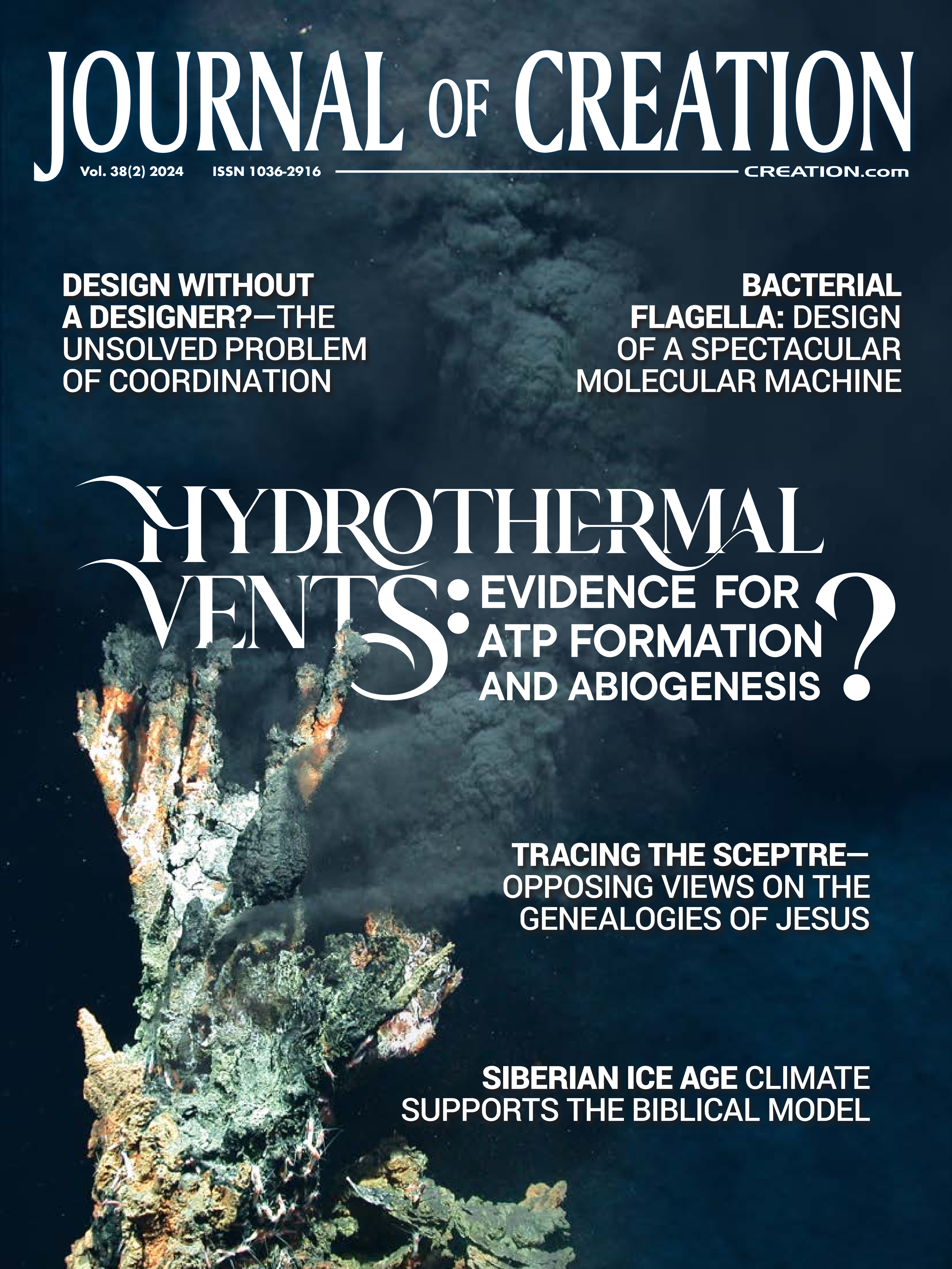
JOURNAL OF CREATION

Vol. 38(2) 2024 ISSN 1036-2916 CREATION.com



DESIGN WITHOUT A DESIGNER?—THE UNSOLVED PROBLEM OF COORDINATION

BACTERIAL FLAGELLA: DESIGN OF A SPECTACULAR MOLECULAR MACHINE

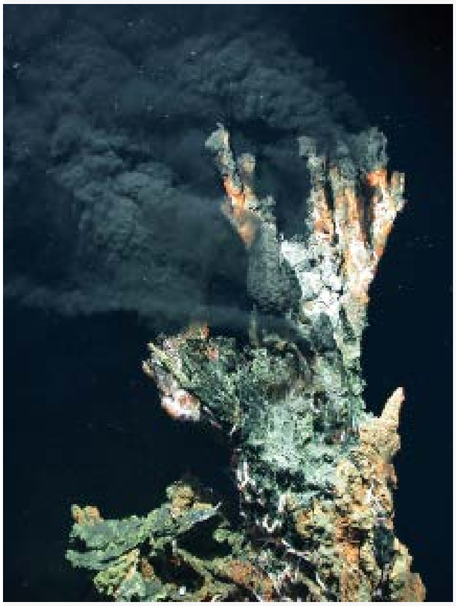
HYDROTHERMAL VENTS: EVIDENCE FOR ATP FORMATION AND ABIOGENESIS?

TRACING THE SCEPTRE—OPPOSING VIEWS ON THE GENEALOGIES OF JESUS

SIBERIAN ICE AGE CLIMATE SUPPORTS THE BIBLICAL MODEL

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: 'Candelabra' black smoker located 3,300 m deep in the Logatchev Hydrothermal Field on the Mid-Atlantic Ridge

IMAGE: © MARUM (University of Bremen), CC-BY-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

