JOURNAL OF CREATION

Vol. 38(1) 2024 ISSN 1036-2916 CREATION.com

ORIGIN OF SATURN'S RINGS AND RING SATELLITES

PLEISTOCENE BODY SIZE REDUCTION: EVIDENCE OF POST-FLOOD DECLINE IN LONGEVITY?

Namib Sand Sea within the **BIBLICAL TIMEFRAME**

MADAGASCAR ENDEMISM BETTER EXPLAINED BY POST-FLOOD RAFTING

REASSESSING **HUMAN–CHIMPANZEE GENETIC SIMILARITY**

JOURNAL OF CREATION

An international journal devoted to the presentation and discussion of technical aspects of the sciences such as geology, biology, astronomy, etc., and also geography, archaeology, biblical history, philosophy, etc., as they relate to the study of biblical creation and Noah's Flood.

COVER: Namib desert
IMAGE: Robur.q © Wikimedia Commons, CC-BY-SA-4.0

Editorial correspondence should be addressed to:

The Editor
Journal of Creation
Creation Ministries International
PO Box 4545
Eight Mile Plains
QLD 4113
AUSTRALIA

Email: journal@creation.com

SUBSCRIPTION INFORMATION

AUSTRALIA
Creation Ministries International
PO Box 4545
Eight Mile Plains, QLD 4113
Phone: (07) 3340 9888
Email: aus@creation.com
Subscription: A$23 (3 issues)

CANADA
Creation Ministries International
300 Mill St, Unit 7, Kitchener, ON
N2M 5G8
Phone: (519) 746 7616
Email: canada@creation.com
Subscriptions and orders only:
1–888–251–5360
Subscription: C$23 (3 issues)

NEW ZEALAND
Creation Ministries International
PO Box 13227, Onehunga
Auckland 1643
Phone: (09) 537 4818
Email: nz@creation.com
Subscription: NZ$27 (3 issues)

SINGAPORE
Creation Ministries International
PO Box 195, Singapore 911207
Email: singapore@creation.com
Subscription: S$23 (3 issues)

SOUTH AFRICA
Creation Ministries International
PO Box 3349, Durbanville 7551
Phone: (021) 979 0107
Email: sa@creation.com
Subscription: R270 (3 issues)

UK and EUROPE
Creation Ministries International
15 Station Street
Whetstone
Leicestershire, LE8 6JS
United Kingdom
Phone: (44) 0116 2848 999
Email: uk@creation.com
Subscription: £15 (3 issues)

USA
Creation Ministries International
PO Box 350
Powder Springs, GA 30127
Phone: 800-616-1264
Email: us@creation.com
Subscription: US$23 (3 issues)

OTHER COUNTRIES
Creation Ministries International
PO Box 4545
Eight Mile Plains, QLD 4113, Australia
Phone: (+617) 3340 9888
Email: aus@creation.com
Subscription: A$23 (3 issues):
Please pay in Australian dollars or
advise MasterCard or Visa details

Printed in Australia
Published by:
Creation Ministries International Ltd
ABN 31 010 120 304

Creation Ministries International (CMI) is a non-profit evangelical group of ministries around the world which, though independent, form an operational unity. We share not only this *Journal of Creation* and the associated *Creation* family magazine, but the same biblical platform, and overall outreach and educational vision. In addition, we communicate and co-operate with bona-fide creationist researchers from all over the world. The expanding effectiveness of these ministries, and the future of quality biblical creation research in general, depends on donations from concerned individuals. These may be made to the CMI office in your country. Alternatively, donations can be made via CMI's webstore at creation.com/donate.

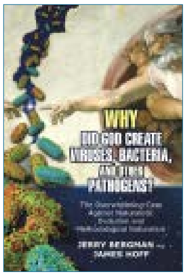
PERSPECTIVES

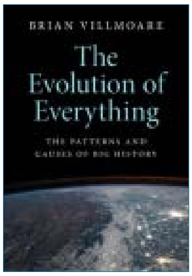
Fossil ranges of several important organisms within the evolutionary story have been pushed back by 'tens of millions' of years.

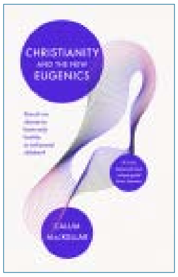
BOOK REVIEWS

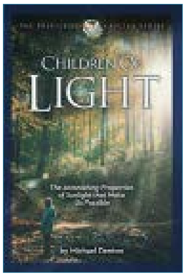
LETTERS

OVERVIEW









PAPERS

Could a panheterozygous ancestor provide a sufficiently large pool of latent traits to produce all the existing species in a family of organisms?

BONUS ARTICLES

ABOUT US

CREATION MINISTRIES INTERNATIONAL

What is Creation Ministries International?

Creation Ministries International is an independent, non-profit, non-denominational organization, controlled by Christians in the fields of science and education, committed to researching, developing, and promoting Christian creationist materials, and Christian school texts and aids. Our work is based on acceptance of:

- The Bible is the written Word of God. It is divinely inspired and inerrant throughout.
- The final guide to the interpretation of Scripture is Scripture itself.
- The account of origins presented in Genesis is a simple but factual presentation of actual events and therefore provides a reliable framework for scientific research into the question of the origin and history of life, mankind, the earth and the universe.
- Scripture teaches a recent origin for man and the whole creation.
- The great Flood of Genesis was an actual historic event, worldwide (global) in its extent and effect.
- The special creation of Adam (as one man) and Eve (as one woman) and their subsequent fall into sin, is the basis for the necessity of salvation for mankind (and thus for the Gospel of Jesus Christ).
- The scientific aspects of creation are important, but are secondary in importance to the proclamation of the Gospel of Jesus Christ as Sovereign, Creator, Redeemer and Judge.

Please note that in all of this, we openly proclaim that our work is centred around Jesus Christ. We are convinced that the real needs of men and women can only be met by reconciliation to God through faith in and commitment to Jesus Christ the Creator, as Lord and Saviour.

For instructions to authors, see the last page.

Highlights from review of genetic research on the Denisovans

Peter Line

In 2008 a scrap of human finger bone was discovered in Denisova Cave, an isolated cave in the Altai mountains of southern Siberia, and its mitochondrial DNA (mtDNA) was sequenced in 2010.[1] The mtDNA analysis of the finger bone (Denisova 3—a proximal fragment of a juvenile manual distal phalanx; see figure 1), allegedly from a layer dated to between 48 and 30 ka ago, reported that Neanderthals and Denisovans differed from modern humans at an average of 202 and 385 nucleotide positions, respectively.[2] From this it was concluded that an "extinct species of human ancestor" had existed in Asia about 40 ka ago, and it was said to be the first time a 'hominin' had "been described, not from the morphology of its fossilized bones, but from the sequence of its DNA."[3] The layer that Denisova 3 was found in was later dated to allegedly 63–55 ka.[4]

Image: Thilo Parg, Wikimedia / CC BY SA 3.0

Figure 1. Replica of Denisovan finger bone fragment (Denisova 3)

Additional bone fragments found

A review paper on the Denisovans was published by me on 28 June 2019, from a non-evolutionary viewpoint.[5] At that time there were seven fragmentary remains attributed to Denisovans. Six fragments were from the Denisova Cave, while one (the Xiahe mandible) was from Baishiya Karst Cave, Xiahe county, China. Soon after this review, on 4 September 2019, it was reported by Bennett *et al*., using ancient DNA analysis, that a distal fragment of a fifth finger (little finger) phalanx from Denisova Cave was the larger, missing part of the fifth finger Denisova 3 proximal fragment of the distal phalanx.[6] Concerning this fragment the authors stated: "Our morphometric analysis shows that its dimensions and shape are within the variability of *Homo sapiens* and distinct from the Neanderthal fifth finger phalanges."[6]

More recently, a comprehensive review by Peyrégne *et al*., in *Nature Reviews Genetics*, collated genetic research on the Denisovans, albeit from an evolutionary perspective.[7] Three undiagnostic bone fragments (Denisova 19, 20, and 21, all from Denisova Cave) had been added to the Denisova sample by the time of this review, bringing the total to ten fragmentary remains, all attributed to Denisovans based solely on molecular information.[8] Denisova 19, 20, and 21 are said to be the oldest of the Denisovan bone fragments, allegedly dated at 217–187 ka, with the youngest being Denisova 3 (genetically dated at 76–52 ka).[9] In their discussion of Denisovan population history, Peyrégne *et al*. also mentioned that the earliest evidence of Denisovan presence is supposedly 250–170 ka ago,[9] based on analysis of DNA (by Zavala *et al*.) in the sediment of Denisova Cave. Zavala *et al*. also reported finding evidence that Denisovans and Neanderthals occupied the site (Denisova Cave) repeatedly, "possibly until, or after, the onset of the Initial Upper Palaeolithic at least 45,000 years ago, when modern human mtDNA is first recorded in the sediments."[10] The Zavala *et al*. study was discussed by me earlier, including the dating methods used, with their associated unreliability and problems.[11] Similarly, the ages presented in this article are unreliable, being based on many unknowns and flawed assumptions, and so are not accepted here, but are given for the reader's information.

Denisovan candidates

Peyrégne *et al*. named 'archaic' remains in Asia that may be Denisovan (Narmada in India, Tam Ngu

Hao 2-1 in Laos, Penghu 1 from the Taiwan Strait, and Xuchang 1, Xuchang 2, Maba, Xujiayao, Harbin, and Jinniushan in China), based on morphology or geographical and temporal origin, although molecular information to confirm this is lacking.[9] According to evolutionists Cartmill and Smith, the Ngandong 'hominins' from Java, Indonesia, are also candidate Denisovans.[12] The Ngandong ('Solo Man') remains are usually classified as *Homo erectus*. Peyrégne *et al.* reported that the Denisovan population size likely remained small throughout most of their history, that they seem to have lived in groups of 100 or more individuals, and that when comparing genomes there was evidence "suggesting that inbreeding was not as prevalent in the population of *Denisova 3* as it was in Neandertals".[13] The sequence divergence between the genomes of Denisovans and Neanderthals is said to indicate they were separated for allegedly at least 300,000 years, although genetic evidence also suggested there was subsequent admixture.[13]

Denisovan ancestry in present populations

The Denisovan genome is said to be unexpectedly divergent to Neanderthals and modern humans in some regions, supporting a superarchaic ancestry presence in the Denisovan genome.[14] The levels of Denisovan ancestry in present populations vary widely, with the highest levels being in Philippine Negritos, who have "30–40% more Denisovan ancestry than Melanesians and Indigenous Australians (~4%)".[14] Denisovan introgression into the ancestors of indigenous Australians and Melanesians has been estimated at allegedly between 54 ka and 44 ka ago, with it also estimated that a "Denisovan-related" population perhaps persisted until supposedly 25 ka in Oceania.[15] According to Peyrégne *et al.*:

> "The presence of *Homo floresiensis* close to the time when modern humans reached this region of the world around 46 ka … raises the possibility that they may have met and mixed, and that *Homo floresiensis* could be related to the population that contributed the highly diverged Denisovan component in present-day Oceanians. There is, however, no evidence of an excess of Denisovan or archaic ancestry among Indigenous populations from Flores … ."[16]

Denisovans and *Homo floresiensis*

Although the pygmy population on Flores Island possessed ancestry from both Denisovans and Neanderthals in their genomes, Tucci *et al.* reported that

> "We found no evidence that unknown sequences in Flores are enriched for older or more divergent lineages … , as would be expected if they contained lineages inherited from a more deeply divergent hominin group, such as *H. floresiensis* or *H. erectus*."[17]

However, the DNA from *H. floresiensis* and *Homo erectus* is currently unknown. Maybe the reason why there is no trace of *H. floresiensis* or *H. erectus* in the genomes of the population from Flores is that some of the specimens classified as *H. erectus* and *Homo heidelbergensis* were Denisovans. The Denisovans appear to have been a diverse group. Because of the "divergent Denisovan ancestry in present-day populations and their large inferred geographical range", Peyrégne *et al.* stated that "it is plausible that there was substantial morphological variability among Denisovans."[18] According to Jacobs *et al.*, there were three Denisovan groups:

> "The genetic diversity within the Denisovan clade is consistent with their deep divergence and separation into at least three geographically disparate branches, with one contributing an introgression signal in Oceania and to a lesser extent across Asia (D2), another apparently restricted to New Guinea and nearby islands (D1), and a third in East Asia and Siberia (D0)."[19]

It may be that the LB1 *H. floresiensis* specimen was a pathological Denisovan (e.g., a pathological *H. erectus*), or the pathological offspring of interbreeding between a Denisovan and 'modern' human. Because the effective population size of Denisovans was believed to be small, Peyrégne *et al.* suggested genetic drift may have resulted in "rapid and random changes in the phenotypic diversity of Denisovan populations", resulting in Denisovan phenotypes that "could have differed greatly between populations."[18] Peyrégne *et al.* commented that *Homo luzonensis*, from the Philippines, may have been related to Denisovans, but that it was not possible to link them without ancient DNA or proteins.[20] Peyrégne *et al.* also listed some of the many challenges in detecting Denisovan ancestry in the genomes of present-day people, including:

> "The panel of archaic reference genomes is small, particularly for Denisovans where there is only a single Denisovan reference genome (*Denisova 3*) compared with three Neandertal genomes (*Denisova 5*, *Vindija 33.19* and *Chagyrskaya 8*). This limited view of the genetic variation among archaic humans complicates comprehensive identification of introgressed archaic segments by limiting the number of known informative variants and their frequency in archaic humans."[20]

Denisovan phenotype

According to Peyrégne *et al.*, differences in gene expression are believed "to account for most phenotypic changes in human evolution", and these involve non-coding sequences, the effect on gene expression (including the Denisovan phenotype) of which is hard to predict.[21] Of course, differences in gene expression do not require an evolutionary explanation. Rather, it can be inbuilt genetic variation (or the inbuilt potential for gene expression to vary) put there by the Creator. This could involve epigenetic modifications, such as differentially methylated regions between different human groups. In discussing this, Peyrégne *et al*. stated that

> "Further description of these differentially methylated regions between modern and archaic humans highlighted anatomical phenotypes that Denisovans may have shared with Neandertals, including a robust jaw, a low cranium, an increased cranial base growth, a low forehead, a thick enamel, a wide pelvis, large femoral articulations, wide fingertips and a large ribcage … ."[21]

However, more Denisovan fossils need to be identified to test the accuracy of phenotypic predictions like the above. It is interesting that the fragment of Denisovan parietal bone found was described as "surprisingly thick, more like cranial bones of Stone Age *Homo erectus*".[22] The Xiahe mandible (figure 2: identified as Denisovan by ancient protein analysis), which has no chin, was described by paleoanthropologist Roberto Sáez:

> "The *mandibular morphology* in general is *primitive*, short and very robust, and close to *Homo erectus* specimens. But the less elongated shape of the dental arcade is closer to that of the earliest Middle Pleistocene specimens of *Neanderthals and Homo sapiens*. The teeth are similar to the Denisovans' from Altai mountains, and their morphology fits within Middle Pleistocene hominin variability [emphases in original]."[23]

While one cannot yet say with certainty that the Denisovans included *Homo erectus* specimens, indications are that they were *erectus*-like, and whether you call them *Homo erectus* or *Homo heidelbergensis* (Middle Pleistocene hominins) is, in many ways, a moot point, as there appears to be little difference between them.

Figure 2. Xiahe Denisovan mandible found on the Tibetan plateau

Image: Dongju Zhang, Wikimedia / CC BY SA 4.0

Comparing genomes

Although also having limitations, phenotypic inferences from Denisovan ancestry in present-day genomes is used to indirectly investigate the Denisovan phenotype. An example is a version of the *EPAS1* gene, inherited by Tibetans, "involved in the physiological response to low concentrations of oxygen at high altitudes".[24] Towards the end of their review paper, Peyrégne *et al*. have a section titled "Insights into modern human evolution from archaic genomes". Here they state:

> "Comparing the genomes of many thousands of present-day humans with those of Neandertals and Denisovans has identified about 30,000 single nucleotide changes, 4,000 small insertions or deletions (indels) and a few copy number differences that all, or nearly all, present-day humans carry, whereas archaic humans carry the ancestral state shared with great apes … ."[25]

However, combining "all, or nearly all" means not all nucleotide changes are fixed, rather some are near-fixation. According to Kuhlwilm and Boeckx:

> "Previously, a number of 31,389 sites has been reported as recently fixed derived in present-day humans, while being ancestral in archaics … . We find a smaller number of only 12,027 positions in the genome, in part due to the inclusion of another archaic individual and different filters, but mainly because of a richer picture of present-day human variation. The 1,000 Genomes Project as well as other sources contributing to the dbSNP database now provide data for thousands of individuals, which results in very high allele frequencies for many loci, instead of full fixation. Indeed, 29,358 positions show allele frequencies larger than 0.995, demonstrating that the level of near-fixation is similar to the level of previously presented fixation. The number of loci with high frequency (HF) changes of more than 90% in present-day humans is an order of magnitude larger than the number of fixed differences. This cutoff is

> somewhat arbitrary and based on previous work … . However, when increasing the frequency cutoff, the number declines sharply, while decreasing it results in a near-linear increase of sites."[26]

Hence, if you only include genetic changes that are fixed in present-day humans, then the number of changes compared to 'archaic' humans will be reduced, perhaps considerably (depending on the HF cutoff associated with near-fixation), compared to also including near-fixation changes in present-day humans. Even what was considered fixed may not be if it does not account for the "richer picture of present-day human variation." And even then, comparing the genomes of thousands of present-day humans to three 'archaic' humans (two Neanderthals and one Denisovan, as in the above study by Kuhlwilm and Boeckx[27]) is unlikely to account for the genetic variation in the latter. As stated by Kuhlwilm and Boeckx:

> "The three archaic individuals carry more than twice as many changes than present-day humans; however, we emphasize that much of this difference is not due to more mutations in archaics, but rather the fact that data for only three individuals is available, compared to thousands of humans. The variation across the archaic population is not represented equally well, which makes these numbers not directly comparable."[26]

The above genetic differences between present-day humans and 'archaic' humans are trivial compared to the differences in the genomes between present-day humans and chimpanzees (chimps). The assertion that human and chimp DNA are 98 to 99% similar is not accurate. Even if it was true, a 99% similarity would be equal to 30 million single nucleotide base pair differences. Even with the false idea of just 1% difference a transition from chimp to human is impossible for mutations to achieve in the time available.[28] As the paper by Carter in this journal shows, however, it is likely that the difference is around 95%.[29] If so, compared to the problem described above for the 99% claim, it worsens the problem for neo-Darwinian evolution fivefold. It requires an *additional* 120 million base pair differences to become fixed in the population through mutation and selection.

In their conclusion, Peyrégne *et al*. reported that evidence gathered on the Denisovans to date included a history of "numerous episodes of interbreeding with Neandertals, as well as with modern humans, and possibly other ancient human groups."[30] However, they acknowledge that questions about the Denisovans still remain unanswered, in particular that little is known of their appearance.[31]

References

1. Dalton, R., Fossil finger points to new human species, *Nature* **464**:472–473, 2010.
2. Krause, J., Fu, Q., Good, J.M. *et al*., The complete mitochondrial DNA genome of an unknown hominin from southern Siberia, *Nature* **464**:894–895, 2010. See also supplementary information, p. 1, for description of manual phalanx.
3. Brown, T.A., Stranger from Siberia, *Nature* **464**:838, 2010.
4. Jacobs, Z., Li, B., Shunkov, M.V. *et al*., Timing of archaic hominin occupation of Denisova Cave in southern Siberia, *Nature* **565**:597, 2019.
5. Line, P., An overview of the Denisovan puzzle, creation.com, 28 Jun 2019.
6. Bennett, E.A., Crevecoeur, I., Viola, B. *et al*., Morphology of the Denisovan phalanx closer to modern humans than to Neanderthals, *Science Advances* **5**(9):eaaw3950:1, 4 Sep2019 | doi:10.1126/sciadv.aaw3950.
7. Peyrégne, S, Slon, V.' and Kelso, J., More than a decade of genetic research on the Denisovans, *Nature Reviews Genetics*, 18 Sep 2023 | doi:10.1038/s41576-023-00643-4.
8. Peyrégne *et al*., ref. 7, pp. 1, 8.
9. Peyrégne *et al*., ref. 7, p. 2.
10. Zavala, E.I., Jacobs, Z., Vernot, B. *et al*., Pleistocene sediment DNA reveals hominin and faunal turnovers at Denisova Cave, *Nature* **595**:399, 2021 | doi:10.1038/s41586-021-03675-0.
11. Line, P., Analysis of mtDNA from sediments in Denisova Cave, *J. Creation* **35**(3):5–7, 2021.
12. Cartmill, M. and Smith, F.H., *The Human Lineage*, 2nd edn, John Wiley & Sons, Inc., Hoboken, NJ, p. 382, 2022.
13. Peyrégne *et al*., ref. 7, p. 3.
14. Peyrégne *et al*., ref. 7, p. 5.
15. Peyrégne *et al*., ref. 7, pp. 8–9.
16. Peyrégne *et al*., ref. 7, pp. 11–12.
17. Tucci, S., Vohr, S.H., McCoy, R.C., *et al*., Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia, *Science* **361**:512, 515, 2018 | doi:10.1126/science.aar8486.
18. Peyrégne *et al*., ref. 7, p. 13.
19. Jacobs, G.S., Hudjashov, G., Saag, L. *et al*., Multiple deeply divergent Denisovan ancestries in Papuans, *Cell* **177**:9, 2019 | doi:10.1016/j.cell.2019.02.035.
20. Peyrégne *et al*., ref. 7, p. 12.
21. Peyrégne *et al*., ref. 7, p. 14.
22. Bower, B., First known fossil of a Denisovan skull discovered in cave, 29 Mar 2019.
23. Sáez, R., Finally, the mandible of a Denisovan! – Nutcracker Man, 1 May 2019.
24. Peyrégne *et al*., ref. 7, p. 15.
25. Peyrégne *et al*., ref. 7, p. 16.
26. Kuhlwilm, M and Boeckx, C., A catalog of single nucleotide changes distinguishing modern humans from archaic hominins, *Scientific Reports* **9**:8463, p. 3, 11 Jun 2019 | doi:10.1038/s41598-019-44877-x.
27. Kuhlwilm and Boeckx, ref. 26, p. 9.
28. Line, P., The myth of ape-to-human evolution, *Creation* **41**(1):44–46, 2019.
29. Carter, R.W., Reassessing human–chimpanzee genetic similarity, *J. Creation* **38**(1):93–103, 2024.
30. Peyrégne *et al*., ref. 7, p. 17.
31. Peyrégne *et al*., ref. 7, pp. 17–18.

The origin of Saturn's rings and ring satellites

Wayne Spencer

Much research has been done on the rings of Saturn since the completion of the NASA *Cassini* mission in 2017. Today there is a consensus among secular scientists that the rings could not have formed at the time Saturn formed. This is borne out of considerations from the data available from the mission.[1] It is clear that Saturn's rings are eroding from micrometeorites and collisions. There is also a significant mass of material falling onto Saturn from the rings, referred to as 'micrometeoroid infall' or 'ring rain'. It was estimated by secular scientists that the time required for the current mass of Saturn's rings to fall into the planet is in the range of 150–400 Ma.[2] This is leading planetary scientists to consider new catastrophic models for the formation of Saturn's rings and some of its moons.

The time for Saturn's rings to fall into the planet (150 to 400 Ma) deserves clarification. Durisen and Estrada[2] estimate the ratio of ejected mass to meteoroid mass when dust particles impact on the ring objects. When this ratio, referred to as the 'ejecta Yield', is larger, it leads to a younger age, such as 15 Ma. But if it is assumed to be smaller, it leads to a larger age for the rings. Considering the Yield value as 10^5 led Durisen and Estrada to the range of 15 to 400 Ma.[2] However, they commented, "The lower bound estimate of 15 Myr seems exceedingly short".[2] Then they considered other analysis from Kempf *et al.*[3] which dealt with quantifying the mass influx to the rings based on the *Cassini* Cosmic Dust Analyzer data. Kempf *et al.* estimated a minimum 'pollution exposure age' from the dust influx to the rings of 100 Ma.[3] Durisen and Estrada thus chose a smaller value for the ejecta yield of 10^4, which increases the lower bound estimate for the ring age to roughly agree with Kempf. Thus, Durisen and Estrada altered their estimated lower bound number from 15 Ma to 150 Ma.[2] This ring age also makes a significant assumption, which is that the rings were significantly more massive in the past than they are observed to be today (up to a few times the mass of Mimas). Various age estimates are possible because of how various parameters must be chosen to make the calculations.

The origin of Saturn's many moons has become another issue of considerable interest since, in recent years, dozens of additional moons have been discovered. Note that some of the newly discovered moons may still have what is referred to as 'provisional' status while additional observations take place to confirm their existence and their orbits. The current total number of moons of Saturn listed by NASA is 146, with the most recent one discovered 8 June 2023.[4] Saturn's moon Pan lies in the outer edge of the Enke division within the A-ring. Moons Atlas, Prometheus, Pandora, Epimetheus, and Janus lie near the F-ring (outside the A-ring) (figure 1). Mimas lies just outside the G-ring, and Enceladus is within the E-ring, which is the outermost ring (table 1). The moons of Saturn consist of a large proportion of ice but also contain some rock. Today's theories on ring formation sometimes incorporate moon formation as part of the models. Various computer simulations are explored to theoretically investigate scenarios for their naturalistic formation from an old age perspective.

TNO breakup

Following are three catastrophic models that have been put forward to explain Saturn's rings since the end of the *Cassini* mission. The first of these involves the tidal disruption of a Transneptunian object (or TNO).[5] This model was proposed in connection with the 'Nice' model that argues that the four outer planets formed closer to the Sun and then migrated outward to their current orbits.[6] The mechanism has the TNO passing very near Saturn, which would cause it to pass within the Roche limit, so it would break up into fragments. One problem with this model is that to connect it with the outer planet migration of the

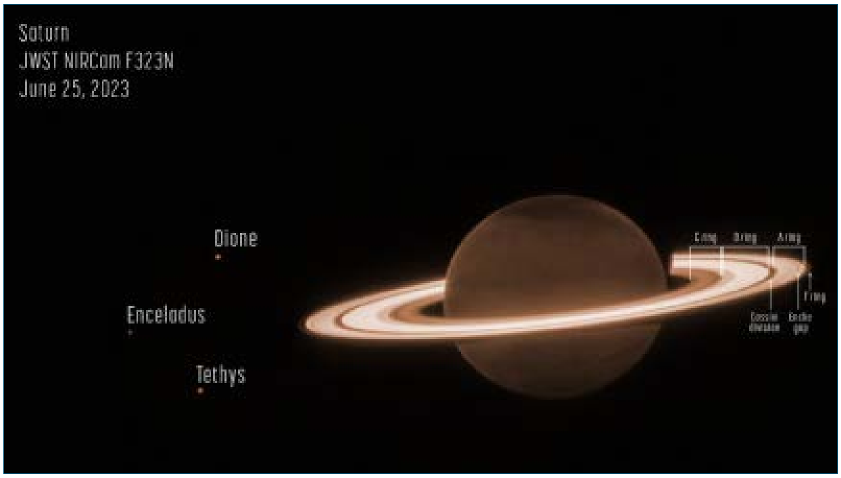


Figure 1. Image is in infrared light from the James Webb Space Telescope, taken 25 Jun 2023 (cropped). Rings appear bright, showing the narrow F ring on the outside and the A, B, and C rings within. The D ring is faint but lies inside the C ring.

Image: NASA and STScI

Table 1. Distances to Saturn's rings and to selected satellites in or near the rings measured from the centre of Saturn. Moons are shown in brackets. Epimetheus and Janus are shown together since they are moons that interchange orbits periodically. Dione, Helene, and Polydeuces all share the same orbit, with Helene and Polydeuces as Trojans with Dione.[9,10]

Ring or orbit location	Distance from the center of Saturn (km)
Saturn equator	60,268
D inner edge	66,900
C inner edge	74,658
Maxwell gap	87,491
C outer edge	91,975
B inner edge	91,975
B outer edge	117,507
Cassini division	117,507–122,340
A inner edge	122,340
Encke gap	133,410
(Pan)	133,600
Keeler gap	136,487
A outer edge	136,780
(Prometheus)	139,400
F ring	139,826
(Pandora)	141,700
(Epimetheus–Janus)	151,400–151,500
G inner edge	166,000
G outer edge	173,000
E inner edge	180,000
(Mimas)	186,000
(Enceladus)	238,400
(Dione–Helene–Polydeuces)	377,700
E outer edge	480,000
(Rhea)	527,200

Nice model puts it at more than 3.5 Ga ago, which is far too long ago to be consistent with the new data on Saturn's rings. If it were later, such as 200 or 400 Ma ago, that timing is unlikely because TNO objects would not be likely to be in an elliptical Saturn-crossing orbit at that time. Also, tidal break-up events such as this tend to form only a limited number of large fragments, not many small objects like in Saturn's rings. Simulations of these types of events also depend greatly on parameters affecting the collision, such as the velocity and angle of incidence.

Comet–moon collision

A second model proposed to explain Saturn's rings is where a comet or centaur object collides with an early moon of Saturn and disrupts the moon.[7] One advantage of making the impacting object a comet or centaur is that its orbit is more elliptical, and so it can be moving at a higher velocity. This moon would have to be a differentiated object (layered with an icy mantle). It would also need to have the majority of its mass as ice. The collision could generate many icy particles and fragments. Also, if a small moon with a rocky core but outer layers of ice should move nearer to Saturn, its own Roche limit would actually depend on its density. Thus, it is thought that the icy mantle of such an object would break up due to tidal forces at a greater distance from Saturn than the rocky core. So, it is thought the rocky core could stay relatively intact while the icy mantle breaks apart.

However, there is more to this model. Saturn spins relatively rapidly, and this creates a torque on moons that tends to cause their orbits to expand. This model proposes that the early moon which was disrupted was in a resonance with Enceladus very close to the Roche limit. This would be approximately at the outer edge of the A-ring today. It is believed that rings always form inside the Roche limit. This moon resonance led to generating heat in Enceladus (to help explain its liquid eruptions)[7] and to the disruption of the other moon. One of the main difficulties with this model is that Saturn's moons are usually believed to have formed with the planet, so a moon that no longer exists must have been present for a long time prior to the rings. This implies the moon that broke up must have remained near the Roche limit for a long time and did not migrate outward. It would generally be considered unlikely for a small moon to remain near the Roche limit because its orbit would become unstable. This model also attempts to explain the formation of Mimas, which has generated considerable debate as well. In this scenario, today's moon Mimas is the re-accreted core of the earlier moon that was disrupted.

Saturn, Neptune, and Chrysalis

A third model was proposed in 2022 which makes use of a spin-orbit resonance between Saturn and Neptune and also involves Saturn's moon Titan and another moon that was disrupted.[9] This model proposes that between Saturn and Neptune there had been a resonant relationship which no longer exists. It also proposes that a moon existed in the past that no longer exists today, unofficially named 'Chrysalis'. This model also suggests that Saturn's moon Titan was once closer to Saturn, and it migrated outward. Theories that attempt to explain Saturn's moons often make use of migration to explain how the moons could form nearer to Saturn and then move outward to their present orbital positions. The spin of Saturn and orbital changes for Saturn's moons are important in this model.

Saturn's spin axis precesses with a period that is close to the precession frequency of Neptune's orbit. Also, the shape and rotation of Saturn are influenced by its moons. Titan, since it is the largest moon, has the greatest influence on Saturn's rotation. In this model, Titan is believed to have once been nearer to Saturn, where it would have altered Saturn's spin axis. Add to this the existence of another moon of Saturn in the past (Chrysalis), which was similar in size, composition, and mass to Iapetus. The proposal is that Chrysalis came into an unstable orbit, likely due to perturbations from other moons, which caused it to come too near to Saturn, and it was disrupted by the tidal forces. The breaking up of Chrysalis would then provide icy material for making up the rings. But this complex scenario also attempts to explain the relatively large tilt of Saturn's spin axis (which is 26.7°) as well as why Saturn and Neptune are not in the spin-orbit resonance today. The loss of the moon Chrysalis would have altered Saturn's tilt and caused Saturn to exit the spin-orbit resonance. This model is supported by calculations and computer simulations.

This model combines multiple *ad hoc* hypotheses to explain Saturn, its rings, Titan, and a possible resonance with Neptune. But this scenario at Saturn requires multiple fortuitous effects to work out properly in order for it to affect the planet's spin axis. It is plausible that moons could influence the spin of Saturn if their mass is sufficient and they are close enough to Saturn. However, a tidal breakup of a moon would not necessarily widely scatter debris in a way that would lead to Saturn's current rings. Scientists tend to assume that long periods of time will lead to the debris settling into a plane and that the objects would naturally distribute themselves into rings, as we see. But long periods of time do not necessarily lead to the right patterns to explain what we see today. The end results of the simulations do not carry all the way through the process because much is not yet sufficiently well understood to model quantitatively. It is generally assumed that once a ring of objects has formed, given time, it will 'evolve' into something similar to Saturn's combination of multiple rings A through E.

Conclusions

Planetary scientists have simulated a variety of collisions which break up moons of Saturn to form its rings. Collisions that are more head-on or at higher speeds tend to disburse the material over a wider range of angles and generate smaller-sized debris. The general process following moon disruption is that the debris tends to spread out along the moon's orbit. Then there would be a long period of the objects spreading out and settling into a flattened disk. It is important to note that the distance from the outer edge of the A-ring to the inner edge of the C-ring is over 62,000 km.[10] This is a broad region that the material coming from a collision or tidal breakup would have to spread across. From simulations, the time for the debris to spread out and settle is generally thought to require tens of to a few hundred million years.

In Saturn's actual rings today there are some notable differences in the composition and thickness of the main rings.[10] Some models employ Centaur or TNO objects because they would be assumed to have a larger proportion of their mass as silicates or other non-icy material. The B-ring is the most massive ring, for example, but the C-ring has more non-icy material in it than the A or B rings. Computer simulations do not usually address these types of differences across the rings. The *Cassini* radiometer and Cosmic Dust Analyzer provide estimates of the non-ice content of the ring objects.[2] For the C-ring, the non-ice fraction was estimated at approximately 1–2%; the A and B-rings were in the range of 0.1–0.5%. However, a notable contrast to this was found when the actual cosmic dust particles (nanometre-sized) were analyzed by the spacecraft. The cosmic dust particles striking the rings were 8–30% silicate. This also suggests a young age since the ring objects are estimated to be 95% water ice.

What should creationists conclude from the new models on the formation of Saturn's rings and moons? It may be that rings made up mainly of small dust particles, such as Saturn's E-ring, could have come about since creation. The same could apply to Jupiter's faint dust ring. There are multiple known ongoing processes causing material to come from certain moons and spread out into rings. On the other hand, the massive scale of Saturn's rings has proved to be very challenging for scientists to explain using naturalistic models. Complex impact and moon-breakup events can be modelled only very roughly and there remain many questions around whether these simulations are realistic. To say God created Saturn's rings with the planet only several thousand years ago is still a legitimate approach for us today. This view would imply the Saturn system has been relatively stable since creation, though changes have taken place in the rings, and some rings may not have existed at creation. Saturn's small moons may have had their orbits altered since creation, and some may have even collided or broken up since creation. Resonance effects between the rings and moons certainly shape the rings and gaps. But it's not clear whether the resonances were created or whether they came about since creation. Saturn's main rings may have come about by intelligent design and God's supernatural action. There is room for creationists to further research the possibilities. More research is needed so that we may understand how the creation shows the glory of God.

References

1. Spencer, W., Saturn's changing rings, *J. Creation* **37**(3):16, 2023
2. Durisen, R.H. and Estrada, P. R., Large mass inflow rates in Saturn's rings due to ballistic transport and mass loading, *Icarus* **400**:115221, 2023.
3. Kempf, S. *et. al.*, Micrometeoroid infall onto Saturn's rings constrains their age to no more than a few hundred million years, *Science Advances* **9**(19), 12 May 2023.
4. SMD content editors, Saturn moons, nasa.gov, updated October 2023.
5. Hyodo, R. and Charnoz, S., Dynamical evolution of the debris disk after a satellite catastrophic disruption around Saturn, *The Astronomical J.* **154**:34–42, 2017.
6. Spencer, W., The proposed origin of our solar system with planet migration; in: Whitmore J.H., (Ed.), *Proceedings of the Eighth International Conference on Creationism*, Creation Science Fellowship, Pittsburgh, PA, pp. 71–81, 2018.
7. Dubinski, J. A recent origin for Saturn's rings from the collisional disruption of an icy moon, *Icarus* **321**:291–306, 2019.
8. Spencer, W., Warm icy moons, *J. Creation* **29**(3):97–103, 2015.
9. Wisdom, J. *et. al.*, Loss of a satellite could explain Saturn's obliquity and young rings, *Science* **377**(6612):1285–1289, 2022.
10. Williams, D.R., Saturnian rings fact sheet, nasa.gov, 17 Jul 1995.
11. Moons of Saturn, wikipedia, 8 June 2023.

The mysterious rings around a trans-Neptunian dwarf planet

Michael J. Oard

Star gazers have always found the rings of Saturn intriguing. They have gone from wondering what they are made of to today's wondering about their age. Just recently, some scientists calculated that the rings may be relatively young, from less than 100 Ma to about 400 Ma within the uniformitarian timescale.[1–3] This result was based on the estimated incoming mass flux of micrometeoroids divided into the estimated number of pollutants in the rings with the assumption that the rings began as water ice.

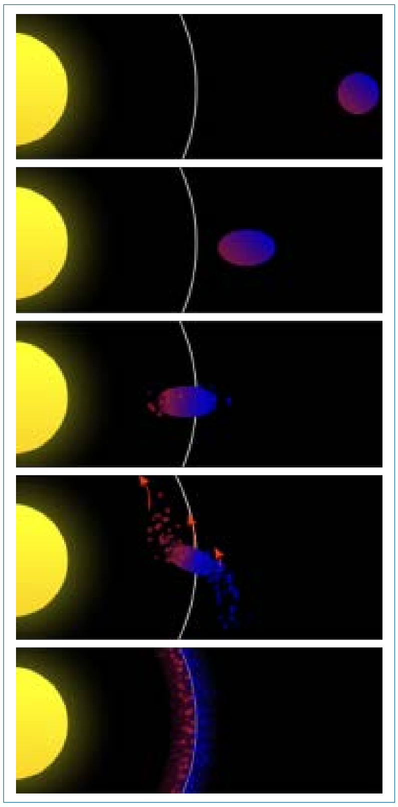


Image: Theresa Knott, Wikimedia | CC BY SA 3.0

Figure 1. Illustration of a disintegrating secondary celestial object approaching a large celestial object when reaching the Roche limit

Other solar system rings

Scientists have discovered that the other gas giants, Jupiter, Uranus, and Neptune, are also surrounded by rings. Narrow rings surround some non-planetary bodies in the outer solar system, including the centaur Chariklo, about 250 km in diameter, and the dwarf planet Haumea, 1,400 km in diameter, which orbits the sun beyond Neptune. Centaurs are icy planetesimals orbiting between Jupiter and Neptune. All of these rings are close or within the Roche limit, the distance from a celestial body within which the tidal force will tear apart a smaller celestial body (figure 1). In this case, the tidal force is greater than the force of gravity of the smaller body. The particles will then begin to rotate around the body, forming a ring. The Roche limit is about 2.5 times the radius of the larger celestial object.

The strange rings around Quaoar

In 2021, a ring was detected around a trans-Neptunian dwarf planet, named 'Quaoar', far outside its Roche limit (figure 2).[4,5] Quaoar has a diameter of about 1,110 km, about half that of Pluto. The first ring discovered is located 4,057 km from Quaoar's centre, approximately 3 times the distance of the Roche limit, estimated to be 1,780 km from Quaoar's centre. A second ring was discovered in 2022 that is 2,520 km from Quaoar's centre, still outside the Roche limit.[6] It has a small moon, Weywot, that is 80 km in diameter and orbits 12 times the diameter of Quaoar. The rings are too narrow to be directly seen, but were inferred from numerous telescopic observations in which the ring material slightly obscured the light of stars that passed near Quaoar. Moreover, different telescopes varied in shape and intensity of the ring material, suggesting the ring's opacity varies along its length, as with the rings of

Saturn and Neptune. Quaoar's rings present a challenge to uniformitarian speculation on ring formation:

> "However, the position of Quaoar's rings is very different from that of any comparably opaque rings, and therefore poses a challenge to standard models of planetary rings."[7]

The opacity of the rings suggests that the rings are relatively dense and that their particles should often collide with one another. These collisions are believed to result in particles breaking up, bouncing off each other, or sticking together. The latter supposedly will occur at lower speeds of collision. Since the collisions dissipate energy, the velocity of the particles should slow down with time. Then the particles will aggregate into larger objects such as moons.

The uniformitarian conundrum

When considering billions of years of uniformitarian time, the question is: why hasn't the ring coalesced into a moon? There are many possibilities. One is that the debris was caused by an impact with another object. This is considered unlikely because it is believed that only a few decades are needed for the debris to reassemble into a moon, but this deduction may rely on hypotheses on how small particles would stick together. Other possibilities are:

1. the particles are more elastic and bounce off each other
2. the particles are moving too fast to coagulate
3. external gravitational forces somehow break apart any aggregated particles
4. the hypothesis that particles will quickly aggregate into larger bodies may be flawed
5. there is some kind of resonance between Quaoar and/or Weymot that keeps particles from coagulating (figure 2).

Morgado *et al.* even suggest maybe "the need for revisiting the Roche limit notion,"[8] which is a strange proposal, since the Roche limit seems to be well supported physically.

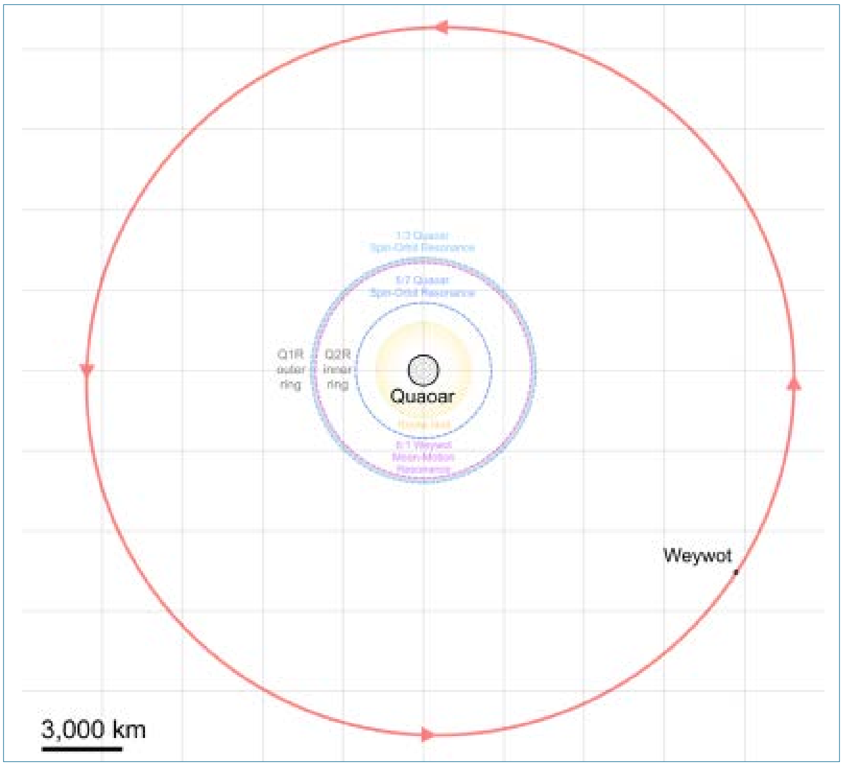


Figure 2. "Diagram of the Quaoar–Weywot system to scale, viewed top-down over Quaoar's north pole". "The radii of dynamical zones (resonances and the Roche limit) are labelled and indicated with dashed circles. Weywot orbits counterclockwise from this perspective."

Image: Nrco0e, Wikimedia | CC BY SA 4.0

How might creation scientists respond?

Creation scientists have several options for explaining Quaoar's strange rings. They could have been recently created, and the uniformitarian hypothesis of the quick coagulation of the particles is flawed. Another option is that an asteroid smashed into one or two moons, and there has not been enough time for the particles to re-aggregate. It is interesting how many uniformitarian solar system conundrums there are, and that many of them can be solved by applying a recent creation.[9–11]

References

1. Kempf, S., Altobelli, N., Schmidt, J., Cuzzi, J.N., Estrada, P.R., and Stama, R., Micrometeoroid infall into Saturn's rings constrains their age to no more than a few hundred million years, *Science Advances* **9**(eadf8537):1–6, 2023.
2. Ogasa, N., Saturn's rings may be relatively young, *Science News* **203**(11):14, 2023.
3. Spencer, W., Saturn's changing rings, *J. Creation* **37**(3):6–8, 2023.
4. Morgado, B.E. *et al.*, A dense ring of the trans-Neptunian object Quaoar outside its Roche limit, *Nature* **614**:239–243, 2023.
5. Hedman, M.M., A planetary ring in a surprising place, *Nature* **614**:232–233, 2023.
6. Pereira, C.L. *et al.*, The two rings of (50000) Quaoar, *Astronomy & Astrophysics* **673**(L4):1–14, 2023.
7. Hedman, ref. 5, p. 232.
8. Morgado *et al.*, ref. 4, p. 241.
9. Psarris, S., *What you aren't being told about astronomy, vol. I—Our Created Solar System*, creationastronomy.com, 2009.
10. Psarris, S., *What You Aren't Being Told About Astronomy, vol. II—Our Created Stars and Galaxies*, creationastronomy.com, 2012.
11. Psarris, S., *What You Aren't Being Told About Astronomy, vol. III—Our Created Universe*, creationastronomy.com, 2016.

Fossil range expansions continue

Michael J. Oard

Creationists have regularly published on fossil range expansions. They have found in the conventional geological literature either fossils that conventional geologists believe are older, or living fossils that extend the fossil range upward in the geological column to the present. The most recent publication was in 2019.[1] Not many of these are major changes in the dates or important fossils in the evolutionary story, but a few are. Regardless, this series of perspective articles shows that the fossils in the geological column appear less ordered than previously thought.

After five years, there are many more fossil range expansions. Several push back the dates by tens of millions of years or are important organisms within the evolutionary story. There are likely more range expansions than reported on here, since these were found only while doing my research.

Earth's earliest metazoan animal?

The beginning of 'complex' animals is debated among evolutionary paleontologists. Igniting further debate is the discovery of what could be sponges or sponge-like animals 890 Ma ago, 350 Ma older than the oldest undisputed sponges from the Cambrian period.[2,3] The 'molecular clock' supports the origin of metazoans back into the early Neoproterozoic, so finding sponges that 'old' is not unexpected. The Neoproterozoic is dated from 1 Ga to 541 Ma BP. It seems typical that molecular clocks indicate that an organism diverged from its supposed ancestor well before its earliest fossil occurrence. The discoverer of the Neoproterozoic sponges is confident the structures are biological sponges, yet others are not. The critics also point out that this so-called ancient life would have to have gone through periods of extremely low oxygen levels and 'snowball Earth' episodes.[3] Others have supported the discoverer by pointing out they have found traces of biological molecules, linked to sponges of that age.[4]

For creation scientists, this would mean that metazoans are much older than the Cambrian. It illustrates that a Precambrian/Cambrian pre-Flood/Flood boundary depends not on the *absence* of metazoan fossils in the Precambrian, but on the great increase in abundance of metazoans at that boundary. This also makes it more plausible to consider pre-Flood boundary locations other than the Precambrian/Cambrian boundary.

Predatory cnidarians pushed 30 Ma earlier into Ediacaran

The origin of jellyfish and corals, or cnidarians, has been a long-standing mystery.[5] A new fossil found in the United Kingdom has now pushed back the origin of cnidarians into the Ediacaran Period, but with a body plan much different from the strange Ediacaran fossils.[6] Since cnidarians are predatory, the discovery also pushes back the origin of predatory behaviour about 30 Ma.

Jawed fish pushed back about 20 Ma

China seems to come up with some amazing fossils. This time the Chinese report that they have found jawed fish, armoured placoderms from the class Chondrichthyes, from the early Silurian.[7,8] This pushes back the origin of jawed fish about 20 Ma. The variety of newly discovered jawed fish presents a puzzle: "How could a group that was already so diversified leave such a meagre record, particularly of whole fishes?"[9] There should be more of them found in the Silurian, and their origin should go back to the Ordovician or even the Cambrian, where none have been found as yet. (Presumably fossil range expansion is tending toward the Cambrian Explosion being more explosive!)

Image: Kennethcgass, Wikemedia / CC BY SA 4.0

Figure 1. The flat, branching bryozoan from Wisconsin, United States

Bryozoans pushed back into the Cambrian from the Ordovician

Bryozoans are a phylum of aquatic invertebrates, nearly all living in sedentary colonies. They are very diverse, with about 6,500 living species and 15,000 fossil species.[10] They are typical Paleozoic fossils (figure 1) from the Ordovician upward in the geological column and are commonly used as index fossils. Typically, the 'molecular clock' claims that bryozoans evolved earlier than their fossil representatives, which were as old as the Ordovician. Moreover, six orders of bryozoans are found in the Ordovician, the variety suggesting that their origins must be in the Cambrian. Therefore, bryozoans should be part of the Cambrian Explosion, but they were not thought to be so until recently. Unequivocal bryozoans have now been found in the early Cambrian in China and Australia, pushing the origin of these animals back about 35 Ma.[11] Thus, fossils and the molecular clock have been reconciled and nearly all animal phyla have their origin in the Cambrian Explosion.

Digestive tracts now found in Ediacaran

'First emergence' dates for animal structures or characteristics are sometimes pushed back. The tube-dwelling *Cloudina* is an index fossil for the Ediacaran period of the late Neoproterozoic. It is considered a 'primitive metazoan'. A new discovery from Nevada, USA, has revealed mineralized soft tissues within the external tubes.[12] The researchers believe that the mineralized soft tissue represents digestive tracts:

> "Although alternative interpretations are plausible, these internal cylindrical structures may be most appropriately interpreted as digestive tracts, which would be, to date, the earliest-known occurrence of such features in the fossil record."[13]

Mineralized soft tissue has already been found from the Ediacaran period, but preserved digestive tracts have now been pushed back to the late Neoproterozoic. The researchers acknowledge that there are numerous reports of mineralized soft tissues: "Although they may be rare, there is no shortage of preserved internal soft-tissue structures reported from the fossil record."[14]

Sound-producing system and tympanal ear in katydids pushed back 100 Ma

Another set of animal structures found in China pushed back in the fossil record is the sound-producing system and tympanal ear in katydids; these have been pushed back about 100 Ma.[15,16] Furthermore, the sensors are identical to those found in today's katydids. And, just as remarkable, such an amazing ability to hear sound is thought to have evolved multiple times: "For example, tympanal ears have evolved at least 18 times independently in diverse taxa of seven extant insect orders … , involving at least 15 body locations".[17] The ability to produce sound has evolved independently in seven different orders of insects. Amazing 'parallel evolution'!

Slime moulds now found in Burmese amber from the Mesozoic

Slime moulds, myxomycetes, which are common in most extant forests, especially in tropical and temperate ones, would be very difficult to preserve in the fossil record. Yet, they have been preserved in amber; for instance, in the early Cenozoic Baltic amber and in the late Cenozoic Dominican Republic amber. Slime moulds are now found in the famous amber in northern Myanmar, which is dated as early Cretaceous, 100 Ma ago.[18] Thus, the existence of slime moulds has been pushed back about 50 Myr in the fossil record. And, just as interesting, there is no change in morphology between these Cretaceous slime moulds and those that exist today. In other words, there is no evidence of morphological evolution. The researchers note that other groups of organisms remarkably show no change over time.

Origin of mammals pushed back 20 Ma

The oldest mammal was considered to be *Morganucodon* that lived about 205 Ma ago. Now a mammal has been found that is claimed to have lived 225 Ma ago, pushing back the origin of mammals 20 Ma.[19] *Brasilodon quadrangularis*, found in southern Brazil, is only 20 cm from head to tail. It is considered difficult to distinguish between Triassic reptiles and mammals, because they are thought not to have diverged/diversified by that point in evolutionary history. Researchers have usually considered three inner ear bones as a diagnostic mammalian trait if they have the fossil material. In this case, the researchers determined that three skulls and associated dentary (lower jaw) bones were from mammals by an ingenious method.[20] Because the dentary bones were of different ages, they concluded that the animals had only two sets of teeth, common in mammals, whereas reptiles can erupt multiple sets of teeth.

Oldest known forest pushed back 2–3 Ma

Land plants are believed to have evolved in the late Precambrian, but the earliest fossil land plants are bryophytes (mosses) from the Ordovician.[21] However, the origin of forests is another matter. They are supposed to have begun in the mid Devonian Period. A new discovery of a forest in New York, USA, pushes back the origin of forests by 2–3 Ma.[22,23] However, the researchers discovered that one of the three tree species pushed back its origin by 20 Ma. This tree is called *Archaeopteris* and has roots that extend 11 m, similar to modern conifers. Researchers did not know that such wide and complex root systems developed that far back: "Here we show that *Archaeopteris* had a highly advanced root system essentially comparable to modern seed plants."[24] They also discovered evidence of the class Lycopsida, pushing these trees back millions of years from the Carboniferous to the Devonian.

Earliest pelican discovered

The earliest fossil record of pelicans had come from the early Oligocene in southeastern France. Scientists have recently found a pelican from the late Eocene in Egypt that pushes back their origin 6 Ma.[25] Moreover, the pelicans indicate no change in beak morphology:

> "This and other fossil pelicans, such as *Miopelecanus* (Cheneval, 1984), are so strikingly similar to modern pelicans they are hypothesized to indicate long-term stasis in feeding morphology."[26]

Conclusions

Many of these newly reported time range extensions do not push the origin date back that far or are in unimportant organisms within the evolutionary story. However, a few are significant, namely the possible 350 Ma extension of sponges into the early Neoproterozoic, extension back into the late Neoproterozoic Ediacaran Period of cnidarians, the extension of the origin of mammals back 20 Ma, and the conclusion that bryozoans are now part of the Cambrian explosion. Also critically, most of these fossils are nearly identical to modern counterparts, showing little or no morphological evolution. Who knows what the fossil record will look like in a hundred or two hundred years.

References

1. Oard, M.J., More expansion of fossil time ranges, *J. Creation* **33**(3):3–4, 2019.
2. Turner, E.C., Possible poriferan body fossils in early Neoproterozoic microbial reefs, *Nature* **596**:87–91, 2021.
3. Kozlov, M., Sponge-like fossil could be earth's earliest known animal, *Nature* **596**:19, 2021.
4. Gold, D.A., Grabenstatter, J., de Mendoza, A. *et al.*, and Summons, R.E., Sterol and genomic analyses validate the sponge biomarker hypothesis, PNAS **113**(10):2684–2789, 2016.
5. LaFlamme, M., Lifting the veil on the oldest-known animals, *Nature* **609**:904–905, 2022.
6. Dunn, F.S., Kenchington, C.G., Parry, L.A. *et al.*, A crown-group cnidarian from the Ediacaran of Charnwood Forest, UK, *Nature Ecology and Evolution* **6**:1095–1104, 2022.
7. Zhu, Y.-an, Li, Q., Lu, J. *et al.*, The oldest complete jawed vertebrates from the early Silurian of China, *Nature* **609**:954–958, 2022.
8. Andreev, P.S, Sansom, I.J., Li, Q. *et al.*, Spiny chondrichthyan from the lower Silurian of South China, *Nature* **609**:969–974, 2022.
9. Friedman, M., Fossils reveal the deep roots of jawed vertebrates, *Nature* **609**:898, 2022.
10. Ernst, A. and Wilson, M.A., Bryozoan fossils found at last in Cambrian deposits, *Nature* **599**:203–204, 2021.
11. Zhang, Z., Zhang, Z., Ma, J. *et al.*, Fossil evidence unveils an early Cambrian origin for Bryozoa, *Nature* **599**:251–255, 2021.
12. Schiffbauer, J.D., Selly, T., Jacquet, S.M. *et al.*, Discovery of bilaterian-type through-guts in cloudinomorphs from the terminal Ediacaran Period, *Nature Communications* **11**:205, 2020.
13. Schiffbauer *et al*., ref. 12, p. 1.
14. Schiffbauer *et al*., ref. 12, p. 7.
15. Xu, C., Wang, B., Wappler, T. *et al.*, High acoustic diversity and behavioral complexity of katydids in the Mesozoic soundscape, PNAS **119**(51):1–8, 2022.
16. De Jesús, E.G., Insect ears go back 160 million years, *Science News* **203**(2):5, 2023.
17. Xu *et al*., ref. 15, p. 1.
18. Rikkinen, J., Grimaldi, D.A., and Schmidt, A.R., Morphological stasis in the first myxomycete from the Mesozoic, and the likely role of cryptobiosis, *Scientific Reports* **9**:19730, 2019.
19. Anonymous, *Brasilodon* is earliest known mammal, new research shows, sci.news,7 Sep 2022.
20. Cabreira, S.F., Schultz, C.L., da Silva, L.R. *et al.*, Diphyodont tooth replacement of *Brasilodon—a* Late Triassic eucynodont that challenges the time of origin of mammals, *J. Anatomy* **241**:1424–1440, 2022.
21. Servais, T., Cascales-Miñana, B., Cleal, C.J. *et al.*, Revisiting the Great Ordovician Diversification of land plants: recent data and perspectives, *Palaeogeography, Palaeoclimatology, Palaeoecology* **534**:109280, 2019.
22. Discovered the oldest forest in the world, dating back 386 million years, thearchaeologist.org, 5 Dec 2022.
23. Stein, W.E., Berry, C.M., Morris, J.L. *et al.*, Mid-Devonian *Archaeopteris* roots signal revolutionary change in earliest fossil forests, *Current Biology* **30**:421–431, 2020.
24. Stein *et al.*, ref. 23, p. 421.
25. El Adli, J.J., Wilson Mantilla, J.A., Antar, M.S.M., and Gingerich, P.D., The earliest recorded fossil pelican, recovered from the Late Eocene of Wadi Al-Hitan, Egypt, *J. Vertebrate Paleontology* **41**:e1903910, 2021.
26. El Adli *et al.*, ref. 25, p. 1.

Amyloids are not sources of information

Royal Truman

Prof. Emer. Peter Maury,[1] from the University of Helsinki, had a distinguished career in medical research focusing on amyloids,[1] amyloidosis, and fibrillogenesis. He is now a leading proponent of the Amyloid World Hypothesis, which recognizes the need to explain the origin of information in biological systems. He claimed, in a 2018 review article, that amyloids produced under allegedly plausible prebiotic conditions performed information processing, information transfer, and error correction. Specifically:

> "The amyloid world hypothesis posits that in the pre-RNA era, information processing was based on catalytic amyloids ... . The new functions include … information transfer ... and error-correcting information-processing system."[2]

Coded symbols are a defining characteristic of informational messages, and this seems to have been taken into account:

> "In the encryption process, environmental information is encoded in the three-dimensional structure of the amyloid conformer. The steric information can then be transferred … generating replicas of the spatially altered amyloid conformer."[2]

That was when the alarm bells went off. *Environmental information*? Deterministic responses to environmental influences and steric shapes do not create information. For example, smoke shapes result from heat and mutual interactions, but this was not the *source* nor the *content* of the information communicated by the native Americans using smoke signals. It is the *implementation*.

Informational messages must meet specific criteria, whether in biological systems, technology, human language, or other examples of information exchange. The smoke signals used pre-agreed-upon symbols (size and duration of individual smoke clouds), a syntax (the order of symbols), a semantic meaning, an intended activity to perform, and an ultimate goal.

Therefore, the native Americans could communicate, for example, over distances where a herd of buffalo had been located, or that enemies were approaching, expecting suitable action to be taken.

Deterministic causes coupled with replication are not information! For example, drops of water dripping down a slope from one stone to another can attract moisture, produce 'daughter' drops, and 'replicate'. This satisfies the evolutionist definition of a *replicator*, whereby some kinds of drops will replicate faster ('natural selection').

Astonishingly, someone as intelligent as Maury indeed made an analogous argument:

> "Information transfer on the early Earth for about 4000 million years ago [sic] occurred, according to the amyloid hypothesis, by means of a β-sheet peptide-based prion-like amyloid system in which *environmentally derived information* encrypted in the β-sheet zipper structure was *transmitted* by a templated conformational *self-replication* mechanism to 'daughter' amyloid entities. Recognition was mediated by amino acid side chain complementarity and *coding* by the β-sheet zipper structure [emphases added]."[2]

Other Amyloid World proponents, like Rout *et al.*, correctly noted that forming highly ordered amyloid aggregates is analogous to crystallization.[3] In crystallization, a seed crystal attracts copies of the same, or similar, molecules to produce larger crystals. The molecules being added are 'moulded' into certain locations by the existing structure, forming the distinctive crystal lattice. Just like water molecules are moulded when attaching to the surface of an existing drop. But is this how RNA and DNA information is *created*? By adding nucleotides through physical interactions, and transferring shape details to produce additional copies?

According to the Amyloid World Hypothesis researchers, yes. In fact, conflating direct physical cause–effect with information is claimed to be advantageous, being faster:

> "The information content of the β-sheet system, though potentially large, is very limited when compared to the virtually unlimited information content of a nucleic acid-based genetic system. The β-system allows, on the other hand, for more rapid responses to environmental changes which would likely have been an advantage during early molecular evolution."[2]

Physical factors causing crystallization, gas expansion, water freezing, etc. are not how coded instructional messages arise. The codons of DNA and mRNA, which specify protein sequences, don't even interact with the activated amino acids (AAs). The meaning of the codons can be assigned arbitrarily.[4] Additional codes specify when to initiate transcription, how proteins are to fold, where they are to be sent, and their half-lives.[5,6]

Without a code, AAs polymerize randomly (if they do at all). However, multiple copies of many kinds of proteins are required for biological processes. These must possess very special sequences to provide enzymatic functions and to create the cytoskeleton. They also transport biochemicals, form sensors, carry signals, etc. Correct function also requires that only a small number of protein surfaces interact with other biochemicals.

Therefore, prebiotic researchers have devoted much effort to finding conditions that produce non-random sequences. This is a misguided endeavour. They wish to avoid any implication of teleology, since natural processes should not display goal orientation. But why should compulsory, miniscule linking preferences among AAs or nucleotides produce *useful* functions? Especially when we see how different the thousands of protein families found in cells are.[7] Therefore, the precise specifications provided by DNA sequences pose a dilemma for materialists.

It is ironic that OoL researchers have been so active in attempting to find natural processes for AAs to self-assemble into large peptides in high concentrations. The fact that AAs do *not link easily* is more than fortunate, since otherwise the sequences specified by DNA would be corrupted by random insertions. This was a central point made by Professor Tan, who pointed out that the *facile ability of AAs to self-link and thereby insert themselves into purposeful protein sequences would prevent life from existing!*[8]

The amyloid experiments

In amyloid experiments, peptide templates were carefully designed which could interact with tailored peptides to form β-sheets, as shown in figure 1.[2,9] Multiple copies could then form conglomerates with a distinctive structure. *This interaction was alleged to produce information*. In addition, when the substrates were one to three residues shorter, specific *activated* AAs were preferentially selected, being able to extend the β-sheet (see figure 1).

Maury explained:

> "From a primordial pool of random uncoded short protopeptides, the adaptive template-directed chiro-selective and error correcting replication cycles generated amyloids that represented the first 'coded' peptide polymers. Direct chemical interaction between amino acids/peptides and ribonucleotides in the primordial environment was probably important [*sic*] the evolution of the genetic code."[2]

This refers to experiments *designed* to avoid side-chain reactions, and others *designed* to add specific AAs, with a slight preferential (or the L-enantiomer) to form β-sheets.[2]

These experiments were not performed under plausible prebiotic conditions.[10–12] Unrealistic details included modification of the peptides with end-capping groups and activated aa. To form long fibrils, impossibly high concentrations of specific pure modified peptides were necessary.[9]

Amyloids are supposed to have produced an RNA world. This is peculiar since the opening paragraph stated that a functional ribonucleotide polymer could not have existed under putative early Earth conditions.[2]

We have frequently encountered the word 'information' being applied to simple deterministic physical effects to then claim that information stored on DNA arose through natural processes. This is a category mistake.[13]

What is information?

Information is used to communicate instructions or understanding between a sender and receiver. Informational messages must meet specific criteria, whether in biological systems, technology, human language, or other examples of information exchange, as we have discussed in depth.[4] Biological systems are incomprehensible without taking information into account, requiring retro-engineering purposes and goals. Hundreds of different programs are used by cells.[5,6]

Professor Gitt's five-level hierarchical model clarifies if coded information is involved, as shown in figure 2.[14,15]

Examples of pragmatics in cells include generating the correct proteins in the proper proportions and locations, followed by carefully choreographed events to repair damaged tissue or

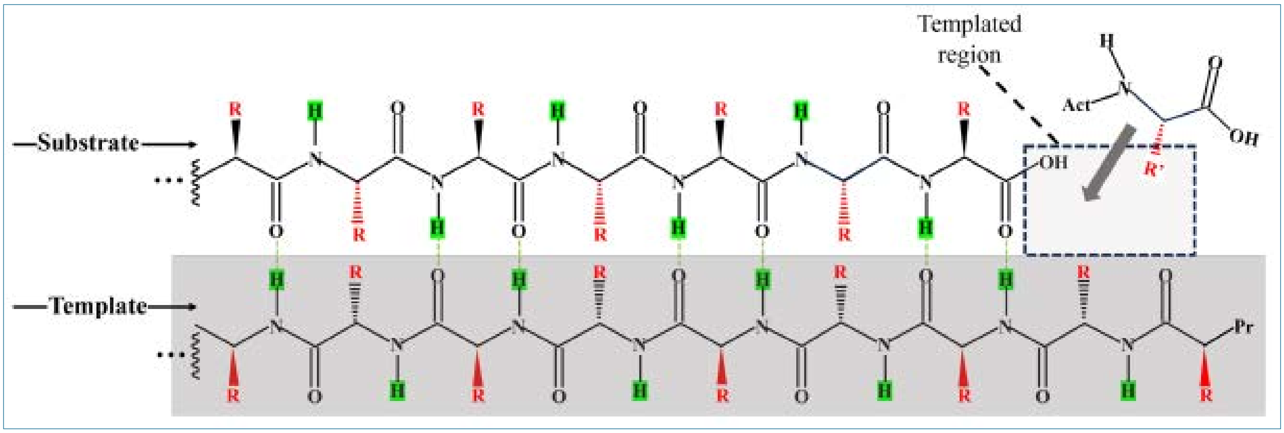


Figure 1. Template and substrate peptides tailored to interact and produce β-sheets. The R groups were not the same, and selected to form β-sheets. Substrates 1–3 residues shorter than their templates preferentially attached specific amino acids. Act = activating group, Pr = protecting group. Figure created by R. Truman.

produce an immune system response. The outcome is *caused* neither by the physical attributes of DNA, mRNA, nor the decoding equipment ribosomes. The achieved purposes include producing a complex organism with hundreds of integrated parts and reproducing.

The amyloid experiments might seem to exemplify aspects of the lowest level, statistics, since a small preference exists to add a particular AA at a specific location. But this is not equivalent to a symbol in a code. All codes are indeed implemented using physical principles, in particular analogue codes. But are three stones and a stick in a hole a code or are they there for physical reasons having no further meaning? It depends on whether a pre–agreed-upon code had been set up between sender and receiver, linked to a process to generate specific outcomes or cognitive understanding.

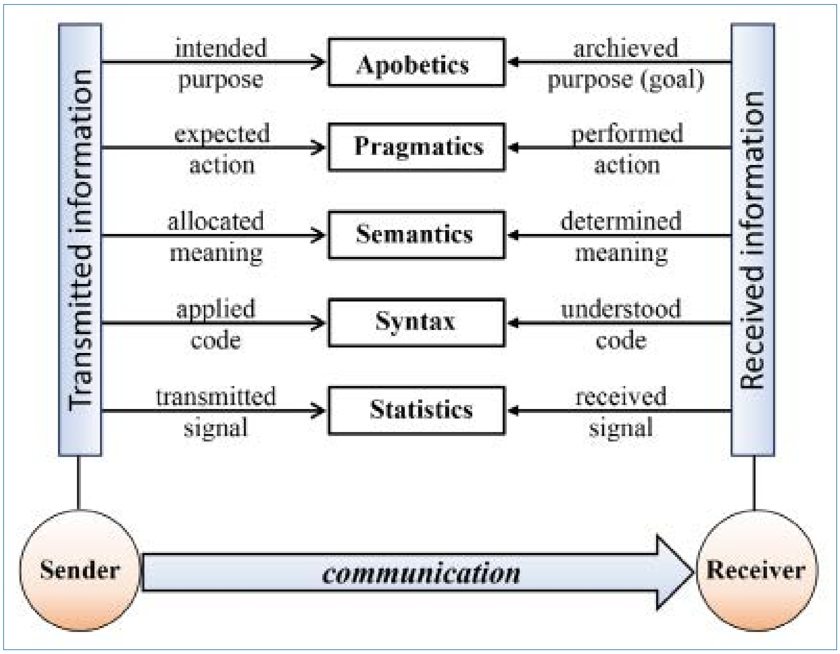


Figure 2. The five hierarchical levels of Universal Information, according to Gitt.[15] Figure recreated and slightly modified by R. Truman.

Mass media, YouTube, and the modern form of (mis)education

Much of the indoctrination in evolution, defined as litter → LUCA → Laureates, is currently being conducted through mass media and YouTubers. Very few read, or are qualified to understand, the primary evolutionary literature. Middlemen produce interpretations, having a veneer of vague, conceptual plausibility, with a generous sprinkle of technical terms thrown in.

One YouTuber who has engaged in many online video debates with creation scientists and Intelligent Design supporters reviewed Maury's paper and educated his followers with the missing details for how amyloids supposedly led to the modern genetic system. Disturbingly, more people see videos like these than are critically evaluating the primary literature.

With supreme confidence, the YouTuber explained:

> "And ATP is another naturally occurring energy source near hydrothermal vents. So, we know that amyloids have ATPase activity they can utilize the energy of ATP to do work. And once you develop this interaction between amyloids and ATP, it's only a matter of time until you start having refinements into the information storing system. The stringing of ATP and different triphosphate nucleotides together into DNA and RNA, the incorporation of lipids which are again found naturally at hydrothermal vents and which spontaneously formed bilayer membranes; as well as the creation of protein enzymes to do specific function."[16]

Addressing all the errors in this one paragraph alone required a full paper.[17] The point was not to single out a particular YouTuber who has put out excellent videos on other topics. Our concern is that careless wording by evolutionary scientists and those embellishing and passing on errors are seriously misguiding many.

Evolution theory and the influence of science fiction

Norbert Wiener, the founder of Control Theory, showed that information is a real entity, and that reality can only be understood by taking the effects of matter, energy, and information into account.[18,19] Downgrading the meaning of *information* instead of using well-understood concepts to describe matter leads to serious mistakes. Not only is what philosophers call a category mistake created, but a tendency is increasing in the origin of life community to replace hard scientific work with vague imagery.

Evolutionary imagery is rampant in science fiction films. In a memorable scene in *Jurassic Park 1*, baby dinosaurs were born without fathers:[20]

> "Henry Wu: Actually, they can't breed in the wild. Population control is one of our security precautions.

> There is no unauthorized breeding in Jurassic Park.
>
> Ian Malcolm: Uh, and how do you know they can't breed?
>
> Henry Wu: Well that's because all the animals in Jurassic Park are female. We've engineered them that way.
>
> ...
>
> Ian Malcolm: John, the kind of control you're attempting here is, uh, it's not possible. If there's one thing that the history of evolution has taught us, it's that life will not be contained. Life breaks free. Expands to new places and crashes through barriers. Painfully, perhaps even dangerously. But ... uh well, there it is.
>
> John Hammond: There it is.
>
> Henry Wu: You're implying that a group composed entirely of females will ... breed?
>
> Ian Malcolm: No, I'm simply saying that *life ... uh, finds a way* [emphasis added]."

The association of *evolution* with *miraculous creative properties* is cemented into technical papers. Whenever complex biological features are found which clearly look designed, standard *pro forma* phrases are inserted, such as 'through evolutionary processes'; 'in the course of evolution'; 'fine-tuned by evolution'; or 'evolutionary pressure caused'.

Or as the YouTuber put it:

> "… it's only a matter of time until you start having refinements into the information storing system."[16]

References

1. Prof. Emer., Clinicum, Peter Maury—publications; researchportal.helsinki.fi. *Amyloids*: Portions of some proteins can sometimes interact to form so-called β-strands, if they have suitable amino acid sequences. When many β-strands aggregate they occasionally form long, stable, insoluble fibers. In abiotic studies, short amino acid sequences are designed which show some characteristics of biological amyloids.
2. Maury, C.P.J., Amyloid and the origin of life: self-replicating catalytic amyloids as prebiotic informational and protometabolic entities, *Cell. Mol. Life Sci.* **75**:1499–1507, 2018 | doi:10.1007/s00018-018-2797-9.
3. Rout, S.K., Friedmann, M.P., Riek, R., and Greenwald, J., A prebiotic template-directed peptide synthesis based on amyloids, *Nat. Commun.* **9**:234–242, 2018 | doi:10.1038/s41467-017-02742-3.
4. Truman, R. Wiebe, P., and Siemens, E., Trivializing information, a cornerstone of reality (in press).
5. Truman, R., Cells as information processors part 1: formal software principles, CRSQ **52**:275–309, 2016.
6. Truman, R., Cells as information processors part 2: hardware implementation, CRSQ **53**:19–41, 2016.
7. Mistry, J. *et al.*, Pfam: the protein families database in 2021, *Nucleic Acids Research* **49**(D1):D412–D419, 2021 | doi:10.1093/nar/gkaa913.
8. Tan, C.L., Facts cannot be ignored when considering the origin of life #1: the necessity of bio-monomers not to self-link for the existence of living organisms, ARJ **15**:25–29, 2022.
9. Nanda, J., Rubinov, B., Ivnitski, D., *et al.*, Emergence of native peptide sequences in prebiotic replication networks, *Nat. Commun.* **8**:434, 2017 | doi:10.1038/s41467-017-00463-1.
10. Truman, R., Non-existence of error correction in plausible prebiotic amyloids (in press).
11. Truman, R. and Basel, C., Prebiotically plausible peptides don't self-assemble to produce useful catalytic amyloids, *J. Creation* **37**(3):135–140, 2023.
12. Truman, R., Amyloids having sequence-, regio-, and stereoselective properties don't form under plausible prebiotic conditions, *J. Creation* **37**(3):128–134, 2023.
13. Category Mistakes, Stanford Encyclopedia of Philosophy, *5 Jul 2019*.
14. Gitt, W., Scientific laws of information and their implications—part 1, *J. Creation* **23**(2):96–102, 2009.
15. Gitt, W., Compton, B. and Fernandez, J., *Without Excuse*, Creation Book Publishers, 2011.
16. Amyloid world hypothesis: the origin of life, youtube.com, 12 May 2023.
17. Truman, R., Amyloids and ATP fictitious chemistry XXX (in press).
18. Wiener, N., *Cybernetics or Control and Communication in the Animal and the Machine*, Hermann et Cie, The Technology Press, Paris, 1948.
19. Wiener, N., *Cybernetics or the Control and Communication in the Animal and the Machine,* The MIT press, 1961.
20. Jurassic Park film transcript, at approximately the 41-minute point of the film.

God’s creation: dealing with apparent malevolent design in nature

Why Did God Create Viruses, Bacteria, and Other Pathogens?
Jerry Bergman and James Hoff
Westbow Press, Bloomington, IN, 2023

John Woodmorappe

Author Jerry Bergman is well known. He is a well-published award-winning author who has taught microbiology, psychology, and other university courses for over 40 years. James Hoff is a computer designer who holds four major patents in computer technology.

By way of introduction, I once heard an atheist say, “Believers like to talk about the beautiful things in nature, such as apple trees. They are silent about the hideous things in nature, such as tapeworms.” In fact, believers have often written about ‘hideous things’. However, notice how the atheist has changed the argument: from the origins of specified complexity, which he cannot explain in a non-theistic framework of thinking, to the alleged malevolence of some of this complexity. The fact of intelligent design should not be confused with the perceived malevolence of some of the designs. These are two separate issues.

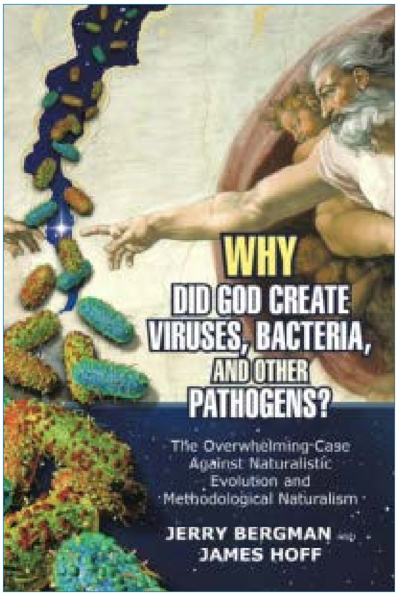
Authors Bergman and Hoff examine some of the things which are sometimes alleged to be incompatible with living things originating from a benevolent creator. The authors do not get into theology, nor do they explicitly suggest why God allowed ‘malevolent’ things in nature to exist. The authors do not factor in the Fall and its consequences. They do not mention Satan or his role as the corrupter and perverter of things that God created. They stick to science.

Bergman and Hoff, rather than trying to ‘figure God out’, go on to re-examine the usual thinking about the existence of perceived malevolent things in nature. To begin with, they show that ‘malevolent’ elements in nature are greatly exaggerated in numbers. In addition, they can be characterized as malfunctions. They are distortions—often minor ones—of neutral or benevolent elements of nature, or a misplacement of one organism in another organism or another ecological system.

Given a benevolent Creator, why are there bacteria?

Surely no loving God would make such ‘loathsome’ creatures. Think again. Bacteria have numerous essential roles in nature. Bergman and Hoff write:

> “Bacteria and most other microbes, often called germs, although often assumed to exist only to cause disease, actually have several critically important functions in our bodies. These include synthesizing vitamins, triggering hormones, and reducing the number of infections caused by harmful bacteria. They also serve numerous critical roles in ecology, such as recycling organic and inorganic materials. Furthermore, they serve other important roles in human life, including synthesizing antibiotics, fixating nitrogen from the air to make fertilizer, and providing a major source of food for humans including yogurt, cheese, and tofu” (p. 59).



How bacteria and viruses acquire pathogenicity

Let us, first of all, keep pathogenic bacteria in perspective. According to the authors (p. 59), less than 8% of all identified species of micro-organisms cause disease, including perhaps 1% of all bacteria (p. 60). The vast majority of bacteria are either directly or indirectly beneficial to humans. Bacteria have a bad reputation because we are prone to single out and study precisely those bacteria that cause disease!

Let us examine how the small percentage of bacteria that are pathogenic got that way. Consider the common innocent intestinal bacterium *E. coli* (figure 1). One variant of it is very harmful. Bergmann and Hoff write:

> “The only difference between the common benign *E. coli* flora in the human large intestine and the savage O157:H7 strain that can cause lethal bloody diarrhea is that the O157:H7 strain carries an island of pathogenicity in its chromosome, the STX gene, and an unusually large extra chromosomal plasmid. These differences produce

> the infamous potentially lethal *E. coli* strain. The O157:H7 bacteria produces actually only one chemical, called shiga [toxin], that destroys blood vessels, first in the intestines, then in the rest of the body" (pp. 68–69).

Viruses can become pathogenic when they change their hosts. Consider HIV. In humans, it is deadly. But in its original host—the monkey and the baboon—this virus appears to be harmless.

Finally, we must remember that all microorganisms live in equilibrium with the immune systems of the hosts. An imbalance in this equilibrium itself can cause pathogenicity. For instance, Bergman and Hoff comment:

> "A critical factor in disease causation is the health of the person infected with microbes. An example is *Candida albicans*, which is a benign yeast that normally lives in the human mouth without problems but can cause disease in immune-suppressed people" (p. 69).

Let us extend the foregoing reasoning. We can visualize organisms once having such strong immune systems that various micro-organisms could freely colonize these organisms without ever causing them illness.

Those pesky mosquitos

The authors keep these reputed repulsive creatures in perspective. Most mosquitos do not suck blood, and even fewer are able to transmit disease. Mosquitos are no 'mistake'. For instance, mosquito larvae serve as a crucial food source for many fish. A set of relatively minor modifications can transform harmless mosquitos into pathogenic ones. Bergman and Hoff conclude:

> "In short, the evidence leads to the conclusion that no mosquitos were able to serve as a vector of human pathogens until mosquito mutations or abnormalities allowed this condition to develop. This supports the belief that, originally, all life was mutation-(corruption-) free and, as is true of humans and all other life, the mutation load has steadily increased since that time" (pp. 116–117).

Why did God create poisons?

The authors answer this trivial objection. Whether something is poisonous or not depends upon its concentration. At very low levels, selenium and chromium are non-toxic. In fact, they are beneficial. Another example is the Shiga toxin mentioned above. It is among the top five known toxins in terms of smallest median lethal dose (2 ng/kg in mice). However, even Shiga toxin has a beneficial usage in the right dosage: it can target stomach cancers, because the cancer cells have a receptor to the toxin that healthy cells don't. At high concentrations, even water and oxygen are poisonous. Does this mean that God made a mistake when He created water and oxygen? Of course not.

Authors Bergman and Hoff support the threshold dose concept of radiation damage. They argue that, below about 100 rems, ionizing radiation is harmless to humans. (Some other scientists would disagree.)

Irreducible complexity and intelligent design

The authors change the subject a bit and focus on intelligent design. The simple mousetrap has been used as an example of irreducible complexity. Either all the components are in place, or else the mousetrap does not function at all. There is no such thing as a 'half mousetrap'. Nor can a mousetrap originate from a step-by-step process. Neither, by analogy, can complex living things arise step-by-step through an incremental evolutionary process.

An argument has been made against the irreducible complexity of the mousetrap by pointing to the fact that its wooden base can be dispensed with if one allows the components to be directly attached to the floor. But this does not eliminate the base: It merely substitutes one wooden base (the floor) for another (the original)! Making a mousetrap while involving a wooden floor is *itself* a form of irreducible complexity just as much as the original mousetrap.

Other evolutionists have made even more bizarre arguments. Some have said that mice can fall in a hole, and this is somehow supposed to disprove the mousetrap as an example of irreducible complexity. However, falling into a hole, even if it were to trap the

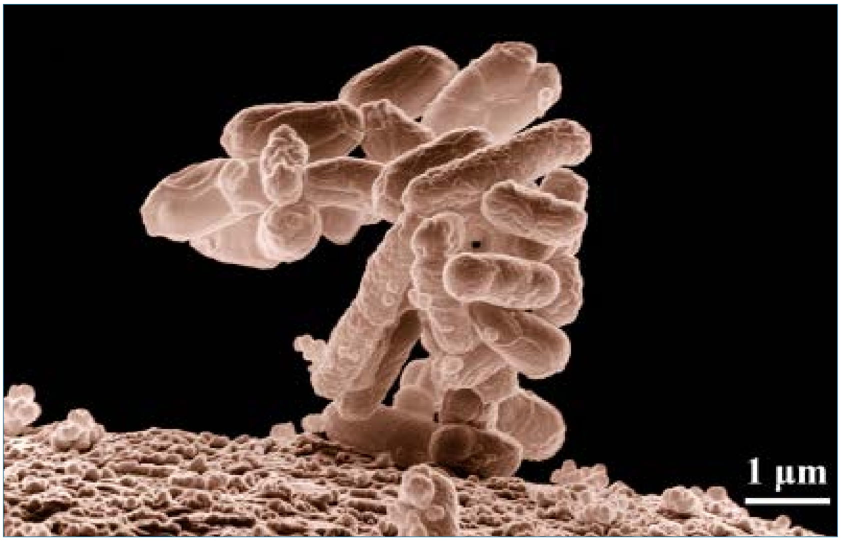


Image: byfkfkrErbe and Christopher Pooley, Wikimedia / Public Domain

Figure 1. *Escherichia coli*, one of the common, usually harmless, intestinal bacteria

mouse, has no relevance to any kind of purported incremental development of any spring-based mousetrap.

Some have argued against irreducible complexity, citing individual structures within the mousetrap that can serve multiple functions, and then become co-opted to serve new functions. However, it is not the individual functions that matter: it is the intelligent design that unites and coordinates all the individual components into a coherent, functioning whole. For example, the spring must be placed in the exact location relative to the other mousetrap elements, and in just the right way, in order for the mousetrap to function at all. Only then can we begin to talk about the function of the spring being 'co-opted' (by the designer, not by blind evolutionary processes). The mere fact that a spring can be used in many other devices and for many other purposes is, by itself, completely irrelevant.

Evolutionary co-option is pure *ad hoc* speculation

The notion that structures can serve multiple functions, and that this can rescue evolutionary explanations, does not even have a leg to stand on, even given the standard evolutionary assumptions. Bergman thus quotes an evolutionist:

> "Among these great innovations in design, the crucial inventions of nature, the earliest have left no trace of their development in the fossil record. The organization of living material in a cell wall and a nucleus, the transmission of the blueprint of its design and its means of self-construction, and the very important device of sexual reproduction, all developed in minute organisms which have left little evidence" (p. 160).

The 'backwards' retina myth

Evolutionists have argued that the human retina is wired 'backwards', and that no Intelligent Designer would make it that way. Once again, the evolutionist is merely stating an opinion, and is changing the argument from the fact of the design (eye) to his opined inefficiency of the design.

According to this dysteological argument, the nerves that are located in the front of the retina block part of the image that falls on the rods and cones. Bergman reminds us that the retina needs a very disproportionately high blood supply, which requires a rich blood supply (choriocapillaris) in contact with the retinal pigment epithelium. If the nerves were behind the retina, there would be no room for the blood supply in front. Blood is almost opaque, while wiring in front of the retina forms a fibre optic plate that improves image sharpness and colour distinction.

However, the question is more basic. Even if, for the sake of argument, the 'backwards' human retina was not quite as visually effective as the 'correctly' wired one, it would still mean nothing. Human eyes are more than adequate just the way they are. Pointedly, there is no scientific or theological reason that obligates the Creator to give human beings eyes that are as visually acute as those, for example, of the eagle. And eagle eyes are backwardly wired too, yet it is hard to call eagle eyes bad! The backwards-retina argument is akin to saying that human legs are 'bad design' because, after all, the human being cannot normally outrun the lion.

Evolution is not consensus science

Nowadays, evolutionists usually just dismiss creationists and proponents of Intelligent Design. They bully dissenters into shame and silence with the 'evolution is consensus science' messaging. Bergman deconstructs this nonsense:

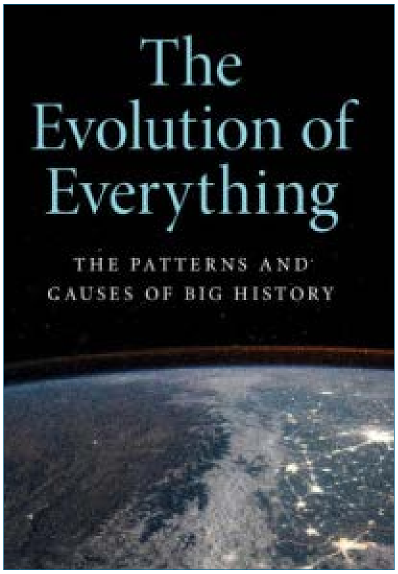
> "First of all, this claim is not true. There exist thousands of scientists that do not accept evolution, many in-the-closet due to the hostility of the Darwinian establishment. Many have lost their academic or research positions due to disputing the so-called 'consensus science'. The consensus that exists is forced; a fact that is well documented in the works listed below. We must not forget that eugenics, scientific racism, use of frontal lobotomies, bloodletting, and other ideas were also once consensus science. They are now an embarrassment to science" (p. 30).

Conclusions

Many items of perceived malevolent design (e.g., pathogenic bacteria) are fairly straightforward modifications of benevolent design (e.g., harmless or helpful bacteria). This leads to a better understanding of such perceived malevolent design—in terms of both theological issues and scientific issues. In either case, we are not in a position where we have to contemplate a creator who made harmful organisms.

By analogy, let us consider the automobile engine that has lost too much of its motor oil. The observer notices that the engine is overheating and will soon destroy itself. Following the atheists, should we conclude that the designer of the engine created the engine parts so that they would torment each other? Absolutely not. The engine is acting in a manner never intended by its designer. In like manner, we should not blame the Creator for the later malfunctions in His creation. If anything, and from a theological point of view, it is more like a question about the Creator's providential care, which is a separate issue. Finally, the central issue of specified complexity remains, even if, for the sake of argument, the 'malevolent' design is not explained to the satisfaction of the critic.

The evolution of a story: weaving a tale that goes far beyond science



The Evolution of Everything: The patterns and causes of big history
Brian Villmoare
Cambridge University Press, 2023

Reed Costello

Brian Villmoare, an Associate Professor in the Department of Anthropology at the University of Nevada, Las Vegas, is a paleoanthropologist working in the Afar region of northern Ethiopia since 2002. In 2013 he was part of the team that discovered allegedly the oldest fossil specimen of our genus, *Homo*. As an undergraduate, he studied philosophy and English literature and has long been interested in how science, society, and philosophy intersect.

His book begins by informing us that the author intends to borrow from the history department in using 'big history', which seeks to give us a broader understanding of the past by utilizing multiple fields of study. He made it clear that this book will be one giant exercise in evolutionary storytelling. That is, not just the grand narrative of evolution, but an attempt to explain most of history and human action in evolutionary terms.

Materialistic bias from the outset

In seeking to explain all of human history through the lens of materialism, which he equates with science, he proceeds to define science for us on page 3:

> "In its most basic form, science simply tries to describe the material world in as objective a way as possible. A scientific statement about the world has several important characteristics:
> 1. Any scientific statement must invoke only forces and causes that can be observed by anyone using empirical methods. Science cannot attribute actions, for example, to 'spirits' that can only be seen by one privileged spiritualist.
> 2. Any statement that one makes … must be testable by other scientists … .
> 3. If there are competing explanations, the one with the fewest assumptions will be accepted."

How much of this is science, and how much is materialistic bias? First, let us examine statement number two. The issue here is the example he gives about scientists examining a crater. While the first scientist makes a claim about a crater that other scientists can look at, the first scientist does not make a testable claim about an observable phenomenon. Only the crater is observable, not its cause. Scientists can develop competing explanations, but none can be properly tested. Nobody looking at this crater can see the event in question. His example of historical science violates the definition of science given.

Operational vs historical science

It is important to distinguish empirical and historical science when defining science. Going forward, we will see that most of his claims about history do not fit the definition of science.

Ernst Mayr (one of the 20th century's leading evolutionary biologists) describes the scientific weakness of evolutionary biology as follows:

> "Evolutionary biology, in contrast with physics and chemistry, is a historical science—the evolutionist attempts to explain events and processes that have already taken place. Laws and experiments are inappropriate techniques for the explication of such events and processes. Instead one constructs a historical narrative, consisting of a tentative reconstruction of the particular scenario that led to the events one is trying to explain."[1]

Jerry A. Coyne (professor in the Department of Ecology and Evolution at the University of Chicago) states:

> "In science's pecking order, evolutionary biology lurks somewhere near the bottom, far closer to phrenology than to physics. For evolutionary biology is a historical science, laden with history's inevitable imponderables. We evolutionary biologists cannot generate a Cretaceous park to observe exactly what killed the dinosaurs; and unlike 'harder' scientists, we usually cannot resolve issues with

> a simple experiment, such as adding tube A to tube B and noting the color of the mixture."[2]

Evolutionary biology and the other topics covered in this book mainly discuss matters of history that should not be conflated with hard sciences. The author fails to provide the crucial distinction, which creates a misconception about the reliability of claims made in these fields.

Since the author is a paleoanthropologist, it makes sense that he would loosely define science, as his field is about as soft as science can be, and the scientific method is applied very loosely. The criteria here claim that any hypothesis must be testable and involve an observable phenomenon using empirical methods. However, this idea is inconsistent with creating narratives about the unobservable and unrepeatable past. There is a philosophical commitment hidden in these criteria.

The philosophical commitment has been admitted before and shows the bias inherent in what many call science today. As revealed by the evolutionary biologist Richard Dickerson:

> "Science is fundamentally a game. It is a game with 1 overriding rule: Rule #1: Let us see how far and to what extent we can explain the physical and material universe in terms of purely physical and material causes, without invoking the supernatural."[3]

An eminent immunologist and Evangelical Christian summarizes the bias as follows:

> "Most important, it should be made clear in the classroom that science, including evolution, has not disproved God's existence because it cannot be allowed to consider it. Even if all the data point to an intelligent designer, such a hypothesis is excluded from science because it is not naturalistic."[4]

The modern institutions of science have an extreme bias that rules out God, and thus the Bible, before the evidence is ever examined, and no matter what evidence is found, God will still be denied.

As a paleoanthropologist (a specialist in the field of paleontology), his field has a severe weakness that shows much of this book should be discarded from the start. Henry Gee, Ph.D. in zoology and the chief science writer for *Nature*, explains the weakness of this field. He tells us that fossils are not found with certificates of authenticity, that you cannot determine ancestry based on fossils; the attribution of ancestry is in our imagination. This gives unlimited freedom to make up plausible-sounding stories and has more to do with our own biases than any evidence. It tells us not what happened but what we think should have happened; and missing links are likewise imaginary. The tales about human evolution are unscientific, and paleontology lacks scientific value.[5]

Science vs beliefs? No, beliefs vs beliefs!

On page 4, Villmoare enters the conflict between 'science' and beliefs. The author wastes no time, targeting creationists specifically and stating:

> "The most well-known such conflict is the debate between the scientific perspective on the evolution of species (including humans) and Creationism. Some interpretations of the Book of Genesis in the Old Testament have humans as the product of divine Creation."

We see the strawman set up with evolution as the objective and scientific explanation, while creation is the barrier to scientific progress. In this short section, he makes no arguments against the position but speaks from the assumption that it is false and describes the issues he believes creationists cause.

On page 5, he mentions that humans are not unique; we are a biological accident. The lack of human value is the other objection to 'science' that he mentions. He recognizes that if humans are just another variety of animals, mere bags of rearranged pond scum, then the value of human life becomes severely undermined. However, this is just an extension of his complaint about creationists. Human life is valuable because God created humanity in His image. The basic idea he outlines is that if evolution was true, then it would essentially be an accident that humans are the dominant intelligent species on the planet. It could have easily been any other. As for morality and the value of humanity, he tosses the issue off because it is outside of science. But this is also true of most of his book.

On page 6, we have some rare points of agreement. He claims that science is not just about learning a set of facts but also about arguing how to interpret them. He believes the explanation with the fewest assumptions is the most scientific. This is a valid point and something CMI often points out. Creationists are not disputing any facts. Instead, we dispute how the secular community *interprets* those facts and the philosophical *assumptions* that guide those interpretations. It is uncommon for those who propagandize evolution to admit that evidence does not speak for itself.

Is evolution necessary for science?

On page 60, Villmoare repeats Theodosius Dobzhansky's assertion beloved by materialists, "Nothing in biology makes sense without evolution." This claim is significant for those who wish to oversell the importance of evolution. However, other evolutionists are more frank about the significance of evolution to biology. The editor of the journal *BioEssays* shines a light on this for us:

> "The subject of evolution occupies a special, and paradoxical, place within biology as a whole. While

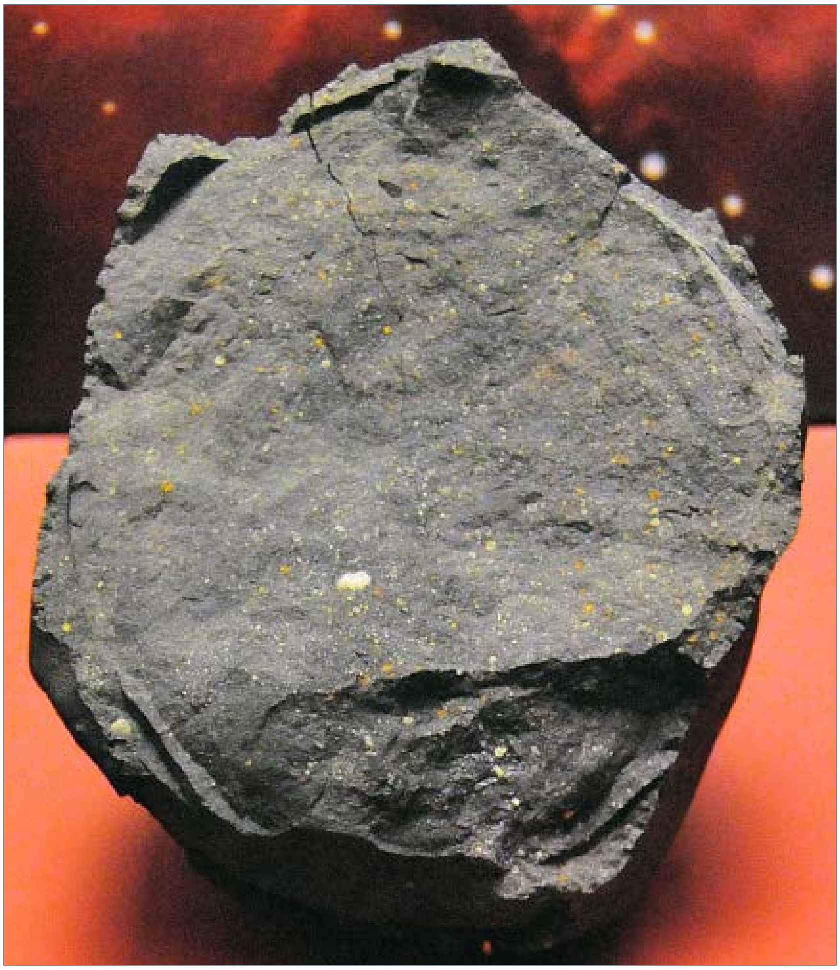


Image: Basilicofresco Wikimedia / CC BY SA 3.0

Figure 1. Although the Murchison meteorite indicates that some basic building blocks of organic life can form abiotically, these are unable to self-assemble into the biomolecules needed for life.

> the great majority of biologists would probably agree … ‘nothing in biology makes sense except in the light of evolution’, most can conduct their work quite happily without particular reference to evolutionary ideas. ‘Evolution’ would appear to be the indispensable unifying idea and, at the same time, a highly superfluous one.”[6]

Dr Marc Kirschner, founding chair of the Department of Systems Biology at Harvard Medical School, makes a similar point:

> “In fact, over the last 100 years, almost all of biology has proceeded independent of evolution, except evolutionary biology itself. Molecular biology, biochemistry, physiology, have not taken evolution into account at all.”[7]

Despite what Villmoare wants us to believe, evolution is critical to a godless worldview, but has no significance to scientific progress.

Chapter 4: Origin of Life

The chapter begins with some grand assertions, claiming that all life on Earth shares a common ancestor because all life has the same DNA molecule, and our degree of relatedness can be determined through genetic comparisons. This grand assertion is not argued for but merely asserted, and he ignores that a common designer can just as easily explain these similarities. The notion that similarity is strictly due to ancestry is hardly demonstrable.

In this chapter, his major argument for abiogenesis is the Miller–Urey experiment, and the Murchison meteorite (figure 1) for panspermia, or at least that the ingredients needed for life to start on Earth come from space.

The meteorite only shows that some of the basic building blocks of organic life can form abiotically, but this hardly suggests they can self-assemble into the massive, complex, and delicate biomolecules needed by all living things, let alone combine them all into a functioning cell, all before the fragile biomolecules break down.

CMI has long addressed the Miller–Urey experiment. This experiment did produce a small number of the simplest amino acids, glycine and alanine, and far greater amounts of tar chemicals that would be toxic to life forming. The spark discharges in this experiment do not produce the cytosine molecules that act as the base for RNA and DNA, and, even if formed, it would be too unstable to matter. A random collection of very simple molecules does not support abiogenesis logically.[8]

On page 54, in box 4.5, the author introduces us to the RNA world. The RNA world is the idea that the first living things were not based on DNA but on RNA (ribonucleic acid). The idea is popular because it is believed that RNA could self-propagate and act as a catalyst for other reactions at the same time (essential features for living things). It was demonstrated that some RNA sequences can function as catalysts,[9] but the good news for that idea stops there.

RNA is a very complex and unstable biomolecule. The idea that it could form in abiotic systems is undemonstrated and has numerous issues. RNA is 100 times more reactive than DNA, and the discovery of DNA's instability was a major topic for the 2015 Nobel Prize in Chemistry.[10] Thus, even if RNA could form abiotically, it would break down quickly. And like any DNA that could hypothetically form, it would lack any special enzymes to maintain it or protect it from hydrolysis and background radiation. The building blocks of RNA—nucleotides—are very complex, and forming them in a laboratory is complicated.

Chapter 5: Evolution of new species/creationist bashing

This chapter has a section dedicated to attacking creation. Given that this is a dedicated section, these arguments should be what the author believes are the most vital points he can make. As such, this is the portion most deserving of a response. He makes many assertions but only makes two attempts at an argument against creation. His first argument is to appeal to the existence of simpler eyes (figure 2). He claims:

> "The eye is an extremely complex organ, and if any one part of the eye is absent, or does not function perfectly, the entire organ is useless. The basic idea is that the eye works as a complete organ or not at all, so there could never have been an intermediate stage in evolution toward the eye. For example, there is no selective advantage to having a focusing lens if there is not already present a retina exactly the right distance away. However, the evolution of the eye is now well known. There are species of primitive animals (flatworms, for example) who have only a light-sensitive patch of skin on the head. In some animals, the importance of light perception is sufficient to put those receptors in a concavity in the skull for protection. Once in a depression, an animal that lives in the water could take advantage of the 'pinhole camera' effect to focus this light by restricting the size of the opening. From here it would be a small step to enclose the water-filled depression and cover it with clear tissue. So, although in a modern eye, if any one part fails to function, the organ is useless, in evolutionary terms the intermediate steps did provide an advantage."

Image: JJ Harrison, Wikimedia / CC BY SA 3.0

Figure 2. The main and secondary eyes of a jumping spider. There is no support for the idea of gradual changes or 'accidents' leading to the evolution of even simpler eyes.

Armin Moczek, a biologist at Indiana University, explains the issue with this narrative:

> "The problem, according to a growing number of scientists, is that it is absurdly crude and misleading. … For one thing, it starts midway through the story, taking for granted the existence of light-sensitive cells, lenses and irises, without explaining where they came from in the first place. Nor does it adequately explain how such delicate and easily disrupted components meshed together to form a single organ. And it isn't just eyes that the traditional theory struggles with. The first eye, the first wing, the first placenta. How they emerge. Explaining these is the foundational motivation of evolutionary biology … . And yet, we still do not have a good answer. This classic idea of gradual change, one happy accident at a time, has so far fallen flat."[11]

Villmoare's primary argument against creationists was that we have a framework or 'lens' that guides how we interpret data, but as shown earlier, the secular community also has a bias. Only naturalistic explanations are allowed, regardless of the evidence.

Chapter 13: Evolution of human behaviour

This chapter is an exercise in evolutionary storytelling and takes evolution as a given when constructing the narrative. The author assumes an evolutionary relationship with animals and then tries to explain humans based on this. Of course, the explanatory power of this is so far-reaching that it is effectively meaningless. In addition, it ignores the obvious alternative: there are similarities between human behaviour and animal behaviour because we share a common designer. And the more similar we are to other members of God's creation, the more we should expect their behaviour to mirror ours. He claims that similar behaviours, between other mammals and humans, fit evolutionary predictions. Now we ask, what does evolution predict?

Leading chemist Dr Philip Skell expresses a similar view:

> "I found that Darwin's theory had provided no discernible guidance, but was brought in, after the breakthroughs, as an interesting narrative gloss … . Darwinian explanations for such things are often too supple: Natural selection makes humans self-centered and aggressive—except when it makes them altruistic and peaceable. Or natural selection produces virile men who eagerly spread their seed—except when it prefers men who are faithful protectors and providers. When an explanation is so supple that it can explain any behavior, it is difficult to test it experimentally, much less use it as a catalyst for scientific discovery. Darwinian evolution … does not provide a fruitful heuristic in experimental biology."[12]

Our answer is that evolution predicts nothing; it simply incorporates anything into the narrative.

Chapter 6: Genetics

At the start, he claims that the genetic code is one of the most potent sources of evidence for universal common ancestry. His first argument is that since the DNA code is universally present in living things, this shows common ancestry, but the claim is also false. It has been known for decades that there are lifeforms that do not use the same code. There are at least 33 different genetic codes discovered among living things.

> "Dobzhansky believed that the common ancestry of all living things could be seen in the universality of the genetic code. … But we now know that the genetic code is not universal. Exceptions have been found among bacteria and other single celled organisms."[13]

The number of exceptions has grown with time and is found among many groups of organisms. The next piece of evidence he puts forward is genetic similarity, which, as before, is just as easily explained by common design.[14] He trots out the disproven claim that the human genome is 98.7% similar to that of chimpanzees.[15] The actual percentage is hard to calculate. Depending on the methods used, it could be lower than 85%, and is probably no higher than 96%.[16]

Closing remarks/summary

The book may be entertaining for the more zealous Darwinists, but it is just evolutionary storytelling. He provides little evidence and few arguments where it counts. The book is narrative first, with outdated evidence and shoddy reasoning. The key portions where the most decisive evidence should be provided contain arguments that were refuted before he published the book.

References

1. Mayr, E., Darwin's influence on modern thought, Lecture 1999; scientificamerican.com, 24 Nov 2009.
2. Coyne, J., The fairy tales of evolutionary psychology, *The New Republic*, 4 Mar 2000.
3. Dickerson, R.E., Random walking, *J. Molecular Evolution* **34**:277–279, 1992; Dickerson, R.E., The game of science: reflections after arguing with some rather overwrought people, *Perspectives on Science and the Christian Faith* **44**:137–138, 1992.
4. Todd, S.C., A view from Kansas on that evolution debate, *Nature* **401**(6752):423, 1999.
5. Gee, H., *In Search of Deep Time: Beyond the fossil record to a new history of life*, The Free Press, New York, pp. 2, 5, 8–9, 1999.
6. Wilkins, A.S., Evolutionary processes: a special issue, *BioEssays* **22**:1051–1052, 2000.
7. Dizikes, P., Missing links, *Boston Globe*, 23 Oct 2005.
8. Sarfati, J., The Miller–Urey experiment revisited, creation.com, 15 Mar 2015.
9. Press release: The 1989 Nobel Prize in Chemistry, nobelprize.org, 12 Oct 1989.
10. Press release: The Nobel Prize in Chemistry 2015, nobelprize.org, 7 Oct 2015.
11. Buranyi, S., Do we need a new theory of evolution? theguardian.com, 28 Jun 2022.
12. Skell, P., Why do we invoke Darwin? Evolutionary theory contributes little to experimental biology, *The Scientist* **19**(16):10, 29 Aug 2005.
13. Elzanowski, A. and Ostell, J., *The genetic codes*, NCBI, ncbi.nlm.nih.gov, 7 Jan 2019.
14. Press Release, PBS charged with false claim on universal genetic code, arn.org, 10 Sept 2001,
15. Cohen, J., Relative differences: the myth of 1%, *Science* **316**(5833):1836, 29 Jun 2007.
16. Luskin, C., Human-chimp similarity: what does it mean?, evolutionnews.org, 20 Oct 2021.

Every life worthy of life

Christianity and the New Eugenics
Calum MacKellar
Inter-Varsity Press, London, UK, 2020

Lucien Tuinstra

Evangelical Christian Dr Calum MacKellar is Director of Research at the Scottish Council on Human Bioethics and the author of *Christianity and the New Eugenics*.[1] Among other things, he is a Fellow with The Center for Bioethics & Human Dignity, and a Visiting Professor in bioethics at St Mary's University in London.

The book's references at the bottom of each page are helpful, and a glossary is included in-between the further reading section and the indices. Its subtitle, "Should we choose to have only healthy or enhanced children?", implies there is an evaluation, a moral choice, a *preference* at stake (p. 88). This seemingly simple question is answered throughout the book, coming from many different angles. The book consists of five chapters. The following review uses the same structure.

Introduction

'Eugenics' is a combination of two Greek words: *eu* (good) and *genos* (birth). It raises the question, 'good birth according to whom?' A historic slogan for eugenics was elimination of 'life unworthy of life', excluding people judged to be inferior from contributing to the human gene pool ('negative eugenics'). As currently understood, new ('positive') eugenics is "the selection of desired heritable characteristics in order to improve future generations, typically in reference to humans".[2] The resulting 'designer babies' idea is a topic explored in Aldous Huxley's dystopian book *Brave New World*, which is set in the 26th century. We have presently already entered the era of tinkering with our progeny.[3] MacKellar quotes the American scientist Lee Silver regarding the risk of the new eugenics:

> "It is individuals and couples who want to reproduce themselves in their own images" (p. 10).[4]

Is humanity poised to fall into error by not learning from the past?

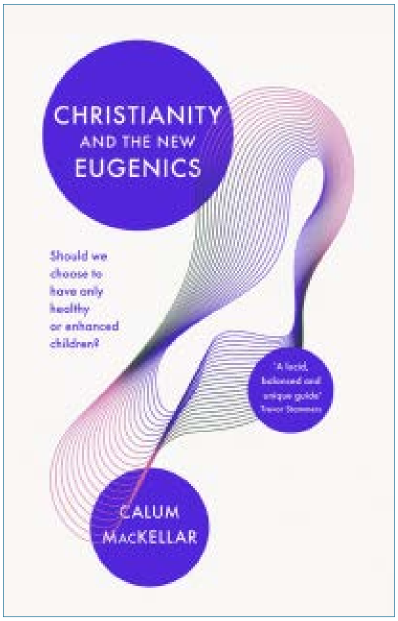
History

Discussing past eugenics, unsurprisingly the author mentions the Nazi regime.[5] However, the Germans were not the frontrunners. "Eugenic ideology seems to have flourished in the USA at the beginning of the twentieth century", according to MacKellar (p. 20). Earlier, it can be traced to Britain, and particularly the late nineteenth-century writings of biologist Francis Galton (figure 1)—a cousin of Charles Darwin—who coined the term 'eugenics'. Its proponents included prominent scientists, some of whom supported it with religious fervour.

Francis Crick (1916–2004), co-discoverer of the helical structure of DNA, was in favour of bribing people who were "poorly endowed genetically" to be sterilized.[6] Sir Julian Huxley, president of the British Eugenics Society from 1959 to 1962, wrote:

> "Once the *full implications of evolutionary biology* are grasped, eugenics will inevitably become part of the future [emphasis added]" (pp. 18–19).[7]

Robert Edwards, 2010 Nobel Prize winner, said:



> "Soon it will be a sin for parents to have a child that carries the heavy burden of genetic disease. We are entering a world where we have to consider the quality of our children" (p. 19).[8]

Edwards developed *in vitro* fertilization (IVF) and linked his work with eugenics. He stated:

> "I wanted to find out exactly who was in charge, whether it was God himself or whether it was scientists in the laboratory." He concluded, "It was us" (pp. 19–20).[9]

MacKellar makes no bones about the fact that there is a worldview connection between abortion and eugenics:

> "… decriminalization of abortion with the UK *Abortion Act 1967* may have been motivated by a willingness to eradicate the disabled and unwanted based on eugenic ideology" (p. 20).

Another Nobel Prize winner, James Watson, recognized this too, but did not have any qualms about 'playing God' through abortion:

> "… we will increasingly have the power, through prenatal diagnosis to spot the good throws and to consider discarding through abortion the bad ones" (p. 4).[10]

Abortion is sometimes 'justified' by people who supposedly should

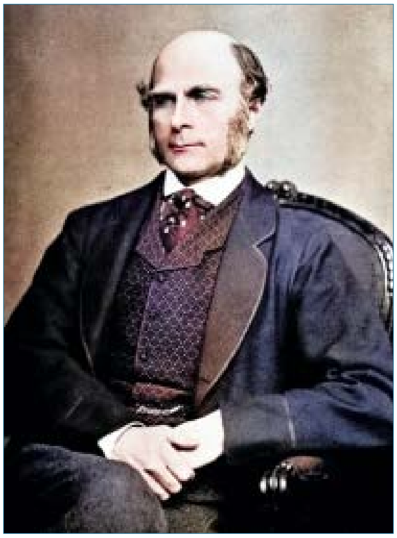


Figure 1. Francis Galton

know better. Ordained as an Episcopal Christian priest, Joseph Fletcher, founder of 'situational ethics', who later in life identified as atheist, was an American bioethicist. He argued, in 1968:

> "People … have no reason to feel guilty about putting a Down's syndrome baby away, whether it's 'put away' in the sense of hidden in a sanitarium or in a more responsible lethal sense. It is sad; yes. Dreadful. But it carries no guilt. True guilt arises only from an offense against a person, and a Down's is not a person" (p. 196).[11]

MacKellar warns his readers not to be misled now that eugenics is resurfacing under the euphemism 'therapeutic genetic selection' (p. 185). Therapy is used to treat a person with some disorder; eugenic selection is to either prevent (genetically) or destroy (by means of abortion) a person with a disorder.

The Christian perspective

Calum MacKellar devotes half of the book to a "Christian enquiry into the new eugenics". He takes a positive approach by discussing the image of God, love and unconditional acceptance of children, and equality of all.

Little is said about the materialism so entrenched in the evolutionary worldview. He hints at it when he says that "all human life (including all adult life) can just be reduced to biochemical molecules" and equates this with "a purely scientific perspective" (p. 102). With that, MacKellar probably means naturalistic science, as later he says that "by suggesting a purely naturalistic explanation of humanity there is a danger that it may be reduced to biological science" (p. 193).

The author clearly delineates that the image of God is not related to "functional aspects, … [as] it would mean that every human being would reflect the image of God to a different degree" (p. 43). Only Jesus "perfectly reflects the love coming from the Father" (p. 39) and this reflection has nothing to do with 'ableism', but the fact that Jesus is without sin. Ableism "includes a number of beliefs, processes, presumptions, and practices that project the normal human standard while devaluing those who do not fulfil these [physical, mental, etc.] characteristics" (p. 94). The key point that MacKellar gets across throughout the book is that all "humans do not simply *bear* the image of God: they *are* the image of God [emphases in original]" (p. 44). He explains that no matter how (un) healthy, suffering or flourishing, short- or long-lived, a child is always loved unconditionally by God, so parents should do likewise. Most parents do so once their child is born, but MacKellar focuses on the decisions made prior to birth, and even before conception. He powerfully states:

> "The concept of *conditional parenthood*, whereby individuals decide to be parents only if their child fulfils certain biological criteria, may then represent a significant misunderstanding of what it means to be a loving parent [emphasis in original]" (p. 59).

He argues that, should such a eugenic decision (which can take several forms, see next section) fail to lead to the desired outcome in the child, the parents could be disappointed. Inevitably, the child who becomes aware of this later on will perceive, at best, that he/she is not living up to expectations and, at worst, that he/she should never have been born. These are "existential questions a child should never have to face" (p. 71). The author discusses the child's longing for unconditional love and acceptance, especially in the context of adoption.

Another point that MacKeller emphasizes is the question of what sort of society (or parents) we become if we try to engineer our offspring; either by selecting out disabilities ('negative' eugenics) or selecting in favoured qualities ('positive'). What message do we send to those who live with those same disabilities? For example, does this not communicate that people with Down's syndrome (figure 2) are less worthy of life? Due to prenatal checks in the UK, 90% of babies with Down's are aborted. Other countries are similarly schizophrenic on this issue.[12] On the one hand, they claim to care deeply about the disabled, but on the other hand they are keen to prevent the existence of future people with Down's syndrome. Rather, our societies ought to be like the examples of the following parents because there are lessons here about unconditional love:

> "You know, I bargained with God. I could handle all this for the next year if he just smiled or if he learned how to walk or talk. A year later he hadn't changed at all. And I remember being hit on this birthday thinking I made this deal and he hasn't changed … . And I look back at that point and realized that nothing had changed, *except that I'd learned to love* him for what [sic] he is [emphasis added]" (p. 78).

Emily Rapp writes about her child dying from Tay Sachs disease:[13]

> "I would walk through a tunnel of fire if it would save my son. I would

> take my chances on a stripped battlefield with a sling and a rock à la David and Goliath if it would make a difference. But it won't. I can roar all I want about the unfairness of this ridiculous disease, but the facts remain. What I can do is protect my son from as much pain as possible, and then finally do the hardest thing of all, a thing most parents will thankfully never have to do. *I will love him to the end* of his life, and then I will let him go [emphasis added]" (p. 79).

And a father of two boys with a genetic disorder confided:

> "…when I ask myself would I rather that Jonathan and Christopher had never been born, the answer is: absolutely not. Though it broke my heart twice to share their sufferings, through them *I know a lot more about love and faithfulness, kindness, gentleness, and humility* than I could possibly otherwise have known [emphasis added]" (p. 99).

Obviously, no parent wishes a genetic disorder for their child. MacKellar explains that proponents of eugenics argue that we need to distinguish between the disorder and the person. But if we are trying to eradicate disorders through eugenic deselection, what does that say about how we perceive those alive now with the same disorders? It is one thing to treat somebody with a disorder, but that "is different from saying that persons with the disorder should not exist" (p. 165). Should we applaud "the National Socialists [who] did more to 'prevent' future generations of Tay Sachs sufferers than all the efforts of science to date" (p. 82)?[14] A genetic disorder is always embodied. Some people *born* with a disorder may view their disability as "part of their very identity and who they are as persons" (p. 83). Consider, for example, the difference between somebody born without limbs and someone who lost them later in life due to a terrible accident. MacKellar explains that eugenic ideology shifts the focus from the worthiness of life to the quality of life. Besides the fact that quality is arbitrary, he makes another important point:

Figure 2. Heidi Crowter, a campaigner against the abortion of babies with Down syndrome

Image: dontscreenusout, Wikimedia / CC BY 2.0

> "It is difficult to see how an individual with the same value system can, in any rational and consistent way, agree that (1) it is acceptable to discriminate between possible future persons but that (2) it is unacceptable to discriminate between existing persons" (p. 86).

Dutch ethical expert on disability, Hans Reinders answers "the only reasonable answer to the question of why a disabled child should not be born is by reference to what one thinks about the lives of people actually living with the same disorder" (p. 89).[15]

MacKellar goes on to say that "a society which believes that life is meaningful only if it has a certain quality" may end up questioning "whether the seriousness of the murder of a person would be dependent on that person's worth as an expression of his or her quality of life" (p. 87). Isn't that often the question regarding abortion and euthanasia? To by-pass this, an oft-used argument by proponents of abortion is that the fetus is not a person and therefore not an object meriting our compassion. British Protestant theologian Oliver O'Donovan confronts this pro-abortion argument with a clincher:

> "It is a strange conclusion indeed, that one may render a service of kindness to a Nobody which it would be immoral to render to a Somebody" (p. 92).[16]

A service of kindness (the subject) is, of course, that which is rendered to another *person* (the object). However, abortion destroys the person, which is immoral indeed. This is why abortion proponents declare the fetus a non-person because 'it' literally is destroyed.

Another discrepancy described by MacKellar is that many people are—rightfully—against abortion if it is because of the baby's sex (i.e., for non-medical reasons), but they advocate it if done because of a disability. Do these people not see their inconsistency when they rail against the abortion of female babies—confirming the personhood of the baby-girl—but they promote abortion when it comes to a baby with a disability? Surely, neither sex nor disability of the baby justifies abortion.

MacKellar makes it clear that the extent to which we decide how far to take eugenics is very subjective and dependent on one's worldview.

Eugenics procedures

The Nazis perpetrated 'negative' eugenics—a horrific crime against humanity that most people are familiar with. Less well-known, but also non-voluntary, was the selection of reproductive partners for SS personnel. A doctor assessed whether the fiancée of the SS member was (deemed) suitable to further the (pro-)creation of the 'master race'. Perhaps surprisingly, immediately following the paragraph describing procedures instigated by Heinrich Himmler, MacKeller relays that Jews practice what he considers to be a sort of voluntary eugenics. That is, two individuals carrying the same mutation, which might result in a child with a disorder, are advised against marriage (p. 126).

Another way that eugenics might be manifested is through selective adoption (p. 129). If people are ok with genetic screening and abortion, would they accept that children with certain disorders are basically not adoptable? Presumably adoption agencies require unconditional acceptance.

MacKellar points out that selection at fertility clinics is common. Sex cells (i.e., eggs and sperm) contributed in lieu of those of the infertile partner, are selected to resemble his/her ethnic background, to avoid social stigma for the child later in life (p. 134). Sometimes such background choices might even include (non-genetic) religious choices!

In contrast to selection from existing sex cells and embryos, a more recent development is the active modification of germlines with CRISPR-Cas9. This has already been condemned by UNESCO as 'contrary to human dignity' as it truly gets into the realm of 'designer babies' (p. 163).[17]

Concluding remarks

MacKellar summarizes that when it comes to eugenic decisions it is critical to assess what moral framework the (potential) parents have. He argues that self-interested aims will likely not produce the kind of parents who will unconditionally love their child (pp. 179, 182): "where choice exists, there is always the possibility of later regretting the choice made!"

The US Protestant ethicist Scott Rae said:

> "In many cases in which abortion is contemplated, the parent may confuse the burden of life for the child with the burden of the parents caring for the child" (p. 190).[18]

MacKellar also quotes Christian bioethicist Agenta Sutton:

> "Any form of eugenics involves discrimination based on the view that some individuals are either unwelcome or less welcome than others. Eugenics, in whatever form it takes, means usurping powers of the lives—and deaths—over others, while failing to recognize our creaturely limitations and the fact that true perfection is not of this world" (p. 196).[19]

Christianity and the New Eugenics is a deep philosophical probe, not least about how we value the life of our neighbour and that of (future) children. Its author ably pinpoints the horns of the dilemma upon which society finds itself: all people are equal, but some people are more equal than others.[20]

References

1. MacKellar, C., *Christianity and the new eugenics*, Inter-Varsity Press, London, 2020.
2. Eugenics, *Encyclopædia Brittanica*, 2023.
3. Grigg, R., Eugenics is back, *Creation* **39**(3):36–38, Jul 2017; creation.com/eugenics-is-back.
4. Silver, L.M., *Remaking Eden*, Phoenix, London, p. 27, 1999.
5. Bergman, J., *Darwinian Eugenics and the Holocaust*, Involgo Press, UK, 2020; reviewed by Woodmorappe, J., The deep and undeniable Darwinian roots of Nazi eugenics, *J. Creation* **35**(1):29–31, 2021.
6. Crick, F., Letter to Dr B. Davis, 22 Apr 1970.
7. Huxley, J.S., Eugenics and society, *Eugenics Review* **28**(1):11–31, 1936.
8. Quintavalle, J., Better by accident than design, quoted in Institute of Ideas, *Designer babies: where should we draw the line?* Hodder & Stoughton, London, p. 73, 2002.
9. Obasogie, O.K., The eugenics legacy of the nobelist who fathered IVF, *Scientific American*, 4 Oct 2013.
10. Watson, J., Values from Chicago upbringing; quoted in: Chambers, D.A., *DNA: The double helix perspective and prospective at forty years*, New York Academy of Science, NY, pp. 194–197, 1995.
11. Bard, B. and Fletcher, J., The right to die, *The Atlantic Monthly* **221**(4):59–64, 1968; reprinted on riverbendds.org/fletcher.html, accessed 27 Nov 2023.
12. Robinson, P., An inconsistent society—An upside down view of Down's syndrome abortion, creation.com/down-syndrome-abortion, 17 Nov 2016.
13. Tay-Sachs is a lethal genetic disease found most commonly among Jews (specifically Ashkenazi Jews).
14. Lewontin, R.C., Science & 'The demon-haunted world': an exchange, *New York Review of Books*, 6 Mar 1997; nybooks.com, accessed 28 Nov 2023.
15. Reinders, H.S., *The Future of the Disabled in Liberal Society: An ethical analysis*, University of Notre Dame Press, Notre Dame, IN, pp. 8–9, 2000.
16. O'Donovan, O., *The Christian and the Unborn Child*, Grove Books, Bramcote, UK, p. 19, 1980.
17. United Nations Educational, Scientific, and Cultural Organization, *The universal declaration on the human genome and human rights*, 11 Nov 1997.
18. Rae, S.B., *Brave New Families: Biblical ethics and reproductive technologies*, Baker Book House, Grand Rapids, MI, p. 200, 1996.
19. Sutton, A., A case against germ-line gene therapy, *Ethics & Medicine* **29**(1):17–22, 2013.
20. As in the Orwellian phrase, "All animals are equal, but some animals are more equal than others", from *Animal Farm*, first published in 1945.

Fine-tuned light

Children of Light: The astonishing properties of sunlight that make us possible
Michael Denton
Discovery Institute Press, Seattle, WA, 2018

Shaun Doyle

Children of Light is the third book in the Privileged Species series by Michael Denton, a Senior Fellow at the Discovery Institute's Center for Science and Culture.[1] He has an M.D. from Bristol University in the UK and a Ph.D. in biochemistry from King's College in London, and has commented extensively (and critically) on evolution.[2]

'The Privileged Species Series' focuses on the empirical fact of *fine-tuning*. There are many factors about our situation that have a 'Goldilocks' property—i.e., if they were even slightly different in any way from what they are, life as we know it would not be possible. In *Children of Light*, Denton focuses on the many facets and functions of visible light that are 'just right' for human life.

Put simply, the book is a *tour de force* on the fine-tuning of light for human-like life. I will simply give the reader a taste of what Denton covers throughout his chapters. I cannot cover all the elements he mentions. But these few details I think show why this is a topic that deserves our full attention. (All quotes, unless otherwise marked, are from *Children of Light*.)

The miracle of sunlight

Many of our ancestors worshipped the sun. Denton agrees with Carl Sagan, who said that "they were far from foolish". They built many monuments to line up with the movement of the sun. This included Stonehenge, the Sphinx, some structures at Angkor Wat, and even whole cities such as Teotihuacan.

Today, we don't worship or build monuments to the sun. Nonetheless, we're still often struck by a sunrise or sunset. And the eerie twilight of a solar eclipse still amazes us. But, compared to so many of the ancients, we don't give the sun much thought. Denton avers that familiarity strips us of our awe. I also suspect a little bit of scientific knowledge does too. We know the sun is 'just' a big ball of plasma like any other star. So, while we know that without it we couldn't live, the sun itself rarely gets much special attention.

However, this underestimates just how special our 'light' circumstances are. As Denton explains:

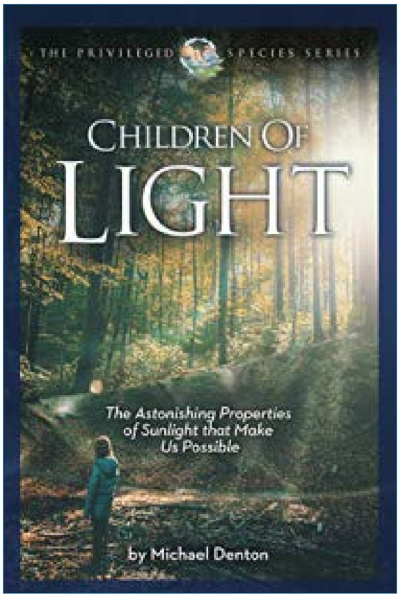
> "Less widely known, however, is the existence of an extraordinary suite of coincidences in the nature of things which render the Earth's surface a supremely fit habitat for advanced carbon-based life forms like ourselves—coincidences that are, on any consideration, ludicrously improbable."

He mentions that the sun has just the right properties for photosynthesis and high-acuity vision. And Denton explains the significance:

> "… these are elements of natural fitness *exclusively for our type of life—for beings possessing the gift of sight, breathing oxygen (aerobic), and inhabiting the terrestrial surface of a planet like the Earth* [emphasis original]."

The light of life

Most stars, including our sun, emit most of their radiation as light and heat. But this very fact is an amazing element of fitness. Electromagnetic



radiation (EMR) of different frequencies interacts with matter in different ways. And the range of EMR frequencies is incredibly large—on the order of 10^{25}. However, visible light makes up an incredibly small portion of that frequency spectrum, falling in a range of about 400–800 nm. This also happens to be roughly the EMR frequency range that enables photochemistry. It is energetic enough to enable most chemical reactions, as well as excite valence electrons to higher orbital levels, as is required for photosynthesis. Higher frequency EMR, such as UV, X-rays, and gamma rays, strip electrons from atoms completely and denature biological molecules. On the other hand, lower frequency EMR, such as far infra-red, microwave, and radio waves, does not have a high enough energy to excite electrons to higher orbital levels; they only vibrate or rotate atoms. Denton notes an important thing to realize:

> "… it is not that life adapted to the right light but *that the right light is the only light that provides the correct energy levels for photochemistry* [emphasis original]."

However, heat is also a significant element of fitness. It warms things well beyond what they would otherwise be without heat radiation. But not

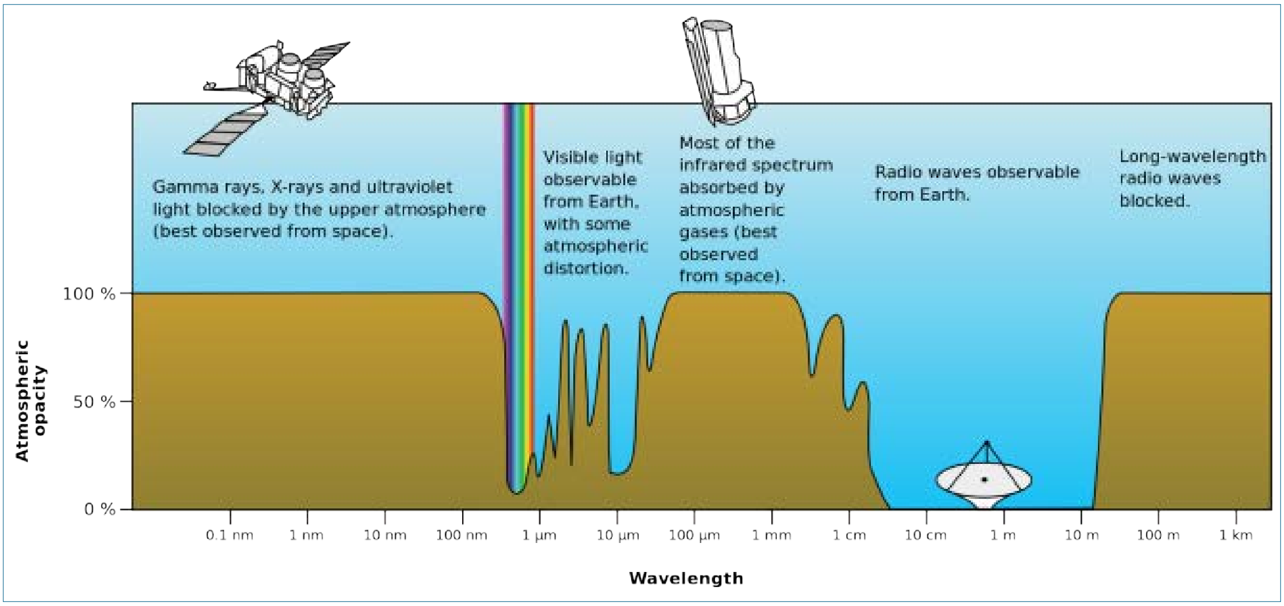


Image: NASA, Wikimedia / Public Domain

Figure 1. Absorbance spectrum of EM radiation by Earth's atmosphere. (It is also Denton's figure 3.2)

too much! If atoms are moving too fast, chemical reactions in organic compounds become too energetic and common to sustain a stable organism. And the most efficient way to supply that heat is precisely the way the sun provides it: in the near-infrared spectrum:

> "The essential heat that prevents the Earth's hydrosphere from freezing solid and that animates matter for chemical reactions is provided by electromagnetic energy in another region of the EM spectrum—the IR region, or more specifically the near infrared. This region lies adjacent to the visual band, between it and the far infrared and microwave regions, or between about 0.8 microns and 14 microns. This is the only region of the EM spectrum which can provide safe heat to warm the Earth, preventing it from freezing, providing sufficient kinetic energy to move molecules and promote chemical reactions but not enough to cause uncontrolled chemistry."

Together, the visual and near-infrared bands of the EM spectrum are extremely small in comparison to the range of possible EM frequencies. Denton's conclusion is apt:

> "That the Sun should emit radiation in the only infinitely small region of the EM of utility to life is a truly extraordinary coincidence!"

Letting the light in

Light in the right EM frequency range is *necessary* for life like us to thrive, but it's not *sufficient*. We also need the *right sort of atmosphere* to let in the right light in the right amounts. As Denton points out:

> "The life-giving light of the Sun must penetrate the atmosphere right down to the ground to work its magic, and a proportion of the Sun's IR radiation (heat radiation) must be absorbed by and held in the atmosphere to warm the Earth above the freezing point of water and animate the atoms of life for chemistry."

And our atmosphere is amply fit for such a task. Notice the ranges over which the atmosphere lets through the most EM radiation (figure 1). It blocks completely any wavelengths shorter than about c. 200 nm (middle of the UV range); is highly (though not completely) transparent to visible light; is 'patchy' in its transparency to infrared light from 0.8–15 µm wavelength, but it blocks infrared wavelengths 15–1,000 µm. It is impervious to all wavelengths longer than this besides long-wave microwave and short-wave radio waves (c. 4 cm–15 m), to which the atmosphere is completely transparent.

If we shift the absorbance spectrum in figure 1 (i.e., if we imagine the absorbance by the atmosphere had covered a slightly different region of the EM spectrum), light eaters would be impossible. Shifting it to the left even a little would expose the surface to much more UV radiation, potentially absorb visible light, and absorb a lot more short-wave infrared radiation. The UV would destroy biological tissues and the increased short-wave IR absorption would heat the atmosphere too much, producing a runaway greenhouse effect and making biochemistry impossible. Shifting it slightly to the 'right' would also result in a lot more visible and near-IR light being absorbed, creating a runaway greenhouse effect that would make biochemistry untenable.

Moreover, *water* displays a similar element of fitness in the atmosphere. Of all wavelengths, it is *most* transparent to *visible light* (figure 2), not

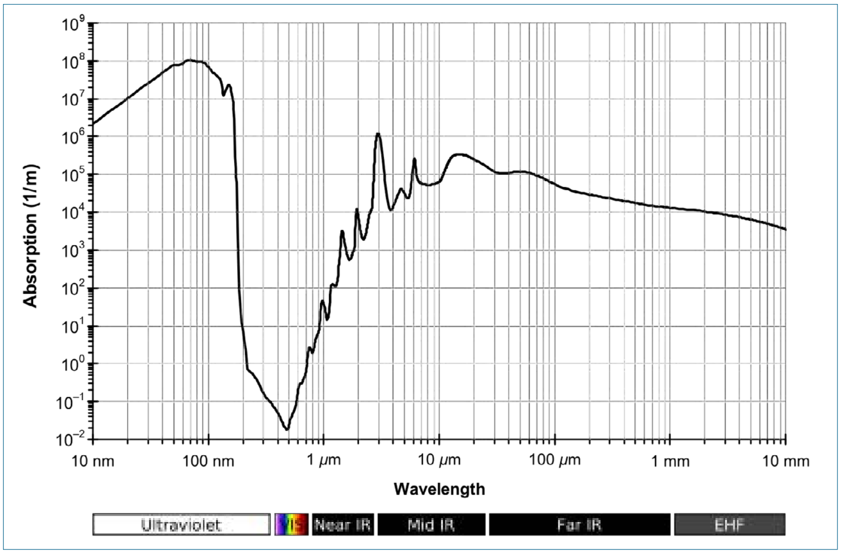


Figure 2. Absorption spectrum of liquid water across a wide wavelength range

Image: Kebes, Wikimedia / CC BY SA 3.0

just as a liquid but also as ice[3] and vapour (figure 3). This means that photosynthesis is possible in the air, in the water, and even under a frozen lake!

In the IR range, however, things are dramatically different from the visible range. There are strong absorption bands in the IR region, with the vast majority of the region completely absorbed by the atmosphere. Denton notes this absorption raises the temperature at the surface about 33°C above what it would otherwise be. Since the average global surface temperature is about 15°C, and absent the atmosphere it would be about –18°C, Earth's atmosphere is the difference between H_2O normally being water rather than ice on the surface! However, it also insulates Earth's surface from extreme daily temperature changes. It protects us both from the heat of the sun in the day and the cold of its absence at night, evening out the temperatures considerably. It's important to note, though, that the parts of the spectrum that let IR radiation *through* are just as important as those that absorb it. This allows much of the Earth's own radiation to escape into space, which helps modulate the temperature.

And to top it all off, the dips in the absorption spectra in the IR region are due to the particular gases in the atmosphere that are essential for the existence of aerobic life for reasons *independent of* their absorbance characteristics. Denton explains:

> "The fact that the combined absorbance characteristics of these five gases provide just the right absorbance characteristics necessary for advanced aerobic life on the earth's surface, letting through the right light for photosynthesis and absorbing sufficient heat to raise the earth's temperature to within the ambient range, is an extraordinary fact—one of the most astonishing elements of fitness for life in all nature. Why? Because the five atmospheric gases N_2, O_2, O_3, H_2O, and CO_2, four of which—N_2, O_2, H_2O, and CO_2—form the bulk of the atmosphere, must exist on any planet hosting complex carbon-based biological life. That their absorbance characteristics should be of such vital benefit for life is therefore a coincidence of stunning fortuity."

The gift of the leaf

One cannot talk about the importance of light for life without talking about photosynthesis. It is practically the sole source of oxygen production for the atmosphere (and long-agers believe photosynthesis was the *origin* of a significantly oxygenated atmosphere).

But Denton focuses his attention on the leaf and its importance for complex terrestrial life like us. As he mentions:

> "By providing reduced carbon fuels for land-based life, the gift of the leaf had the enormous consequence of enabling aerobic life forms not only to leave the water, but to become air-breathing—taking up oxygen directly from the atmosphere."

Indeed, air-breathing is an important precondition for complex life. Denton explains:

> "Only by taking in oxygen directly from an atmosphere enriched in oxygen (as is our current atmosphere on Earth) can we obtain the necessary 250 milliliters of oxygen we need every minute even at rest.
>
> "And there is little doubt that this requirement (being air-breathing) will also apply to all advanced, complex carbon-based aerobes throughout the universe. … It is far more difficult to obtain oxygen from water than from air, and this puts a ceiling on the metabolic rate aerobic water-breathing organisms can attain and on the consequent complexity (in the broadest sense) that aquatic organisms may achieve compared with air-breathing organisms."

High oxygen levels in the air is a precondition for complex life. Moreover, photosynthesis is a precondition for the maintenance of high levels of oxygen in the atmosphere, and photosynthetic *plants* are the food necessary for terrestrial aerobes to survive and thrive. Therefore, photosynthesis and plants are necessary for complex terrestrial life like us.

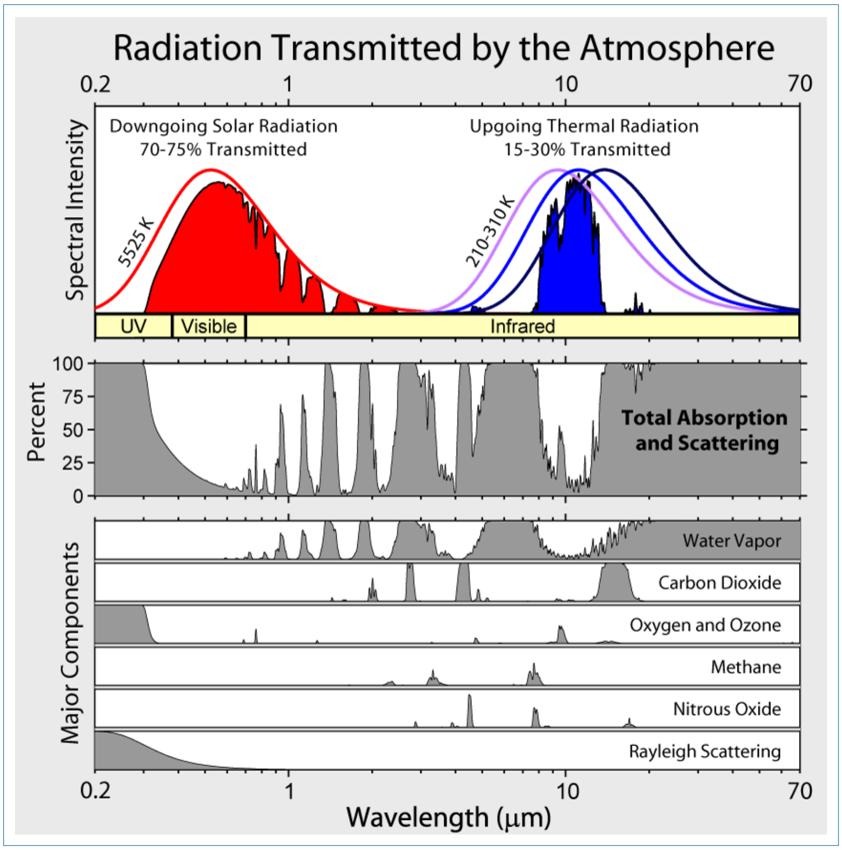


Image: Global Warming Art, Wikimedia / CC BY SA 3.0

Figure 3. The absorption spectrum of Earth's atmosphere (middle panel) (absent cloud cover), and the effect that this has on both solar radiation and upgoing thermal radiation (top panel). Individual absorption spectra for major greenhouse gases plus Rayleigh scattering are shown in the lower panel. Note the absence of absorption by water vapour in the visible range.

Denton then proceeds to briefly explain the amazing phenomenon of photosynthesis. He offers a helpful summary:

> "In essence, the process involves the use of light energy to draw electrons and protons (H^+) from water (H_2O), oxidizing the water to oxygen (O_2) which is released into the atmosphere, and reducing carbon dioxide to sugars and various reduced carbon compounds (CH). The overall reaction can be written thus:
>
> $$CO_2 + H_2O \Rightarrow CH + O_2$$".

He notes that it is an incredibly complex and specific process and cannot fully describe it in a short book like this. However, it relies on many specific preconditions to be possible. Some have already been mentioned, such as the particular radiation properties of the sun and the absorbance properties of the atmosphere. But it is crucially dependent on *liquid water* as well—not just its optical properties, but many others Denton explored in the second book of this series *The Wonder of Water*.[4] Water alone exists in all three phases at ambient temperatures, and has appropriate viscosity to produce and maintain soil, the matrix in which most terrestrial plants grow. The surface tension and viscosity properties of water also make plant transpiration possible, which is a much more efficient means of transporting water from the soil to the atmosphere than mere soil evaporation.

The complex web of interlocking preconditions needed for photosynthesis and the physical structure of plants, which, in turn, provide the preconditions for complex aerobic life, are so fortuitously aligned that it looks rigged.

Fitness for vision

Sight is so crucial to understanding the world around us that 'to see' is often synonymous with 'to understand'. Specifically, *high-acuity* vision of the camera eye (made up of a lens, retina, and tubes filled with photon-detecting molecules) allows us to see to a far horizon, to focus on fine details up close, or to observe stars light-years away from us, and everything in between. While there are some other cool ways of sensing the world around us in the animal kingdom (e.g., echolocation), they would be useless for mastering fire or cataloguing the movements of the heavens, which formed the prelude for science.

But vision shares a commonality with photosynthesis, as Denton explains:

> "All biological light-detecting devices depend on the fundamental fact that the energy levels of EM radiation in the visual region are just right for photochemistry."

However, there are other properties of visible light that make it uniquely fit for high-acuity vision. Our eyes are marvellous seeing devices, capable of handling trillion-fold changes in luminescence (i.e., the difference between a fresh snowfield on a clear day and on a moonless night). However, they have limits. For instance, they are *diffraction* limited. When light is focused through a small opening, it interacts with the edges of the opening and creates an interference pattern on the opposite side of the opening, called an 'Airy disc' (figure 4). As Denton explains:

> "The formation of the disc, whether in the eye or a telescope, reduces the resolving power of the optical device, because, when two point

> sources in the visual field are close together, their Airy discs may overlap and the two sources cannot be resolved."

What's crucial about this is that the Airy disc diameter provides a physical limit to the image-resolving capacity of a camera, and it is dependent on several parameters, such as the aperture diameter, the focal length (the distance between the aperture and the retina), and *the wavelength of the light*. Denton points out that it roughly corresponds to this formula:

> Airy disc diameter (in microns) = 2.44.λ.F/A (Where λ is wave length, F is focal length and A is aperture).

From this, we can calculate that the maximum resolving power of the human eye corresponds to an Airy disc diameter around 2.5 µm. This corresponds well to the diameter of many photoreceptors, which ranges from c. 1.5–6 µm.[5] And few animals on Earth have better resolving power than humans—raptors (birds of prey) and the like are among the few.

But if our eyes responded to shorter wavelengths, could we have higher-acuity vision? No. First, shorter wavelengths (into the UV range and beyond) excite electrons too much for photon-detecting molecules to function properly. Second, to increase the resolving power, we'd need to keep the same number of photosensitive chemicals per cell while reducing the size of the cells. But that's physically impossible because we can't reduce the size of the photo-sensitive molecules. This would seriously reduce, for example, the span of luminescence over which our eyes could function. Plus, it's simply not possible, given the size of atoms, to make all the complex biochemical processes occur in a vessel much smaller than photoreceptors actually are.

But maybe we could achieve better acuity with longer wavelengths? No. Greater wavelengths mean greater Airy diameters, and thus decreased resolving power. Plus, to function as our eyes do, eyes would have to be orders of magnitude larger than they are. That creates clear biomechanical problems according to the square cube law, where an object's surface area increases by n^2 as its volume increases by n^3. As Denton summarizes:

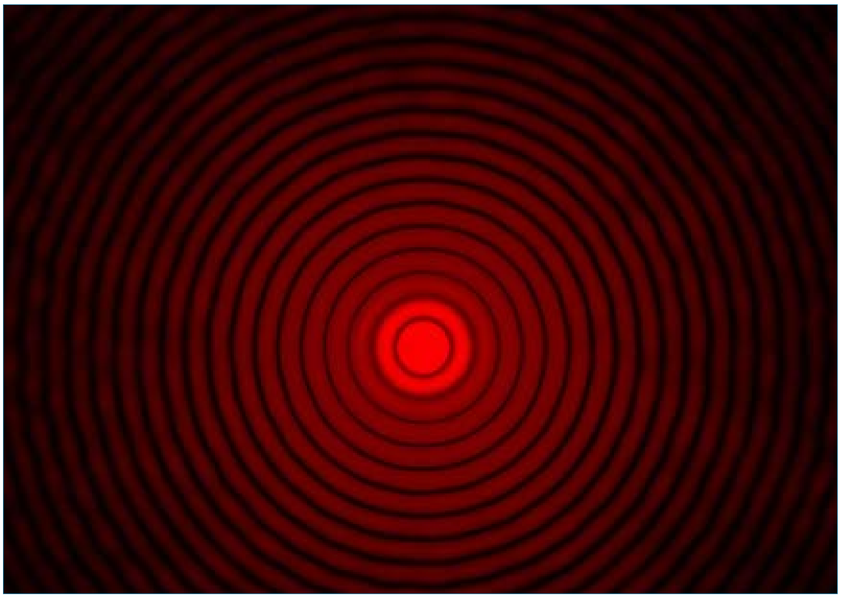


Image: Bautsch, Wikimedia / CC0 1.0

Figure 4. Airy disc effect created by passing a red laser beam through a 90-µm pinhole aperture with 27 orders of diffraction

> "In short, given the basic constraints of biology, the wavelength of light is almost exactly what it needs to be for high-acuity vision in organisms of our approximate size and biological design, inhabiting a planet of the right size and gravity to maintain an oxygen-rich atmosphere capable of sustaining advanced carbon-based life."

The anthropocentric thesis

Science fiction loves to imagine the possibility of life of all sorts of shapes, sizes, and biochemistries being possible. However, Denton points out a key underlying assumption of such ideas:

> "Such scenarios are, of course, pure science fiction, but the underlying notion that the cosmos is fit for a vast zoo of alien life-forms of wildly differing biologies and biochemistries as well as intelligent mechanical forms, is not science fiction but a world view that suggests *that there is no special fitness in nature for intelligent, conscious agents like ourselves* [emphasis in original]."

This sort of materialistic anti-teleology is the key assumption of our culture. However, the more we look into the amazingly improbable confluence of conditions necessary for the existence of advanced 'light eaters' capable of technology, the more absurd this thesis becomes. As Denton says:

> "No matter how unfashionable the notion may be in many intellectual circles, the evidence is unequivocal: Ours is a cosmos in which the laws of nature appear to be specially fine-tuned for our type of life—for advanced, carbon-based 'light eaters' who possess the technologically enabling miracle of sight!"

What about dark life?

It may be that more than half of the biomass on Earth actually doesn't need light to run. Denton mentions the life-forms deep underground and at the bottom of the oceans that live exclusively apart from the light. They don't even need to interact with any 'light eaters' to survive! However, a curious fact about these organisms is that *they are almost all unicellular*. Denton explains:

> "We now know there can be a cosmos replete with carbon-based life; yet, without the additional elements of fine tuning for us energy-hungry aerobes, it would be devoid of complex, advanced, carbon-based organisms remotely comparable with ourselves."

Assessment

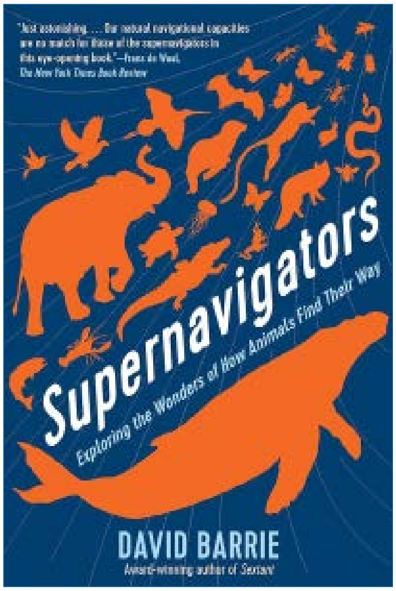
As with the previous books in the Privileged Species series, Denton stops short of affirming a personal designer, and often relies on a long-age framework to make his case. However, the long-age emphasis in *Children of Light* is somewhat muted relative to *Fire Maker* and *The Wonder of Water*. Meanwhile, the key strength of those books shines through this one too: Denton has assembled an amazing array of scientific facts to support his foundational conclusion that our conditions are fine tuned for advanced life like us. I have only briefly surveyed a few that Denton speaks of. And these alone would make Denton's case. However, the book mentions so many more. That alone makes the book worth the read.

References

1. See my reviews of the previous two in Doyle, S., Fine-tuned fire, *J. Creation* **37**(2):22–25, 2023; and Doyle, S., Fine-tuned water, *J. Creation* **37**(3):29–32, 2023.
2. See, for example, Denton, M., *Evolution: A theory in crisis*, Adler & Adler, MD, 1985; Denton, M., *Nature's Destiny: How the laws of biology reveal purpose in the universe*, Free Press, New York, 1998; Denton, M., *Evolution: Still a theory in crisis*, Discovery Institute Press, Seattle, WA, 2016.
3. Warren, S.G. and Brandt, R.E., Optical constants of ice from the ultraviolet to the microwave: a revised compilation, *J. Geophys. Res.* **113**:D14220, 2008 | doi:10.1029/2007JD009744.
4. Denton, M., *The Wonder of Water*, Discovery Institute Press, Seattle, WA, 2016.
5. Kolb, H., Photoreceptors; in: Kolb, H., Fernandez, E. and Nelson, R. (Eds.), *Webvision: The organization of the retina and visual system*; webvision.med.utah.edu, Jul 2013.

Supernaturally designed navigators

Supernavigators: Exploring the wonder of how animals find their way (originally published in Great Britain as ***Incredible Journeys***)
David Barrie
The Experiment, New York, 2019



Arthur Manning

I believe that one of the most compelling pieces of evidence of the intelligent design of animals is the ability of many of them to perform amazing feats of navigation. If you think there are only a few examples of such behaviour among living animals, this book will completely extinguish such a notion.

Barrie, a navigator himself, spent four years travelling around the world, witnessing research scientists in their efforts to decipher the mysterious navigational abilities of numerous different kinds of animals. He also consulted the biological literature (I counted more than 350 sources in his endnotes), and interviewed dozens of researchers involved in investigating these phenomena. So, if you are looking for a great overview of animal migration, this book is the place to start.

Huge variety of navigation systems

It contains a wealth of information that any biology teacher, like me, can include in lectures when covering the various groups of animals. Each day's lesson can be a time of wonder by including one of the mysteries or discoveries discussed herein.

I counted about 62 different kinds of organisms, the amazing abilities of which were described within these pages. They span the gamut from bacteria to protozoans to slime moulds to round worms to cnidarians (jellyfish, corals, etc.) to mollusks to insects to crustaceans to fish to amphibians to reptiles to birds (Barrie claims that about half of all bird species migrate, p. 77) to mammals to humans. There is also a representative of a group not mentioned, arachnids. The spider, *Leucorchestris arenicola*, wanders in the night looking for a female and then returns to his burrow by a direct route in the dark, a round trip of 800 metres.[1]

Some kinds of organisms are only briefly mentioned while a good number of others are dealt with more thoroughly. In addition, each chapter ends with an example of animal navigation, which he includes to "help to entertain the reader, while also revealing how many mysteries remain to be solved" (p. xii). The book is written for the general reader, without a lot of technical jargon and details. *Supernavigators* includes a bibliography and an index. Finally, it ends with an interesting interview with the author.

Here is a brief sampling of some 'supernavigators':

- The bar-tailed godwit, a land bird that cannot soar or swim, flies non-stop from Alaska to New Zealand (p. 53).
- The young of the European cuckoo flies unaccompanied from Europe to Africa to join its parents, which have left earlier (p. 78).
- The monarch butterfly is described by Barrie as having an "extraordinarily complex and sophisticated system …" (p. 134).
- The ancient murrelet, a seabird, is the only bird known to migrate east to west across the Pacific Ocean—why it does so is a "mystery, as indeed is its method of navigation" (p. 142).
- The bogong moth uses "both visual and magnetic 'snapshots' …" (p. 154), and also orients with "the help of the Milky Way. Wow!" (p. 304).
- Three-striped poison frogs, when transported 800 metres from their homes:

  > "… were not only able to find their way back, but followed quite direct routes, even though their journeys sometimes lasted several days. Given that the rainforest is such a cluttered environment, full of noises, smells, and obstacles, and offering little access to the sky, it is very hard to understand how they do this" (p. 230).

Evolutionary storytelling

Sadly, Barrie gives the credit for these wonders to evolution, so I cannot recommend this book for children. But the great majority of the book is devoted to the navigational behaviours of animals and the experiments that have been conducted to explain them.

Let us consider some of Barrie's statements that relate to the question of origins:

> "But whether you are an arctic tern flying from one end of the earth to the other, or a desert ant dashing back to its nest with a dead fly in its jaws, you must be able to find your way. It is quite simply a matter of life and death" (p. ix).

So, if an animal is not successful in its migration, there will be no next generation to make necessary corrections. How could such a complex behaviour have slowly evolved over many generations? A partially evolved navigational system could be fatal to its owner.

Barrie does not get involved in evolutionary speculations about the origin of animal navigation. He apparently accepts evolution as scientific dogma, and therefore navigational systems must be the result of it, regardless of how counterintuitive that would seem. He recounts the evolution of life from simple to complex, and, since navigation is present to some degree in microscopic life, he concludes that this behaviour appeared quite early in evolution: "the first life forms that emerged on our planet were very small indeed, and they were the pioneers of navigation" (p. 5). Barrie then goes on to describe navigation in some simple lifeforms. It seems he assumes this behaviour evolved, along with the lifeforms that possessed it, from simple to more complex.

However, there is an enormous unbridgeable gap between prokaryotes (bacteria) and simple eukaryotes (like choanoflagellates).[2] There are no known intermediates between these major groups in nature nor in the fossil record. In addition, evolutionists don't believe that sponges (the possessors of choanocyte cells which resemble choanoflagellates) have evolved into any other kind of animal.[3]

When discussing how some animals can navigate by the sun, Barrie commented, "you should never underestimate the power of natural selection, especially in the case of creatures that have been around for hundreds of millions of years" (p. 32). I suppose that, unfortunately, Barrie, being a student of psychology and philosophy, is unaware of the nature and limitations of natural selection.

Darwin believed that variation within a kind had no limits. He should have known better. When farmers chose certain individuals with desirable traits to produce offspring (Darwin called this 'artificial selection'), there was always a limit to the extent of that trait that future matings could not go beyond (for instance, producing cows which have more meat or give more milk). One could mate the longest-necked horses for many generations and eventually produce a horse with a very long neck, but you will never get a horse with a neck like a giraffe. You would need new, 'giraffe' genes that would produce the structures resulting in a giraffe neck, which has distinct features that horse necks do not possess.

Modern evolutionists believe that natural selection acts on new traits produced by mutations which are caused by environmental damage to DNA. However, these traits are often deleterious to the organisms, sometimes (if minor) neutral, and, rarely, beneficial even though the mutated DNA results in the degradation of a trait. Millions of generations of mutations would never result in the kinds of changes that would transform a bacterium into a human. But the accumulation of minor negative mutations over many generations would swamp any beneficial ones, driving the species to extinction. Experiments with numerous generations of bacteria and fruit flies have resulted in lots of deformed bacteria and fruit flies, but no new, improved kinds of either.

Jean-Henri Fabre and insect design

In chapter two Barrie discusses Jean-Henri Fabre, the French scientist whom some consider to be the father of the science of entomology (insect study).

> "I have a soft spot for the French entomologist, Jean-Henri Fabre (1823–1915) … . His major work … became that most unusual publishing phenomenon: a bestseller all about arthropods. Not only did he write some of the most lyrical and entertaining descriptions of insect life in any language, but he was also a pioneer of animal navigation studies. Fabre was far from being a conventional scholar, but his exceptional powers of observation were coupled with the curiosity, patience and ingenuity that are the hallmarks of a true scientist" (pp. 15–16).

High praise, but no mention of the fact that Fabre was a lifelong opponent of evolution.

Experimental investigation

Barrie describes many experiments that have been conducted to elucidate the mechanisms of animal navigation. It seems that there is a variety of strategies utilized among different species, and sometimes within a single species. He describes navigation that apparently is the result of cues obtained by the sense of sight (landmarks); sound (crashing waves on an island); smell (peculiar smells from certain regions due to plant life, etc.); relying on the sun, moon, and stars; and combinations of some of these in a single animal.

> "Although the matter is not yet settled, we now have, for the very first time, strong if not decisive evidence that a bird can solve the longitude problem using geomagnetic and celestial cues in parallel" (p. 177).

Image: AlejandroLinaresGarcia, Wikimedia / CC BY SA 4.0

Figure 1. Newly hatched loggerhead turtles use three different navigational systems.

Loggerhead turtles

In addition, Barrie describes experiments which strongly suggest that hatchling loggerhead turtles (figure 1) use three different cues to successfully navigate in their first few critical moments after hatching. The researcher, Ken Lohmann, explained that when they emerge from the nest, they follow the light from the sky (sense of sight). Then, upon entering the sea, they orient at right angles to the oncoming waves (sense of touch). Then when they get into deeper water, they "switch over to use their magnetic compass …" (p. 200).

Navigation behaviour is sophisticated enough to warrant the conclusion that it is not the result of accumulations of accidental genetic changes. But three different navigational behaviours in one organism is most astounding! Lohmann's interpretation of sea turtle navigation is that

> "… the hatchlings are born with an inbuilt sensitivity to the characteristic signatures of the earth's magnetic field around the gyre [circular ocean current], defined by specific combinations of magnetic intensity and inclination [dip of the earth's magnetic field compared to the surface of the earth]. These signatures act like 'open sea navigational markers' that trigger a hardwired automatic response, which sends the turtles off in a direction that will tend to keep them well within the gyre" (p. 203).

Such a system, if integrated into a robot, would indeed be a remarkable accomplishment for any engineer. Barrie poses the question:

> "How could such a system be established? That is not a question that anyone can answer confidently. Turtles and their kin have been around for a hundred million years or more … . Natural selection has therefore had plenty of time to perform its magic and must have favored the survival of animals carrying genes that enable them to identify key decision points along their migratory route" (p. 204).

Again, natural selection is simply a culling process. It produces nothing new. What is the probability of chance genetic changes producing highly sensitive sensory systems and the neural systems that are integrated with them to detect and respond to environmental changes by making fine adjustments to the appropriate muscular motions and to continually track the resultant changes of direction and to make any compensatory motions? I believe the most reasonable answer is zero. Time is not the hero. There are so many negative mutations that would be made in millions of years that the turtles would have gone extinct long before these systems would have come about by chance. In addition, the fossil record is completely contrary to the evolutionary origin of turtles.[4]

Magnetic navigation

Barrie asserts that "representatives of such widely different animal groups [fish, reptiles, and arthropods] all share an ability to make use of the earth's magnetic field to perform complex feats of navigation …" (p. 209). He continues:

> "Whether the various different forms of magnetic navigation emerged at some very early stage in the evolution of life and proved so valuable that they have been widely conserved, or whether they have been repeatedly 'reinvented,' is as yet unknown" (p. 209).

However, there are major problems with both scenarios. If, such behaviour "emerged at some very early stage in the evolution of life", then the enormous periods of time supposedly needed for natural selection would not have been available. On the other hand, many diverse kinds of organisms independently evolving this behaviour would also be highly unlikely. It would be unlikely to have evolved once by chance, so the probability of it happening numerous times by chance is vanishingly small. The more reasonable explanation is that these 'complex feats of navigation' in diverse groups are the result of intelligent design by a single designer.

Human navigation

Barrie continues his book by discussing the fascinating topic of human navigation. Then he concludes the book by warnings against 'anthropocentrism' and the overuse of technology to the detriment of our brains. In seeking to convince the reader of the validity of his views, he not only gives his reasons, but does so, for the most part, in a measured, respectful manner. I heartily concur with his warning about the overuse of technology, which results in brain atrophy.

However, in his denunciation of 'anthropocentrism', Barrie decries the view of "Our special status … enshrined in the book of Genesis, where it is proclaimed that God 'created man in his own image' and gave him 'dominion over … every living thing that moveth upon the earth'" (p. 252). He then refers to St Augustine's view that we have no moral duty to animals. However, he did not condemn evolutionists for using their theory to justify attempts to eliminate creatures deemed to be 'less fit' so that the 'fittest' can survive, e.g., the attempts to eradicate the Aboriginal people in Australia.

In addition, he failed to mention the views of modern Bible believers on this subject. The current views of Bible scholars might best be called 'theocentric', that is that God should be the centre of all things, not man or the animals or nature in general. Today, biblical scholars would unanimously agree that our dominion should be one of wise and caring stewardship.[5] "God … took the man, and put him into the garden of Eden to dress it and to keep it" (Genesis 2:15). This has also been translated as, "to care for it and to maintain it" (New English Translation). In addition, we see God's concern for the animals in the Mosaic Law. Moses commanded that not only humans but the farm animals were also to have a seventh day of rest (Exodus 23:12). Proverbs 12:10 tells us, "A righteous man regardeth the life of his beast." Finally, we are told in the book of Revelation that God will "destroy them that destroy the earth" (Revelation 11:18).

Barrie judges that "Those who regard Biblical revelation as a more reliable source of information about the world than science have little hope of understanding, let alone solving, the many practical problems that face us." (p. 253). However, he gives no explanation as to why this is supposedly true. The Bible is not antiscience. Unfortunately, some Bible believers have been antiscience, but many of the founders of modern science believed the Bible. This list would include Kepler, Pascal, Boyle, Newton, Linnaeus, Faraday, Dalton, Mendel, Pasteur, Maxwell, Fabre, and George Washington Carver. In addition, Abraham Trembley, who has been called the 'father of experimental zoology', should be of interest to the reader of this book. Trembley's faith was no hindrance to his science. In fact, it may be said that his faith was the basis of his science.[6]

Supernavigators is a highly informative and enjoyable read. Barrie is a talented writer. His passion for the preservation of nature is admirable. But his attack on religion is most likely counterproductive. He would be advised to seek to enlist the religious to his cause, rather than casting them as the enemy. I believe that Mr Barrie would benefit from exposure to the scientific case for creation and against evolution. There are many good resources available.

References

1. Foelix, R., *Biology of Spiders*, Oxford University Press, Oxford, p. 131, 2011.
2. Bergman, J., Research has overturned endosymbiosis: the unbridgeable chasm between prokaryotes and eukaryotes remains*, J. Creation* **35**(1):38–47, 2021.
3. Margulis, L. and Schwartz, K., *Five Kingdoms: An illustrated guide to the phyla of life on earth,* W. H. Freeman and Co., New York, p. 217, 1998.
4. Catchpoole, D., Turtles at loggerheads with evolution, *Creation* **33**(3):28–31, 2011.
5. Wilson, G., Caring past our prejudice, *Answers* **15**(4):23–25, 2020.
6. Manning, A., Abraham Trembley and the hydra, CRSQ **37**(4):222–225, 2001.

Did the post-Flood North American mammals live above their dead Flood relatives?

Mike Oard's most recent publication[1] attempts to answer my 2012 article[2] on fossils and the post-Flood boundary. By replicating my study, his analysis supports my original conclusions that a post-Flood boundary located in upper Cenozoic deposits is untenable. Oard, however, concludes the exact opposite. The stark contrast of the data he presents vs his interpretations, his failure to verify citations, and his numerous biological and paleontological errors raise broader questions.

Oard's data vs interpretation

Space forbids a detailed evaluation of Oard's paper, so I will focus on ramifications of the data presented in tables 2, 3, and 4. These tables document the presence of genera among three mammal families (Bovidae, Felidae, and Gomphotheriidae) in Tertiary vs Pleistocene sediments. These sediments serve as a proxy for the post-Flood boundary, though Oard does not view this boundary as globally, or even regionally, equivalent to the post-Flood boundary.[3] His evaluation results in multiple genera from each family recovered in both his Flood and post-Flood sediments, and this negates Oard's argument for an upper-Cenozoic post-Flood boundary for two reasons.

First, the presence of numerous boundary-crossing genera necessitates that the genus is the taxonomic unit of the kind, not the family, resulting in vastly larger numbers of animals brought aboard the Ark. In Oard's table 3, 12 of 15 felid genera cross his post-Flood boundary (13, actually, as *Leopardus* does as well).[4] Most of these are extant (currently living) genera, which are all connected via a network of hybridization. Of course, hybridization is considered key evidence that organisms belong to the *same* created kind rather than *different* kinds. Arguing for a post-Flood boundary around the Pliocene–Pleistocene division requires us to believe that Noah brought more than a dozen pairs of interfertile cats aboard the Ark (and likely many more). The situation is actually far worse. Arment has demonstrated that hundreds of ruminant kinds, representing *thousands* of individuals, must be brought aboard the Ark, given an upper-Cenozoic post-Flood boundary.[5] Oard's stated affirmation of the family as the kind is admirable but wholly inconsistent with the actual results of his own analysis.[6]

Second, an upper-Cenozoic post-Flood boundary exacerbates the return of organisms to the places where their pre-Flood kin were buried. Continuing with the cats from table 3, Oard's results require that pre-Flood *Leopardus* are buried in South America, and post-Flood *Leopardus* return to South America and North America, but not to Asia, Europe, or Africa.[7] Pre-Flood *Smilodon* are buried in North and South America, and post-Flood *Smilodon* return only to North America. Pre-Flood *Lynx* returns to each of the four continents where its pre-Flood kin are buried, yet nowhere in Oard's data is there a pre-Flood cat from, say, Africa, the post-Flood fossils of which are only in North America, or vice versa. Instead, their biogeographic distributions remain effectively the same or involve minor expansions or reductions in neighboring regions. Oard further notes that there are numerous mammal families with endemic (continent-specific) genera, which he admits is "a situation that still needs an explanation" in his model.[8] It is for these and other reasons that the Cenozoic mammal record is best interpreted as the diversification and migration from family-level kinds taking place entirely after the Flood, not genus-level kinds consistently returning to the Flood-generated graveyards of their kin.

Placing the post-Flood boundary at variable positions in the late Cenozoic, as Oard is wont to do, is inconsistent and arbitrary, and does nothing to solve these problems. His approach 1) fails to avoid the calamity of genus-level kinds; and 2) cannot mitigate the statistical unlikelihood of rampant post-Flood return migrations, which are all the more unlikely due to the massive changes in climate, habitat, and continental distributions between the pre-Flood and post-Flood worlds. Dismissing the Cenozoic mammal fossil record as 'equivocal' merely reflects Oard's poor grasp of the tangible, and gives empirical data which make an upper-Cenozoic post-Flood boundary untenable. Oard's frequent appeals to '33 geological criteria' of his own creation neither answers nor nullifies these challenges.

Oard's unread citation

Oard makes much of a putative antilocaprid (pronghorn antelope) from Japan as evidence against this family's North American endemism.[9] I knew of this entry and excluded it from my 2012 article because *the fossil does not exist.* No antilocaprids are catalogued in the paper,[10] nor in a recent compendium of mammal fossils of Asia.[11] Oard's use is ironic, because he has claimed that I uncritically accept data presented in the PBDB.[12] Yet, when tempted by a clearly anomalous record that he believed was a useful counterexample to my analysis, it is Oard who accepted the PBDB's entry without due diligence. Oard also cited this paper in a 2013 exchange with me, unaware that it makes no such claims.[13] He did not read the paper then, and he has not read the paper now.

Marcus Ross
Lynchburg, VA
UNITED STATES of AMERICA

References

1. Oard, M.J., Did the post-Flood North American mammals live above their dead Flood relatives? *J. Creation* **36**(3):106–113, 2022.
2. Ross, M.R., Evaluating potential post-Flood boundaries with biostratigraphy—the Pliocene/Pleistocene boundary, *J. Creation* **26**(2):82–87, 2012.
3. Oard, ref. 1, p. 106.
4. See paleobiodb.org/classic/basicCollectionSearch?collection_no=13907.
5. Arment, C., Ruminating on created kinds and ark kinds, ARJ **15**:391–404, 2022.
6. Oard, ref. 1, p. 107, 112.
7. None of the felids travel to Australia or Antarctica, nor are they found in either continent as fossils.
8. Oard, ref. 1, p. 109.
9. Oard, ref. 1, pp. 109–110.
10. Hirota, K., A list of vertebrate fossils from Shimane Prefecture, Japan, *Fossil Club Bulletin* **12**:21–27, 1979. Translated for the Smithsonian Institution Libraries, 1983; electronic copy produced in 2008. This paper is easily found online by searching for its title: LINK.
11. Wang, X., Flynn, L., and Fortelius M. (Eds.), *Fossil Mammals of Asia*, Columbia University Press, New York, 2013.
12. Oard, M., Geology Indicates the terrestrial Flood/post-Flood boundary is mostly in the late Cenozoic, *J. Creation* **27**(1):119–127, 2013.
13. Ross, M. vs. Oard, M., The Flood/post-Flood Boundary, comment and reply, *J. Creation* **27**(2):43–45, 2013.

» Michael J. Oard replies:

I appreciate Dr Ross for engaging in a discussion of the fossils and the upper diluvial boundary with me. Although his response is highly critical, at least I am responding to Arment[1] and his fossil arguments.[2] As a result, four papers have recently been published in this journal on the topic. I essentially agree with Arment that Australian marsupials are post-Flood. A deeper analysis, however, reveals they were first dated Pleistocene by secular science, but, because of ‘primitive’ features and their dating method based on the ‘stage of evolution’, the marsupials were pushed back to as old as Late Oligocene.

Sadly, Ross so far has refused to seriously examine the 35 criteria that Dr Clarey and I have developed that strongly indicate the boundary is in the Late Cenozoic. These criteria are developed mainly from various geological and climatological aspects. Ross surprisingly dismisses them by saying, “Oard’s frequent appeals to ‘33 geological criteria’ of his own creation neither answers nor nullifies these challenges.” I can assure the reader that these are not of my own creation but simply Cenozoic ‘history’. These 33 criteria (Clarey added two more) went through peer review and were published in this journal. Each one of these 35 criteria provides powerful evidence for the late Cenozoic boundary, which should nullify his one argument based only on fossils.

Two of the 35 criteria are challenges to the K/Pg boundary using mammals, the subject of this discussion. Those who believe in a K/Pg boundary must believe that few mammals were buried and fossilized during the Flood, but after the Flood tens of millions were buried and fossilized all over the earth. Could the conditions of fossilization even occur after the Flood? Secondly, Ross must explain the hundreds of sudden appearances of Tertiary mammal and the subsequent sudden extinctions at precise Tertiary times all over the globe, assuming the geological column. These two features alone should be enough to reject the K/Pg boundary model.

I have examined Ross’s arguments for North American mammals that he claimed left North America, arrived at the Ark, then returned to the continent over the Bering Land Bridge, and ended up living above their dead pre-Flood ancestors.[3] Using the Paleobiology Database (PBDB), I found substantial changes in nine years to the classification. Some even genera were transferred into different genera, making one wonder what precisely is a genus. Although there were still many genera of mammals that cross the Tertiary/Pleistocene boundary, *the trend of the data* was to decrease the number. Moreover, most of these mammals are not unique to North America, neither in the Tertiary (assume buried pre-Flood animals) nor in the Pleistocene (assumed post-Flood).

This brings up another point of contention, and that is I do not accept the subjective uniformitarian Tertiary/Pleistocene boundary as the upper Flood boundary, which should eliminate many more boundary crossing genera, especially when I have determined that the boundary is in the mid Pleistocene on the High Plains of the United States.[4,5] The Pleistocene does not necessarily cover the same timeframe as the uniformitarian Ice Age, although it includes it. There are places with hundreds, and sometimes thousands, of metres of Pleistocene strata. Ross claims that to use a floating boundary is inconsistent and arbitrary. The history of uniformitarian dating and classification of fossils necessitates it. Two examples are pushing back the Australian marsupials from the Pleistocene to as old as the late Oligocene and increasing the age of the Antarctic Ice Sheet by ten times. I believe it is a mistake to take the Cenozoic part of the geological column as an *absolute* for biblical chronology.

Ross exaggerates my supposed failure to verify citations, which is true of only *one*. I simply trusted the PBDB on the Miocene Antilocapridae (pronghorn) from Japan, which is still on the PBDB. Must I examine and verify the hundreds of other citations that are used in the PBDB? Has Ross done this? I am thinking that we do need to examine the observations of the fossils and geology closer in the referenced articles.

Therefore, I examined the data a little deeper and after eliminating the example claimed for Japan, I concluded Antilocapridae do exist in the Tertiary and Pleistocene only on North America. But this can be analyzed even further. First, the fossils need to be accurately classified and dated. Often the fossils are pieces of jaws and teeth and the dates are based on fossils. I even found one Antilocapridae genus that was reclassified into a different genus. Another factor is that the pronghorn is so close to an antelope that many people consider them antelopes. The only difference seems to be that pronghorns lose their horns. I wonder how many of the extinct pronghorns are known to lose their horns and are really pronghorns? So, if we consider the pronghorn as an antelope (a subfamily of Bovidae), then these mammals are not unique just to North America, since antelopes are found as fossils on all the continents except South America in the Tertiary and Pleistocene.

Ross and Arment[6] use the family as the kind level, which I also believe as an average, and then discuss boundary crossing genera, which I did admit still needs explaining. But the classification system is at a much finer scale below the order: infraorder, superfamily, family, subfamily, tribe, and finally genus. So, there are more degrees of freedom in analyzing mammals. It is interesting that Ross mentions *Smilodon* (saber-toothed cat), which is found in the Pleistocene of North and South America with four locations in the Tertiary of North America, which seems to verify his claims. However, the four Tertiary examples in North America were all dated as Blancan, which can be either late Pliocene or early Pleistocene, so could all be post-Flood. More analysis is required. But if we go one small step up in the classification system of saber-toothed cats to the tribe Smilodontini, saber-tooth cats are found on all continents for both the Tertiary and Pleistocene, except in the Tertiary of South America.

The really substantive argument is: Can the same 'genera' of a 'family' exist both before and after the Flood? I do not think either Ross or Arment have proven that this cannot happen.

Dr John Reed was mentioned as a reviewer in the acknowledgments only because he improved my English.

Michael J. Oard
Bozeman, MT
UNITED STATES of AMERICA

References

1. Arment C., To the Ark, and back again? Using the marsupial fossil record to investigate the post-Flood boundary, ARJ **13**:1–22, 2020.
2. Ross, M.R., Evaluating potential post-Flood boundaries with biostratigraphy—the Pliocene/Pleistocene boundary, *J. Creation* **26**(2):82–87, 2012.
3. Oard, M.J., Did the post-Flood North American mammals live above their dead Flood relatives? *J. Creation* **36**(3):106–113, 2022.
4. Oard, M.J., Were the Wind River terraces caused by multiple glaciations? CRSQ **50**(3):154–171, 2014.
5. Oard, M.J., Relating the Lava Creek ash to the post-Flood boundary, *J. Creation* **28**(1):104–113, 2014.
6. Arment, C., Ruminating on created kinds and Ark kinds, ARJ **15**:391–404, 2022.

Possible myths in geology

Michael J. Oard

Some well-known geoscientists believe that there are widely held myths in the earth sciences. The myths pointed out by geologists Garzanti and Dickinson are suspect terranes, mantle plumes, global sequence stratigraphy, Wilson cycles, and snowball Earth. One of the most pervasive myths is that sand becomes more 'mature' as it undergoes many processes, mainly river transport and beach turbulence. Garzanti and colleagues claim this belief is falsified by their research in southwest Africa where the climate is so dry that chemical weathering can be eliminated as a complication. Based on sand transported 2,000 km down the Orange River and then an additional 1,800 km northward along the coast to southwest Angola, they concluded mineralogical maturity is not occurring. Moreover, while water transport does not cause textural maturity, transport in an eolian environment sometimes does. There likely are other myths believed by earth scientists, such as the Milankovitch mechanism. Such myths that are often dogmatically believed by many uniformitarian geologists should caution creation scientists to be careful accepting these and other uniformitarian deductions. We should examine carefully the supporting data and the assumptions.