CREATION.com

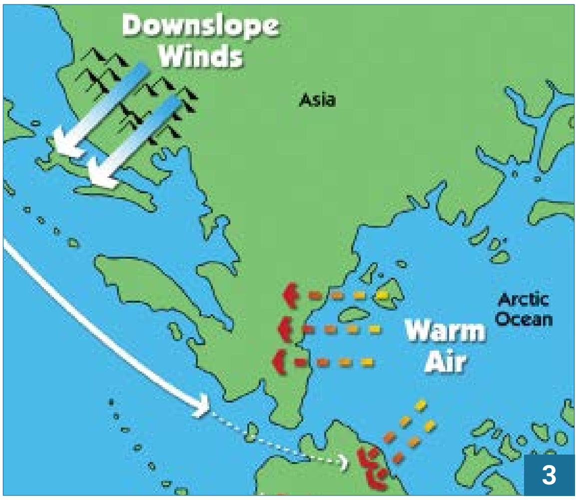
Printed in Australia
Published by:
Creation Ministries International Ltd
ABN 31 010 120 304

CREATION MINISTRIES INTERNATIONAL
Worldwide Outreach

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

LETTERS

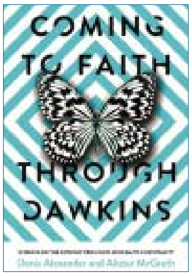


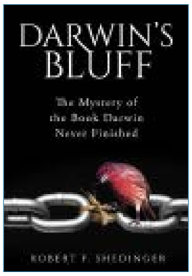
Did humans migrate and settle in Siberia during a period of harsh Ice Age climate?

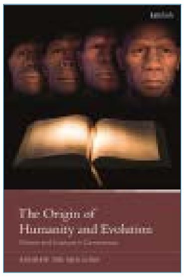
BOOK REVIEWS

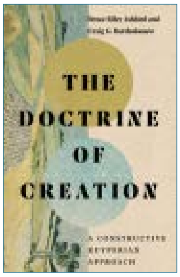
VIEWPOINT

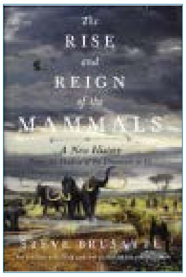
ESSAYS









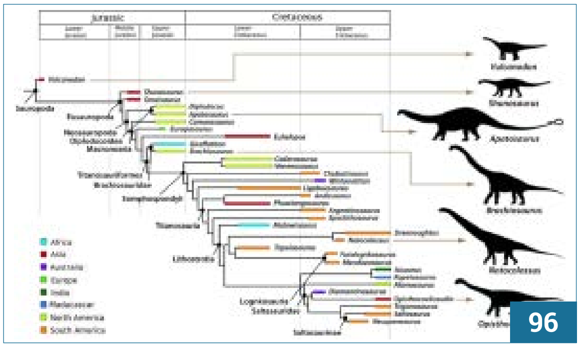


PAPERS

BONUS ARTICLES

78

Evidence for a seven-day week in the Ancient Near East.