It is rare when uniformitarian geologists come to understand that some of their long-held cherished beliefs are myths. They also comment on the philosophy and psychology behind myth making. Well-known USGS geoscientist Warren Hamilton, in his long swan song, published posthumously in *Earth-Science Reviews*, wrote about groupthink, defective assumptions, untested beliefs, lack of objective science, the lost art of crucial testing, etc. in the geosciences.[1] Sandstone specialist Eduardo Garzanti, from the Department of Earth and Environmental Sciences in Milano, Italy, also pointed out several geological myths, focusing on the origin of some types of sandstone.[2] He also references a similar paper by William Dickinson, late professor emeritus at the University of Arizona.[3] Garzanti writes that myths are relatively common in geology:

> "A myth … is a powerful traditional narrative involving symbols that evoke legendary meanings about the mysterious origin and functioning of nature. Although we are unwilling to admit it, mythical thinking plays a conspicuous part in geological research. It helps us feel more comfortable while exploring with our inadequate tools the depths of geological time. It substitutes processes we fail to understand with a friendly image."[4]

Garzanti also states that myths are commonly intertwined with 'truth': "Truth and myth are commonly intertwined in theories about the functioning of the Earth."[5] Although believing geomyths stimulate mental activity, Dickinson would add that it can be difficult to separate myth from science: "Distinguishing between myth and science is subtle, for both seek to understand things around us."[6] This has become more pronounced over the past decades with less separation between data and interpretation than in the 1950s.

Garzanti and Dickinson's geological myths

Garzanti challenges several long-accepted geological myths: "We often resort to mythical thinking in the face of natural phenomena that we hardly understand. Sedimentary petrology has several long-standing myths."[4] The geological myths he mentions in particular are geosynclines (which are no longer accepted because of plate tectonics); suspect terranes that amalgamated to a continent during plate convergence; mantle plumes in which hot partially molten rock rises from the core/mantle boundary to the surface; global sequence stratigraphy; tectonic reunification of supercontinents, like Rodinia and Pangea, called Wilson cycles; and climatic revolutions such as 'snowball Earth'.[2]

Suspect terranes

Suspect and exotic terranes are posited to be pieces of continental or ocean lithosphere that might have been (suspect terranes) or likely were (exotic terranes) plastered onto a continent during plate collision. Much of western North America is a collage of about 50 of these terranes.[7] One of the reasons geologists propose exotic terranes is that one or more of the rock data, fossil data, absolute dates, paleomagnetism, etc. do not agree with the current location of the terrane. Hence it is believed that a particular terrane must have originated somewhere else and been transported by plate tectonics. Such a belief has brought up challenges for geology,[8] especially when paleomagnetism contradicts geology, like in the Baja-BC controversy. Some geologists have questioned the whole concept of suspect terranes.[9,10]

William Dickinson also wrote about myths in earth science, including most of those Garzanti mentioned.

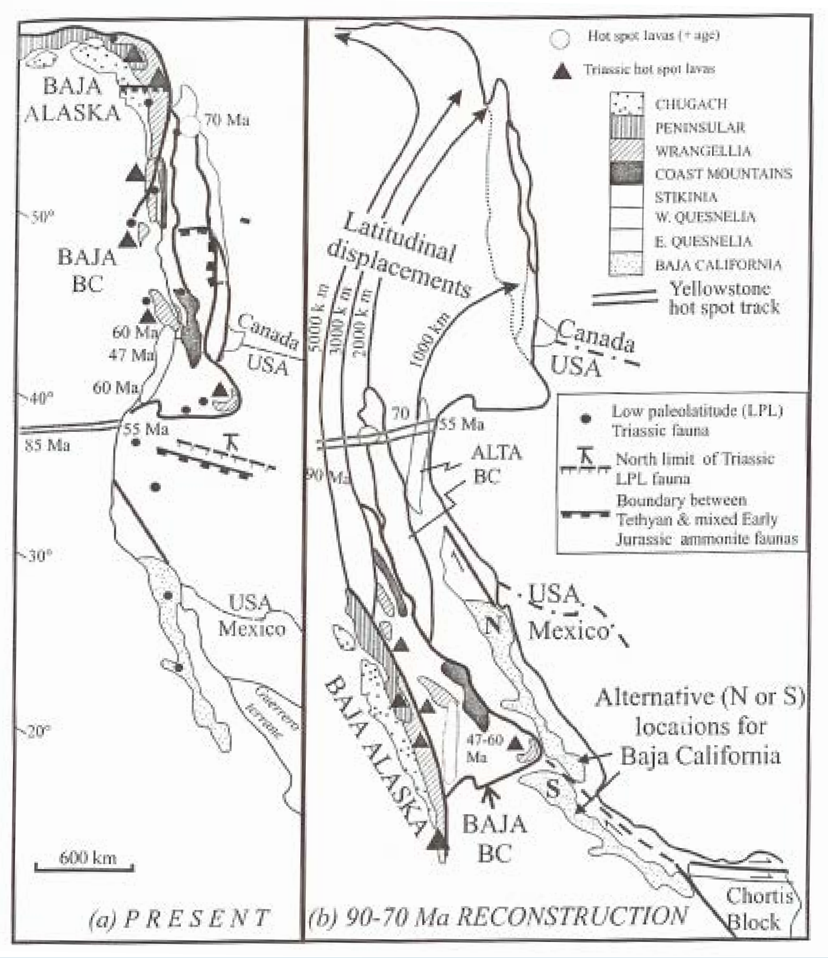


Figure 1. Locations of various superterranes 70 to 90 Ma ago in accordance with the standard geological timescale as suggested by Keppie and Dostal.[14]

Figure 2. The Columbia River Basalt area, including the Steens Mountain volcanics

Dickinson added that blindly accepting paleomagnetism over other rock evidences for defining suspect terranes, and in spite of reasons to doubt the results of the paleomagnetic studies, is mythical thinking.[3] In regard to suspect terranes, Dickinson may be referring to the Baja-BC controversy, which exhibits contrasting paleomagnetic solutions. The Baja-BC controversy is the belief by some geologists, based on shallow paleomagnetic inclinations, that the suspect terranes of western North America (see below) were first plastered onto Baja, California, during the Upper Cretaceous and Lower Tertiary. Then they moved northward 1,000–5,000 km along strike-slip faults to western British Columbia and Southeast Alaska (figure 1).[11,12] Many geologists see little evidence of such movement based on lithology and fossils and explain away the positive evidence for the hypothesis, such as low paleomagnetic inclinations.[13] The controversy shows that there are still some glaring contradictions in the earth sciences.

Mantle plumes

Garzanti,[2] Hamilton,[1] and Dickinson[3] all mention mantle plumes as mythological. Well-known geophysicist, the late Don Anderson, also believed mantle plumes were a myth.[15] Hotspots within plates are evident from intraplate volcanism, but it is the interpretation of hotspots that is controversial. Dickinson amplifies by questioning the idea that hotspots are a result of hot mantle rising from the core/mantle boundary; i.e., mantle plumes, and whether these plumes could migrate hundreds of kilometres laterally below the subsurface. Dickinson believes many hotspots and hotspot tracks fail predictions for deep mantle plumes:

> “Geometric analysis has shown repeatedly that all oceanic hotspots cannot be fixed relative

> to one another, because mutually fixed hotspots would generate hotspot tracks at azimuths incompatible with established relative plate motions (Norton, 2000). Moreover, some Pacific island-seamount chains are the products of multiple or migratory hotspots, or involve eruptions distinctly out of age-space sequence (Dickinson, 1998).”[16]

Dickinson adds that many believe the myth that hot spot lavas can move horizontally hundreds of kilometres below the surface (presumably in the mantle) before erupting. He may have been thinking of one explanation offered for the Columbia River Basalts in the northwest United States (figure 2). These massive lava flows erupted from dikes in southeast Washington, western Idaho, and eastern Oregon. According to some interpretations,[17] magma had to travel hundreds of kilometres northward under the surface from the supposed Yellowstone hotspot that tracked from southwestern Idaho to Yellowstone National Park, northwest Wyoming, USA.[18] One problem with the Yellowstone hotspot track toward the northeast is that another hotspot moves from southeast Oregon west-northwest, the opposite of the claimed plate motion.[18]

Foulger indicates that numerous assumptions and variables enter into the interpretation of hotspots and hotspot tracks (figure 3).[19] The Hawaiian Island-Emperor Seamount hotspot track, if the relative dates are to be believed, may be the ideal, but there are other complications and problems with other hotspot tracks that do not line up with plate tectonics.[20–23] For instance, the Line Islands in the central Pacific Ocean lack a predictable age progression as the plate moves over a hotspot, although researchers are trying to solve this problem.[24] Others emphasize that these features may be caused by ‘hot lines’ or ‘hot cracks’ in which volcanism occurs at the same, or

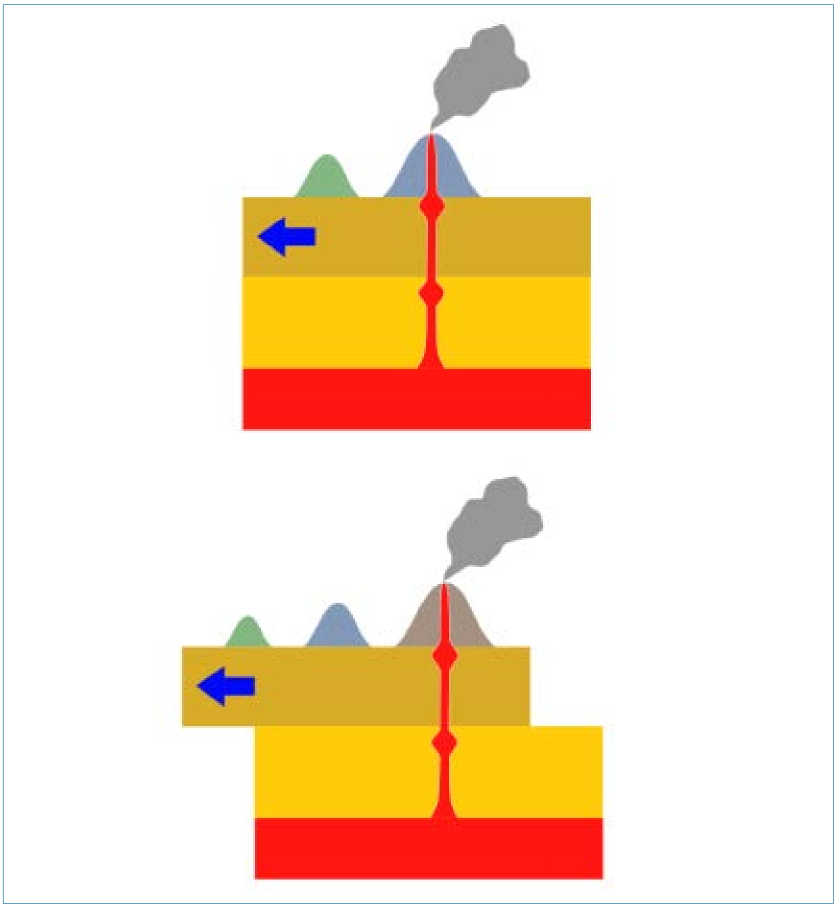


Image: Los688, Wikipedia / PD-self

Figure 3. Drawing showing a cross-section though the earth’s lithosphere (brown) moving relative to the rest of the upper mantle (yellow) and lower mantle (red) with magma rising from the lower mantle. The moving lithosphere produces a hotspot track.

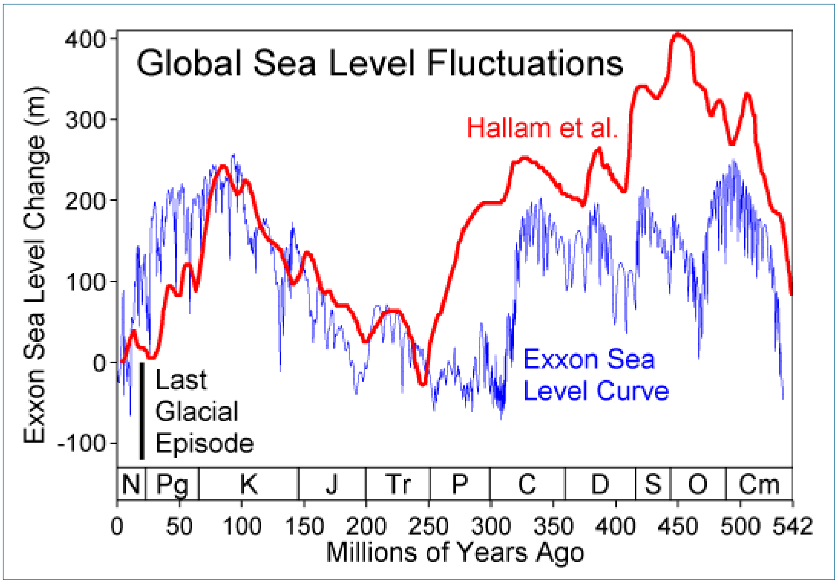


Image: Robert A. Rohde, Wikimedia / CC-BY-SA-3.0

Figure 4. Comparison of two sea level reconstructions during the last 500 Myr. The black bar shows the magnitude of sea level change during the Quaternary glaciations of the past few million years, but the bar is offset further in the past for readability.

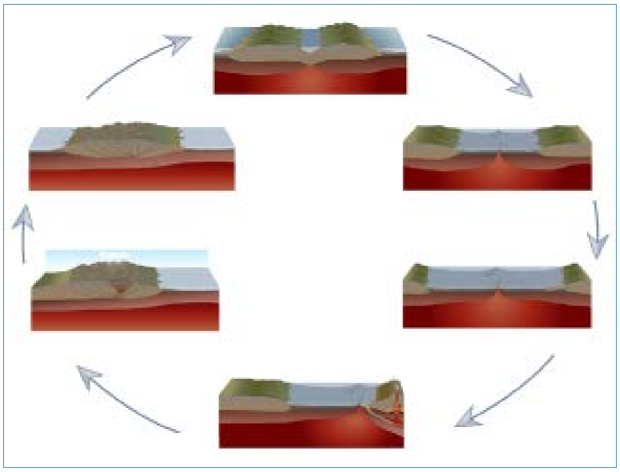


Image: Fabrichter, Wikimedia / CC-BY-SA-4.0

Figure 5. A Wilson cycle in which supercontinents split apart into separate plates, starting at the top figure and going clockwise, until they crunch back together to form another supercontinent

nearly the same, time over a long distance along a tension crack in the lithosphere.[25,26]

Many do not believe mantle plumes are a myth.[27–29] Despite mantle plumes being theoretically predicted, seismic studies have not been able to image mantle plumes, as stated by McNamara in 2019: "Unfortunately, although many seismic studies provide hints and glimpses of plumes, we do not yet have complete, incontrovertible evidence of their existence."[30] One of the main reasons for the lack of observations is that mantle plumes are narrow. And they are composed of magma, which has no seismic reflectors. Maybe someday geophysicists will gain seismic evidence and mantle plumes will be shown to not be a myth after all. But their existance is still unproven.[31–34] Guimarães *et al*. state:

> "Intraplate magmatism is enigmatic in origin despite its importance in our understanding of crustal cycling through the deep mantle. A mantle plume origin is justified for some intraplate magmatism, but not in the case of a large number of occurrences."[35]

Global sequence stratigraphy

Garzanti[2] follows Dickinson[3] in mentioning that global sequence stratigraphy involves 'mythic' thinking (i.e., proceeds on the basis of untestable assumptions). It is based on the idea that major unconformities can be correlated *globally* based on the global rises and falls in sea level usually related to increases and decreases in seafloor spreading activity, glaciation, and/or the volume of the ocean basins with time (figure 4).[36,37] Some secular scientists even think sequence stratigraphy is better than uniformitarian stratigraphy based on fossils, mainly because the subsurface can be imaged over large areas by seismic methods and biostratigraphy only samples widely scattered locations. However, some secular scientists question sequence stratigraphy.[38–40]

The first problem they identify is that local and regional tectonics and a change in sediment supply can cause unconformities in sediments.[41] Also, as sediment accumulates, accommodation space must be provided by subsidence.[42] Moreover, the method is mainly two-dimensional, while the three-dimensional architecture can be quite variable, and the sequences must be correlated with other basins to develop a global pattern.[42]

Many aspects of global sequence stratigraphy, both its philosophical foundations and its empirical cogency, have been discussed in the creationist literature.[43,44] Some elements of sequence stratigraphy that are empirical may be valuable for Flood geology research.[45–48] Recent work on a global scale has argued for the validity of global stratigraphic correlation in a biblical context[49] and has made much use of global sequence stratigraphy,[50] though it has also called some aspects of its uniformitarian context into question.[51] However, other creationists have continued to register concerns with sequence stratigraphy.[52–54] For instance, faulty radiometric and biostratigraphic dating, evolutionary biases, and the Milankovitch mechanism can enter into sequence stratigraphy. It behoves creation scientists who are using sequence stratigraphy[50] to take seriously these concerns and make sure that uniformitarian assumptions are weighted carefully.

Wilson cycles

Wilson cycles are cycles in plate spreading and converging back into a supercontinent (figure 5). Uniformitarian scientists have claimed to have identified about a half dozen of these cycles. The last is the convergence of plates to form the supercontinent Pangea at about 335 Ma ago, which split apart to form the current continental configuration, starting at about 175 Ma ago. The supercontinent Pannotia formed about 600 Ma ago and broke apart 560 Ma ago. And going back to the third from the last Wilson cycle, plates came together about 1 billion years ago to form the supercontinent Rodinia, which split about 700 Ma ago. Few geologists have a problem with supercontinents breaking up and spreading into many plates. However, Garzanti thinks it is mythological thinking for plates to converge back together, although he does not explain why.[4] Some creation scientists commonly use two Wilson cycles in the Catastrophic Plate Tectonics (CPT) model.[55] Although mechanisms for plate spreading have been formulated, the mechanism for causing plates to converge again does not seem to have been worked out. It is more logical to me that within the CPT model there was only one splitting with no convergence from previous Wilson cycles, as Clarey proposes.[50]

Snowball Earth

Garzanti also lists as myth climatic revolutions such as snowball Earth in which the whole world was glaciated.[4] This idea came about from the analysis of what are considered ancient marine ice age deposits within tropical paleomagnetic latitudes. Thus, uniformitarian geologists have been *forced* to claim the outrageous hypothesis that the earth was totally or almost totally glaciated in the Neoproterozoic—about three separate times![56–58] Of the many problems with this hypothesis is that with a snow-covered global surface, the earth would probably cool 100°C[59] due to the high reflectivity (albedo) of snow and the lack of heat sources (other than the sun). Second, just as outrageous is that a mechanism is needed to melt a snow-covered earth when air temperatures would have been much below freezing. Furthermore, the melting has to occur when solar luminosity was supposedly 10–30% less than it is today, according to the uniformitarian big bang theory.[60,61] This is called the faint young sun paradox.[61] This makes their assertion even more difficult to justify.

The maturity myth in sedimentary petrology

Garzanti, an expert in the petrology of sand and sandstones, focused on the myth that sediment increases its maturity with time via water transport:

> "One is that sediments increase their 'maturity' through time by winnowing and sorting, physical wear, chemical weathering, diagenesis, and recycling, as if their destiny were to reach a final stage of perfection represented by quartz spheres of equal size."[4]

A mature or supermature sand is defined as one that has reached pure quartz spheres of about equal size. This sand would essentially be well-sorted with well-rounded quartz grains, called a 'quartz arenite', that has greater than 90–95% quartz grains. Maturity involves two processes: (1) textural maturity that is believed to be caused by mechanical wear, winnowing, and sorting and (2) mineralogical maturity in which the more labile minerals are broken up or dissolved and the harder, more chemically resistant, minerals remain. Such maturity does not apply to finer-grained sand because the small size of the framework grains does not have enough momentum during transport to cause damage when the grains collide, both in water and in air. Mineralogical maturity is a rather vague concept that expresses the ratio between relatively durable detrital grains, such as quartz, chert, zircon, tourmaline, and rutile, and other less mechanically or chemically resistant minerals, such as feldspar, amphibole, pyroxene, and olivine.[62]

Water transport barely changes the maturity of sand

Garzanti amplifies on why many of the processes he mentions do not increase textural or mineralogical maturity in water transport. He claims that sand transported 2,000 km westward down the Orange River, South Africa, and then northward in the littoral zone up to 1,800 km along the coast does not change the textural maturity.[63] This was demonstrated observationally in 1937 by Russell on sand transport 1,740 km down the Mississippi River from Cairo, Illinois, to the Gulf of Mexico.[64] It was also shown experimentally in 1959 by Kuenan in his sand flume experiment.[65]

During littoral transport in southwest Africa, some of the sand is blown from the beach east onto the Namib Desert, where generally southerly winds transport the sand mainly north. In eolian desert transport, Garzanti and colleagues show that textural maturity does increase rapidly,[66] but mineralogical maturity does not increase in air or in water: "Quartz and other stable minerals do not increase significantly in abundance even after thousands of kilometers of high-energy fluvial, littoral, or eolian transport".[66] However, eolian transport of sand does cause a decrease in unconsolidated or soluble grains, such as shale, siltstone, sandstone, and gypsum.[67] Sands occasionally become 'less mature' during transport. Furthermore, rounding is extremely slow in water[67] but considered 100 to 1,000 times more effective in air.[68,69]

It had been assumed by geologists that when sand is eroded and transported by water, less resistant minerals, such as olivine, pyroxene, amphibole, and feldspar, are eventually eliminated by erosion.[62] The remaining quartz would then become progressively rounded by water action. Garzanti believes that these and other myths are "instilled routinely in undergraduate students' minds."[4]

Exceptions to the maturity rule have been simply given a name, 'textural inversions', and dismissed.[5] Papering over difficulties with nominal hypotheses is a common tactic used to explain a host of anomalies, but when many anomalies are found and detailed explanations are not given, it is time to question the hypothesis. It seems that few secular earth scientists are aware of how many myths they might have believed.

Hydrological sorting

Hydraulic sorting is a complicated process and can modify the mineralogical composition of a sediment locally, but this does not necessarily mean the sediment becomes more 'mature' or well-rounded or well-sorted. In a traction current, the larger-grained heavy minerals can be winnowed out and can result in a greater or lesser quartz content.[70] Smaller-grained heavy minerals will often still be deposited with the lighter quartz, feldspar, and calcite.[70]

Image: Verisimilus, Wikimedia / CC-BY-3.0

Figure 6. Miocene cyclic deposits, considered of Milankovitch origin, from the Tabernas basin of southern Spain. Prominent beds are approximately 0.5 m in width.

Recycling

Some think that recycling, or reworking of previously deposited sediment, will increase textural and mineralogical maturity.[71] However, the effect of recycling is variable, depending upon the lithology of the added detritus.[71] If the lithology of the new detritus is from a quartz arenite that is already mature, the new sediment will become more mineralogically and texturally mature. But if detritus comes from many other types of rock, such as basalt, the percent of quartz is likely to decrease.[72]

Chemical weathering

In both the Orange River watershed and along the southwest African coast, chemical weathering is very low because the climate is arid.[73] So, just the effects of mechanical weathering in water and air can be isolated, showing that the idea of mineralogical maturity without chemical weathering during transport is mythological.

On the other hand, a warm, wet climate with little relief causes strong chemical weathering. Prolonged feldspar hydrolysis and weathering of unstable lithic fragments in a granitic or gneissic terrane can result in a high quartz sand (mineralogically mature),[74] such as in the Amazon drainage.[75] Central Africa also seems like an ideal location for mineralogical maturity by chemical weathering, but the area also has numerous quartz arenite outcrops that are being eroded. Although the sand is quartz rich, textural mineralogy is likely caused by recycling quartz arenites.[76]

Likely even more myths

I believe secular geologists believe in many other myths; for instance, naturalism, deep time, uniformitarianism, and evolution. There are many reasons that secular scientists believe these myths, but one of the reasons would be the dominance of these myths in the culture and the disdain for creation, the global Flood, Christianity, and the truth of God's Word.

I would also include the astronomical theory of ice ages (cyclostratigraphy) or the Milankovitch mechanism as mythical. These cycles supposedly explain Pleistocene glacial/interglacial oscillations as well as cycles of pre-Pleistocene sedimentation (figure 6).[77–80] The Milankovitch cycles are too weak to produce these dramatic effects. The changes in solar radiation integrated over the warm or cold half year for a whole hemisphere are small. Uniformitarian scientists use Milankovitch cycles to date a wide range of climatic data sets, including ice cores, deep-sea cores, pollen cores, and continental basin cores. The myths consciously or unconsciously influence observations and then conclusions as scientists interweave observations with myth.

Discussion

Not including the myths I added, the above myths are, of course, Garzanti and Dickinson's opinions, but new information may possibly verify the 'myth'. But the crucial papers are still recent, and deductions are not changing that fast. Garzanti's paper was published in 2017, and Dickinson paper was published in 2019, and even more recent papers from other authors would support Garzanti and Dickinson; for instance, with mantle plumes.

One point of bringing these myths up is because it appears that many of the concepts that uniformitarian scientists passionately believe could be wrong. It should be a caution for all scientists to hold their deductions loosely. It seems that geologists, like other human beings, jump to conclusions too quickly, without weighing all the evidence; or if there is not enough evidence, make a stand for a particular theory.

Creation scientists should take a lesson from the considerations of Garzanti and Dickinson. It should tell us that we should be careful of our interpretations of data. If the data and deductions come from uniformitarian scientists, we should thoroughly examine the deductions and the assumptions behind them. When I do this, I often find problems; for instance, with plate tectonics and CPT, and with the idea that the geological column is an exact global sequence of burial within biblical Earth history. These concepts maybe true, but they need more support and research on seeming contradictions.

In regard to the geological column, Reed and I edited a book in which advocates of three positions presented their case with the others critiquing them, followed by answers to those critiques.[81] The three positions are: 1) the geological column is mythical, 2) the geological column is an absolute global time sequence within biblical Earth history, and 3) the geological column is a general fossil order with exceptions.

Garzanti claimed that it was a myth that a sand does not reach mineralogical maturity or textural maturity in water. However, we have such sandstones in abundance in the Precambrian and Paleozoic. They are called quartz arenite. How did these sandstones become mature? It is possible that strong currents and turbulence during the Flood can cause quartz arenite. This is the subject of a future paper. If we compare the other sandstones in the rock record, they also present challenges to the uniformitarian principle, especially arkose and graywacke.

Conclusions

Some secular scientists admit that many myths interact and are intertwined with observations in the earth sciences, creating false paradigms. Some of these are suspect terranes, mantle plumes, global sequence stratigraphy Wilson cycles, and snowball Earth. An additional myth, emphasized by Garzanti, is that sand becomes more 'mature' with transport in a river and during longshore transport. Maturity in a sand or sandstone is defined as quartz-rich (mineralogical maturity) with well-rounded grains (textural maturity). When chemical weathering can be mostly eliminated, like in southwest Africa, the mechanical maturity concept can be better tested. Garzanti and colleagues show that mineralogical maturity changes little by water or by wind transport. Textural maturity also changes little in water transport, but it can occur rapidly by wind transport. Eolian action seems to be the only mechanism that efficiently rounds sand in today's environment.

These perceived myths are the opinions of two well-respected geologists, but with time they may prove to not be myths at all. Regardless, creation scientists can learn from their expertise and be careful of the concepts we accept. It behoves us to thoroughly research the data and the assumptions.

References

1. Hamilton, W.B., Toward a myth-free geodynamic history of Earth and its neighbors, *Earth-Science Reviews* **198**(102905):1–49.
2. Garzanti, E., The maturity myth in sedimentology and provenance analysis, *J. Sedimentary Research* **87**:353–365, 2017.
3. Dickinson, W.R., The place and power of myth in geoscience: an associate editor's perspective, *American J. Science* **303**:856–864, 2003.
4. Garzanti, ref. 2, p. 353.
5. Garzanti, ref. 2, p. 354.
6. Dickinson, ref. 3, p. 856.
7. Coney, P.J., Jones, D.L., and Monger, J.W.H., Cordilleran suspect terrances, *Nature* **288**:329–333, 1980.
8. Le Grand, H. and Glen, W., Choke-holds, radiolarian cherts, and Davy Jones's locker, *Perspectives in Science* **1**(1):24–65, 1993.
9. Blodgett, R.B. and Stanley Jr, G.S. (Ed.), The terrane puzzle: new perspectives on paleontology and stratigraphy from the North American cordillera, *Geological Society of America Special paper 442*, Geological Society of America, Boulder, CO, 2008.
10. Hudson, T.L., Suspect philosophy? *Geology* **15**(12):1177, 1987.
11. Keppie, J.D. and Dostal, J., Evaluation of the Baja controversy using paleomagnetism and faunal data, plume magmatism, and piercing points, *Tectonophysics* **339**:427–442, 2001.
12. Oard, M.J., The Baja-British Columbia controversy, *J. Creation* **18**(2):8–10, 2004; dl0.creation.com/articles/p025/c02556/j18_2_8-10.pdf.
13. Housen, B.A. and Beck, Jr, M.E., Testing terrane transport: an inclusive approach to the Baja B.C. controversy, *Geology* **27**(12):1143–1146, 1999.
14. Keppie, J.D. and Dostal, J., Evaluation of the Baja controversy using paleomagnetic and faunal data, plume magmatism, and piercing points, *Tectonophysics* **339**:429, 2001.
15. Anderson, D.L., The persistent mantle plume myth, *Australian J. Earth Sciences* **60**:657–673, 2013.
16. Dickinson, ref. 3, p. 859.
17. Camp, V.E. and Wells, R.E., The case for a long-lived and robust Yellowstone hotspot, *GSA Today* **31**(1):4–10, 2021.
18. Kincaid, C., Druken, K.A., Griffiths, R.W., and Stegman, D.R., Bifurcation of the Yellowstone plume driven by subduction-induced mantle flow, *Nature Geoscience* **6**:395–399, 2013.
19. Foulger, G.R., Are 'hot spots' hot spots? *J. Geodynamics* **58**:1–28, 2012.
20. Clouard, V. and Bonneville, A., How many Pacific hotspots are fed by deep-mantle plumes? *Geology* **29**(8):695–698, 2001.
21. White, S.M., Umino, S., and Kumagai, H., Transition from seamount chain to intraplate volcanic ridge at the East Pacific Rise, *Geology* **34**(4):293–296, 2006.
22. Ballmer, M.D., Conrad, C.P., Smith, E.I., and Harmon, N., Non-hotspot volcano chains produced by migration of shear-driven upwelling toward the East Pacific Rise, *Geology* **41**(4):479–482, 2013.
23. Guimarães, A.R., Fitton, J.G., Kirstein, L.A., and Barfod, D.N., Contemporaneous intraplate magmatism on conjugate South Atlantic margins: a hotspot conundrum, *Earth and Planetary Science Letters* **536** (116147):1–8, 2020.
24. Pockalny, R., Barth, G., Eakins, B., Kelley, K.A., and Wertman, C., Multiple melt source origin of the Line Islands (Pacific Ocean), *Geology* **49**:1358–1362, 2021.
25. Lynch, M.A., Linear ridge groups: evidence for tensional cracking in the Pacific Plate, *J. Geophysical Research* **104**(B12):29321–29333, 1999.
26. Harmon, N., Forsyth, D.W., Weeraratne, D.S., Yang, Y., and Webb, S.C., Mantle heterogeneity and off axis volcanism on young Pacific lithosphere, *Earth and Planetary Science Letters* **311**:306–315, 2011.
27. Hand, E., Mantle plumes seen rising from Earth's core, *Science* **349**:1,032–1,033, 2015.
28. Chase, A. and Wessel, P., Analysis of Pacific hotspot chains, *Geochemistry, Geophysics, Geosystems* **23**(e2021GC010225):1–25, 2022.
29. Nelson, P.L. and Grand, S.P., Lower-mantle plume beneath the Yellowstone hotspot revealed by core waves, *Nature Geoscience* **11**:280–284, 2018.
30. McNamara, A.K., A review of large low shear velocity provinces and ultra low velocity zones, *Tectonophysics* **760**:203, 2019.
31. Bao, X., Lithgow-Bertelloni, C.R., Jackson, M.G., and Romanowicz, B., On the relative temperatures of Earth's volcanic hotspots and mid-ocean ridges, *Science* **375**:57–61, 2022.
32. Marignier, A., Ferreira, A.M.G., and Kitching, T., The probability of mantle plumes in global tomographic models, *Geochemistry, Geophysics, Geosystems* **21**(e2020GC009276):1–17.
33. Fletcher, M., Wyman, D.A., and Zahirovic, S., Mantle plumes, triple junctions and transforms: a reinterpretation of Pacific Cretaceous–Tertiary LIPs and Laramide connection, *Geoscience Frtontiers* **11**:1133–1144, 2020.
34. Jiang, Z., Li, S., Liu, Q., Zhang, J., Zhou, Z., and Zhang, Y., The trials and tribulations of the Hawaii hot spot model, *Earth-Science Reviews* **215**(103544):1–23, 2021.
35. Guimarães, A.R., Fitton, J.G., Kirstein, L.A., and Barfod, D.N., Contemporaneous intraplate magmatism on conjugate South Atlantic margins: a hotspot conundrum, *Earth and Planetary Science Letters* **536**(116147):1–8, 2020.

36. Haq, B.U., Hardenbol, J., and Vail, P.R., Chronology of fluctuating sea levels since the Triassic, *Science* **235**:1156–1166, 1987.
37. Hallam, A., Pre-Quaternary sea-level changes, *Annual review of Earth and Planetary Science* **12**:205–243, 1984.
38. Miall, A.D. and Miall, C.E., Sequence stratigraphy as a scientific enterprise: the evolution and persistence of conflicting paradigms, *Earth Science reviews* **54**:321–348, 2001.
39. Burgess, P.M., The future of the sequence stratigraphy paradigm: dealing with a variable third dimension, *Geology* **44**(4):335–336, 2016.
40. Miall, A.D., Eustatic sea level changes interpreted from seismic stratigraphy: a critique of the methodology with particular reference to the North Sea Jurassic record, *American Association of Petroleum Geologists Bulletin* **70**(2):131–137, 1986.
41. Miall, A.D., Exxon global cycle chart: an event for every occasion? *Geology* **20**:787–790, 1992.
42. Burgess, P.M., The future of the sequence stratigraphy paradigm; dealing with a variable third dimension, *Geology* **44**(4):335–336, 2016.
43. Klevberg, P., The philosophy of sequence stratigraphy-part I: philosophic background, CRSQ **36**:72–80, 1999.
44. Klevberg, P., the philosophy of sequence stratigraphy-part II: application to stratigraphy, CRSQ **37**:36–46, 2000.
45. Froede Jr, C.R., Sequence stratigraphy and creation geology, CRSQ **31**:138–147, 1994.
46. Davison, G.E., The importance of unconformity-bounded sequences in Flood stratigraphy, *J. Creation* **9**:223–243, 1995.
47. Bartlett, A.C., Sequence stratigraphy: value and controversy—for whom? CRSQ **34**:5–22, 1997.
48. Klevberg, P., The philosophy of sequence stratigraphy-part III: application to sequence stratigraphy, CRSQ **37**:94–104, 2000.
49. Clarey, T.L. and D.J. Werner, Global stratigraphy and the fossil record validate a Flood origin for the geologic column; in: Whitmore, J.H. (Ed.), *Proc. 8th ICC*, Creation Science Fellowship, Pittsburgh, PA, pp. 327–350, 2018.
50. Clarey, T., *Carved in Stone: Geological evidence of the worldwide Flood*, Institute for Creation Research, Dallas, TX, 2020.
51. Clarey, T.L. and Werner, D.J., The sedimentary record demonstrates minimal flooding of the continents during Sauk deposition, ARJ **10**:271–283, 2017.
52. Froede Jr, C.R., Akridge, A.J., and Reed, J.K., Can 'megasequences' help define biblical geologic history? *J. Creation* **29**(2):16–25, 2015.
53. Reed, J.K. and Oard, M.J., The meaning of unconformities, *J. Creation* **32**(1):92–99, 2018.
54. Reed, J.K., Changing paradigms in stratigraphy—*another* 'new uniformitarianism'? *J. Creation* **32**(3):64–73, 2018.
55. Snelling, A.A., *Earth's Catastrophic Past: Geology, creation & the Flood*, Institute for Creation Research, Dallas, TX, 2009.
56. Oard, M.J., 'Snowball Earth'—a problem for the supposed origin of multicellular animals, *J. Creation* **16**(1):6–9, 2002.
57. Oard, M.J., Uniformitarian scientists claim that 'snowball Earth' caused the Great Unconformity, *J. Creation* **34**(3):12–14, 2020.
58. Isaacs, E., 'Snowball earth' out with a bang? *J. Creation* **34**(3):5–7, 2020.
59. Budyko, M.I., The heat balance of the earth; in: Gribbin, J. (Ed.), *Climatic Change*, Cambridge University Press, London, p. 95, 1978.
60. Faulkner, D., The young faint sun paradox and the age of the solar system, *J. Creation* **15**(2):3–4, 2001.
61. Oard, M.J., Is the faint young sun paradox solved? *J. Creation* **25**(2):17–19, 2011.
62. Garzanti, ref. 2, pp. 354–355.
63. Garzanti, E., Resentini, A., Andò, S., Vezzoli, G., Pereira, A., and Vermeesch, P., Physical controls on sand composition and relative durability of detrital minerals during ultra-long distance littoral and aeolian transport (Namibia and southern Angola), *Sedimentology* **62**:971–996, 2015.
64. Russell, R.D., Mineral composition of Mississippi River sands, *GSA Bulletin* **48**:1307–1348, 1937.
65. Kuenen, Ph.H., Experimental abrasion 3. fluvial action on sand, *American J. Science* **257**:172–190, 1959.
66. Garzanti, ref. 2, p. 362.
67. Garzanti, ref. 2, p. 355.
68. Garzanti, ref. 2, p. 360.
69. Kuenen, Ph.H., Experimental abrasion 4: eolian action, *J. Geology* **68**:427–429, 1960.
70. Garzanti, ref. 2, pp. 355–356.
71. Garzanti, ref. 2, p. 356.
72. Garzanti, ref 2., p. 356–357.
73. Garzanti, E., Andò, S., Vezzoli, G., Lustrino, M., Boni, M., and Vermeesch, P., Petrology of the Namib Sand Sea: long-distance transport and compositional variability in the wind-displaced Orange Delta, *Earth-Science Reviews* **112**:173–189, 2012.
74. Garzanti, ref. 2, p. 357.
75. Potter, P.E., Modern sands of South America: composition, provenance and global significance, *Geologische Rundschau* **83**:212–232, 1994.
76. Garzanti, E., Vermeesch, P., Vezzoli, G., Andò, S., Botti, E., Limonta, M., Dinis, P., Hahn, A., Baudet, D., and De Grave, J., Congo river sand and the equatorial quartz factory, *Earth-Science Reviews* **197**:102918, 2019.
77. Reed, J.K. and Oard, M.J., Cyclostratigraphy, part I: what is cyclostratigraphy? CRSQ **52**(2):95–105, 2015.
78. Reed, J.K., and Oard, M.J., Cyclostratigraphy part II: history of the method, CRSQ **53**(2):103–109, 2016.
79. Oard, M.J. and Reed, J.K, Cyclostratigraphy, part III: critique of the Milankovitch Mechanism, CRSQ **56**(3):132–142, 2020.
80. Oard, M.J. and Reed, J.K., Cyclostratigraphy and astrochronology part IV: is the pre-Pleistocene sedimentary record defined by orbitally-forced cycles? CRSQ **56**(4):234–242, 2020.
81. Reed, J.K. and Oard, M.J. (Eds.), *The Geologic Column: Perspectives within diluvial geology*, Creation Research Society, Glendale, AZ, 2006.

Michael J. Oard *has an M.S. in atmospheric science from the University of Washington and is now retired after working as a meteorologist with the US National Weather Service in Montana for 30 years. He is the author of* Frozen in Time, Ancient Ice Ages or Gigantic Submarine Landslides?, Flood by Design, Dinosaur Challenges and Mysteries, *and* Exploring Geology with Mr Hibb. *He is a fellow of the Creation Research Society.*

Enantiomeric amplification of L-amino acids: part 7—using aspartic acid on an achiral Cu surface

Royal Truman

A study is critically evaluated here which reported an enantiomeric excess (e.e.) of aspartic acid when sublimed at low pressures and ~460 K when deposited on achiral Cu(111) surfaces. Different levels of initial e.e. increased or decreased when continually exposed to the sublimate, converging to a D/L ratio of 16. This was claimed to offer a possible natural solution for the origin of L-only amino acids (AAs) in proteins. The study used a single AA known to be among the few able to crystallize as conglomerates. However, the results only occurred upon careful guidance by chemists. A very high concentration of Asp was necessary but would not have arisen naturally at 2×10^{-10} torr and 460 K in any plausible terrestrial setting. No e.e. was observed at temperatures around 400 K and a few degrees above 460 K, Asp degraded thermally. Therefore, the experiments were deliberately terminated within 55 minutes at an optimal temperature. Availability of sizeable amounts of an ideal pristine surface in contact with the sublimate is not realistic. Furthermore, such homochiral clusters do not form for most other biogenetic AAs. Crucially, contact with water at this high temperature would have subsequently rapidly racemized the e.e., especially in the presence of Cu^{2+} chelating metal.[1,2]

Auto-amplification of aspartic acid on an achiral Cu surface

This is part 7 of a series critiquing possible explanations for a natural origin of the L-amino acids (AAs) needed to form proteins. In 2015, Yun and Gellmann published the results of a study they believed was the first example of auto-amplification of enantiomeric excess (e.e.) of a chiral molecule on an *achiral* metal surface.[3] Gas-phase mixtures of aspartic acid (Asp) having an excess of D or L enantiomer were exposed to an achiral crystalline metal surface known as Cu(111). This concentrated the enantiomer provided in excess on the surface (e.e._s). The experiments extend earlier work by Hazen *et al.* which showed that enantiomers of amino acids (AAs), such as Asp, adsorb preferentially on the *chiral* surfaces of calcite.[4]

A different *chiral* surface $\text{Cu}\{3,1,17\}^{R\&S}$ was already known to adsorb Asp enantiomers selectively at 460 K with an e.e._s (*s* for surface) of about 39%.[5] Specifically, D-Asp selectively adsorbed on the $\text{Cu}\{3,1,17\}^{S}$ surfaces and L-Asp on the $\text{Cu}\{3,1,17\}^{R}$ surfaces.[4]

Amplification of biological AAs in aqueous solution which already possessed an e.e. is already known to occur for a small minority of AAs which crystallize as conglomerates (i.e., physical mixtures of enantiomerically pure individual crystals), instead of forming racemates (i.e., individual crystals containing equimolar quantities of both enantiomers).[6] Like these studies, the effect found by Yun and Gellmann on the Cu(111) surface was interpreted as caused by stronger interactions between the same enantiomer types. As mentioned in part 6 of this series, this is known to occur for only the biogenetic AAs Asp, Asn, Thr, Glu, and Asn.[7] I pointed out that different very unusual and narrow environmental conditions were necessary for these five AAs to form conglomerates and that the e.e. which could be produced in a laboratory would be short-lived in nature before remixing or destruction occurred.

Initially, the D/L proportion of Asp absorbed on the Cu(111) surface at 400 K was found to match the proportion in the gas phase.[2] No e.e. was observed. Therefore, further experiments were conducted. Initial proportions D/L = 78, 16, 6.8, and 0.10 were allowed to reach saturation at 400 K. This required about 20 minutes. The surface was then slowly heated to 460 K and exposed to atmospheres of 1:2, 1:1, and 2:1 D/L Asp; see figure 1.[2] Using a racemic proportion always led to no enantiomeric excess, as shown by the yellow boxes in figure 1.

The data in figure 1 show that initially saturated adsorptions having more D- than L-Asp converge over time to a D/L ratio of 16. Using an initial excess of L-Asp instead produced the mirror effect.[2] It is important to note that Weiss *et al.* showed that Asp decomposes thermally at quite low temperatures (see figure 2).[8] In the experiments reported by Yun and Gellmann, however, Asp is expected to adsorb on the Cu(111) surface as biaspartate ($^{-}O_2C\text{–}CH(NH_2)CH_2\text{–}CO_2^{-}$). On Cu surfaces, biaspartate loses CO_2, $N{\equiv}CCH_3$ and H_2.

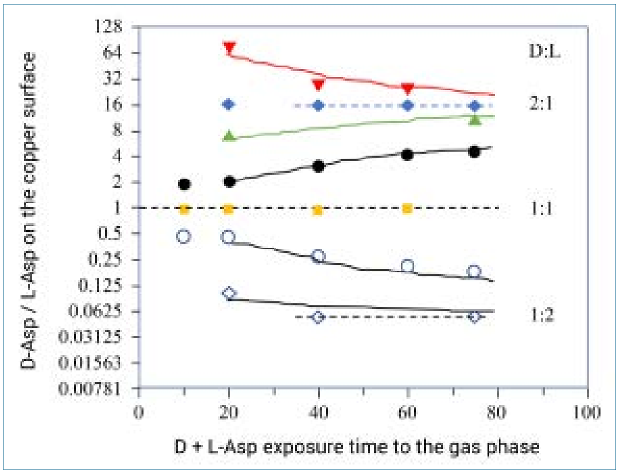


Figure 1. D/L ratios of Asp absorption on an achiral Cu(111) crystal surface over time at 400 K beginning with D/L values of 78 (▼); 16 (◆); 2 (●); 6.8 (▲); ½ (○) or 0.10 (◇). After reaching equilibrium in 20 minutes the surface was exposed to gas phase ratios D/L Asp of 1/2, 1, or 2/1.[2] (After figure 2 in ref. (2)).

Figure 1 of their paper shows that biaspartate decomposition also began at temperatures above 493 K.[2]

Therefore, after the initial absorption at 400 K for 20 minutes, further exposure at 460 K was discontinued after only 55 minutes. Figure 1 implies that, under these unique conditions, if exposure had continued for much longer, then auto-amplification could have increased from lower e.e. levels to up to a maximum of 88% (D-Asp / L-Asp = 16).[9] This was not actually demonstrated beginning with D/L ratios lower than 16, in the experiments (with D/L of 6.8 and 2.0). Perhaps the very long times needed at 460 K or higher destroyed all, or almost all, the Asp. In addition, extrapolating these two curves in figure 1 suggests the maximum D/L would level off significantly under a D/L ratio of 16.

The favoured concentration of homochiral AAs seems to be due to non-bonding AA clusters forming on surfaces. Glycine is known to form trimer rings through hydrogen bonding on the Cu(111) surface at 400 K.[10] Alanine forms a hexagonal complex on Cu(111) at 473 K, also using hydrogen bonding.[11] What is noteworthy in the report by Yun and Gellmann is that clusters could be selectively homochiral rather than racemic for some AAs under special conditions.

It is interesting how the e.e. of the sublimate phase at low pressure produced the opposite outcome reported by Tarasevych *et al.*, as discussed in part 6. In those experiments, pure L-enantiomers of Asn, Thr Asp, Glu, and Asn were mixed individually in 97.5:2.5 weight ratios with some more-volatile aliphatic AAs having a small e.e. of L-enantiomer. The sublimate generated under low pressure conditions decreased the e.e. of the L-enantiomer in the sublimate.[12]

If all these kinds of experiments reported could have occurred naturally (and if not, what would the purpose be for publishing the results in the origin of life (OoL) literature?), then their effects would tend to annul each other.

Critique of this study

- The enantiomeric separation on the crystal face required careful cleaning and preparation of the crystal face to optimize condensation and formation of crystals.
- It is implausible that such a Cu^{2+} surface, able to effectively absorb biaspartate, would happen to be exposed to such high concentrations of Asp at such extreme low pressure.
- An ultrahigh vacuum pressure of 2×10^{-10} torr was used.[2] Since 1 torr ≈ 0.00133 bar, the experiments were conducted at around 3×10^{-13} bar.[13] For comparison purposes, atmospheric pressure on Earth is ~1 bar and on the moon ~3×10^{-15} bar.[14] What primordial terrestrial environment could have resembled this? A putative Late Heavy Bombardment between ca. 4.0 and 3.8 billion years ago as claimed would have eliminated an e.e. in AAs.[15]
- The Asp molecules had to densely coat the surface to permit complexes to form, but where would all this pure AA have come from? No e.e. resulted at 400 K, so the temperature had to be raised to near 460 K. At such a temperature, and close to vacuum pressure, the AAs would have long since sublimed and dissipated instead of being suddenly concentrated onto such a hot surface.
- The suitable temperature range was very narrow. At only a slightly higher 493 K (220°C) Asp begins to decompose.[16,17] Higher temperatures would have been necessary for sublimation to occur under more realistic terrestrial pressures instead of the experimental 2×10^{-10} torr. I pointed out in part 4 that Weiss *et al.* analyzed the thermal decomposition of all 20 proteinogenic AAs using calorimetry, thermogravimetry and mass spectrometry.[7,18] For the 8 AAs they reported on in detail, the decomposition temperatures ranged from 185 to 280°C, with an average of 235°C.

They concluded that their results “put constraints on hypotheses of the origin, state and stability of amino acids in the range between 200°C and 300°C.”

- The amplified Asp would have been short-lived and of insignificant quantity under natural conditions. Asp sublimate formed would have remained for some time located in the low-pressure environment and near the heat source. Remixing of both enantiomers would have soon occurred.
- A steady supply of L-enantiomer excess in the gas phase would have been necessary for OoL purposes. L-enantiomer absorbed on the crystals, however, would have depleted the e.e.$_L$ remaining in the gas phase.
- High excesses of one enantiomer were used both to coat the crystal surface and then in the gas phase at 460 K. This unrealistic environment was required to form the Asp clusters in short time scales.

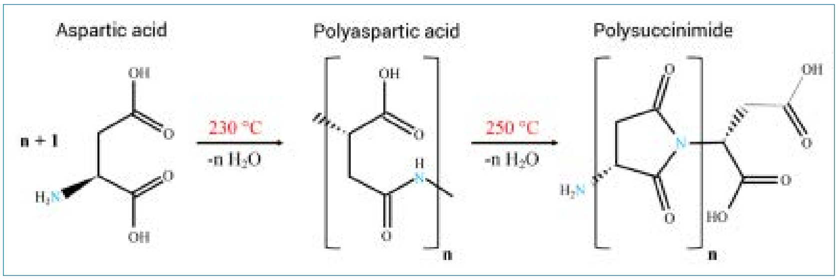


Figure 2. Two steps in the thermal decomposition of aspartic acid.[7] The maximum point of degradation for these two steps occurred at ~503 K (230°C) and ~523 K (250°C) with the loss of water molecules.[2]

- The amplification effect seems to occur for very few biological AAs. In addition, we saw in other parts of this series that sometimes an e.e. was amplified for the enantiomer initially in excess, and in other conditions it was depleted. The authors have not offered a plausible natural means to generate only enantiomers used by proteins.
- The amplification is symmetrical, so an excess of L-enantiomer somewhere would be offset by an excess of D-enantiomer elsewhere. For example, depletion in the gas phase to create an e.e. in the sublimate would provide a mechanism for the mirror image effect to now occur nearby.
- Polypeptides don't form from dilute AAs adsorbed on faces of crystals. The AAs would have had to eventually desorb and dissolve in water to be relevant for OoL purposes, whereupon racemization and mixing would eliminate the e.e. Crystals at near 460 K imply a hot environment, and racemization of AAs in hot water is very fast.[19] Note also that Cu^{2+} and other cationic metals are known to chelate AAs, facilitating loss of the α-proton, thereby further increasing the rate of racemization.[1,2]

This study illustrates the deep knowledge and technical expertise physical chemists have brought to bear to find a natural means to amplify L-AAs, a prerequisite to form proteins. The 'low-hanging' potential processes seem to have been exhausted, leaving ever more unlikely scenarios to be examined. The reader should not be misled to think that the large number of publications are an indication of progress, or, as Blackmond has claimed, that now researchers are spoiled by the large number of promising opportunities to further explore.[5] The effects are achieved under very unnatural conditions that do not even exist in the various putative early earth environments, and the results are short lived.

References

1. Buckingham, D.A., Marzilli, L.G., and Sargeson, A.M., Proton exchange and mutarotation of chelated amino acids via carbanion intermediates, *J. Am. Chem. Soc.* **89**:5133–5138, 1967 | doi:10.1021/ja00996a009.
2. Bada, J.L., Kinetics of the nonbiological decomposition and racemization of amino acids in natural waterss; in: Hem, J.D. (Ed.), *Nonequilibrium Systems in Natural Water Chemistry*, Advances in Chemistry vol. 106, American Chemical Society, Washington, DC, chap, 13, pp. 309–331, 1971 | doi:10.1021/ba-1971-0106.ch013.
3. Yun, Y. and Gellman, A.J., Adsorption-induced auto-amplification of enantiomeric excess on an achiral surface, *Nature Chemistry* **7**:520–525, 2015 | doi:10.1038/NCHEM.2250.
4. Hazen, R.M., Filley, T.R., and Goodfriend, G.A., Selective adsorption of L- and D-amino acids on calcite: implications for biochemical homochirality, PNAS **98**:5487–5490, 2001 | doi:10.1073/pnas.1010859.
5. Yun, Y. and Gellman, A.J., enantioselective separation on naturally chiral metal surfaces: D,L-aspartic acid on Cu(3,1,17)$^{R\&S}$ surfaces, *Angew. Chem. Int. Ed.* **52**:3394–3397, 2013. | doi:10.1002/anie.201209025.
6. Blackmond, D.G. and Klussmann, M., Spoilt for choice: assessing phase behavior models for the evolution of homochirality, *Chem. Commun.* **37**:3990–3996, 2007 | doi:10.1039/B709314B.373.
7. Truman, R., Enantiomeric amplification: part 6—sublimation using Asn, Thr, Asp, Glu, Ser mixtures, *J. Creation* **37**(3):90–92, 2023.
8. Weiss, I.M., Muth, C., Drumm, R., and Kirchner H.O.K., Thermal decomposition of the amino acids glycine, cysteine, aspartic acid, asparagine, glutamic acid, glutamine, arginine and histidine, *BMC Biophysics* **11**(2), 2018 | doi:10.1186/s13628-018-0042-4.
9. e.e. = (D – L)/(D + L) = 0.88, where (D + L) = 1. Then D – (1 – D) implies 2D = 1.88. Therefore, D/L = 0.94 / 0.06 = 16.
10. Zhao, X.Y., Yan, H., Zhao, R.G., and Yang, W.S., Self-assembled structures of glycine on Cu(111), *Langmuir* **19**:809–813, 2003 | doi:10.1021/la0267037.
11. Yitamben, E.N., Niebergall, L., Rankin, R.B. *et al.*, Tracking amino acids in chiral quantum corrals, *J. Phys. Chem. C* **117**:11757–11763, 2013 | doi:10.1021/jp400074r.
12. Tarasevych, A.V., Sorochinsky, A.E., Kukhar, V.P., and Guillemin, J-C., Deracemization of amino acids by partial sublimation and via homochiral self-organization, *Orig. Life Evol. Biosph.* **43**:129–135, 2013 | doi:10.1007/s11084-013-9333-6.
13. $(2 \times 10^{-10}$ torr$)(1.33 \times 10^{-3}$ bar/torr$) \approx 3 \times 10^{-13}$ bar.
14. Stern, S.A., The lunar atmosphere: history, status, current problems, and context, *Reviews of Geophysics* **37**(4):453–491, 1999 | doi:10.1029/1999RG900005.
15. Claeys, P. and Morbidelli A., Late Heavy Bombardment; in: Gargaud M. *et al.* (Eds.) *Encyclopedia of Astrobiology*, Springer, Berlin, Heidelberg, 2015 | doi:10.1007/978-3-662-44185-5_869.
16. Weiss, I.M., Muth, C., Drumm, R., and Kirchner, H.O.K., Thermal decomposition of the amino acids glycine, cysteine, aspartic acid, asparagine, glutamic acid, glutamine, arginine and histidine, *BMC Biophys.* **11**(2):1–15, 2018 | doi:10.1186/s13628-018-0042-4.
17. More specifically, the value of 493 K or 220°C for beginning of thermal degradation of Asp was taken from figure 3 in Weiss *et al.*, ref. 16.
18. Truman, R., Enantiomeric amplification of L-amino acids: part 4—based on subliming valine, *J. Creation* **37**(3):79–83, 2023.
19. Truman, R., Racemization of amino acids under natural conditions: part 1—a challenge to abiogenesis, *J. Creation* **36**(1):114–121, 2022.

***Royal Truman** has bachelor's degrees in chemistry and in computer science from State University of New York; an M.B.A. from the University of Michigan (Ann Arbor); a Ph.D. in organic chemistry from Michigan State University; and a two-year post-graduate 'Fortbildung' in bioinformatics from the Universities of Mannheim and Heidelberg. He works in Germany for a European-based multinational.*

Enantiomeric amplification of L-amino acids: part 8—modification of eutectic point with special additives

Royal Truman and Chris Basel

About a third of biological amino acids (AAs) form racemic crystals which are less soluble than homochiral crystals in aqueous solutions. In principle, this allows a solution with an initial excess of one enantiomer to be further enriched. Some dicarboxylic acids increase or decrease the solubility of these racemic crystals, affecting the maximum enantioenrichment achievable. A study is critiqued here in which the enrichment effects were achieved by using unrealistic conditions, beginning with saturated solutions of concentrated amino acids at a fixed, controlled temperature with stirring. Under natural conditions, the proposed cycles of enrichment through cooling and desiccation, followed by partial dissolution in rainwater, would have rarely separated enriched solutions and instead would have diluted any co-solvent which raised the eutectic point. The maximum enantiopurity theoretically obtainable would have only been high enough to be biologically relevant for two AAs. However, no net increase in the L enantiomer would have resulted throughout nature. Instead, the initial enantiomeric excess needed for each amplification cycle would have racemized and mixed over time.

In this series, we have been evaluating various proposals from the Origin of Life (OoL) community on how a small enantiomeric excess (e.e.) of D- or L-amino acid (AA) could have been amplified naturally. In other words, a mixture already contained an excess of one enantiomer, and a method was proposed on how it might have been locally enriched. For two enantiomers, L and D, % enantiomeric excess (e.e.) is defined as (L – D)/(L + D) × 100.

One hypothesis for creating e.e. postulates preferentially extracting more of the desired enantiomer in some manner. Another hypothesis involves removing as much racemic mixture as possible, thereby concentrating the AA already present in excess. The total and average amount of D- and L-AA throughout nature would remain unchanged, but the goal is to separate the initial excess of L into another location. The fundamental question is whether the proposed methods leading to enrichment would occur naturally.

Enantiomeric amplification in the crystal phase

Pre-existing e.e. of AAs dissolved in water can sometimes be separated if racemic DL crystals are more or are less soluble than the homochiral crystals.[1–3] Of the 19 proteinogenic amino acids containing an *α*-chiral carbon, two (threonine and asparagine) crystallize as conglomerates of distinct D and L crystals in equal amount.[4–6] Isovaline, which is not part of the genetic code, has been identified in meteorites[7] and also forms conglomerates of mixed D and L crystals.[4] If an excess of the L enantiomer is present in solution, then slow cooling will cause the L crystal to crystallize first. If these crystals could be carefully separated before large amounts of D or racemic crystals form, then an e.e.$_L$ would be obtained.

Extracting enriched L-AA crystals in this manner would work for only two biological AAs, and the precisely controlled conditions necessary indicate that this would not occur naturally. Worse, nothing would prevent enriched L-AA crystals from redissolving later. If they never dissolved, they would have remained in crystal form and therefore be irrelevant for OoL speculations.

Enantiomeric amplification in the solution phase

The other seventeen biological AAs having D and L enantiomers form racemic crystals; i.e., the individual crystals contain the same amount of D and L enantiomers. Therefore, if a solution begins with an excess of L-AA and is carefully cooled so that DL racemic material crystallizes from solution, then the supernatant solution will be enriched in L enantiomer. The maximum ratio of L/D in the original solution for which the racemic crystal would still form first will determine the highest solution e.e.$_L$ attainable. Klussmann *et al.* called this the *eutectic point* for that AA at 25°C.[8,1,9] At higher L/D ratios, racemic crystals won't form first, so solution e.e. cannot be further enriched.

In experiments reported by Klussmann *et al.*, saturated aqueous AA solutions containing 0 to 100% e.e.$_L$ were stirred for several hours or days at 25°C, producing the results

Table 1. Distribution of D- and L-histidine in water at 25°C, beginning with an excess of L. Data from ref. 1 supporting information.

No.	e.e.$_0$(%) [a]	e.e.$_{solution}$(%) [b]	[His] [c]	[L-His] [d]	[D-His] [d]	[His] (mg/g) [e]
1	0	0.4	1.78	0.89	0.89	15.4
2	65.4	76.3	2.78	2.45	0.33	24.1
3	94.9	91.9	4.58	4.39	0.19	39.6
4	83.4	92.4	4.83	4.65	0.18	41.8
5	94.9	94.9	4.75	4.63	0.12	41.1
6	100.0	100.0	4.66	4.66	0	40.3
7 [f]		93.7	4.79	4.64	0.15	41.5

[a] Initial e.e. before crystallization; [b] e.e. measured in solution after equilibration and formation of some racemic crystals; [c] total solution concentration in 10^{-3} molar fractions; [d] solution concentration of pure enantiomer in 10^{-3} molar fractions; [e] total solution concentration in mg/g solvent; [f] average eutectic, experiments 3 and 4 according to the paper. Experiments 4 and 5 were probably meant.

Table 2. Distribution of D- and H-isoleucine in water at 25°C, beginning with an excess L-enantiomer. Data from ref. 1 supporting information.

No.	e.e.$_0$(%) [a]	e.e.$_{solution}$(%) [b]	[His] [c]	[L-His] [d]	[D-His] [d]	[His] (mg/g) [e]
1	0	0.4	1.78	0.89	0.89	15.4
2	65.4	76.3	2.78	2.45	0.33	24.1
3	94.9	91.9	4.58	4.39	0.19	39.6
4	83.4	92.4	4.83	4.65	0.18	41.8
5	94.9	94.9	4.75	4.63	0.12	41.1
6	100.0	100.0	4.66	4.66	0	40.3
7 [f]		93.7	4.79	4.64	0.15	41.5

[a] Original e.e. before crystallization; [b] e.e. measured in solution after equilibration and formation of some racemic crystals; [c] total solution concentration in 10^{-3} molar fractions; [d] solution concentration of pure enantiomer in 10^{-3} molar fractions; [e] total solution concentration in mg/g solvent; [f] average eutectic, experiments 4 and 5.

shown in table 1 and table 2. Samples from the liquid phase were analyzed over time (after stirring for a few hours or days) using RP-HPLC (reverse phase high-pressure liquid chromatography) until equilibrium was established.[1] The solution e.e. was then measured and compared to the initial e.e. (see table 1, table 2, and figure 1).

The saturated data points were used to create ternary phase diagrams (see figure 1). If a eutectic point existed, it would lie on the phase diagram curve.

The average of experiments 3 and 4 in table 1 is not 93.7% as reported, and presumably the researchers calculated the eutectic value from the average of experiments 4 and 5. Perhaps they discarded experiment 3 since the e.e. decreased with respect to the initial e.e. of the saturated solution when equilibration was complete.

The data in table 2 provide another example of the experimental concept. The researchers only tested an excess of L-AA and assumed quite reasonably that the D-AAs would provide the mirror image results in the phase diagrams.

Klussmann and collaborators provided a summary of the eutectic points they found for various biological AAs, as shown in table 3.[8]

Klussmann *et al.* also used the solubility ratio α [1] of AAs to predict the eutectic points reasonably well.[10]

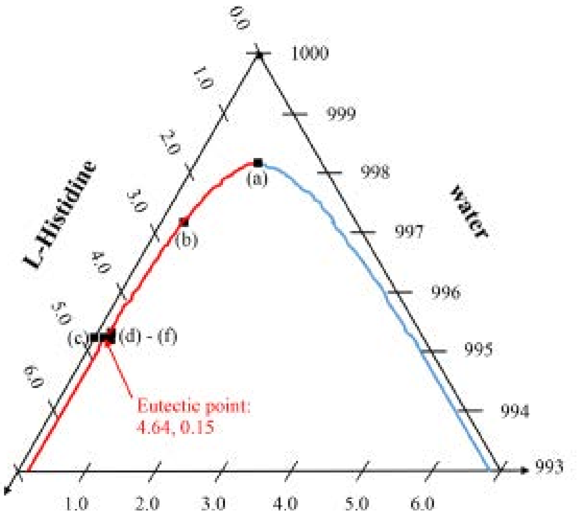
$$\alpha = [\mathrm{rac}]/[\mathrm{ep}] \qquad [1]$$

where [rac] and [ep] are the solubility of racemic and enantiopure mixtures.

The enrichment concept proposed was that even if the solution e.e. should be initially small, if racemic crystals could be removed through careful cooling, the solution would be enriched. By repeating this process several times, the e.e. at the eutectic point could be achieved.

Critique of these studies

- Only two of the nineteen relevant AAs could be theoretically enriched to beyond an e.e. of 90%. Almost all would have remained unsuitable for biological purposes.[11]
- Stirring was required at a fixed temperature for some days to produce the crystals.
- The crystallization process would have required a large initial enantiomer excess in saturated concentration levels of AAs, completely unrealistic to have occurred naturally.
- In nature, cooling would have had to occur very slowly and then cease at just the right time before the homochiral crystals would begin to form.
- The liquid phase and crystals would somehow have to have completely separated from each other. The researchers deliberately began the next cycle with manually separated enantiomerically enriched solutions. How is this supposed to have occurred naturally? The solution phase would have mixed eventually with racemic AA dissolved elsewhere. In addition, the enriched solution phase and racemic crystals would have subsequently encountered rainwater, snow, hail, tides, dew, groundwater, water vapour, etc., leading to remixing.
- The theoretical maximum number of DL crystals would not have been removed each cycle; nor would both phases have been 100% separated naturally, as was done in the experiments. The *total amount* of extra L-enantiomer present in the solution phase at the end of each cycle would have steadily decreased, ending in insignificant amounts at any location. The researchers, however, concentrated L-enantiomer in one location by beginning each cycle with a new prepared solution having the eutectic e.e.$_L$.
- Over geologic time, the racemic crystals would have had countless opportunities to redissolve, in particular due to temperature fluctuations. A single remixing event could have undone the effects of multiple enrichment cycles. Even neglecting contamination with AAs from the environment, remixed AAs possessing an e.e.$_L$ would have then been more likely to precipitate together, given the difficulty of forming only DL crystals. Furthermore, evaporation of the water would have occurred. In these more plausible scenarios, pure L would not have been separated to become available for prebiotic chemistry.
- The higher the e.e.$_L$ achieved, the more difficult it would have become in subsequent cycles to naturally remove racemic crystals. With no rapid stirring it would have become ever easier for homochiral crystals to accompany the racemic ones, given that L–L interactions would have been statistically so much more likely to form than L–D ones. The researchers used saturated solutions at a fixed 25°C to facilitate equilibration between the two phases. In nature, indiscriminate cooling, such as during night time or winters, would not have continually extracted only pure racemic crystals.



Initial concentrations of L-His and D-His in the solution phase:
(a) 0.89, 0.89
(b) 2.45, 0.33
(c) 4.66, 0.0
(d) – (f) 4.39, 0.19; 4.65, 0.18; 4.63, 0.12
Based on data and a diagram in ref. 1.

Figure 1. Ternary phase diagram of histidine in water at 25°C constructed with L-enantiomer in excess (red). The mirror image was predicted (blue).[1]

Table 3. Solution enantiomeric excess at the eutectic point in water at 25°C for some proteinogenic amino acids.[8]

Amino acid	e.e. of solution at eutectic (%), 25 °C, in water
Threonine	0
Valine	46
Alanine	60
Phenylalanine	83
Methionine	85
Leucine	87
Histidine	93
Serine	>99

- Under natural, instead of guided, conditions, any theoretical enriched solutions combined would have remixed over long time periods during which any e.e. built up would have racemized.

Modification of eutectic composition via additives

Laboratory experiments demonstrated that co-crystallization of some small molecules with AAs could alter the

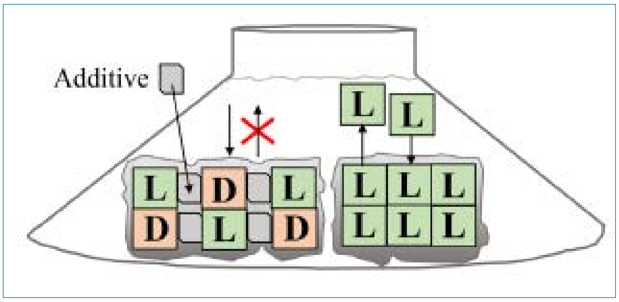


Figure 2. A co-solvate can sometimes enrich an initial enantiomeric excess in the solution phase by decreasing the solubility of the racemic compound. An example is the incorporation of CH_3Cl into DL proline crystals.[12]

Table 4. Solution enantiomeric excess at the eutectic for amino acids in aqueous solution in the presence of carboxylic acid additives at 25°C. The row labelled 'none' shows e.e. values without the carboxylic acid additive for comparison purposes.[10] D or L % enantiomeric excess effects were assumed to be symmetric.

	% e.e. at the eutectic Amino acid							Average Δe.e.
Additive	thr	val	Ile	met	phe	leu	his	
none	0	47	52	85	88	88	94	—
oxalic acid	50	66	82	43	23	98	63	−4.8
malonic acid	11	50	51	69	86	91	91	−0.8
succinic acid	2	93	52	42	79	89	56	−6.8
maleic acid	34	69	71	55	7	81	82	−9.2
fumaric acid	24	99	59	72	99	92	98	14.8
adipic acid	0	48	51	66	94	92	77	−4.3
							Average:	−2.0

relative heterochiral/homochiral solubility and thus tune the eutectic composition.[1,10] For example, when valine co-crystallized with fumaric acid, its eutectic increased from 46% to 99% e.e. Similarly, proline's eutectic composition increased from 50% to 99% e.e. when chloroform co-crystallized with the racemic compound, see figure 2.

Modification via additives

More than 80% of known chiral compounds crystallize as racemic mixtures instead of individual enantiopure solids. Therefore, the resolution of a chiral compound generally requires chiral acids or bases to form diastereomers with differing solubilities or methods to inhibit crystallization of the racemic compound.[13]

When a small e.e.$_L$ of an AA is dissolved, preferential precipitation of racemic crystals will automatically increase the e.e. of the solution phase. Separation of the just enriched solution followed by further precipitation of more racemic crystals will further increase the e.e. In the ideal case, enrichment of the solution could be steadily increased until the eutectic composition of D and L is reached. At that point, any more L present would be counterproductive, leading to L crystals precipitating first instead of racemic ones.

Sometimes solvent molecules can be incorporated into the crystal using hydrogen bonding to form solid structures known as solvates. In rare cases, mixed DL-AAs and added solvent molecules will be especially stable and thus less soluble in water. Therefore, solutions containing an initial excess of D- or L-enantiomer could be enriched in the liquid phase by crystallizing racemic mixtures.[10]

A series of molecules of putative prebiotic relevance were tested by Klussmann *et al.* to determine whether the e.e. of the eutectic is modified. They reported that

> "Neither urea nor thiourea, nor any of a series of heterocyclic bases (cytosine, guanine, thymine, or uracil) had any effect on amino acid eutectic ee values in aqueous solution."[10]

An effect was found for some dicarboxylic acids though, see table 4.

In these experiments, typically ~50% e.e. of the AA being tested was combined with various proportions of additive at 25°C in aqueous solutions. The eutectic point represents the proportion of additive with AA leading to the highest % e.e. in the solution phase. Some additives lowered the AA solubility of pure D, pure L, and the DL racemic mixture, but of special interest was when the depression was greater for the racemic crystals.

In the case of threonine (thr) in table 4, the eutectic point contained no excess of L, meaning D and L were present in identical amounts. Beginning with more L than D in solution would have reduced the e.e. after crystallization, since for thr these crystals would be all L instead of racemic. But all the dicarboxylic acids shown in the table raised the eutectic point % e.e. of thr or had no affect (i.e., adipic acid), so now enrichment of the solution phase could occur by precipitating racemic crystals instead. This poses the obvious dilemma for the OoL community that the exact opposite effect would occur when the initial excess would be of D-thr.

The authors claimed

> "… that the eutectic ee can change significantly in the presence of some acids, with solution enantioenrichment observed in many cases, except for methionine and histidine."[10]

This is a somewhat misleading claim. In 12 cases (yellow boxes in table 4) the authors believe enantiomeric *enrichment* in solution occurred (being outside of measurement error) but we see that a *depletion* in e.e. was reported for thirteen cases (blue boxes in table 4).

Using all the data reported, one finds that the average e.e. in the presence of dicarboxylic acids was actually −2%,

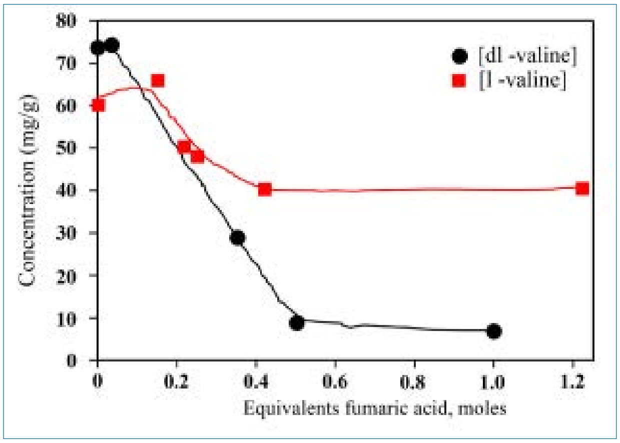


Figure 3. Solution concentration of valine as a function of equivalents of fumaric acid added: (O) L-valine; (●) DL-valine. Figure redrawn from a diagram in ref. 10.

see table 4, rightmost column. The outcome of multiple 'enrichment' cycles would have produced a *lower* final e.e. than without the additives. Suppose that only one of the dicarboxylic acids had been present, would this help? No, from the rightmost column of table 4 we see that for all the additives except fumaric acid the net effect is to *decrease* the eutectic point. Furthermore, it would be unhelpful to explain the origin of only L biological AAs if an additive able to increase the eutectic point of some AAs would simultaneously decrease it for other ones.

The team found that enantiopure and racemic valine both produced crystals with fumaric acid using hydrogen bonding in a 2:1 ratio and that enantiopure and racemic phenylalanine produced crystals with fumaric acid in a 1:1 ratio.[10] As shown in figure 3, at least ~20% as much fumaric acid as valine on a molar basis had to be present to obtain a discernible shift in eutectic at all, and valine displayed the strongest effect; i.e., the eutectic of 47% e.e. with no additive was increased to 99% with fumaric acid.

Solution phase enantioenrichment resulted when the solubility of the racemate was strongly suppressed relative to that of the enantiopure system. It is important to emphasize that racemic valine crystal solubility was lower under these conditions than the homochiral crystals *only* when ~20% or more moles of the solution was fumaric acid (see figure 3).

As explained above, higher eutectic points would have permitted higher e.e. to be achieved if repeated crystallization and decanting were carried out, in each case after carefully isolating the solution phase. The OoL notion was that cycles of rain and evaporation might have occurred in pools containing AAs and appropriate hydrogen-bonding partners if an $e.e._L$ of the AA had been present initially. But how would this work? Evaporating the contents of a pool of water and then redissolving with new water would not change anything. The slightly enriched solution would have to be separated from the racemic crystals formed. But this necessary mobility of the solution phase would surely have diluted it with racemic AA found throughout nature. The racemic crystals formed would eventually also tend to redissolve over time.

Another obvious fact is that rainwater would dilute any other co-solvents present. Furthermore, multi-additive systems such as described above allegedly mimic the complex mixtures extracted from meteorites, including the dicarboxylic acids shown in table 4, but in nature the mixtures would have been vastly less concentrated.

Critique of these studies

- The proposed enantiomer enrichment mechanism would apply to only about a third of the biological AAs, and in almost all cases the best theoretical outcome would have produced too low an e.e. to be biologically useful.
- In about half the cases the eutectic would be lowered instead of raised, decreasing the maximum e.e. achievable for those AAs. However, to form viable proteins all the biological AAs except glycine would have to have been present in L form only.
- DL crystallization would have required considerably higher aqueous concentrations of AAs than expected to form under abiotic conditions. Bada estimated that the maximum concentration of AAs in ancient oceans would have only been about 10^{-8} g/l, which corresponds to a concentration of ~10^{-10} M.[14]
- Unrealistic high concentration of co-solvents like fumaric acid (the most promising additive found) was necessary to obtain a discernable shift in eutectic. Although the enrichment cycles could allegedly occur under natural conditions through partial redissolving with rainwater, followed by desiccation, this would have diluted the co-solvent throughout all the cycles.
- Enriched solutions would eventually have had to be translated far from the racemic crystals to avoid remixing, somewhere amenable to further relevant biochemical reactions.
- Desiccation would have produced a slurry of chemicals with very little AA present instead of pure racemic AA crystals.
- The slurry would not have been carefully cooled, nor a stirring mechanism have been provided by nature, to optimize the separation of DL and enantiopure crystals. During some cycles, very little racemic crystal might have precipitated; other times, a considerable number of the L crystals might have formed, but often some, or all, the material would have redissolved. Obtaining enriched solutions somewhere by chance would have required an enormous number of trials-and-errors during which much could have gone wrong, such as contamination with close to racemic AAs.
- A more plausible scenario would assume an initial $e.e._L$ of ~2% in the initial solution instead of ~50%, and a much lower amount of diacid in the aqueous solution, mixed with many other chemicals. Obtaining >50% e.e. solutions

under such more plausible natural conditions is not credible. During the endless cycles of forming and dissolving these slurries over vast time periods, any putative increase in e.e. would have simply accelerated the L → D enantiomeric inversion, eliminating the original L excess.

Final comments

These papers illustrate a common principle found in OoL publications, discussed by Truman in this journal.[15] Experiments were executed under conditions that could not have occurred naturally, which the researchers knew were most likely to produce the desired results. Using realistic conditions would have consumed considerable research time, but nonetheless it would have been easy to perform some experiments which permitted extrapolation towards realistic conditions. The optimized results were claimed to support the possibility of abiogenesis, but this is not what objective evaluation of the data suggests. Experiments discussed above can be used to illustrate this principle.

Saturated AA solutions of ca. 10^{-3} M were used.[1] However, Basa estimated AAs in prebiotic oceans would have concentrations of about 10^{-10} M.[14] Stirring of a saturated AA solution at a controlled fixed temperature of 25°C maximized separation of racemic from homochiral crystal by facilitating rapid equilibration. Why were no experiments reported at lower initial AA concentrations, like 10^{-4} M (still a factor of 10^6 too high), with no stirring and using cooling cycles instead of a fixed temperature to reflect day vs. night temperatures and winter vs summer cycles? If after perhaps a year the researchers obtained no crystals, nor change in e.e., then this should have been reported and its significance for OoL purposes evaluated.

Other conditions should also be modified. Starting with absurdly high concentrations of dicarboxylic acid in water saves research time, but what happens at more realistic concentrations, like 1% – 10% of those used? Rainwater, tides, dew, etc. would have diluted the initial dicarboxylic acid and also during the subsequent cycles. Furthermore, AAs and dicarboxylic acids concentrated through evaporation would have been mixed with many other chemicals. Would pure racemic AA crystals form upon desiccation, or rather an amorphous slurry having no change in e.e.? Experiments could have been carried out by including many of the chemicals that the researchers reported as not affecting the eutectic. These chemicals dissolve in water and allegedly would have also been present under abiogenesis conditions.

Ironically, time is the evolutionists' great enemy, as these multiple parameter adjustments made to reflect a more plausible natural setting would have dramatically hindered selective loss of racemic AA crystals from a solution. During the immense time intervals, the e.e. would have racemized and would also have mixed with racemic AA from elsewhere.

References

1. Klussmann, M., White, A.J.P., Armstrong, A., and Blackmond, D.G., Rationalization and prediction of solution enantiomeric excess in ternary phase systems, *Angew. Chem. Int. Ed.* **47**:7985–7989, 2006 | doi:10.1002/anie.200602520.
2. Breslow, R. and Levine, M., Amplification of enantiomeric concentrations under credible prebiotic conditions, PNAS **103**:12979–12980, 2006 | doi:10.1073/pnas.0605863103.
3. Breslow, R. and Cheng, Z-L., On the origin of terrestrial homochirality for nucleosides and amino acids, PNAS **106**:9144–9146, 2009 | doi:10.1073/pnas.090435010.
4. Viedma, C., Enantiomeric crystallization from dl-aspartic and dl-glutamic acids: implications for biomolecular chirality in the origin of life, *Origins Life Evol. Biosph.* **31**:501–509, 2001 | doi:10.1023/a:1012790523136.
5. Ref. 8 claims the two exceptions are threonine and arginine.
6. Tarasevych, A.V., Sorochinsky, A.E., Kukhar, V.P. and Guillemin, J-C., Deracemization of amino acids by partial sublimation and via homochiral self-organization, *Orig. Life. Evol. Biosph.* **43**:129–135, 2013 | doi:10.1007/s11084-013-9333-6.
7. Glavin, D.P., Elsila, J.E., McLain, H.L. *et al.*, Evidence for extraterrestrial l-amino acid excesses in the CM2 Aguas Zarcas and Murchison Carbonaceous Chondrites: predictions for Ryugu and Bennu, *51st Lunar and Planetary Science Conference*, 2020.
8. Klussmann, M., Iwamura, H., Mathew, S.P., Wells, D.H. Jr, Pandya, U., Armstrong, A., and Blackmond, D.G., Thermodynamic control of asymmetric amplification in amino acid catalysis, *Nature* **441**:621–623, 2006 | doi:10.1038/nature04780.
9. Chemists almost always used the term 'eutectic' in a different manner; see Eutectic, britannica.com. This makes Klussmann's papers difficult to understand.
10. Klussmann, M., Izumi, T., White, A.J.P., Armstrong, A., and Blackmond, D.G., Emergence of solution-phase homochirality via crystal engineering of amino acids, *J. Am. Chem. Soc.* **123**:7657–7660, 2007 | doi:10.1021/ja0708870.
11. Truman, R., Racemization of amino acids under natural conditions: part 1—a challenge to abiogenesis, *J. Creation* **36**(1):114–121, 2022.
12. Blackmond, D.G., The origin of biological homochirality, *Cold Spring Harb. Perspect. Biol.* **11**:a032540, 2019 | doi:10.1101/cshperspect.a032540.
13. Jacques, J., Collet, A., and Wilen, S.H., *Enantiomers, Racemates and Resolution*, Krieger Publishing Company, Melbourne, FL, 1991.
14. Bada, J.L., Amino acid cosmogeochemistry, *Phil. Trans. R. Soc. Lond. B* **333**:349–358, 1991 | doi:10.1098/rstb.1991.0084.
15. Truman, R., 'Cleaning up' and analyzing small data sets can distort conclusions, *J. Creation* **36**(2):66–71, 2022.

Royal Truman *has bachelor's degrees in chemistry and in computer science from State University of New York; an M.B.A. from the University of Michigan (Ann Arbor); a Ph.D. in organic chemistry from Michigan State University; and a two-year post-graduate 'Fortbildung' in bioinformatics from the Universities of Mannheim and Heidelberg. He works in Germany for a European-based multinational.*

Chris Basel *has a bachelor's degree in chemistry from William Jewell College, a master's degree in analytical chemistry from the University of Kansas, and a certificate in ADMET Process (pharmacology) from the University of California-San Diego. He worked as a research manager in the pharmaceutical industry for 30 years and now serves as an associate professor of chemistry and department chair at a Christian university in Missouri.*

Late Pleistocene body size reduction: evidence of a post-Flood decline in longevity?

Jake Hebert

Even after the Flood, the Genesis patriarchs routinely experienced lifespans of hundreds of years (Genesis 11). Hence, biblical creationists should be interested in possible scientific corroboration for this extreme longevity. Whatever factor or factors enabled extreme human longevity also likely enabled greater animal longevity. Longevity studies have shown that greater longevity is often associated with larger adult body sizes and prolonged intervals of maturation. Hence, one might expect longer-lived people and animals to be larger than those with shorter lifespans. Thus, the ubiquity of giantism in the fossil record is noteworthy, as is evidence of decreasing body sizes during and after the post-Flood Ice Age. This evidence of body size reduction is worldwide and especially strong for mammals, but there is some evidence for body size reduction in other taxa. Because Pleistocene giantism was found even in places far from the high-latitude ice sheets, Bergmann's rule, in and of itself, is likely an insufficient explanation. Because of the body size/longevity link, body size reduction is likely indirect evidence of declining longevity in the immediate post-Flood world.

Ancient humans routinely experienced lifespans of hundreds of years (Genesis 5 and 11), and creationists should be interested in possible scientific corroboration of this great longevity. Greater longevity in animals is often associated with larger adult body sizes and prolonged maturation intervals.[1,2] The larger one's adult body size and the greater the amount of time to attain that adult body size, the longer one's lifespan will tend to be. Equivalently, reduced longevity is associated with smaller adult body masses and shorter maturation intervals (figure 1).

Most of the studies linking longevity to body size and maturation time have included organisms from across multiple higher taxonomic groupings; for example, families, classes, and/or orders within the Linnaean classification system. But of much greater interest to creationists is whether these trends hold *within* a particular Genesis 'kind' or baramin. Suppose a member of a particular baramin were raised under conditions that somehow caused it to attain to a much larger body size than other members of its baramin, and over a much longer time interval. Would the larger creature live longer?

The Genesis kind likely corresponds to the Linnaean genus or family.[3] Hence, intra-species or intra-genus longevity-size correlations are almost guaranteed to apply within a Genesis kind. Though it is not as abundant, some such intra-species and intra-genus correlations do exist and are discussed in other papers.[1,2] Also, a theory of ontogenetic growth predicts that the age at skeletal maturity, t_{maturity}, should be proportional to adult body mass, M, raised to the one-fourth power:[4]

$$t_{maturity} = kM^{1/4} \qquad (1)$$

The derivation of Eq. (1) implicitly assumes that environmental conditions are held constant. So a change in those conditions could change the age at maturity, with a corresponding change in adult body mass, *M*.

Eq. (1) is in agreement with observations that biological timescales in general tend to be proportional to body mass raised to the ¼ power.[5–7]

Creationists have long noted the ubiquity of giantism in fossil creatures, and some have suggested a link between this giantism and longevity.[8–15] Eq. (1) and the observations linking greater longevity to greater ages at maturity provide that linkage.

In this light, it is striking that 65 is the earliest age at which a Genesis 5 patriarch is listed as having a son (Genesis 5:15, 21). Although Genesis does not tell us whether or not the listed sons were firstborn, it seems likely that at least some of them were. Given the strength of the human sex drive, it seems very unlikely that the Genesis patriarchs were all deciding to postpone marriage for five decades! It is far more likely that they were becoming sexually mature at much greater ages than do humans today. Given the above discussion, one would expect very long-lived humans to take a greater amount of time to mature than humans with shorter lifespans. But this immediately begs another question: *Were ancient humans bigger than we are?* We briefly return to this question in the concluding remarks.

General evidence for post-Flood body reduction

If extant versions of creatures are smaller than the fossil versions, then it is obvious that a reduction in size *must* have occurred, even if that reduction is not necessarily documented

Figure 1. Greater longevity is often positively correlated with greater adult body masses and longer maturation intervals. Likewise, one would expect reduced longevity to be associated with smaller body masses and shorter maturation intervals.

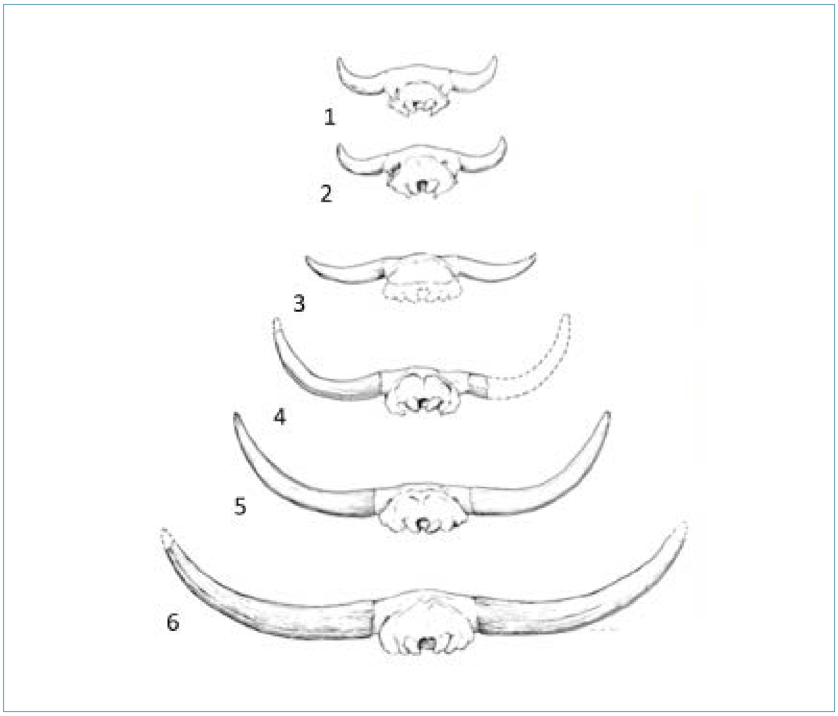


Figure 2. Diminution of Pleistocene and Holocene North American bison horn sizes. In reverse numerical and stratigraphic order, these are (6) *Bison latifrons* (classic phase), (5) *Bison latifrons* (advanced phase), (4) *Bison alleni*, (3) *Bison antiquus barbouri*, (2) *Bison antiquus taylori* (advanced phase), and (1) the modern *Bison bison bison*. From figure 2 in Schultz and Hillerud (1978). '[F]ree and open access' provided by the Nebraska Academy of Sciences at DigitalCommons@University of Nebraska-Lincoln.

in the fossils themselves. However, in many cases the size reduction *is* revealed in the fossils. This paper describes both: general evidence for giantism and evidence that this giantism diminished or disappeared after the Flood.