96

Is Mendelian speciation consistent with a straightforward reading of Genesis and rapid speciation in a young earth?

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.

Siberian Ice Age climate supports the biblical model

Michael J. Oard

Uniformitarian scientists have conventionally predicted very cold temperatures, winter and summer, and low precipitation during their last ice age, including in Siberia. The paleoenvironment in Siberia would have been a polar desert:

> "Were the last glacial landscapes of Siberia treeless and sparsely vegetated and the climate colder all year round than at present, as suggested by some key reconstructions … and climate model simulations, or do these conventional views require adjustment and revision?"[1]

Tarasov *et al.* view the Ice Age climate during the Upper Paleolithic (UP) from 50,000–10,000 years differently than most other conventional scientists. They have macrofossils, the stomach contents of frozen animals, pollen cores from lakes, etc. to back up their claims.

Many more questions for uniformitarian scientists

Siberian researchers have produced many confusing interpretations with a growing number of questions:[2] "However, the list of questions has not become shorter and the gap between 'what do we know and what would we like to know' is far from being closed."[1] I also have many questions of the uniformitarian scenario, such as:

- Why would there be a grassland environment with a huge number and diversity of mammals?
- Why would humans migrate through the far north under very cold conditions 10–50 kyr ago as believed by conventional scientists?
- Why would some people settle in Siberia during the UP?
- Could the huge variety of animals, many of them now extinct or living farther south, have lived in Siberia during the paleoclimate and paleoenvironment envisioned by uniformitarian scientists?

These sorts of unanswered questions do not unilaterally overthrow the whole long-age approach to ice ages. However, in revealing potential inadequacies in their current climate models, they also help generate concept space for considering other interpretive frameworks, such as a biblical approach to ice age data.

Accurate 'ages' required

Part of uniformitarian scientists' problem is their 'dates'. Accurate dates are required in order to understand the history of events in Siberia, and if they are not correct, the secular history of events is also inaccurate:

> "Robustly dated continuous (or even semi-continuous) terrestrial proxy records, which represent environmental and climatic conditions of Northern Asia ca. 50–10 cal kyr BP, are rare. … The problems of generating such records [terrestrial proxy records], however, are manifold, including chronological control … significant technical challenges, financial considerations, labour and time investments necessary for sediment core recovery and detailed analysis."[3]

Based on their dates, Tarasov *et al.* showed other surprising climatic paradoxes, such as that the Mediterranean Sea area supposedly became depopulated during the Ice Age, while Siberia increased its population.[1] They asked, "Were the last glacial environments in Siberia less hostile to UP hunter-gatherers than those in the Mediterranean region?"[1] And their tentative solution to this question involved precise age determinations for climatic regimes:

> "The episode of further cooling and drying of the regional climate ca. 49–47.7 cal kyr BP … could have been a potential factor that triggered the movement of a part of the AMH population north-eastwards."[4]

Paleoenvironmental information contradicts uniformitarian climate models.

Uniformitarian climate simulations produce very cold winter and summer temperatures and dry conditions, with ice often over the lowlands of Siberia and Alaska. For instance, one model produced temperatures 20–40°C colder over the ice sheets than those areas today, with up to 20°C colder temperatures over large areas south of the ice sheets.[5]

However, the data on the ground in Siberia tell a different story, as indicated by Tarasov *et al*. A wealth of paleoenvironmental data is available for the UP in Siberia. Most of the proxy data show a huge number of diverse mammals that do not agree with the assumed very cold ice age paleoclimate:

> "However, the fossil animal records from the northern and southern regions [of Siberia] are in line with the botanical and aDNA [ancient DNA] records in *not* supporting desert environments in Northern Asia between 50 and 10 cal kyr BP [before present], not even during the LGM [Last Glacial Maximum]."[6]
>
> "The existence of such environments [ice free and well vegetated with a large number of animals] in Siberia particularly in its coldest northern regions, during the UP *cannot* be adequately explained by the still widely accepted 'year-round colder-than-present climate scenario' [emphasis added]."[6]

The number of animals has been compared to the enormous number of animals in the Serengeti of Africa:

Image: Andrey Giljov, Wikimedia / CC BY SA 4.0

Figure 1. The saiga antelope

> “We calculate, based on animal skeleton density in frozen soils of northern Siberia, that mammoth-steppe animal biomass and plant productivity, even in these coldest and driest of the planet’s grasslands were close to those of an African savanna.”[7]

For creation scientists, we can take the pollen data from two lakes[8] in a relative sense, since the deeper parts of the cores are older than the shallower parts. A core from southern Siberia shows mostly sagebrush and grass with more tree pollen toward the bottom and the top. Another core from central Siberia was dominated by grass and sedges throughout, with more tree pollen at the top. Many grass roots are found in the yedomas: “in yedoma numerous thin grass roots are preserved”.[9] This means that when the loess of the yedoma was being deposited, grass was growing.

It all adds up to the conditions suggested by Guthrie of the ‘mammoth steppe’.[10] Such an environment occurred over a wide area: “Their results confirm that large areas of Northern Asia presently occupied by boreal forests … were much more open.”[11]

Uniformitarian scientists attempt to claim such a grass environment was from a cold steppe and tundra climate, but the pollen data can be interpreted differently, for instance a mild steppe climate:

> “However, pollen-based temperature reconstructions for the glacial period are inconclusive, since herbaceous pollen taxa identified at the genus or family level have very broad bioclimatic tolerances and can be found in cold and warm climates.”[6]

Such a grassland with diverse mammals, as many as 40 species, required diverse types of ground vegetation.[12] Zimov *et* al. reinforce this conclusion and add that the soils were fertile.[7] Practically all the mammals were grazers, eating grass. Those that fed from a more swampy environment, such as reindeer and moose, did not arrive until the end of the Ice Age.[13] It was the end of the Ice Age when Siberia had a radical climate change at the Pleistocene/Holocene transition.[12] Many of the 40 types of animals indicated warmer conditions than today, especially in winter. Although there are local areas of grass in Siberia today, most of it is swampy. It is the permafrost that causes the swamps, and the grassland implies little or no permafrost early in the Ice Age, as expected within the biblical Ice Age model.[16,17]

One of the most tell-tale mammals is the Saiga antelope (figure 1) that is found in Siberian permafrost, as well as in unglaciated areas of Alaska and the Yukon territory, while today they inhabit the steppes of Kazakhstan and vicinity. The Saiga antelope has small hooves and cannot negotiate permafrost areas with bogs; this implies wide open, solid plains.

Humans supposedly migrated and settled in Siberia during the harshest Ice Age climate.

Scientists believe UP humans migrated to all continents 10–50 ka ago, when the climate was the harshest:

> “The Upper Palaeolithic (UP) period, broadly dated to between 50,000 and 10,000 years ago, is of particular interest … as it witnessed the climatically harshest and most variable part of the last glacial epoch … when AMH [anatomically modern humans] spread to all continents, with the exception of ice-covered Antarctica.”[14]

During the whole UP interval, humans continued to move and even settle in Siberia with the *greatest concentration at the LGM*, which is implausible given the conventionally assumed very cold and harsh desert paleoclimate and paleoenvironment.

> “This reconstruction [cold, desert paleoenvironment] shows hostile environments that are unsuitable for large herbivores, but also for human habitation during the entire MUP [Middle Upper Paleolithic 28/25–19/18 kyr BP] and, thus, contradicts

the recent archaeological site date for this interval."[15]

It does not seem feasible that humans would migrate through Siberia into Alaska and down the ice-free corridor of the Yukon Territory and Alberta, Canada, into the central United States during the very cold, polar desert uniformitarian ice age conditions. They certainly would not settle in Siberia.

Creation science model of the Ice Age

I have suggested a much different climate for the Ice Age from uniformitarian conceptions.[16,17] It would start out with mild winters, cooler summers, and much more precipitation early in the Ice Age caused by warm oceans from pole to pole and top to bottom and much Flood and post-Flood volcanism. Mild winters result from a warm ocean and the release of latent heat during condensation. This would probably be greatest during winter due to greater storm activity. The warmer the sea surface temperature, the greater the evaporation at mid and high latitudes compared to today. Volcanic aerosols in the stratosphere and volcanic ash on the ground would reflect a proportion of sunlight back to space, cooling the land, especially during summer. Minimal cooling would occur over the oceans because of its high heat capacity. Abundant mid- and high-latitude moisture would produce heavy snowstorms at high latitudes and certain mid-latitude areas. Heavy rain would occur over most non-glaciated land.