There is very strong evidence for a 'high' Flood/post-Flood boundary in the rocks; generally speaking, high or higher than the Mid-Pleistocene.[16–19] For this reason, this study confines itself primarily to evidence of body size reduction that occurred, by evolutionary reckoning, in the Late Pleistocene or Holocene. However, I also agree with Oard[20] that Ice Age deposits will not necessarily always be classified as 'Late Pleistocene' on the uniformitarian timescale. Thus, a more thorough review of the stratigraphy surrounding the examples cited below could result in the removal of some of these examples, as well as the addition of some examples not included here.

Body reduction size in mammals

North America

Alaskan horse metacarpal bones decreased in length by 13.5% during the Late Pleistocene, implying a 'dramatic' and 'unexpected' body size decline prior to their extinction.[21] Likewise, North American bighorn sheep are apparently the direct descendants of larger fossil sheep that underwent a body size reduction:

> "A direct ancestor-descendant relationship between modern and the fossil sheep in North America seems probable. Reduction of body size seems likely to have occurred at the end of Pleistocene or the beginning of Holocene time."[22]

Bighorn sheep are found in the North American great plains, and Oard has recently argued that Great Plains fossils may be Flood, rather than post-Flood.[20] In any case, morphological shrinkage of North American Bighorn sheep has occurred, and the same is true of North American bison, although there is disagreement among evolutionary scholars about the details.[23]

Extant North American bison (*Bison bison*) are comprised of the plains bison (*B. bison bison*) of the Great Plains and the wood bison (*B. bison athabascae*) of Canada and Alaska. Morphological shrinkage for the plains bison is illustrated[24] in figure 2. Although some of the variation in horn size depicted in figure 2 could represent mere in-kind variation, analysis of post-cranial bison fossil data also implies that a true body size reduction did occur.[25] The bison shown in figure 2 are in stratigraphic sequence, although evolutionists do not necessarily believe all the bison shown are in a direct lineage.

A giant version of the steppe bison *Bos priscus* (figure 3) is thought to have come to North American from Eurasia via the Bering Land Bridge, becoming the ancestor of *B. latifrons*. Some claim that *B. antiquus* is descended from *B. latifrons*, as is *B. occidentalis*.[26] In turn, extant bison *B. bison* are descended from *B. antiquus*,[27] possibly via hybridization with *B. occidentalis*:

> "Likely, *B. antiquus* and *B. occidentalis* did not go extinct, but through phenotypic and morphologic adaptation to changing climatic conditions, evolved into what is traditionally referred to as *B. bison* that we have throughout the Holocene … ." [28]

Interestingly, Late Pleistocene fossils of smaller *B. priscus* bison are also found in North America, suggesting that this larger steppe bison also became smaller over time.[29]

The Pleistocene and Holocene glyptodont *Doedicurus* sp. was a one-ton armadillo-like creature (figure 4), recently shown by DNA analysis to actually be a *genuine* armadillo.[30,31] Late Pleistocene North America was home to the giant beavers *Castoroides dilophidus* and *Castoroides ohioensis*. Despite their claim that modern and giant beavers were unrelated, evolutionists have acknowledged, "Even so, the shapes of their bones look a lot like those of a modern beaver, only much larger."[32]

Europe and Asia

Fossil evidence implies the extant wild boar (*Sus scrofa*) underwent a Holocene or Late Pleistocene body size reduction in both Italy and Japan.[33,34] The European badger (*Meles meles*) in southern Italy also apparently became smaller in size during the Late Pleistocene.[35] Walvius noted that western European red deer are about one third smaller than their 'neolithic' forebears.[36]

The Middle to Late Pleistocene *Palaeoloxodon namadicus* from India[37]

Figure 3. A mummified steppe bison on display at the University of Alaska's (Fairbanks) Museum of the North.

Image: Bernt Rostad, Wikimedia / CC BY 2.0

Figure 4. Glyptodon (*Doedicurus*) museum display in Brazil

Image: Wilson Dias/Abr, Wikimedia / CY BY 3.0 BR

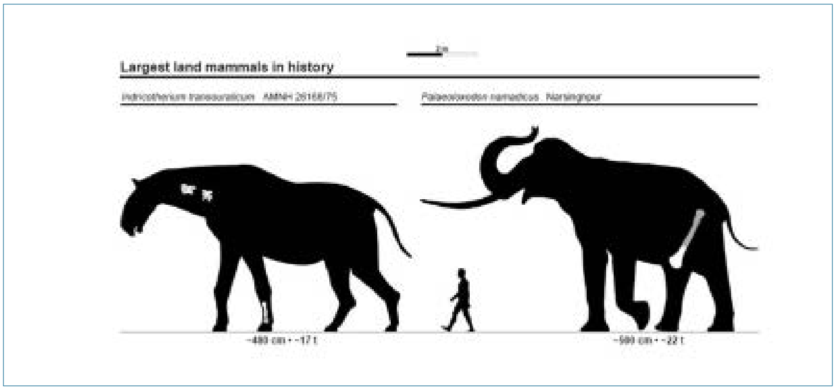


Figure 5. The estimated size of the elephantine *Palaeoloxodon namadicus* compared to an extant human. The Oligocene mammal *Indricotherium transouralicum*, thought to be the largest mammal that ever lived, is also shown.

Image: A. Larramendi, Wikimedia / CY BY SA 4.0

Image: DiBgd, Wikimedia / CY BY SA 3.0

Figure 6. Life reconstruction of Miocene South American megafauna, including the giant ground sloth *Megatherium*, with two glyptodons in the foreground and the giant teratorn *Argentavis* in the background. Although *Argentavis* is thought to have become extinct in the Miocene, glyptodons and Megatherium are thought to have survived until the Late Pleistocene.

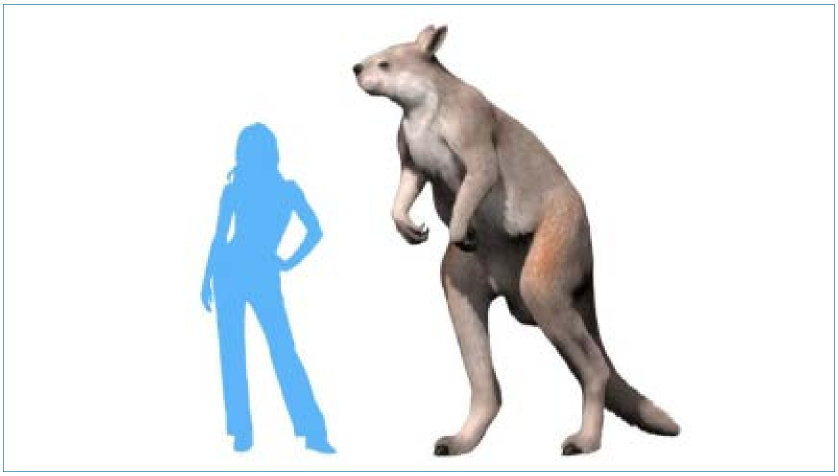


Image: Nobu Tamura, Wikimedia / CY BY SA 4.0

Figure 7. The giant short-faced kangaroo *Procoptodon goliah* compared to an extant woman.

is clearly a member of the Genesis 'elephant kind', but it was much larger than extant elephants (figure 5), and the giant beaver *Trogontherium cuiveri* lived in Late Pleistocene China.[38]

Davis (1981) cites evidence that on the uniformitarian timescale the majority of large animals in Israel, including foxes, wolves, boars, aurochs, and goats, became smaller 12,000 years ago, and some animals then underwent another size reduction due to domestication.[39]

In 2006 bones of an enormous Late Pleistocene camel, "double the size of a modern-day camel" were unearthed near the village of El Kowm in Syria.[40] In the Late Pleistocene, giant camels lived in Mongolia,[41,42] and the giant ape *Gigantopithecus blackii* is thought to have inhabited Southeast Asia.[43] In passing it is worth noting that fossils of giant camels have also been found in North America, although these specimens are found in rocks that may be from the Flood.[44]

South America

Although South America has no extant megafauna, many large mammals existed in Pleistocene South America that can aptly be called giants:

> "Bears, sabertooth cats, enormous capybaras, and llamas roamed across South America, as well as other bizarre creatures including massive terrestrial sloths, armored glyptodonts (hippo-sized animals closely related to armadillos), and peculiar animals reminiscent of camels and rhinoceroses (macrauchenids and toxodonts). These enigmatic animals were decimated during the Quaternary—all South American mammal species larger than 100 kg were lost. The mystery surrounding their extinction has yet to be fully resolved, and is a topic of considerable debate ... ."[45]

These extinct South American megafauna, thought to have survived until the mid-Pleistocene or Holocene, include the giant ground sloth *Megatherium*[46] and the giant glyptodon armadillos[47] (figure 6).

Africa

Pleistocene and early Holocene Africa, too, had larger versions of extant creatures, including the bovine *Megalotragus*, with body similarities to the extant hartebeest and wildebeest in the bovid subfamily *Alcelaphinae*.[48] It is not difficult to imagine that *Megalotragus* was simply a larger ancestor of these smaller extant alcelaphines. Pleistocene Africa was home to other megafauna, such as *Dinopithecus ingens* ('gigantic terrible ape') twice the size of an extant baboon,[49] the East African lion *Panthera leo*,[50] and the giant Olduvai buffalo *Pelorovis oldowayensis*.[51] These last three examples are Early- or Mid-Pleistocene and thus may represent Flood fossils. However, it is not difficult to imagine that extant African species are descended from these larger animal forms. Moreover, Beasley suggested that evolutionists could be mistaking giant African fossil apes for alleged 'ape-men'.[12]

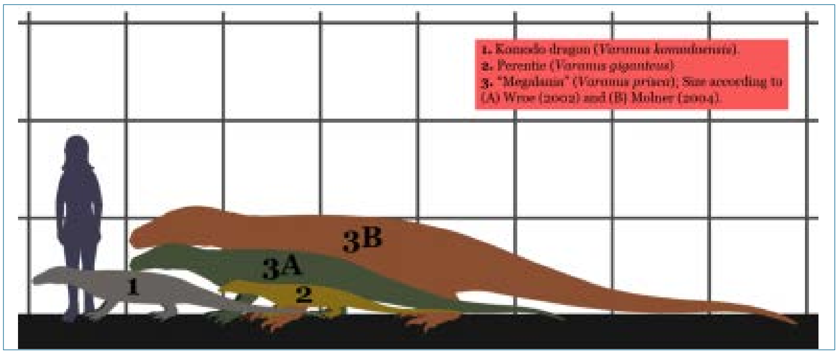


Figure 8. Two body size estimates (3A and 3B) for the Late Pleistocene giant monitor lizard *Varanus prisca*, compared to the extant (1) Komodo dragon *Varanus komodoensis*, and the extant (2) *Varanus giganteus*.

Image: Conty, Wikimedia / CY BY 3.0

Australia

Some Australian megafauna are likely the ancestors of smaller extant fauna. Oard and Arment agree that Australian marsupial fossils (excluding those from the early Cenozoic) are post-Flood.[20,52,53] These included the giant wombat *Phascolonus gigas*. Extant wombats still live in Australia, but they are much smaller. Australia was also once home to giant kangaroos, including the giant short-faced kangaroo *Procoptodon goliah* (figure 7), and *Macropus titan*, very similar to the extant eastern grey kangaroo, except for its 30% larger size.[54] The giant wallaby *Protemnodon anak*, named after the biblical giants the Anakim (Deuteronomy 2:11, 21, 9:2), also lived in Late Pleistocene Tasmania.[55]

In light of this worldwide data, it is hardly surprising that Davis wrote:

> "[Finnish paleontologist Björn] Kurtén (1965) discovered that most carnivores in Israel and Lebanon underwent a considerable size reduction at the end of the Pleistocene. The dwarfing of fossil mammal lineages at the end of the late Quaternary was *probably world-wide* [emphasis added]… ."[39]

Counterexamples

Of course, there are counterexamples to this trend. Mountain gazelles in the Levant apparently become larger from the Late Pleistocene to Early Holocene.[56] Likewise, aurochs (*Bos primigenius*) in Italy became smaller from the Late Pleistocene through to the Holocene, but this was preceded by an apparent *increase* in size from the Early to Mid-Pleistocene.[57] I believe this is likely an artifact due to the chaotic nature of the Flood, but it could be argued that this is evidence against this paper's thesis. Likewise, there are examples of island dwarfism during the Pleistocene,[58,59] including some examples from the Early and Mid-Pleistocene.[60] Likewise, Davis reported that recent gazelles in northern Israel were larger than Early Holocene specimens.[39] Nevertheless, a Late Pleistocene body size reduction seems to be the general rule.

Bergmann's Rule not an adequate explanation

Bergmann's Rule[61] asserts that mammals and birds, and perhaps other organisms, living at higher, colder latitudes tend to be larger than organisms living at lower latitudes, presumably as an adaption for conserving body heat. Since the Genesis Flood caused an Ice Age,[62] this seems at first glance to be a reasonable explanation for both large mammal body sizes during the Ice Age and the diminution of those body sizes as the Ice Age came to an end. However, Bergmann's rule is somewhat controversial[63] and is not a completely adequate explanation even if it is correct. Bergmann's rule can perhaps explain some post-Flood giantism, but it does not explain the pre-Flood giantism of creatures which both creationists and evolutionists agree were living under warmer climatic conditions, such as dinosaurs in the pre-Flood world. Nor does it explain, in the creation model, the large sizes of Ice Age animals living far from the high-latitude ice sheets, since the Flood Ice Age model posits a more equable climate.[64] It seems more likely that Bergmann's rule is a second-order effect modulating body size, with some other, more fundamental cause (increased longevity?), resulting in giantism in general.[65]

Body size reduction in other taxa?

There is some evidence that other taxa also underwent a size reduction toward the end of the Ice Age. The giant monitor lizard *Megalania* (or *Varanus priscus*) lived in Australia during the Late Pleistocene,[66] dwarfing even the extant *Varanus giganteus* and Komodo dragon *Varanus komodoensis* (figure 8).[67,68] South African fur seals, angulate tortoises and granite limpets underwent an apparent size reduction from the Middle Stone Age (250 to 200 ka) to the Later Stone Age (50 to 40 ka).[69] Likewise, the southern African tick shell, *Nassarius kraussianus*, used by early humans for ornamentation, decreased in size from the

Pleistocene to the Holocene, prompting evolutionists to ask, *Why were the shells of mankind's earliest ornament larger in the Pleistocene than in the Holocene?*[70]

Concluding remarks

Given the trends noted in the Introduction, a general decrease in animal body size makes sense if longevity was decreasing during the post-Flood Ice Age. This was suggested by Greg Beasley in this very journal more than thirty years ago:

> "The fossilised remains of both flora and fauna are, as a rule, significantly larger in the past than in their extant counterparts. One possible explanation for this 'shrinkage' over time is that the growth potential of living organisms has been impeded through **earlier maturation and declining longevity**; a consequence of changes in the prevailing biospheric conditions during the earth's recent past. It is proposed that these changes were brought about by, and as a consequence of, geophysical, atmospheric and biological changes, initiated during the Flood. The writer proposes that morphological shrinkage is *primarily a phenomenon of the post-Flood period, as was declining longevity and earlier skeletal maturation* [bold added, italics original emphasis]."[12]

I believe Beasley was absolutely correct. What is more, the budding field of sclerochronology is now providing both indirect and direct evidence in support of his proposal, only some of which has as of yet been discussed in the creation literature.[1,2]

It is worth noting that large and small animals are often found together at Late Pleistocene sites. [36,71,72] Carter has noted that very old members of a population tend to be far less numerous than younger members of that population.[73] Could it be that the smaller animals were juveniles living alongside the larger adults?

Of course, as noted at the beginning of this paper, this discussion absolutely begs the question, *Did humans, like animals, also undergo a body size reduction after the Flood?* There is *much* scientific and cultural evidence that they did, which I briefly discussed in a recent short article.[74] However, that subject deserves a much more in-depth treatment that must await a separate paper.

References

1. Hebert III, L., Allometric and metabolic scaling: Arguments for design … and clues to explaining pre-Flood longevity? in: *Proc. 9th ICC*, Cedarville University, OH, pp. 206–227, 2023.
2. Hebert, J., Sherwin, F.J., and Overman, R., *Crassostrea* oysters: evidence for extreme longevity in the pre-Flood world? CRSQ, in press.
3. Woodmorappe, J., *Noah's Ark: A feasability study*, Institute for Creation Research, Santee, CA, 1996.
4. West, G.B., Brown, J.H., and Enquist, B.J., A general model for ontogenetic growth, *Nature* **413** (6856):628–631, 2001.
5. Calder, W.A. III., *Size, Function, and Life History*, Harvard University Press, Cambridge, MA, 1984.
6. Lindstedt, S., Body size, physiological time, and longevity of homeothermic animals, *The Quarterly Review of Biology* **56**(1):1–16, 1981.
7. Schmidt-Nielsen, K., *Scaling: Why is animal size so important?* Cambridge University Press, Cambridge, 1986.
8. Woetzel, D., *Chronicles of Dinosauria*, Dobbs, R. illust., Master Books, Green Forest, AR, 2013.
9. Coppedge, D.F., Life is devolving from a past world of giants; crev.info, accessed 20 Mar 2023.
10. Nelson, V., *Monumental Monsters*, Untold Secrets of Planet Earth Publishing Company, Red Deer, Alberta, Canada, 2017.
11. Patten, D.W., The longevity accounts in ancient history, CRSQ **19**(1):40–52, 1982.
12. Beasley, G., Pre-Flood giantism: a key to the interpretation of fossil hominids and hominoids, *J. Creation* **4**(1):5–55, 1990.
13. Taylor, P.S., *The Great Dinosaur Mystery and the Bible*, Master Books, El Cajon, CA, 1987.
14. Cuozzo, J.W., Neandertal children's fossils: reconstruction and interpretation distorted by assumptions, *J. Creation* **8**(2):166–178, 1994.
15. Line, P., Explaining robust humans, *J. Creation* **27**(3):64–71, 2013.
16. Holt, R.D., Evidence for a late Cainozoic Flood/post-Flood boundary, *J. Creation* **10**(1):128–167, 1996.
17. Oard, M.J., Dealing carefully with the data, *J. Creation* **16**(1):68–72, 2002.
18. Oard, M.J., Geology indicates the terrestrial Flood/post-Flood boundary is mostly in the late Cenozoic, *J. Creation* **27**(1):119–127, 2013.
19. Clarey, T.L., Werner, D.J., and Tomkins, J.P., Globally extensive Cenozoic coals indicate high post-Flood boundary, *J. Creation* **36**(1):13–15, 2022.
20. Oard, M.J., The Central and Southern High Plains animals likely buried in the Flood, CRSQ **59**(4):228–240, 2023.
21. Guthrie, R.D., Rapid body size decline in Alaskan Pleistocene horses before extinction, *Nature* **426**(6963):169–171, 2003.
22. Wang, X., Systematics and population ecology of Late Pleistocene Bighorn Sheep (*Ovis canadensis*) of Natural Trap Cave, Wyoming, *Transactions of the Nebraska Academy of Sciences* **XVI**:173–183 (esp. p. 173), 1988.
23. Martin, J.M., Mead, J.I., and Barboza, P.S., Bison body size and climate change, *Ecology and Evolution* **8**:4564–4574, 2018.
24. Schultz, C.B. and Hillerud, J.M., Climatic change and the extinction of large mammals during the Quaternary, *Transactions of the Nebraska Academy of Sciences and Affiliated Societies* **VI**:95–105, 1978.
25. Martin, J.M., Mead, J.I., and Barboza, P.S., Bison body size and climate change, *Ecology and Evolution* **8**:4564–4574, 2018.
26. Berg, F. and Fink, R., The incredible shrinking buffalo–buffalo tales and trails, buffalotalesandtrails.com, accessed 10 Aug 2022.
27. Wilson, M.C., Hills, L.V., and Shapiro, B., Late Pleistocene northward-dispersing *Bison antiquus* from the Bighill Creek Formation, Gallelli Gravel Pit, Alberta, Canada, and the fate of *Bison occidentalis*, *Canadian J. Earth Sciences* **45**(7):827–859, 2008.
28. Martin *et al.*, ref. 25, p. 4,565.
29. Froese, D., Stiller, M., Heintzman, P.D. *et al.*, Fossil and genomic evidence constrains the timing of bison arrival in North America, PNAS **114** (13):3457–3462, 2017.
30. Anonymous, Extinct glyptodonts really were gigantic armadillos, ancient DNA shows, Phys.org, 22 Feb 2016.
31. Delsuc, F., Gibb, G.C., Kuch, M. *et al.*, The phylogenetic affinities of the extinct glyptodonts, *Current Biology* **26**(4):155–156, 2016.
32. Giant beaver | Yukon Beringia Interpretive Centre; beringia.com, accessed 6 Oct 2023.
33. Iannucci, A., Sardella, R., Strani, F., and Mecozzi, B., Size shifts in late Middle Pleistocene to Early Holocene *Sus scrofa* (Suidae, Mammalia) from Apulia (southern Italy): ecomorphological adaptations? *Hystrix* **31**(1):10–20, 2020.
34. Fujita, M., Yamasaki, S., Sugawara, H., and Eda, M., Body size reduction in wild boar (*Sus scrofa*) from the late Pleistocene Maehira Fissure Site in Okinawa-jima Island, Japan, with relevance to human arrival, *Quaternary International* **339–440**:289–299, 2014.

35. Iurino, D.A., Body size reduction and tooth agenesis in Late Pleistocene *Meles meles* (Carnivora, Mammalia) from Ingarano (Southern Italy), *Rivista Italiana di Paleontologia e Stratigrafia* **120**(1):109–118, 2014.
36. Walvius, M.R., A discussion of the size of recent red deer (*Cervus elaphus* L.) compared with prehistoric specimens, *Beaufortia* **97**(9):75–82, 1961.
37. Jukar, A.M., Lyons, S.K., Wagner, P.J., and Uhen, M.D., Late Quaternary extinctions in the Indian subcontinent, *Palaeogeography, Palaeoclimatology, Palaeoecology* **562**:110137, 2021.
38. Yan, Y., Li, Q., Fostowicz-Frelik, Ł., and Ni, X., Last record of *Trogontherium cuvieri* (Mammalia, Rodentia) from the late Pleistocene of China, *Quaternary International* **513**:30–36, 2019.
39. Davis, S.J.M., The effects of temperature change and domestication on the body size of Late Pleistocene to Holocene mammals of Israel, *Paleobiology* **7**(1):101–114, 1981.
40. Anonymous, Giant camel fossil found in Syria; bbc.co.uk, accessed 10 Oct 2006.
41. Anonymous, Last of the giant camels and archaic humans lived together in Mongolia until 27,000 years ago, Phys.org, 24 Mar 2022.
42. Klementiev, A.M., Khatsenovich, A.M., Tserendagva, Y. *et al.*, First documented *Camelus knoblochi* Nehring (1901) and Fossil *Camelus ferus* Przewalksi (1878) from Late Pleistocene archaeological contexts in Mongolia, *Frontiers in Earth Science* **10**, Article 861163, 2022.
43. Carey, B., Gigantic apes coexisted with early humans, study finds, LiveScience, 7 Nov 2005.
44. Barbour, E.H. and Schultz, C.B., A new giant camel, *Titanotylopus nebraksensis*, gen. et sp. nov, *Bulletin of the Nebraska State Museum* **1**(36):291–294, 1934.
45. Samonds, K.E., Book Review: *Megafauna: Giant Beasts of Pleistocene South America,* by Fariña, R.A., Vizcaíno, S.F., and Iuliis, G.D., *J. Mammalogy* **95**(6):1308–1309, 2014.
46. Zurita, A.E., Carlini, A.A., Scillato-Yané, G.J., and Tonni, E.P., The extinct mammals of the Quaternary of Chaco Province, Argentina, and its relationship with those of the east of the pampean area and Chile, *Revista Geológica de Chile* **31**(1):65–87, 2004.
47. Mitchell, K.J., Scanferla, A., Soibelzon, E. *et al.*, A., Ancient DNA from the extinct South American giant glyptodont *Doedicurus* sp. (Xenarthra: Glyptodontidae) reveals that glyptodons evolved from Eocene armadillos, *Molecular Ecology* **25**(14):499–508, 2016.
48. Brink, J.S., The evolution of the black wildebeest, *Connochaetes gnou*, and modern large animal faunas in central southern Africa, Ph.D. dissertation, University of Stellenbosch, pp. 107, 125, 2005
49. Delson, E., Terranova, C.J., Jungers, W.L. *et al.*, Body mass in Cercopithecidae (Primates, Mammalia): estimation and scaling in extinct and extant taxa, *American Museum of Natural History Anthropological Papers* **83**:1–159, 2000.
50. Manthi, F.K., Brown, F.H., Plavcan, M.J., and Werdelin, L., Gigantic lion, *Panthera leo*, from the Pleistocene of Natodomeri, eastern Africa, *J. Paleontology* **92**(2):305–312, 2018.
51. Martinez-Navarro, B., Pérez-Claros, J.A., Palombo, M.R., Rook, L., and Palmqvist, P., The Olduvai buffalo *Pelorovis* and the origin of *Bos*, *Quaternary Research* **68**(2):220–226, 2007.
52. Oard, M., Australian marsupials: there and back again? *J. Creation* **36**(1):99–106, 2022.
53. Arment, C., To the Ark, and back again? Using the marsupial fossil record to investigate the Flood/post-Flood boundary, ARJ **13**:1–20, 2020.
54. Anonymous, Small(er) is beautiful; museumvictoria.com.au, accessed 9 Oct 2023.
55. Buckley, M., Cosgrove, R., Garvey, J., and Prideaux, G.J., Identifying remains of extinct kangaroos in Late Pleistocene deposits using collagen fingerprinting, *J. Quaternary Science* **32**(5):653–660, 2017.
56. Munro, N.D., Lebenzon, R., Sapir-Hen, L., Revisiting Late Pleistocene-Early Holocene mountain gazelle (*Gazella gazella*) body size change in the southern Levant: A case for anthropogenic impact, PLoS ONE **17**(8), e0273024, 2022.
57. Pandolfi, L., Petronio, C., and Salari, L., *Bos primigenius bojanus*, 1827 from the early Late Pleistocene deposit of Avetrana (southern Italy) and the variations in size of the species in southern Europe: Preliminary Report, *J. Geological Research*, Article ID 245408:1–11, 2011.
58. Sen, S., Barrier, E., and Crété, X., Late Pleistocene dwarf elephants from the Aegean islands of Kassos and Dilos, Greece, *Annales Zoologici Feenici* **51**(1–2):27–42, 2014.
59. Croitor, R., Bonifay, M.-F., and Bonifay, E., Origin and evolution of the Late Pleistocene island deer Praemegaceros (Nesoleipoceros) Cazioti (Depéret) from Corsicana and Sardinia, *Bulletin of the Museum of Prehistoric Anthropology of Monaco* **46**:35–68, 2006.
60. van der Geer, A., Lyras, G.A., and Volmer, R., Insular dwarfism in canids on Java (Indonesia) and its implications for the environment of *Homo erectus* during the Early and earliest Middle Pleistocene, *Palaeogeogrpahy, Palaeoclimatology, Palaeoecology* **507**(1552):168–179, 2018.
61. Bergmann, C., *Ueber die Verhältnisse der Wärmeökonomie der Thiere zu ihrer Grösse* (On the relationship between the heat economy of animals and their size), *Göttinger Stud*. **3**:595–708, 1847.
62. Oard, M.J., *An Ice Age Caused by the Genesis Flood*, Institute for Creation Research, El Cajon, CA, 1990.
63. Bogin, B., Hermanussen, M., and Scheffler, C., Bergman's rule is a 'just-so' story of human body size, *J. Physiological Anthropology* **41**(1):1–13, 2022.
64. Oard, M.J., *Frozen in Time*, Master Books, Green Forest, AR, 2006 edn.
65. Or perhaps it was the other way around: perhaps greater longevity was the effect of larger body sizes.
66. Price, G.J., Louys, J., Cramb, J. *et al.*, Temporal overlap of humans and giant lizards (Varanidae; Squamata) in Pleistocene Australia, *Quaternary Science Reviews* **125**:98–105, 2015.
67. Wroe, S., A review of terrestrial mammalian and reptilian carnivore ecology in Australian fossil faunas, and factors influencing their diversity: the myth of reptilian domination and its broader ramifications, *Australian J. Zoology* **50**:1–24, 2002.
68. Molnar, R.E., *Dragons in the Dust: The paleobiology of the giant monitor lizard megalania*, Indiana University Press, Bloomington, IN, 2004.
69. Klein, R.G., Why anatomically modern people did not disperse from Africa 100,000 years ago; in: Akazawa, T., Aoki, K., and Bar-Yosef, O. (Eds.), *Neanderthals and Modern Humans in Western Asia*, Plenum Press, New York, pp. 509–521, 1998.
70. Teske, P.R., Papadopoulos, I., McQuaid, C.D., Newman, B.K., and Barker, N.P., Climate change, genetics or human choice: why were the shells of mankind's earliest ornament larger in the Pleistocene than in the Holocene? PLoS ONE **7**, e614, 2007.
71. Martini, P., Camel fossils from the El Kowm Basin, Syria. Diversity and evolution, Ph.D. dissertation, University of Basel, Switzerland, p. 162, 2019.
72. Gruber, K., Giant prehistoric kangaroos walked, not hopped; australiangeographic.com, 15 Oct 2014.
73. Carter, R., The extreme rarity of long-lived people in the post-Flood era, *J. Creation* **37**(2):63–67, 2023.
74. Hebert, J., Rarity of long-lived post-Flood human fossils? *J. Creation* **37**(3):1–2, 2023.

***Jake Hebert** earned a B.S. from Lamar University, an M.S. from Texas A&M University, and a Ph.D. from the University of Texas at Dallas (all degrees in physics). His Ph.D. research was a cutting-edge study of the possible link between solar activity, cosmic rays, and weather and climate. He is a research scientist at the Institute for Creation Research, where he has been employed since 2011. He has a general interest in apologetics, although his primary research areas are climates before and after the Flood and possible evidence for antediluvian and immediate post-Flood longevity.*

Madagascar endemism better explained by post-Flood rafting

Michael J. Oard

The biogeography of Madagascar provides a great opportunity to demonstrate the superiority of the biblical/creation model over the uniformitarian/evolutionary model. Particularly, evolutionists find it impossible to explain the many different kinds of vertebrates found on Madagascar, some of which appear to be more closely related to those in Asia than Africa. According to their models, these animals first evolved millions of years after Madagascar separated from Africa and India, and therefore cannot have been split from their ancestral populations by plate tectonics. Evolutionists themselves will admit that they face seemingly insurmountable difficulties in arguing for the only alternative; this being dispersal across water (via land bridges, 'island hopping', or rafting). Biblical creationists can argue convincingly that plants and animals rafted to Madagascar on massive log/vegetation mats left over from the Genesis Flood. The great diversity of species can be explained by rapid post-Flood diversification.

Madagascar biogeography

Biogeography is the study of the distribution of plants and animals throughout the world. Other than the straightforward mechanisms of migration, such as birds and bats flying to distant lands with attached seeds, migration over a land bridge, seeds and insects spread by the wind, etc., biogeography is full of mysteries.[1] It is complicated with many variables, unknowns, and preconceived ideas based on one's worldview.

The island of Madagascar off southeast Africa (figure 1) represents the most outrageous example of island endemism. Endemism is the idea that plants and animals are found only in a particular geographical area and not others. Madagascar is the fourth largest island in the world covering about 590,000 km^2, slightly larger than France or the state of California. A plateau lies in the centre of the island, at 750–1,500 m above sea level (asl) with a steep escarpment on the east side. The highest peak is Moromokotro at 2,876 m asl. Because of the southeasterly trade winds, the eastern side of the island is a tropical rain forest, while the western side is a tropical savanna. Madagascar is 430 km east of continental Africa. It is separated from the continent by a deep ocean channel, the Mozambique Channel, which is commonly over 2,000 m deep.[2]

The endemic animals of Madagascar

The animals, both living and as subfossils in the Late Pleistocene and Holocene, on Madagascar are amazing in their isolation; most are exclusive to the island.[3] These include the lemurs, which have diversified into numerous species, some of which are extinct.[4] The percentage of Madagascar land mammals that are unique to the island ranges from 84% to 100%.[5,6] A more recent estimate is 88%.[7] Dwarf hippo bones have been found with likely butcher marks on them with a ^{14}C date of about 2,000 years ago (figure 2).[7] Some non-marine invertebrates are highly unique to Madagascar.[8] Certain freshwater fish are also highly unique to Madagascar.[9] Practically all Madagascar amphibians are endemic: "The amphibian fauna of Madagascar is highly exceptional, with more than 99% of the species endemic to this 'micro-continent' and its offshore islands."[10] Madagascar has an incredible diversity of reptiles, more than 90% of which are found only on Madagascar.[11] Birds are species poor and not so unique, but still with 51% found only on Madagascar.[12] Other animals existed on Madagascar from the late Ice Age up to about 2,500 years ago.[13] The bones of the extinct animals, especially lemurs,[14] are not fossilized or permineralized, and man appears to be the reason for these extinctions. I will focus on the endemic mammals and how they arrived on Madagascar, assuming that the same mechanisms would be the cause of endemism in other animals.

Vicariance rejected because of 'molecular clocks'

The mysterious biota of Madagascar came to the attention of zoologists back in the mid-1800s with the first hypothesis that the animals dispersed across a vast, now destroyed, continent named 'Lemuria'.[15] Then, when plate tectonics was accepted in the 1960s and 1970s, biogeographers thought they had a solution in vicariance when the southern supercontinent, Gondwana, separated into the southern continents we have today. This idea came crashing down when 'molecular clocks', mainly DNA comparisons,

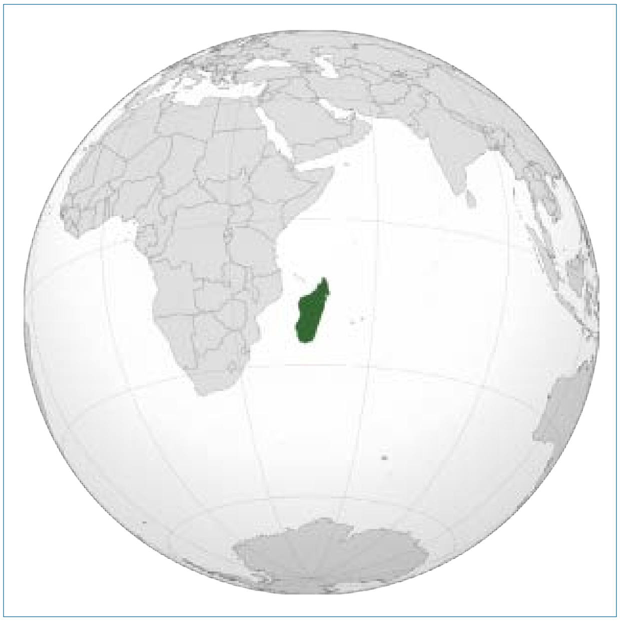


Image: M. Bitton, Wikimedia / CC BY SA 4.0

Figure 1. The island of Madagascar (green) in relation to Africa

Image: FunkMonk, Wikimedia / CC BY SA 3.0

Figure 2. Hippopotamus skeleton from Madagascar at the Museum für Naturkunde, Berlin

indicated that most evolution from a common ancestor occurred *after* Madagascar became isolated. It is postulated that Madagascar split from Africa about 160 Ma and from India about 65–80 Ma ago.[16] Others claim the separation from India was 88 Ma ago.[17] So, the last land connection was well before the majority of the animals arrived. The molecular clock timing is claimed to be 18–60 Ma ago, well after Madagascar separated from India.[3]

Molecular clocks are widely used by uniformitarian scientists to estimate the time of origin for almost all organisms. Crottini *et al.* believe these molecular clocks have started to resolve the biogeography of Madagascar, considered one of the greatest mysteries of natural history.[2] These clocks suggest that the Madagascar fauna predominantly originated in Africa and were dispersed by claimed favourable paleocurrents, which would have to have been very different to today's currents, which flow from the east.

These molecular clocks, of course, assume evolution and deep time. They assume that the closeness of the molecular data, mainly the DNA, of two organisms, the closer they are related by a common ancestor. The 'age' of fossils is sometimes used to 'calibrate' molecular clocks.[18]

However, molecular clocks have problems too.[19] Warren *et al*. admit that numerous assumptions attend molecular studies and clocks:

> "The calibration of molecular clocks (or relaxed clocks) is always based on numerous assumptions that may … or may not have been explicitly stated, and may or may not be valid. Therefore, the divergence time estimates they yield should be viewed with caution."[20]

One problem is that different molecular clocks give different divergence times, hampering the exact timing of colonizing. Regardless, molecular clocks conclude that the divergence times of most animals on Madagascar occurred after the island became isolated. Thus, the ancestral animals had to arrive by over-water dispersal 18 to 60 Ma ago and diverged into numerous species and genera on Madagascar.[4] This conclusion is also a global explanation for dispersal:

> "Such conclusions are consistent with a growing body of molecular phylogeographical studies worldwide that support oceanic dispersal rather than vicariance in explaining geographical disturbance."[15]

Uniformitarian problems with dispersal over water

The rejection of vicariance has caused uniformitarian scientists to look for other solutions; the only one being over-water dispersal, either on long-destroyed land bridges, island hopping, or on vegetation rafts. Island hopping is the idea that animals spread across oceanic barriers by migrating from one island to another across smaller oceanic barriers.

Problems with land bridges and island hopping

Some biogeographers favour now-sunken land bridges or islands for island hopping. Although most biogeographers believe the animals came from Africa, the closest continent,[21] a few suggest that the animals reached Madagascar and other islands in the western Indian Ocean from India on a series of islands stretching from India to Madagascar when sea level was much lower.[41] There are several island archipelagos in the western Indian Ocean, as well as a few submerged banks such as Saya de Malha and Nazareth, which are about 80 m deep along the route from India to Madagascar. These banks would have been islands during the uniformitarian sea level falls of over 100 m during their multiple ice ages. Still, there would be long stretches of deep water between islands and banks. Warren *et al*. also claim that the bathymetry could have been much shallower in the western Indian Ocean more than 5 Ma ago, which would not only aid island hopping, but also the idea of sunken land bridges.[21] Of course, there is no evidence of this.

In a recent review, Ali and Hedges list numerous problems with the ideas of land bridges and island hopping.[22] They only go into the common belief of origin from Africa, but do not seem to entertain the idea that the majority of the biota could have come from Asia. The most obvious possibility for a land bridge or island hopping is a route across the east–west Comoros Islands archipelago (figure 3). However, it is believed that these volanic islands are too young and the arrival of most vertebrates is considered much older.[23] Ali and Hedges challenge the latest claim of a land bridge or a series of islands on the Davie Fracture Zone that is believed to have stretched from Africa to southwest Madagascar and is claimed to have been exposed three different times in the Cenozoic.[2,24] This fracture zone forms a northwest–southeast ridge over 1,300 km long with segments rising 2,500 m above the floor of the Mozambique Channel to within 500 m of the surface.[2] With briefly lower sea level in the past and/or postulated tectonic uplift, some believe that the islands along the fracture zone would have been either seamounts or atoll crowns that could be used for island hopping. But animals would have found it difficult to survive on these postulated, isolated islands. Besides, there is apparently no evidence for the existence of these ancient atolls. The hippopotamus could not navigate across these deep channels (see below).

There are further problems with island hopping. Regardless of postulated islands along the Davie Fracture Zone, the Mozambique Channel is still deep, even between 'islands'. Ali and Hedges also state that if land bridges once existed there should be many more animals that migrated from Africa to Madagascar than the ones found there today. Furthermore, some of the endemic fauna should have travelled from Madagascar to Africa, but this is not the case.

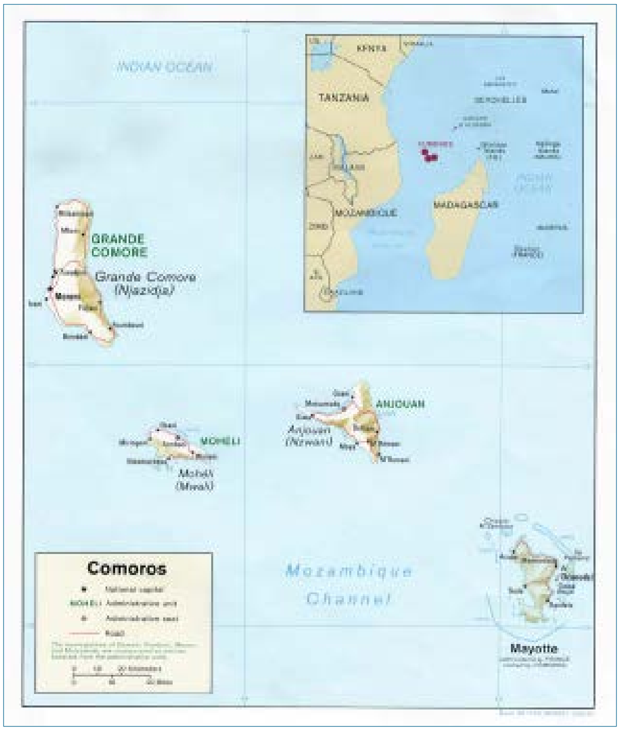


Figure 3. The Comoros Islands west of the northern tip of Madagascar

Image: United States CIA's World Factbook, Wikimedia / Public Domain

Both sides of the issue are confronted by many animals that could not make it over a land connection: "However, the majority of the species that colonize remote islands are neither migratory, nor nomadic, and do not get there across land-bridges."[25] One example is the burrowing and blind snakes, small worm-like snakes with reduced vision. They are found not only on Madagascar, but also on the southern landmasses of the former Gondwanaland.[26] Ali and Hedges 'solve' the problem by claiming that these snakes evolved early and ended up where they are found by vicariance.[27] However, Vidal *et al.* claim that several overwater dispersals also are required to reach Madagascar, and to spread blind snakes all over the world, a transatlantic journey from Africa to South America must have occurred. One problem is that the snakes, as well as all the present fauna, lack a fossil record to verify their old molecular dates.

Numerous challenges also for overwater dispersal by vegetation mats

Therefore, overwater dispersal on vegetation rafts seems to be the only way for most of the mystery animals to arrive on Madagascar.[23] This seems to be the consensus view of uniformitarian scientists at the moment.[28,29] But the issue is far from resolution, although Ali and Hedges have high hopes that they have solved the mystery, as they end with, "Hopefully, the analysis presented above brings closure to this matter."[30]

Table 1. Variables listed in Mazza *et al.*[32] for successful rafting

Biological variables	
1.	Starvation
2.	Dehydration
3.	Temperature and humidity
4.	Salt intake
Vegetation mat characteristics	
1.	Provide the needed resources
2.	Large enough
3.	Shaped to minimize drag through the water
Physical variables	
1.	Wind and currents favourable
2.	Problem of ocean eddies
3.	Problem of tsunamis and storms

Critics of rafting believe the hypothesis is fatally flawed,[31,32] especially because the journey would be too long with a lack of food and water, and there would be a lack of genetic diversity.[33] Of course, at least one male and female must make the journey or a pregnant female. It would be much better for more than one pair to make the journey. Mazza *et al*. list numerous variables that *all* must be satisfied for a successful colonization by rafting, but they can be grouped into three main considerations: biological variables, vegetation mat characteristics, and physical variables (table 1).[32] Nonetheless, these variables do not exhaust the number of challenges.

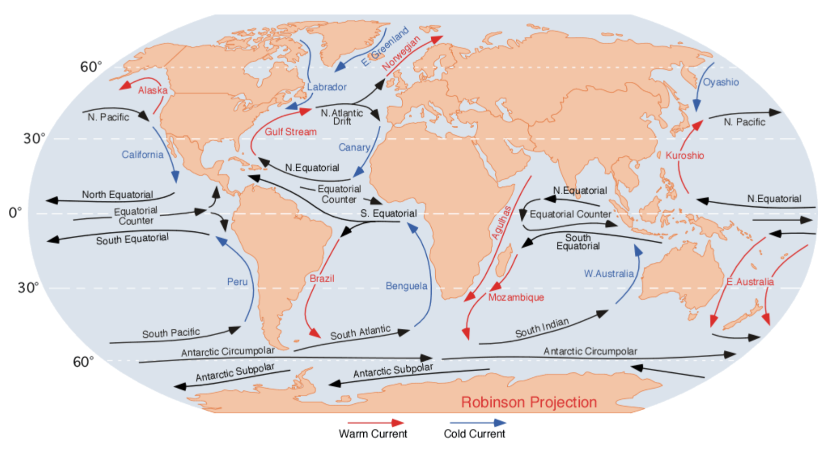


Figure 4. Surface ocean currents of the world

Image: Dr Michael Pidwirny, Wikimedia, Public Domain U.S. Government

Just considering the vegetation mat, it must be able to provide enough food and fresh water, be capable of staying afloat until it reaches the new location, and be carried by the right currents. Natural rafts that have all these characteristics have never been observed. It also has been noted that floating islands descending to the ocean from rivers are quickly broken up by waves.[32] If a floating island reached the open ocean, it would not last long. Mazza *et al*. summarize the many difficulties:

> "Nonetheless, given the many complex, intricate and interdependent variables involved in over-sea dispersal of terrestrial mammals, the probability that they could reach remote islands by this means [vegetation rafts] appears vanishingly small."[34]

Ali and Hedges have countered many of these arguments, especially referencing when the animals had one or more characteristics that would aid dispersal, such as small body mass, low energy requirements, and the ability to go into torpor.[23] However, it looks like some large animals must also have been rafted to Madagascar, such as the hippo, which arrived in the late Pleistocene/Holocene. Hippos are notoriously poor swimmers, and their feet make poor paddles. The barrel shape could cause them to roll over, and they cannot cross a channel deeper than 4 m.[25] The hippos would also need 43–72 litres of fresh water per day and are highly sensitive to prolonged exposure to salt water and sunlight.[35] It is unlikely that hippos could have arrived on Madagascar on the puny rafts envisioned by biogeographers.

Moreover, ocean currents are not favourable today (figure 4) and presumably in the Cenozoic, although Ali and Huber believe they were favourable during the Palaeogene.[36] Ali admits that the present currents cannot bring any of the animals from Africa to Madagascar: "it is now almost impossible for adrift mammals to float to the island from Africa, or for that matter any of the other large Indian Ocean landmasses."[37] Animals set adrift on a vegetation mat from Africa would end up on the African coast to the south (figure 4):

> "Our estimates of current and wind trajectories show that the most likely fate for a raft emerging from an estuary on the east coast of Africa is to follow the Mozambique current and become beached back on the African coast."[38]

I do not think there is any evidence for reversed currents in the Palaeogene; it appears to be purely an *ad hoc* hypothesis.

To make matters worse, Ali and Hedges claim that there were *multiple* dispersals by rafts, as if one successful over-water dispersal is not improbable enough.

A major uniformitarian mystery

Therefore, island endemism on Madagascar represents one of the most difficult enigmas of biogeography. Its origin is "the most difficult enigma in zoological geography" and "one of the greatest unsolved mysteries of natural history."[21] Yoder and Nowak are dismayed: "These biotic enigmas have inspired centuries of speculation relating to the mechanisms by which Madagascar's biota came to reside there."[39] It is a centuries-old debate with a huge literature.

To make matters worse, Madagascar violates a basic rule of island biogeography that islands are largely colonized from the nearest mainland. In the case of Madagascar, however, the biota has a strong Asiatic flavour.[40] India is 3,796 km away, while Africa is only 430 km away. The nearest distance to India compares to the Hawaiian Islands, another huge mystery in which the closest land is 3,675 km away! But winter winds from India point toward Madagascar, and winds and ocean currents at other times of the year generally flow from the east (figure 4).[36]

Creation science solution

Creation scientists are also challenged by the endemic animals on Madagascar but have additional options that can potentially explain the mystery of Madagascar animals. But one major challenge is that mammals and birds must start from the Ark that landed in the 'mountains of Ararat' and make it to southwest Asia. The fact that the animals seem to have come from Asia and not Africa would support a more direct route from the 'mountains of Ararat'.

But not all Madagascar animals needed to migrate from the Ark. Some semi-aquatic animals may have survived outside the Ark and would not need to have travelled far to make it to Madagascar. It is possible that many amphibians did not need to start from the Ark landing site. Amphibians begin their lives as a larval stage in water, and because of this many amphibians may have survived outside the Ark.[41,42] And some reptiles are aquatic, like tortoises, or semi-aquatic, like crocodiles, so were likely not needed on the Ark to survive.

Flood and post-Flood fossils on Madagascar

One favourable feature in the biblical model is that we can easily determine the animals that made it to Madagascar by knowing the Flood/post-Flood boundary. This is a problem for other landmasses, such as Australia.[43] All fossils on Madagascar date from the late Pleistocene or Mesozoic: "Reconstructing the temporal pattern of this striking biotic turnover is hampered by the almost complete lack of post-Cretaceous and pre-Pleistocene terrestrial fossil deposits."[44] Masters *et al*. complain, "Deciphering the origins of Madagascar's biota is greatly impeded by the absence of Cenozoic fossils older than 80 ka."[45] They blame it on highly acidic soils. Therefore, the Mesozoic fauna would be from the Flood, and the very late Pleistocene, Holocene, and present-day animals are from the post-Flood period.

Figure 5. A large duck-billed dinosaur track found on top of a coal mine in Utah

A land bridge or island hopping very unlikely

Post-Flood land bridges and island hopping are very unlikely, even more so than the uniformitarian model. In the biblical model, sea level would have started out 66 m higher than today because there would be no Greenland and Antarctic Ice Sheets.[46] Because of thinner ice sheets during the Ice Age,[47,48] sea level would have dropped to only 50–55 m below that of present day.[49] This is not nearly as low as postulated by uniformitarian scientists in their ice age model. Moreover, lower sea level would have occurred well after the Flood, around 500–700 years after, which would have been too late for animal dispersal.

Post-Flood log mats vastly superior to uniformitarian vegetation mats

The only option seems to be dispersal on log/vegetation mats. This is a second favourable feature in the biblical model since post-Flood log/vegetation mats, henceforth referred to as 'log mats', would have been much larger than the postulated uniformitarian vegetation mats. Uniformitarian scientists postulate that their vegetation mats would have originated from storms that ripped up vegetation that floated down a river to the ocean; this is fraught with fatal or near-fatal problems (see above). The vegetation mats would be

Figure 6. A plant growing from a vertical log. I have also seen them growing on horizontal, floating logs.

inadequate, although uniformitarian scientists have a few examples of successful rafting, but only of small animals. For instance, small lizards swept off Caribbean islands by hurricanes floated over 100 km on vegetation to nearby islands.[50,51]

Pre-Flood biomass enormous

Creation scientists have difficulty envisioning huge post-Flood log mats, but deductions from the amount of pre-Flood biomass, the potential thickness of the log mats, a few of the animals that would have needed oceanic transport, and modern observations of floating mats can help us understand.

Post-Flood log rafts would have been much larger, and hence more stable, than the small vegetation mats envisioned by uniformitarian scientists.[52–55] The estimated amount of carbon in the pre-Flood biosphere, based on the amount of coal, is about eight times the carbon in the current biosphere.[56] This would mean that the pre-Flood world was rich in trees and plants. As the Flood progresses, more and more of this vegetation is ripped up with much of it floating on the floodwaters. Most of this biomass probably was deposited in the sediments, later becoming coal, but much of it would have continued floating on the post-Flood oceans. Therefore, it is reasonable that the post-Flood log mats would be large and locally thick —thick enough to be stable and likely support a few large animals.

Possible evidence for the existence of post-Flood thick log mats comes from thick, nearly pure, coal seams. Some coal seams can be explained by the beaching of log mats on BEDS (Briefly Exposed Diluvial Sediments),[57] since some coal seams have dinosaur tracks on top (figure 5).[56] Dinosaurs evidently walked on top of the beached vegetation before another rise in the Flood level pinned the vegetation and covered the top with sediments. The fact that some of these coal seams are thick would mean that during the Flood some log mats must have been thick, and hence, by extension, that some post-Flood log mats would have been thick also; for instance, 10 or more metres thick and covering tens of square kilometres. Present day vegetation mats flowing down rivers to the ocean would be mostly broken up by the surf, but post-Flood log mats would not have passed through the surf zone. Such thick log mats would have been capable of transporting a few larger animals, although small animals would be much more favoured.

Post-Flood log mats could float a long time, similar to the numerous logs still floating on Spirit Lake dozens of years after the May 1980 eruption of Mount St Helens. During the first 20 years, it is estimated that about half the Spirit Lake logs sank,[58] but the ‘half-life’ (the time it would take for half the logs to sink) of Douglas Fir was estimated to be 75 years. After 75 years, half the Douglas Firs would still float; after 150 years, there would be 25% left; and after 225 years, there would be 12.5% left, if the half-life concept still applies after 75 years.

Some large animals needed to be transported on log mats

It may be difficult to envision how a large animal could possibly walk onto a log mat, and the mat to be stable enough to carry the animal over a long distance. A thick log mat would be more stable and easier to walk on when beached than while floating. Biogeography shows that in some cases large animals would have needed to be rafted.[59] Most of the animals rafted to Madagascar likely were small, but the hippopotamus was not, and there is no other way for this animal to end up on Madagascar, except by rafting. Some of the marsupials rafted to Australia could also have been large.[44] Small ground sloths were rafted to the West Indies,[60] since there does not seem to be any other way for them to have arrived on these isolated islands.

Modern observations of floating islands

A few observations show that floating islands can occur with live trees and bushes growing:[61]

> “Perhaps a more useful model can be drawn from present-day phenomena. Krause (1997a) reviews contemporary reports of floating ‘islands’ of vegetation, often with standing trees and mammalian inhabitants, observed in remote oceanic locations, tens and hundreds of kilometers from land.”[62]

Trees and bushes can even grow on the logs (figure 6). I have seen other bushes growing from horizontal floating logs. This vegetation would provide food for the animals. Numerous insects would still be on the log mats for carnivores to eat. With much more rain during the Ice Age,[50,63] fresh water could have been available, although the log mats were mostly porous. Van Duzer has documented many small floating islands today, sometimes with trees growing on them.[64] A floating island with vertical trees with monkeys has been observed on isolated water bodies adjacent to the Magdalena River of northwest Columbia.[65,66] If such floating islands can occur today on a small scale, is it possible that millions to possibly billions of floating logs could exist right after the Flood?

With vegetation, insects, and microorganisms already repopulating the land masses, the Ark’s survivors would have been able to spread rapidly outward from the ‘mountains of Ararat’. There would have been a population explosion as a host of new habitats lay open and waiting for residents with few, if any, predators, at least at the beginning. If log mats temporarily beached in coastal areas, some animals could have unknowingly climbed onto the log mats and been carried across seas and oceans to islands or other continents after the log mat broke free of the land (figure 7). Shorelines with significant tides would have been good candidates for temporary grounding of mats. And if ocean currents were somewhat similar to today in the Indian Ocean, currents from India would have favoured dispersal to Madagascar (figure 4).

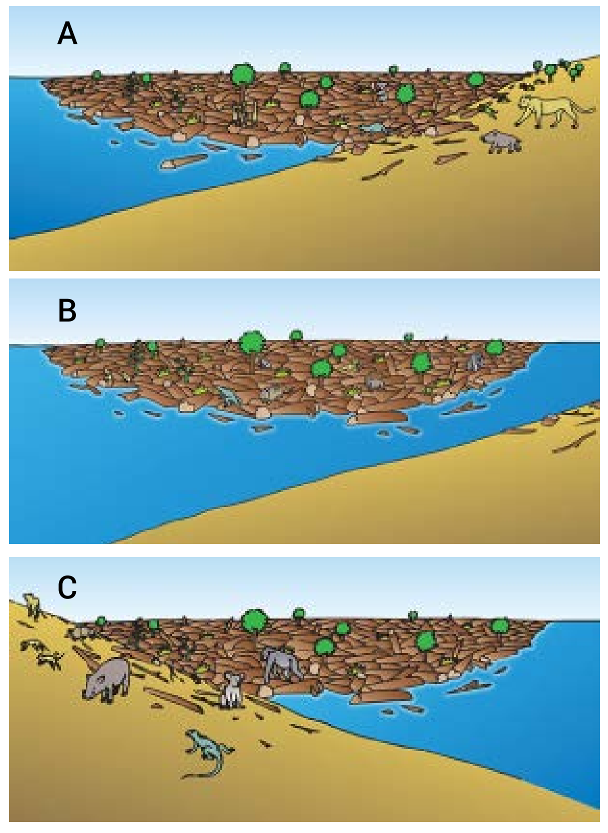


Figure 7. Schematic of a log mat beached on one landmass (A), floating away with animals on top (B), and ending up on another landmass (C) (drawn by Keaton Halley).

Diversification of Ark kinds causes island endemism

Another favourable feature of the biblical model is that creation scientists can also explain rapid formation of endemic animals on Madagascar and other isolated islands, based on the diversification of the Ark kinds. These kinds would have had great potential to diversify, since God no doubt would have picked pairs with such potential. Observations on the Galápagos Islands indicate that diversification can occur rapidly.[67] This is illustrated by the creation orchard of life (figure 8). It is the Ark kinds that spread all over the earth,[68,69] and depending upon the level of the kinds with respect to the biological classification system, endemism can occur where the animals land and diversify over time.

Endemism on Madagascar can be at the species, genus, family, or order level, or within the subdivisions of this classification, such as superfamily, infraorder, etc. It makes a difference whether the endemism is at the species/genus level or the family/order level, since baraminologists estimate the average Ark kind at the family level.[54] It is well known that many species can interbreed, so the boundaries of the kind are almost always at a higher taxonomic level. One taxonomical problem is that the definition of a species is subjective and unknown in many instances:

> “However, it can be challenging to determine whether island forms are sufficiently distinct from one another and/or from mainland forms, to justify being designated as separate species. … There are in fact numerous operational definitions of the species unit. Singh (2012) lists 23 species concepts, while Lomolino *et al.* (2017) pick out six. … Traditionally, morphology was the principal basis for species recognition. … Hence, there can be uncertainty as to what constitutes a species.”[70]

The same can likely be said for the genus and family levels, also, which is one reason that creation scientists believe the kind averages at the family level.

This means that if endemism is only at the species/genus level, but not at the family level, a particular family

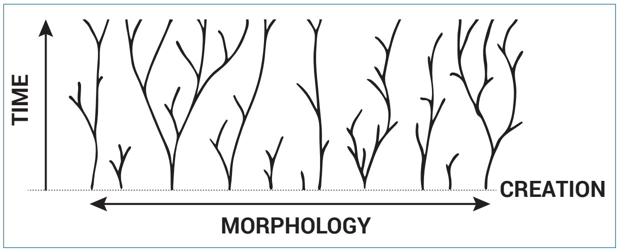


Figure 8. The creation orchard of life


Image: Stevencdickson, Wikimedia / CC-BY-SA-4.0

Figure 9. A taxidermy mount of a tenrec from the Horniman Museum and Gardens, London


Image: Adrian Pingstone, Wikimedia / PD-user).

Figure 10. Madagascar giant rat *Hypogeomys antimena* from subfamily Nesomyinae in the Bristol Zoo, England

could have spread from the Ark, hopped on a log mat, and diversified into different genera and species after the log mat arrived on the new land. Any species or genus level endemism from this particular family would be no big deal on Madagascar or anywhere. On the other hand, if the endemism is at a higher level on Madagascar, then it would appear that a particular Ark kind made it to Madagascar and nowhere else, and from there diversified into various species, genera, or even families. This is not evolution, or even microevolution, but diversification of Ark kinds from the variety already built in.

Analysis of mammal diversification in Madagascar

Madagascar diversification can be illustrated by the endemic mammals. There are four major types of mammals on Madagascar: (1) euplerid carnivores, (2) lemurs, (3) tenrecs, and (4) nesomyine rodents. This does not include the hippopotamus. The original mammals that landed on Madagascar would have been able to easily diversify because of the extremely variable habitats on the island,[29] and the inbuilt capacity for variation that God programmed into plants and animals at creation.

Euplerid carnivores, the mongooses, have been organized into ten species and seven genera that are endemic at the family level.[71] However, another compilation has only seven species in six genera, indicating problems in taxonomy.[72] It is interesting that the euplerid carnivores belong to the suborder Feliformia and, according to the Paleobiology Database (PBDB), have numerous representatives on all continents, except Antarctica, in the Paleogene and Neogene. So, it is unlikely that the Madagascar mongooses represent one Ark kind at the family level. Regardless, one member of the suborder made it to Madagascar and diversified.

One classification has five endemic lemur families within the superfamily Lemuroidea of the primate order that represent 67 species on Madagascar (figure 2).[73] However, if we go to the next taxonomic level, the infraorder Lemuriformes, there is one fossil claimed in the Fayum of northeast Egypt, but many of the Fayum mammals are mainly teeth[74] and the claim may be spurious. It is interesting that the latest Wikipedia entry has eight lemur families, emphasizing taxonomic issues. Regardless, the superfamily Lemuroidea may be the Ark kind, which made it only to Madagascar.

Tenrecs, shrew-like mammals (figure 9), are endemic on Madagascar but only at the genus level. The family Tenrecidae occurs at other locations in southwest Africa. So, as shrews spread and diversified from the Mountains of Ararat, one particular family or subfamily, the tenrecs, arrived on Madagascar and continued to diversify into various genera and species.

The nesomyine rodents (figure 10) come from the subfamily Nesomyinae with nine genera[75] endemic to Madagascar, while the PBDB shows that the family Nesomyidae occur over Africa with one location in Spain. These rodents have been placed in the superfamily Muroidea, which has a wide distribution on the earth. The Ark kind for these rodents must have been at a higher taxonomic level than the subfamily Nesomyinae, which would have been the particular rodent or group of rodents to end up on Madagascar.

Within the biblical model, God created each kind of animal and plant with the internal potential to diversify into varieties within the kind. The biological classification system definitions seem arbitrary and subjective in some cases.[76] The age and even the location of a fossil is considered a taxonomic variable, which would result in differently named animals. I have witnessed such variability in the taxonomy of organisms in the Paleobiology Database.[77] Ali and Vences comment that "An obvious limitation to ALTS is the fact that it is based on taxonomic information, which is an imperfect representation of evolutionary history and age."[78] They then give the example of changing classification of certain frogs on the Seychelles Islands and skinks over the world.

Conclusions

The numerous endemic animals on Madagascar represent a major uniformitarian mystery. Vicariance has been rejected, leaving dispersal as the only mechanism. One group of researchers shows that dispersal by land bridges or island hopping is very unlikely, if not impossible, while another group lists numerous reasons to reject dispersal on vegetation mats. It does not appear that any uniformitarian mechanism can explain this mystery.

But creation scientists have more options. First, we can determine what animals were dispersed, and that most dispersal to remote islands must have been on thick log/vegetation mats that would be much larger than uniformitarian vegetation mats. The ancestors of the Madagascar fauna likely arrived from Asia, not Africa, as some uniformitarian scientists believe.[33,79] This deduction is reinforced by the fact that no Madagascar endemic vertebrates are found on Africa.[23] The animals must have quickly migrated to southwest Asia from the 'mountains of Ararat', although some Madagascar amphibians and reptiles may not have originated from the Ark. Ocean currents would also favour an origin from India. With the creation orchard of life, we can understand how certain unique animals, whether an Ark kind or not, made it to Madagascar and rapidly diversified into various endemic species, genera, and even families. With very thick and extensive post-Flood log mats, creation scientists have the potential to explain the mysteries of biogeography for not only Madagascar, but also other continents and isolated islands, and even for the most remote islands of Hawaii.

References

1. Statham, D., Phytogeography and zoogeography—rafting vs continental drift, *J. Creation* **29**(1):80–87, 2015.
2. McCall, R.A., Implications of recent geological investigations of the Mozambique Channel for the mammalian colonization of Madagascar, *Proceedings of the Royal Society of London B* **264**:663–667, 1997.
3. Yoder, A.D. and Nowak, M.D., Has vicariance or dispersal been the predominant biogeographic force in Madagascar? Only time will tell, *Annual Review of Ecology, Evolution, and Systematics* **37**:412, 2006.
4. Karanth, K.P., Delefosse, T., Rakotosamimanana, B., Parsons T.J., and Yoder, A.D., Ancient DNA from giant extinct lemurs confirms single origin of Malagasy primates, PNAS **102**:5090–5095, 2005.
5. Goodman, S.M. and Benstead, J.P., Updated estimates of biotic diversity and endemism for Madagascar, *Oryx* **39**(1):73–77, 2005.
6. Goodman, S.M., Ganzhorn J.U., and Rakotondravony, D., Mammals, chap. 13; in: Goodman, S.M. and Benstead J.P. (Eds.), *The Natural History of Madagascar*, The University of Chicago Press, Chicago p. 1159–1422, 2003.
7. Whittaker, R.J., Fernández-Palacios, J.M., and Matthews, T.J., *Island Biogeography: Geo-environmental dynamics, ecology, evolution, human impact, and conservation*, Oxford University Press, Oxford, p. 83, 2023.
8. Paulian, R. and Viette, P., Invertebrates, chap. 8; in: Goodman, S.M. and Benstead J.P. (Eds.), *The Natural History of Madagascar*, The University of Chicago Press, Chicago, p. 505, 2003.
9. Sparks, J.S. and Stiassny, M.L.J., Fishes, chap. 9; in: Goodman, S.M. and Benstead J.P. (Eds.), *The Natural History of Madagascar*, The University of Chicago Press, Chicago, p. 850, 2003.
10. Glaw, F. and Vences, M., Amphibians, chap. 10; in: Goodman, S.M. and Benstead J.P. (Eds.), *The Natural History of Madagascar*, The University of Chicago Press, Chicago, p. 883, 2003.
11. Raxworthy, C.J., Reptiles, chap. 11; in: Goodman, S.M. and Benstead J.P. (Eds.), *The Natural History of Madagascar*, The University of Chicago Press, Chicago, p. 934, 2003.
12. Hawkins, A.F.A. and Goodman, S.M., Birds, chap, 12; in: Goodman, S.M. and Benstead J.P. (Eds.), *The Natural History of Madagascar*, The University of Chicago Press, Chicago, p. 1019, 2003.
13. Crowley, B.E., A refined chronology of prehistoric Madagascar and the demise of the megafauna, *Quaternary Science Reviews* **29**:2591–2603, 2010.
14. Godfrey, L.R., Jungers, W.L., and Burney, D.A., Subfossil lemurs of Madagascar; in: Werdelin, L. and Sanders, W.J. (Eds.), *Cenozoic Mammals of Africa*, University of California Press, Los Angeles, CA, pp. 351–367, 2010.
15. Warren, B.H., Strasberg, D., Bruggemann, J.H., and Prys-Jones, R.P., Why does the biota of the Madagascar region have such a strong Asiatic flavour? *Cladistics* **26**:527, 2010.
16. Crottini, A., Madsen, O., Poux, C., Strauß, A., Vieites, D.R., and Vences, M., Vertebrate time-tree elucidations the biogeographic pattern of a major biotic change around the K-T boundary in Madagascar, PNAS **109**(14):5358–5363, 2012.
17. Cox, C.B., Ladle, R.J., and Moore, P.D., *Biogeography: An ecological and evolutionary approach*, 10th edn, John Wiley & Sons, Hoboken, NJ, p. 339, 2020.
18. Whittaker *et al.*, ref. 7, p. 198.
19. Masters, J.C., Génin, F., Zhang, Y., Pellen, R., Huck, T., Mazza, P.P.A., Rabineau, M., Doucouré, M., and Aslanian, D., Biogeographic mechanisms involved in the colonization of Madagascar by African vertebrates: rifting, rafting and runways, *J. Biogeography* **48**:494, 2021.
20. Warren *et al*., ref. 15, p. 529.
21. Joseph, G.A. and Seymour, C.L., Why have Madagascar's mammals, despite being closely-related to African open habitat specialists, failed to radiate into open grasslands? *J. Biogeography* **50**:622–627, 2023.
22. Ali, J.R. and Hedges, S.B., A review of geological evidence bearing on proposed Cenozoic land connections between Madagascar and Africa and its relevance to biogeography, *Earth-Science Reviews* **232**:1–19, 2022.
23. Rabinowitz, P.D. and Woods, S., The Africa–Madagascar connection and mammalian migration, *J. African Earth Sciences* **44**:270–276, 2006.
24. Masters *et al*., ref. 19, pp. 492–510.
25. Whittaker *et al.*, ref. 7, p. 62.
26. Vidal, N., Marin, J., Morini, M., Donnelian, S., Branch, W.R., Thomas, R., Vences, M., Wynn, A., Cruaud, C. and Hedges, S.B., Blindsnake evolutionary tree reveals long history on Gondwana, *Biology Letters* **6**:558–561, 2010.
27. Ali and Hedges, ref. 22, p. 12.
28. Kuhn, A., Gehara, M., Andrianarimalala, M.S.M., Rabibisoa, N., Randriamahatantsoa, B., Overcast, I., Raxworthy, C.J., Ruane, S., and Burbrink, F.T., Drivers of unique and asynchronous population dynamics in Malagasy herpetofauna, *J. Biogeography* **49**:600–616, 2022.
29. Lawton, G., On a raft and a prayer, *New Scientist* **3365/3366**:50–52, 18/25 Dec 2021.

30. Ali and Heges, ref. 22, p. 17.
31. Mazza, P.P.A., Buccianti, A., and Savorelli, A., Grasping at straws: a re-evaluation of sweepstakes colonization of islands by mammals, *Biological Reviews* **94**:1364–1380, 2019.
32. Stankiewicz, J., Thiart, C., Masters, J.C., and de Wit, M.J., Did lemurs have sweepstake tickets? An exploration of Simpson's model for the colonization of Madagascar by mammals, *J. Biogeography* **33**:221–235, 2006.
33. Ali and Hedges, ref. 22, p. 2.
34. Mazza *et al.*, ref. 31, pp. 1374–1375.
35. Masters *et al.*, ref. 18, p. 497.
36. Ali, J.R. and Huber, M., Mammalian biodiversity on Madagascar controlled by ocean currents, *Nature* **463**:653–656, 2010.
37. Ali, J.R., Islands as biological substrates: continental, *J. Biogeography* **45**:1012, 2018.
38. Stankiewicz *et al.*, ref. 32, p. 221.
39. Yoder and Nowak, ref. 3, p. 405.
40. Warren, *et al.*, ref. 20, pp. 526–538.
41. Woodmorappe, J., *Noah's Ark: A feasibility study*, chap. 18, Institute for Creation Research, Dallas, TX, 1996
42. Swenson, K.W., Amphibian responses to the 1980 eruption of Mount St Helens—implications for Noahic Flood recovery, *J. Creation* **34**(3):45–52, 2020.
43. Oard, M.J., When and how did the marsupials migrate to Australia? *J. Creation* **36**(2):90–96, 2022.
44. Crottini *et al.*, ref. 16, p. 5,358.
45. Masters *et al.*, ref. 24, p. 494.
46. Oard, M.J., (ebook), Earth's surface shaped by Genesis Flood runoff, 2013; michael.oards.net/genesisfloodrunoff.htm.
47. Oard, M.J., Non-glacial landforms indicate thin Scandinavian and British-Irish ice sheets, *J. Creation* **31**(2):119–127, 2017.
48. Oard, M.J., Evidence strongly suggests the Laurentide Ice Sheet was thin, *J. Creation* **30**(1):97–104, 201.
49. Oard, M.J., *How Noah's Flood Caused a Single Ice Age*, Creation Book Publishers, Powder Springs, GA (in press).
50. Calsbeek, R. and Smith, T.B., Ocean currents mediate evolution in island lizards, *Nature* **426**:552–555, 2003.
51. Censky, E.J., Hodge, K., and Dudley, J., Over-water dispersal of lizards due to hurricanes, *Nature* **395**:556, 1998.
52. Snelling, A.A., *Earth's Catastrophic Past: Geology, creation & the Flood*, Institute for Creation Research, Dallas, TX, pp. 163–182, 2009.
53. Wood, T.C. and Murray, M.J., *Understanding the Pattern of Life: Origins and organization of the species*, Broadman & Holman Publishers, Nashville, TN, pp. 187–203, 2003.
54. Wise, K.P. and Croxton, M., Rafting: a post-Flood biogeographic dispersal mechanism; in: Ivey, Jr., R.L. (Ed.), *Proceedings of the Fifth International Conference on Creationism*, technical symposium sessions, Creation Science Fellowship, Pittsburgh, PA, pp. 465–477, 2003.
55. Oard, M.J., (ebook), *The Genesis Flood and Floating Log Mats: Solving geological riddles*, Creation Book Publishers, Powder Springs, GA, chapter 8, 2014.
56. Archer, D., *The Global Carbon Cycle*, Princeton University Press, Princeton, NJ, 2010.
57. Oard, M.J., *Dinosaur Challenges and Mysteries: How the Genesis Flood makes sense of dinosaur evidence—including tracks, nests, eggs, and scavenged bonebeds*, Creation Book Publishers, Powder Springs, GA, 2011.
58. Morris, J. and Austin, S.A., *Footprints in the Ash: The explosive story of Mount St. Helens*, Master Books, Green Forest, AR, p. 97, 2003.
59. Wood and Murray, ref. 53, p. 193–195.
60. Steadman, D.W., Martin, P.S., MacPhee, R.D.E., Jull, A.J.T., McDonald, H.G., Woods, C.A., Iturralde-Vinent, M., and Hodgins, G.W.L., Asynchronous extinction of late Quaternary sloths on continents and islands, PNAS **102**:11763–11768, 2005.
61. Snelling, ref. 52, p. 172.
62. Yoder and Nowak, ref. 3, p. 423.
63. Oard, M.J., *Frozen in Time: Woolly mammoths, the Ice Age, and the biblical key to their secrets*, Master Books, Green Forest, AR, 2004.
64. Van Duzer, C., *Floating Islands: A global bibliography*, Canto Press, Los Altos Hills, CA, 2004.
65. Ali, J.R., Fritz, U., and Vargas-Ramírez, M., Monkeys on a free-floating island in a Columbian river: further support for over-water colonization, *Biogeographia –J. Integrative Biogeography* **36**(a005):1–8, 2021.
66. Oard, M.J., A growing island with monkeys and trees observed, *J. Creation* **36**(3):17–18, 2022.
67. Carter, R., Galápagos finches, rapid speciation, and recent creation; creation.com.
68. Statham, D., Biogeography, *J. Creation* **24**(1):82–87, 2010; creation.com/biogeography.
69. Statham, D., Plants and animals around the world: why are they found where they are? *Creation* **32**(4):45–47, 2010.
70. Whittaker *et al*., ref. 7, pp. 195, 196.
71. Ali, ref. 38, pp. 1003–1018.
72. Mittermeier, R.A., Langrand, O.M., Wilson, D.E., Rylands, A.B., Ratsimbazafy, J., Reuter, K.E., Andriamanana, T., Louis Jr, E.E., Schwitzer, C., and Sechrest, W., *Mammals of Madagascar*, Lynx Press, Barcelona, Spain, pp. 125–127, 2021.
73. Mittermeier *et al.*, ref. 72, pp. 38–82.
74. Gagnon, M., Ecological diversity and community ecology in the Fayum sequence (Egypt), *J. Human Evolution* **32**:133–160.
75. Jansa, S.A., Goodman, S.M., and Tucker, P.K., Molecular phylogeny and biogeography of the Native rodents of Madagascar (Muridae: Nesomyinae): a test of the single-origin hypothesis, *Cladistics* **15**:253–270, 1999.
76. Vences, M., Guayasamin, J.M., Miralles, A., and De La Riva, I., To name or not to name: criteria to promote economy of change in Linnaean classification schemes, *Zootaxa* **3636**(2):201–244, 2013.
77. Oard, M.J., Did post-Flood North American mammals live above their dead Flood relatives? *J. Creation* **36**(3):106–113, 2022.
78. Ali, J.R. and Vences, M., Novel summary metrics for insular biotic assemblages based on taxonomy and phylogeny: biogeographical, palaeogeographical and possible conservational applications, *J. Biogeography* **46**(12):2735–2751, 2019; p. 2744.
79. Warren *et al.*, ref. 20, pp. 526–538.

__Michael J. Oard__ has an M.S. in atmospheric science from the University of Washington and is now retired after working as a meteorologist with the US National Weather Service in Montana for 30 years. He is the author of Frozen in Time, Ancient Ice Ages or Gigantic Submarine Landslides?, Flood by Design, Dinosaur Challenges and Mysteries, *and* Exploring Geology with Mr Hibb. *He is a fellow of the Creation Research Society.*

Mendelian speciation: part 2—latent genetic information

Nigel E.A. Crompton, Thomas Sprague, Royal Truman, and Reinhard Junker

Dominance, epistasis, and transposition are all mechanisms able to keep genetic information in a latent state. *Dominant* genes suppress recessive alleles when present in the heterozygous state. *Epistasis* is a form of gene–gene (often protein–protein) interaction which can keep individual genes in a latent state—as well as entire developmental programs if the suppressed (hypostatic) gene is a key regulatory gene. *Transposition* of transposable elements can reversibly activate and deactivate genes. Loss of heterozygosity can cause a variety of latent traits to be expressed. When such traits are phenotypically significant, or sufficient new ones accumulate, novel species are observed to have arisen within a genetic family. A pan-heterozygous ancestor would provide a large pool of latent traits sufficient to produce all the existing species in a family of organisms. This completely circumvents the necessity for new genes to arise, vast numbers of random mutations to accumulate, or for millions of years to elapse.

Mendel's law of exponential trait combinations was presented in part 1 of this series, which described how latent (hidden, or cryptic) genetic information is employed to produce enormous potential for phenotypic variation. *Latent or cryptic information is also a defining characteristic of all organisms* that undergo sequential developmental processes, that are able to respond to internal and external cues, and that pass on lifetime experiences to help their offspring survive, as discussed in Appendix 1.

The existence of latent information is well known, undisputed, and indispensable for survival. Therefore, it comes as no surprise that (1) it is present and that (2) it is able to be quickly expressed as novel combinations of traits producing new species that are potentially better adapted to their environment.

But how are the pre-existent, created genetic programs kept latent, and how are they subsequently expressed? Different combinations of biallelic gene traits produce the different species phenotypes within a genetic family (baramin). How is the information to produce alternate traits stored unexpressed in the genome?

Latent information: dominance, epistasis, and transposition

At least three mechanisms are known to maintain information in a latent state: dominance, epistasis, and transposition.

Dominance

Dominance is observed in hybrids when both traits of a character are present but only one, the dominant trait, is seen; the other, the recessive trait, is not seen, but is 'latent' in the hybrid.[1,2] 'Recessive' describes those traits which disappear completely in the hybrids but reappear unchanged in subsequent generations. Figure 1 displays the offspring of a cross between two types of canids, which was undertaken at the University of Kiel, Germany. The top panel shows the parents, king poodles and a wolf (top panel). The middle panel shows their offspring (F1), which all look alike. The bottom panel shows the grandchildren (F2), the offspring of a cross between the F1s. A variety of recessive traits, hidden in the F1 offspring, suddenly appear, revealing even in this simple example the significant genetic potential that can be held latent (not expressed) in the F1 animals. Dominant traits result from functional proteins; however, recessive traits can result from alternative proteins, or from impaired proteins, or perhaps no protein is translated at all.

Epistasis

Epistasis is a more complex genetic scenario than simple dominant vs. recessive alleles. Epistasis is a consequence of interaction between genes. Gene interaction (technically interaction of their proteins) was first observed in the expression of rooster's combs by Bateson and Punnett in 1905.[3] Roosters use their combs for cooling and to attract mates.

The four rooster comb traits were *Walnut*, *Rose*, *Pea*, and *Single*. Because hybrids with only *Walnut* and *Single* offspring were never observed in crossbreeding attempts, character interaction was proposed to have taken place.[3] Shown in figure 2 are the offspring of the self-cross of *Walnut*, which itself resulted from a cross between *Rose* and *Pea*. The various combs are predicted to occur at the Mendelian ratio of 9:3:3:1.

Figure 1. A king poodle and a wolf (top: parental generation) produced hybrid offspring (centre, F1 = first generation) where many of the traits of the parents are hidden. Various latent traits were expressed and observed when the hybrids mated. They were present in trait combinations not seen in either of the grandparents (lower image, F2 = second generation).

Two genes, each with two alleles, produce four traits of a character as shown in figure 2. *Single* is the standard eye-catching rooster comb. The irregular *Rose* and *Pea* combs are dominant over *Single*. They are believed to be due to mutations caused by inappropriate over-expression of two genes, *MRN2* and *SOX5*, in the embryo's head.[4,5] *Rose* and *Pea* interact to form the greatly reduced *Walnut* comb.

Multiple traits (character alternatives) resulting from gene interactions are now considered unremarkable by biologists, because most characters arise from the activity of not one but a suite of genes. The example in figure 2 is our starting point, and is not an example of epistasis. In this example, two genes interact to produce four traits, in the Mendelian phenotypic ratio of 9:3:3:1. *Epistasis* occurs when at least one of the four possible traits is missing. This results in a phenotype ratio which, missing a trait, is shorter (e.g., 9:3:4 or 12:3:1). Epistasis differs from dominance, where the dominant trait of a character silences the recessive trait of the same character. In epistasis, the presence of one character, referred to as *epistatic*, masks the traits of another character, referred to as *hypostatic*. Epistasis still follows Mendelian genetics; therefore, examples of both dominant and recessive epistasis are observed.

Recessive epistasis

Recessive epistasis occurs when both alleles of the epistatic gene must be recessive in order to suppress expression of it. Coat colour in Labrador dogs is the classic example of this. Coats can be black, brown, or golden, as shown in figure 3. Again, as two genes are involved, one expects four traits, but because only three are observed it suggests epistasis occurring. Labrador coats can be black or brown (the latter is recessive). However, when both alleles of the epistatic gene are recessive, only the golden coat colour is seen. Black and brown Labradors are never seen in self-crosses of golden Labradors. Nevertheless, the information for black and brown coat colours remains latent in their genomes and can be expressed in suitable hybrids.

The example illustrated in figure 3 is based on two genes, both of which display dominance: B (B is dominant over b) and E (E is dominant over e). If at least one B is present, the fur is black. Only if b is doubly recessive (bb) is the fur brown.

Gene E determines whether the coat is dark (black/brown) or light (red/yellow). If at least one dominant E allele is present, the coat is dark. However, if E is doubly recessive (ee), then the coat is light (golden). The light colour is due to the fact that in the absence of dominant E only phaeomelanin is formed. Eumelanin must be produced for the dark colour to develop. In golden Labradors, black and tan traits are still present but latent.

E is thus recessive epistatic over B, because it silences B when doubly recessive (ee). Under these conditions the B traits are present but remain latent in the genome and are not expressed.

Dominant epistasis

Dominant epistasis occurs when a single dominant allele of an epistatic gene is sufficient to prevent expression of both alleles of the hypostatic gene. A classic example is seen in the colour of pumpkin skins. These can be yellow, green, or white. Since the colour trait is determined by two genes, one would expect four traits; but since only three are observed, it suggests epistasis is occurring. The presence of at least one dominant-epistatic allele results in only white fruit being formed. Furthermore, when the dominant-epistatic allele is homozygous (fixed), only white fruit are observed in self-crossing offspring, and yellow and green fruit are never produced (expression of these colours is suppressed). Nevertheless, the information for yellow and green fruits remains latent in the genome and can be expressed in suitable hybrids with pumpkins with the recessive-epistatic allele.

The effects of epistasis are occasionally observed among members of geographically dispersed species. For example, in crosses in which double recessive epistasis occurs, as seen in some ducks (figure 4).

The European shoveler (*Spatula clypeata*, figure 4 A) and the Cinnamon duck (*S. cyanoptera*, figure 4 B) are distinct species. Interestingly, their hybrids look like a third species, the Australian shoveler (*S. rhynchotis*, figures 4 C, D). Particularly interesting is the striking vertical, white eye-stripe seen in the hybrids, which is present in neither parent species, the result of a double epistasis. Information for the expression of the white eye-stripe is latently available in both parent species.[6]

Another example of epistasis is seen in *Arabidopsis thaliana*, a small herbaceous plant of the crucifer family (Brassicaceae). If two key epistatic suppressor genes are knocked out, the offspring take on the form of a shrub similar to an Azalea (figure 5).[7]

The information for the woody trait already exists in *Arabidopsis thaliana*, but is held latent, awaiting expression through epistatic rescue.

Of about 150 crucifer plant species in Central Europe, only one, the rock candytuft (*Iberis saxatilis*), native to Europe and northwest Africa, has a woody phenotype. However, invasion of islands by herbaceous species, from many different families, has led to the unexpected appearance of over 1,000 novel woody phenotypes;[8] and also to the appearance of other latent phenotypes, such as new flower colours and inflorescences (the form the flowers, as a group, take on any single plant).[9,10] This indicates that the lignification (wood-forming) program, as well as other programs, are often held latent but can be expressed when epistatic suppression is turned off.

Why is epistasis so important for Mendelian speciation? In simple dominance situations, one of the two traits of a single character is typically non-functional (e.g., colour is lost) and is not apparent in a recessive state. However, when epistasis is present, entire developmental programs can be held latent, provided the hypostatic gene is a regulatory gene, and release of epistasis can reactivate these programs, which can give rise to even complex novel phenotypes.

Transposition

Transposition refers to when DNA sequences move from one location within the chromosomes of a genome

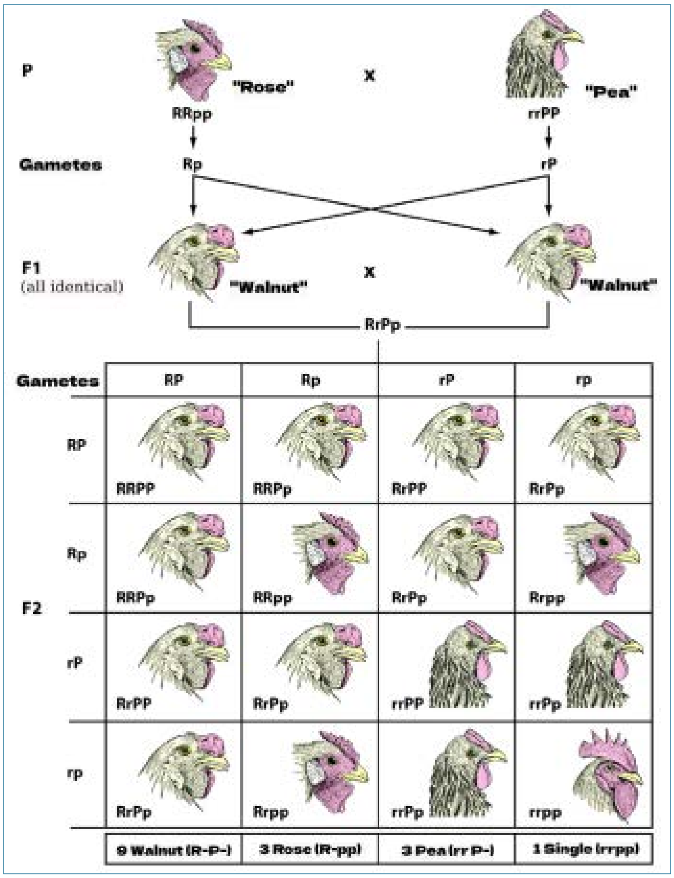


Figure 2. Two genes (each having two alleles) interact to form four rooster-comb traits, so-called gene interaction, documented by geneticists Reginald Punnett and William Bateson of Cambridge University.[3] All four traits are observed. This is gene interaction, not epistasis.

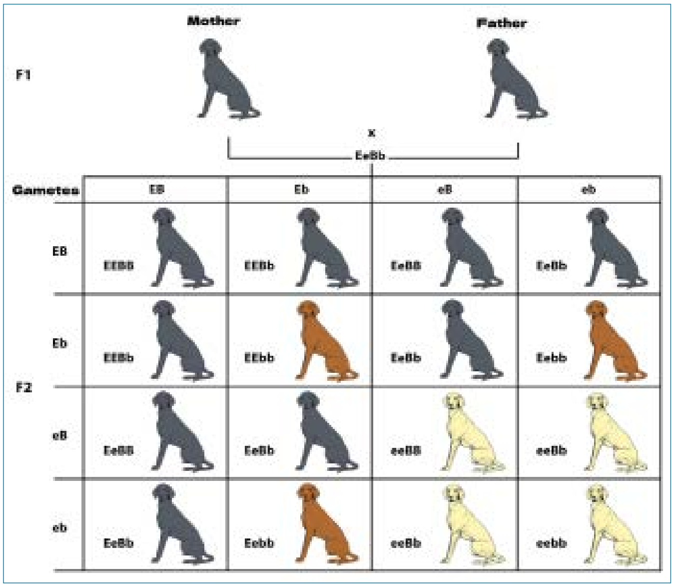


Figure 3. Recessive epistasis using the example of coat colour: dark (black or brown) and light (gold) in Labrador retrievers. Notice that in this example only three traits (not four) are seen.

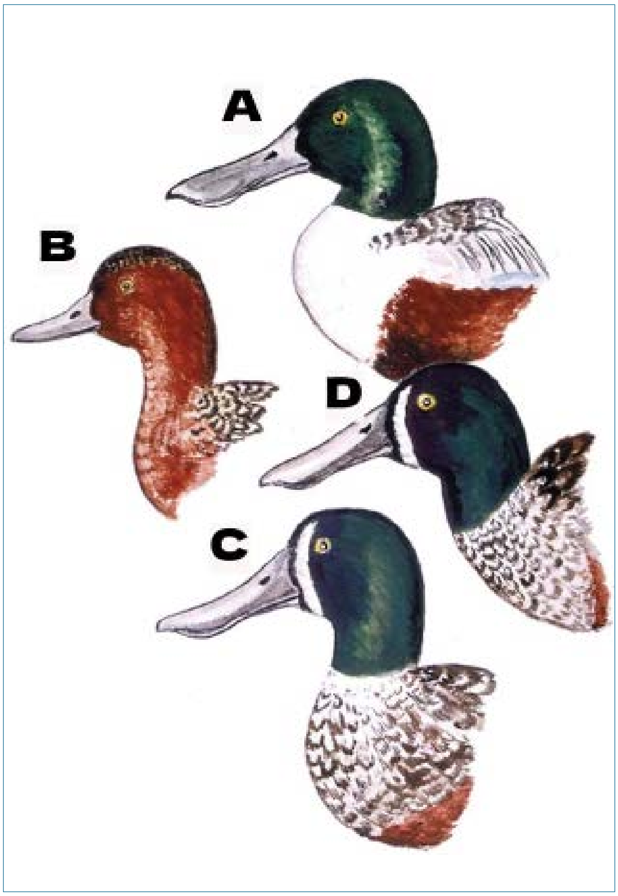


Figure 4. Different phenotypes found in shovelers. A and B are the parents of hybrid C, which looks like D, an unrelated species.

Figure 5. Variants of *Arabidopsis thaliana*. Middle: Cushion-like forms of plant growth of a *soc1-3* and *ful-2* double mutant after 8 months of growth under short-day conditions. Lower left insert: typical appearance of the normal non-mutated, non-woody plant. Lower right insert: lignification (wood) in the *Arabidopsis thaliana* double mutant. (From: ref. (7), reprinted with permission)

to another (figure 6). More often than not this is due to the activity of a transposon. These can move to another position in the genome either by excising and reinserting themselves (DNA transposons) or by first producing an RNA copy of themselves (via transcription) and then inserting a DNA copy of this (via reverse transcription) elsewhere in the genome (retrotransposons). These processes are typically regulated epigenetically by DNA methylation.

These genetic elements are either DNA transposons (Class II TEs) or retrotransposons (Class I TEs), depending on their mechanism of transfer. Expression of novel phenotype traits, and even characters, can be regulated by such relocations, and transposons play an important role in the generation of phenotype diversity.[11] Transposition is responsible for at least one of the features studied by Mendel (seed shape), as discussed in Appendix 2.

The difference between red and white wine is caused by a retrotransposon called ‘Gret1’, which is inserted near a gene responsible for regulating the production of the red anthocyanin pigment in grapes.

Gret1 blocks the expression of this gene, which encodes the transcription factor VvmybA1. When the gene is switched off by the retrotransposon, anthocyanin is no longer produced and the grapes do not turn red. Since only one functional copy of *VvmybA1* is required for the synthesis of anthocyanin, both copies of the gene must be switched off (which could result from self-crossing) to produce the homozygous form with both copies of *VvmybA1* silenced by *Gret1*. This is the case with white wine varieties, see figure 7.

However, when *Gret1* moves away (jumps out), the *VvmybA1* allele regains activity and red pigment is produced again.[12]

Another notable example of transposition-induced trait expression is industrial melanism in peppered moths (*Biston betularia*), which results from the insertion of a large transposon into the first intron of the *cortex* gene. In this case, the transposon causes an increase in *cortex* expression and thereby a darker variant of the peppered moth, as shown in figure 8.[13]

Transposons and Mendelian speciation

Why are transposons important for Mendelian speciation? Unlike traits resulting from irreversible loss of genetic information (e.g., through homozygosity), transposons come and go, thereby fully deactivating or fine-tuning gene expression. In these cases the trait information is not lost, even when genes appear to be ‘fixed’ in the homozygous state. When the transposons move away from their position, the information previously suppressed is reactivated. Transposition allows for the temporary suppression of genetic information for one or many generations, as well as its subsequent re-release.

Dominance, epistasis, and transposition collaborate to produce many alternative traits. Recessive traits can appear by simple inactivation of the dominant trait, such as by base pair substitution (i.e., a mutation). Far more flexible is the use of inserted genetic elements like transposons.

Extensive research has shown that epigenetic modifications can regulate the dosage of a particular function (or trait). They can be activated in specific locations in organs and tissues in a regulated manner in response to internal and external cues.[11] These genetic modifications are not necessary for the development of the characters themselves, but they can elegantly give rise to their alternative manifestations (traits).

Species and genetic families

Many definitions of species have been proposed in the history of biology. Some of these are based on genetics. However, objective definition uses combinations of traits. *De facto*, (in practice) a species is defined—more or less—by a unique set of traits.

In general, individual minimal trait differences are not sufficient to define a species (e.g., only pink versus red petals). Mendel commented that well-defined species differ in many characters. However, he conceded that some pea variants are sometimes classified as independent species. He acknowledged that some workers use sharp demarcation criteria to separate species, even single trait differences being considered sufficient justification for identifying a species; though most workers considered these varieties.[14]

Sometimes it is not clear what exactly defines a separate species. The famous silversword alliance of Hawaii is a plant group of three genera and 30 species in the sunflower family (Asteraceae). They are all so closely related they all easily form hybrids. All apparently belong to a genetic family, since they can all interbreed.[15,16] However, species within genetic families can differ in many significant characters and show exceptionally different morphologies. This is typical for many eukaryotic species, e.g., cats,[17] and dogs;[18] waterfowl (reference 6), and birds of paradise[19].

This raises the question about mechanisms of speciation. Attributing speciation to accrual of gene changes (mutations) is popular in mainstream science. Evidence for it, however, is scanty, and it has the potential to encourage eugenics. A gene change in *MC1R* results in red hair,[20] in *SLC24A5* results in light skin,[21] and in *HERC2* results in blue eyes.[22] However, people expressing from one to all three of these genetic changes / features even after very many generations, are neither a new species nor shifting toward one but remain *Homo sapiens*. Healthy new traits do not simply give rise to new species. More unusual mutations such as hypertrichosis (super-abundant hair), coloboma (iris distortion), sickle-cell

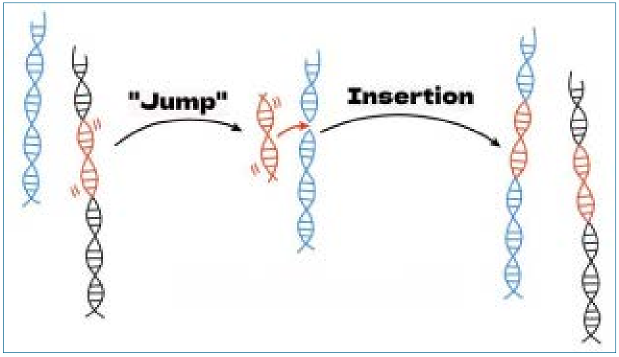


Figure 6. Schematic representation of the transposition of a transposon. Shown are two different chromosomes (blue and black) with a transposon (left, red). When 'jumping', the transposon locates next to the blue chromosome (middle) and inserts into this chromosome (right, blue chromosome). Both chromosomes possess a copy of the transposon after this form of transposition, which involves making a DNA copy of the original transposons' RNA.

Left: U.S. Department of Agriculture—Agricultural Research Service / Public Domain;
Right: Kuschti / Public Domain

Figure 7. Red and white grape varieties are due to the action of retrotransposons (see text).

Figure 8. The light and dark forms of the peppered moth (*Biston betularia*) are due to the effect of a retrotransposon.

anaemia, or Down syndrome do not reflect incipient novel speciation events. The fruit fly, *Drosophila melanogaster*, can be extensively mutated, even as far as causing organs to appear in abnormal locations, yet a new species is not observed, it remains *Drosophila melanogaster*.

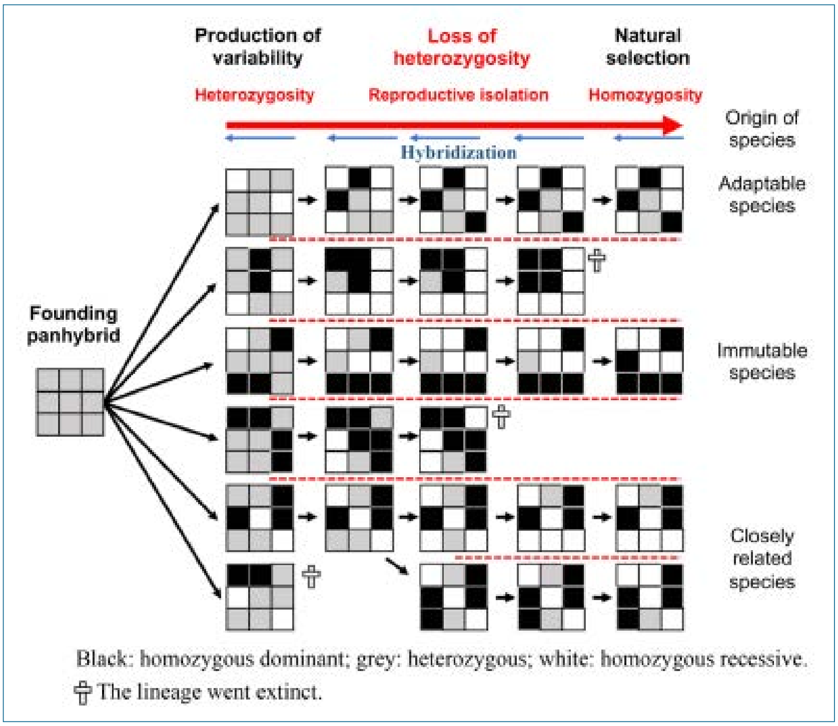


Figure 9. Loss of heterozygosity using a hypothetical nine-trait organism as an example. The initial panhybrid generates new lineages, which then produces distinct new species via meiosis and reproductive isolation. Populations (species) may become extinct for various reasons, rows 2, 4 and 6 (✝). The red-dashed lines separating the lineages indicate reproductive isolation.

Simple random mutations are implausible speciation events. Multiple allele differences typically distinguish separate species. Mules and ligers (crosses between horses and asses, and lions and tigers, respectively) are hybrids with the complete genomes of both parent species mixed together. By using established crossing techniques, both parental species (and potentially other alternatives) could be selected from the mix. Various hybrids actually look like, or are, third species, e.g., the Australian shoveler (figure 4), and the gray snub-nosed monkey.[51] Meiosis (cell division associated with gamete formation and a halving of the chromosome complement) segregates unique multiple allele combinations and can give rise to an abundance of potential species (figure 1). Both hybridization and meiosis affect multiple genes simultaneously, and within a single event. More importantly, the new allele combinations these processes give rise to are expected to be functional combinations; as opposed to mutated DNA sequences, which are expected to be detrimental changes, as exposure to mutagens confirms.

Loss of heterogeneity

Hybridization promotes heterozygosity. Conversely, reproductive isolation results in loss of heterozygosity. Loss of heterozygosity leads to unique combinations of homozygous dominant and recessive traits, i.e., the emergence of species, as shown in figure 9.

The last column in figure 9 represents extant populations (species). Most have retained some heterozygosity and potential for diversification. One species (3rd row) is fully homozygous 'constant'. Hybridization can partially reverse the loss of heterozygosity (chain of blue arrows).

The loss of mixed alleles gradually leads to new (homozygous) combinations of characters. Mendel's law of exponential trait combinations indicates that n unique, pure-breed characters can give rise to 2^n different trait combinations, only one of which is identical to the original parent hybrid.[29] The offspring retain the same number of characters (genes). It is the combinations of dominant and recessive traits that differ, and it is these that give rise to new species.

As mixed inheritance is lost, the previous heterozygous (varying) traits become more homozygous (constant) with each generation. When a new population having an appropriate (species-defining) mixture of homozygous (constant) traits arises, a new species has come into existence. To emphasize: it is the loss of heterozygosity that enables hybrids to form novel homozygous trait combinations, and because these are reproductively isolated, they are new species.

Prior to whole genome sequencing, hybridization was considered to play a negligible, if any, role in speciation, especially among animals. This was because some hybrids are sterile, e.g., mules and hinnies, and also because of Mayr's definition of species, "Species are groups of interbreeding natural populations that are reproductively isolated from other such groups."[23] If species are reproductively isolated, then hybrids must be unusual and counter-productive. However, since genome sequencing, hybridization is now confirmed to be a highly critical component of speciation and adaptive radiations;[24] examples include Darwin's finches,[25] cichlid fish,[26] as well as other fish,[27] and postman butterflies.[28]

Discussion

Extensive phenotypic variation is a natural consequence of meiosis, as well as its propensity to convert heterozygous into homozygous genes, which inexorably leads to new species (figure 9) as described in detail in Part 1 of this series.[29] The alternative mechanism for explaining the origin of species, discussed in genetic and biological textbooks based on Darwinian assumptions, is random mutations. In theory, numerous beneficial mutations could potentially bring about profound changes. Mathematical models of how long this might take indicate billions of generations.[30] Undisputed natural examples of multiple beneficial, information-increasing mutations are essentially unknown in eukaryotes.[31] This has always been an Achilles' heel of evolution theory. Mutations are primarily associated with functional losses, a point thoroughly explored by John Sandford[32] and Michael Behe.[33]

Latent genetic information or numerous mutations as the basis for speciation?

In general, the following two observations are repeatedly made: mutations do not form new phenotypic characters (traits, yes; characters, no); and mutations do not form new distinct species. Multiple beneficial mutations would be required to create a new beneficial character, a highly improbable scenario.

However, multiple mutations cause significant genetic and phenotypic collateral damage, since mutations that accumulate in latent (recessive) characters as genetic variants are a source of ultimately damaging change.[33] Accumulating mutations tend to degrade genetic information.[34,35] Mutation is primarily a consequence of entropy in the biological world, which is predicted to inexorably purge biological information, particularly latent genetic information, in eukaryotes.[32]

Processes that contribute to speciation

There are three processes that contribute to speciation:

- Meiotic recombination of existing trait information (segregation)
- Reproductive isolation
- Selection

The first process, meiotic recombination of existing trait information, produces numerous novel trait combinations. The second process, reproductive isolation, is necessary to avoid hybridization (i.e., restoration of heterozygosity), which causes characteristic recessive traits to once again become latent and removes barriers to species separation. The third process, selection, leads to the 'favoured races' of Darwinian philosophy.[36]

The first process discovered by Mendel (and now known as *meiotic recombination*) enables latent phenotypic traits to be expressed.[1] His studies of hybrids were carried out on closely related plants with different alleles for one, two, or three genes.

However, hybrids can also occur between individuals of different genera, even if these differ by numerous alleles. Species within genetic families share compatible genes, and interbreeding can occur naturally. However, species from separate genetic families are thought likely to possess incompatible sets of genes; so that any crosses in the wild would not result in viable hybrids.

The second process, repr*oductive isolation*, is important to maintain new trait combinations and, therefore, novel species. These arise as novel combinations of dominant and recessive traits, as will be further elaborated on in Part 3 of this series.

The third process, *selection*, made famous by Darwin, is inevitable.[36] Selection comes in different forms referred to as natural, artificial, and sexual selection. However, selection offers no explanation for the *emergence* of novel phenotypic characters—it can eliminate existing varieties, but it *cannot create* them. Therefore, selection does not explain the origin of species. However, once novel combinations of traits appear, if those combinations (phenotypes) are advantageous (more fit), selection will favour them over other phenotypes (said to be less fit) within a population.

However, if the traits lead to net disadvantaged individuals, then selection will work against them, eliminating their deleterious phenotypes from a population.

Latent genetic information as a crucial source of novelty

Latent genetic information (Mendel's recessive elements) remains the decisive source of phenotypic novelty. The scientific community is increasingly recognizing this. In cases where features are irreducibly complex (i.e., a number of functioning components must be present simultaneously), they must be able to interact with each other for the whole to function. It is obvious that mutation events cannot satisfactorily explain how such irreducibly complex features can arise.

In such cases, it has been proposed that existing information is co-opted; that is, reused to overcome the impossible number of complementary beneficial mutations necessary to produce *de novo* information. It is important to understand that the term 'co-option' is being used here simply as another way of saying 'use of pre-existing genetic programs' makes speciation possible. Indeed, the extraordinary radiation of the cichlids of the African Great Lakes has been attributed to pre-existing sources of genetic variation.[37] In other words, the majority of the thousands of speciation events that took place in these fishes resulted from pre-existing genetic programs, which were already present in the cichlid genome.[26]

Part 3 of this series will address the contribution of reproductive isolation to speciation once pre-existing genetic programs have recombined to produce a plethora of novel phenotypes.

It has been asked, what would the founding generation of a new species look like? This is obviously a highly speculative question. Mendel's peas were self-pollinating; theoretically a single pan-heterozygous plant would rapidly give rise to a plethora of different genera and species. However, many plants and most animals have two genders. Due to genetic drift, loss of heterozygosity and speciation still take place. However, in this case it requires more generations, depending on the population size. If such populations were initiated with a pan-heterozygous founding pair, each gene could be represented with four alleles, and double the diversity potential. This potential would increase as the number of founding members, and specifically as the number of different alleles of each gene, increased in any family of organisms.

Appendix 1. Latent (cryptic) information is a characteristic of all organisms

The existence of latent genetic information is well established. There are many methods to extract and implement coded instructions, as reported by Truman since 2012 under the term 'Coded Information Systems'.[38,39]

Case 1. Latent information expressed during different periods in a multicellular eukaryotic organism's lifetime.

- Zygotes already contain information which can be activated at the right time to produce the variety of cell types found in a multicellular organism.
- Metamorphoses are dramatic examples whereby the same genomes produce different organisms having entirely different body parts and behaviours.
  - » Butterflies: egg → larva (caterpillar) → pupa (chrysalis) → butterfly
  - » Frogs: egg → tadpole → frog
  - » Beetles: egg → grub (maggot) → beetle
  - » Schistosoma parasite: egg → miracidia (free-swimming) → sporocysts (within a host snail) → cercariae (tadpole-like larva engulfed by a piscine host) → schistosomulae (within mammalian host) → male and female worms which mate to form new eggs.[40] Even the ability to produce both genders has been latently conserved!

Case 2. Latent information expressed rapidly in response to input from cellular sensors.

- Immune system defences when under attack.
- Repair of damaged tissue.
- Regeneration of entire missing limb, including the bones, muscles, and nerves. Many organisms like salamanders do this very effectively.
- Stress responses to temperature extremes, nutrient deprivation, or exposure to toxins.
- Dormancy and germination in which seeds of plants and spores of fungi are maintained in a dormant state until activated by specific cues.
- Diapause, a state of suspended development or dormancy particularly for insects, to halt or slow down development in response to unfavourable environmental conditions.
- Phenotypic plasticity to respond to environmental cues in a coordinated manner. For example, plants can produce different leaf shapes or flowering patterns based on cues from light intensity or nutrient availability.

Case 3. Latent information passed down generations.

- Examples have been presented in this 3-part series which conform to Mendel's rules.
- Transgenerational epigenetic changes have been reported, which result from parental experiences like diet, stress, or toxins. Germ cell DNA and proteins can be tagged with special informative ligands.
- Epigenetic silencing sometimes occurs when transposable elements jump between sites in the genome.[11]
- Paramutation involves transfer of an allele's silent state to also silence its active homologue allele. Although poorly understood at this time, it has been observed in pea, maize, tomato, worm, fruit fly, and mouse.[41] A silencing RNA mechanism may be involved in some cases.

Appendix 2. Mendel's experimental results from today's perspective

The molecular biology basis for dominance, epistasis and transposition were unknown to Mendel. Still, he wrote about the 'internal makeup' in his plant hybrids (their genotype), and what was passed on to the offspring, which he called 'elements', corresponding to what is now understood to be genes or alleles. He clearly recognized that hybridization at fertilization was due to the material nature and arrangement of his so-called 'elements', which came into viable union in the zygote.

What do we know today about the physical nature and arrangement of what Mendel called 'elements', the alternative alleles? Mendel studied seven pea characters.

The molecular basis of Mendel's characters must be understood in their biological context. The characters are represented by varieties of Garden Peas. They are the result of numerous generations of self-pollination; therefore, the characters will have become completely homozygous, any heterozygosity will have been lost. How can alternative traits exist under such conditions? They arise in one of two ways, by transposition or by mutation. In either case, if these processes have resulted as a consequence of the Fall (and not as part of the original design), then the traits that arise are expected to reflect loss of functional information.

The first feature was seed *shape*. Ripe seeds are either round or wrinkled in shape. Wrinkled peas are more commercially attractive because they are sweeter than round peas. The wrinkled form is recessive (r/r). It is caused by a transposon that is inserted into the gene that encodes the starch-splitting enzyme. This insertion leads to an accumulation of simple sugars, which eventually leads to enhanced cotyledon shrinkage and a wrinkled pea.[42,43]

The second character was *seed colour*. The seeds are either yellow or green. The green form is recessive (i/i). It results from the insertion of six nucleotides, knocking out the *sgr* gene, which is responsible for the cleavage of chlorophyll molecules associated with senescence.[44,45,46] This insertion of six nucleotides is evidence of a transposon having once been present but now removed from that gene location, leaving six nucleotides.[47]

The third character was *seed coat colour*—which also defines *flower colour*. The flowers are either purple or white. The white form is recessive (a/a). It results from a mutation, namely a guanine to adenine transition at a splice site in the dominant *A* gene, resulting in a truncated transcription factor. This factor is used to regulate the expression of genes required for the synthesis of anthocyanin (violet pigment).[48]

The fourth, fifth, and sixth traits have not yet been sufficiently studied at the molecular level. The seventh character was *stem length*. Plants are either normal height or dwarf. The dwarf form is recessive (le/le). It results from a transition from guanine to adenine, which leads to a substitution of the amino acid alanine to threonine. As a result, a 3b-hydroxylase enzyme (= 3-oxidase) is no longer able to form active gibberellin hormone, which results in inhibited growth.[49,50]

These are four instructive examples. Three changes resulted from information loss, underscoring just how damaging mutational events are.[33] However, Mendel's first feature arose from a transposition event. In this case the information was not lost. Even if a population of such plants was isolated and the r/r homozygous state was fixed, movement of the transposon could restore the function of the original dominant *R* gene at any subsequent generation.

Transposons are ubiquitous and account for a large proportion of the DNA in most organisms. It is reasonable to assume that they play an important role in phenotypic diversity.[11]

References

1. Mendel, G., Versuche über Pflanzenhybriden, *Verh. Naturforsch. Vereins Brünn* **4**:3–47, 1866; link.springer.com/book/10.1007/978-3-663-19714-0.
2. Mendel, ref. 1, p. 11.
3. Bateson, W. and Punnett, R.C., A suggestion as to the nature of 'walnut' comb in fowls, *Proc. Camb. Phil. Soc.* **13**:165–168, 1905.
4. Boije, H., Harun-Or-Rashid, M. *et al.*, Sonic Hedgehog-signalling patterns the developing chicken comb as revealed by exploration of the pea-comb mutation, PLoS One **7**:e50890, 2012 | doi:10.1371/journal.pone.0050890.
5. Imsland, F., Feng, C. *et al.*, The Rose-comb mutation in chickens constitutes a structural rearrangement causing both altered comb morphology and defective sperm motility, *PloS Genet* **8**:e1002775, 2012 | doi:10.1371/journal.pgen.1002775.
6. Scherer, S. and Hilsberg, T., Hybridisierung und Verwandtschaftsgrade innerhalb der Anatidae—eine systematische und evolutionstheoretische Betrachtung, *Ornithol.* **123**:357–380, 1982 | doi:10.1007/BF01643271.
7. Melzer, S., Lens, F., Gennen, J., Vanneste, S., Rohde, A., and Beekham, T., Flowering-time genes modulate meristem determinacy and growth form in Arabidopsis thaliana, *Nature Genet.* **40**:1489–1492, 2008 | doi:10.1038/ng.253.
8. Zizka, A., Onstein, R.E., Rozzi, R., Weigelt, P., Kreft, H., Steinbauer, M.J., Bruelheide, H. and Lens, F., The evolution of insular woodiness, PNAS **119** e2208629119, 2022 | doi:10.1073/pnas.2208629119.
9. Carlquist, S., Wood anatomy of Macaronesian and other Brassicaceae, *Aliso* **7**:365–384, 1971 | doi:10.5642/aliso.19710703.09.
10. Carlquist, S., *Island Biology*, Columbia University Press, New York, 1974.
11. Borger, P., *Darwin Revisited: Or how to understand biology in the 21st century,* Scholar's Press, 2018.
12. Kobayashi, S., Goto-Yamamoto, N., and Hirochika, H., Retrotransposon-induced mutations in grape skin colour, *Science* **304**:982, 2004 | doi:10.1126/science.1095011.
13. Van't Hof, A.E., Campagne, P., *et al.*, The industrial melanism mutation in British peppered moths is a transposable element, *Nature* **534**:102–105, 2016 | doi:10.1038/nature17951.
14. Mendel, ref. 1, p. 6.
15. Crompton, N.E.A., Die Radiation der Silberschwert-Gruppe. 1. Indizien für präexistente genetische Programme, *Stud. Integr.* **29**(32):80–89, 2022.
16. Crompton, N.E.A., Die Radiation der Silberschwert-Gruppe. 2. Hybriden und die Geschichte der Silberschwerte, *Stud. Integr.* **30**(1):13–19, 2023.
17. Pendragon, B., and Winkler, N., The family of cats—delineation of the feline basic type, *J. Creation* **25**(2):188–124, 2011.
18. Pendragon, B., A review of selected features of the family Canidae with reference to its fundamental taxonomic status, *J. Creation* **25**(3):79–88, 2011.
19. Crompton, N.E.A., Die Paradiesvögel. 1. Farbenpracht, Vielfalt, und Einheit; und ihre Hybriden, *Stud. Integr.* **25**(2):88–97, 2017.
20. Valverde, P., Healy, E., Jackson, I., Rees, J.L. and Thody, A.J., Variants of the melanocyte–stimulating hormone receptor gene are associated with red hair and fair skin in humans, *Nat. Genet.* **11**:328–330, 1995.
21. Lamazon, R.L., Mohideen, M.P.K., Mest, J.R., Wong, A.C. *et al.*, SLC24A5, a putative cation exchanger, affects pigmentation in zebrafish and humans, *Science* **310**:1782–1786, 2005 | doi:10.1126/science.1116238.
22. Sturm, R.A., Duffy, D.L., Zhao, Z.Z., Leite, F.P.N., Stark, M.S., Hayward, N.K., Martin, N.G., and Montgomery, G.W., A Single SNP in an Evolutionary conserved region within Intron 86 of the HERC2 gene determines human blue–brown eye color, *Am. J. Human Genet.* **82**:424–431, 2008.
23. Mayr, E., *Systematics and the Origin of Species*, Columbia University Press, New York, 1942.
24. Kagawa, K., and Takimoto, G., Hybridization can promote adaptive radiation by means of transgressive segregation, *Ecology Letters*:**21**:264–274, 2018.
25. Lamichhaney, S., Berglund, J., Almen, M.S., Maqbool, K., Grabherr, M., Martinez-Barrio, A., Promerova, M., Rubin, C., Wang, C., Zamani, N., Grant, B.R., Grant, P.R., Webster, M.T., and Andersson, L., Evolution of Darwin's finches and their beaks revealed by genome sequencing, *Nature* **518**:371–375, 2015.
26. Meier, J.I., Marques, D.A., Mwaiko, S., Wagner, C.E., Excoffier, L., and Seehausen, O., Ancient hybridization fuels rapid cichlid fish adaptive radiations, *Nature comms*. 814363, 2017 | doi:10.1038/ncomms14363.

27. Herder, F., Nolte, A.W., Pfaender, J., Schwarzer, J., Hadiaty, R.K., and Schliewen, U.K., Adaptive radiation and hybridization in Wallace's dreamponds: evidence from sailfin silversides in the Malili Lakes of Sulawesi, *Proc. Royal Soc. B* **273**:2209–2217, 2006.
28. Dasmahapatra, K.K., Walters, J.R., Briscoe, A.D., Davey, J.W., Whibley, A. *et al.*, Butterfly genome reveals promiscuous exchange of mimicry adaptations among species, *Nature* **487**:94–98, 2012.
29. Crompton, N.E.A., Mendelian speciation: part 1—what is the abundant source of significant biodiversity? *J. Creation* **37**(3):110–120, 2023b.
30. Hössjer, O., Bechly, G., and Gauger, A., On the waiting time until coordinated mutations get fixed in regulatory sequences, *J. Theor. Biol.* **524**:110657, 2021 | doi:10.1016/j.jtbi.2021.110657.
31. Multiple beneficial mutations are required simultaneously to enable a new function. If they occur successively, they would have to be coordinated and be selectable at any time. For probabilistic reasons this is not plausible and has never been observed in practice. For each new advantageous mutation, the probability of that organism benefitting is exponentially less likely for each additional suitable mutation.
32. Sanford, J.C., *Genetic Entropy and the Mystery of the Genome*, Ivan Press, 2005.
33. Behe, M.J., *Darwin Devolves: The new science about DNA that challenges evolution*, New York, 2019.
34. Schoen, D.J., David, J.L., and Bataillon, T.M., Deleterious mutation accumulation and the regeneration of genetic resources, PNAS **95**:394–399, 1998 | doi:10.1073/pnas.95.1.394.
35. Uchimura, A., Higuchi, M., *et al.*, Germline mutation rates and the long-term phenotypic effects of mutation accumulation in wild-type laboratory mice and mutator mice, *Genome Res.* **25**:1125–1134, 2017 | doi:10.1101/gr.186148.114.
36. Darwin, C., *On the Origin of Species by Means of Natural Selection, or the Preservation of Favoured Races in the Struggle for Life*, John Murray, London, 1859.
37. Brawand, D., Wagner, C.E. *et al.*, The genomic substrate for adaptive radiation in African cichlid fish, *Nature* **513**:375–381, 2014 | doi:10.1038/nature13726.
38. Truman, R., Information Theory—Part 3: introduction to Coded Information Systems, *J. Creation* **26**(3):115–119, 2012; creation.com/cis-3.
39. Truman, R., Information Theory—part 4: fundamental theorems of coded information systems theory, *J. Creation* **27**(1):71–77, 2013.
40. McManus, D.P., Dunne, D.W., Sacko, M. *et al.*, Schistosomiasis, *Nat. Rev. Dis. Primers* **4**(13):1–19, 2018 | doi:10.1038/s41572-018-0013-8.
41. Gouil, Q., Baulcombe, D.C., Paramutation-like features of multiple natural epialleles in tomato, *BMC Genomics* **19**(203):1–15, 2018 | doi:10.1186/s12864-018-4590-4.
42. Bhattacharyya, M., Smith, A.M., Ellis, T.H.N., Hedley, C., and Martin, C., The wrinkled-seed character of pea described by Mendel is caused by a transposon-like insertion in a gene encoding starch-branching enzyme, *Cell* **60**(1):115–122, 1990 | doi:10.1016/0092-8674(90)90721-p.
43. Reid, J.B. and Ross, J.J., Mendel's genes: toward a full molecular characterization, *Genetics* **189**(1):3–10, 2011 | doi:10.1534/genetics.111.132118.
44. Armstead, I., Donninson, I., Aubry, S., Harper, J., Hörtensteiner, S., James, C., Mani, J., Moffet, M., Ougham, H., Roberts, L., Thomas, A., Weeden, N., Thomas, H., and King, I., Cross-species identification of Mendel's I locus, *Science* **315**:73, 2007 | doi:10.1126/science.1132912.
45. Sato, Y., Morita, R., Nishimura, M., Yamaguchi, H. and Kusaba, M., Mendel's green cotyledon gene encodes a positive regulator of the chlorophyll-degrading pathway, PNAS **104**:14169–14174, 2007 | doi:10.1073/pnas.0705521104.
46. Aubry, S., Mani, J. and Hörtensteiner, S., Stay-green protein, defective in Mendel's green cotyledon mutant, acts independent and upstream of pheophorbide α-oxygenase in the chlorophyll catabolic pathway, *Plant Mol. Biol.* **67**:243–256, 2008 | doi:10.1007/s11103-008-9314-8.
47. Scott, L., Lafoe, D. and Weil, C.F., Adjacent sequences influence DNA repair accompanying transposon excision in maize, *Genetics* **142**:237–246, 1996 | doi:10.1093/genetics/142.1.237.
48. Ellis, T.H.N., Hofer, J.M.I., Timmerman-Vaughan, G.M., Coyne, C.J., and Hellens, R.P., Mendel, 150 years on, *Trends Plant Sci.* **16**:590–596, 2011 | doi:10.1016/j.tplants.2011.06.006.
49. Lester, D.R., Ross, J.J., Davies, P.J., and Ried, J.B., Mendel's stem length gene (Le) encodes a gibberellin 3β-hydroxylase, *Plant Cell* **19**:1435–1443, 1997 | doi:10.1105/tpc.9.8.1435.
50. Martin, D.N., Proebsting, W.M., and Hedden, P., Mendel's dwarfing gene: cDNAs from the Le alleles and function of the expressed proteins, PNAS **94**:8907–8911, 1997 | doi:10.1073/pnas.94.16.8907.
51. Wu, H., Wang, Z., Zhang, Y., Frantz, L., Roos, C., Irwin, D.M., Zhang, C., Liu, X., Wu, D., Huang, S., Gu, T., Liu, J., and Yu, L., Hybrid origin of a primate, the gray snub-nosed monkey, *Science* **380**:926, 2023 | doi:10.1126/science.abl4997.

Nigel E.A. Crompton *has a Ph.D. in biology from the University of Giessen, Germany, and a D.Sc. from the University of Zurich, Switzerland. He worked in mutation and cancer research for twenty years in Germany, the United States, and Switzerland. He was called to teach at Cornerstone University in Grand Rapids, Michigan, where he lectures in biology, genetics, molecular cell biology, and neuroscience.*

Thomas Sprague *has a Ph.D. in mathematics and computer science from Western Michigan University and a masters degree in biblical studies from Dallas Theological Seminary. Prior to retirement, he was a data analyst for a regional affiliate of Feeding America after a thirty-year academic career, most recently as Professor of Mathematics at Cornerstone University in Grand Rapids, Michigan.*

Royal Truman *has bachelor's degrees in chemistry and in computer science from State University of New York; an M.B.A. from the University of Michigan (Ann Arbor); a Ph.D. in organic chemistry from Michigan State University; and a two-year post-graduate 'Fortbildung' in bioinformatics from the Universities of Mannheim and Heidelberg. He works in Germany for a European-based multinational.*

Reinhard Junker *studied biology, mathematics, and theology and gained a Ph.D. in interdisciplinary theology. He has worked as a research assistant at Studiengemeinschaft Wort und Wissen e. V. in Baiersbronn (Black Forest/Germany) for almost 40 years, mainly in the areas of design theory, comparative biology, and palaeontology. He is co-author of* Evolution—a critical textbook *and author of numerous specialist publications and popular books on biological and theological topics.*

How is the Namib Sand Sea explained within the biblical timeframe?

Michael J. Oard

The Namib Sand Sea in west-central Namibia has formed on a pediment between the ocean and the Great Escarpment, which rings southern Africa. Based on present sand delivery rates from the littoral zone, it should have taken over one million years to accumulate the sand. However, three other possible sources exist: the Tsondab Sandstone below the sand sea, the hinterland to the east, and the Sperrgebiet (an extensive rocky and sand-covered plain south of the Namib Desert). West-to-east changes in mineralogy and colour suggest sand from these sources. The Flood and a post-Flood rapid Ice Age can account for the volume of sand in the Namib Sand Sea.

Garzanti[1] and Dickinson[2] point out several myths in the earth sciences, including suspect terranes, mantle plumes, global sequence stratigraphy, Wilson cycles, and snowball Earth. Garzanti, a specialist in sands and sandstones, focuses on the myth that sands become more mineralogically and texturally mature through mechanical and chemical weathering. As proof, he points to the dry climate of southwest Africa in which chemical weathering can be eliminated, leaving just mechanical weathering. He notes no trend of textural and mineralogic maturity over 2,000 km of transport down the Orange River and 1,800 km of littoral transport northward from the Orange River to Angola. However, as sand is blown inland, wind rapidly rounds grains, resulting in textural maturity, especially for medium-large grain sizes.

Namib Sand Sea

The 'Namib Desert' is a coastal desert in southwest Africa, stretching 1,800 km from the Olifants River of northwestern South Africa northward through Namibia into Angola (figure 1). In Namibia, the desert (erg; a desert composed mostly of sand dunes) or Namib Sand Sea stretches 600 km along the coast, covering 34,000 km^2 between Luderitz and the Kuiseb River. The Namib Sand Sea has been well studied.[3–9] It extends 100–150 km inland to the base of the Great Escarpment (figure 2).[3] The Kuiseb River flows annually past Gobabeb but then diminishes and vanishes in the desert. It is known to have reached the Atlantic Ocean only 15 times between 1837 and 1989. Southerly winds have pushed the desert sands and the river northward 30 km, which is why the river takes a north-west turn from near Gobabeb to the coast.

The Great Escarpment is the semi-continuous coastal escarpment outcropping over 3,500 km around southern Africa (figure 3).[10,11] Planation surfaces have also formed on the plateau above the Great Escarpment from the Escarpment to the coast. In Namibia, the Great Escarpment rises from about 1,000 m at its base to 1,500–2,500 m above sea level (asl). The origin of the escarpment is a uniformitarian mystery. It is thought to have retreated inland from the coast at a rate of 5–7.5 km/Myr.[12]

Several rivers flow off the escarpment but do not extend very far out into the sand sea. The Tsondab and Tsahchab Rivers flow ephemerally today but have well defined valleys cut 80 to 200 m into the underlying Tsondab Sandstone, indicating greater flow during the past. These rivers penetrate west into the Sand Sea for 40–80 km, then disappear among the dunes in extensive playas.

South of the Namib Desert is the Sperrgebiet, an extensive rocky and sand-covered plain with some sand dunes. It runs from the coast to the Great Escarpment and from the Orange River northward to the dry Koichab River. 'Sperrgebiet' is a German word for 'prohibited area' after the discovery of alluvial diamonds at the mouth of the Orange River.

The surface below the Sand Sea is a large planation surface or pediment with inselbergs, such as the 600 m high Spitzkoppe (figure 4). The pediment was eroded into the Tsondab Sandstone, which, in turn, overlies Precambrian bedrock.[13] The Tsondab Sandstone is 45–220 m thick, and its dates have historically varied. Lancaster thought it Oligocene, but mammal fossils in nearby formations suggest it is Miocene or Pliocene.[14] Ward thought the sand was early- to mid-Cenozoic.[15] It is now dated Miocene, based on biostratigraphy.

The climate of the Namib Desert is arid to hyper-arid. Temperatures are hot near the Great Escarpment but relatively cool with fog and related light drizzle near the coast, due to the cold Benguela Current offshore. Rainfall increases northwards into Angola. The southern part of the Sand Sea has little rainfall, although winter storms that affect the

Image: Jeff Schmaltz, MODIS Land Rapid Response Team, NASA GSFC; Wikimedia / Public Domain (modified)

Figure 1. The Namib Sand Sea with the Orange River to the south

Image: Heyheyuwb, Wikimedia / CC BY SA 3.0

Figure 2. The Great Escarpment of Namibia in the background with inselbergs in the foreground

southwestern Cape might move as far north as into southern Namibia. Mean annual rainfall ranges from 15 mm or less at the coast to 27 mm at Gobabeb and 87 mm at Ganab near the Escarpment. The wind is generally from the south to southwest, but sometimes shifts and becomes strong from the east to northeast during winter, especially in the eastern Namib Desert.[16]

Some of the largest sand dunes in the world occur here. About 75% of the dunes are linear (figure 5), with the rest being crescentic or star dunes.[17] The dunes start right at the coast (figure 6). The linear dunes rise up to 180 m above the interdune areas, while star dunes are up to 200–350 m high. It is interesting that linear dunes are the most widespread type of desert sand dune today but rare in the geological record.[18] Wind energy and sand transport decrease eastward.[19]

The sand believed to have collected over a million years

The sand today is believed to be the Orange River sediment that is transported down its 2,000 km length, then spread northward by a 3-km-wide littoral transport system along the coast.[19] This sand is then moved inland by south to southwest winds. A small volume of sand is also contributed by the ephemeral rivers off the Escarpment.

Researchers have calculated how long it would take to accumulate the sand in the Namib Sand Sea by dividing the total volume by the annual input. The volume of sand has been variably estimated at 375–1,020 km^3.[19] A later estimate was 773–1,020 km^3.[20] Sand is added at about 400,000 m^3/yr. If these assumptions are correct, the desert has been operating for over 1 million years, assuming zero sand at the beginning and uniform rates for the replenishment system.

The aridity of the area supposedly goes back to the Miocene, greater than 5 Ma, as verified by cosmogenic nuclide dating.[21] However, regarding the dunes themselves, optical stimulated luminescence gave dates of 5.7 to 43 ka.[19] Bristow *et al*. state, "The oldest sands within the dune are 5,700 yr old, indicating complete turnover of sand during the Holocene."[22]

Four possible sources for the Namib sand

Researchers have recognized three possible sources of sand for the Namib Desert: (1) northward littoral transport from the Orange River delta, (2) the Tsondab Sandstone below the erg, and (3) rivers and ephemeral streams from the Great Escarpment.[21] A fourth possibility, not considered by current researchers, is from the Sperrgebiet to the south.

The Orange River source

The source of Namib sand was poorly constrained in 2010: "The Namib Sand Sea is one of the world's oldest and largest sand deserts, yet little is known about the source of the sand in this, or other large deserts."[23] However, Garzanti *et al*. claim that 90% of the sand is from the Orange River, which starts in eastern South Africa, near Lesotho, and flows 2,000 km to the Atlantic Ocean (figure 7).[20] This would be a present-day estimate, but in the past, other sources could have added much sand, and because of uniformitarianism, they are not considered significant. It must be remembered that research usually only studies the tops of the sand dunes that are probed,[24] which would be expected to have originated from the Orange River delta after the Flood. But the deeper sand may show evidence of having originated from other sources.

The Tsondab Sandstone

The Tsondab Sandstone has often been considered a possible source, especially in the east.[21] It is only partially lithified,[19] so it would erode easily. The Tsondab Sandstone is reddish due to an iron oxide coating; the grains are mostly fine to medium quartz, subangular to rounded, well to poorly sorted, with one location showing the foreset dips oriented to the north to northeast.[25] However, other researchers state that the dominant dip direction is toward the south.[13]

The Tsondab Sandstone is quite similar to the desert sand,[20] so some of the sand of the Namib erg is likely reworked from erosion of this formation. Garzanti *et al.* state that the sand and the Tsondab Formation are quite similar:

> "A major potential source of recycled sand is the up to 220 m-thick Tsondab Sandstone, underlying much of the modern sand sea (Ward, 1988). This unit displays quite similar morphology, geometry and mineralogy of modern linear dunes, and represents a Miocene analogue of the present erg."[26]

Garzanti *et al*. later state:

> "A major potential source of recycled sand for the Namib dunes is the partially lithified Tsondab Sandstone, which underlies much of the moderns and sea [refs]. … Textural and mineralogical evidence thus fully supports the very close analogy between the ancient fossil desert and the modern active one [refs]. Virtually identical textural and mineralogical features unfortunately prevent the present authors from establishing how much mobile sand is recycled from the underlying aeolianites."[27]

Garzanti *et al*. still later reinforced the point:

> "As documented by the Tsondab Sandstone, which underlies most of the modern Namib Erg and represents its Miocene predecessor characterized by impressively similar sedimentological and mineralogical features."[28]

The Tsondab Sandstone has been considered an earlier version of the Namib Sand Sea,[13] but it cannot be an older analogue for the Namib Desert sand since the leeward side of dunes dips predominantly in the opposite direction.[13] Because the Tsondab Sandstone is so similar, researchers do not know how much of the Tsondab Sandstone was added to the Namib Sand Sea. It could have been substantial in the past, accounting for a large part of the sand. At least the

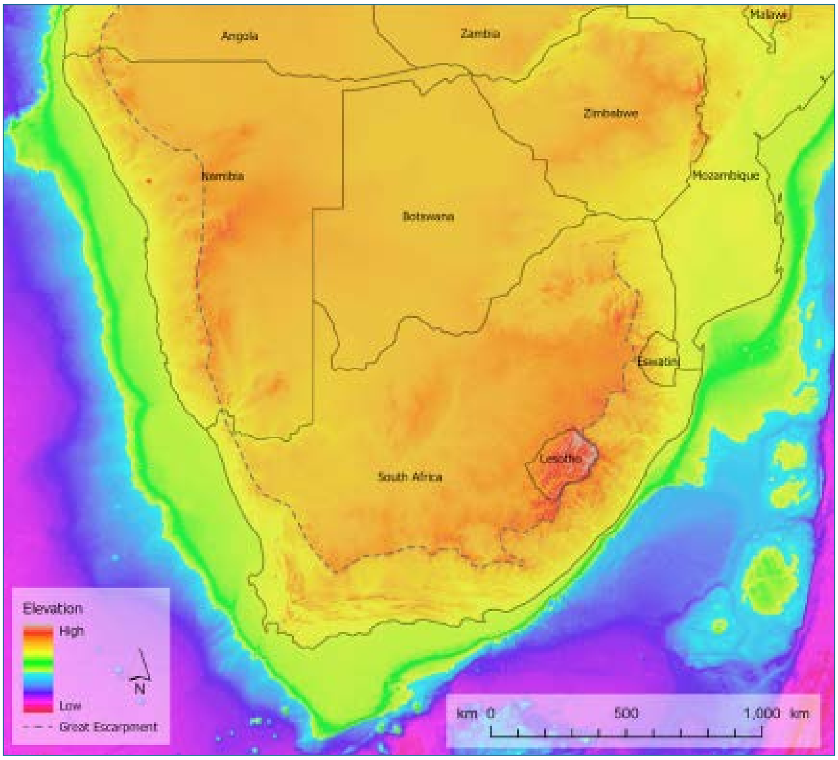


Figure 3. The Great Escarpment that parallels most of the coast of southern Africa

Figure 4. Spitzkoppe Peak, a 600-m tall inselberg on the coastal planation surface in the Namib Desert, Africa

Image: Daniel Kraft Wikimedia / CC BY SA 3.0

Image: ESA, Wikimedia / CC BY SA 3.0 IGO

Figure 5. Linear dunes of the Namib Sand Sea

Image: Robur.q, Wikimedia / CC BY SA 4.0

Figure 6. Coastal dunes of the Namib Sand Sea

researchers acknowledge that some of the Namib sand comes from the Tsondab Formation.

The eastern hinterland

Several researchers have suggested that there is a hinterland source from the Great Escarpment and the terrain to the east. Sand could come from the ephemeral rivers, as observed today. But the conditions likely were much different in the past, as indicated by the depth of erosion in the river valleys. So, this source could have potentially added much of the total volume of sand.

Sperrgebiet, to the south

Researchers do not think much sand came from the south, since there is very little sand there today. But it is possible that in the past, especially when considering Flood runoff, more sand existed in that region. The prevailing winds from the south to southwest would then have carried it to the Namib Sand Sea.

The west to east changes in mineralogy and colour in the Sand Sea

The sand in the Namib Sand Sea is not homogeneous, as would be expected if the source was nothing but the Orange River. One would expect that the coastal dunes would have the same lithology as the Orange River sands, and this is true.[19] Feldspar, volcanics, and heavy minerals are the same for the Orange River and coastal Namib sand. However, there is a west-to-east change in lithology, from the coast to the Great Escarpment, including an increase in quartz and a decrease in volcanic lithic fragments and pyroxene.[19] The eastern dunes reflect more the Tsondab Sandstone and the hinterland to the east. In addition, grain size decreases and sorting increases from west to east.

There is also a gradient in colour. Lancaster writes that the colour increases from pale in the coastal zone to red in the east, because of a thicker iron-oxide coating on the grains.[3] The colour may represent different sand sources, with the red sand originating from the red Tsondab Sandstone.

Possible Flood/post-Flood solution to Namib Desert sand

How can over one million years of sand in the Namib Desert be explained during biblical earth history? Like many challenges from the secular world, this challenge initially seems powerful. But the Flood and the post-Flood rapid Ice Age can explain the volume of sand within the short biblical earth history.

Tremendous erosion in southwest Africa

From a biblical point of view, we need to include the Flood in any discussion of the origin of the sand and the geomorphology of Namibia. Based on the amount of offshore sediment from Walvis Ridge to the Falkland/Agulhas fracture zone (figure 8), about 2,400 m of erosion is estimated to have occurred across southwest Africa![12] During this time, the Great Escarpment formed, probably by retreating inland during Flood erosion. So, the Namib Desert and its surrounding areas were greatly eroded during the Flood.

Planation surfaces formed above and below the Great Escarpment, likely by fast-flowing Flood runoff.[29,30] The planation surface above the Great Escarpment is either part of one African surface that covers much of the continent or a series of planation surfaces separated by erosional scarps and dissected by valleys that are now occupied by rivers and ephemeral streams.[11] New research indicates that the African surface may not be one large continent-scale planation surface that was later faulted or folded to different elevations, as some uniformitarian scientists believe.[31,32]

Sand left over after Flood erosion

I suggest that a large volume of sand in this desert was left as a lag during Flood runoff. Evidence for fast Flood runoff is the existence of coarse gravel at the base of the Tsondab Sandstone.[13] This gravel is predominantly resistant quartz and chert.[33] Some of the sand above the coastal pediment became partially lithified to form the Tsondab Sandstone, while unlithified sand remained on the surface to 'jump start' the Namib Sand Sea. The predominantly south-dipping foresets in the Tsondab Sandstone, different from the foresets of the Namib Sand, do not support an origin of the Tsondab Sandstone from the Orange River Delta. Instead, it was a lag deposit of waning Flood currents flowing off southwest Africa as the continent was uplifted late in the Flood.[29,30]

The east-to-west change in the sand is further evidence that much of the sand was deposited as a lag during Flood runoff, especially the sand to the east. Besler writes that some researchers do not believe the source of the sand for the Tsondab Sandstones is from the Orange River, and that it could have come from the Gamsberg quartzite to the east.[34] The sand in the west may have accumulated after the Flood from the present transport system during and after the Ice Age.

Figure 7. Map of the Orange River and its major tributaries

Image: Keenan Pepper, Wikimedia / CC BY SA 4.0

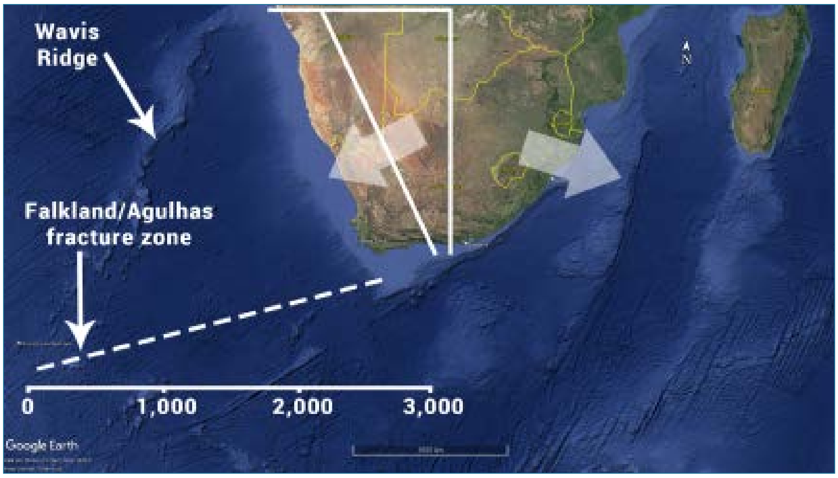


Figure 8. Map of southern Africa and the adjacent oceanic margin (annotations by Melanie Richard). Large arrows show direction of runoff during the uplift of southern Africa. Lines in southwest Africa show the two areas of estimated continental erosion of that area.

Image: Data SIO, NOAA, US Navy, NGA, GEBCO / Public Domain (modified)

Ice Age sand input

The Ice Age would have delivered a little sand to the Sand Sea to add to the lag left by receding floodwater. It is difficult to know the set of ocean currents during the Ice Age, but it is reasonable to infer that the northward Benguela Current and the southerly trade winds developed soon afterward, beginning to transport Orange River Delta sediments north. Sand from the delta would take a fair amount of time to be transported 300–900 km to reach the Namib Desert. Garzanti *et al.* estimate that with a velocity of 1 mm/sec, currents could transport a single sand grain 1,800 km to Angola in only 57 years.[20] Another estimate gives a minimum of 450 to 3,600 years. Regardless, it does not seem that the Ice Age, which lasted about 700 years,[35] would have been a significant source of sand.

Conclusions

The Namib Sand Sea in west-central Namibia is claimed to have over one million years' worth of sand, believed to have originated from the Orange River Delta. However, much of that sand could have come from the underlying Tsondab Sandstone or from the eastern highlands. A third source, not considered, could be the Sperrgebiet to the south.

During the Flood, 2,400 m of erosion occurred over southwest Africa. Such erosion likely left a lag of sand on the pediment that extends from the Great Escarpment to the ocean. The lag would consist of a fining up sequence of conglomerate and breccia forming the base of the Tsondab Sandstone. This sandstone is weakly lithified, transitioning to the unconsolidated sand of the Sand Sea. Ice Age input from the Orange River sands along the coast would have added a little more sand, especially near the coast and atop that deposited during the Flood. The combination of sand sources can account for the west-to-east change in sand properties. We do not need a million years for the sand to accumulate in the Namib Sand Sea. The Flood and post-Flood Ice Age can explain the volume of sand just as readily.

References

1. Garzanti, E., The maturity myth in sedimentology and provenance analysis, *J. Sedimentary Research* **87**:353–365, 2017.
2. Dickinson, W.R., The place and power of myth in geoscience: an associate editor's perspective, *American J. Science* **303**:856–864, 2003.
3. Lancaster, N., *The Namib Sand Sea: Dune forms, processes and sediments*, A.A. Balkema, Rotterdam, Netherlands, 1989.
4. Teller, J.T. and Lancaster, N., Lacustrine sediments in Narabeb in the central Namib Desert, Namibia, *Palaeogeography, Palaeoclimatology, Palaeoecology* **56**:177–195, 1986.
5. Bierman, P.R. and Caffee, M., Slow rates of rock surface erosion and sediment production across the Namib Desert and escarpment, southern Africa, *American J. Science* **301**:326–358, 2001.
6. Chase, B.M., Meadows, M.E., Scott, L., Thomas, D.S.G., Marais, E., Sealy, J., and Reimer, P.J., A record of rapid Holocene climate change preserved in hyrax middens from southwest Africa, *Geology* **37**(8):703–706, 2009.
7. Feder, A., Zimmermann, R., Stollhofen, H., Caracciolo, L., Garzanti, E., and Andreani, L., Fluvial-aeolian sedimentary races, Sossusvlei, Namib Desert, *J. Maps* **14**(2):630–343, 2018.
8. Rowell, A., Thomas, D., Bailey, R., Stone, A., Garzanti, A., and Padoan, M., Controls on sand ramp formation in southern Namibia, *Earth Surface processes and Landforms* **43**:150–171, 2018.
9. Eitel, B., Blümel, W.D., Hüser, K., and Mauz, B., Dust and loessic alluvial deposits in Northwest Namibia (Damaraland, Kaokoveld): sedimentology and palaeoclimatic evidence based on luminescence data, *Quaternary International* **76/77**:57–65, 2001.
10. Ollier, C.D. and Marker, M.E., The Great Escarpment of Southern Africa, *Zeitschrift für Geomorphologie N. F.* **54**:37–56, 1985.
11. Oard, M.J., Passive margins explained by Flood runoff, *J. Creation* **35**(2):3–4, 2021.
12. Oard, M.J., Tremendous erosion of continents during the Recessive Stage of the Flood, *J. Creation* **31**(3):74–81, 2017.
13. Kocurek, G., Lancaster, N., Carr, M., and Frank, A., Tertiary Tsondab Sandstone Formation: preliminary bedform reconstruction and comparison to modern Namib Sand Sea dunes, *J. African Earth Sciences* **29**(4):629–642, 1999.
14. Lancaster, ref. 3, p. 13.
15. Ward, J.D., Eolian, fluvial and pan (playa) facies of the Tertiary Tsondab Sandstone Formation in the central Namib Desert, Namibia, *Sedimentary Geology* **55**:143–162, 1988.
16. Rowell, A., Thomas, D., Bailey, R., Stone, A., Garzanti, E., and Padoan, M., Controls on sand ramp formation in southern Namibia, *Earth Surface Processes and Landforms* **43**:150–171, 2018.
17. Lancaster, ref. 3, pp. 20–46.
18. Bristow, C.S., Duller, G.A.T., and Lancaster, N., Age and dynamics of linear dunes in the Namib Desert, *Geology* **35**(6):555–558, 2007.
19. Garzanti, E., Andò, S., Vezzoli, G., Lustrino, M., Boni, M., and Vermeesch, P., Petrology of the Namib Sand Sea: long-distance transport and compositional variability in the wind-displaced Orange Delta, *Earth-Science Reviews* **112**:173–189, 2012.
20. Garzanti, E., Dinis, P., Vermeesch, P., Andò, S., Hahn, A., Huvi, J., Limonta, M., Padoan, M., Resentini, A., Rittner, M., and Vezzoli, G., Sedimentary processes controlling ultralong cells of littoral transport: placer formation and termination of the Orange sand highway in southern Angola, *Sedimentology* **64**(July):1–30, 2017.
21. Vermeesch, P., Fenton, C.R., Kober, F., Wiggs, G.F.S., Bristow, C.S., and Xu, S., Sand residence times of one million years in the Namib Sand Sea from cosmogenic nuclides, *Nature Geoscience* **3**(12):862–865, 2010.
22. Bristow *et al.*, ref. 18, p. 555.
23. Vermeesch *et al.*, ref. 21, p. 862.
24. Lancaster, ref. 3, p. 67.
25. Lancaster, ref. 3, p. 13.
26. Garzanti *et al.*, ref. 19, p. 183.
27. Garzanti, E., Resentini, A., Andò, S., Vezzoli, G., Pereira, A., and Vermeesch, P., Physical controls on sand composition and relative durability of detrital minerals during ultra-long distance littoral and aeolian transport (Namibia and southern Angola), *Sedimentology* **62**:988, 2015.
28. Garzanti *et al*., ref. 20, p. 23.
29. Oard, M.J. (ebook), *Earth's Surface Shaped by Genesis Flood Runoff*, 2013.
30. Oard, M.J., *Flood by Design: Receding water shapes the earth's surface*, Master Books, Green Forest, AR, 2008.
31. Burke, K. and Gunnell, Y., The African Erosion Surface: A continental-scale synthesis of geomorphology, tectonics, and environmental change over the past 180 million years, *GSA Memoir 201*, Geological Society of America, Boulder, CO, pp. 1–66, 2008.
32. Oard, M.J., The remarkable African planation surface, *J. Creation* **25**(1):111–122, 2011.
33. Bierman, P.R. and Caffee, M., Slow rates of rock surface erosion and sediment production across the Namib Desert and escarpment, southern Africa, *American J. Science* **301**:326–358, 2001.
34. Besler, H., The Tsondab Sandstone in Namibia and its significance for the Namib erg, *South African J. Geology* **99**:77–88, 1996.
35. Oard, M.J., *How Noah's Flood Caused a Single Ice Age*, Creation Book Publishers, Powder Springs, GA (in press).

Michael J. Oard *has an M.S. in atmospheric science from the University of Washington and is now retired after working as a meteorologist with the US National Weather Service in Montana for 30 years. He is the author of* Frozen in Time, Ancient Ice Ages or Gigantic Submarine Landslides?, Flood by Design, Dinosaur Challenges and Mysteries, *and* Exploring Geology with Mr Hibb. *He is a fellow of the Creation Research Society.*

Reassessing human–chimpanzee genetic similarity

Robert W. Carter

The similarity of the human and chimpanzee genomes is a critical question in the creation–evolution debate. Tomkins estimated the two genomes were on the order of 85% similar. In his 2018 paper, he took 18,000 long chimpanzee sequence reads ('contigs') and compared them to the chimpanzee and human genomes using BLAST. He determined a percent similarity of 84%, but this was generated by taking the average of a demonstrably non-normal distribution. Worse, the percent identities were bimodally distributed, with strong peaks in the high 60 and high 90 percent range. There were almost no matches in the 84% range. In the present study, BLAST was found to frequently identify best matches on the incorrect chromosome. Additional questions arose when performing searches that do and do not allow for the insertion of gaps. By comparing those same contigs to older and newer chimpanzee and human genomes, including the first fully complete human genome, most of the percent identity scores were found to be higher than in his original study. BLAST does point us in the right direction, but it is an inadequate program for assessing percent similarity.

The question of how similar humans are to other species has been debated for centuries. In the early 20th century, most scientists assumed that proteins were the carrier of genetic information, and so the protein content of humans and, for example, apes was assumed to be highly divergent. The discovery that many proteins were similar among the various species, sometimes even identical, came as a shock to many. When molecular methods were first being developed, there was quite a contention within the scientific community, with most thinking that our closest 'relative' was the gorilla (*Gorilla gorilla*) and some believing it was the orangutan (*Pongo pygmaeus*). King and Wilson published the first human–chimp DNA hybridization experiments in 1975.[1] Sibley and Ahlquist[2] followed up with more detailed experiments in 1984.[3] They showed quite clearly that human DNA was most similar to, first, chimpanzee (*Pan troglodytes*), then to gorilla, then to orangutans, but this was not universally accepted; they were still defending their results as late as 1990.[4] The earliest DNA sequencing data concentrated on specific protein-coding genes, which were found to be highly similar in the two species. It was from these earlier studies that we obtained the '98% or 99%' similarity figures that are so often cited. Yet, the true similarity is less than that, a fact that has been known for quite some time.[5] The notion of a high similarity between the two species is bolstered by the fact that there are, indeed, large areas of high similarity, specifically in the protein-coding regions. Yet, much of the discussion has centred around these places to the exclusion of other genomic compartments that are much less similar.

Worse, DNA hybridization can only test similarity among sequences *that will align*. When heating up DNA in solution, the strands will separate at a given melting temperature that varies with GC content. The opacity of melted DNA is significantly less than that of aligned DNA, meaning the process can easily be studied in a spectrophotometer. If the DNA of individuals from two different species is mixed and heated, a non-linear reassociation curve with multiple plateaus will be noted as the solution cools and the strands begin to align. By applying a set of complex formulae, and after chemically removing the highly repetitive DNA, the percent similarity of the two species can be estimated.

When Ahlquist realized that he could not tell us how *different* two species were, only how similar certain portions of their genomes were, he understood that DNA hybridization and reassociation kinetics was extremely limited.[6] Yes, humans and chimpanzees obviously share a significant portion of highly similar DNA, and estimates put much of that in the 98% similarity range, but there was a large portion of the two genomes that were necessarily excluded from these analyses.

The discussion changed significantly when the first human and chimpanzee genomes were published in 2001[7] and 2005,[8] respectively. Various estimates indicated genomic similarity in the 98% range once again. Yet, the human genome was not complete, and the chimpanzee genome was intentionally built using the human genome as a scaffold. The first human genome had 318 long blocks with nothing but the letter 'N' (28,000 Ns per block, on average). These spaces mostly covered highly repetitive stretches of DNA that the sequencing technology of the day was unable to handle. The spaces were added to the genome with the hopes that they could later be filled in when better sequencing technology came along. Currently, the most up-to-date

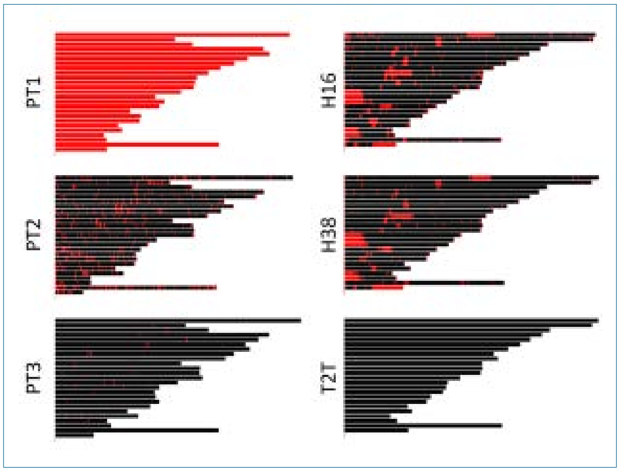


Figure 1. Chromosome maps for chimpanzee (left column) and human (right column) genomes. The autosomes are in numerical order, so chimp chromosomes 2A and 2B follow chromosome 1. The autosomes are followed by the X, Y, and mitochondrial chromosomes. PT1 was assembled before chimpanzee chromosomes 12 and 13 were renumbered 2A and 2B, respectively, but the chromosomes were reordered to match the other genomes. Each chromosome was binned into 250,000-bp sections and any bin that contained an N was coloured red.

version (GRCh38) from the Human Genome Project (HGP) still contains 151 MB of unaligned sequence (approximately 5% of the genome) that has yet to be incorporated into the chromosomes, and the centromeric sequences are fake. That is, “The centromeric alpha satellite arrays are represented as computationally generated models of alpha satellite monomers to serve as decoys for resequencing analyses.” The short arm of chromosome 21 is plagued with problems, and there is evidence of a genome-wide deletion bias.[9]

This hope for a fully sequenced human genome was not realized for over 20 years after the first draft was published (30+ years since the initiation of the HGP). In the summer of 2023, the Telomere-to-Telomere Project (T2T) finally published the full sequence of the last remaining human chromosome, Y.[10]

The original chimpanzee genome included the 318 spacer regions seen in the first human genome plus an additional *295,000* smaller ones (average = 51 Ns, calculations below). This was because many short indels (insertions and deletions) must be added if one is to align the two genomes, and the short chimpanzee sequence reads were lined up on the human genome. Coupled to the fact that the first chimpanzee genome was only lightly sequenced (the average coverage was ~5-fold compared to ~30-fold for the human genome), that first attempt gave us a very poor representation of the chimp genome.

Since then, better chimpanzee genomes have been assembled. The first several updates still suffered from the problem of ‘humanization’, but it was eventually assembled without (direct) reference to the human genome. In 2018, Kronenberg *et al*. published a curated set of nearly 80,000 high-quality chimpanzee contigs (i.e., contiguous stretches of DNA). They used Pac-Bio long-read sequencing technology to get through many of the problematic sections of the chimpanzee genome. Combined with millions of short reads from shotgun sequencing and the testing of specific letters with old-fashioned Sanger sequencing, they managed to achieve approximately 65-fold coverage.[11] These contigs were taken from a chimpanzee named Clint. The Clint_PTRv2 (aka panTro6) genome was the assembled version of those contigs. Tomkins used a randomly selected set of 18,000 of these chimpanzee contigs and compared them to the assembled genome in his 2018[12] paper. In the meantime, the human genome has gone through multiple rounds of improvement, culminating with T2T (figure 1).

The BLAST program (Basic Local Alignment and Search Tool) is a mainstay of modern genetics. First developed in the early 1990s for searching protein databases for similar sequences, it was rapidly adopted for use with DNA sequences individually (BLASTn) or in batches (MegaBLAST). It uses a heuristic method to make educated guesses about local areas of alignment and is able to find areas of significant similarity about 50 times faster than other, more comprehensive, search algorithms (e.g., Smith-Waterman).

In 2011, Tomkins used BLAST to query 40,000 raw chimpanzee sequence reads against the human genome.[13] Excluding the areas that did *not* line up, he estimated 86–89% similarity. Given that BLAST only identifies regions of *best* alignment, the true similarity should have been less than that. However, it is unclear if those raw sequences reflected an unbiased sampling of the chimpanzee genome.

Tomkins (2011),[14] Tomkins and Bergman (2012),[15] and Bergman and Tomkins (2012)[16] discussed the art of genome construction and multiple frustrations they had with the way the evolutionary community was approaching the subject. In 2013, Tomkins used BLAST to reassess human–chimpanzee sequence similarity.[17] He reached a figure of about 70%. This, however, was due to a glitch in the software being used, as one skeptic claims to have pointed out to Tomkins.[18] By working with the software developers, however, Tomkins was able to get the problem fixed. He then reproduced his original study, this time using a non-buggy algorithm, and arrived at an estimate of 88%.[19] In 2016, he assessed human–chimp similarity by examining 101 trace read data sets from multiple chimpanzee sequencing projects, ‘blasting’ them against the human genome and arriving at an 85% similarity figure.[20] In all this work, he was trying to avoid using the chimpanzee genome, since it was demonstrably ‘humanized’. Raw sequence reads might be affected by selection bias and they might have a higher error rate, but they are closer to the source than the assembled genome.

In his latest paper on the subject, Tomkins used BLAST to search for areas of significant similarity using a selection of Kronenberg *et al*.'s chimpanzee contigs. It took six months of computing time to complete a search of these contigs in the human genome and two versions of the chimpanzee genome. He placed summary tables on GitHub so that anyone could check his results.[21] By averaging the percent identity (*pident*) column, he arrived at human–chimpanzee similarity of 85%.

Around this same time, evolutionary geneticist Richard Buggs came out with an estimate of 84.4% similarity, but this was only published in a blog post.[22] Later, Seaman and Buggs (2020) published a revised figure of 96.6% using fully aligned genomes, but only after cutting out the centromeres, telomeres, copy number variations, about 300,000 small indels (accounting for about two million letters in each genome), and an additional percentage of DNA that resisted alignment.[23] This 'apples-to-apples' comparison is the most robust performed to date, but since they deliberately excluded the most variable portions of the two genomes, the true similarity is necessarily less than 96.6%. How much less is a matter of active investigation.

Several skeptics of Tomkins' work have complained that he needed to weight his results before calculating any percent similarity.[24] While they are technically correct, they have suggested an incorrect method of weighting. Specifically, they noted that Tomkins' results contained both short and long matches. He simply took the average of all the matches and failed to account for the total length. By taking the total number of aligned bases and dividing by the total match lengths, he would have arrived at a figure closer to 96%. A better method would be to take the match percentage and (conservatively) apply it to the whole contig (not just the matched area), but this produces a comparable similarity score, or one perhaps a few percentage points lower. Even so, both weighting schemes ignore the significant percentage of the genomes that fail to align in BLAST searches.

Yet, any weighting strategy would be inappropriate if the contigs do not represent a fair sampling of the chimpanzee genome. If the database was skewed toward one sequence class over another,[25] no amount of 'weighting' will help. Thus, instead of weighting by the length of each match, an estimate of the relative frequency of each sequence class represented by the contigs was called for but not performed.

Another major objection is that Tomkins, prior to 2018, chose to use the *ungapped* feature of BLAST exclusively. This is faster but produces shorter matching regions. However, his critics have promulgated a surprising misunderstanding among themselves. Worse, their purported results seem to back up this misunderstanding, casting doubt on all their calculations and conclusions. Williamson produced an early example which has since been duplicated and even expanded on by others. In an unpublished manuscript[26] and a follow-up video,[18] Williamson showed an alignment of two nearly identical short sequences. The only difference was that one had an 'A' in the middle, causing the alignment to be perfect for the first half and completely off in the second half (figure 2). He claimed that this would produce a total alignment score of 46%. By inserting a gap in the shorter sequence, however, the alignment score is increased to 92%. Putting aside the fact that he missed one alignable letter (the red line in figure 2), BLAST would actually report a higher percent similarity for the misaligned sequence pair. The algorithm searches for areas with the best *local* alignment. Thus, it would report back that it had found an area of 100% match for the first sequence pair and only 92% for the other. BLAST does not generally work with such short sequence pairs, but the illustration still holds.

```
GTCGTAATGATTA    GTCGTAATGATTA
||||||    |      |||||| ||||||
GTCGTATGATTA     GTCGTA.TGATTA
```

Figure 2. A false understanding of how the BLAST algorithm works. In the alignment on the left, 7 out of 13 nucleotides match (a 54% similarity). In the alignment on the right, 12 out of 13 nucleotides match (92% similarity) after allowing for gaps. In reality, the BLAST algorithm would report a 100% similarity for the sequence on the left, but with a *match length* of only six letters. The red line in the left-hand alignment indicates a matching nucleotide pair that was missed by Roohif and, later, by Gutsick Gibbon in their videos on the subject.

The assertion is that, by disallowing gaps in the search protocol, Tomkins was biasing his results downward. However, there are other reasons why his results are biased downward, and the objection shows a complete misunderstanding of how BLAST works. First, short sequences like this are disqualified. If the matching sequences do not score above some preset minimum (*-culling* is set to 44 by default), a null result is returned. Second, the *-word_size* parameter sets the initial minimum match length (default = 11). Once a matching 'word' is found, the area is extended to the left and to the right. Each matching letter found increases the score by a set amount (*-reward* = 2 by default) while each mismatch decreases the score (*-penalty* = 3 by default). Thus, the bitscore for the match starts out with a value of 22 (word size of 11 × 2 points per matching letter pair) and increases as the alignment is extended. When the score drops to a set amount (*-xdrop_ungapped* = 20 by default) from any local maximum, the algorithm stops searching, rolls back to the area with the highest score, and reports back that area of alignment only. Thus, it is expected that 'ungapped' BLAST searches should produce slightly higher similarity scores than 'gapped' searches (figure 3), contrary to Tomkins' detractors.

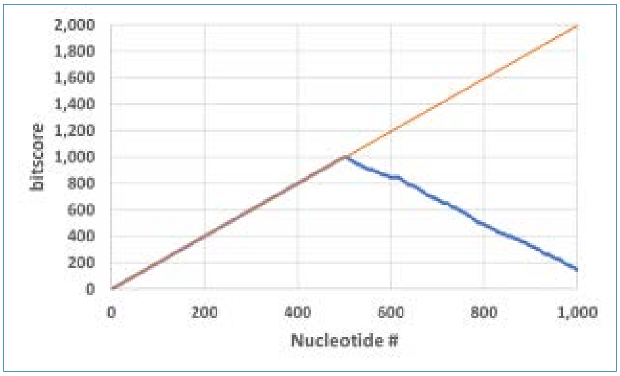


Figure 3. An explanation of how BLAST calculates *bitscore*. Two identical sequences with 1,000 random nucleotides were created and a single extra nucleotide was added at position 501 in the second string. Blue line: in an ungapped search, BLAST would report a 100% match over the first 500 nucleotides. Red line: in a gapped search, BLAST would report a 99.9% match over 1,000 nucleotides. The descending blue line represents a misunderstanding. Many confuse the total alignment in the misaligned sequence pair (62.3%) with the shorter match that will be reported by BLAST. The point at which the algorithm breaks away in an ungapped search depends on the setting of *-x-drop*, which is set to 20 by default.

An example of scoring in a BLAST search can be seen in figure 3. Here, two identical 1,000-nucleotide sequences were created. An extra letter was then inserted after position 500 in the second string, which threw off the second half of the otherwise perfect alignment. Using *-ungapped*, BLAST would calculate a maximum score of 1,000 (blue line) and report back a 100% percent identity value for the two strings over a match length of 500. After a single gap is inserted in the shorter string, BLAST would calculate a maximum score of 1,995 (red line) and report back a 99.9% percent identity for the two strings over a match length of 1,000. The descending blue line represents the mistaken notion that BLAST will iterate across the entire query string, in which case it would (falsely) report a *bitscore* below 200 and a percent identity of 62.3%. However, due to the *-x_drop* parameter, BLAST will stop searching when the score drops to less than 20 below some local maximum. In this case, the algorithm stops when the score reaches 980, rolls back to the place with the highest score, and reports that it found a 100% match over the first 500 letters. The second half of the string is not tested at all.

BLAST is not intuitive. It takes a brute force approach for finding matches. It will often locate a high-scoring match on the wrong chromosome, and gapped vs ungapped searches will often hit on very different areas of the genome (see Results). And since the *bitscore* can rise even when traversing a 'gappy' area with relatively poor alignment, searches that allow for gaps will also often return hits with a lower percent identity than searches that don't allow for gaps. For these reasons, one must be very careful when trying to estimate total sequence similarity using this program. Worse, BLAST cannot find a sequence match in areas masked-out by the letter 'N'. Thus, when using a database of sequences that are not incorporated into a genome (e.g., many of the 18,000 contigs used by Tomkins in his 2018 paper had yet to be added to the human genome), BLAST will fail to identify the real matching sequence and will settle on the next-best region, driving down the overall percent similarity. Thus, top-level genomes (which contain only the canonical chromosomes) and full genomes (which also contain unassembled accessory sequences) will not yield the same answers. This is something that has been missed by Tomkins' detractors. Most of their efforts have focused on top-level genomes while he made certain to include *all* the sequence data available.

Methods

The sequences in the contig database used by Tomkins (2018) were obtained from the European Nucleotide

Table 1. Statistics for the various genomes used in this study

Dataset	Nickname	Species	Year	Sequences	Size (GB)	Ns (MB)	N Blocks
18k Contigs	18K	Chimpanzee	2018	17,990	0.57	0	0
PanTro1	PT1	Chimpanzee	2004	26	3.08	672	295,020
Clint_PTRv2/panTro6	PT2	Chimpanzee	2018	26	2.81	28.0	24
PanTro3-v1.1	PT3	Chimpanzee	2023	26	3.14	2.90	28
NCBI34/hg16	H16	Human	2004	25	3.07	227	377
GRCh37/hg19	H37	Human	2009	25	3.10	234	328
GRCh38.p13	H38	Human	2019	25	3.08	150	799
Telomere-to-Telomere	T2T	Human	2023	25	3.11	0	0

Table 2. The main BLAST parameters

Parameter	Typical	Description
-evalue	0.1	The expect value, or how often the match is expected due to chance
-outfmt	10	Output format, 10 = comma separated list of specified fields
-max_target_seqs	1	The number of target sequences included in the output file
-max_hsps	1	The number of high scoring sequence pairs included in the output file
-perc_identity	50	Minimum percent identity to be included in the output file
-word_size	11	The size of the seed words used to initiate matching
-num_threads	8	The number of parallel operations to perform (machine specific)
-gapopen	3	A penalty for opening a gap
-gapextend	3	A penalty for extending any gap
-reward	2	A reward for matching a letter in the query and target sequences
-penalty	3	A penalty for mismatching a letter in the query and target sequences
-xdrop_ungap	20	Search cuts off if score drops below this level from any local maxima
-xdrop_gap	30	Search cuts off if score drops below this level from any local maxima
-xdrop_gap_final	100	A maximum xdrop for gapped sequences
-dust	yes/no	Mask highly repetitive sequences in the query sequence?
-soft_masking	true/false	Mask letters specified in lowercase?
-ungapped	[blank]/ungapped	Allow for indels or perform an ungapped search?

Table 3. Output parameters

Variable	Description
Qid	The name of the query sequence
Qlen	The length of the query sequence
Sseqid	The name of the target sequence
Sstart	The starting location of the match within the target sequence
Send	The ending location of the match within the target sequence
Pident	The percent identity between the matching area of the query and target sequence
Nident	The number of identical letters in the match
Length	The length of the match
Mismatch	The number of non-identical letters in the match
Gapopen	The number of gaps
Gaps	The sum of gap lengths
Evalue	The expect score
Bitscore	The total score for the match, according to the BLAST parameters

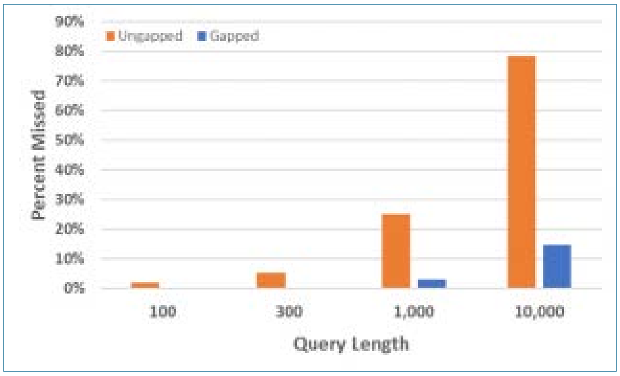


Figure 4. Percent of query sequence included in a match vs. query length for ungapped and gapped BLAST searches. These data were obtained by taking the longest chimpanzee contig (2.7 MB), breaking it into pieces (according to the lengths given), and blasting the pieces against PT2 chromosome 3. Error bars are not shown.

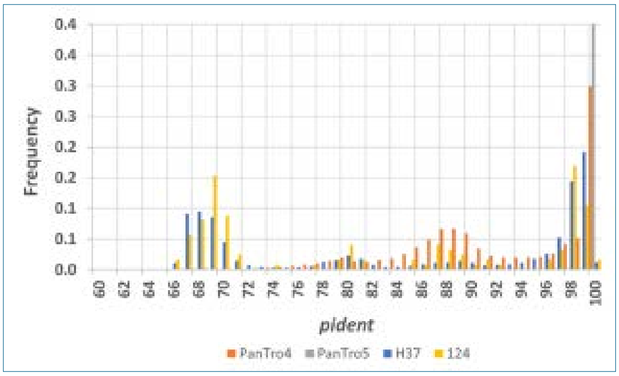


Figure 5. Normalized *pident* scores from Tomkins' (2018) accessory data. 18K chimpanzee contigs were blasted against three different genomes, one human and two chimpanzee. Also included is a selection of 124 short contigs (e.g., a subset of the H37 results) that were used extensively in the current study. The distributions for H37 and the 124 contigs were highly similar, both visually and statistically, so the latter was treated as a fair subsampling of the former. The names of the chimpanzee genomes do not reflect the naming conventions used in this study; and note that the y-axis is truncated at 0.4, cutting off the PanTro5 results.

Archive[27] according to the list he provided. Multiple versions of the chimpanzee and human genomes were obtained (table 1), including the original chimpanzee genome (PanTro1, hereafter PT1),[28] the Clint_PTRv2 genome (aka panTro6, hereafter PT2),[29] and the most recent version of the chimpanzee genome (panTro3.1.1, hereafter PT3).[30] Top-level Genbank version chromosomes were downloaded individually. An additional bulk data download produced an additional 4,300 and 1,446 unaligned sequences for PT2 and PT3, respectively. An early human genome (NCBI34/hg16, hereafter H16),[31] a similar version to the one Tomkins used (GRCh37.71, hereafter H37),[32] a more recent human genome (GRCh38.p13, hereafter H38),[33] and the Telomere-to-Telomere human genome (hereafter T2T)[34] were also obtained. After unzipping, if necessary, chromosome data were concatenated into single FASTA files. Two BLAST databases were created for each genome (one for the chromosomes and one for the unassembled sequences) using the command line.[35]

The number of N blocks and the total number of Ns were counted for each genome. Using a custom Python script, maps were created for each genome that showed the chromosome lengths and the locations and lengths of all N blocks (figure 1).

Thousands of BLAST searches were performed using a series of custom Python programs. These required the submission of a query sequence, identification of the target database, and the setting of various input parameters (table 2). There are other options available, but not all were tested. Of particular importance was the difference between searches that allowed or disallowed gaps. A 'gapped' search is the default, but sending the command *-ungapped* turns it off. Gapped searches were noticeably slower. The *-output_fmt* string was set to "10 qid qlen sseqid sstart send pident nident length mismatch gapopen gaps evalue bitscore" (table 3), where '10' just specifies a comma separated string. The query id, starting location, and length were specified in the BLAST report file name.

In many cases, both ungapped and gapped BLAST searches were performed and compared side-by-side. First, to assess the results of Tomkins (2018), a selection of 150 of the smaller contigs were blasted against PT1, PT2, PT3, H16, H37, H38, and T2T. Several of the most highly repetitive contigs were removed to speed up the analysis (e.g., the time to search varied from a few seconds to a few hours, depending on the repetitiveness of the query). This left 124 contigs and a runtime of approximately 9 hours per genome compared. Second, a 10,000-bp snippet of the longest chimpanzee contig was blasted against PT3 online.[26] This localized it to chimpanzee chromosome 3, so an additional BLAST database was created for this chromosome only. The longest contig (in its entirety) was broken up into pieces 100-, 300-, 1000-, and 10000-bp long and blasted against PT3 chromosome 3. Third, random subsequences of various lengths were chosen from each genome and blasted against other genomes and the parent genome, using a variety of parameter settings. Fourth, the first 500,000 nucleotides of T2T chromosome 22 were broken up into 300-bp and 1,000-bp bins and blasted against PT3 using gapped and ungapped searches.

The Shapiro–Wilk test for normality was applied to the lengths of the contigs, the lengths of the matches in H37, and the *pident* values for H37 reported by Tomkins (2018) using a Python plugin. A Mann–Whitney U test was used to

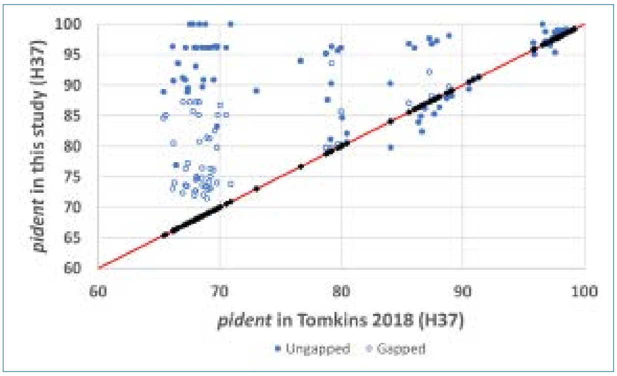


Figure 6. Replicating Tomkins' 2018 BLAST results. These *pident* values were obtained by blasting 124 short chimpanzee contigs against the H37 human genome, using both ungapped and gapped searches. The *pident* values from the (gapped) BLAST results in Tomkins (2018) are shown on the diagonal.

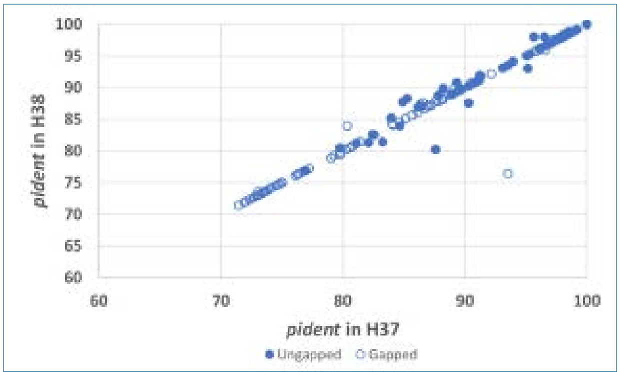


Figure 7. Gapped and ungapped *pident* values obtained by blasting 124 short chimpanzee contigs against H37 and H38 reveal very similar results, but gapped searches had lower *pident* values in general.

test for similarity in the normalized *pident* histograms of the 18,000 contigs and the 124 shorter contigs.

Results

Each of the three tests for normality in Tomkins' 2018 'homo' data table returned a probability of 0.0. Even though one contig was 2.7 million bases long, the contig lengths were highly skewed toward shorter lengths, with a mode of 1,004 base pairs. The match lengths were equally skewed. The longest match was only 342,000 nucleotides (in a query of nearly two million bp). Matches averaged 62.3% (± 0.31 SD) of the query length, with no clear relationship between query length and match length. The fraction of the query sequence included in the match, however, was highly contingent upon the length of the query and whether or not the search was ungapped or gapped (figure 4). There were zero Ns both among the chimpanzee contigs and within the T2T human genome. The other genomes did not contain any small, sporadic N blocks, as seen in the original chimpanzee genome (table 1). Genome maps are shown in figure 1.

When examining the raw data from Tomkins 2018, the similarity scores seem to come in equally spaced waves, perhaps indicating algorithmic artifacts (figure 5). PanTro4 and PanTro5 were versions of the chimpanzee genome that were and were not, respectively, assembled using the human genome as a guide. H37 and panTro4 have peaks in highly similar places. Tomkins reported an average *pident* score for Pantro5 of 100%. This could not be replicated either.