However, the post-Flood Ice Age climate was highly dynamic. As volcanism waned, summers would warm. Evaporation and conductive cooling would cool the oceans with time, causing less evaporation and precipitation. By the end of the Ice Age, winters would be much colder than those today, with warming summers and little precipitation. Little snow would be added to the ice sheets during the year, and summer temperatures would melt much ice. I have roughly estimated that the time for glacial maximum would be about 500 years, and the time to melt the ice sheets about 200 years for a post-Flood rapid Ice Age of roughly 700 years.

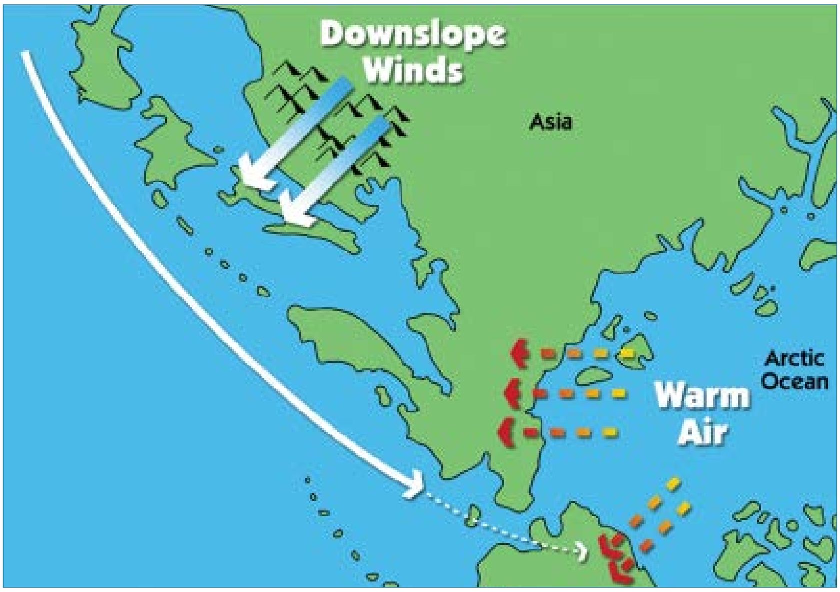


Figure 2. Map of Siberia and Alaska showing onshore flow of warm, moist air from the Arctic Ocean and the North Pacific. The long arrow off Asia represents a main storm track, becoming dashed into the Bering Sea as the track weakens. General downslope flow off the eastern Asian Mountains results in only mountain glaciation in eastern Asia. (From Oard, ref. 16, figure 14.2)

After the ice sheets melted, temperatures warmed in the early Holocene, melting some of the permafrost in places, forming a thermokarst terrain with hills (yedomas) and basins (alases), sometimes with lakes.[18]

Ice Age modelling

Gollmer has attempted to model ice sheet growth based on a warm ocean and various volcanic aerosol loading scenarios, using the Goddard Institute of Space Studies (GISS) model.[19–21] His model has progressed over the years, and the latest presentation was run out to 397 years with no initial Greenland and Antarctic ice sheets.[21] The average ocean temperature was set at 24°C, since he previously found that 30°C seemed too warm. The volcanic aerosol loading had a perpetual optical depth of 2.0, which means that only 1/5 of the solar radiation hits the earth's surface. The latest model was even further from creating an ice age in that the high latitude oceans cooled rapidly, with sea ice quickly forming and becoming extraordinarily thick. The many millions of animals in Siberia, Alaska, and the northwest Yukon Territory contradict this finding. Something seems wrong in the sea ice module. No land bridge is formed between Siberia and Alaska for animal migration. Ice thickness builds up to only 5 m, far from what occurred during the Ice Age.

Gollmer's model strongly shows the effect of the warm ocean, which, in his model, causes the continents to be too warm for glaciation. However, there seems to be a problem in his model with the initial condition of the volcanism. Nonetheless, it is very difficult to know what exactly to use for a volcanic initial condition. Only two modifications seem able to cause the higher continental latitudes to be cold enough to build the ice sheets: (1) a higher albedo (reflectivity) of snow, especially fresh snow; and (2) an increase of the albedo of the continents, since researchers discovered that volcanic ash on the ground is about as reflective as snow.[22] The initial aerosol optical depth can then be greatly reduced, so that more sunshine penetrates the surface but much of it is reflected back, which has the added benefit of not retarding photosynthesis. I look forward to more iterations of his model, which will undoubtedly change some of the aspects of my Ice Age model.