The *pident* scores were not skewed; when plotted as a histogram, they were fully bimodal (figure 4, H37). Tomkins took the average of these values and reported a human–chimpanzee similarity of 84% without accounting for the strange data distribution or the expected genomic frequency of the respective sequence classes within the two main peaks. There were very few values near the 'average'.

The subset of 124 random small contigs had a highly similar *pident* distribution to the full collection of 18,000 (figure 4). After normalization, a Mann–Whitney U test performed on the two distributions reported a p-value <0.00001, meaning the two distributions are essentially identical. Thus, this can be considered a 'fair sampling' of the parent distribution and any analyses performed with the subsample should be applicable to the larger set. However, the original numbers could not be validated. When blasted against H37 (the same or similar version of the human genome Tomkins used), most contigs attained a higher *pident* (figure 6). The results for H37 and H38 were highly similar (figure 7), so the difference between the results of Tomkins (2018) and this study are not likely due to differences in the genome version used. Neither is it expected that different versions of BLAST would produce highly different results (barring programmatic bugs). This discrepancy remains unresolved, although gapped searches did generate results that were closer to Tomkins' numbers, and he used gapped searches in that study. In essence, the *pidents* of all low-scoring matches were found at much higher frequencies, especially when using the *-ungapped* parameter, which he used in earlier studies. Did his use of the gapped parameter drive down the human–chimpanzee similarity in his 2018 study? Attempts were made to recreate his results using various settings of *-dust*, *-soft_masking*, and gapping (with identical parameter settings to his 2018 paper). The other user-defined parameters were not expected to make much of a difference.

When plotted against Tomkins' results, many of the new values were higher than he reported (figures 5, 7, and 8). Tomkins' 2018 data file also does not identify *where* the matches were located on the human genome, so this cannot

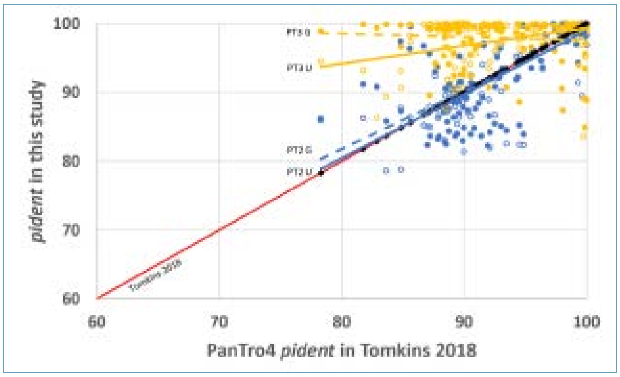


Figure 8. Results of blasting a set of 124 chimpanzee contigs on two chimpanzee genomes. Tomkins' original percent identity values (black diamonds) lie along the diagonal red line and came from panTro4, a predecessor to PT2. The average percent identity values for the chimpanzee genomes shifted upward from PT2 to PT3, but ungapped and gapped searches returned very similar values for each genome. Note the lines are provided for visual aid only. Variances were high and error bars are not shown.

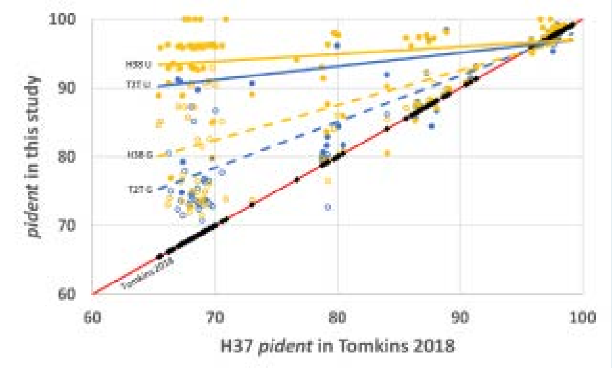


Figure 9. Results of blasting a set of 124 chimpanzee contigs on two human genomes. Tomkins' original percent identity values (black diamonds) lie along the diagonal red line and were obtained using H37. The average percent identity values for the human genomes shifted upward from H38 (H37 is not shown, but results were similar) to T2T, but ungapped and gapped searches were split. Tomkins used gapped searches in his 2018 study, which would have biased his results downward. Again, the lines are provided for visual aid only.

be double checked. Also, the current study was unable to reproduce the bimodal peak seen in his data.

Gapped and ungapped searches for matches to those 124 chimpanzee contigs returned nearly identical results for the individual chimpanzee genomes, but the values for PT2 were generally lower than for PT3 (figure 8). It is assumed that this was due to the greater degree of completion of the PT3 genome. Many values went from the 70% range to a full 100% match as the gaps were filled in. Yet, both genomes contained unassembled sequences. It is assumed that the more complete PT3 genome was created by folding in some of the unassembled sequences found in PT2. Thus, the contigs that matched a gap in PT2 should have been located in the accessory sequence data. The reason for the jump in similarity scores is thus unexplained. The ungapped and gapped searches in the two human genomes, however, were split (figure 9). The two ungapped searches were similar and were generally higher than the results for the gapped searches.

Blasting against the various genomes returned high average *pident* scores. These scores were even higher after weighting was applied (table 4). However, the average length of the matches was drastically different. For the two chimpanzee genomes, a large fraction of the contig was found, on average, to match a section of the chimpanzee genome, though ungapped searches returned smaller match lengths than did gapped searches. For the human genomes, only about a third of the contig, on average, was matched using ungapped searches and just over half of the average contig was captured with gapped searches. Also, many potential matches failed to reach the *-culling-limit*, the score that must be reached for BLAST to include it on the list of potential hits (default = 44). Being that the *-word-size* was set to 11, any initial matches automatically start with a score of 22. Only 11 additional matching letters must be added to the seed word to reach a score of 44 (more if mismatches or gaps are found). Fully 14% of ungapped searches against the human genome failed to find any significant matches. In other words, the sequences represented by those contigs *do not even exist in the human genome*.

Importantly, when blasting a query against its parent genome, BLAST always returned a 100% match, for both gapped and ungapped searches.

Many inconsistencies in genome location were noted among the results reported above, so a systematic study of the first 500,000 nucleotides in the T2T chromosome 22 was undertaken. The results of ungapped and gapped searches of T2T against PT3, with two different bin sizes, were highly consistent, but most of the reported 'best' matches were not for chromosome 22 (figure 10). Some of this might be due to the translocation of genomic segments among the chromosome arms (whether due to evolution or design). Some might be due to highly similar stretches of DNA being found in more than one place. Much of it might be due to the presence of long and abundant repeats (e.g., Alu elements) that are scattered about the genome. Without a thorough understanding of how BLAST finds comparable sequences, most of the results are probably inapplicable for studying human–chimp differences. Mapping the matches from this section of T2T chromosome 22 onto the PT3 genome reveals the issue starkly (figures 11 and 12). BLAST located parts of this human genome on multiple chimpanzee chromosomes, including several places where consecutive 1,000-bp sections of the two genomes line up beautifully and other places where

Table 4. Results of blasting 124 small contigs on the various genomes. Not all searches returned a value that was above the culling limit. Av Len = the average length of the matching region. % Len = the percent of the query contig that was included in the match. Unweighted = the simple, average of all *pident* scores. Weight1 = sum(*num_iden*)/sum(*len*). Weight2 = sum(*pident* x qlen)/sum(qlen).

					Average pident		
Genome	**Method**	**Returned**	**Av Len**	**% Len**	**Unweighted**	**Weight1**	**Weight2**
PT2	Ungapped	124	2,841.5	75.8	92.91	97.96	99.42
	Gapped	124	10,040.6	95.1	92.72	98.86	98.97
PT3	Ungapped	124	2,582.1	85.6	97.73	99.14	99.76
	Gapped	122	7,171.9	96.5	97.64	99.14	99.31
H16	Ungapped	107	682	35.1	94.06	95.71	95.09
	Gapped	122	2088	52.9	86.43	94.86	82.61
H38	Ungapped	108	913.7	37.9	94.59	96.63	98.30
	Gapped	120	4,210.1	57.4	86.95	96.52	96.46
T2T	Ungapped	107	857.2	38.4	94.03	96.48	98.31
	Gapped	122	4,501.6	57.8	86.65	96.54	96.79

consecutive 1,000-bp sections of the human genome (falsely) map to the same location in chimpanzee. Worse, that section of overlapping windows moved to another chromosome when switching to a gapped search. These areas (PT3 chromosomes 9:63,565,920–63,566,109 and 14:3,929,276–3,929,593) have been flagged by RepeatMasker.[36] BLAST can filter for repetitive sequences (e.g., by setting *-dust* = yes or *-soft_masking* = true), if the sequences are masked (often by setting certain sections to lowercase), but doing so had little effect on the results reported above (data not shown).

Discussion

The high similarity of human and chimpanzee genomes is uncontestable. The evolutionary community has taken this as demonstrable proof of common ancestry. They have a flexible system, though. The date to our most recent common ancestor can shift (and has by several million years over the past several decades), based on fossil or genetic evidence. Yet, being that God clearly created along hierarchical lines,[37] there was nothing stopping Him from creating humans and chimpanzees as similar or as dissimilar as He liked. However, chimpanzees and humans have similar behaviours, similar morphology, similar food preferences, and similar temperature requirements. On first principles, therefore, one would expect them to also be similar to us genetically. The answer to the question is not critical for either side, but it is something that many people want to know.

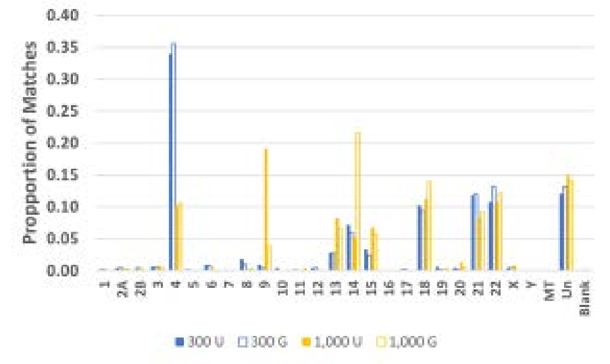


Figure 10. Locating sections of the T2T chromosome 22 on the PT3 genome using BLAST. Two different bin sizes were used, and both ungapped and gapped searches were performed. Most of the 'best' hits did not locate to chromosome 22. This raises serious questions about using BLAST to assess human–chimpanzee genetic similarities.

Tomkins' low estimates were partially driven by incomplete genomic data, but that was all he had to work with at the time. When repeating his methods on more modern genomes, the percent identity of chimpanzees and humans is clearly higher than 85%. The unnoticed bimodal distribution in his *pident* values should have indicated a problem, but after taking 18,000 readings he felt confident that he had a reasonable sample size, and thus a reasonable average. He also performed a reasonable control test, blasting the contigs against several versions of the chimpanzee genome. With PT2/panTro6, he attained a 100% match average, which is a little strange. When repeated with a smaller sample size

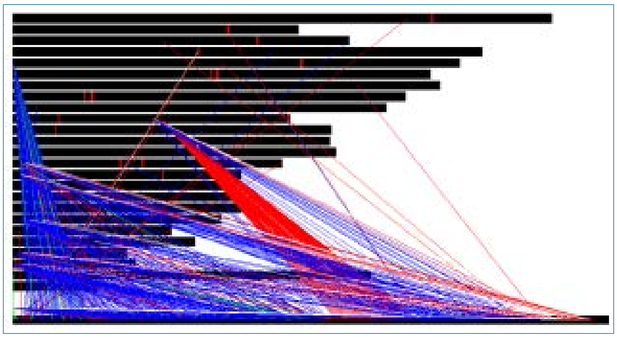


Figure 11. Mapping the first 500,000 nucleotides of T2T chromosome 22 onto the PT3 genome, bin size of 1,000, ungapped search. The bottom line represents an expanded view of this part of the test chromosome. For each bin, a line connects that section of the human chromosome to the place where BLAST found the highest-scoring hit. The lines are coloured according to *pident* (green ≥ 99%, blue ≥ 95%, red ≥ 90%, white < 90%). There are some sections where consecutive bins on the human chromosome line up with consecutive bins on the chimpanzee genome (e.g., at the beginning of PT3 chromosome 4) and other places where consecutive bins on the human chromosome all point to the same place on PT3 (e.g., the series of red lines pointing to the middle of chromosome 9).

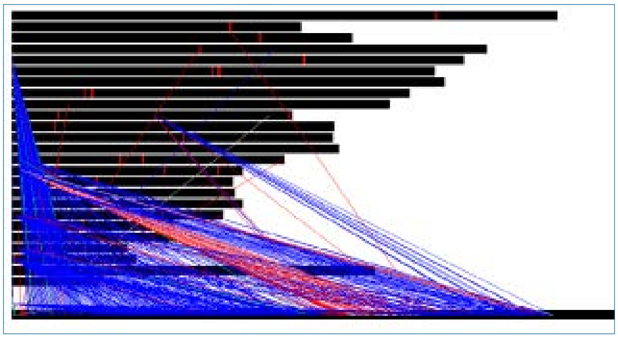


Figure 12. Same as figure 10, but for a gapped search. The large section of overlapping matches on chromosome 9 have moved to chromosome 14 and are still overlapping.

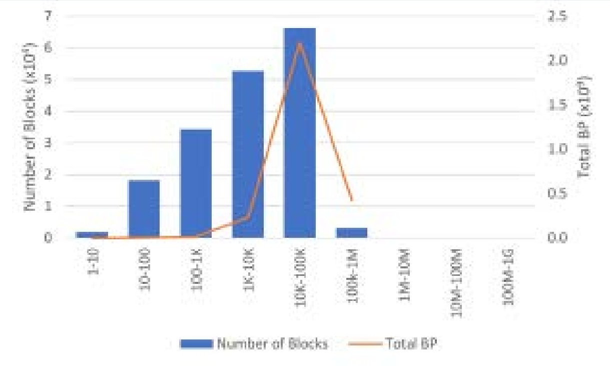


Figure 13. LASTZ comparison of the number of shared blocks and the total number of nucleotides within each block category, H38 v PT3 (data obtained from ref 41).

of contigs against PT2, many contigs did display a 100% match identity, but certainly not all (table 4, figure 7). The current study also failed to find the peak in *pident* values he reported that were in the high 60% range when comparing the chimpanzee contigs to human. This was true even when examining the same human genome he used (H37) and a reasonable sampling of his contig database. To date, these discrepancies are unexplained.

His detractors have focused on his lack of weighting and his use of ungapped BLAST searches, but the former is being applied incorrectly, and the latter biases the similarity upward. Gapped searches produce worse matches, as clearly demonstrated here. What is needed is a more comprehensive DNA alignment system. Several have been developed, including Mummer 4,[38] LASTZ,[39] and Fluent DNA,[23] but these all suffer from assumptions, free parameters, and user input requirements (e.g., gap opening penalties, sensitivity thresholds, and scoring matrixes). They do not just magically pop out the perfect alignment. There is still much 'art' to the science of genomic comparison.

LASTZ is probably the most common method used today. Multiple examples of full genome LASTZ alignments can be found online. The data suggest that log stretches of DNA are shared by humans and chimpanzees (figure 13).[40] Fluent DNA will only compare genomes that have previously been aligned with other software, but the output data are useful. In their description paper, Seaman and Bugs (2020) presented multiple views and statistics that help us to better assess human–chimpanzee similarity. The oft-cited number from their paper is '96.66%', but that only comes after excluding the centromeres (6.2% of the human genome[41]), telomeres (10–15 kb each), copy number variations, masked regions of the input genomes (they compared H38 and PT2, which contained 158 MB and 28 MB of masked region, respectively), unalignable sequence areas, and all indels (over 2.1 million gaps must be added to each side to align the two genomes). The ignored fraction of the genome totals many millions of bases. The alignment length is only 95.57% of the total reference genome length (H38), so they started off with a substantial difference before the similarity statistic was calculated. Fully 98.65% of the aligned region is identical between humans and chimpanzees. Multiplying these values, approximately 94.27% of the two genomes are identical, and even that needs to be taken with a grain of salt.

BLAST is an inappropriate software platform for making genome-to-genome comparisons, for several reasons. First, it only identifies local matching areas within any given query string, sometimes dropping a significant proportion of the query from the analysis. Second, searches using consecutive strings from the query chromosome do not necessarily locate consecutively on the target chromosome and searches involving highly repetitive sequences will often overlap on the target chromosome. Third, due to the large number of indels that must be added to any multi-species alignment, allowing for gaps in the reported match is necessary, but this tends to lower the average percent similarity. Once a chimpanzee genome is completed in full, it will be possible to create a full-scale alignment between the two genomes. This would need to be manually curated and differences (i.e., translocations, segmental duplications, gene copy number and placement) would need to be carefully mapped. Additionally, interspecies differences would need to be catalogued. At that point, it would be possible to calculate the full genomic difference between humans and chimpanzees. The value will probably be closer to 95% than to 85%, but as of now there remains a large degree of statistical uncertainty.

References

1. King, M.C. and Wilson, A.C., Evolution at two levels in humans and chimpanzees, *Science* **188**(4184):107–116, 1975.
2. Wieland, M., Convert to creation: Margaret Wieland interviews bird expert and former renowned evolutionist Dr Jon Ahlquist, *Creation* **40**(3):36–39, 2018; creation.com/jon-ahlquist.
3. Sibley, C.G. and Ahlquist, J.A., The phylogeny of the hominoid primates, as indicated by DNA-DNA hybridization, *J. Mol. Evol.* **20**(1):2–15, 1984.
4. Sibley, C.G., Comstock, J.A., and Ahlquist, J.E., DNA hybridization evidence of hominoid phylogeny: a reanalysis of the data, *J. Mol. Evol.* **30**(3):202–236, 1990.
5. Cohen, J. Relative differences: the myth of 1%, *Science* **316**:1836, 2007.
6. Ahlquist, personal communication.
7. International Human Genome Sequencing Consortium, Initial sequence and analysis of the human genome, *Nature* **409**(6822):860–921, 2001; Venter, J.C. *et al*., The sequence of the human genome, *Science* **291**(5507):1304–1351, 2001.
8. The Chimpanzee Sequencing and Analysis Consortium, Initial sequence of the chimpanzee genome and comparison with the human genome, *Nature* **437**:69–87, 2005.
9. Nurk, S. *et al.* The complete sequence of a human genome, *Science* **376**(6588):44–53, 2022.
10. Rhie, A. *et al*., The complete sequence of a human Y chromosome, *Nature* **621**:344–354, 2023.
11. Kronenberg, Z.N. *et al*. High-resolution comparative analysis of great ape genomes, *Science* **360**(6393):eaar6343, 2018.
12. Tomkins, J., Comparison of 18,000 *de novo* assembled chimpanzee contigs to the human genome yields average BLASTN alignment identities of 84%, ARJ **11**:205–209, 2018.
13. Tomkins, J.P., Genome-wide DNA alignment similarity (identity) for 40,000 chimpanzee DNA sequences queried against the human genome is 86–89%, ARJ **4**:233–241, 2011.
14. Tomkins, J., How genomes are sequenced and why it matters: implications for studies in comparative genomics of humans and chimpanzees, ARJ **4**:81–88, 2011.
15. Tomkins, J. and Bergman, J., Genomic monkey business—estimates of nearly identical human–chimp DNA similarity re-evaluated using omitted data, *J. Creation* **26**(1):94–100, 2012; creation.com/human-chimp-dna-similarity-re-evaluated.
16. Bergman, J. and Tomkins, J. Is the human genome nearly identical to chimpanzee?—a reassessment of the literature, *J. Creation* **26**(1):54–60, 2012; creation.com/human-chimp-dna-similarity-literature.
17. Tomkins, J., Comprehensive analysis of chimpanzee and human chromosomes reveals average DNA similarity of 70%, ARJ **6**:63–69, 2013.
18. 'Roohif', Creationist peer review is utter, utter poo, youtube.com/watch?v=D117oXq8yT4, 14 Sep 2018.
19. Tomkins, J.P., Documented anomaly in recent versions of the *BLASTN* algorithm and a complete reanalysis of chimpanzee and human genome-wide DNA similarity using *Nucmer* and *LASTZ*, ARJ **8**:379–390, 2015.
20. Tomkins, J.P., Analysis of 101 chimpanzee trace read data sets: assessment of their overall similarity to human and possible contamination with human DNA, ARJ **9**:294–298, 2016.
21. github.com/jt-icr/chimp_contigs.
22. Buggs, R., How similar are human and chimpanzee genomes? 2018; richardbuggs.com/index. php/2018/07/14/how-similar-are-human-and-chimpanzee-genomes/.
23. Seaman, J. and Buggs, R., FluentDNA: nucleotide visualization of whole genomes, annotations, and alignments, *Frontiers in Genetics* **11**:292, 2020.
24. E.g., 'Gutsick Gibbon', '80% chimpanzee' | The bogus creationism of Jeffery Tomkins, youtube.com/watch?v=QtTHlqhRQi0, 26 May 2023.
25. Potential biases can be introduced methodologically, instrumentally, during quality control, or by human curation of the final dataset. We will assume that Tomkins' selection of the 18,000 contigs was done randomly.
26. This is from an unpublished manuscript by Williamson that he claims was rejected by ARJ. I have a copy in my possession. Gutsick Gibbon showed screen shots of it in at least one of her videos and duplicated the faulty alignment on her own.
27. www.ebi.ac.uk.
28. PT1: hgdownload.soe.ucsc.edu/goldenPath/panTro1/chromosomes.
29. PT2: ncbi.nlm.nih.gov/datasets/genome/GCF_002880755.3.
30. PT3: ncbi.nlm.nih.gov/datasets/genome/GCF_028858775.1.
31. H16: hgdownload.soe.ucsc.edu/goldenPath/hg16/chromosomes.
32. H37:hgdownload.soe.ucsc.edu/goldenPath/hg19/chromosomes.
33. H38: ncbi.nlm.nih.gov/genome/guide/human/; a list of genome versions and release dates can be found at ncbi.nlm.nih.gov/datasets/genome/GCA_000001405.14/.
34. T2T: s3-us-west-2.amazonaws.com/human-pangenomics/T2T/CHM13/assemblies/analysis_set/chm13v2.0.fa.gz.
35. Make BLAST database command: >makeblastdb -in "{input_fna}" -dbtype nucl -out "{output_db}"
36. RepeatMasker is a program that screens DNA sequences for interspersed repeats and low complexity DNA sequences. It is commonly used in the genomics community. See repeatmasker.org.
37. Cserhati, M. and Carter, R., Hierarchical clustering complicates baraminological analysis, *J. Creation* **34**(3):41–50, 2020; creation.com/hierarchical-clustering-baraminology-analysis.
38. Marçais, G. *et al*., MUMmer4: A fast and versatile genome alignment system, *PLoS Computational Biology* **14**(1):e1005944, 2018.
39. Harris, R.S., Improved pairwise alignment of genomic DNA. Ph.D. Thesis, The Pennsylvania State University, 2007.
40. E.g., Human vs chimp LASTZ alignment data can be found at useast.ensembl.org/info/genome/compara/mlss.html?mlss=1098.
41. Altemose, N. *et al.*, Complete genomic and epigenetic maps of human centromeres, *Science* **376**(6588):eabl4178, 2022.

Robert W. Carter *received his Bachelor of Science in Applied Biology from the Georgia Institute of Technology in 1992 and his Ph.D. in coral reef ecology from the University of Miami in 2003. He has studied the genetics of fluorescent proteins in corals and sea anemones and holds one patent on a particular fluorescent protein gene. His current research involves looking for genetic patterns in the human genome and the development of a biblical model of human genetic history. He works as a speaker and scientist at CMI-US.*

Whales designed or evolved: part 2—anatomy and genetics

Marc Surtees

Darwin suggested that whales might have descended from bear-like creatures. However, until the 1980s there was no fossil evidence to support the evolution of whales from terrestrial mammals. In the last few decades, paleontologists have discovered fossil 'walking whales' and other 'archaeocetes'. They have been claimed to be the key steps in the transition from fully terrestrial into obligate marine animals. Advocates of this evolutionary transition support their theories with various lines of evidence. These include: (i) fossil archaeocetes (ancient whales); (ii) hind-limb vestiges in modern whales, and (iii) teeth buds and pseudogenes in baleen whales.

The fossil evidence was reviewed in part one of this article. This second part examines some anatomical genetic evidence and design features for which there is no adequate evolutionary explanation. There are no viable evolutionary theories to explain the appearance of the features which fit whales for life in the sea. Therefore, the biological evidence is consistent with the design hypothesis.

Whales, for example the blue whale (figure 1), are marine mammals which are extremely well designed for life in the sea. Some of the features which make these beautiful creatures so superbly fitted to life in the ocean include:

- streamlining
- hairlessness
- blubber (for insulation)
- tail fluke (plus muscles and bones) for propulsion
- flippers for directional control
- heat exchanger circulatory system
- blowhole (muscles and nerves)
- specialized respiratory system (oxygen storage, lung collapse, heart rate suppression)
- salt elimination system
- echolocation system (toothed whales)
- baleen (food extraction system)
- underwater birth and suckling
- specialized ear morphology.

These features provide considerable evidence of design. However, evolutionists claim, "The origin of whales (order Cetacea) is one of the best-documented examples of macroevolutionary change in vertebrates."[1] The fossil evidence which evolutionists point to was evaluated previously. [2] This article focuses on the design features that are a major challenge to evolutionary claims that terrestrial quadrupeds evolved into fully marine-adapted creatures with flukes and flippers.

Living whales are of two types: those with teeth and those with baleen. These are very different, yet according to evolutionists, the baleen whales (mysticetes) and toothed whales and dolphins (odontocetes) we see today evolved from a common ancestor with teeth, something like *Dorudon* (figure 2) a so-called ancient whale.

Echolocation

Dolphins, porpoises, and toothed whales (i.e., odontocetes) all have an echolocation system made up of various parts (figure 3). They all work together to enable these creatures to effectively 'see' using sound. The echolocation system of odontocetes is possibly the most significant difference between them and other mammals, apart from bats. However, the bats' system differs remarkably from that in odontocetes—although evolutionists believe "200 genes had independently changed in the same ways."[3] This is a huge problem for evolution, because these common genes are *homoplastic*. That is, there is no possible way they came from a common echolocating ancestor.[4]

The dolphin's echolocation system has features found only in these creatures, which enable them to locate things in the water, including a double-beam system. [5,6] The components of the echolocation system, or biosonar system, can be thought of as three subsystems: sound production, projection, and signal detection.

All whales have a blowhole through which they breathe. In odontocetes, the blowhole is a part of a complex sound production system which allows these creatures to produce sounds which are used to echolocate. The blowhole is not connected to the buccal cavity (the inside of the mouth). Instead, it leads to a number of airsacs which have a vital role in the echolocation system.

Image: Archibald Thorburn / PD

Figure 1. Blue whale

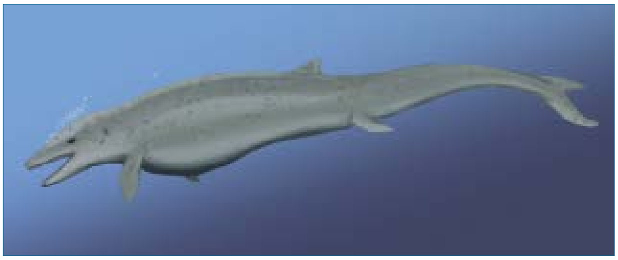


Image: Nobu Tamura, Wikimedia / CC BY 3.0, (redrawn by Caleb)

Figure 2. *Dorudon* was a fully marine creature, claimed to be an evolutionary ancestor of living whales.

Air from the blowhole passes through this system of air sacs, allowing air to be moved across 'phonic lips' to produce sounds, which the dolphin uses for echolocation. The airsacs mean that the dolphin can generate sound within a closed system underwater while the blowhole is shut. This is unique to cetaceans, since all other animals can only produce sound by breathing in or out, which is not possible while underwater. The odontocetes have two pairs of phonic lips which reserach suggests can produce different frequencies of clicks, simultaneously.

The melon in the forehead is filled with lipids (fats) that have about the same density as sea water, which is essential for effective functioning of the system. If the fat was a different density, the sound waves would be refracted, which would make directing the sound waves more difficult. However, the melon contains various lipids with different ultrasound refractive indices, in the right sequence so the melon acts as an ultrasound lens. The lipids are different from blubber lipids, and are made by different and complex enzyme pathways.[7]

Thus, the melon organ projects the sounds, and dolphins can change the shape of the melon to focus and direct the sounds. The presence or absence of the melon in extinct odontocetes is obvious from the shape of the skull, which has a large indentation to accommodate it. The complexity and functioning of the dolphin's amazing system for producing sound beams far exceeds any human-designed sonar.[8]

The sound collection part of the echolocation system is in the lower jaw. Incoming sound is transmitted through the jaw via the fat-filled acoustic window (which is similar to the melon) to the middle ear. The auditory nerve transfers the signal from the middle ear to a specialized area of the brain which processes the signals and interprets them into a 'soundscape'.

The echolocation system is so well designed that the dolphin can sense the density of objects, as well as discriminate between objects of differing compositions. The echolocation clicks can even penetrate soft structures like sand to detect objects buried there.

There is no evidence-based evolutionary explanation for the origin of the various unique components of this biosonar system through a process of random mutation and natural selection. Even the earliest fossils of echolocating cetaceans show that the echolocating system is fully formed—the same applies to bats.

Baleen

Baleen (figure 4), the filter system used to capture small creatures such as krill, is another example of an optimally designed system for which there is no evolutionary explanation. That fact notwithstanding, evolutionists have tried to explain the origin of baleen by mutation and natural selection, but the story is rather confusing.

Back in 2008 there was a report of a creature called *Aetioceus weltoni*, which was described as a toothed mysticete,[9] whereas a mysticete is, by definition, toothless. This creature is believed, by evolutionists, to have lived about 26 Ma ago. The skull resembles that of a creature like *Dorudon*, but it is claimed to be a mysticete. The reasons for the claim are features of the skull and fine details of openings and channels in the skull. Although they are much smaller than those found in mysticetes, they are believed to be homologous with similar features found in living mysticetes. The authors imagine that this creature had both teeth and baleen, which seems highly unlikely from a functional point of view.

Intermediate lacking both teeth and baleen?

More recently, the evolutionary story appears to have changed, as shown by a report published in 2018, of *Maiabalaena*, which is described as the 'sucking whale'.[10] This creature was supposed to have lived about 30 Ma ago and we are assured that this is a stage in the evolution of baleen. It had neither teeth nor baleen; instead, it apparently sucked in its food. *Maiabalaena* is presented as evidence that whales went through a toothless stage before evolving baleen.

At the same time, the authors wrote of their surprise at this intermediate stage between modern filter-feeding whales and their toothed ancestors. We are told that even though this was an efficient suction feeder, it was an intermediate between toothed whales and baleen whales.

This story is perhaps more convincing than the idea that there was a stage with both teeth and baleen. Indeed, the authors wrote, “Previous hypotheses for the origin of baleen have attempted to infer the presence of baleen in fossils from osteological correlates.” They then go on to explain why these theories are inadequate, writing:

> “In crown mysticetes, deep palatal sulci on the ventral surfaces of the maxillae accommodate structures that innervate and vascularize the tissue overlying the baleen; identical sulci are absent in stem mysticetes, although much smaller foramina in the same area have been proposed as homologs, concurrent with the presence of multicusped, adult teeth on the lateral margins. However, these foramina are not present in all taxa within the relevant clades, and they differ from the sulci of baleen-bearing mysticetes in size, orientation, and overall morphology. Moreover, similar foramina have been described in the basilosaurid *Dorudon atrox*.”

However, we are assured that a suction feeder evolved baleen, without any evidence showing that this happened, or how.

Other claimed supporting evidence is that baleen whale embryos have ‘tooth buds’, which proves that they evolved from whales with teeth. These ‘tooth buds’ appear at an early stage and are ‘resorbed’ and replaced with baleen.[11]

There are, however, problems with this story. One might imagine that if one looked at the jaw of the embryo one would see little tooth buds in the embryo jaw, which later disappear to be replaced by baleen. But this is not what you see. The ‘buds’ are not like that at all. They appear as areas inside the jaw which can be distinguished from the surrounding tissues using histological stains.

They do have some features in common with teeth at an early stage of development. This could be because teeth and baleen share common developmental pathways in the early stages, which is consistent with design.

In particular, these buds are not consistent with a transition from teeth to baleen because there are too many of these tooth buds for them to be some sort of evolutionary vestige. The toothed whales from which they are supposed to have evolved had no more than a maximum of 30 teeth in the upper jaw. The embryos of modern whales have as many as 80 ‘tooth buds’. Evolutionists have no explanation as to why or how whales with relatively few teeth gained a lot more teeth and then lost them as baleen evolved.

The evolutionists’ belief in a naturalistic explanation for the origin of baleen must be taken on trust. The best explanation is that baleen was designed to give these whales an efficient feeding system, and they were created with baleen.

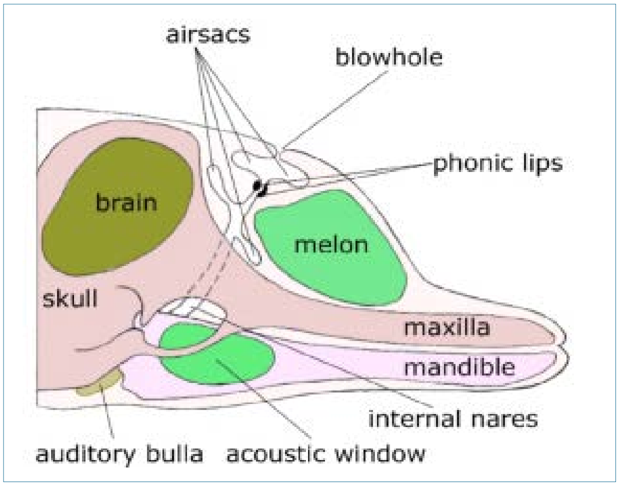


Image: Marc Surtees

Figure 3. A simplified diagram showing parts of the dolphin echolocation system

Image: PeakPX.com | CC0

Figure 4. Humpback whale mouth showing the baleen plates

Reproduction

Whale reproduction provides remarkable evidence which is consistent with creation biology and impossible to explain by slow, gradual evolution. The reproductive systems of whales have some amazing features which enable them to successfully reproduce.[12] Whales live their whole life in the sea and therefore face some unique challenges when it comes to reproduction, especially because of their streamlined shape and means of propulsion. In order to optimize speed and efficiency, the male reproductive organs of whales are completely internalized to minimize drag.

The body temperature of whales is 35–38°C. However, the production of mammalian sperm occurs most efficiently at temperatures around 32–33°C. This is why most terrestrial mammals have external testicles. If whale testicles were at

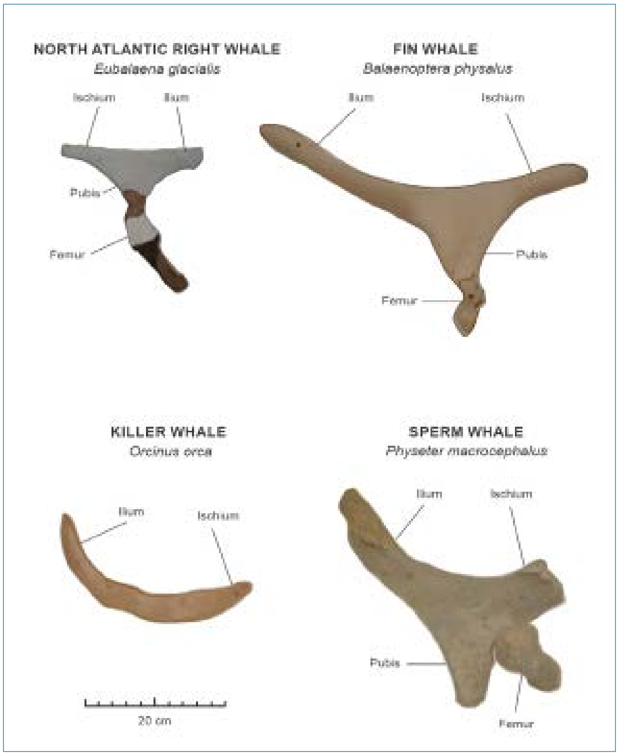


Figure 5. 'Pelvic' bones from a right whale, a fin whale, a killer whale, and a sperm whale (after um.uib.no, redrawn by Caleb Salisbury)

the same temperature as the rest of the body, spermatogenesis would be very inefficient.

There is an additional challenge because the internal testicles are next to main muscles which propel the whale through the ocean. Such active muscles generate much heat, raising the temperature to even higher levels. The insulating blubber only makes things worse because it keeps that heat inside the body. Therefore, without some counter measures, spermatogenesis would effectively stop and whales would be extinct!

The solution is the *countercurrent heat exchange* blood flow system. The blood vessels of the whale are arranged so that cooler blood from the outside of the body cools the blood flowing into the testicles. Other mammals have a single testicular artery, but whales have 20 to 40 coming from the aorta. These arteries run alongside a similar number of veins carrying cooler blood from the dorsal fin and flukes. The direction of venous flow is the opposite of the direction of flow of the arteries. This countercurrent heat exchanger cools the arterial blood before it reaches the testicles so that the internal testicles are cool enough for spermatogenesis to proceed.

Female whales also have a countercurrent heat exchanger to keep the fetal whale from overheating. This is vital to the survival of the fetus since the growing fetus produces heat, and there is no way for the heat to escape because of the insulating blubber. The female also has to deal with the same source of heat as the male—the muscles used to propel the whale. Without the countercurrent heat exchanger, the fetus would suffer from fatal overheating. Female whales have 20 to 40 arteries providing blood to the uterus, which run parallel to the veins carrying cooler blood from the dorsal fin and fluke, which keeps the fetus at the ideal temperature.

Another design feature concerns the specialized bones supporting the reproductive organs. Evolutionists claim that these bones are vestiges of the hips and legs of the whales' ancestors. This is an appeal to homology which is not well supported by the evidence (see below). These bones are not similar to hip bones despite the fact that evolutionists label different areas with the same names as part of the pelvic girdle of tetrapods. They are essential parts of the cetacean urogenital system in both the male and female, which is designed to ensure successful reproduction of whales.

Vestigial legs?

Evolutionists claim that the existence of whales with vestigial leg and hip bones is proof of evolution from terrestrial quadrupeds. Before the claim can be evaluated, we need to define what is meant by an evolutionary vestige. One definition of a vestigial organ is a reduced organ that serves a different function from the original in an evolutionary ancestor. A vestige will also be homologous with the structure from which it was supposedly derived. Homology is established on the basis of the following:

1. same fundamental structure
2. same relationship to surrounding characters
3. same embryonic development.

The claim that living whales have vestigial hips and legs will only be proven if these three requirements are met. The strongest evidence is the presence of bones which are often called 'pelvic' bones and sometimes associated bones referred to as a 'femur'. However, in 1998, Pabst *et al.* wrote: "the exact identity and development of the elements of the pelvic vestige of extant cetaceans [i.e., are they ischium, ilium, or pubis?] have not been established. Such identification is critical to fully understanding the events underlying the evolution of the cetacean pelvis."[13] This is still the case. These bones are embedded in the abdominal wall and connected via muscles to the reproductive organs. They are essential to the function of the reproductive organs. This is not consistent with them being vestiges, since the pelvic and leg bones of land mammals are not embedded in the abdominal wall and are not directly connected to the reproductive organs. For example, in the male whale, there are muscles linking the bone to the penis.[12] Also, these bones do not appear to have the same fundamental structure as the hip and leg bones of land animals, as shown in figure 5.

Notice that while labels are used to suggest that they are the vestiges of hip and thigh bones, there is nothing to prove that the various parts are related in any way to the ilium, ischium, pubis, and femur. This seems to be a clear case of confirmation bias and a prior commitment to evolution. This is particularly true for the labels on the two ends of the killer whale bone. How does anyone know which end is the 'ilium' and which is the 'ischium'? It is far from obvious that these bones have the same fundamental structure as hips and legs. Furthermore, they do not have the same relationship to surrounding tissues. The bones are located within the body wall of the abdomen or the reproductive organs, which disqualifies them from being vestigial legs, since they are differently located with respect to other parts of the body.

There have also been reports of atavistic hind-limbs dating from the late 19th and early 20th century. (*Atavism:* the reappearance of something lost during evolution). But these historical accounts of atavistic legs have not been verified and there are no recent reports. In addition, the whole idea that evolution can be verified by atavistic features is fraught with problems. [14] Interestingly, there was a report of a dolphin with hind-fins which some have claimed proves that dolphins evolved from land animals.[15] But since they are clearly not legs, this implies that dolphins went through a stage with four fins. There is no evidence for this. It is more likely that this was the result of a developmental defect which caused the growth of extra fins.

Genetics

Genetics of limb loss

Bejder and Hall reviewed the evidence for the genetic control of limb development in lizards, chickens, and mice; and the theory of limb loss in snakes.[16] They believe that limb loss and body elongation are linked, and discuss the role of Hox genes. The position of limbs in normal chicks is specified by the pattern of expression of HoxC-6 and HoxC-8 to 10 genes, during development. Differences in the expression pattern in pythons, however, do not prevent the initiation of limb buds and they conclude that other factors are responsible for the failure of fully developed hind-limbs. Others have shown that there are variations in regulatory sequences controlling the expression of Hox genes. These are believed to be responsible for the different positions of limbs in the mouse and chicken. This finding and the fact that regulatory sequences in five species of baleen whales are different from those of artiodactyls prompt Bejder and Hall to suggest that similar regulatory changes may have caused body elongation and, secondarily, limb loss. However, they also acknowledge that the equivalent regulatory sequences in 12 other whales are conserved. They conclude that "A simple evolutionary change in Hox gene expression or Hox gene regulation is unlikely to have driven loss of hindlimbs in cetaceans … ." The fact that they are unable to provide a genetic basis for limb loss is easy to explain if limb loss never occurred.

Pseudogenes

Evolutionists like to point to the existence of pseudogenes of genes which are part of the developmental pathway of teeth development. It is claimed that these pseudogenes are found in baleen whales because they evolved from toothed whales. It is much more likely that these are fully functional regulatory elements which are part of the developmental pathway for baleen formation. If these are evolutionary relics, as some claim, then that raises the question as to why 30 Myr of natural selection has not resulted in the elimination of the useless pseudogenes along with the 'tooth bud' stage mentioned above?

Waiting time problem

One big problem with the proposed evolution of whales is that the window of time available for the transition from terrestrial to fully marine creatures is far too short to allow for the origin and spread of the required genetic changes. Table 1 below shows the approximate ages assigned by evolutionists to the various key fossil intermediate steps in the evolution of whales from the hypothetical ancestors and highlights this problem.

When interpreted within the evolutionary paradigm, the fossil record indicates that the evolutionary transition, from terrestrial to fully aquatic, took about 10 Myr. This rapid evolution is clearly difficult to reconcile with slow, gradual

Table 1. Approximate evolutionary ages of hypothetical fossil intermediates in the evolution of whales

Name	Evolutionary 'age' / Ma
Pakicetus	50
Ambulocetus	50
Rodhocetus	50
Maiacetus	47
Indohyus	47
Dorudon	40
'Modern' whales	30

neo-Darwinian evolution. This 'waiting time problem' is because the mathematical principles of population genetics place severe constraints on the rate at which new genes can originate and spread. Yet evolutionists never question the soundness of their belief that a sufficient number of mutations could have accumulated to produce the required optimally designed body systems of whales in a relatively short period of time. One possible solution is that whale ancestors existed many millions of years before the fossils listed above. This allows more time but is based on belief that the creatures in question were not fossilized.

Discussion

Previously, we have examined the fossil archaeocetes and concluded that there is not enough fossil evidence for the proposed evolutionary transition from a terrestrial quadruped like *Pakicetus* to obligate marine creatures. However, the biggest challenge to the evolutionary account of the origin of whales is not the inadequate fossil evidence but rather the origin of the integrated systems which enable life in the sea.

The three features reviewed herein—echolocation (odontocetes), filter feeding (mysticetes)—and the reproductive system, reveal a high degree of design. This, together with the lack of evidence for the evolutionary origin of these novel features, means that the evolution of whales must be taken on the word of people with *a priori* commitment to evolution.

The genetic evidence for the supposed loss of the hind limbs is also inconsistent and therefore inconclusive, as is the argument for vestigial hind limbs. There is also the waiting time problem. Even allowing them 10 Myr, evolutionists cannot account for the development of one of these unique features, required for life in the sea, by a process of mutation and natural selection. The problem is further compounded by the requirement to explain things such as osmoregulation, the cardiovascular system, and the respiratory system, which also show exquisite design. There is not enough time in the evolutionary account of whale evolution for the fixation of the genes and genetic regulatory pathways which are required to produce the systems which are essential for life in the sea. Evolutionists just have to believe that given enough time new genetic networks, not just mutations in one or two genes, can originate and produce the unique design features of whales.

Conclusions

Having reviewed the evidence, it seems that the evolutionary origin of the design features mentioned herein is far from proven. Even allowing evolutionists the hypothetical 10 Myr assumed within the evolutionary paradigm, they cannot show how the echolocation system, baleen, or the countercurrent cooling system of whale reproductive organs could have evolved.

The design of these creatures clearly reveals the wisdom of God, who created them for life in a marine environment.

References

1. Nummela, S., Thewissen, J.G.M., Bajpai, S., Hussain, S.T., and Kumar, K., Eocene evolution of whale hearing, *Nature* **430**:776–778, 2004.
2. Surtees, M., Whales designed or evolved: part 1—the fossils, *J. Creation* **37**(3):121–127, 2023.
3. Pennisi, E., Bats and dolphins evolved echolocation in same way, Science, 4 Sep 2013.
4. Sarfati, J., Echolocation homoplasy, creation.com, 3 Oct 2013.
5. Cranford, T., Elsberry, W., Van Bonn, W. *et al.*, Observation and analysis of sonar signal generation in the bottlenose dolphin (*Tursiops truncatus*): evidence for two sonar sources, *J. Experimental Marine Biology and Ecology* **407**(1):81–96, 2011.
6. Starkhammar, J., Moore, P., Talmadge, L., and Houser, D., Frequency-dependent variation in the two-dimensional beam pattern of an echolocating dolphin, *Biology Letters* **7**(6):836–839, 2011.
7. Varanasi, U., Feldman, H.R., and Malins, D.C., Molecular basis for formation of lipid sound lens in echolocating cetaceans, *Nature* **255**(5506):340–343, 1975.
8. Sarfati, J., Dolphin sonar (still) far better than man's, *Creation* **41**(1):51, 2019.
9. Deméré, T.A. and Berta, A., Skull anatomy of the Oligocene toothed mysticete *Aetioceus weltoni* (mammalia; Cetacea): implications for mysticete evolution and functional anatomy, *Zoological J. Linnean Society* **154**(2):308–352, 2008.
10. Peredo, C.M., Pyenson, N.D., Marshall, C.D., and Uhen, M.D., Tooth loss precedes the origin of baleen in whales, *Current Biology* **28**(24):3992–4000, 2018.
11. Deméré, T.A., McGowen, M.R., Berta, A., and Gatesy, J., Morphological and molecular evidence for a stepwise evolutionary transition from teeth to baleen in mysticete whales, *Systematic Biology* **57**(1):15–37, 2008.
12. Rommel, S.A., Pabst, D.A., and McLellan, W.A., Functional anatomy of the cetacean reproductive system, with comparisons to the domestic dog; in: Miller D.L. (Ed.), *Reproductive Biology and Phylogeny of Cetacea, Whales, Porpoises and Dolphins*, CRC Press, Boca Raton, FL, pp. 127–145, 2016.
13. Pabst, D.A., Rommel, S.A., and McLellan, W.A., Evolution of thermoregulatory function in cetacean reproductive systems; in: Thewissen, J.G.M. (Ed.), *The Emergence of Whales: Evolutionary patterns in the origin of Cetacea*, Springer, New York, pp. 379–397, 1998.
14. Wieland, C., The strange tale of the leg on the whale, *Creation* **20**(3):10–13, 1998.
15. Wieland, C., A dolphin with legs—NOT!, creation.com, 8 Nov 2006.
16. Bejder, L. and Hall, B.K., Limbs in whales and limblessness in other vertebrates: mechanisms of evolutionary and developmental transformation and loss, *Evolution & Development* **4**(6):445–458, 2002.

Marc Surtees *earned a Ph.D. in Zoology for his original research in the hormonal control of seasonal breeding. He lives in Angus, Scotland. Marc worked for the pharmaceutical industry for more than 30 years, mainly in medical research. He is now retired and has more time to pursue his interest in evidence-based creation biology, fossils and geology.*

What's wrong with being wrong: part 6—a more than cursory look into evolutionary ethics

Marc Kay

In previous parts I addressed the chief evolutionary explanations for morality's and altruism's appearance and spread. Although group selection, kin selection and reciprocal altruism are by far the most popular accounts, there are other options evolutionists have offered as support for an evolutionary understanding of morality. Three are examined here, a further four in the subsequent part.

Evolutionary explanations are fluid, sufficiently flexible to accommodate inconvenient data.[1] In this sixth paper, and the sequel, the seventh, several additional evolutionary accounts for morality's and altruism's appearance are examined. Few are necessarily to the exclusion of any other, with evolutionists hedging bets and combining the explanatory worth of several accounts. Empirical validation is commonly thin and the combinatory thread of just-so stories and conjectured genetic mechanisms is advanced to shore up scientific respectability.

Goodness[2]

Though an exhaustive review of evolutionists' explanations of humans' inherent goodness is beyond this paper, they all follow naturalistic[3] paths and arrive at a shared destination. At their core is agreement that 'machinery' exists which allows the 'good' to materialize. What form this 'machinery' takes is moot; central is the belief that humans possess an innate, evolutionary drive to seek this 'good', the inconvenient psychopath notwithstanding.[4]

Primatologist and ethologist Frans De Waal (figure 1) proposes that humans have inherited a good nature from our non-human ancestors.[5] Our sense of right and wrong arose as an extension of social instincts of our primate relatives. More specifically, our ability to discern between good and evil is sourced from higher primates' putative ability to express emotions, detect them in others and respond empathetically, punishing transgressors.

To shrink the discontinuity between human and non-human requires some verbal 'fudging', as philosopher Richard Joyce (figure 2) labels de Waal's approach:[6]

> "In discussing what constitutes morality, the actual behavior is less important than the underlying capacities. For example, instead of arguing that food-sharing is a building block of morality, it is rather the capacities thought to underlie food-sharing (e.g., high levels of tolerance, sensitivity to others' needs, reciprocal exchange) that seem relevant. … whether animals are nice to each other is not the issue, nor does it matter much whether their behavior fits our moral preferences or not. The relevant question rather is whether they possess capacities for reciprocity and revenge, for the enforcement of social rules, for the settlement of disputes, and for sympathy and empathy."[7]

Not to put too fine a point on it, de Waal cheats. His studies assume chimps, his primary animal subject, are a rudimentary source of human morality in hominid evolution. While not denying the evolutionary relationship, Joyce nevertheless accuses him of blurring the evaluative distinction between the predictive and/or instrumental, and truly moral. Predictive 'oughts/shoulds' "suggest the likelihood of something occurring" (e.g., given today's hot weather, it should rain this evening), while instrumentals entertain a hypothetical end (e.g., 'If I want to pass my exam, I should study'). Joyce then undermines de Waal's entire project with a single remark:

> "… though it may be permissible to ascribe animals certain mental states whose contents involve the word 'ought' or 'should' [in the predictive and instrumental connotation], this may do nothing to establish the legitimacy of ascribing to them *moral* judgments [emphasis in original]."[8]

Joyce's criticism draws our attention to fundamental epistemic difficulties of assigning moral appraisal to behaviour, particularly whether the normative can be in virtue of, or grounded by, non-moral or natural properties.[9] De Waal fails to observe the metaphysical boundary separating these two worlds, which facilitates his Trojan Horse descriptive smuggling the normative inside its belly. By conveniently underplaying the moral quiddity imbedded in human "reciprocity and revenge, for the enforcement of social rules, for the settlement of disputes, and for sympathy and empathy", he can present them as morally neutral in

Image: Chowbok, Wikimedia / CC BY SA 3.0

Figure 1. Primatologist and ethologist Frans De Waal postulates human morality evolved from primate co-operation and the like. However, he doesn't distinguish between the good of instrumental ends and the non-instrumentality of true morality.

chimps, by labelling them 'capacities', which ultimately carry into the human line.

Discharging one's burden of proof for any claim, especially extraordinary ones, is a well understood principle. It is an uncontroversial epistemic duty, if not a moral one.[10] De Waal loses sight of his obligation to explain why reciprocity, tolerance, punishment, and the like, involve a capacity for moral deliberation. De Waal does not provide a single justification for this overextended assertion. To imply that apparent analogous behaviours in humans and chimps are for the same ends, without considering they may be better explained by dissimilar causes and goals, begs the question by assuming that these chimp behaviours possess a latent moral quality (or in his words, "a building block of morality") which was the evolutionary antecedent for human morality.

Joyce reproaches de Waal for categorizing chimp behaviour as 'accepted' and 'unaccepted'. These descriptors fail to come to terms with the truly moral. As Joyce points out:

> "Th[ese are] very different from an awareness of accept*able* and unaccept*able* behaviors—the difference being that the former implies only knowledge that certain behaviors *will* provoke hostility, whereas the latter implies a judgment that these behaviors *merit* hostility … the notions of *merit* and *desert* lie close to the heart of the moral judgment. Without them there can be no sense of justice, no guilt, and no moral conscience [emphases in original]."[11]

Central to his explanation is the hegemonic position emotions play in underpinning morality, what Kitcher calls an 'alliance between Darwin and Hume'.[12] Normally seen as the counterpoint to rationality, de Waal argues that emotions dominate and shoulder rational decision-making:

> "People can reason and deliberate as much as they want, but ... if there are no emotions attached to the various oppositions in front of them, they will never reach a decision or conviction. This is critical for moral choice, because if anything morality involves strong convictions. These convictions don't—or rather can't—come about through a cool rationality: they require caring about others and powerful 'gut feelings' about right and wrong."[13]

Neuroscientist Antonio Damasio (figure 3) is likewise optimistic about man's innate goodness. That man acquired this positive, life-affirming quality through an evolutionary struggle which eliminated the genetically inferior is beside the point. His metaethic of emotivism[14] consigns 'self' to an evolutionary neuronal scaffolding process which has built the complexity of consciousness (not 'mind'—he is, after all, a materialist!) from smaller parts, establishing a beachhead of 'goodness' while surrounded by a 'nature, red in tooth and claw'.

Despite his sanguine expectation, Damasio is not blind to the abject mire in which humans are engulfed. While accepting the ubiquity of death, he longs for that salvatory truth, love. However, rather than discovering the good in the transcendent, he installs it in the biological, an inevitable outcome of his materialism and the evolutionary process:

> "Does this mean that love, generosity, kindness, compassion, honesty, and other commendable human characteristics, are nothing but the result of conscious but selfish, survival-orientated neurobiological regulation? ... . That is definitely *not* the case. Love is true, friendship sincere, and compassion genuine, if I do not lie about how I feel, if I *really* feel loving, friendly, and compassionate … . Realizing that there are biological mechanisms behind the most sublime human behavior does not imply a simplistic reduction to the nuts and bolts of neurobiology … . The picture I am drawing for humans is that of an organism that comes to life designed [*sic*] with automatic survival mechanisms and to which education and acculturation add a set of socially permissible and desirable decision-making strategies that, in turn, enhance survival, remarkably improve the quality of that survival, and serve as the basis for constructing a *person* [last emphasis added]."[15]

His argument is best understood as an attempt to bridge the gap between the body and metaphysics of ethical inquiry by relocating (Kant's) noumenal to the phenomenal: "For most ethical rules and social conventions, regardless of how elevated their goal, I believe one can *envision* a meaningful link to simpler goals and to drives and instincts [emphasis in original]."[16]

His isn't a novel idea: Complex neural networks, fashioned over millions of years produce and link the social rules and conventions. No need to connect the dots, and the entire process, its cumulative history, can be skipped.

These criticisms notwithstanding, his whole project grounds itself on an epistemic rock: it coheres only on the basis that ethical rules and socially permissible strategies are themselves ethical. This not only question-begs their ethical value, but also misses the burden of how their 'moral point of view', to use his wording, came into existence.

Dennett complained that creationists routinely invoked a supernatural skyhook to explain apparent design. *Mutatis mutandis*, I fail to see how Damasio has escaped Dennett's criticism. Creationists' 'skyhook' is recognition that creation is miraculous, the existence of which requires a creator. Damasio's account, however, demands an infinity of natural-law-violating events elevated by a myriad of chimeric cranes.[17,18]

Ridley also explains human 'goodness' as an inevitable product of a lengthy evolutionary journey: "it would be simply inconceivable", he muses, "to imagine … a world without obligations to reciprocate, deal fairly, and trust other people."[19] While acknowledging individuals and whole societies[20] are capable of heinous crimes and selfishness (he lists many), Ridley, fuelled by an unwarranted optimism, opines that

> "The roots of social order are in our heads, where we possess the instinctive capacities for creating not a perfectly harmonious and virtuous society, but a better one than we have at present. We must build our institutions in such a way that they draw out those instincts."[21]

Pirating the language of revelation, Hauser champions the idea that humans are "handed down from on high" a culturally universal Golden Rule. This, he argues, is something which "emerges as an obligatory outcome" whenever "humans live in social groups".[22] Borrowing from Chomsky's language acquisition thesis, and quasi-teleological in its confabulatory just-so account, Hauser sets out a case for millions of years of natural selection imbedding a cerebral universal moral grammar. This allows us to reconcile ethical dilemmas through relying on the 'good' part of ourselves: "Humans appear to be uniquely endowed with a capacity that enables large-scale cooperation among unrelated individuals, and to support stable relationships that rely on reciprocity."[23] Darwin, he said, "was correct in thinking that along the evolutionary path to our moral sense, nature must have added some extra accessories to the core, allowing individuals not only to care for others but to know why caring is the right thing to do, while harming is often the wrong thing to do."[24]

Image: Puku999, Wikimedia / CC0

Figure 2. Richard Joyce is critical of De Waal for relaxing the moral categories of 'unacceptable' and 'acceptable' behaviour by redefining them as 'unaccepted' and 'accepted'.

Baron-Cohen, hardly alone in his belief, holds that inner goodness has a material location: "there are *genes for empathy*". This bedrock of evolutionary thought is the materialists' cash-cow meme. The proof?

> "… scientists are starting to discover particular genes that in far-reaching ways influence our empathy. I restate that these are *not* genes for empathy per se but are genes for proteins expressed in the brain that—through many small steps—are linked to empathy. These steps are still to be clarified, but we can already see from statistical analyses that genes exist that are *associated* with empathy [a] discovery [which] will upset those who want to believe empathy is wholly environmental [emphases in original]."[25]

Emotions and feelings[26,27]

Primate behaviouralists argue that non-human primates do not always act from purely selfish motives but can recognize others' needs and adjust their desires and emotions to match their conspecifics. Empirical data drawn from primate interaction (figure 4) indicate an animal will assist another experiencing distress. The anxious animal communicates its unease through noise or facial expression, which induces a similar emotion in a conspecific, leading the latter to aid the former. This mirroring effect is labelled 'emotional contagion'.[28] Some believe this ability laid the foundation for a complete moral faculty to evolve in humans:

Image: Fronteiras do Pensamento, Wikimedia / CC BY SA 2.0

Figure 3. According to Antonio Damasio, man is innately good, and became so through an obscure evolutionary 'pulling-oneself-up-by-one's-bootstraps' neural scaffolding process.

> "With increasing differentiation between self and other, and an increasing appreciation of the precise circumstances underlying the emotional states of others, emotional contagion develops into empathy. Empathy encompasses—and could not possibly have arisen without—emotional contagion, but it goes beyond it in that it places filters between the other's and one's own state ... . Selection must have favoured mechanisms to evaluate the emotional states of others and quickly respond to them. Empathy is precisely such a mechanism. In human behaviour, there exists a tight relation between empathy and sympathy, and their expression in psychological altruism. It is reasonable to assume that the altruistic and caring responses of other animals, especially mammals, rest on similar mechanisms."[29]

Early experiments involving rhesus monkeys[30] discovered that individuals would starve themselves after pulling a chain which delivered food to them but simultaneously electrocuted a conspecific. This appeared to demonstrate primate empathy, an embryonic altruism. On such experiments the assumed evolutionary nexus between higher order primates and humans for the rise of morality was hoisted. This conclusion is not unequivocal. It is possible the monkeys were perfunctorily reacting to the distress, not consciously effecting solidarity with the sufferer.

To further support his thesis De Waal appealed to experiments carried out by Premack and Woodruff in which apes appear to altruistically help conspecifics. He cited the case of an older female in a zoo enclosure having a problem removing a tyre at the bottom of a six-tyre-deep pile. Eventually it gave up, and a juvenile, previously under its care, removed the tyres on top until it could free the one the female wanted and gave it to her.[31] Kitcher, while conceding that the youngster was capable of a moderately intense psychological altruistic response, however argued that "there was little cost in interrupting his activities to help with the tires ... in a context where not much else was going on."[32]

It is interesting that one key reason de Waal rejects the Veneer Theory, which posits people as basically selfish and morality masks this fact, is that morality would be "reduced to calculations and reasoning, [and] we would come close to being psychopaths, who indeed do not mean to be kind when they act kindly."[33] Yet, his explanation seems incapable of escaping that which he finds so abhorrent:

> "It should further be noted that the evolutionary pressures responsible for our moral tendencies may not all have been nice and positive … . In our own species, nothing is more obvious than that we band together against adversaries. In the course of human evolution, out-group hostility enhanced in-group solidarity to the point that morality emerged … . And so, the profound irony is that our noblest achievement—morality— has evolutionary ties to our basest behavior—warfare."[34]

Any explanation must avoid circular reasoning. Placing emotion at the centre of morality fails this criterion: evolution occurred, so empathy must have arisen from more primitive emotions, and, since evolution has given humans morality, our empathic faculties arose from more primitive emotions.

Others are more candid concerning the link between evolution and how our emotions arose. Wright bluntly states:

> "According to evolutionary psychology, human emotions were 'designed' by natural selection to serve the strategic interests of individual human beings ... . In the case of friendly feelings, we are 'designed' to

warm up to people who share our opinions on contentious issues because, during evolution, these are people it would have been advantageous to form alliances with. This is the generic reason that it is often hard for an outside observer to say whether a given human behaviour was driven more by strategic calculation or by emotions: *because many emotions are proxies for strategic calculations*. (As for why natural selection created these proxies for strategic calculation: these emotions evolved, presumably, either before our ancestors were very good at conscious strategic calculations or in cases where conscious awareness of the strategy being pursued was disadvantageous) [emphasis in original].”[35]

Creationists should not have a problem with emotions playing an important aiding role in moral decisions. Anger at an immoral act, which then spurs us into action, is appropriate. However, we should object to non-human emotion as an explanation for human morality. Being aggrieved about something, without rationality’s input as to *why* that something is morally wrong, is inadequate justification for moral disapprobation. ‘Aggrieved’, when applied to an animal’s response to its witnessing suffering in a conspecific, appears anthropomorphic and empirically unfalsifiable. It also begs the question of a pre-existing moral standard causing the emotion.

Image: USAID Africa Bureau, Wikimedia / CC0

Figure 4. Without the presumed evolutionary link to non-human primates and their capacity for co-operation, a materialist explanation for human morality has no purchase.

Selfishness

What seems in odd opposition to what goodness intrinsically is, one school of thought proposes morality appeared because of a lengthy history of selfish behaviour. This idea is that human ‘goodness’ is merely a biologically induced means to less selfless ends. Human ‘goodness’ is a veneer masking a Hobbesian brute.[36] Man’s true nature is summed up in the cynicism of Ghiselin: “Scratch an ‘altruist’, and watch a ‘hypocrite’ bleed.”[37]

Wright echoes Ghiselin, believing that a hypocritical veneer[38] of respectability conceals an underbelly of immorality and egoistic intentions:

> “The pretense of selflessness is about as much part of human nature as its frequent absence. We dress ourselves up in tony moral language, denying base motives and stressing our at least minimal consideration for the greater good; and we fiercely and self-righteously decry selfishness in others.”[39]

Wright’s dystopian view is a bitter pill. All our lives, all our life, are as much mirage as they are true. Nothing is as it appears, and first impressions are, in all likelihood, lies and deception.

To balance this crushing pessimism, Wright frequently invokes an objectivist moral benchmark, without ever saying where this standard is located. Using expressions such as ‘truly moral’, he thinks that our moral ‘infrastructure’ is subjected to systematic ‘corruption’ causing humans to stray from ‘true morality’, and that this ‘corruption’ is “rooted in the genes (and is so rooted because it served the Darwinian interests of our ancestors during evolution).”[40] And again:

> “I do believe that some of our genetically based moral intuitions are (*sometimes*) subject to subtle biases that steer them away from the truly moral [and] I believe these biases to be themselves grounded in the genes, not mere ‘cultural overlay’ [emphasis in original].”[41]

Wright’s ultimate reliance on the gene and selfishness giving rise to a facade of selflessness is echoed by the philosopher Michael Ruse. He writes that morality is not objective according to any realist metaethic but is "a collective illusion foisted upon us by our genes".[42] Ruse, an atheist, understands well that eliminating God undermines any epistemic foundation to ethical objectivity. He 'knows' that rape and paedophilia are morally wrong, yet understands that one requires more than an appeal to emotions to condemn these heinous acts. What's left is an illusion of objectivity masking morality's actual state of subjectivity: "not only is Darwinian ethics a subjectivist ethics, it is one which positively excludes the objectivist approach … there are no objective ethics."[43]

Richard Alexander, despite his focus on the group as the principal level for selection, in contrast to Dawkins' emphasis on the gene, shares common ground with Ruse concerning human 'disingenuousness'. In the penultimate paragraph of his seminal paper, Alexander writes:

> "In human societies there is the additional problem of what motivations one communicates to his fellows, who should view with favor any evidently altruistic actions, including group-sustaining behavior, even if such actions are in reality ultimately selfish to the actor because of their group-maintaining aspects. It is not necessary that an appropriately selfish (i.e., maximally reproductive) individual be aware either of his motivations or of all of the consequences of his actions. Indeed, we frequently exhort our children to be (consciously) unselfish altruists, even though such tendencies would consistently be selected out of human populations, except for one paradoxical and crucial fact—that actions which would otherwise be truly altruistic may increase the reproduction of their bearer if they are viewed as true altruism by his fellows. If it is reasoned that parental exhortations to unselfish altruism have during human history led human progeny to reproductive success, then it might be argued that sincerity represents a valuable social asset even when it derives from a real failure to recognize the reproductively selfish background and effects of one's own behavior."[44]

Conclusion

I have examined three additional accounts for the rise of morality and altruism. There is a common misunderstanding to all three. Grounded meaning is replaced with question-begging descriptions of (presumed) good qualities: generosity, altruism, honesty, trust, and so forth. Giving examples of 'goodness' assumes a prior definition of 'goodness'. What is missing is an answer to the question: what is goodness *qua* the good? This oversight is lost in the forest of just-so stories entertaining us about how it appeared in humans.

As with the three major explanations of group selection, reciprocal altruism and kin selection, these supplementary explanations suffer from another deficiency. There is a fundamental reliance on a genetic source for the 'good'. This is yet another 'missing link' in the evolutionary tale. A related problem is their dependence on anthropomorphic descriptions of animal behaviour. Human emotions are read back into animals to unite the two genetic histories.

Finally, there is an epistemic oversight. There is a vast divide separating the ethical from the non-ethical. Assuming, rather than demonstrating, that the ethical can be grounded by matter not only fails to explain its origin, but, more importantly, is not a reason that we should believe it.

Creationists are encouraged to use this dearth of explanation as an apologetic against the evolutionary worldview.

In the next paper, I will review another set of evolutionary arguments advanced to explain morality's and altruism's origin.

Acknowledgments

I would like to thank two anonymous reviewers for their suggestions. I also wish to thank David Green for his input.

References

1. For example, to excuse its invisibility, some argue that "The types of genetic mutations that eventually lead to macroevolutionary changes are rare, and this accounts for the slow pace of evolutionary development" (Can evolution be observed, creation.com, accessed 10 Nov 2022, which cites biologos.org/questions/what-is-evolution. However, BioLogos has since removed this entry). Others have described it as so ubiquitous that it is impossible to go unnoticed, yet, if not observed, it must have happened too quickly to be seen: "Evolutionary change is so nearly the universal rule that a state of motion is, figuratively, normal in evolving populations … . The most slowly evolving groups do all seem to be very highly and specifically adapted to a particular zone. Their typical history is one of rather rapid shift into a new, stable and persistent zone" (Simpson, G.G., Horotely, Bradytely, and Tachytely; in: Major Features of Evolution, Columbia University Press, New York, 1953, archive.org; accessed 10 Nov 2022.) It's easy to overlook Simpson's tautology. Substitute with a synonym and its vacuity comes to light: "Evolutionary change is so nearly the universal rule that a state of change is, figuratively, normal in changing populations." Or perhaps the entirely incomprehensible Dawkin-speak, "Evolution has been observed, it's just that it hasn't been observed while it's happening." (Bill Moyers interviews Richard Dawkins, Now, 3 Dec 2004, PBS network, accessed 10 Nov 2022.)
2. I've intentionally left out a discussion of what 'good' means. I will address this Pandora's box in a later paper. I will simply note that evolutionists' use is highly malleable.
3. Ethical philosophers divide meta-ethics into two camps: theories which claim there are no ethical facts and that moral statements bear no ontological implications (i.e., non-cognitivism) and cognitivist theories which argue for the opposite. The latter is subdivided into subjectivist and objectivist theories. Evolutionists rarely opt for the former; the majority, as far as I can understand, stand in the objectivist camp. Within this category lie two further subdivisions, leaving the evolutionist little option. Ethical Naturalism, the belief that moral properties are reducible to biological and/or psychological phenomena, is the preferred theory. Ironically, by virtue of their metaphysical worldview, this 'choice' has already been made for the evolutionist.

   However, a minority of evolutionists who, faced with the epistemological and logical problems a purely naturalistic metaphysic imposes upon ethical

theory, opt for a non-naturalism theory. Here, moral facts and properties are irreducible to natural facts of the universe. This is arguably the most popular Christian meta-ethic. Shafer-Landau and Cuneo are notable, contemporary bearers of this meta-ethic. Theirs, while intellectually impressive, contains serious flaws, and while I do address these in a later paper, for now two brief comments.

Landau is committed to an evolutionary explanation for morality. He takes issue with a class of proposed ethical antirealist defeaters against ethical realism, whose central argument is this: given the truth of realism and evolutionary adaptative pressures, it would take a miracle for our doxastic faculties to reliably track these stance-independent moral truths. This reasonable criticism of evolutionary ethical realism brings me to my second remark.

Landau acknowledges the force of the antirealist objection, but his evolutionary worldview limits his options. He recognizes the danger of accepting ethical naturalism in which moral beliefs are reduced to natural phenomena. In a further concession, there is a very clear likelihood that this tracking process is unreliable if chained to ethical naturalism. And this is where his best option proves inadequate. Principal among his failings is Landau's almost total reliance on a specimen of metaphysical bruteness. He claims that certain moral answers are grounded in their being so self-evident that to deny them would indicate a person's irrationality. These simple moral facts require no further explanation and are abstract and mind-independent, hence their existing as inhabitants in a non-natural orb: "assume that the moral fixed points are true of conceptual necessity [and then] assume that these truths are constituted by moral concepts, which are nonnatural [and so] moral fixed points are true in virtue of their constituent concepts, some of which are nonnatural." (Cuneo, T. and Shafer-Landau, R., The moral fixed points: new directions for moral nonnaturalism, *Philosophical Studies* **171**(3):399–443, 2014; p. 412).

4. Sometimes a mechanism by proxy is factored in e.g., epigenetic rules—to be addressed in a subsequent paper. In addition, the 'mechanics' is rarely without its own just-so history. In an upcoming part I address these psychological aberrations, specifically with respect to the argued-for neuroscience supposedly evidencing these.
5. De Waal, F., *Primates and Philosophers: How morality evolved*, Princeton University Press, Princeton, NJ, pp. 3–58, 167–175, 2006.
6. Joyce, R, *The Evolution of Morality*, MIT Press, Cambridge Ma, 2007, p. 77.
7. De Waal, ref. 5, p. 16.
8. Joyce, ref. 6, p. 78. For further elaboration on the difference between these disparate 'oughts', see pp. 78ff.
9. I visit this discussion in a subsequent paper, but it is worth mentioning the Naturalistic Fallacy. Championed by G.E. Moore, he drew attention to the problematic exercise of cashing out the non-natural, morality, in terms of the natural. Also apposite is Hume's Guillotine, the problems involved deriving a moral 'ought' from a non-moral 'is'. This too will be covered in a follow-up paper.
10. Wrenn makes a valuable contribution to this issue by arguing that our hitherto epistemic duties are better understood to be moral duties. (Wrenn, C.B., Why there are no epistemic duties, *Dialogue: Canadian Philosophical Review* **46**(1):115–136, 2007.)
11. Joyce, ref. 6, p. 80.
12. Kitcher, P., Ethics and evolution: how to get here from there; in: de Waal, ref. 5, p. 124.
13. De Waal, ref. 5, p. 18.
14. Emotivism is a meta-ethical theory that there are, inter alia, no ethical facts or knowledge, and that "Ethical statements are neither true nor false but express emotions, desires or attitudes." (Mautner, T. (Ed.), *The Penguin Dictionary of Philosophy*, Penguin Books, London, pp. 164–165, 2000.) Or as Ayer, an early exponent of this system of evaluation, argued: "in every case in which one would commonly be said to be making an ethical judgement, the function of the relevant ethical word is purely 'emotive'. It is used to express feeling about certain objects, but not to make any assertion about them. It is worth mentioning that ethical terms do not serve only to express feeling. They are calculated also to arouse feeling, and so to stimulate action … it is impossible to find a criterion for determining the validity of ethical judgements. It is not because they have an 'absolute' validity which is mysteriously independent of ordinary sense-experience, but because they have no objective validity whatsoever … . They are pure expressions of feelings and as such do not come under the category of truth and falsehood. They are unverifiable for the same reason as a cry of pain, or a word of command is unverifiable— because they do not express genuine propositions." Ayer, A.J., *Language, Truth and Logic*, Dover Publications, New York, pp. 108–109, 2014 (1946).
15. Damasio, A., *Descartes' Error: Emotion, reason, and the human brain*, Quill, New York, pp. 125, 126, 2000. It is significant that his 'love' and the other desirable traits of human goodness exist to "enhance survival, [and] remarkably improve the quality of that survival" are reduced to an instrumental value and end rather than love *qua* love.
16. Damasio, ref. 15, p. 125.
17. For more supposed delineation of skyhooks and cranes, see Dennett, D., *Darwin's Dangerous Idea: Evolution and the meanings of life*, The Penguin Press, London, pp. 74ff and passim, 1995. To appreciate just how unintelligent his case for materialism is, note the following definition, replete with straw men and the contradictory notion that design is ateleological and without thought: "Let us understand that a skyhook is a 'mind-first' force or power or process, an exception to the principle that all design, and apparent design, is ultimately the result of mindless, motiveless mechanicity" (p. 76).
18. Despite being a thorough-going materialist, and thus eschewing the non-material soul, Damasio fails to escape from what he calls Descartes' error, the title of his best-seller. Attempting to integrate the neurobiological facts to a resilient whole, Damasio uses the language of a theatre-attending homunculus, in which 'someone' views what's going on in the brain. Naturally he doesn't state this so overtly; nonetheless the ghost in the machine has bought his ticket and watches the movie progress: "A large part of such knowledge is recalled in the form of images at many brain sites rather than a single site. Although we have the illusion that everything comes together in a single anatomical theater, recent evidence suggests it does not … the images over which we reason (images of specific objects, actions, and relational schemas, of words which help translate the latter into language form) not only must be 'in focus' … but also must be held active in mind … the brain holds and retrieves knowledge in spatially segregated rather than integrated manner, they also require attention and working memory so that the component of knowledge that is retrieved as a display of images can be manipulated in time … . Brains [must possess] the ability to display images internally and to order those images in a process called thought. (The images are not solely visual; there are also 'sound images', 'olfactory images', and so on.) … having a mind means that an organism forms neural representations which can [sic] become images" (Damasio, ref. 15, pp. 84, 89, 90.)

    The materialist labyrinth is best understood when we ask who is the 'who' who is viewing the images? And, ever deeper into the rabbit hole, who is the 'who' viewing the 'who' who is viewing the images? Nowhere is this explained. Images require a viewer external to the image; hence, the exigency for an internal homuncular by proxy. All that is served up is rehash, what he later terms 'visual dispositional representation' of "a complex neural machinery of perception, memory, and reasoning … [amounting to] patterns of activity occurring in … visual cortical circuitry" (pp. 97, 103), This vacuous circularity ends in epistemological nihilism: "If our organisms were designed [there's that word again!] differently, the constructions we make of the world around us would be different as well. We do not know, and it is improbable that we will ever know, what 'absolute' reality is like" (p. 97).
19. Ridley, M., *The Origins of Virtue*, Softback Preview, p. 143, 1997.
20. On this he mentions Cook's and de Galaup's eventual disillusionment with the 'utopian' Pacific Islands. The former, on his second voyage, was exposed to the sacrificial infanticide, misogyny, and ubiquitous theft, while the latter wrote: "The most daring rascals of all Europe are less hypocritical than the natives of these islands. All their caresses were false." Ridley, ref. 19, p. 255.
21. Ridley, ref. 19, p. 264.
22. Hauser, M.D., *Moral Minds: How nature designed our universal sense of right and wrong*, HarperCollins, New York, p. 358, 2006.
23. Hauser, ref. 22, p. 411.
24. Hauser, ref. 22, p. 309. His sanguinity extends to the final sentence of his book, a conclusion that only an armchair scientist-cum-philosopher could utter: "Appreciating the fact that we share a universal moral grammar and that at birth we could have acquired any of the world's moral systems, should provide us with a sense of comfort, a sense that perhaps we can understand each other" (p. 426). To be fair, Hauser expresses some reservation humans are strictly good (which is richly ironic given he was dismissed from Harvard for research misconduct, code for fudging his experiment findings. See: Marc Hauser 'engaged in research misconduct', *Harvard Magazine*, 5 Sep 2012, accessed 6 June 2023. However, the 'good' is always determined in terms of the genetic good, whether for the group's or the individual(s)'s best interests. Explanations which reduce the ethical to the natural run afoul of Moore's Naturalistic Fallacy, a defeater for any evolutionary ethical meta-ethics. Very few materialists give Moore's criticism its due, an issue I take up in a subsequent part.
25. Baron-Cohen, S., *The Science of Evil: On empathy and the origins of cruelty*, Basic Books, New York, p. 151, 2011. Italics are Baron-Cohen's. Notice the flim-flam: "scientists are starting to discover particular genes" quickly reduces to "Though still to be clarified … we can already see from statistical analyses that genes exist that are *associated* with empathy". Jay Joseph, in his remarkable book-length criticism of twin studies which are used to support the genetic explanation for 'everything', quotes Ken Richardson on genetic statistical modelling to explain behaviour: "never before in any field of science have so many arbitrary assumptions been gathered together, in full knowledge of their invalidity, as the basis of substantive claims about the nature of people,

with so many potentially dire consequences for them.” (Richardson, K., *The Origins of Human Potential*, Routledge, London, p. 135, 1998; in: Joseph, J., *The Trouble with Twin Studies: A reassessment of twin research in the social and behavioral sciences*, Routledge, New York, p. 86, 2015.)

26. Before Darwin, David Hume was the most celebrated advocate of emotion as the prime mover of moral sentiments. In a lengthy, much relied upon passage, Hume famously distils his thesis: “Take any action allowed to be vicious: Wilful murder, for instance. Examine it in all lights, and see if you can find that matter of fact, or real existence, which you call vice. In which-ever way you take it, you find only certain passions, motives, volitions and thoughts. There is no other matter of fact in the case. The vice entirely escapes you, as long as you consider the object. You never can find it, till you turn your reflexion into your own breast, and find a sentiment of disapprobation, which arises in you, towards this action. Here is a matter of fact; but ’tis the object of feeling, not of reason. It lies in yourself, not in the object. So that when you pronounce any action or character to be vicious, you mean nothing, but that from the constitution of your nature you have a feeling or sentiment of blame from the contemplation of it. Vice and virtue, therefore, may be compared to sounds, colours, heat and cold, which, according to modern philosophy, are not qualities in objects, but perceptions in the mind.” Hume, D., *A Treatise of Human Nature*, III.I.I, J.M. Dent and Sons Ltd., London, pp. 167–168, 1956 (1739–1740). Darwin was certainly familiar with Hume as he references him in his *Descent*, citing Hume’s *An Enquiry Concerning the Principles of Morals*. See Darwin, C., *The Descent of Man, and Selection in Relation to Sex*, Penguin Books, p. 132, footnote 23, 2004 (1879, 2nd edn).
27. Hume did not altogether lock the door against reason: he exalted emotion, which had the effect of putting reason in its proper place. For example, “Since morals, therefore, have an influence on the actions and affections, it follows, that they cannot be derived from reason; and that because reason alone, as we have already proved, can never have any such influence. Morals excite passions and produce or prevent actions. Reason of itself is utterly impotent in this particular. The rules of morality therefore, are not conclusions of our reason. No one, I believe, will deny the justness of this inference; nor is there any other means of evading it, than by denying that principle, on which it is founded. As long as it is allowed, that reason has no influence on our passions and action, it is in vain to pretend, that morality is discovered only by a deduction of reason. An active principle can never be founded on an inactive; and if reason be inactive in itself, it must remain so in all its shapes and appearances, whether it exerts itself in natural or moral subjects, whether it considers the powers of external bodies, or the actions of rational beings. It would be tedious to repeat all the arguments, by which I have proved, that reason is perfectly inert, and can never either prevent or produce any action or affection, it will be easy to recollect what has been said upon that subject. I shall only recall on this occasion one of these arguments, which I shall endeavour to render still more conclusive, and more applicable to the present subject. Reason is the discovery of truth or falsehood. Truth or falsehood consists in an agreement or disagreement either to the real relations of ideas, or to real existence and matter of fact. Whatever, therefore, is not susceptible of this agreement or disagreement, is incapable of being true or false, and can never be an object of our reason. Now it is evident our passions, volitions, and actions, are not susceptible of any such agreement or disagreement; being original facts and realities, complete in themselves, and implying no reference to other passions, volitions, and actions. It is impossible, therefore, they can be pronounced either true or false, and be either contrary or conformable to reason. This argument is of double advantage to our present purpose. For it proves directly, that actions do not derive their merit from a conformity to reason, nor their blame from a contrariety to it; and it proves the same truth more indirectly, by shewing us, that as reason can never immediately prevent or produce any action by contradicting or approving of it, it cannot be the source of moral good and evil, which are found to have that influence. Actions may be laudable or blameable; but they cannot be reasonable: Laudable or blameable, therefore, are not the same with reasonable or unreasonable. The merit and demerit of actions frequently contradict, and sometimes control our natural propensities. But reason has no such influence. Moral distinctions, therefore, are not the offspring of reason. Reason is wholly inactive, and can never be the source of so active a principle as conscience, or a sense of morals.” Hume, ref. 26, p. 177.
28. Hatfield, E., Cacioppo, J.T., and Rapson, R.L., Emotional contagion, *Current Directions in Psychological Science* **2**(3):96–99, 1993.
29. De Waal, ref. 5, pp. 26–28.
30. See Wechkin, S., Masserman, J.H., and Terris, W., Shock to a conspecific as an aversive stimulus, *Psychonomic Science* **1**(2):47–48, 1964, and Masserman, J., Wechkin, M.S., and Terris, W., Altruistic behavior in Rhesus monkeys, *American J. Psychiatry* **121**:584–585, 1964. In De Waal, ref. 5, p. 29.
31. De Waal, ref. 5, pp. 31–32. See Premack, D. and Woodruff, G., Does the chimpanzee have a theory of mind?, *Behavioral & Brain Sciences* **1**(4):515–526, December 1978.
32. Kitcher, P., *Ethics and Evolution: How to Get Here from There*, in: De Waal, ref. 5, pp. 130–131.
33. De Waal, ref. 5, p. 52.
34. De Waal, ref. 5, pp. 53, 54, 55.
35. Wright, R., ‘The Uses of Anthropomorphism’; in: De Waal, ref. 5, pp. 87–88.
36. Thomas Hobbes was a 17th-century English political philosopher. He held that the natural state of man was self-regarding, each man seeking to satisfy his own desires, one against the other in this pursuit of individual happiness and survival. Two passions stand out in Hobbes: fear of death and a desire for power. Both are related by any one man’s constant suspicion of another, and that that other will either seek his demise or, more broadly, disempower him.
37. Ghiselin, M., *The Economy of Nature and the Evolution of Sex*, University of California Press, Berkley, p. 247, 1974.
38. For further discussion on the Veneer Theory, its history, and, in particular, its origin with Thomas Huxley, see scattered references and explanations in De Waal, ref. 5.
39. Wright, R., *The Moral Animal: The new science of evolutionary psychology*, Pantheon, New York, p. 344, 1994.
40. Wright, ref. 35, p. 95.
41. Wright, ref. 35, p. 94.
42. Ruse, M., *Taking Darwin Seriously: A naturalistic approach to philosophy*, Basil Blackwell, Oxford, p. 253, 1986. I devote more attention to his lengthy argument in a subsequent paper. What has perhaps troubled me more than Ruse’s arguments—they’re simply thin on science and epistemic purchase—is the alacrity of Christians accepting them or being blinded to the self-immolating implications for Christianity itself. For example, the neo-orthodox Australian Centre for Public Christianity interviewed Ruse without raising any contrary argument. This is hardly surprising given both interviewer and interviewee are evolutionists. For example, Denis Alexander, Alister McGrath, Simon Conway-Morris, John Lennox are all given opportunity to white-ant Christianity. For short interviews with Ruse, see, for example, A Ruse on Easter from Darwin’s lapdog and Culture Clash.
43. Ruse, ref. 42, p. 254. Despite his atheism, and yet oddly consistent with it, (the illusion/delusion of) God does have at least one function: “He backs up the objective, binding status of morality” (p. 254).
44. Alexander, R.D., The evolution of social behaviour, *Annual Review of Ecology and Systematics* **5**:325–383, 1974; p. 377.

***Marc Kay** has a bachelor’s degree in philosophy, religious studies, and Indo-Malay; postgraduate certification in TESOL. He was previously a teacher, and mental health and youth worker. He is now a fulltime stay-at-home dad while his wife pursues her academic career. He commits any free time to street evangelism.*

What's wrong with being wrong: part 7—a more than cursory look into evolutionary ethics (contd)

Marc Kay

In part 6, I examined three further arguments employed by evolutionists to explain morality's and altruism's origins. These are in addition to the more standard accounts of group selection, kin selection, and reciprocal altruism. This paper surveys another four. Collectively, these ten do not exhaust evolutionary responses. However, they capture the lack of clarity and explanatory power in ethical philosophy and science and their shared inability to give a logical account for morality and goodness.

This paper surveys another four arguments employed by evolutionists to explain the origins of morality and altruism. To help recap the previous articles, table 1 summarizes the evolutionary options and approaches discussed in this series so far.

Sex sells

Darwin wrote:

> "There are many other structures and instincts which must have been developed through sexual selection … . It is clear that these characters are the result of sexual and not of ordinary selection, since unarmed, unornamented, or unattractive males would succeed equally well in the battle for life and in leaving a numerous progeny, but for the presence of better endowed males."[1]

Hitching his carriage to sex, Darwin's 'other theory', evolutionary psychologist Geoffrey Miller (figure 1) ascribes quasi-panacea qualities to sexual selection, asserting that it can explain the perpetuation of artistic attributes, intelligence, and, most oddly, moral virtues because these traits were sexually attractive. However, there is a rider: Miller denies sexual selection created the virtues. He defends the position they merely built on what our simian ancestors already possessed: "sexual selection amplified our standard social-primate virtues into uniquely elaborated human forms."[2]

According to Miller, "sexual selection can 'supercharge' other evolutionary processes by adding positive feedback dynamics that tend to trigger evolutionary innovation and speciation."[2] 'Traditional mechanisms' involved in social selection, like kin selection and reciprocal altruism, when compared with sexual selection, have limited effect on how they produce and shape the evolution of moral virtues: "Nonsexual forms of social selection can shape morality only insofar as they confer fairly concrete survival benefits (e.g., shared food, protection from predators) on the morally virtuous."[2] However, in combination with, for example, considerations of mate choice, sexual selection will "anticipate, sharpen, and amplify the social selection pressures to produce a more extreme, costly, prosocial version of the moral virtue than social selection could achieve alone."[2]

Driscoll offers several valuable criticisms of Miller's argument, including the all-important: How would moral virtues have spread in a group of non-moral individuals to obtain the "required something to break the non-moral equilibrium that existed in groups before morality arose"?[3] She rightly points out that within groups a novel virtuous mutant would be eliminated, eliminated by its ruthless and amoral neighbours. It would require an already virtuous group to safeguard the survival and spread of virtue. This highlights the problem of the non-equilibrium hurdle as it ignores how the group went from zero to virtuous uniformity.