Where do the warmer summers fit in the biblical Ice Age?

The lake cores indicate the grass, sedges, and sagebrush paleoenvironment changed at the end of the Ice Age. More tree pollen shows up in southern Siberia based on the top of their pollen interval at 10 ka. The researchers do conclude:

> "This contradicts earlier reconstructions of very low summer temperatures (i.e., close to 0°C) during the last cold stage across the northern Siberian lowlands … . Using an indicator-species approach, Kienast *et al.* (2005) reconstructed mean July temperatures above 12°C for most of the last cold stage in the study area, where modern mean July temperatures are about 7°C."[4]

The uniformitarian time period of 10–50 kyr ago could apply to the middle and end of the post-Flood Ice Age. The animals would be especially numerous during the middle Ice Age but be dying out or migrating out of Siberia at the end of the Ice Age because of the winters becoming much colder than those today with the rapid increase in permafrost. Continents over the earth would have cooler summers during the early part of the Ice Age, but this would apply mainly to the interiors far from warm onshore flow from off the warm oceans. This could be the case with Siberia with warm onshore flow from the Arctic and north Pacific Oceans (figure 2).

Conclusions

Tarasov *et al.* have made a compelling case for a fundamental contradiction between conventional long-age ice age climate models and the paleoclimatic data in Siberia. Their climate models clearly need revision. However, the paleoclimate data they cite matches what we would expect from mid-to-late Ice Age conditions in the biblical framework.

References

1. Tarasov, P.E., Leipe, C., and Wagner, M., Environments during the spread of anatomically modern humans across Northern Asia 50–10 cal kyr BP: what do we know and what would we like to know? *Quaternary International* **596**:155–170, 2021; p. 156.
2. Tarasov *et al*., ref. 1, pp. 155–170.
3. Tarasov *et al*., ref. 1, p. 159.
4. Tarasov *et al*., ref. 1, p. 166.
5. Charbit, S., Ritz, C., Philippon, G., Peyaud, V., and Kageyama, M., Numerical reconstructions of the Northern Hemisphere ice sheets through the last glacial-interglacial cycle, *Climates of the Past* **3**:15–37, 2007.
6. Tarasov *et al*., ref. 1, p. 165.
7. Zimov, S.A., Zimov, N.S., Tikhonov, A.N., and Chapin III, F.S., Mammoth steppe: a high-productivity phenomenon, *Quaternary Science Reviews* **57**:26–45, 2012; p. 26.
8. Tarasov *et al*., ref. 1, p. 161.
9. Zimov *et al*., ref. 7, p. 43.
10. Guthrie, R.D., *Frozen Fauna of the Mammoth Steppe: The story of Blue Babe*, The University of Chicago Press, Chicago, IL, 1990.
11. Tarasov *et al*., ref. 1, p. 163.
12. Davydov, S., Davydova, A., Schelchkova, M., Makarevich, R., Fyodorov-Davydov, D., Loranty, M., and Boeskorov, G., Essential mineral nutrients of the high-latitude steppe vegetation and the herbivores of mammoth fauna, *Quaternary Science Reviews* **228**(106073):1–15, 2020.
13. Zimov *et al*., ref. 7, p. 27.
14. Tarasov *et al*., ref. 1, p. 155.
15. Tarasov *et al*., ref. 1, p. 160.
16. Oard, M.J., *Frozen in Time: Woolly mammoths, the Ice Age, and the biblical key to their secrets*, Master Books, Green Forest, AR, 2004.
17. Oard, M.J., *How Noah's Flood Caused a Single Ice Age*, Creation Book Publishers, Powder Springs, GA (in press).
18. Brosius, L.S., Walter Anthony, K.M., Treat, C.C., Lenz, J., Jones, M.C., Bret-Harte, M.S., and Grosse, G., Spatiotemporal patterns of northern lake formation since the Last Glacial Maximum, *Quaternary Science Reviews* **253**(106773):1–12, 2021.
19. Gollmer, S.M., Initial conditions for a post-Flood rapid Ice Age; in: Horstemeyer, M. (Ed.), *Proceedings of the Seventh International Conference on Creationism*, Creation Science Fellowship, Pittsburgh, PA, Article 18, 2013.
20. Gollmer, S.M., Effects of aerosol distribution on precipitation patterns needed for a rapid ice age; in: Whitmore, J.H. (Ed.), *Proceedings of the Eight International Conference on Creationism*, Creation Science Fellowship, Pittsburgh, PA, pp. 695–706, 2018.
21. Gollmer, S.M., A feasibility of a rapid Ice Age and transition to ice sheet growth; in: Whitmore, J.M. (Ed.), *Proceedings of the Ninth International Conference on Creationism*, Cedarville University, Cedarville, OH, pp. 267–279, 2023.
22. Jones, M.T., Sparks, R.S.J., and Valdes, P.J., The climatic impact of supervolcanic ash blankets, *Climate Dynamics* **29**:553–564, 2007.

Contamination of meteorite samples with terrestrial amino acids

Royal Truman and Chris Basel

Meteorites, the source of most extraterrestrial material, are believed to have provided a wide variety of proteinogenic amino acids (AA) according to Origin of Life researchers. The chemicals identified from fragments are listed, but, until recently, little or no effort has been dedicated to quantifying how much was due to terrestrial contamination, although contamination is considered to be inevitable.

In 2021, Glavin *et al.* analyzed three fragments from the Aguas Zarcas meteorite, which landed in Costa Rica in 2019 (*UA* samples, from the University of Arizona).[1] In addition, 10 g were extracted and ground to a powder from a single fragment of the Murchison meteorite, which had landed in Australia in 1969; individual portions (0.08 g and 1.0 g) were analyzed separately. The results, shown in table 1, provided insights about

Table 1. Nanomoles amino acid / g meteorite from Aguas Zarcas (UA) and Murchison (Mur.) meteorite fragments and soil samples from near the landing sites. Data extracted and reorganized from table 1 and 2 in Glavin *et al.* (2020).[1]

	Aguas Zarcas meteorite								**Murchison meteorite**					
Amino acid	**UA 2741 0.08 g** [1,2]		**UA 2741 0.5 g** [1,3]		**UA 2746 0.52 g** [1,3]		**UA soil** [1,3]		**Mur. 0.08 g**[1,2]		**Mur. 1 g** [1,3]		**Mur. soil** [4]	
	L	D	L	D	L	D	L	D	L	D	L	D	L	D
glycine	75		20		158		425		40		32		667	
alanine	18.4	3.7	3.5	1.6	38	17	213	74.3	3	2.2	8.2	8.3	356	47
glutamic acid	19.7	2.2	3.7	0.59	36	10.3	119	28	6.3	1.03	7.6	2.7	269	19
serine	18	3.4	1.5	0.3	6.6	1.9	91.3	16.9	3.5	0.13	0.6	0.4	199	15
threonine	14.8	0.01	28	0.2	56	0.7	107	4.2	2.21	0.02	0.32	0.17	0	0
aspartic acid	10.1	2.4	0.5	0.16	27	15.1	120	50	3	0.59	1.7	0.95	314	72
2-a-3-mba (valine isomer)	20.1	0.92	1.2	0.35	27	3.6	204	10	2.8	0.55	0.93	0.62	97	4
α-isovaline	5	4	3.5	2.8	3.9	2.9	0.1	0.1	11.8	10	11.5	9.5	0	0.1
α-aminoisobutyric acid (α-AIB)	4.6		5.6		52		1		11.4		10.4		0.1	
γ-amino-n-butyric acid + D,L-β-AIB	3.9		1.4		6		25.2		2.4		2		4.9	
β-alanine	3.4		0.9		10		26		6		16		8	
δ-5-apa	2.6		1		1.8		0.01		1.8		2.2		0	
γ-D,L-4-apa	2.1		0.8		0.7		0.01		2.9		0.9		0	
γ-D,L-4-a-2-mba	2.1		1		1.1		0.01		2.1		1.56		0	
D,L-α-amino-n-butyric acid	1.8		1.4		2.9		4		2		2.4		0.7	
β-3-a-3-mba	1.3		0.47		1		0.01		4.76		5.2		0	
α-norvaline (L-2-apa)	0.56	0.45	0.5	0.5	0.16	0.15	0.17	0.08	0.05	0.1	0.25	0.25	0	0
β-amino-n-butyric acid	0.26	0.33	0.19	0.19	0.3	0.34	0.6	0.48	1.6	1.8	1.2	1.2	0	6
β-3-a-2,2-dmpa	0.47	0.47	0.18		0.17		1		1.9		1.73		0	
ε-amino-n-caproic acid (EACA)	0.4		0.7		1.8		1.4		2.2		2.2		0	
γ-D,L-4-a-3-mba	0.31		0.06		0.04		0.01		0.42		0.07		0	
β-D,L-3-apa	0.27		0.6		0.9		0.5		2.7		2.5		0	
β-D,L-3-a-2-epa	0.1		0.1		0.1		0.1		0.3		0.3		0	
β-D,L- and allo-3-a-2-mba	0.04		0.8		1.4		0.01		0.29		0.3		0	