To overcome this, Miller suggests mate preferences for the virtuous. Their attractive character would grant a reproductive advantage. But why would a non-virtuous individual find virtue compelling? After all, not only is the virtuous 'freak' less fit, its offspring will be also?

Miller's answer is that moral virtues telegraph more than probity, having "evolved to advertise individual fitness".[2] Displaying a positive virtue, like empathy, is a reasonable indication of all-round health, what he calls 'neurogenetic warranty'.[4] These sexually selected signals advertise, and are linked to, good genes, which are also indicators of, inter alia, a low 'mutational load' (i.e., fewer than average errors in DNA replication),[4] and higher intelligence. They are thus a predictor of stable marriages, empathy, exercising, eating well, social, economic, and aesthetic success.[5] Despite their cost (e.g., exposing the virtuous individual to cheating and other sociopathic acts), displays of virtue are a guarantee of superior genes for other reproductively valuable characteristics. Acting virtuously communicates

Table 1. Evolutionary options and approaches discussed in earlier parts of this series.

Idea/Approach	Description	Criticisms
Group selection	An individual organism will surrender its own best interests so that the probability of extinction of the group or species is minimized.	Difficult, if not impossible to quantify Opposes Darwinism's central principle of the individual's role in adaptation and survival, interpreted at the gene level. Fails to account for cheats who parasite off the goodness of others. Genetic drift eliminates the required and hypothetical novel altruistic gene(s)
Kin selection	Sacrifices one's own interests by promoting the fitness of genetically related others. A little bit of the genetic "you" will spread to the broader relative gene pool.	The math equations fail to capture real life conditions. Population genetics, allele frequencies, mutation rates, epistasis, migration, and group size are omitted in calculations.
Reciprocal altruism	Under certain conditions natural selection will favor these altruistic behaviours directed toward distantly related and non-related members because in the long run they benefit the organism performing them.	Cheats can prosper by not returning their 'debt' to the 'altruist'. Ignores the problem of the altruistic gene's origin. Subverts the sense of altruism. Relies on tendentious and anthropomorphic animal studies.
Sociobiology in general	The systematic study of the biological basis of all social behaviour.	Dependence upon bizarrely incorrigible and immoral human societies. The individual organism counts for almost nothing and a person is only DNA's way of making more DNA. Rejects ethical realism, and holds that genes have tricked humans into believing morals are objective and from God.

that brain, body, and mind are working as a harmonious unit, a combination all too alluring to pass up.

While rejecting the claim that handsome and smart people are necessarily virtuous, Miller ties virtuous behaviour to other attractive qualities:

> "… good genes virtues should correlate positively with other well-established fitness indicators, such as physical and mental health, longevity, fertility, body size and symmetry, as well as intelligence … . In particular, genuine phenotypic correlations should exist between good genes virtues, physical attractiveness, social status, and charisma, not just stereotyped 'halo effects' in which more physically attractive people are seen as virtuous."[6]

Miller seems to be saying what he originally denies; surely 'attractive' qualities, such as body symmetry, personality and the like are what makes one person more desirable than another and that these qualities are more than likely found in virtuous persons (figure 2). As Miller himself remonstrates, no-one would accept the shallow assertion that a person is necessarily moral because she is 'drop-dead gorgeous'; but this correspondence doesn't want to disappear, because elsewhere he writes:

> "… there is an evolutionary deep relationship between moral goodness and aesthetic beauty, as reflected in the overlap between virtue ethics and the recent revival of Darwinian aesthetics … [having its] intellectual roots in late nineteenth-century evolutionary biology, when mate choice for sexual ornaments was seen as the central evolutionary process that creates organic beauty … . Beauty is thus an emergent property of coevolution between a signaling system (the beauty cues displayed by some individuals) and a receiver system (the aesthetic judgment system in other individuals)."[7]

Miller's claims are fluid and hard to pin down. He vacillates between one idea and its contradictory. On one hand Miller claims male sociopathic and anti-social personality types have a reduced long-term mating success; yet, in tacit recognition that cheats can, and do, prosper, he gives a free pass to the counterfactual 'if virtue is good, why do the pathologically dishonest and mean proliferate?' He claims they, too, are 'sexy':

> "… there is substantial overlap between sexually attractive personality traits and human moral virtues, but does not pretend that all sexually attractive traits are virtues, or that all virtues are sexually attractive under all conditions. Some individuals may feel most aroused by potential mates who show Machiavellian cunning … or rampant promiscuity … . To argue that

> some moral virtues evolved through mate choice is not to argue that vice is never attractive."[8]

Despite Miller's special pleading, other studies have argued that a clear genetic evolutionary advantage does accrue to these not-so-nice individuals because of their potential reproductive success through having multiple partners. For example, MacMillan *et al.* contend that:

> "Rather than viewing antisocial personality as maladaptive, it might be considered one end of a continuum of adaptive strategies for maximizing fitness … . We believe antisocial personality disorder describes individuals who have, within the reproductive limits of the human species, chosen [to] maximiz[e their] number of offspring by courting and copulating with multiple mates [thus decreasing time and energy available for protection and provision of relatives, leading to reduced survival of relatives, including offspring]."[9]

A common weakness in evolution-based explanations is that they are so accommodatingly malleable they cannot be falsified. Closely related to this is that Miller's thesis has zero predictive value, rendering it worthless to demonstrate any evolutionary history, and it's between a costly signalling trait and its genetically related phenotypic partner. Responding to Driscoll's apt objection, Miller comments:

> "… signal evolution is highly stochastic … . Sexual selection is a major source of biodiversity precisely because the demands of costly signaling vastly underspecify the precise design details of fitness indicators. Any indicator will do, as long as it is costly, complex, and hard to fake. This is a strength of costly signaling theory because it gives the theory very broad applicability, but it is a weakness because it makes almost impossible any a priori predictions about the design details of indicators in particular species. We can recognise an indicator post hoc when we see one, but we may have never been able to predict which indicators would evolve in which lineages."[10]

If we can't predict any relationship beforehand, there is a logical possibility there is not one. More importantly, any other explanation may be of equal, if not superior, value to Miller's, including the Christian conclusion of there being no genetic component to ethics and that its origin lies in the immaterial.

Suspect links aside, morality, to Miller, is, again, just another means to an amoral end, not a stand-alone, unique faculty: "moral capacities … [are] costly, conspicuous signals to increase individual reproductive prospects."[11] Evolution struggles to provide justification for moral behaviour being good in and of itself because everything must be referenced back onto reproductive success.[12] Nothing novel here.[13]

Image: Rebel Wisdom, Wikimedia / CC BY 3.0

Figure 1. The unfalsifiable: According to Geoffrey Miller (pictured), not only do beautiful people telegraph moral probity, but the psychopathic can be reproductively advantageous.

Parental manipulation

Theorists argue groups form and persist because there is a reproductive gain for all their members. Alexander argues an exception: situations when altruism between siblings is controlled to further the reproductive interests of the parent(s). Humans, Alexander claims, "are parental manipulators par excellence".[14] He terms this manipulation a type of fraud, though he is at pains to distinguish it from any conscious or purposeful deception by the parent:

> "Parental manipulation of progeny refers to parents adjusting or manipulating their parental investment, particularly by reducing the reproduction (inclusive fitness) of certain progeny in the interests of increasing their own inclusive fitness via other offspring … parental care evolves, not because it increases the reproduction of individual offspring, but because it increases the reproduction of the parent."[15]

Parental manipulation is an alternative explanation to kin selection. Lauded as an explanation for such diverse phenomena as homosexuality, when parents supposedly transform the child into, and raise him as, a homosexual, certain insects feeding undeveloped eggs to other offspring, cannibalism of the youngest by older aboriginal children during food shortages, polyandrous societies and for "teaching

Image: Thomas Wolf, www.foto-tw.de, Wikimedia/CC BY-SA 3.0

Figure 2. Some evolutionists argue that good 'beauty' genes in people communicate not just physical attractiveness but superior moral qualities as well. Hollywood is where the 'beautiful' people go yet Hollywood is a morass of immorality (!?).

children things like honesty, decency, generosity [because it] driv[es] the children to support the parents' biological interests",[16] parental manipulation of offspring holds great appeal for evolutionary pundits to make sense of the counter-intuitive and biologically inexplicable.

In addition to being devoid of empirical basis,[17] the proposal that parents manipulate offspring in order to maximize the former's fitness, while suppressing the progeny's, surreally turns any commonsense understanding of altruism on its head. To make sense of this Humpty Dumpty world, one must believe 'altruism' has nothing to do with a psychological (or spiritual) unselfish regard for others. It has, however, everything to do with biology and increasing an actor's reproductive success, even if that (inevitably) entails being at the expense of others' success.[18] Only this fundamental principle makes 'sense' of the paradox in Alexander's following claim: "the entire parent-offspring interaction has evolved because it benefited one of the two individuals—the parent."[19] His explanation runs something like this.

Consider two adult organisms: one possesses a gene enabling it to manipulate one of its offspring to become an altruist with respect to its other offspring, the other adult without it. And suppose—a word with inexhaustible ontological swagger!—this offspring's aiding its sibling(s) increases the siblings' reproductive capacity. Combine these two causes, and despite the altruist offspring being effectively sterile, ceteris paribus, "these genes for altruism through parental manipulation will be promoted because [the manipulating organism] is twice as fit, biologically speaking, as [the parent without the manipulating genes]."[20]

As an explanation to account for increasing progeny's survival and reproduction, it offers some traction, but as an explanation for altruism's extending to future generations, it is dead in the water. After all, on the rational assumption the altruistic offspring does not reproduce, how does 'altruism' spread if it is found only in the helping offspring?

But what happens if a mutation causes one offspring to manipulate its parent to increase its own reproductive fitness? Alexander proposes two get-out-of-jail cards. If the mutant successfully gains more parental benefits than its siblings, thus lowering the parent's fitness, not only will this increase his fitness, but his offspring will carry the manipulative allele in greater numbers. However, once it is an adult, its own inclusive fitness will be reduced because its offspring will be more manipulative than he: "no individual can receive a net benefit from possessing such an allele, and genetic lines will win that lack alleles disrupting in this fashion the parent-offspring interaction."[19]

Second, with a few caveats, by withholding parental care or punishing (or even eliminating!) the manipulative offspring, the parent sees a net reproductive gain. Benefit accrues only if: (i) the negative effects incurred by the other offspring act against the manipulative offspring; (ii) it is combined with the cost of energy and decrease to the parent's fitness controlling the same manipulative offspring; and (iii) it does not exceed what would have been the detrimental consequences upon the parent if no action had been taken against the offspring's adversarial behaviour. Furthermore, if cheating (and, if I correctly understand Alexander, this entails, for example, deceit by the mutant offspring toward its parent and sibling) by the mutant is trivial, "individual offspring should evolve to allow" the parent to always win because the negative cost to the mutant (maximally death at the hands of the parent), resulting from detrimental action taken against its parent, will eclipse any gain to its inclusive fitness.[21]

Compulsion

The imposition of force on the weak by the strong other is perhaps the most counter-intuitive of evolutionists' explanations for altruism's existence. However, given the redefining of altruism as nothing more than reproductive success, cases such as a male chimpanzee's aggressive demand for meat from a subordinate or forcing an impala to the edge of a herd to act as a sentry, causing it to be more alert for its own safety as well, can all be squeezed under the rubric of biological altruism.

Non-adaptive altruism-beneficial acts forced onto an 'altruist' by unrelated companions, such as slave ants working for their masters (figure 3), are regarded as examples of biological altruism because the reproductive capacity of the imposer increases at the expense of the 'altruistic' provider.[22]

Figure 3. Evolutionists can flip the normal meaning of altruism on its head by redefining it as a means by which one creature can increase its own reproductive capacity at the expense of another. Master and enslaved ants are a commonly cited example of this now rebadged biological altruism.

Image: Adrian A. Smith, Wikimedia/CC BY 2.5

There are two other explanations on offer. If a punisher of a cheat does not subsequently interact with that individual, and the defector, as a result, switches to cooperation with others, this comes at a cost to the punisher and therefore is regarded as an act of altruism. In other words, the punisher has put himself at risk by being the 'cop on the block' to enforce community rules and expectations but his efforts have turned into a loss.

A second narrative accounts for a 'variety' of altruism by having the punisher subsequently interact with the cheat, gaining a benefit after this punishment through the community perceiving him as unselfish because he has risked everything for them. However, he collects the unwelcome reputation as an enforcer, always on the alert for rule-breakers.[23]

Reason

According to animal rights activist and Princeton academic Peter Singer (figure 4), it is the evolutionary acquisition of reason which underlies morality impartiality. Reason, he argues, can explain the emergence of psychological altruism. Reason's objectivity, in not allowing self-interest to count more than another's, enabled true altruism to appear:

> "Nor ... is it irrational for people to prefer their own interests and those of their families to the interests of strangers. Yet it remains true that there is no magic in the pronoun 'my' which gives greater intrinsic importance to my interests, or those of my father, relatives, friends, or neighbours. Hence when I ask myself what it would really be best for me to do—best not in terms of my own interests and desires, but best from an objective point of view—the answer must be that I ought to do what is in the interests of all, impartially considered."[24]

Without reason, non-reciprocated acts of kindness put individuals at a disadvantage. Reason would be selection advantage:

> "… if the capacity for reasoning brings with it an appreciation of the reasons for extending to strangers the concern we feel for our kin and our friends, evolution would not eliminate this rational appreciation of the basis of ethics ... . The evolutionary advantages of the capacity to reason would outweigh the disadvantages of occasional actions which benefit strangers at some cost to oneself."[25]

Is Singer being disingenuous or has he missed the epistemological problem? Singer's intention is clear: he wants to present a deductive syllogism (after all, empirical verification is impossible) in which objective reason adjudicates, leading to the conclusion that a person must act disinterestedly with respect to weighing his own and others' needs. But has Singer successfully prosecuted his case?

At best, it is a triviality; at worst, it is a circular argument as he has said nothing more than what is already in his initial premise. To claim that self-interest should not trump another's is what it means to be impartial. This makes evident his question begging that there is no genuine intrinsic importance to my desires over and above any other's. Shouldn't Singer initially provide a reason why everyone's rights are to be equally considered rather than assuming it? Isn't the ethical egoist or hedonist[26] equally entitled to point out that her wants are more important than anyone else's because of the very fact that they are hers? After all, *ceteris paribus* and reason notwithstanding, according to evolutionary orthodoxy, nature's genealogy is one 'red in tooth and claw'.

Image: Mal Vickers, Flickr/CC0

Figure 4. Peter Singer argues that "Understanding the origins of morality, therefore, frees us from two putative masters, God and nature." (Singer, P., *Practical Ethics*, Cambridge University Press, Cambridge, p. 5, 2011).

In any case, people serially ignore reason's rule. Singer's explanation, just one of multiple evolutionary narratives, is that feelings controlling actions arose before reason appeared. An internal struggle between younger reason and older passion now grips the human psyche, with people often opting for action that takes no account of others' needs or interests.[27] The ancients understood this failure of the intellect and conscience as akrasia;[28] we moderns, as cognitive dissonance. Singer's ivory tower idealism glosses over this counterfactual by special pleading: "most of us have too much natural sympathy for others, and too many emotional ties with our community, to take this course."[29] This is hardly a formidable ethical defeater of the egoistical who may regard these 'ties' as an instrumental means to their own self-interested ends!

And in a very strange, almost Machiavellian, twist, Singer virtually commits himself to the position of which he is so vocally disdainful. While there was once an evolutionary advantage to seeking our own happiness, reason defeated self-indulgence by finding meaning in the ethical life and concern for others' interests. It is odd that the ultimate justification for seeking the well-being of others was humans realizing that self-interest resulted in "boredom and loss of interest in life".[30] Seeking another's happiness only because it results in a more interesting and meaningful life, goals of self-gratification, is hardly self-denying altruism.

At the end of his seminal best seller, Singer asks the only important question: "Why act morally?" A convincing response, you would think, should epistemically attract an ethical answer; but this just doesn't happen: "It is not a question within ethics, but a question about ethics." In its place comes the non-moral, universalizability: "Taking ethics as in some sense necessarily involving a universal point of view seems to me a more natural and less confusing way of discussing these issues."[31]

Laying your own concerns aside and constructing judgments from a disinterested spectator's vantage is the key component of morality for Singer.[32] But this summons a further relevant demand: "Why should ethics be universalizable?" In one sense it would seem there is no ready answer. After all, to whom or what is an appeal for information made within an evolutionary worldview? For Singer there is no warrant: the reason one must appeal to universalization of anything ethical is that it just is the (rational) case that such must be appealed to. This seems to be a claim to bruteness, that universalization just is, in no need of further grounding.

No one, as far as my understanding of Singer's atheism goes, can reasonably indict him for inconsistency. His rejection of God entails the embrace of a surrogate to explain existence; and Singer quite predictably adopts evolution and its philosophical bed-fellow, metaphysical naturalism, as God's subrogation. Trading the transcendent personal for the subaltern and immanent impersonal comes at great cost:

> "When we reject belief in a god, we must give up the idea that life on this planet has some preordained meaning. Life as a whole has no meaning. Life began, as the best available theories tell us, in a chance combination of molecules; it then evolved through random mutations and natural selection. All this just happened; it did not happen for any overall purpose."[33]

By asking us to take our own viewpoint "to a standpoint like that of the impartial spectator",[34] an inescapable problem surfaces. In a naturalistic, evolutionary world, his 'friend' who subs for the Creator is a figment of atheist wishful thinking: the atheist cosmos does not speak. And this hitch rudely surfaces when Singer accepts that an egoistic rational agent, one who subscribes to the maxim 'Let everyone do what is in my interests', is rationally entitled to cheat the other to obtain his ends. Singer can't appeal to any moral proscription because such objectivity is non-existent.

After almost 300 pages of argument for reason serving as the key to an ethical life, Singer concludes with the anticlimactic:

> "It cannot be proven that we are all rationally required to reduce pain and suffering and make the world a better place for others … . We will probably always need the sanctions of the law and social pressure to provide additional reasons against serious violations of ethical standards."[35]

Out of what would seem desperation, Singer opts for a society run by rules which take into account both our selfish nature, as inherited from the evolutionary past, and a utilitarian greater good decided by a quasi-mystical impartial point of view. A rule-based ethics, however, has no infrangible absolutes, as Singer concedes, and thus can be abandoned whenever the situation demands. Why this can be done is that we are social creatures and must make concessions to the majority or some principles that "are no more than relics from our evolutionary and cultural history and can be discarded without cost."[36]

Conclusion

I have examined four additional accounts for the rise of morality and altruism. All share an appeal to just-so stories which lend a façade of intellectual credence to the explanation. Related to this is the failure to solve the problem of altruism and goodness being reproductively disadvantageous to any individual in whom these characteristics first appear. As many evolutionists have noted, being unethical can pay dividends: cheats can, and do, prosper.

As with part 6's three explanations, there is an elusive (and illusory) genetic piece to the puzzle. The necessary empirical verification is missing. In its place is the assumption that evolution has caused the moral gene(s) to arise because we would not be moral creatures if evolution had not caused this. This is a spectacular example of question begging.

Again, creationists are encouraged to underscore the lack of scientific and historical data in ethical philosophy and use this vacuum as an apologetic against the evolutionary worldview.

In the following papers I will review evolutionary arguments for metaethics, a subdivision of ethics. Simply put, metaethics asks what is going on in ethical discourse. In addition, I will unpack several contemporary ethical philosophers' attempts to vindicate a metaethics grounded on evolution.

I would like to thank two anonymous reviewers for their suggestions. I also wish to thank David Green for his input.

References

1. Darwin, C., *The Descent of Man, and Selection in Relation to Sex*, Penguin Books, p. 243ff, 2004 (1879, 2nd edn). As an aside, Darwin, in what appears to be a 'scientific' justification for marrying his first cousin Emma, wrote in the concluding passages to his Descent: "Both sexes ought to refrain from marriage if in any marked degree inferior in body or mind; but such hopes are Utopian and will never be even partially realised until the laws of inheritance are thoroughly known … . When the principles of breeding and of inheritance are better understood, we shall not hear ignorant members of our legislature rejecting with scorn a plan for ascertaining by an easy method whether or not consanguineous marriages are injurious to man" (p. 688). Darwin's jibe against the politicians would seem to be a less than disguised attack on Christianity's proscription against incest.
2. Miller, G., Sexual Selection for Moral Virtues, *The Quarterly Review of Biology* **82**(2):97–125, 2007; p. 98.
3. Driscoll, C., Why moral virtues ate probably not sexual adaptations; in: Sinnott-Armstrong, W. (Ed.), *Moral Psychology, vol.1; The Evolution of Morality: Adaptations and innateness*, The MIT Press, Cambridge, MA, p. 246, 2008.
4. Miller, ref. 2, p. 101.
5. Miller, ref. 2, p. 108. On the other hand, lower intelligence, having an underlying genetic dimension, is a predictor of "murder, rape, assault, alcoholism, drug addiction, absenteeism, child abuse and neglect, passing along sexually transmissible infections, and causing fatal traffic accidents" (p. 108).
6. Miller, ref. 2, p. 113.
7. Miller, G., Kindness, fidelity, and other sexually selected virtues; in: Sinnott-Armstrong, ref. 3, p. 232. As Christians, we argue that beauty in the creation is a result of God being beautiful. For pagans, as demonstrated by Miller's propositions, the creation itself must engender it. Of course, this raises many philosophical problems, especially when the evolutionary spin rules. Very little, if anything at all, has been written on this subject of beauty in Christian thought and how evolution cannot explain what it is. Why is beauty beautiful?
8. Miller, ref. 2, p. 99. In an energetic bout of anthropomorphic depiction, according to Miller even "animals often have incentives to lie about their own qualities to attract more mates" because "Most animal communication is relentlessly narcissistic" (p. 100).
9. MacMillan, J. and Kofoed, L., Sociobiology and antisocial personality: an alternative perspective, *J. Nervous and Mental Disease* **172**(12):701–706,1984; pp. 701, 702. A 'random' maximizing of your reproductive fitness has long been given the 'moral' thumbs-up through sperm donor banks. There are multiple reports of men who, for egoistic calculations, 'fathered' 100's, if not 1,000's of children. See, for example, Sperm donor alleged to have fathered 550 children faces legal action, accessed 3 Jul 2023; and Ari Nagel, accessed 3 Jul 2023. I explore the world of the psychopath, and the plethora of evolutionary explanation associated with it, in far more detail in a subsequent paper. For now, the alacrity exhibited by supporters for the genetic and biochemical basis for sociopathy and the like is unwarranted.
10. Miller, G., Response to comments; in: Sinnott-Armstrong, ref. 3, p. 265. I have a sneaking suspicion the *post hoc, ergo propter hoc* fallacy is also rearing its ugly head here!
11. Sinnott-Armstrong, ref. 3, p. 211.
12. While not on board with Miller's enthusiastic support for sexual selection of the virtues, Driscoll nevertheless concedes that preferences for moral mates "involve simple self-interest" (Sinnott-Armstrong, ref. 3, p. 250).
13. There is a more disturbing footnote to Miller's argument that virtues are a good gene indicator. Miller endorses the work of Arthur Jensen and J. Philippe Rushton. Up to their deaths, these two psychologists promoted the very dangerous idea that the difference in IQ scores between black and white American could be substantially put down to genetics. In a 2008 article, they wrote: "Despite repeated claims to the contrary, there has been no narrowing of the 15- to 18-point average IQ difference between Blacks and Whites (1.1 standard deviations). The differences are as large today as when first measured nearly 100 years ago. Racial group differences, and the associated gaps in living standards, education levels, etc., are rooted in factors that are largely heritable, not cultural" (Rushton, J.P. and Jensen, A., James Watson's most inconvenient truth: race realism and the moralistic fallacy, *Medical Hypotheses* **71**(5):638, 2008). Both supported a eugenics program.

    Another problem for Miller is his dependence on twin studies. (It was Darwin's cousin, the eugenicist Francis Galton, who initiated twin research in the 19th century.) While a full examination is impossible in an endnote (it would require, minimally, a separate paper), twin studies received an exhaustive and highly critical exposé in Joseph, J., *The Trouble with Twin Studies: A reassessment of twin research in the social and behavioral sciences*, Routledge, New York, 2015. What can only be described as scandalous, all

twin studies which pushed a genetic causation for behaviour are riddled with methodological errors, including consciously tendentious ones. These include, but are not limited to:

i. lack of control groups

ii. assuming separated monozygotic twins had been truly separated when in fact they were not and had had contact and shared a common cultural, and often a geographic, environment

iii. late separation

iv. the lack of reliability and validity of the characteristic under study,

v. bias in favour of a genetic interpretation

vi. subject recruitment done through media which produced a biased sampling due to the twins having to have known each other to respond, thus excluding twins who truly had had no contact

vii. subjects given expensive gifts to participate

viii. twins lying and comparing notes

ix. twins adopted by different branches of the same family

x. drawing conclusions from an extremely limited sample size

xi. question begging the genetic explanation for the similarities

xii. investigator fraud

xiii. data not being made available to examine

xiv. questionable statistical practices, including upward adjustments, and

xv. subjects chosen because they were so alike.

14. Alexander, R.D., The evolution of social behaviour, *Annual Review of Ecology and Systematics* **5**:367, 1974.
15. Alexander, ref. 14, p. 337.
16. Ruse, M., *Sociobiology: Sense or nonsense?* D. Reidel Publishing Company, Dordrecht, Holland, pp. 63,67–69, 1985. As an explanation for homosexuality, see Kirby, J., A new group-selection model for the evolution of homosexuality, *Biology and Philosophy* **18**(3):689–690, 2003.
17. Alexander admits that actually measuring fitness shifts is extremely problematic. He writes, "This problem could scarcely be pointed up better than by the difficulty in deciding whether a particular aspect of human culture is increasing or decreasing the reproduction of its bearers" (Alexander, ref. 14, p. 374).
18. For further explanation on this division, see Kay, M., What's wrong with being wrong: a closer look at evolutionary ethics—part 1, *J. Creation* **36**(2):120, 2022.
19. Alexander, ref. 14, p. 340.
20. Ruse, M., Sociobiology: a philosophical analysis; in: Caplan, A.L. (Ed.), *The Sociobiology Debate: Readings on the ethical and scientific issues concerning sociobiology*, Harper & Row, New York, p. 359, 1978.
21. Alexander, ref. 14, pp. 340, 342. Dawkins has contested Alexander's contention that parents must always win in conflicts with their offspring. Whether Dawkins' rebuttal is successful remains an open question. After all, both he and Alexander depend on arcane entities, namely, gene(s) for altruistic and selfish behaviour, the one essential item which seems to have been given a free ontological pass. However, as I read it, Dawkins 'strawmans' Alexander's premise. The latter proposes the offspring possesses a newly fashioned mutant gene not inherited from the parent and which gives it an advantage over its siblings (and the parent) while Dawkins alters the terms: "The fact that Alexander is considering a newly mutated gene is not fundamental to the argument. It is better to think of a rare gene inherited [my italics] from one of the parents." See Dawkins, R., *The Selfish Gene*, Oxford University Press, Oxford, pp. 135ff, 2006. As an aside, much of Dawkins' rebuttal suffers from his belief that the individual gene is all that matters, when it is the entire 23/46 chromosome makeup which is inherited, warts and all, not a single gene. Bertram is also adamant Alexander's case is invalid, despite conceding "parents may often be able to manipulate their offspring in practice in such a way as to compel them to be more altruistic than those offspring would otherwise be [for example,] if a mother is able to partially castrate some of her offspring, they are in effect compelled to be altruistic toward their kin as their only way of reproducing." Bertram, B.C.R., Problems with altruism; in: King's College Sociobiology Group (Ed.), *Current Problems in Sociobiology*, Cambridge University Press, Cambridge, p. 260, 1982.
22. For more examples, see Bertram, ref. 21, pp. 259–261.
23. For elaboration on the mechanics, so-called, see Stevens, J.R., The selfish nature of generosity: harassment and food sharing in primates, *Proceedings: Biological Sciences* **271**(1538):451–457, 2004. Somewhat in opposition to this is a bizarre experiment in which subjects' brains are scanned to see what was occurring when they punished defectors in a game of economic exchange. The authors concluded from the produced images that "Altruistic punishment is probably a key element in explaining the unprecedented level of cooperation in human societies [due to] altruistic punishment provid[ing] relief or satisfaction to the punisher and activat[ing] … reward-related brain regions" (de Quervain, D., Fischbacher, U., Treyer, V., Schellhammer, M., Schnyder, U., Buck, A. and Fehr, E., The Neural basis of altruistic punishment, *Science, New Series* **305**(5688):1258, 2004). It needs be pointed out that this form of altruism is not the psychological variety but the reinterpreted biological type. After all, how could this be genuine altruism if someone obtains personal gratification?
24. Singer, P., *The Expanding Circle: Ethics, evolution, and moral progress*, Princeton University Press, Princeton, p. 153, 2011.
25. Singer, ref. 24, pp. 139–140. Singer is not alone in his apotheosis of reason as the basis of morality. Kant pressed reason to this end. Kant quickly becomes turbid and unreadable, so for a bitesize, digestible analysis of his *Fundamental Principles of the Metaphysics of Morals, in* Lindsay, A.D., *Kant*, Oxford University Press, London, pp. 162ff, 1936.
26. One definition of ethical egoism is "each person has a moral duty to follow those, and only those, moral rules that will be in the agent's maximal self-interest over the long haul" (Craig, W.L. and Moreland, J.P., *Philosophical Foundations for a Christian Worldview*, IVP, Downers Grove, Il, p. 426, 2003). Ethical hedonism is the principle that pleasure is the highest good.
27. Perhaps the most salient example of this is abortion. No matter what 'justification' a person may proffer for the pro-death argument, ultimately it comes down to the mother's interests at the expense of the child's.
28. The original extended discussion of this occurs in Book 7 of Aristotle's *Nicomachean Ethics*. However, the Apostle Paul eloquently and succinctly—in opposition to Aristotle's prolixity—notes the psychological phenomenon: "My own behaviour baffles me. For I find myself not doing what I really want to do but doing what I really loathe … . I often find that I have the will to do good, but not the power. That is, I don't accomplish the good I set out to do, and the evil I don't really want to do I find I am always doing" (Romans 7). The pagan Greek had no solution to this 'wretched' state; but Paul did: "Who will deliver me from this body of death? I thank God there is a way out through Jesus Christ our Lord." (Romans 7:24–25)
29. Singer, ref. 24, p. 145.
30. Singer, ref. 24, p. 146.
31. Singer, P., *Practical Ethics*, Cambridge University Press, Cambridge, p. 277, 2011.
32. Kant was probably the most famous proponent of the truth of reason, leading to his categorical imperative, or the universality of moral prescriptions: "Act only in accordance with that maxim through which you can at the same time will that it become a universal law" (Kant. I., *Groundwork of the Metaphysics of Morals*, Cambridge University Press, Cambridge, p. 31, 2006 (1785)).
33. Singer, ref. 31, p. 291.
34. Singer, ref. 31, p. 279.
35. Singer, ref. 31, p. 295.
36. Singer, ref. 31, p. 167.

***Marc Kay** has a bachelor's degree in philosophy, religious studies, and Indo-Malay; postgraduate certification in TESOL. He was previously a teacher, and mental health and youth worker. He is now a fulltime stay-at-home dad while his wife pursues her academic career. He commits any free time to street evangelism.*

Insignificant concentrations of peptides form in water: part 1—using hot temperatures or high pH

Royal Truman and Charles McCombs

Large peptides (proteins) must satisfy 10 requirements concurrently to be relevant for origin of life (OoL) models. One requirement is that they be large polymers despite the strong tendency to hydrolyse. This will not occur in natural environments under hydrothermal vent-like temperatures and pressures since amino acids (AAs) are chemically degraded and peptides hydrolyze rapidly via the diketopiperazine (DKP) pathway. OoL experiments are expertly designed to circumvent these problems in three ways: 1) by using very high concentrations of pure aa, pumped into preheated high-pressure reactors; 2) by terminating the experiments quickly before tiny peptides, typically only up to about 3 AA residues long, are completely degraded; and 3) by meticulously eliminating multiple contaminants which accelerate hydrolysis and thermal degradation of AAs. These contaminants are ubiquitous in hydrothermal vents. Experiments to prevent rapid hydrolysis at high temperatures via the DKP pathway by using very high pH are not reflective of near-neutral pH hydrothermal environments. We conclude that hydrothermal conditions are not suitable to form large peptides in high concentrations contra to what is often claimed.

Living organisms cannot exist without large numbers of specialized proteins, and these proteins with their linked amino acids (AAs) are coded for by DNA. Not surprisingly, large peptides (proteins) play an indispensable role in most naturalist evolutionary scenarios shown in figure 1. For example, conglomerates of peptides allegedly might have interacted with RNA strands during a theoretical RNA world phase and protected them from degradation.[1]

For decades, evolutionists have been claiming that polypeptides form readily and naturally in water. In the opening sentence in a 1996 *Nature* publication, Lee *at al.* stated confidently that "The production of amino acids and their condensation to polypeptides under plausibly prebiotic conditions have long been known", with references which go back to the 1970s.[3]

In a 2022 mini review paper, Fried *et al.*[4] stated multiple times that polypeptides form *readily*. For example:

> "In sum, we shed light on the role of early peptides and small proteins *before* and *during* the nucleotide world, in which nascent life fully grasped the potential of primordial proteins [emphasis in the original]."

And that their arguments

> "… lend credence to the idea that early peptides served many central prebiotic roles before they were encodable by a polynucleotide template."

Origin of Life (OoL) researchers have been unable to offer credible narratives for how relevant large peptides could have formed in the absence of a cellular genetic system. The conundrum is that peptides, like proteins, must fulfil the 10 properties summarized in table 1 *concurrently*. (Peptides consist of 2–50 aa whereas proteins typically have ≥50 aa and usually a specific 3-dimensional folded structure). An analogous list could be made for other biopolymers such as RNA, DNA, and lipids.

There are many contradictory trade-offs in the requirements shown in table 1. For example, extremely hot aqueous temperatures used in hydrothermal vent simulations to increase the length of peptides (requirement 1) would accelerate racemization of the reacting AA, hindering linking of only L-enantiomers (requirement 2). As another example, some models, like the Amyloid World hypothesis, ameliorate the need for very long peptide chains (requirement 1), but these proposals now require a much greater number of identical peptides (requirement 6) which must be co-located (requirement 7).

The fact that so many prerequisites can't be met by chance is dealt with in OoL research by designing experiments which address and optimize only one of the ten properties. For example, to sidestep the need for having only L-enantiomer polymerizing, glycine is the only biological AA used. And since it lacks a chiral carbon, it is therefore unable to produce D- and L-enantiomers (requirement 3). Using glycine, which does not have any sidechain, also camouflages the need to prevent sidechains from being integrated into peptides (requirement 3), without which requirement 5 cannot be fulfilled.

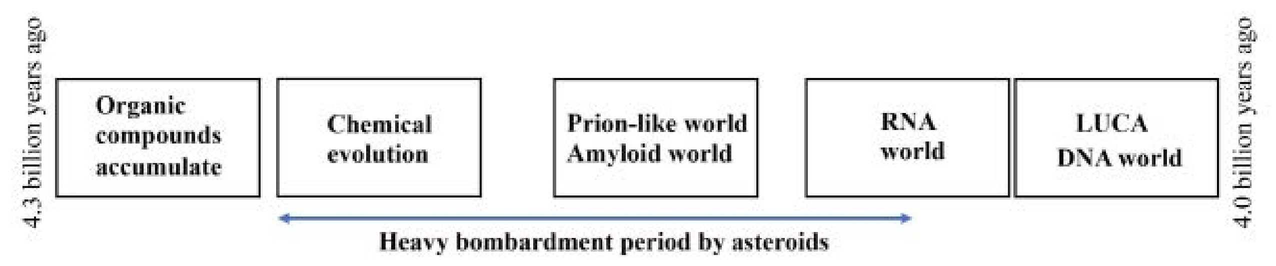


Figure 1. Hypothetical evolutionary stages preceding the Last Universal Common Ancestor (LUCA). For example, see ref. 2.

Table 1. Properties which all prebiotically relevant peptides must fulfil

Nr	Requirements that large peptides / proteins must fulfil for life to be possible
1	Many amino acids must be linked together, about 300 on average for proteins.
2	Only the L-amino acid enantiomers must be included.
3	Only the linear polymers must form; i.e., the side chains of amino acids must not react.
4	Precise sequences of amino acid residues must form to perform useful functions.
5	The long chains must adopt a suitable 3-dimensional structure.
6	A vast number of peptide copies must be produced continually for millions of years.
7	The correct proportion of peptides having a specific sequence must be co-located.
8	Other molecules, including non-biological amino acids, must be avoided in the peptides.
9	The entire system or organism must self-replicate, including all necessary peptide copies.
10	The polymers and 3-dimensional structure must be formed under relevant conditions.

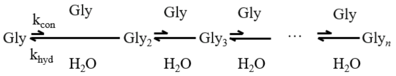
Another trick used by OoL chemists is to chemically modify and protect the side chains of AAs to prevent them from reacting (requirement 3). Yet another example of intelligent guidance to obtain the desired outcome involves chemically activating the aa to obtain relevant quantities of peptides to satisfy requirements 1 and 6.

The order in table 1 reflects the effort OoL scientists have devoted to addressing these constraints in our experience, whereas the last four requirements have been almost entirely ignored in the evolutionary literature. Despite the irrelevance of experiments which are incapable of satisfying the 10 requirements concurrently, even those which addressed only one of the constraints have been repeatedly shown to lack substance. Some of the individual requirements have been analyzed in this journal. Attempts by evolutionists to solve constraint 2 (formation of L-only chains) have been countered by Truman in a series of papers dealing with the racemization of AAs and peptides after they form.[5–10] Furthermore, the evolutionist notion that an initial enantiomeric excess of AA was later amplified has also been shown to be absurd.[11–18]

The need for long peptides to form suitable 3-dimensional structures (constraint 5) has been countered by demonstrating that the vast majority of random peptide sequences do not fold into reliable 3-dimensional sequences.[19–24] This will also be addressed in the current two-part series, although our focus here will be on requirements 1 and 6: peptides of significant length and concentration must be found in water. In the current 2-part series, we will show that only tiny peptides would form naturally and in insignificant concentrations. This is important to evaluate the plausibility of OoL models such as the Amyloid World hypothesis, which require very concentrated peptides about nine AAs long.[25]

Peptide formation in water is thermodynamically unfavourable

Thaxton, Bradley, and Olsen pointed out, in 1992, that condensation of peptide bonds, as shown in eqn (1), would be thermodynamically unfavourable in water by about 3.0 kcal/mole per bond at ambient temperatures.[26]



$$\mathrm{Gly} \underset{k_{hyd}}{\overset{k_{con}}{\rightleftharpoons}} \xrightarrow[\mathrm{H_2O}]{\mathrm{Gly}} \mathrm{Gly}_2 \rightleftharpoons \xrightarrow[\mathrm{H_2O}]{\mathrm{Gly}} \mathrm{Gly}_3 \rightleftharpoons \xrightarrow[\mathrm{H_2O}]{\mathrm{Gly}} \cdots \rightleftharpoons \xrightarrow[\mathrm{H_2O}]{\mathrm{Gly}} \mathrm{Gly}_n \qquad (1)$$

The rate constant k_{con} refers to condensation and k_{hyd} to hydrolysis.

Chemists are aware that AAs will not spontaneously form in water and that hydrolysis of peptides is catalyzed by acids and bases. Therefore, evolutionists have devised special experimental conditions to obtain peptides, including wet–dry cycling (also called ‘freeze–thaw cycles’); the use

Table 2. Literature values for condensation and hydrolysis glycine $\leftrightarrows$ diglycine. A: Rate constants; B: free energies.

A	**Rate constants in $mol^{-1}s^{-1}$**			
25°C	25°C	140°C	150°C	140°C
k_{hyd} (a)	k_{con} (b)	k_{hyd} (c)	k_{hyd} (a)	k_{con} (c)
6.3×10^{-11}	1.6×10^{-13}	4.0×10^{-6}	8.9×10^{-6}	4.3×10^{-8}

B	**Free energy in kcal/mole**	
25°C	25°C	374°C
ΔG_{con} (d)	ΔG_{con} (e)	ΔG_{con} (d)
+3.4	+3.6	+1.2

(a) Radzicka and Wolfenden (1996) ref. 31.

(b) $K_{eq} = 400 = k_{hyd}/k_{con}$; so $k_{con} = k_{hyd}/400 = 1.6 \times 10^{-13}$.

(c) Sakata *et al.* (2014) ref. 35.

(d) Lemke *et al.* (2009) ref. 36.

(e) Martin *et al.* (1998) ref. 37.

of clay and mineral surfaces; concentration by evaporation; and eutectic freezing of dilute aqueous solutions.[27]

We will not evaluate all these scenarios in this series but mention that these experiments inevitably used highly pure AAs in unrealistically high concentrations under multiple prebiotically unrealistic conditions. Why are we focusing here on condensation of AAs and hydrolysis of the resulting peptides in water? It is because any peptide formed would have been produced in irrelevantly low amounts and either remained worthlessly entombed (for OoL purposes) in the environment proposed or flushed into an ocean, where they would have been diluted and hydrolyzed.[28]

Thorough mixing of all peptides formed would have been virtually guaranteed, especially when the putative ancient oceanic conditions are considered. OoL models envision violent conditions on Earth about 4 Ga ago, caused by a moon at only ⅓ today's distance, which would have created tides over 30 times higher.[29] This would imply average terrestrial differences in *height* between high and low tide of about 90 m.[30] In addition, the earth would have rotated twice as fast, and the moon would have orbited the earth every five days, causing these huge tides to occur every few hours.[26] The pools of evaporating water where oceanic AAs allegedly could have concentrated would have mixed with sea water eventually. All OoL scenarios must assume water was not present, which would automatically hydrolyze peptides.

Therefore, we will also examine, in part two of this series, peptide formation and degradation at moderate temperatures in water, where virtually all peptides would eventually have resided. Overall, peptide bonds in water are estimated to have a half-life at 25°C of between about 350 and 600 years *per bond*, so large peptides would not have built up in oceans no matter how they were produced.[31] In addition, circulation of the entire oceanic water through ancient hydrothermal vents would have regularly destroyed both amino acids and peptides.[32–34]

Furthermore, Radzicka and Wolfenden pointed out that peptide hydrolysis is catalyzed by acids, bases, and metal complexes which are ubiquitous in the environment.[31] This explains the elaborate laboratory efforts to exclude impurities otherwise present everywhere in nature. For example, diglycine (also called glycylglycine and abbreviated Gly_2 in this paper), is hydrolyzed with a half-time of only about 2 days in 1 M NaOH and 150 days in 1 M HCl, at 25°C.[31] Therefore, essentially all AAs in a hypothetical ancient prebiotic world would have been in the oceans. In part 2 we will analyze the maximum concentration of AAs possible and their buildup over time under the most optimistic assumptions for OoL purposes.

Higher temperatures to produce larger peptides

OoL researchers have focused on higher temperatures and pressures to produce peptides, arguing that these conditions might resemble those found in, or near, hydrothermal vents. Glycine (Gly) is almost always used in these experiments, and we will focus on this AA also, since the preponderance of data available is limited to this AA. Chain elongation $Gly_n + Gly \rightarrow Gly_{n+1}$ would occur more easily at higher rather than lower temperatures (table 2 A).

From table 2 B, we see that the condensation reactions at around 25°C are endothermic (unfavourable) but less so at the higher temperature. The decreased ΔG_{cond} at higher temperature implies that the K_{eq} for the equilibrium $2\ Gly \leftrightarrows Gly_2$ will now become > 1/400; and for $Gly_n + Gly \leftrightarrows Gly_{n+1}$ K_{eq} will now become > 1/50, where $n \geq 2$. It is important to understand that K_{eq} refers to standard conditions of 1 M Gly, which is far too high for OoL models (we take this into account in part 2 of this series).

Another attractive consideration for experimenting at higher temperatures is that the faster equilibration process, $Gly_n + Gly \leftrightarrows Gly_{n+1}$, would require less time to approach equilibrium, an experimental convenience. But would higher temperatures be a good strategy to increase yields of peptides? Sun *et al.*[38] pointed out, in 2020:

> "No previous studies on peptide cleavage have considered atmospheric pressure and temperatures below 100°C."

Indeed, many experiments have been performed at high temperatures and pressures using extremely high aqueous concentrations of glycine. The yields of peptides are extremely

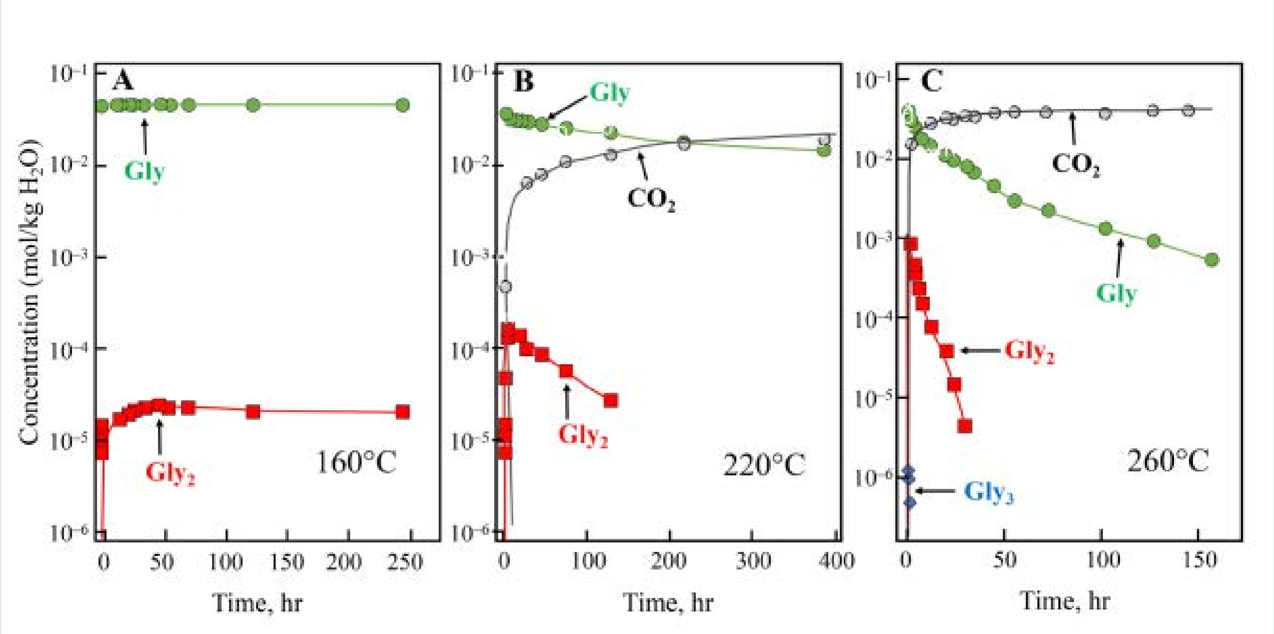


Figure 2. Formation of small peptides in gold hydrothermal cells at pH 6.85 and 200 bar aqueous solutions. Shown are glycine (green circle), diglycine (red square), triglycine (blue diamond), and CO_2 (grey open circle) concentrations. (A) 160°C, (B) 220°C, and (C) 260°C. Redrawn by R. Truman with slight modifications from ref. 36.

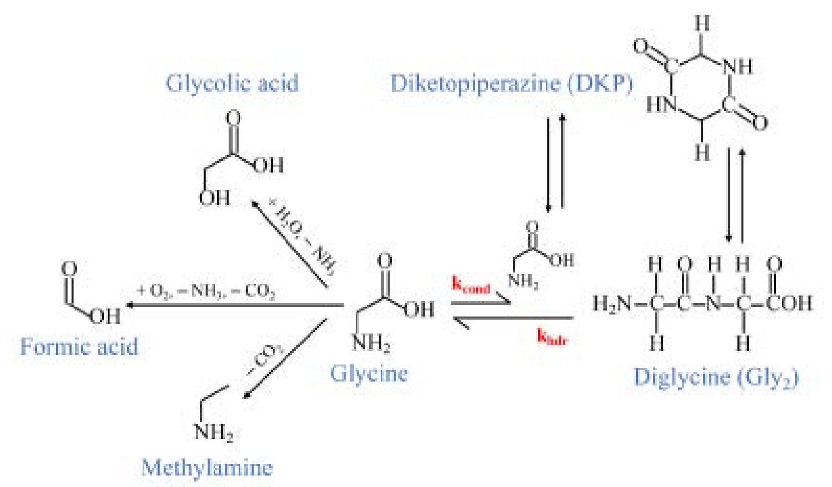


Figure 3. Degradation pathways for glycine under hydrothermal conditions. Drawn by R. Truman using data from figures found in refs. 36 and 39.

low, however, due to thermal degradation processes. Then why are these conditions used for OoL research? Bada[2] explains:

> "The model experiments published to date use short exposure times (i.e., 1+ h) at high temperatures compared to 1–30+ years associated with actual hydrothermal systems."

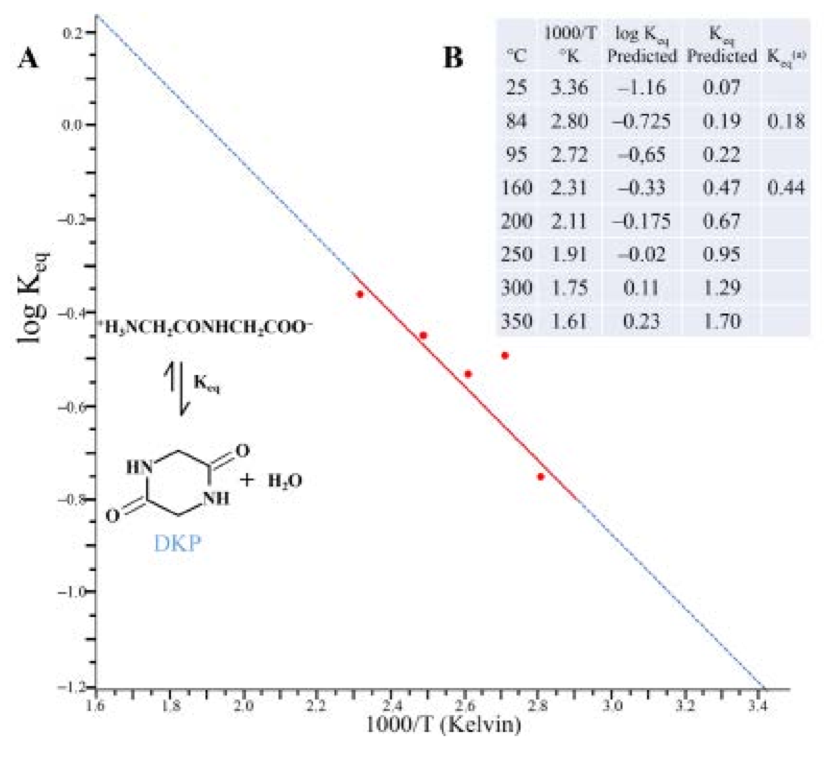
In other words, all the experiments were terminated after very short (and at just the right) times to obtain any peptide at all. As we will see below, to obtain any Gly_3, the reactions were discontinued after very short reaction times as the experimental temperatures were increased. Arguably the most promising results were published in a 2009 study by Lemke *et al.*, who began by documenting how almost all the preceding studies by others had failed to produce Gly_2 from glycine using a variety of high temperature and pressure reactors.[36]

The key results are shown in figure 2. At 260°C (figure 2C) the maximum concentration of Gly_2 was achieved within a few seconds when the experiment was initiated with [Gly] ≈ 0.1 M. But instead of remaining at 10^{-3} M, the concentration of Gly_2 dropped one hundred-fold to ≈ 10^{-5} M within only a day. Clearly all the Gly_2 would have been destroyed under conditions and residence times resembling a hydrothermal vent.

Comparing figures 2A, B, and C shows that ever more Gly_2 decomposes over time as the temperature increases. This is bad news for high temperature scenarios to form peptides. In addition, only at ≥ 220°C was any Gly_3 formed, but it only survived for some minutes before being totally decomposed. High temperature conditions to produce larger peptides are of no value for OoL purposes (even though the peptides appear sooner) since they don’t survive. What is the chemical explanation for this effect?

Figure 2 shows that [Gly] decreases with time far more rapidly than can be accounted for through formation of [Gly_2] plus other peptides, and, simultaneously, [CO_2] was found to increase over time. These two trends correlated with increased temperature. Clearly, glycine was being rapidly decomposed thermally. Initially, the Gly which had been forced into the pre-heated reactor under high pressure would have been highly concentrated, leading to a fast reaction, 2 Gly ⇆ Gly_2, but this slowed down as Gly was steadily decomposed. Higher temperature not only accelerated the reverse reaction, Gly_2 → 2 Gly, but also the rate of thermal degradation of the regenerated Gly. Over time, the necessary Gly feedstock to form Gly2 steadily decreased!

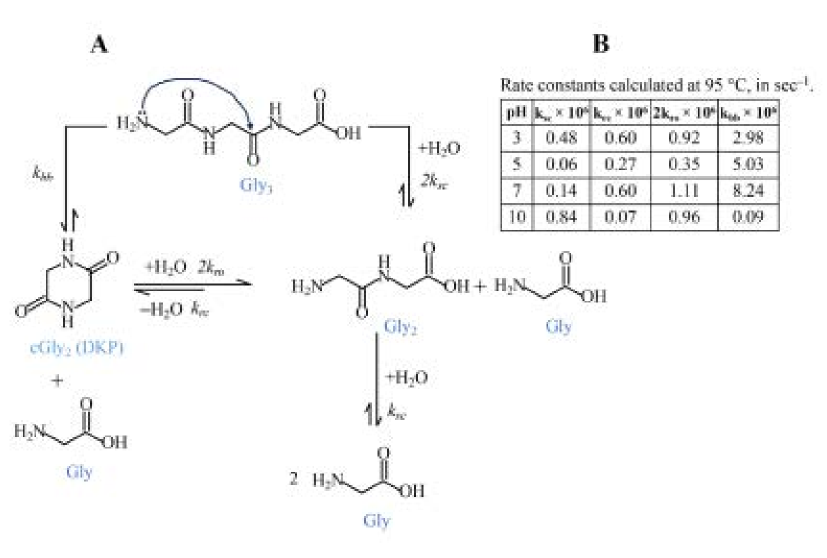
Although the results reported by Lemke *et al.* demonstrated the unfeasibility of producing high concentrations of large peptides in hydrothermal vents (they obtained nothing larger than triglycine), why did they obtain some short-lived peptides at all where other experiments failed? It was not because they had managed to simulate hydrothermal vents more accurately, because OoL experiments do not become more successful by mimicking natural conditions better.[38] Lemke *et al.* realized that even trace amounts of many substances naturally present in hydrothermal vent regions accelerate destruction of Glycine. Consequently, they had a custom-designed gold hydrothermal reaction cell manufactured[39] and pretreated all the components with a 6 N HCl solution at 90°C, and then baked the reactor at 600°C for 6 hours to remove contaminants.[36]



°C	1000/T °K	log K_{eq} Predicted	K_{eq} Predicted	K_{eq} $^{(a)}$
25	3.36	−1.16	0.07	
84	2.80	−0.725	0.19	0.18
95	2.72	−0,65	0.22	
160	2.31	−0.33	0.47	0.44
200	2.11	−0.175	0.67	
250	1.91	−0.02	0.95	
300	1.75	0.11	1.29	
350	1.61	0.23	1.70	

Figure 4. Extrapolation of K_{eq} values to other temperatures for the reaction Gly_2 ⇆ DKP. A: Plot obtained from Radzicka and Wolfenden.[31] The original van ’t Hoff plot (lnK_{eq} vs 1/T in degrees Kevin) shown in red, was extrapolated manually. B: Our estimated predicted K_{eq} values were obtained by estimating log K_{eq} at each 1,000/T value from the extrapolated line.[31]

(a) Measured value.



Rate constants calculated at 95 °C, in sec^{-1}.

pH	$k_{sc}\times10^6$	$k_{rc}\times10^6$	$2k_{ro}\times10^6$	$k_{bb}\times10^6$
3	0.48	0.60	0.92	2.98
5	0.06	0.27	0.35	5.03
7	0.14	0.60	1.11	8.24
10	0.84	0.07	0.96	0.09

Figure 5. Forming cyclic diketopiperazines (DKPs) from triglycine (Gly_3) at 95°C and different pH values. A) Back-biting and direct scission reactions. B) Measured rate constants obtained from table S13 in the Supplementary Information of ref. 41.

Abbreviations for rate constants k_{sc}, k_{rc}, k_{ro}, k_{bb}: sc = scission; bb = back-biting; rc = ring closing; ro = ring opening.

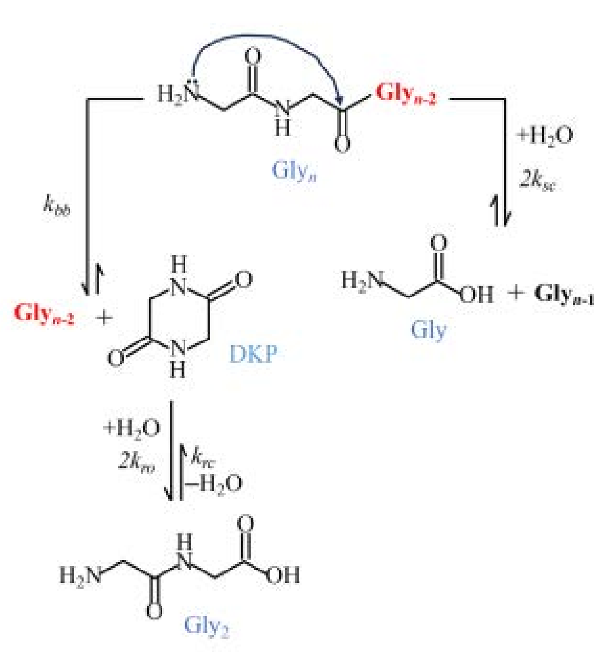


Figure 6. Formation of cyclic diketopiperazines (DKPs) from peptides having ≥ 4 residues. Degradation to form cyclic diketopiperazines (DKPs) is a dominant reaction in high-temperature aqueous solutions for peptides longer than three amino acids. The back-biting reactions convert Gly$_n$ into Gly$_{n-2}$ and DKP, which hydrolyses to Gly$_2$. Abbreviations for rate constants k_{sc}, k_{rc}, k_{ro}, k_{bb}: sc = scission; bb = back-biting; rc = ring closing; ro = ring opening.

Peptide degradation at higher temperatures

In 2021 Körner documented the multiple degradation pathways for AAs and peptides under hydrothermal conditions.[40] These are shown in figure 3 for glycine, which is likely the most stable biological AA. Of particular interest is the formation of diketopiperazines (DKP) at high temperatures, since this lowers the concentration of Gly$_2$ and larger Gly$_n$.

Degradation of diglycine (Gly$_2$) to form DKP

In addition to degrading amino acids, high temperatures also degrade peptides by forming cyclic diketopiperazine (DKP). We'll focus for now on how this decreases the amount of Gly$_2$ available, the precursor for larger peptides. Radzicka and Wolfenden measured K_{eq} values for the reaction Gly$_2$ ⇆ DKP at five temperatures and neutral pH and published the van 't Hoff plot ($\Delta G = -RT\ln K_{eq}$) shown in the grey box of figure 4A.[31] We extended this plot manually to extrapolate linearly between 25°C and 350°C. This led to the predicted K_{eq} shown in column 5 of figure 4B.[41]

Radzicka and Wolfenden calculated that diglycine would degrade rapidly to form DKP with a half-life of $t_{1/2}$ ~ 1 year at 25° and pH 7. We confirmed, from our extended plot in figure 4, their estimate at 25°C, $K_{eq} < 0.08$. This low value indicates that hydrolysis of DKP is favoured in the case of

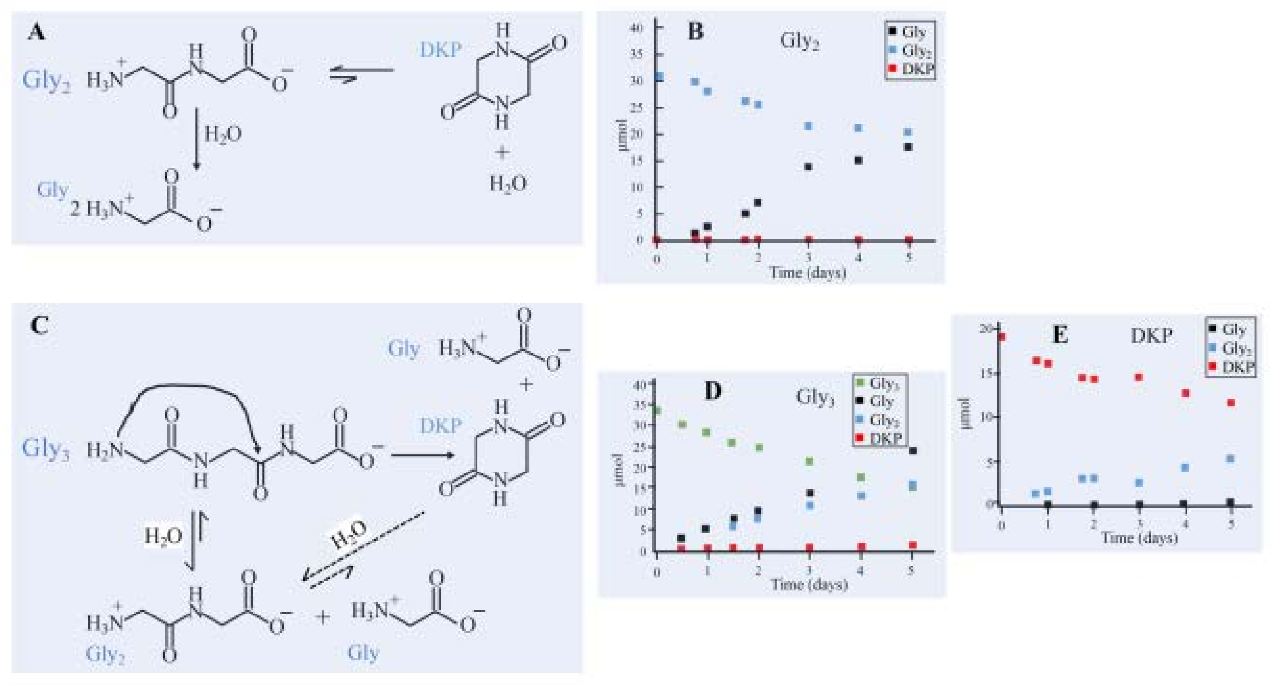


Figure 7. Degradation of diglycine (Gly$_2$) and triglycine (Gly$_3$) at 95°C and pH 10. Redrawn from parts of figures 5 and 11 of ref. 41. A, B: degradation pathways for Gly$_2$. C, D: degradation pathways for Gly$_3$. E: DKP degrades to form Gly$_2$.

Gly_2, since thermodynamically stable ions form in water, and much water is present.[31] Therefore, degradation of Gly and Gly_2 would be minimal via the DKP pathway at low temperatures such as 25°C. But, as we see from figure 4, at ≈ 250°C, $K_{eq} = 0.95$, meaning that about half the $[Gly_2]$ would be converted to [DPK], the proportion rises with temperature.

Degradation of triglycine (Gly_3) to form DKP

Equilibrium constants for the reaction $Gly_n \leftrightarrows DKP + Gly_{n-2}$ are not available for $n \geq 3$, but we do know that at even modest temperatures Gly_3 is degraded to DKP kinetically far more rapidly than by hydrolysis (see the reactions in figure 5A).[41]

The data in figure 5B shows that at 95°C and pH = 7 formation of DKP is about 30 times faster than direct hydrolysis via scission (i.e., $k_{bb} = 8.24 \times 10^{-6}\ s^{-1}$ and $2 \times k_{sc} = 2 \times 0.14 \times 10^{-6}\ s^{-1}$), whereas the reverse reaction, DKP + Gly → Gly_3, is much slower. In addition, hydrolysis (ring opening) is about 4 times faster than the reverse ring closing reaction (i.e., $2 \times k_{ro} = 2.22 \text{ x } 10^{-6}\ s^{-1}$ and $k_{rc} = 0.6 \times 10^{-6}\ s^{-1}$).[41]

Degradation of tetraglycine (Gly_4) and larger peptides to form DKP

In the case of Gly_3, hydrolysis of the DKP generated would produce linear Gly_2 so the net outcome via either the direct scission or indirect back-biting pathway would both be $Gly_3 \rightarrow Gly_2 + Gly$. Since the two products could (re) condense to form Gly_3, destruction of Gly_3 via the back-biting mechanism would be partially offset by the linear Gly_2 formed, which could (re) condense, since [Gly] is high (i.e., ≈ 10^{-4} M). In the case of Gly_n where $n \geq 4$ and after hydrolysis of the generated DKP, the net outcome would be $Gly_n \rightarrow Gly_{n-2} + Gly_2$. Now (re) condensation via $Gly_{n-2} + Gly_2 \rightarrow Gly_n$ would be comparatively far slower (than for Gly_3), since $[Gly_2] << [Gly]$ (see figure 6).

The fact that the back-biting reaction $Gly_n \rightarrow Gly_{n-2}$ + DPK is essentially non-reversible for $n \geq 3$ is one reason researchers have so much trouble obtaining glycine chains of size 4 and larger at high temperatures. Another reason is that at this temperature hydrolysis could occur at all positions. Using the data for pH = 7 and 95°C from figure 5B, direct hydrolysis would occur at a rate of about $(n - 1) \times k_{sc} = (n - 1) \times 0.14 \times 10^{-6}\ s^{-1}$. The equilibration process would hydrolyze much faster at high temperatures than anticipated if one only considered hydrolysis via the scission pathway.

After the systematic experiments on glycine polymerization (which led to a master's degree financed by the NSF Center for Chemical Evolution), Sun *et al.* concluded from the above experiments that

> "The ease of formation and the stability of the cyclic dimers presents one of the greatest obstacles in our understanding of the prebiotic origin of polypeptides. Once formed, the cyclic dimer is extremely stable and presents a dead-end for further polymerization under plausible prebiotic conditions."[41]

Their data confirms this completely, but the authors offered a potential solution:

> "However, as shown here, basic conditions can be used to retard the ring-closure reaction."[41]

In other words, at around pH 10, formation of DKP would be hindered. This is reasonable for Gly_2, which, at pH 10, would have a terminal carboxylate anion that would hinder nucleophilic attack by the end amino group, as shown in figure 7A.

However, surely high pH would be less effective for Gly_n peptides larger than Gly_2, since the carboxylate anion would not be near the reaction site, as illustrated in figure 7C. Let's review the data provided by Sun *et al.*[41] At pH ≤ 7, Gly_2 produced much DKP (according to figure 5 of ref. 41). At pH 10, almost no DKP was found, as shown in our figure 7B. The Gly formed at pH 10 would have been due to the scission reaction. We agree that high pH would hinder formation of DKP from Gly_2 at 95°C. As expected, $k_{bb} > k_{sc}$ at 95°C only for pH experiments at pH ≤ 7, as summarized in figure 5B. At pH ≤ 7 Gly_3 produced much DKP (according to figure 11 of ref. 41, and the DKP remained stable. Figure 7D shows that very little DKP was found at pH 10, but a little more than from Gly_2. This seems consistent with Sun *et al.*'s statement:[41]

> "The ring opening reaction of diketopiperazines is very slow at all pH values considered."

However, although DKP was indeed shown to be stable at pH ≤ 7, it is *not* true for the relevant case, pH 10, as shown in figure 7E: OH^- in water rapidly opened the ring to form Gly_2! Goolcharran and Borchardt also found that Phe-Pro-DKP was stable at pH values between 3 and 8, but hydrolyzed rapidly to the dipeptide Phe-Pro-OH, at pH greater than 8.[42]

Comparing figure 7B and E reveals that the rate of DKP → Gly_2 is about the same as Gly_2 → Gly (in both cases about ⅓ is hydrolyzed within 5 days). The rate of hydrolysis of Gly_2 and Gly_3 at 95°C will be about the same, so we conclude that the rate of hydrolysis of DKP and Gly_3 will be quite similar.

Since the carboxylate group for Gly_3 is far from the back-biting location, we suspect that formation of DKP is *not* being prevented for poly-glycine larger than diglycine at high pH, as Sun *et al.* assumed, but was *not detected* due to its rapid hydrolysis, as shown by our dotted line in figure

7C. Should hydrolysis of DKP be occurring so fast that not much is observed in the products, then high pH would *not* slow down formation of DKP in larger Gly_n and thus retard their rapid hydrolysis. Also, at high pH, more of the N-terminal amino group would be unprotonated and thus reactive for the back-biting reaction, see figure 7C.[40] Having analyzed the reactions at pH 3, 5, and 7, it is unfortunate that no experiments were reported for pH 9; far more relevant for OoL purposes than pH 10.

Would higher pH conditions facilitate producing larger peptides?

At a pH = 10 and 95°C (far cooler than OoL experiments claiming to mimic hydrothermal vent conditions), Sun *et al.* did not find decomposition products of Gly for experiments lasting up to 120°C. However, they did *not observe any linear polymerization*, only hydrolysis of Gly_2, Gly_3 and Ala_3 (tri-alanine) after these had been rapidly *forced into the reactors under high pressure*. In these experiments, they also obtained very little DKP, as shown in figures 5 and 11 of ref. 41, but, as we will explain next, pH = 10 is not a realistic pH for effluents at or near hydrothermal vents.

pH values in hydrothermal vents at high temperatures

An important question for OoL chemistry is, what pH should be assumed in and near hydrothermal vents? Many alkaline hydrothermal chimneys have been found, but their origin needs to be understood.[43] Li *et al.* measured *in situ* pH values in 2023 at the Okinawa Trough hydrothermal fields, based on a new Raman spectrum quantitative calibration model. These pH values were calculated based on concentrations of H_2S and HS^-, together with temperature data.[43] At the Jade site, a pH of 6.3 was calculated at 273°C and 133 bar pressure. Other studies referenced from this location had reported an average pH of 4.9 at 25°C for samples collected and measured in laboratories. This represents an increase in pH of about 1.4 for an increase of 248°C; interesting, but not a large effect.

For the Biwako site, Li *et al.* calculated a pH of 5.3 *in situ*, at 169°C and 152 bar pressure.[43] Other studies had reported an average pH = 5.0 at 25°C using samples from the same site. This represents an increase in pH of only about 0.4 when the temperature was increased 144°C. Earlier *in situ* studies for these two sites, using similar methodologies, provided almost identical pH values.[43] Slightly *acidic* pH values for hydrothermal vents have also been reported by others. Ding *et al.* studied 10 vents at different mid-ocean ridge locations having vent fluid temperatures ranging from 180 to 384°C and pressure between 220 and 250 bar. *In situ* pH of the highest temperature vent fluid had a pH of about 5.1–5.4, and distinctly more acidic values occurred at the seawater/vent-fluid interface.[44] Two other hydrothermal vents analysed had *in situ* pH values of 4.88 and 4.94 at temperatures of 300˚C and 333˚C, respectively.[45]

So why are hydrothermal chimneys considered alkaline when the vent fluids are reported to be slightly acidic? Apparently hydrothermal fluids contain the weakly *acidic* H_2S which reacts with dissolved Cu, Zn, Fe, and Pb to form minerals such as chalcopyrite, sphalerite, pyrite, pyrrhotite, and gelenite. Upon mixing with icy oceanic water, these minerals precipitate, tying up sulfur and releasing protons, thereby lowering the pH of the surrounding water but with the *opposite* effect on the precipitate.[43] The extrapolated pH values calculated suggested that at the highest hydrothermal vent temperatures (up to 400°C) the water spewing out of the vent openings would have pH values slightly > 7. Remarkably, though, the Raman spectrum of the fluids studied at the Jade and Biwako sites mentioned above indicated that the fluids had not mixed with seawater.[41] This would imply that the original water would have been nearly neutral. The exact values from different vent openings aren't known exactly, but certainly the pH would *not* be around the value of pH = 10 used in experiments like those reported by Sun *et al.*[41]

The precipitation of sulphides is likely the main cause of the enhanced acidity of hydrothermal fluids at high temperature, but Li *et al.* also pointed out that the Jade hydrothermal fluid pH of 6.3 may have been raised due to ammonia sourced from the thermal decomposition of *organic matter*.[43] This suggests that under prebiotic conditions the pH would have been even lower, acidic, and not alkaline.

As mentioned above, the pH values of around 10 that were suggested would hinder production of DKPs and thus the major degradation path of peptides. We see, however, that the very hot water under high pressure would have been about neutral or slightly acidic. The chimneys themselves would presumably have an alkaline surface, but only at *icy temperatures* where the key mineral precipitates would have been produced. Relevant concentrations of large peptides are not going to form at near freezing water temperatures.

High temperature conditions inimical to forming large peptides

In all hydrothermal experiments, Gly_3 and larger peptides could only be obtained transiently under carefully designed conditions. Allowing these peptides to remain under those conditions would degrade them quickly. Sakata *et al.* experimented with several metal ions at 140°C and confirmed that they *promoted hydrolysis* instead of oligomerization.[32,35] These results were consistent with all the former studies Sakata *et al.* referenced. Gly_3 could only be obtained in miniscule amounts when in the presence of Cu^{2+}.[35] This led them to write:

> "Our conclusion that deep-sea hydrothermal systems are not favorable environments for even simple peptides is in good agreement with Cleaves et al."[35]

We agree, for the several reasons presented, which include:

- Due to thermal decomposition, the amount of Gly would have been insignificant. Lemke *et al.* had to inject a prebiotically unrealistically high concentration of Gly using syringe pumps into the preheated fluid already at 200 bar pressure.[36]
- The minerals found in hydrothermal vents would have accelerated destruction of Gly (in addition to peptides formed), as shown by all the experiments, which also demonstrated CO_2 was being produced at a rapid rate, but virtually no Gly_2 or Gly_3 was formed.
- Peptides formed under any hypothetical favourable local conditions would have been diluted in huge oceans and simply hydrolyzed over time.
- Around neutral pH values, formation of DKP provides a much faster pathway to degradation of peptides than the direct hydrolysis (scission) pathway.

Icy temperatures are also not feasible to form peptides

We have shown that the claim peptides would have formed easily in or near hydrothermal vents naturally is absurd. For completeness, the opposite kinds of conditions would also be unsuitable. Leading OoL researcher Bada claimed that terrestrial oceans would have been covered by a thick sheet of ice during most of the prebiotic and early biotic history.[2] However, condensation of amino acids frozen in ice or at near freezing temperatures would have been impossibly slow. This is why we postulated a more suitable temperature of about 25°C in part 2 of this series to test prebiotic chemistry more favourably. This temperature avoids both degradation pathways for amino acids, such as shown in figure 3, and formation of DKP, which would hinder formation of peptides.

It is worth mentioning that if peptides had formed somehow the putative Late Heavy Bombardment (LHB), claimed to have occurred approximately 4.0 to 3.8 Ma ago, would have destroyed most amino acids and peptides as well as leading to the complete racemization of any surviving molecules.[46]

Concluding comments

OoL models require peptides or proteins to satisfy 10 requirements concurrently under the same natural environmental conditions. Here in Part 1, we have shown that experiments conducted under high aqueous temperatures only formed tiny peptides in irrelevantly low concentrations. In addition, any peptides exposed to high temperatures would have been rapidly hydrolyzed. This is due to the favourable free energy of hydrolysis; high rate constants of peptide hydrolysis; and degradation of the AA building blocks. High-temperature origin of life scenarios include hydrothermal vents and the effects of large meteor impacts. In part 2 we will also demonstrate that only insignificant equilibrium concentrations of peptides would have formed under moderate aqueous conditions.

References

1. Jheeta, S., Chatzitheodoridis, E., Devine, K., and Block, J., The way forward for the origin of life: prions and prion-like molecules first hypothesis, *life (Basel)* **11**(9):872, 2021 | doi:10.3390/life11090872.
2. Bada, J.L., How life began on Earth: a status report, *Earth Planet, Sci. Lett.* **226**:1–15, 2004 | doi:10.1016/j.epsl.2004.07.036.
3. Lee, D.H., Granja, J.R., Martinez, J.A., Severin, M.K., and Ghadiri, R., A self-replicating peptide, *Nature* **382**:525–528, 1996 | doi: 10.1038/382525a0.
4. Fried, S.D., Fujishima, K., Makarov, M., Cherepashuk, I., and Hlouchova, K., Peptides before and during the nucleotide world: an origins story emphasizing cooperation between proteins and nucleic acids, *J. R. Soc. Interface* **19**:20210641, 2022 | doi:10.1098/rsif.2021.0641.
5. Truman, R., Can ligating homochiral polypeptides explain the origin of homochiral biomolecules?, *J. Creation* **36**(1):74–80, 2022.
6. Truman, R., Racemization of amino acids under natural conditions: part—a challenge to abiogenesis, *J. Creation* **36**(1):114–121, 2022.
7. Truman, R., Racemization of amino acids under natural conditions: part 2—kinetic and thermodynamic data, *J. Creation* **36**(2):72–80, 2022.
8. Truman, R., Racemization of amino acids under natural conditions part 3—condensation to form oligopeptides, *J. Creation* **36**(2):81–89, 2022.
9. Truman, R. and Schmidtgall, B., Racemization of amino acids under natural conditions: part 4—racemization always exceeds the rate of peptide elongation in aqueous solution, *J. Creation* **36**(3):74–81, 2022.
10. Truman, R., Racemization of amino acids under natural conditions: part 5—exaggerated old age dates, *J. Creation* **37**(1):64–74, 2023.
11. Truman, R., The origin of L-amino acid enantiomeric excess: part 1—by preferential photo-destruction using circularly polarized light?, *J. Creation* **36**(3):67–73, 2022.
12. Truman, R., Enantiomeric amplification of L amino acids part 1—irrelevant and discredited examples, *J. Creation* **37**(2):96–104, 2023.
13. Truman, R., Enantiomeric amplification of L amino acids part 2—chirality induced by D-sugars, *J. Creation* **37**(2):105–111, 2023.
14. Truman, R. and Basel, C., Enantiomeric amplification of L amino acids part 3—using chiral impurities, *J. Creation* **37**(2):120–111, 2023.
15. Truman, R., Enantiomeric amplification of L amino acids: part 4—based on subliming valine, *J. Creation* **37**(3):79–83, 2023.
16. Truman, R. and Grocott, S., Enantiomeric amplification of L amino acids: part 5—sublimation based on serine octamers, *J. Creation* **37**(3):84–89, 2023.
17. Truman, R., Enantiomeric amplification of L amino acids: part 6—sublimation using Asn, Thr, Asp, Glu, Ser mixtures, *J. Creation* **37**(3):90–92, 2023.
18. The remaining six parts of the Enantiomer amplification of L-amino acids series are currently in press.
19. Truman, R., The proportion of polypeptide chains which generate native folds—part 1: analysis of reduced codon set experiments, *J. Creation* **25**(1):77–85, 2011.

20. Truman, R., The proportion of polypeptide chains which generate native folds—part 2: theoretical studies, *J. Creation* **25**(2):99–105, 2011.
21. Truman, R., The proportion of polypeptide chains which generate native folds—part 3: designed secondary structures, *J. Creation* **25**(3):102–105, 2011.
22. Truman, R., The proportion of polypeptide chains which generate native folds—part 4: reusing existing secondary sequences, *J. Creation* **25**(3):106–108, 2011.
23. Truman, R., The proportion of polypeptide chains which generate native folds—part 5: experimental extraction from random sequences, *J. Creation* **26**(1):76–85, 2012.
24. Truman, R., The proportion of polypeptide chains which generate native folds—part 6: extracting from random sequences, *J. Creation* **26**(1):86–93, 2012.
25. Maury, C.P.J., Self-propagating β-sheet polypeptide structures as prebiotic informational molecular entities: the amyloid world, *Origins of Life and Evol. Biosph.* **39**:141–150, 2009 | doi:10.1007/s11084-009-9165-6.
26. Thaxton, C.B., Bradley, W.L., and Olsen, R.L., *The Mystery of Life's Origin: Reassessing current theories*, Lewis and Stanley, p. 142, 1992.
27. See extensive references in: Brigiano, F.S., Gierada, M., Tielens, F., and Pietrucci, F., Mechanism and free-energy landscape of peptide bond formation at the silica−water interface, *ACS Catal.* **12**:2821−2830, 2022 | doi:10.1021/acscatal.1c05635.
28. To avoid mixing with sea water, one could envision a small peptide remaining isolated indefinitely somewhere. The molarity of NaCl in sea water is about 55.5 M, and the highest concentration of AA proposed by evolutionists in prebiotic oceans is 10^{-4} M, of which only a small fraction would have been found as a peptide. Therefore, each peptide would be surrounded by millions of NaCl molecules, frozen solid instead of mixing with water. This would be of no value for OoL purposes.
29. Delsemme, A.H., Cosmic origin of the biosphere; in: Brock, E. (Ed.), *The Molecular Origins of Life*, Cambridge University Press, Cambridge, pp. 100–119, 1998.

30 Tide: the magnitude and effects of tidal ranges, The Columbia Electronic Encyclopedia, 6th edn, Columbia University Press, 2023.

31. Radzicka, A. and Wolfenden, R., Rates of uncatalyzed peptide bond hydrolysis in neutral solution and the transition state affinities of proteases, *J. Amer. Chem. Soc.* **118**(26):6105–6109, 1996 | doi:10.1021/ja954077c.
32. Holm, N.G. and Anderson, E.M., Hydrothermal systems; in: Brock, E. (Ed.), *The Molecular Origins of Life*, Cambridge University Press, Cambridge, pp. 86–99, 1998.
33. Martin, W., Baross, J., Kelley, D. *et al.*, Hydrothermal vents and the origin of life, *Nat. Rev. Microbiol.* **6**:805–814, 2008 | doi:10.1038/nrmicro1991.
34. Wagner, A., Arrival of the fittest: solving evolution's greatest puzzle, OneWorld, 2015; p. 51.
35. Sakata, K., Kitadai, N., and Yokoyama, T., Effects of pH and temperature on dimerization rate of glycine: evaluation of favorable environmental conditions for chemical evolution of life, *Geochimica et Cosmochimica Acta* **74**(23):6841–6851, 2010 | doi:10.1016/j.gca.2010.08.032.
36. Lemke, K.H., Rosenbauer, R.J., and Bird, D.K., Peptide synthesis in early Earth hydrothermal systems, *Astrobiology* **9**(2):141–146, 2009 | doi:10.1089/ast.2008.0166.
37. Martin, R.B., Free energies and equilibria of peptide bond hydrolysis and formation, *Biopolymers* **45**:351–353, 1998 | doi:10.1002/(SICI)1097-0282(19980415)45:5<351::AID-BIP3>3.0.CO;2-K.
38. The use of a gold-plated reactor provided an additional big benefit: it is very unlikely any other researchers could afford to conduct additional experiments such as for longer time durations, which would emphasize that larger peptides don't form under realistic prebiotic scenarios.
39. Körner, P., Hydrothermal degradation of amino acids, *Chem. Sus. Chem.* **14**(22):4947–4957, 2021 | doi:10.1002/cssc.202101487.
40. Radzicka and Wolfenden only provided two Keq values, 0.44 at 160°C and < 0.18 at 84°C but offered a graphic with five values in total, measured at different temperatures, see ref. 31.
41. Sun, Y., Frenkel-Pinter, M., Liotta, C.L., and Grover, M.A., The pH dependent mechanisms of non-enzymatic peptide bond cleavage reactions, *Phys. Chem. Chem. Phys*. **22**:107–113, 2020 | doi:10.1039/C9CP05240B.
42. Goolcharran, C. and Borchardt, R.T., Kinetics of diketopiperazine formation using model peptides, *J. Pharm. Sci.* **87**(3):283–2888, 1998 | doi:10.1021/js970325m.
43. Li, Lianfu *et al.*, Direct H_2S, HS^- and pH measurements of high-temperature hydrothermal vent fluids with in situ raman spectroscopy, *Geophys. Res. Lett.* **50**(9):e2023GL103195, 2023 | doi:10.1029/2023GL103195.
44. Ding, K., *et al.*, The in situ pH of hydrothermal fluids at mid-ocean ridges, *Earth and Plan. Sci. Lett.* **237**(1–2):167–174 | doi:10.1016/j.epsl.2005.04.041.
45. Ding, K., Seyfried, W.E., Jr, Tan, C., Schaen, A.T., and Luhmann, A.J., Recent investigation of in-situ ph in hydrothermal vent fluids at main endeavour field (MEF) and ASHES vent field (ASHES): Implications for dynamic changes in subseafloor hydrothermal system, *American Geophysical Union, Fall Meeting 2014*, abstract id. V21A-4738 | ui.adsabs.harvard.edu/abs/2014AGUFM.V21A4738D/abstract.
46. Claeys, P. and Morbidelli, A., Late heavy bombardment; in: *Encyclopedia of Astrobiology*, Springer, Berlin, Heidelberg, 2015 | doi:10.1007/978-3-662-44185-5_869.

***Royal Truman** has bachelor's degrees in chemistry and in computer science from State University of New York; an M.B.A. from the University of Michigan (Ann Arbor); a Ph.D. in organic chemistry from Michigan State University; and a two-year post-graduate 'Fortbildung' in bioinformatics from the Universities of Mannheim and Heidelberg. He works in Germany for a European-based multinational.*

***Charles McCombs** has a bachelor's degree in chemistry from California State University of Long Beach (1973) and a Ph.D. degree in Organic Chemistry from UCLA (1978). He worked for Tennessee Eastman Company for 21 years as a research chemist, receiving 20 patents. He and his wife started Genesis Christian Academy in Englewood, Florida, and he is currently President of Genesis Ministries Inc., and President and Professor of Creation Studies at SouthWest Florida Bible Institute.*

Insignificant concentrations of peptides form in water: part 2—using moderate temperatures

Royal Truman, Change Tan, and Charles McCombs

Most origin of life (OoL) models require long peptides to be present in water. The Amyloid World Hypothesis assumes these could have been as short as about nine residues long, dissolved in water at moderate temperatures. We analyzed the buildup of equilibrating peptides using kinetic and thermodynamic data with computer simulations and the simplest amino acid (AA), glycine (Gly). We found that with a high initial [Gly] = 10^{-4} M at ≈ 25°C a system of peptides about nine residues long reaches equilibrium between condensation and hydrolysis in about 5,000 years. Furthermore, the maximum concentrations achievable are exceedingly low; for $n > 2$ residues, $[Gly_n]_{eq} \approx 2 \times 10^{-6}$ of $[Gly_{n-1}]_{eq}$. Tens of thousands of terrestrial prebiotic oceans would not have sufficed to obtain a single Gly_9 molecule at equilibrium. The algorithms demonstrated that even an unrealistically high initial concentration of 10^{-4} M AAs would only have led to very short peptides, in trace concentrations.

Living organisms depend on a wide variety of proteins, each found in multiple copies. Origin of life (OoL) researchers have been attempting for many decades to find natural circumstances under which large polypeptides could have become present in a prebiotic Earth. In part 1 of this series, we explained why high temperature conditions, such as in, or near, hydrothermal vents would have decomposed amino acids (AAs) and accelerated hydrolysis of peptides, especially via the diketopiperazine (DKP) pathway.[1] Alternatively, at icy or frozen water temperatures, formation of peptides would have been too slow and in too small a concentration to be relevant for OoL purposes.

Here, in part 2, we will examine the feasibility of forming peptides at moderate aqueous temperatures; that is, ≈ 25°C ± 15. In theory, these conditions may have been present in some locations, including boundaries between hydrothermal vents and cold ocean water.

Many evolutionists continue to claim that large peptides formed *easily* and are present in water in high concentrations. In a 2022 mini review Fried *et al.* [2] referred to

> "… the *simple* synthesis of amino acids, the *facile* nature of their activation and condensation [emphasis added]."

adding that

> "… amino acids dominated the portion of the primordial soup destined to become biotic."

Moderate temperature conditions are used explicitly in experiments allegedly relevant to support the Amyloid World Hypothesis.[3] One advantage at such temperatures is that decomposition of peptides by forming DKP would play only a minor role. Therefore, we analyzed the buildup of equilibrating peptides at moderate temperatures in this paper. The algorithms developed here can also be applied to higher temperatures if the relevant rate constants for the equilibrium $AA_n + AA \leftrightarrows AA_{n+1}$ are known, where *n* refers to the number of AA residues.

The concentration of peptides formed in water

Following the practice of most OoL experiments, we will focus on glycine (Gly) to represent biological AAs. Gly is the simplest AA, does not have a side chain, cannot form distinct L- and D-enantiomers, cannot undergo the variety of thermal decompositions other AAs can, and is generally the AA produced in highest concentration in OoL experiments.

In figure 1 the side groups R_1 and R_2 are hydrogen in the case of glycine. Shown are various processes a dipeptide could undergo once formed. Side chain degradation reactions of R_1 and R_2 are not shown.

Note that in aqueous solution, at around physiological pH, amino acids exist as zwitterions; that is, as dipolar ions with both the amino- and carboxyl groups in charged states, so the overall structure is $NH_3^+{-}CHR{-}CO_2^-$; the 'neutral forms' $NH_2{-}CHR{-}CO_2H$ are not present to any measurable degree.[8] Consequently, the overall free energy change of hydrolysis, ΔG_{hyd}, (the reverse of condensation) is the consequence of two effects:

$$\Delta G_{hyd} = \Delta G_m + \Delta G_i \qquad (1)$$

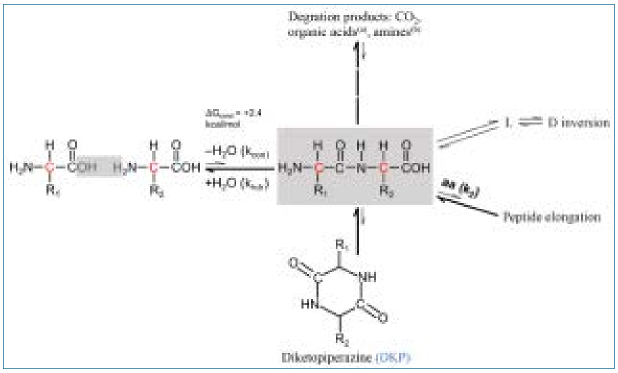


Figure 1. Formation and degradation of a dipeptide. Amino acids form very little dipeptide in water since the reverse hydrolysis reaction is strongly favoured thermodynamically. The actual ionic state will depend on the pH. ΔG_{con} = +2.4 kcal is from Martin, measured at 25°C.[4] Peptides can also degrade chemically, especially at high temperatures, using chemical pathways which depend on the particular amino acids.[5–7] In addition, the D- and L-enantiomers racemize within the peptides. Chiral carbons are shown in red.
[(a)] Organic acids: formic acid, glycolic acid, acetic acid, carbonic acid.
[(b)] Amines: ammonia and methyl amine.

Table 1. Free energy of hydrolysis of glycine-based peptides in water at 4.5 < pH < 7.5 under standard conditions (i.e., [Gly] = 1 M at room temperature).[4]
Gly = glycine. The subscripts refer to the number of residues in the peptide.

Entry	Reaction	ΔG_i	ΔG_m	G_{hyd}	K_{hyd}, M^c
1	$Gly_2 \rightarrow Gly + Gly$	−9.9	6.3	−3.6^b	373 ≈ 400
2	$Gly_3 \rightarrow Gly + Gly_2$	−7.8	5.3	−2.5	61 ≈ 50
3	$Gly_3 \rightarrow Gly_2 + Gly$	−8.8	6.3	−2.5	61 ≈ 50
4	$Gly_4 \rightarrow Gly + Gly_3$	−7.6	5.3	−2.3	44 ≈ 50
5	$Gly_4 \rightarrow Gly_3 + Gly$	−8.7	6.3	−2.4	52 ≈ 50
6	$Gly_4 \rightarrow Gly_2 + Gly_2$	−6.7	5.3	−1.4	10
7	$Gly_n \rightarrow Gly + Gly_{n-1}$	−7.6	5.3	−2.3	44 ≈ 50
8	$Gly_n \rightarrow Gly_{n-1} + Gly$	−8.7	6.3	−2.4	52 ≈ 50

[a] Free energy change (ΔG_{hdr}) in kcal/mole at 25°C to 37°C. The change in temperature does not affect the values within the measurement uncertainties of about 0.2 kcal/mole.
ΔG_{hyd} is the free energy of amide hydrolysis.
ΔG_m is the free energy of hydrolysis of the amide bond to uncharged products.
ΔG_i is the free energy of ionization; i.e., interaction of charged groups with water.
[b] Experimental value; all other values in the last two columns were calculated by Martin.
[c] Equation for calculation: $-\Delta G_{hyd} = 2.3RT\log K_{hyd} \approx 1.4\log K_{hyd}$ kcal/mole.

where ΔG_m is due to hydrolysis of the amide bond to uncharged products (with a positive free energy change, thermodynamically unfavourable) and ΔG_i is the free energy of their ionization (with a negative free energy change, thermodynamically very favourable in water).

Table 1 summarizes some thermodynamic values using glycine (Gly) as an example AA. Martin found that the ΔG_h values at 25°C and 37°C were about the same, within experimental error.[4]

Table 1 shows that AA dimerization is the most unfavourable step in forming peptides (row 1). This is because the amino and carboxylic ends of the peptide form ionic zwitterions, which are very stable in water. Furthermore, a peptide can be hydrolyzed either at its ends or internally, with the latter less thermodynamically favourable (compare rows 2 to 5 with row 6).

Martin calculated the equilibrium constant for hydrolysis of a diglycine, K_{hyd22}, using equation (2).[4]

$$-\Delta G_{hyd} = 2.3RT\log K_{hyd} \approx 1.4 \log K_{hyd} \text{ kcal/mole} \tag{2}$$

where he approximated 2.3RT ≈ 1.4 for temperatures between 25°C and 37°C. As documented in table 1, this led to

$$K_{hyd11} = [Gly][Gly] / [Gly_2] \approx 400 \tag{3}$$

where the square brackets indicate concentration. Martin calculated the equilibrium constant for hydrolyzation of larger peptides using $\Delta G_h = -2.4$ kcal/mol, leading to

$$K_{hyd1n} = [Gly_{n-1}][Gly] / [Gly_n] \approx 50 \tag{4}$$

for $n > 2$ under the standard conditions, including [Gly] = 1 M.[4] The coupled reactions are shown in equation eqn 5, along with the equilibrium constants under the standard condition.

(5)

$[Gly_2]_{eq}$ is needed to calculate $[Gly_3]_{eq}$, which is then used to calculate $[Gly_4]_{eq}$ and so on stepwise. Equation 3 can be rearranged to produce

$$[Gly_2]_{eq} = [Gly]^2_{eq}/K_{hyd11} \tag{6}$$

Prebiotic steady state concentration of glycine and polyglycines

A fundamental question in OoL speculations is, what value should be assumed for $[Gly]_{eq}$ under prebiotic conditions? That is, what steady state concentration of glycine should OoL researchers use for their theories to reflect conditions in the time period 4.4—3.8 Ga ago in terrestrial oceans? Note that glycine can decompose readily to the thermodynamically more favourable methylamine and carbon dioxide, especially under hot conditions. Furthermore, other isomers with the same composition as glycine are thermodynamically more stable in both the gas phase and in water, such as: n-methylcarbamic acid, methyl carbamate, and 2-hydroxyacetamide.[9]

A range of Gly concentrations have been advanced by OoL chemists. Bada estimated, in 1991, that the concentration of all AAs together in ocean waters would have been ≈ 10^{-10} M, consisting primarily of glycine.[10] This estimate took into account chemical decomposition caused by ocean water circulating entirely about every 10 Ma through hydrothermal vents, as Stribling and Miller have also assumed.[10,11]

Lazcano and Miller, however, estimated, in 1996, that the concentration may have been higher, between 10^{-8} and 10^{-4} M.[12]

A detailed analysis by Truong *et al.*, in 2019, found that biologically relevant AAs on solar planets and moons having hydrothermally active oceans (including Enceladus and Europa) would have been destroyed in < 1 Ma, *contra* Bada's estimated 10 Ma. They concluded that

> "… if amino acids are detected at above a concentration of 1 nM, they should have been formed recently."[13]

A concentration of 1 nM (i.e., 10^{-9} M) is close to the estimate of 10^{-10} M by Bada, mentioned above.

Others, however, have calculated that more than 200 km^3 ocean water flows every year through the thousands of fuming hydrothermal vents which exist. They have estimated that all the ocean's water would circulate through one vent or another every 100,000 years. Cold water sinks until coming into contact with giant magma chambers, which quickly heat water to far above 100°C, destroying AAs and peptides.[14–16] Perhaps 10^{-10} to 10^{-9} M is too high an estimate?

In 2023, Kobayashi *et al.* published an extensive study (summarized in Appendix 1) on all the possible sources of AAs and carboxylic acids during the relevant young sun period (4.4 to 3.8 Ga) when life was supposed to have arisen.[17] During that period, solar super flares are claimed to have produced SEPs (solar energetic particles) which could have broken nitrogen, leading to the formation of AAs, assuming enough methane (CH_4) would have been present. Afterwards, under the lower levels of SEP expected to have been present, the rate of destruction of complex molecules would have been at least as high as the rate of their production. Figure 8 in their paper implied that about 10^9 kg Gly may have been formed per year, taking all sources into account, as also elaborated on in our Appendix 1.[17]

To arrive at an estimate for the concentration for glycine, should we assume that it would have survived, on average, for 0.1, 1, or 10 Ma before being thermally degraded? The highest survival time estimate is the oldest one reported but, unlike the later estimates, the detailed basis for the claim was not provided. In addition, very rapid mixing of oceanic water would have occurred due to the assumed violent tidal activity 4 Ga ago.[18]

We decided to select the most favourable assumption OoL scientists would prefer and used Bada's estimate of complete oceanic circulation every 10^7 years. The maximum amount which could have accumulated would have been about

$$\text{Gly} \approx 10^9 \text{ kg / year} \times 10^7 \text{ years} \times 1{,}000 \text{ gm / kg} = 10^{19} \text{ gm.} \quad (7)$$

Based on a molecular weight of 75 for Gly and the amount of water in today's oceans ≈ 1.3×10^{21} litres, the molarity would have been about

$$[\text{Gly}]_{\text{eq}} \approx 2.5 \times 10^{-4} \text{ M (i.e., } (10^{19} / 75) / 1.3 \times 10^{21}) \quad (8)$$

which is similar to the highest estimate proposed by Lazcano and Miller (10^{-4})[12] and the estimate of 3×10^{-4} M proposed by Stribling and Miller.[11] It is worth emphasizing that these estimates apply to glycine and not to all biological AAs. Examination of the chromatographic data in Lazcano and Miller's paper revealed that about 10,000 times more glycine would have been produced than all the other AAs combined; that is, all the biological plus interfering non-biological AAs combined.[12]

We can now solve eqn 6 using $[\text{Gly}]_{\text{eq}} = 1 \times 10^{-4}$ M:

$$[\text{Gly}_2]_{\text{eq}} = [\text{Gly}]^2_{\text{eq}}/K_{\text{hyd11}} = [10^{-4}\,\text{M}]^2/400 \approx 2.5 \times 10^{-11} \text{ M.} \quad (9)$$

For comparison purposes, using a more representative value from the OoL literature of [Gly] ≈ 10^{-7} M would predict $[\text{Gly}_2]_{\text{eq}} = [10^{-7}\,\text{M}]^2/400 \approx 2.5 \times 10^{-17}$ M.

For the peptide condensation reaction $\text{Gly}_n + \text{Gly} \leftrightarrows \text{Gly}_{n+1}$, Martin reported that $K_{\text{con1}n} = [\text{Gly}_{n+1}] / [\text{Gly}_n][\text{Gly}] \approx 1/50$ at 25–37°C for $n > 2$.[4] Therefore, the molar concentration (M) of Gly_{n+1} at equilibrium ($[\text{Gly}_{n+1}]_{\text{eq}}$) can be derived by noticing the pattern for $n > 2$:

$$[\text{Gly}_3]_{\text{eq}} = K_{\text{con1}n}[\text{Gly}]_{\text{eq}}[\text{Gly}_2]_{\text{eq}}$$

$$[\text{Gly}_4]_{\text{eq}} = K_{\text{con1}n}[\text{Gly}]_{\text{eq}} \times [\text{Gly}_3]_{\text{eq}} = K_{\text{con1}n}[\text{Gly}]_{\text{eq}} \times (K_{\text{con1}n}[\text{Gly}]_{\text{eq}}[\text{Gly}_2]_{\text{eq}}) = (K_{\text{con1}n}[\text{Gly}]_{\text{eq}})^2[\text{Gly}_2]_{\text{eq}}$$

$$[\text{Gly}_5]_{\text{eq}} = K_{\text{con1}n}[\text{Gly}]_{\text{eq}} \times [\text{Gly}_4]_{\text{eq}} = K_{\text{con1}n}[\text{Gly}]_{\text{eq}} \times (K_{\text{con1}n}[\text{Gly}]_{\text{eq}})^2[\text{Gly}_2]_{\text{eq}}) = (K_{\text{con1}n}[\text{Gly}]_{\text{eq}})^3[\text{Gly}_2]_{\text{eq.}}$$

Since $K_{\text{con11}} = 1 / K_{\text{hyd11}}$, eqn 3 can be used to replace $[\text{Gly}_2]_{\text{eq}}$ by $K_{\text{con11}}[\text{Gly}]^2_{\text{eq}}$. This leads to the general relationship,

$$[\text{Gly}_n]_{\text{eq}} = (K_{\text{con1}n}[\text{Gly}]_{\text{eq}})^{n-2} \times K_{\text{con11}}[\text{Gly}]^2_{\text{eq}} \text{ or}$$

$$[\text{Gly}_n]_{\text{eq}} = 1/400[\text{Gly}]^2_{\text{eq}} \times (1/50[\text{Gly}]_{\text{eq}})^{n-2} \quad (10)$$

for $n > 2$. Since the poly-glycine peptides arise from condensation of Gly, eqn 10 shows how its concentration determines the concentration of its derivatives.

In this paper, $[\text{Gly}]_{eq}$ will usually be set to 10^{-4} M. From eqn. 10, this leads to $[\text{Gly}_n]_{eq} = 2.5 \times 10^{-11} \times (2 \times 10^{-6})^{n-2}$, and the equilibrium concentration of a peptide decreases by a factor of about 2 × 10^{-6} for each increase of one residue.

For an initial concentration $[\text{Gly}]_i = 10^{-4}$ M, virtually none would have been consumed after attaining the equilibria chain shown in eqn 5. Hence, we can approximate $[\text{Gly}]_{eq} \approx [\text{Gly}]_i$.[19] For triglycine eqn 10 leads to:

$$[\text{Gly}_3]_{eq} = 2.5 \times 10^{-11}\,\text{M} = 5 \times 10^{-17}\,\text{M}. \quad (11)$$

As stated above, each peptide concentration will be about K_{con1n} $[\text{Gly}]_{eq}$; i.e., 2 × 10^{-6} M lower than that of the smaller peptide from which it was derived. *Because of this very small consumption needed to form larger peptides, $[\text{Gly}]_{eq}$ will remain almost identical to $[\text{Gly}]_i$, the concentration before any condensation occurs.* We will see this 2 × 10^{-6} M factor again later when we simulate the buildup of peptides from first principles.

Experiments related to the Amyloid World Hypothesis use peptides about nine residues long.[3] The Gly_9 steady-state concentration would therefore have been about

$$[\text{Gly}_9] = [\text{Gly}_2]\,(K_{con1n}[\text{Gly}])^7 \times = (1/50 \times 10^{-4})^7 \times 2.5 \times 10^{-11}\,\text{M} = 5 \times 10^{-51}\,\text{M}. \quad (12)$$

Although this is an absurdly dilute concentration, the other non-Gly biologically relevant AAs would have been even less available than Gly.[12] But how dilute is 5 × 10^{-51} M? Even 400,000 terrestrial oceans would have been insufficient to form one nonapeptide, despite the overly generous assumptions made![20]

Equations 9 and 10 reveal why OoL chemists use such high initial concentrations of aa like Gly in their experiments. Recall that $[\text{Gly}]_{eq}$ will be only a miniscule concentration lower than $[\text{Gly}]_i$. Suppose that a chemist used $[\text{Gly}]_{eq}$ = 0.1 M (instead of 10^{-4} M). Equation 10 now predicts:

$$[\text{Gly}_3] = 5 \times 10^{-8}\,\text{M (i.e., } K_{con1n}[[\text{Gly}]) \times [\text{Gly}_2] = (1/50 \times 0.1) \times 1/400(0.1)^2 \quad (13)$$

which is significantly more than the 5 × 10^{-17} M shown in eqn 11, and enough to be detectable in laboratory experiments.

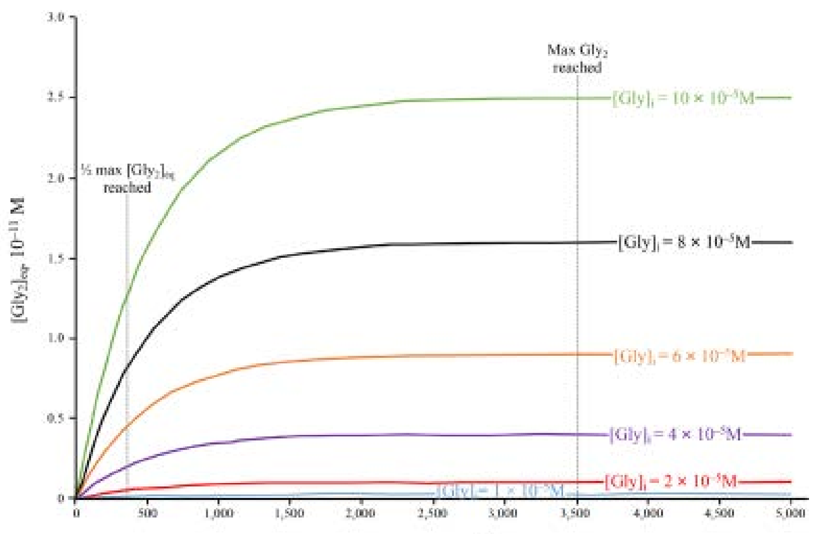


Figure 2. Increase in diglycine (Gly_2) over time via the equilibrium reaction 2 Gly ⇆ Gly_2, assuming no Gly_2 initially. Different initial concentrations of glycine ($[\text{Gly}]_i$) were modelled, using $k_{con} = 5 \times 10^{-6}\,\text{yr}^{-1}\text{mol}^{-1}$ and $k_{hyd} = 2 \times 10^{-3}\,\text{yr}^{-1}\text{mol}^{-1}$ at 25°C, with the algorithm explained in Appendix 2. Data available in Supplementary Material II, sheet 'Gly2 Res_2'.

Time course to build up diglycine at 25°C

The equilibration reactions shown in (5) imply that Gly_{n-1} could only arise from the equilibrium reaction Gly_{n-1} + Gly ⇆ Gly_n. However, Gly_n could also be produced through the condensation of two smaller peptides: $\text{Gly}_x + \text{Gly}_y \leftrightarrows \text{Gly}_n$ (where $x + y = n$). To illustrate, Gly_4 could also arise from the equilibrium reaction 2 Gly_2 ⇆ Gly_4.

To address this concern, we demonstrated in Supplementary Material I that the net outcome of such internal peptide bond condensation and hydrolysis is to *lower* $[\text{Gly}_n]_{eq}$. We call *Full Models* the case where all these additional internal amide-hydrolyzing equilibria are taken into account, and *Reduced Models* when only the most important end groups are taken into account. As shown in Supplementary Material I, large Full Models lead to serious mathematical difficulties; these could not be handled by any of the systems of equation solvers we examined.

For OoL purposes, it makes no practical difference whether a Full or Reduced Model is used; both demonstrate that not a single peptide as small as Gly_9 would have been produced in a prebiotic ocean, and far less larger peptides. Therefore, attempting to find highly precise hypothetical concentrations of large peptides is not necessary.

In this paper, we work with Reduced Models, like others who have pointed out that formation of large peptides in water is thermodynamically strongly unfavourable.[21] Note that all $[\text{Gly}_n]_{eq}$ calculated by Reduced Models will be too high, since the additional hydrolyzing pathways were neglected. These pathways would facilitate the formation

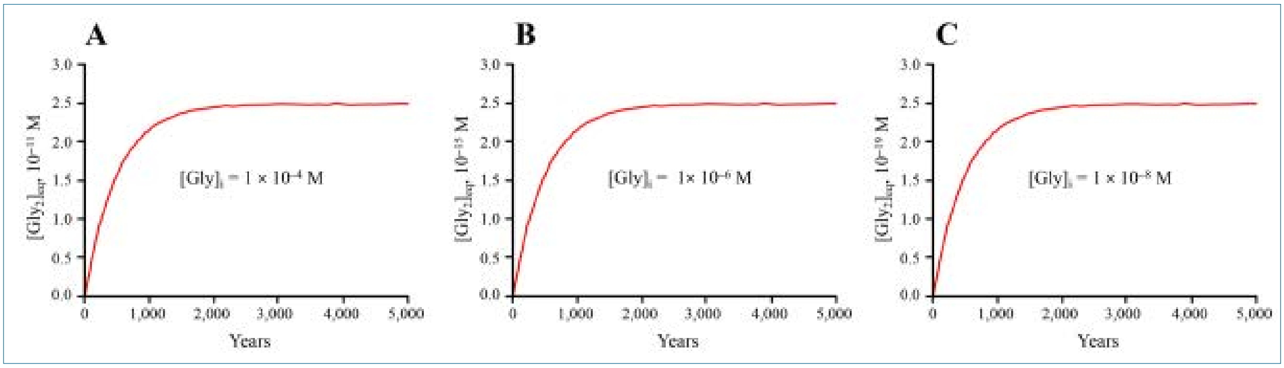


Figure 3. The amount of diglycine (Gly_2) at equilibrium decreases by a factor of 10^4 per factor 10^2 decrease in initial concentration of glycine (Gly). The conditions are the same as for figure 2. Data available in Supplementary Material II, sheet 'Gly2 Res_1'.

Table 2. Literature values for condensation and hydrolysis equilibrium reaction Gly + Gly ⇆ Gly_2 + H_2O. A: Rate constants; B: free energies.

A Rate constants in $mol^{-1}s^{-1}$				
25°C	25°C	140°C	150°C	140°C
k_{hyd11} $^{(a)}$	k_{con11} $^{(b)}$	k_{hyd11} $^{(c)}$	k_{hyd11} $^{(a)}$	k_{con11} $^{(c)}$
6.3×10^{-11}	$1.6 \times 10^{-13\,(f)}$	4.0×10^{-6}	8.9×10^{-6}	4.3×10^{-8}

B Free energy in kcal/mole		
25°C	25°C	374°C
ΔG_{con11} $^{(d)}$	ΔG_{con11} $^{(e)}$	ΔG_{con11} $^{(d)}$
+3.4	+3.6	+1.2

(a) Radzicka and Wolfenden (1996), ref. 22.

(b) K_{hyd11} = 400 M = k_{hyd11} / k_{con11}; k_{con11} = k_{hyd11} / 400 = 1.6×10^{-13} M.

(c) Sakata *et al.* (2014), ref. 24.

(d) Lemke *et al.* (2009), ref. 5.

(e) Martin *et al.* (1998), ref. 4.

of the thermodynamically stabler smaller members of the equilibria.

Equation 10 allows upper limit concentrations to be calculated for peptides once equilibrium has been reached. But it is also of interest to simulate the buildup of peptides from none initially. We explain in Appendix 2 the algorithm used to calculate $[Gly_2]$, the first condensation product, through the equilibration process 2 Gly ⇆ Gly_2 over time.

The resulting curves in figure 2 show how a small increase in $[Gly]_I$ leads to an over- proportionally higher $[Gly_2]_{eq}$. These results are based on the rate constants $k_{con} = 5 \times 10^{-6}$ and $k_{hyd} = 2 \times 10^{-3}$ $yr^{-1}mol^{-1}$ from Radzicka and Wolfenden at 25°C and neutral pH, as explained in Appendix 2.[22] We also assumed that $[Gly]_{eq} \approx [Gly]_i$, since an insignificant amount is consumed.[19]

The relationship between $[Gly]_i$ and equilibrium $[Gly_2]_{eq}$ can be estimated from $K_{con11} = [Gly_2]_{eq} / [Gly]^2_{eq} = 1/400$. Rearranging, $[Gly_2]_{eq} = [Gly]^2_{eq} \times 1/400$ at 25°C – 37°C. Since $[Gly]_i \approx [Gly]_{eq}$, a ten-fold decrease in $[Gly]_i$ will decrease $[Gly_2]_{eq}$ by about a factor of 10^2, as shown in figure 3, neglecting other larger products formed, such as condensation to form Gly_3. This reinforces why very high, prebiotically implausible concentrations of initial AAs must be used in experiments to obtain larger peptides, such as 10^{-1} M Gly.[23]

Figure 2 and figure 3 show that the maximum $[Gly_2]$ is reached quickly, in about 3,500 years, independent of $[Gly]_i$. This might seem like a relatively short time, but recall from eqn. 9 that only 10^{-11} M of Gly_2 must be produced at equilibrium, since build-up of Gly_2 is prevented by rapid hydrolysis, as shown in figure 4. In fact, about half the maximum $[Gly_2]_{eq}$ is reached within only about 400 years.

Time course to build up polypeptides (Gly_n) for $n \geq 2$ at 25°C

From Table 1 the hydrolysis equilibrium reaction

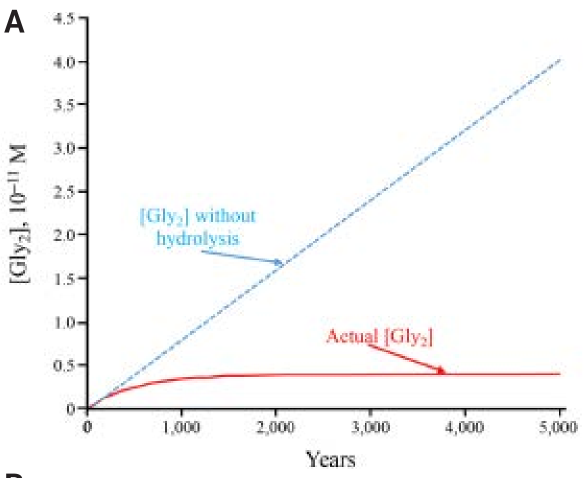
$$Gly_2 + H_2O \leftrightarrows Gly + Gly. \quad (14)$$

has $K_{hyd11} \approx 400$ at 25 to 37°C, whereas the hydrolysis equilibrium reaction

$$Gly_3 + H_2O \leftrightarrows Gly_2 + Gly \quad (15)$$

has $K_{hyd12} \approx 50$ in this temperature range.

In both cases, the equilibrium constant is the ratio of rate constants for hydrolysis and condensation, but only k_{hyd} for equilibrium (14) has been experimentally determined. However, since $K_{hyd11} = 400$ is known, this permitted k_{con} to be calculated directly. These rate constants are shown in table 3A, columns 1 and 2.



B

Time, yr	$[Gly_2]_f$ without hydrolysis	$[Gly_2]_f$
1	5.0000000000 × 10^{-14}	4.990000 × 10−14
2	9.9999999900 × 10^{-14}	9.970020 × 10−14
3	1.4999999970 × 10^{-13}	1.494008 × 10^{-13}
4	1.9999999940 × 10^{-13}	1.990020 × 10^{-13}
5	2.4999999900 × 10^{-13}	2.485040 × 10^{-13}
6	2.9999999850 × 10^{-13}	2.979070 × 10^{-13}
7	3.4999999790 × 10^{-13}	3.472112 × 10^{-13}
8	3.9999999720 × 10^{-13}	3.964167 × 10^{-13}
9	4.4999999640 × 10^{-13}	4.455239 × 10^{-13}
10	4.9999999550 × 10^{-13}	4.945329 × 10^{-13}
11	5.4999999450 × 10^{-13}	5.434438 × 10^{-13}
12	5.9999999340 × 10^{-13}	5.922569 × 10^{-13}
13	6.4999999220 × 10^{-13}	6.409724 × 10^{-13}
14	6.9999999090 × 10^{-13}	6.895904 × 10^{-13}
15	7.4999998950 × 10^{-13}	7.381113 × 10^{-13}
16	7.9999998800 × 10^{-13}	7.865350 × 10^{-13}
17	8.4999998640 × 10^{-13}	8.348620 × 10^{-13}
18	8.9999998470 × 10^{-13}	8.830922 × 10^{-13}
19	9.4999998290 × 10^{-13}	9.312261 × 10^{-13}
20	9.9999998100 × 10^{-13}	9.792636 × 10^{-13}
...	...	...

Figure 4. Rapid hydrolysis of diglycine (Gly_2) prevents high concentrations from forming. A: Equilibrium is reached in about 3,500 years. B: $[Gly_2]_f$ is the final concentration of Gly_2 at the end of each one-year interval in the simulations shown in Appendix 2. Column two was simulated assuming no hydrolysis, and column three includes hydrolysis. Data available in Supplementary Material II, sheet 'Gly2 Res_0'.

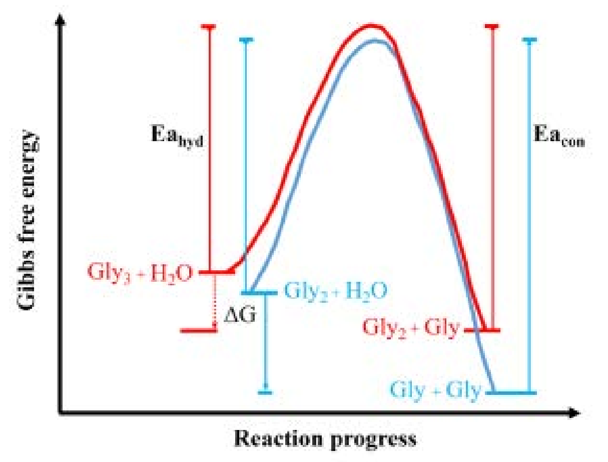


Figure 5. Comparison of the relative Gibbs Free energy (ΔG) and energy of activation (E_a) for the reversible hydrolysis and condensation reactions, $Gly_3 + H_2O \leftrightarrows Gly_2 + Gly$ (red) and $Gly_2 + H_2O \leftrightarrows Gly + Gly$ (blue). Relative differences between both equilibrium reactions are not drawn to exact scale. The transition state of the reaction $Gly_2 + H_2O \rightarrow Gly + Gly$ would have two partial stable zwitterion characters, lowering the energy of its transition state.

In Appendix 2, we multiplied these rate constants by 31,557,600 sec/year to use values easier to visualize: $k_{con11} = 5 \times 10^{-6}$ $yr^{-1}mol^{-1}$ and $k_{hyd11} = 2 \times 10^{-3}$ $yr^{-1}mol^{-1}$. Unfortunately, neither a value for k_{hyd12} nor k_{con12} could be found in the literature for equilibrium reaction 15 $Gly_3 + H_2O \leftrightarrows Gly_2 + Gly$. So we resorted to chemical reasoning to arrive at reasonable estimates.

From table 1, $\Delta G_{hyd} = -3.6$ kcal/mol for equilibrium (14) $Gly_2 + H_2O \leftrightarrows Gly + Gly$ and –2.5 kcal/mol for each end of the Gly_3 molecule for reaction (15). This difference in ΔG_{hyd} is reasonable, since, in the case of 14, the two glycine ions formed are strongly solvated. Given that the transition state structures for reactions 14 and 15 will be similar, the rate constants will correlate with the energy of activation, E_a, required for the various reactions. Considering the stability of each starting molecule in water we conclude that the equilibria (14) and (15) will resemble the diagram shown in figure 5.

Since the hydrolysis reactions ($Gly_2 + H_2O \rightarrow Gly + Gly$ and $Gly_3 + H_2O \rightarrow Gly_2 + Gly$) are energetically more similar than the reverse condensation reactions, the hydrolysis process will be used to estimate one of the missing rate constants, namely k_{hyd}.

A reasonable estimate for k_{hyd} can be made. Since water could hydrolyze Gly_3 at two positions, whereas Gly_2 only could at one position, k_{hyd} for Gly_3 should be about twice as fast. Also taking into account that the Gly_3 to be hydrolyzed would be less strongly solvated initially than Gly_2, thereby leading to a lower total E_a, it is reasonable to assume that

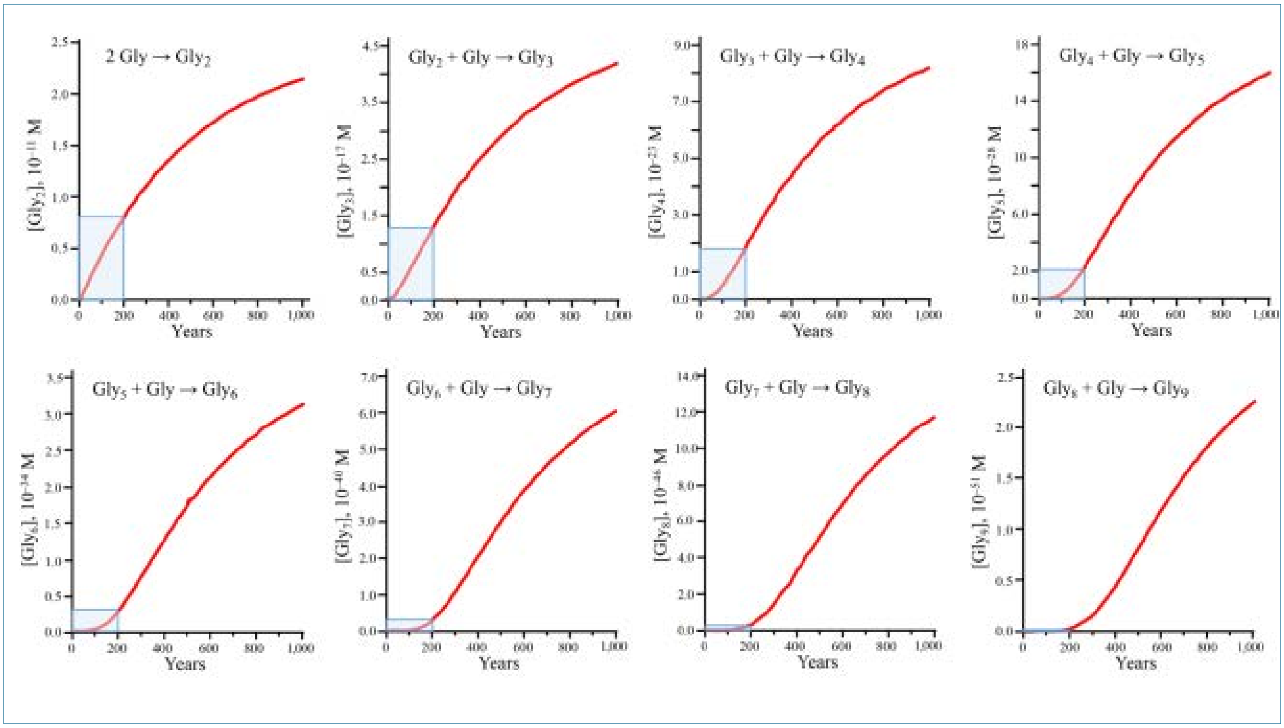


Figure 6. Concentration buildup of peptides after 1,000 years using the assumptions described in the main text and the algorithm explained in Appendices 2 and 3. Systematic time lags are apparent for peptide formation, the longer the peptide, the bigger the lag. Data available in Supplementary Material II, sheet 'Gly2–9'.

k_{hyd} for Gly_3 should be about ten times higher than for Gly_2. Therefore, we estimated that

$$k_{hyd13}\ (\text{for Gly}_3) \approx 2 \times 10^{-2}\ \mathrm{yr}^{-1}\mathrm{mol}^{-1} \qquad (16)$$

i.e., $10 \times k_{hyd11}$ (for Gly_2).

Since $k_{con13} = k_{hyd13} / K_{hyd13}$, we then obtained

$$k_{con13}\ (\text{for Gly}_3) \approx 4 \times 10^{-4}\ \mathrm{yr}{-}\mathrm{mol}^{-1} \qquad (17)$$

i.e., $2 \times 10^{-2} / 50$.

We used $k_{hyd13} = 2 \times 10^{-2}\ \mathrm{yr}^{-1}\mathrm{mol}^{-1}$ and $k_{con13} = 4 \times 10^{-4}\ \mathrm{yr}{-}^{1}\mathrm{mol}{-}^{1}$ in a modified bootstrap method, explained in Appendix 3, to simulate condensation of $\mathrm{Gly}_n \leftrightarrows \mathrm{Gly}_{n+1}$ during the same time intervals as the reaction $2\ \mathrm{Gly} \leftrightarrows \mathrm{Gly}_2$. As we demonstrate in Appendix 3, even large errors in our estimate for k_{con13} and k_{hyd13} would not affect any of the conclusions in this paper, as long as k_{con13} / k_{hyd13} matches the known value for K_{hyd13}.

Figure 6 shows the buildup of peptides after 1,000 years. As expected, the Reduced Model reveals there are systematic time lags that increase with peptide chain length, as illustrated in the period between 0 and 200 years (figure 6, blue boxes). These lags occurred because $[\mathrm{Gly}_n]$ must build up for Gly_{n+1} to form. Note that the scales of the Y-axes are different; that of $[\mathrm{Gly}]_{n+1}$ is a million times lower than that of $[\mathrm{Gly}]_n$, because $[\mathrm{Gly}_{n+1}]$ is about 2×10^{-6} M lower than $[\mathrm{Gly}_n]$ for $n > 2$, as discussed above. Thus, the scale of the first panel ($[\mathrm{Gly}_2]$) is 10^{-11}, of the second panel ($[\mathrm{Gly}_3]$) is 10^{-17}, and so on. The scale of the last panel ($[\mathrm{Gly}_9]$) is 10^{-51}. Although Gly_2 and larger peptides would form after 200 years, their hypothetical final (equilibrium) concentration would be exceedingly low.

Figure 7 shows the concentration buildup of glycine polymers (up to nine residues) after 5,000 years to show how equilibrium is approached with time. Larger peptides took systematically slightly longer to reach a concentration after which further increases were negligible. For the equilibrium reaction, $2\ \mathrm{Gly} \leftrightarrows \mathrm{Gly}_2$, this took about 3,500 years, and for $\mathrm{Gly}_8 + \mathrm{Gly} \leftrightarrows \mathrm{Gly}_9$, about 5,000 years. Therefore, after about 5,000 years, these eight peptides would have reached their *de facto* equilibrium concentrations.

Final comments

Glycine was used as a representative AA, with an initial concentration of 10^{-4} M. To our knowledge, this is some orders of magnitude higher than OoL researchers have been assuming for any other AA, far less for *all* those necessary for their models. Since the side chain groups of AAs are far removed from where the condensation reactions occur, the equilibrium constants and rate constants at a given temperature would be similar for the 20 proteinogenic

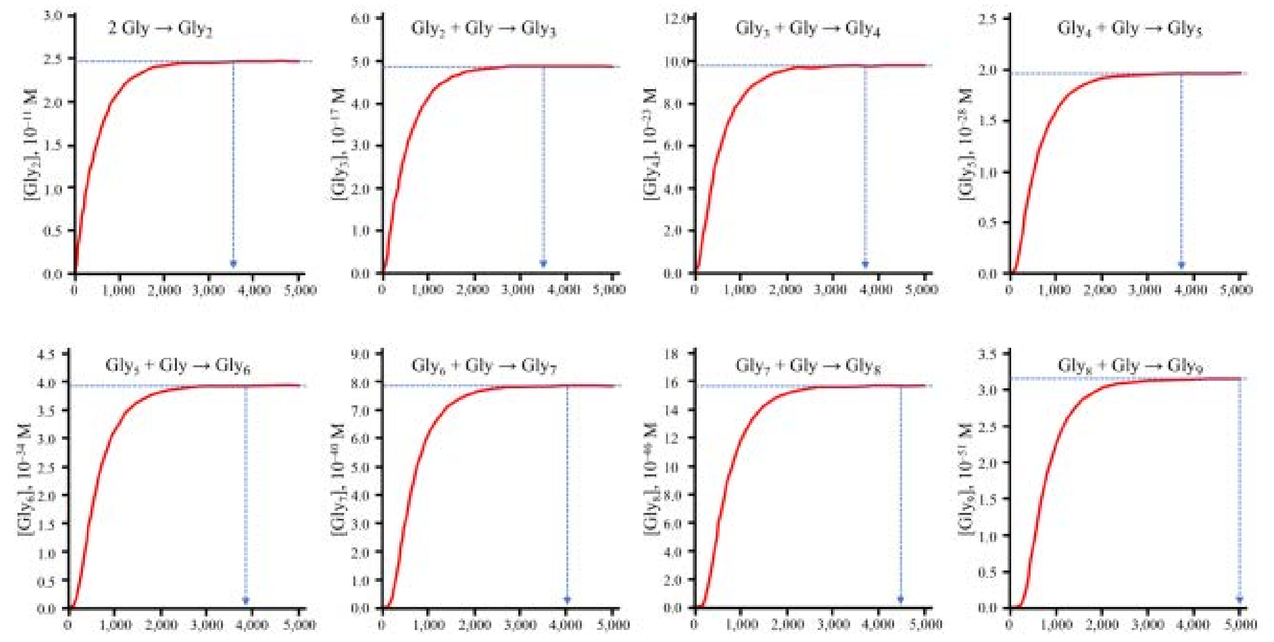


Figure 7. Concentration buildup of peptides after 5,000 years, using the assumptions described in the main text and the algorithm explained in Appendices 2 and 3. The larger peptides took systematically slightly longer to reach a concentration essentially equivalent to the equilibrium point. Data available in Supplementary Material II, sheet 'Gly2–9'.

Table 3. Molar concentration of Gly_n after 10,000 years, simulated using the Customized Algorithms, based on different initial concentrations of glycine. The calculations were performed using the Supplementary Material II Excel file with sheet 'Gly2–9' by entering different $[Gly]_{i,\,t=0}$ values in cell 'B2'. For the equilibrium 2 Gly ⇆ Gly_2 rate constants $k_{con} = 5 \times 10^{-6}$ $yr^{-1}mol^{-1}$ and $k_{hyd} = 2 \times 10^{-3}$ $yr^{-1}mol^{-1}$ were used and for the equilibria Gly_{n-1} + Gly ⇆ Gly_n rate constants $k_{con} = 4 \times 10^{-4}$ $yr^{-1}mol^{-1}$ and k_{hyd} 2×10^{-2} $yr^{-1}mol^{-1}$.

$[Gly]_i$, t=0	$[Gly_2]_{final}$	$[Gly_3]_{final}$	$[Gly_4]_{final}$	$[Gly_5]_{final}$	$[Gly_6]_{final}$	$[Gly_7]_{final}$	$[Gly_8]_{final}$	$[Gly_9]_{final}$
1.0×10^{-4}	2.49×10^{-11}	4.90×10^{-17}	9.80×10^{-23}	1.96×10^{-28}	3.92×10^{-34}	7.84×10^{-40}	1.57×10^{-45}	3.14×10^{-51}
1.0×10^{-5}	2.49×10^{-13}	4.90×10^{-20}	9.80×10^{-27}	1.96×10^{-33}	3.92×10^{-40}	7.84×10^{-47}	1.57×10^{-53}	3.14×10^{-60}
1.0×10^{-6}	2.49×10^{-15}	4.90×10^{-23}	9.80×10^{-31}	1.96×10^{-38}	3.92×10^{-46}	7.84×10^{-54}	1.57×10^{-61}	3.14×10^{-69}
1.0×10^{-7}	2.49×10^{-17}	4.90×10^{-26}	9.80×10^{-35}	1.96×10^{-43}	3.92×10^{-52}	7.84×10^{-61}	1.57×10^{-69}	3.14×10^{-78}
1.0×10^{-8}	2.49×10^{-18}	4.90×10^{-29}	9.80×10^{-39}	1.96×10^{-48}	3.92×10^{-58}	7.84×10^{-68}	1.57×10^{-77}	3.14×10^{-87}
1.0×10^{-9}	2.49×10^{-21}	4.90×10^{-32}	9.80×10^{-43}	1.96×10^{-53}	3.92×10^{-64}	7.84×10^{-75}	1.57×10^{-85}	3.14×10^{-96}
1.0×10^{-10}	2.49×10^{-23}	4.90×10^{-35}	9.80×10^{-47}	1.96×10^{-58}	3.92×10^{-70}	7.84×10^{-82}	1.57×10^{-93}	3.14×10^{-105}

AAs. Therefore, we can use the Customized Algorithm explained in Appendix 2 for the equilibrium process: 2 Gly ⇆ Gly_2, together with Customized Algorithm II, explained in Appendix 3, for the equilibria: Gly_{n-1} + Gly ⇆ Gly_n available in the Supplementary Material II Excel file, using sheet 'Gly2–9' to calculate peptide concentrations, using other assumed average $[Gly]_{i,\,t=0}$ values. The results have been summarized in table 4. Each ten-fold decrease in the initial glycine concentration leads to a 10^9-fold decrease in $[Gly_9]$ at equilibrium. This is a sobering fact to consider when evaluating OoL experiments which rely on very high concentrations of even small peptides.

From Avogadro's number, a 1-M solution of Gly_9 would contain about 6×10^{23} molecules per litre, so a final theoretical $[Gly_9]_{eq} \approx 3 \times 10^{-51}$ M means that not a single Gly_9 would have been present in a prebiotic ocean after the steady state was reach in a few thousand years. Additional time would not permit the concentrations to increase. Furthermore, taking all hydrolyzing processes available according to the Full Model would both decrease the maximum concentrations achievable and reach the final equilibrium state in a shorter timespan.

Suppose peptides had formed in one of the exotic environments evolutionists have proposed, such as wet–dry cycling, clay or mineral surfaces, concentration by evaporation or by eutectic freezing of dilute aqueous solutions, through activation with small molecules (e.g., COS), salt-based deliquescence, catalytic peptide ligation, or condensation reagents.[25,26]

Under the violent asteroid impact and tidal conditions assumed to have existed long ago, most peptides that formed elsewhere would eventually have been flushed into oceanic water.[18] All Ool scenarios claim biological life arose in an aqueous environment anyway. But peptide bonds in water are estimated to have a half-life of between about 350 and 600 years *per bond* at 25°C.[22] Assuming a half-life of 500 years, after only 10,000 years (i.e., 20 half-lives) the proportion of unhydrolyzed peptide bonds would have been $(½)^{20}$, less than one in a million.

Worse, our analysis, above, demonstrated that the equilibrium concentration of large peptides formed though condensation of amino acids would have been essentially zero. Therefore, concentrated peptides from any source would have been rapidly diluted. To complete their destruction, oceanic water flow through ancient hydrothermal vents would have regularly destroyed any surviving peptides and amino acids.[14–16]

Taken together, our analyses indicate that even relatively small peptides would not form prebiotically in relevant concentrations.

It is ironic that OoL researchers have been so active attempting to find some natural process for amino acids to self-assemble into large peptides in high concentrations. The fact that amino acids do *not link easily* is fortunate, since it is actually a requirement for biological life to function. As Tan pointed out in 2022, cells must be able to manufacture large proteins at the right time and location, and in the right proportion. These must have specific sequences to provide the myriad of cellular functions, and the sequence information is encoded on DNA. *Facile ability of amino acids to self-link to form functional protein sequences contra genetically coded instructions would prevent life from existing*![27]

Appendix 1. Availability of prebiotic amino acids

In 2023, Kobayashi *et al*. published an extensive study on all the possible sources of AAs and carboxylic acids during the relevant young sun period (4.4 to 3.8 Ga).[17] Various mixing ratios of carbon dioxide, methane, nitrogen, and water were tested, to model the atmosphere composition believed to have existed then. Assumed energy sources which were simulated in laboratory experiments included galactic cosmic rays (GCRs); solar energetic particles (SEPs) associated with superflares; spark discharges (simulation of lightning flashes); and solar ultraviolet light (UV).[17]

The assumed atmospheric composition was based on photochemical studies which showed that ammonia or methane would have been quickly destroyed by UV emissions from the young sun.[28,29] Geochemical studies also implied that the atmosphere would have been composed of almost entirely N_2 and CO_2.[30–33]

Miller–Urey-type experiments, using a predominantly N_2-CO_2 atmosphere with spark discharges and UV irradiation, could only produce a handful of biologically relevant molecules in trace concentrations too low to be of any relevance for OoL purposes.[34–37]

The ratio of methane (rCH_4, i.e., proportion of CH_4 to $CH_4 + CO_2 + N_2$) in the early Earth's atmosphere was estimated by Catling and Zahnle to have been very low, with rCH_4 being far less than 0.05.[38] Using a value of rCH_4 between 0.01 and 0.05 in figure 8 of Kobayshi *et al*.[17] implies Gly would have formed at a rate of about 10^9 kg/year.

Figure 2d of ref. 17 showed that only Gly and Ser were produced from among the biological AAs, *in a proportion Gly/Ser ≈ 10,000:1*. Non-biological α-ABA + β-ABA(ABA means aminobutyric acid) were produced in much higher concentration than Ser.

Consistent with this, figure 4 of ref 17 shows the concentration of four major products obtained using rCH4 = 0.05: Gly (6×10^{-6}) > α-ABA (0.25×10^{-6}) > β-Ala (0.025×10^{-6}) > γ-ABA $(<1 \times 10^{-9})$. Importantly, besides Gly, no biological AA was found among the top 4 products.

Not to be overlooked is that after the intense radiation experiments almost no Gly and Ser themselves were obtained, but the undefined material produced had to be acid-hydrolyzed at 110°C for 24 h in 6 M HCl. This would have reduced the average concentration of free Gly (and other AAs) available prebiotically.

Appendix 2. Rate of buildup of diglycine (Gly_2) at a moderate temperature

Mathematically, the equilibrium reaction 2 Gly ⇆ Gly_2 is a system of two ordinary differential equations (ODEs). Let's define X = Gly and Y = Gly_2 to express the equations in a more familiar form. This leads to:

$$dX'(t) = -2k_{con}X(t) + 2k_{hyd}Y(t)$$
$$dY'(t) = k_{con}X(t) - k_{hyd}Y(t)$$

where t refers to time. The effects of X and Y on each other occur simultaneously. Unfortunately, none of the tools available to us were able to find an analytic solution. Therefore, we decided to use a bootstrap simulation to build up Gly (i.e., X) and Gly_2 (i.e., Y) starting from $t = 0$, using small time intervals. To do this, values for k_{con} and k_{hyd} at ≈ 25 – 37°C were needed.

Rate constant k_{con} for the condensation reaction 2 Gly → Gly_2 at 25°C

We could not find low-temperature kinetic rate constants for the condensation reaction 2 Gly → Gly_2. Data was available, however, for the reverse hydrolysis reaction, Gly_2 → 2 Gly.

At equilibrium the rate of forward and backward reaction must match $k_{hyd}[Gly_2] = k_{con}[Gly]^2$. Therefore,

$$K_{hyd11} = k_{hyd11} / k_{con11} = [Gly]^2 / [Gly_2]. \quad (19)$$

Radzicka and Wolfenden reported a value of $k_{hyd11} = 6.3 \times 10^{-11}$ $sec^{-1}mol^{-1}$ at 25°C at pH 6.822 and Martin a $K_{hyd11} = 400$.[4] This allows us to calculate

$$k_{con11} = k_{hyd11} / K_{hyd11} = k_{hyd11} / k_{con11} \quad (20)$$

which leads to $k_{con11} = 1.6 \times 10^{-13}$ $sec^{-1}mol^{-1}$ (i.e., 6.3×10^{-11} $sec^{-1}mol^{-1}$ / 400), shown in column 2 of table 3.

Is a $k_{hyd11} / k_{con11} \approx 400$ plausible? From columns 3 and 4 of table 3, we observe that $k_{hyd11} / k_{con11} \approx 100$ at 140°C from a different study. Consistent with this factor four difference, at higher temperatures, the forward and backward reactions will be more similar than at lower temperatures.

Selecting an environment having a temperature of ≈ 25°C would allow OoL scenarios to neglect the decomposition pathways available to Gly shown in figure 1, especially the formation of cyclic DKP, as discussed in part 1 of this series.[1] Even if some DKP formed, it would not decrease [Gly] enough to affect $[Gly_2]$ appreciably at this temperature. This allows us to focus on the equilibrating reaction 2 Gly ⇆ Gly_2, without concerning other reactions shown in figure 1.

Since the highest concentration for Gly assumed by any reputable source from the OoL community in oceans is $[Gly] = 10^{-4}$ M, and virtually none would have been consumed to form $[Gly_2]$ at the equilibrium point, we can use eqn. (19) to calculate $[Gly_2]$ at equilibrium:

$$[Gly_2]_{eq} = [Gly]^2_{eq} / K_{hyd11} \quad (21)$$

which gives $[Gly_2]_{eq} = 2.5 \times 10^{-11}$ M (i.e., $(10^{-4})^2 / 400$). In our model, initial $[Gly_2]$ would be about 0, and, through condensation of Gly, it would eventually achieve a *maximum* of 2.5×10^{-11} M at equilibrium. Therefore, at all times $[Gly_2] \ll [Gly]$ (i.e., 2.5×10^{-11} M $\ll 10^{-4}$ M), and hence hydrolysis of Gly_2, would have virtually no effect on [Gly] during the equilibration process. Our simulation described below and other analysis discussed in the Supplementary Material 1 demonstrates that $[Gly]_i \approx [Gly]_{eq}$.

Runge Kutta bootstrap solution

We used the well-known Runge Kutta algorithm to interpolate values in interval time periods of size h per interval to solve the system of ODEs.[39] The analysis and python code we developed are provided in file Supplementary Material III and the data and diagrams are available in file Supplementary Material IV. A step size of $h = 0.00001$ gave good results but was computationally demanding, since the computations had to be repeated $1/h = 10^5$ times per time interval $t = 1$ year.

Free online servers which run python code timed out long before executing these long runs, so we had to use a high-quality desktop PC (12th Gen Intel(R) Core i7-12700F, 12 Cores(s), 12 Logical Processors and 32 GB memory using the Windows 11 operating system) to perform the calculations. Therefore, the Runge Kutta algorithm was not the technique chosen in this paper for further analysis.

Customized Algorithm bootstrap implemented in Excel and Python

We developed a 'Customized Algorithm' which calculates the cumulative concentrations of [Gly] and $[Gly_2]$ over time. Excel and Python implementation are provided in file Supplementary Material II and Supplementary Material V, respectively.

The iterations began with $[Gly]_i = 10^{-4}$ M and $[Gly_2]_i = 0$ at time = 0 (t_0). The algorithm calculates $[Gly]_f$ and $[Gly_2]_f$ at the end of discrete time intervals, as shown in table 4. The subscript 'i' refers to initial, and 'f' refers to final, concentrations for each time interval, 't'. To simplify

Table 4. Bootstrap algorithm to calculate concentration of Glycine (Gly) and dipeptide (Gly_2) after discrete time intervals

$$\boxed{\mathrm{Gly + Gly} \underset{k_{hdr}}{\overset{k_{con}}{\rightleftharpoons}} \mathrm{Gly_2}}$$

Time, t	$[Gly]_i$	$[Gly]_{lost}$	$[Gly]_f$	$[Gly_2]_i$	$[Gly_2]_{lost}$	$[Gly_2]_f$
0			1×10^{-4}			0
1	$[Gly]_{f,\ (t-1)}$	$2k_{con}\ [Gly]_i^2$	$[Gly]_i - [Gly]_{lost} + 2[Gly_2]_{lost}$	$[Gly_2]_f$ at (t-1) + $k_{con}[Gly]_i^2$	$k_{hyd}[Gly_2]^i$	$[Gly_2]_i - [Gly_2]_{lost}$
2	$[Gly]_{f,\ (t-1)}$	$2k_{con}\ [Gly]_i^2$	$[Gly]_i - [Gly]_{lost} + 2[Gly_2]_{lost}$	$[Gly_2]_f$ at (t-1) + $k_{con}[Gly]_i^2$	$k_{hyd}[Gly_2]^i$	$[Gly_2]i - [Gly_2]_{lost}$

Using time in years, $k_{con11} = 5 \times 10^{-6}\ yr^{-1}\ mol^{-1}$.[a)] $k^{hyd11} = 2 \times 10^{-3}\ yr^{-1}\ mol^{-1}$.[b)] produces the following results.

0			0.0001			
1	$1.00000000 \times 10^{-4}$	$1.00000000 \times 10^{-13}$	$9.99999999 \times 10^{-5}$	$5.00000000 \times 10^{-14}$	$1.00000000 \times 10^{-16}$	$4.99000000 \times 10^{-14}$
2	$9.99999999 \times 10^{-5}$	$9.99999998 \times 10^{-14}$	$9.99999998 \times 10^{-5}$	$9.98999999 \times 10^{-14}$	$1.99800000 \times 10^{-16}$	$9.97001999 \times 10^{-14}$
3	$9.99999998 \times 10^{-5}$	$9.99999996 \times 10^{-14}$	$9.99999997 \times 10^{-5}$	$1.49700200 \times 10^{-13}$	$2.99400399 \times 10^{-16}$	$1.49400799 \times 10^{-13}$
4	$9.99999997 \times 10^{-5}$	$9.99999994 \times 10^{-14}$	$9.99999996 \times 10^{-5}$	$1.99400799 \times 10^{-13}$	$3.98801598 \times 10^{-16}$	$1.99001997 \times 10^{-13}$
5	$9.99999996 \times 10^{-5}$	$9.99999992 \times 10^{-14}$	$9.99999995 \times 10^{-5}$	$2.49001997 \times 10^{-13}$	$4.98003994 \times 10^{-16}$	$2.48503993 \times 10^{-13}$
6	$9.99999995 \times 10^{-5}$	$9.99999990 \times 10^{-14}$	$9.99999994 \times 10^{-5}$	$2.98503993 \times 10^{-13}$	$5.97007985 \times 10^{-16}$	$2.97906985 \times 10^{-13}$
7	$9.99999994 \times 10^{-5}$	$9.99999988 \times 10^{-14}$	$9.99999993 \times 10^{-5}$	$3.47906984 \times 10^{-13}$	$6.95813968 \times 10^{-16}$	$3.47211170 \times 10^{-13}$
8	$9.99999993 \times 10^{-5}$	$9.99999986 \times 10^{-14}$	$9.99999992 \times 10^{-5}$	$3.97211169 \times 10^{-13}$	$7.94422339 \times 10^{-16}$	$3.96416747 \times 10^{-13}$

the notation, we will not include the subscript (t) unless ambiguity demands it.

For each time = t interval the following calculations are performed:

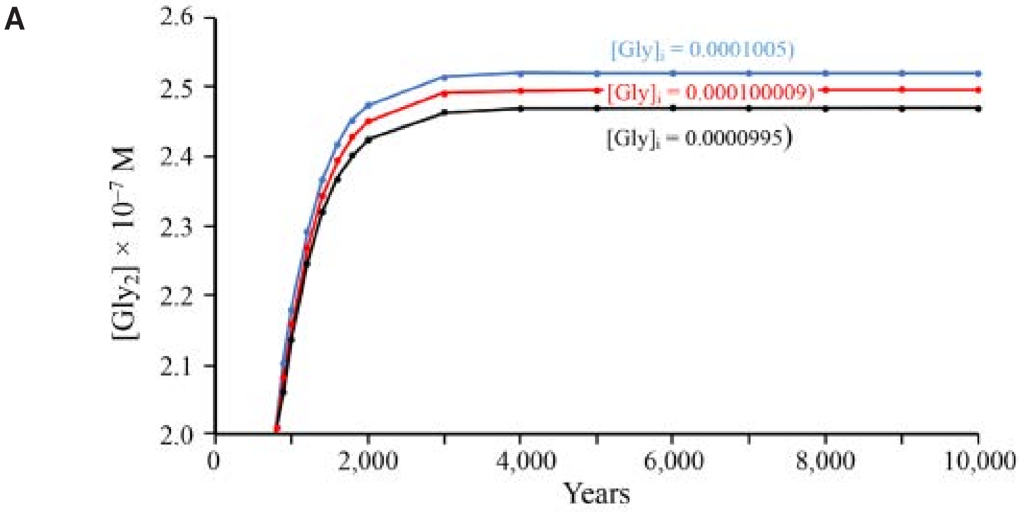
- $[Gly]_i = [Gly]_{f,\ (t-1)}$
- $[Gly]_{lost}$ is the amount lost due to condensation (taking into account that two molecules of Gly are consumed per Gly_2 formed): $[Gly]_{lost} = k_{con} \times 2 \times [Gly]_i^2$
- $[Gly]_f$ is the amount present at the beginning of the time interval, minus 2 × the amount which condensed, plus 2 × the amount of $[Gly_2]$ which is hydrolyzed back: $[Gly]_f = [Gly]_{i,\ (t)} - [Gly]_{lost} + 2 \times [Gly_2]_{lost}$
- $[Gly_2]_i$ is the amount from the end of the preceding time plus the amount condensed: $[Gly_2]_i = [Gly_2]_{f,\ (t-1)} + k_{con} \times [Gly]_i^2$
- $[Gly_2]_{lost}$ is the amount lost due to hydrolysis: $k_{hyd} \times [Gly_2]_i$
- $[Gly_2]_f$ is the initial amount present plus the amount which condensed minus the amount which hydrolyzed: $[Gly_2]_f = [Gly_2]_i - [Gly_2]_{lost}$.

Note that the amount of Gly regenerated can be neglected since it represents an insignificant proportion of the amount already present, whereas the loss of Gly_2 over time (although very small) is a relatively significant factor.

Using time intervals of one second duration (the usual time units in which rate constants are reported) would require considerable computational effort and not be possible with Excel. We decided to work with a more convenient time interval without losing much accuracy, and needed to determine what interval size would be appropriate.

From eqn 21, at equilibrium $[Gly_2]_{eq} = 2.5 \times 10^{-11}$ M. Ignoring the back hydrolysis process for the moment, how long would it take to produce this concentration? Using $k_{con} = 1.6 \times 10^{-13}\ sec^{-1} mol^{-1}$ from eqn. (20), it would take about 1.6×10^{-10} sec (i.e., 2.5×10^{-11} M / $(1.6 \times 10^{-13}\ s^{-1} M^{-1}\ [10–^4]^2)$) to reach equilibrium. Dividing by 31,557,600 secs / yr gives about 500 years.

Therefore, we decided to use time intervals of one year and adjust k_{con} and k_{hdr} by multiplying both by the number



B

	$[Gly]_{initial}$ = 0.9950 × 10^{-4} M		$[Gly]_{initial}$ = 1.000 × 10^{-4} M		$[Gly]_{initial}$ = 1.00009 × 10^{-4} M		Gly]$_{initial}$ = 1.0050 × 10^{-4} M	
Years	$[Gly]_{final}$, × 10^{-4} M	$[Gly_2]_{final}$, × 10^{-11} M	$[Gly]_{final}$, × 10^{-4} M	$[Gly_2]_{final}$, × 10^{-11} M	$[Gly]_{final}$, × 10^{-4} M	$[Gly_2]_{final}$, × 10^{-11} M	$[Gly]_{final}$, × 10^{-4} M	$[Gly_2]_{final}$, × 10^{-11} M
3,000	0.994997	2.46401	0.999997	2.48884	1.00009	2.48929	1.00500	2.51379
10,000	0.994990	2.47007	0.999991	2.49495	1.00008	2.49540	1.00499	2.51996
20,000	0.994980	2.47002	0.999980	2.49490	1.00007	2.49535	1.00498	2.51991

Figure 8. The initial concentration of glycine ([Gly]$_i$) changes very little to produce the equilibrium concentration of Gly$_2$, [Gly$_2$]$_{eq}$. Simulations based on the Customized Algorithm. The data used is available in the Supplementary Material II file, sheet 'Gly2 Res_3'. A: Resulting [Gly$_2$] caused by small changes in [Gly]$_i$ near the assumed concentration of 10^{-4} M used in this paper. B: Values of [Gly] and [Gly$_2$] after 3,000, 10,000, and 20,000 years.

of seconds per year, producing $k_{con} = 5 \times 10^{-6}$ yr^{-1}mol^{-}1 and $k_{hyd} = 2 \times 10^{-3}$ yr^{-1}mol^{-1}.

A valid model requires that all the initial glycine $[Gly]_{i, (t=0)}$ be correctly accounted for by the concentration of the various molecules during every time interval. The mass balance check adds ($[Gly]_f + 2[Gly_2]_f$) at the end of each time interval and compares it to $[Gly]_{I, (t=0)}$, which we have set to 1×10^{-4} M in this paper. The last column of table IVA in the file Supplementary Material V shows that the discrepancy in Gly Mass Balance represents a mere proportion of 1.6×10^{-7} of the concentration of $[Gly_2]_f$ after 3,000 years (and only 1.1×10^{-7} after 20,000 years). This is a considerable improvement over the proportion of 4.7×10^{-3} obtained by the Runge Kutta algorithm after 3,000 years using the very small parameter $h = 0.00001$, as shown in the last column of table IVB.

We can now use this algorithm to re-examine our assumption that $[Gly]_i \approx [Gly]_{eq}$.

Effect of assuming $[Gly]_i \approx [Gly]_{eq}$

Since, proportionally, so little of the Gly is consumed for Gly$_2$ to reach equilibrium in our calculations, we assumed that $[Gly]_i = [Gly]_{eq}$ in calculations involving K_{hyd11}. We tested different values of $[Gly]_i$ to see what value leads to $[Gly]_{eq} \approx 1.0 \times 10^{-4}$ M, as shown in figure 8 and found $[Gly]_i < 1.001 \times 10^{-4}$ M, as shown in figure 8.

Beginning the simulation with $[Gly]_i = 1.00009 \times 10^{-4}$ M resulted in $[Gly]_{eq} = 1.00008 \times 10^{-4}$ and $[Gly_2]_{eq} = 2.49540 \times 10^{-11}$ M, according to figure 8 B, columns 6 and 7 at 10,000 years, by which time equilibrium had been reached. Obviously, 1.00009×10^{-4} M $\approx 1.00008 \times 10^{-4}$ M; i.e., very little Gly was consumed.

We can compare this to our assumption throughout this paper that $[Gly]_i \approx [Gly]_{eq}$. Beginning the simulation with $[Gly]_i = 1 \times 10^{-4}$ M led to, after 10,000 years: $[Gly]_{eq} = 0.999991 \times 10^{-4}$ M, which is essentially $\approx 1 \times 10^{-4}$ M; and $[Gly_2]_{eq} = 2.49495 \times 10^{-11}$ M, which is essentially at $\approx 2.5 \times 10^{-11}$ M, as shown in figure 8 B, columns 4 and 5. Clearly the assumption $[Gly]_i \approx [Gly]_{eq}$ is justified.

Appendix 3. Rate of buildup of Gly_3 to Gly_9 under moderate temperature

We calculated the concentrations of $[Gly_n]$ over time, where $n > 2$ is the number of residues in a peptide, until equilibrium has been reached, beginning from time zero (t_0) over discrete intervals t_1, t_2, etc. The logic is similar to that used in Appendix 2, but with some simplifications, so we will call this the 'Customized Algorithm II'.

Since the concentration of $[Gly_n]$ formed and hydrolyzed are so many orders of magnitude lower than the initial Gly concentration $[Gly]_{i,\,t=0}$, the concentration of Gly_i at the beginning of each time interval was treated as invariant when $n \geq 3$.

For each time = t the following calculations were performed:

- $[Gly_n]_i = [Gly_n]_f$ from the end of the preceding time interval plus the amount produced by condensation: $[Gly_n]_i = [Gly_n]_{f,\,(t-1)} + k_{con} \times [Gly]_{f,\,(t-1)} \times [Gly_2]_i$
- $[Gly_n]_{lost}$ is the amount lost due to hydrolysis: $[Gly_n]_{lost} = k_{hyd} \times [Gly_n]_i$
- $[Gly_n]_f = [Gly_n]_i - [Gly_n]_{lost}$.

The amount of Gly_{n-1} replenished through hydrolyzation of Gly_n was neglected when $n \geq 3$, since $[Gly_{n-1}]$ is about 10^6 times greater than $[Gly_n]$. The effect on [Gly] from hydrolysis is even less than that, and therefore also neglected.

The condensation process $Gly_2 + Gly \rightarrow Gly_3$ can be simulated by analyzing a long series of short time intervals. We used $k_{hyd13} = 2 \times 10^{-2}\ yr^{-1}mol^{-1}$ and $k_{con13} = 4 \times 10^{-4}\ yr^{-1}mol^{-1}$ from eqns 16 and 17 also for peptides Gly_4 to Gly_9. The reason is that the reaction profiles will be so similar, as shown in figure 5 for $Gly_3 \leftrightarrows Gly_2$ and $Gly_4 \leftrightarrows Gly_3$. At moderate temperatures, the internal amide bonds would be less reactive than the two end ones, so the greater number of hydrolyzable positions in larger peptides should not have much of an effect.

As a test for the accuracy of the algorithm and assumptions, we checked the mass balance for all glycine-containing molecules equilibrating with nonaglycine. The initial $[Gly]_{i,\,t=0}$ (i.e., 10^{-4} M) must be accounted for by all the molecules it is present in. After *t* intervals, the Gly molecules will be distributed as: $[\text{total Gly}] = [Gly]_f + 2[Gly_2]_f + 3[Gly_3]_f + 4[Gly_4]_f + 5[Gly_5]_f + 6[Gly_6]_f + [Gly_7]_f + 8[Gly_8]_f + 9[Gly_9]_f$.

The fraction discrepancy is given by: $([Gly]_{i,\,t=0} - [\text{Total Gly}]) / [Gly]_{i,\,t=0}$.

After 5,000 intervals, the fraction discrepancy was found to be $< 1.6 \times 10^{-12}$, and after 20,000 intervals $\approx 1.7 \times 10^{-12}$. The data for these calculations are available in file Supplementary Material II, sheet 'Gly2–9', columns 'AN' and 'AO'.

As mentioned in the main text, even a sizeable error in our estimate of k_{con} and k_{hyd} would not change any of the conclusions in this paper as long as k_{hyd} / k_{con} reflects the correct K_{hyd}. The value of K_{hyd11} determines the final $[Gly_n]_{eq}$ of all the peptides. We show in the Supplementary Material 6 file the effects of increasing and decreasing k_{hyd} by a factor of 5, see figure III and figure IV. The calculated data are available in Supplementary Material 7. Buildup simulations show that initially $[Gly_3]$ will increase much more rapidly for larger k_{con} values and vice versa. This is expected, since hydrolysis will hardly matter until the peptide has first built up. This effect is propagated for each $n + 1$–size peptide. Nevertheless, within the accuracy of the algorithm, the same $[Gly_9]_{eq} \approx 3 \times 10^{-51}$ M was obtained within 5,000 years.

References

1. McCombs, C. and Truman, R., Insignificant concentrations of peptides formed in water—part 1. Using hot temperatures or high pH, in press.
2. Fried, S.D., Fujishima, K., Makarov, M., Cherepashuk, I., and Hlouchova, K., Peptides before and during the nucleotide world: an origins story emphasizing cooperation between proteins and nucleic acids, *J. R. Soc. Interface* **19**:20210641, 2022 | doi:10.1098/rsif.2021.0641.
3. Maury, C.P.J., Liljeström, M., and Zhao, F., Was the first molecular replicator on the primitive Earth an informational amyloid? EGGSVVAAD, a prebiotically plausible peptide, spontaneously forms amyloid assemblies, *J. Biol. Res.* **18:**332–335, 2012.
4. Martin, R.B., Free energies and equilibria of peptide bond hydrolysis and formation, *Biopolymers* **45**:351–353, 1998 | doi:10.1002/(SICI)1097-0282(19980415)45:5<351::AID-BIP3>3.0.CO;2-K.
5. Lemke, K.H., Rosenbauer, R.J., and Bird, D.K., Peptide synthesis in early Earth hydrothermal systems, *Astrobiology* **9**(2):141–146, 2009 | doi:10.1089/ast.2008.0166.
6. Faisal, M., Daimon, H., and Fujie, K., Hydrolysis of glycylglycine in subcritical water conditions, *J. Phys. Conf. Ser.* **121**:082002, 2008 | doi:10.1088/1742-6596/121/8/082002.
7. Sato, N., Daimon, H., and Fujie, K., Decomposition of glycine in high temperature and high pressure water, *Kagaku Kogaku Ronbunshu* **28**(1):113–117, 2002 | doi:10.1252/kakoronbunshu.28.113.
8. Steinhardt, J. and Reynolds, J.A., *Multiple Equilibria in Proteins*, Academic Press, New York, pp. 176–221, 1969.
9. Szőri, M., Jójárt, B., Izsák, R., Szőri, K., Csizmadiaad, I.G., and Viskolcz, B., Chemical evolution of biomolecule building blocks. Can thermodynamics explain the accumulation of glycine in the prebiotic ocean? *Physical Chemistry Chemical Physics* **13**(16):7449–7458, 2011 | doi:10.1039/c0cp02687e.
10. Bada, J.L., Amino acid cosmogeochemistry, *Phil. Trans. R. Soc. Lond. B* **333**:349–358, 1991 | doi:10.1098/rstb.1991.0084.
11. Stribling, R. and Miller, S.L., Energy yields for hydrogen cyanide and formaldehyde syntheses: The hcn and amino acid concentrations in the primitive ocean, *Orig. Life Evol. Biosph.* **17**:261–273, 1987 | doi:10.1007/BF02386466.
12. Lazcano, A. and Miller, S.L., The origin and early evolution of life: prebiotic chemistry, the pre-RNA world, and time, *Cell* **85**(6):793–798, 1996 | doi:10.1016/S0092-8674(00)81263-5.
13. Truong, N., Monroe, A.A., Glein, C.R., Anbar, A.D., and Lunine, J.I., Decomposition of amino acids in water with application to in-situ measurements of Enceladus, Europa and other hydrothermally active icy ocean worlds, *Icarus* **329**:140–147, 2019 | doi:10.1016/j.icarus.2019.04.009.
14. Holm, N.G. and Anderson, E.M., Hydrothermal systems; in: Brock, E. (Ed.), *The Molecular Origins of Life*, Cambridge University Press, Cambridge, pp. 86–99, 1998.
15. Martin, W., Baross, J., Kelley, D. *et al.*, Hydrothermal vents and the origin of life, *Nat. Rev. Microbiol.* **6**:805–814, 2008 | doi:10.1038/nrmicro1991.
16. Wagner, A., Arrival of the fittest: solving evolution's greatest puzzle, OneWorld, 2015. See p. 51.

17. Kobayashi, K., Ise, J.-i., Aoki, R., Kinoshita, M., Naito, K., Udo, T., Kunwar, B., Takahashi, J.-i., Shibata, H., Mita, H., *et al*., Formation of amino acids and carboxylic acids in weakly reducing planetary atmospheres by solar energetic particles from the young sun, *Life* **13**:1103, 2023 | doi:10.3390/life13051103.
18. Delsemme, A.H., Cosmic origin of the biosphere; in: Brock, E. (Ed.), *The Molecular Origins of Life*, Cambridge University Press, Cambridge, pp. 100–119, 1998.
19. We can calculate values for [Gly] and [Gly_2] for the equilibrium 2 Gly ⇆ Gly_2. Define G = $[Gly]_{eq}$ and D = $[Gly_2]_{eq}$. $K_{con11} = 1/400 = D/G^2$; but also $G + 2D = 10^{-4}$ M, since total glycine must be conserved. We solve $G + 2D = G + 2(G^2/400) = G + (G^2/400) = 10^{-4}$ M. Using the quadratic formula gives $G = 0.999995 \times 10^{-4}$ M, almost identical to 10^{-4}. We then solve $D = K_{con11}(G^2) = 2.4999975 \times 10^{-11}$, almost identical to 2.5×10^{-11}. Therefore, $[Gly]_i$ is almost identical to $[Gly]_{eq}$.
20. Total number of Gly_9 = L in ocean × Nr. oceans × Molarity Gly_9 × molecules / mol; $(1.310^{21}) \times (400{,}000) \times (3 \times 10^{-51}) \times (6 \times 10^{23}) = 0.94$.
21. Thaxton, C.B., Bradley, W.L., and Olsen, R.L., *The Mystery of Life's Origin: Reassessing current theories*, Lewis and Stanley, 1992.
22. Radzicka, A. and Wolfenden, R., Rates of uncatalyzed peptide bond hydrolysis in neutral solution and the transition state affinities of proteases, *J. Amer. Chem. Soc.* **118**(26):6105–6109, 1996 | doi:10.1021/ja954077c.
23. Imai, E.-I., Honda, H., Hatori, K., Brack, A., and Matsuno, K., Elongation of oligopeptides in a simulated submarine hydrothermal system, *Science* **283**:831–833, 1999.
24. Sakata, K., Kitadai, N., and Yokoyama, T., Effects of pH and temperature on dimerization rate of glycine: Evaluation of favorable environmental conditions for chemical evolution of life, *Geochimica et Cosmochimica Acta* **74**(23):6841–6851, 2010 | doi:10.1016/j.gca.2010.08.032.
25. See extensive references in: Brigiano, F.S., Gierada, M., Tielens, F., and Pietrucci, F., Mechanism and free-energy landscape of peptide bond formation at the silica−water interface, *ACS Catal.* **12**:2821−2830, 2022 | doi:10.1021/acscatal.1c05635.
26. Arguably the best example of using condensing reagent to form peptides was reported by Greenwald, Friedmann, and Riek.

    Greenwald, J, Friedmann, M.P., and Riek, R., Amyloid aggregates arise from amino acid condensations under prebiotic conditions, *Angew. Chem. Int. Ed.* **55**(38):11609–11611, 2016 | doi:10.1002/anie.201605321.

    1 mM Ala was mixed with 50 nm borate buffer at pH 9.2 (!) with a stirring bar. A large molar excess of the volcanic gas carbonyl sulfide (COS), many orders of magnitude more concentrated than conceivable prebiotically, was forced into the solution under pressure, leading to a reactive thiocarbamate. In a *separate* spatial temporal reaction, the activated AA was added dropwise to a solution of 1 M potassium ferricyanide ($K_3Fe(CN)_6$), leading to Ala_n, $n = 2 – 6$. This can hardly be considered a prebiotically plausible experiment.

    In a second reaction, 2 M Gly, 1 M Ala, 0.5 M Asp and 0.33 M Val were mixed and then activated with carbonyldiimidazole (CDI) on ice. However, the authors admitted that CDI cannot be considered a realistic prebiotic activating agent.
27. Tan, C.L., Facts cannot be ignored when considering the origin of life #1: the necessity of bio-monomers not to self-link for the existence of living organisms, ARJ **15**:25–29, 2022.
28. Lasaga, A.C., Holland, H.D., and Dwyer, M.J., Primordial oil slick, *Science* **174**:53–55, 1971 | doi:10.1126/science.174.4004.
29. Kasting, J.F., Stability of ammonia in the primitive terrestrial atmosphere, *J. Geophys. Res.* **87**:3091–3098, 1982 | doi:10.1029/JC087iC04p03091.
30. Matsui, T. and Abe, Y., Evolution of an impact-induced atmosphere and magma ocean on the accreting earth, *Nature* **319**:303–305, 1986 | doi:10.1038/319303a0.
31. Matsui, T., and Abe, Y., Impact-induced atmospheres and oceans on Earth and Venus, *Nature* **322**:526–528, 1986 | doi:10.1038/322526a0.
32. Kasting, J.M., Bolide impacts and the oxidation state of carbon in the earth's early atmosphere, *Orig. Life Evol. Biosph.* **20**:199–231, 1990 | doi:10.1007/BF01808105.
33. Catling, D.C. and Casting, J.F., *Atmospheric Evolution on Inhabited and Lifeless Worlds*, Cambridge University Press, Cambridge, UK, 2017.
34. Miller, S.L. and Urey, H.C., Organic compound synthesis on the primitive earth, *Science* **130**:245–251, 1959 | doi:10.1126/science.130.3370.2.
35. Schlesinger, G. and Miller, S.L., Prebiotic synthesis in atmospheres containing CH4, CO, and CO2: I. amino acids, *J. Mol. Evol.* **19**:376–382, 1983 | doi:10.1007/BF02101642.
36. Schlesinger, G. and Miller, S.L., Prebiotic synthesis in atmospheres containing CH4, CO, and CO2: II hydrogen cyanide, formaldehyde, and ammonia, *J. Mol. Evol.* **19**:383–390, 1983 | doi:10.1007/BF02101643.
37. Stribling, R. and Miller, S.L., Energy yields for hydrogen cyanide and formaldehyde syntheses: The HCN and amino acid concentrations in the primitive ocean, *J. Mol. Evol.* **17**:261–273, 1987 | doi:10.1007/BF02386466.
38. Catling, D. and Zahnle, K., The Archean atmosphere, *Sci. Adv.* **6**:eaax1420, 2020 | doi:10.1126/sciadv.aax1420.
39. Press, W.H., Flannery, B.P., Teukolsky, S.A., and Vetterling, W.T., 'Runge-Kutta Method' and 'Adaptive Step Size Control for Runge-Kutta', §16.1 and 16.2 in *Numerical Recipes in FORTRAN*: *The art of scientific computing*, Cambridge University Press, Cambridge, pp. 704–716, 1992.

__Royal Truman__ has bachelor's degrees in chemistry and in computer science from State University of New York; an M.B.A. from the University of Michigan (Ann Arbor); a Ph.D. in organic chemistry from Michigan State University; and a two-year post-graduate 'Fortbildung' in bioinformatics from the Universities of Mannheim and Heidelberg. He works in Germany for a European-based multinational.

__Change Tan__ received a B.S. in chemistry from Hunan Normal University, an M.S. in organic chemistry from Nan Kai University, a Ph.D. in biochemistry from the University of Pennsylvania, and completed postdoctoral training in genetics at Harvard Medical School. She worked as an assistant and later an associate professor of biological sciences at the University of Missouri from 2005 to 2021. Her research interests include genetics, developmental biology, molecular biology, origin of life, and origin of biodiversity. She teaches molecular biology, signal transduction, and general biology to graduate and undergraduate students.

__Charles McCombs__ has a bachelor's degree in chemistry from California State University of Long Beach (1973) and a Ph.D. degree in Organic Chemistry from UCLA (1978). He worked for Tennessee Eastman Company for 21 years as a research chemist, receiving 20 patents. He and his wife started Genesis Christian Academy in Englewood, Florida, and he is currently President of Genesis Ministries Inc., and President and Professor of Creation Studies at SouthWest Florida Bible Institute.

Instructions to Authors

JOURNAL OF CREATION is dedicated to upholding the authority of the 66 books of the Bible, especially in the area of origins. All our editors adhere to the *Creation Ministries International* (CMI) Statement of Faith and most papers will be designed to support this. Rarely, other papers may be accepted for publication on merit so that certain issues can be clarified. The views expressed in the papers are those of the authors and not necessarily those of CMI.

Because the scope of this journal is broad, we welcome articles on any topic that is relevant to biblical creation. This includes the sciences such as geology, chemistry, biology, astronomy, etc., and also archaeology, theology, hermeneutics, biblical history, geography, linguistics, ethics and society, philosophy, law, etc. Potential authors should familiarise themselves with the journal and its position and style before submitting articles. Authors should also indicate if their manuscript has been submitted elsewhere, address previous articles on the topic, and ensure the work of others is properly acknowledged.

Word length: Shorter articles are more likely to be read so preference will be given to publishing them. All articles, including letters, may be edited for brevity and clarity. Perspectives: 1,000–2,000 words; Book reviews: 1,500–3,000 words, but please enquire first. You may be asked to scan the cover of the book; Letters to the editor: 1,000 words. We will publish critical letters on articles already published, but a reply will usually follow the criticism; Papers, Overviews, Countering the Critics, Viewpoints and Essays: <5,000 words.

Articles must be written clearly and concisely and should be focused on only one topic/subject. The most readable articles are those with an average sentence length of about 17 words, with one idea per sentence. Do not use too many big or extra words such as “in spite of the fact that” when “although” would do. Please use first person sparingly and do not use “this present writer”, which is verbose, false modesty, and ambiguous. Care with spelling is crucial, and British spelling generally applies. Personal invective or similar comments against others are not acceptable.

Specialist technical terms and abbreviations should be defined the first time they are used. If many technical terms are used, these should be included in a glossary. SI units should be used in scientific papers.

Abstract: All articles except Perspectives, Letters and Book Reviews should be preceded by an Abstract, which should not exceed 200 words and must be without abbreviations and reference citations. The Abstract should summarise the key points of the paper and be comprehensible to readers before they have read the paper.

References should be indicated in the main text by superscript numbers in sequence and then listed in numerical order at the end of the text (End Notes). Full details of all references are required, including all authors and their initials, the full title of the paper or book, the full title of the journal or its accepted abbreviation, the volume number, the page number(s), the editor(s) of the book or proceedings (if applicable), the publishers and place of publication (in the case of a book), and the year of publication. If a citation is repeated, then the same superscript number should be used (a cross reference).

Quotes must be verbatim, with omissions clearly shown by ellipsis (…). Even erroneous grammar and spelling in the original must be reproduced, and indicated by [sic]. Any additions or explanations within a quote need to be placed in square brackets [ ]. Primary sources are preferred, but if a secondary source must be used, the reference format must be [primary source], as cited in [secondary source]. For internet URLs the date last downloaded should be included.

Tables should be embedded in a Microsoft Word document, with brief, self-explanatory titles, and captions if an explanation is essential to understanding the table. Tables should be numbered according to their sequence in the text and all should be referred to in the text, e.g. (see table 1).

Graphics should be supplied electronically on CD or by email to journal@creation.com as 300dpi *.TIF, *.EPS, *.PSD, *.AI, *.JPG, *.PDF or *.BMP files, not embedded into a document file. They can be sent in colour (preferred) or greyscale. Graphics should have a minimum size of 1024 x 768 pixels.

Figures should be numbered according to their sequence in the text. References should be made in the text to each figure. In planning images and figures, the page format and column widths of the journal should be kept in mind and should allow for the possibility of reduction. Each illustration should have a self-explanatory caption. The captions should be collected together at the end of the article document file. If graphics are not provided with a manuscript, authors may be asked to submit suggestions and possible sources of non-restricted material.

Copyright ownership for each and every graphic must be specified and any relevant permissions and or credit requirements given in writing. If you are not the copyright owner, please supply written permission (preferably with an original signature) from the copyright owner. If you are the copyright owner, your submission of a graphic will be taken to grant us permission to use the image in the journal and also any other publications or on our website, unless you specify otherwise.

Biography: Papers, Overviews, Countering the Critics, Forums, Viewpoints, Research Notes and Essays should include a biography of no more than 100 words for each author. It should include the authors’ qualifications and experience, and involvement in creationist work.

Please also:

- send documents in Rich Text (*.rtf) or Word (*.doc) format, not Publisher (*.pub) format. Excel (*.xls) is also acceptable for complicated tables.
- type left-justified without hyphenation except for compound words
- input text continuously; only insert hard returns at the end of sections, lists, etc.
- use single spaces after each sentence within a paragraph
- use Times New Roman 10.5 font and use the word processing formatting features to indicate bold, italics, Greek, Hebrew, maths, superscript and subscript characters
- submit complex mathematical formulas or equations using MathType according to the guidelines in our “Equations layout guide”, which can be obtained by contacting us
- insert captions for graphics at the end of your manuscript
- type references in the correct order and style of the journal using the word processing “Endnotes” and “Cross-references” features to link references to the text correctly.

Photographs and/or CDs may be sent to:journal@creation.com

The Editor,
Journal of Creation
Creation Ministries International
P.O. Box 4545
Eight Mile Plains QLD 4113
AUSTRALIA

NOTE: Papers prepared according to these instructions are more likely to be considered.

<©iStockphoto.com/Imagez>

Creationist research NEEDS YOU

Christians need to keep on providing scientific answers within a biblical framework, and refining our case (including exposing whatever flaws there may be in old arguments). We also need to be ready to respond to challenges by critics.

Faith-funded creationist ministries like *Creation Ministries International* (CMI) can only do so much, not having access to taxpayer dollars.

Creationist membership societies with hundreds of scientist members are encouraging by their very existence. But they are usually just as hampered by funding constraints, and would dearly love more of their members to get involved in actively helping the creationist model.

We have many qualified scientists and other educated professionals on our mailing lists, and we would like to encourage more of you to each give just a little bit of spare time to creation research issues.

GETTING INFORMED

Start by getting as informed as possible through the existing literature. CMI can provide up-to-date catalogues.

JOINING THE NETWORK

Consider researching a particular area with a view to producing a paper. *Journal of Creation* is a great place to air it. CMI is more than willing to provide refereeing through our contacts. If you are concerned that publishing in a creationist journal might affect your employment, for example, a pseudonym may be acceptable. If you are keen to write, see our instructions to authors opposite.

Remember that the creation/evolution issue is often not so much about *facts* as about their *interpretation*. Often the research results produced by secular institutions operating within an evolutionary framework can be just as useful in providing answers for creationists—it just needs someone to go to the trouble of working it through. We can provide some guidance about how you can draw your research into a suitable paper.

NO CONTRIBUTION TOO SMALL

Even producing a brief Perspective item on a specialist area, if it will teach and inform *Journal of Creation* readers, and enable them to share with others, is a worthwhile contribution.

AND FINALLY …

You might want to consider a donation earmarked specifically for creationist research. If so, you could direct it to any of the CMI offices listed at the front of this journal. Such donations may be tax deductible in certain countries.

CREATION MINISTRIES INTERNATIONAL
CREATION.com

THE FAMILY COMPANION TO
JOURNAL OF CREATION

CREATION
magazine

IN A WORLD FLOODED WITH ANTI-CHRISTIAN MEDIA, it's nice to come home to a publication that upholds the truth of God's Word ... all the way from Genesis. Packed full of fascinating articles and beautiful full-colour photography. Creation appeals to both young and old.

Enjoy subjects ranging from the wonders of nature to creation/evolution, archaeology and practical Christian living.

Special children's section sure to interest your younger family members.

Join subscribers across the globe and let *Creation* magazine be your family's life-changing experience too!

// 56
PAGES OF FULL
COLOUR
[NO PAID ADVERTISING]

Subscribe via CREATION.com, mail or phone
(see inside front cover for contact details).

ISSN 1036-2916