[1] Flame-sealed in a glass ampoule with water and extracted at 100°C for 24 h
[2] Hydrolysis using 6 M HCl at 150°C for 3 h
[3] Acid-hydrolysis under HCl vapour
[4] Unpublished analysis of soil 20–30 cm underground using LC-FD (high performance liquid chromatography with fluorescence detection) by Reid R. Keays from The University of Melbourne. Further details not provided.

Table 2. Based on data from table 1. The 'Total' columns sum the D- and L-enantiomers, and the 'Aver.' column is the average from the different samples from the same meteorite. The 'Prop.' column is the relative proportion compared to the total nmol of all AA.

	Aguas Zarcas meteorite										Murchinson meteorite								
	UA 2741 0.08 g^2		UA 2741 0.5 g^3		UA 2746 0.52 g			UA soil ^{1,3}			Mur. 0.08		Mur. 1 g			Mur. soil		
Amino acid	Total	Prop.	Total	Prop.	Total	Prop.	Aver.	Total	Prop.	Soil/ Aver.	Total	Prop.	Total	Prop.	Aver.	Total	Prop.	Soil/ Aver.
glycine	75	33.7%	20	23.7%	158	36.1%	84.3	425	27.9%	5.0	40	30.3%	32	23.5%	36.0	667	32.1%	18.5
alanine	22.1	9.92%	5.1	6.05%	55	12.6%	27.4	287	18.9%	10.5	5.2	3.94%	16.5	12.1%	10.9	403	19.4%	37.1
glutamic acid	21.9	9.83%	4.29	5.09%	46.3	10.6%	24.2	147	9.65%	6.1	7.33	5.56%	10.3	7.57%	8.8	288	13.9%	32.7
valine	21	9.44%	1.55	1.84%	30.6	6.99%	17.7	214	14.1%	12.1	3.35	2.54%	1.55	1.14%	2.5	101	4.86%	41.2
serine	21.4	9.61%	1.8	2.14%	8.5	1.94%	10.6	108	7.10%	10.2	3.63	2.75%	1	0.73%	2.3	214	10.3%	92.4
threonine	14.8	6.65%	28.2	33.5%	56.7	12.9%	33.2	111	7.30%	3.3	2.23	1.69%	0.49	0.36%	1.4	0	0.00%	—
aspartic acid	12.5	5.61%	0.66	0.78%	42.1	9.61%	18.4	170	11.2%	9.2	3.59	2.72%	2.65	1.95%	3.1	386	18.6%	123.7
Proteinogenic:	188.7	84.7%	61.6	73.1%	397	90.7%	215.8	1,464	96.0%	6.8	65.0	48.3%	64.0	46.8%	64.9	2,059	99.0%	
α-isovaline	9	4.04%	6.3	7.47%	6.8	1.55%	7.4	0.2	0.01%	0.03	21.8	16.5%	21	15.4%	21.4	0.1	0.00%	0.0
α-aminoisobutyric acid (α-AIB)	4.6	2.07%	5.6	6.64%	5.2	1.19%	5.1	1	0.07%	0.19	11.4	8.65%	10.4	7.64%	10.9	0.1	0.00%	0.0
γ-amino-n-butyric acid + D,L-β-AIB	3.9	1.75%	1.4	1.66%	6	1.37%	3.8	25.2	1.65%	6.69	2.4	1.82%	2	1.47%	2.2	4.9	0.24%	2.2
β-alanine	3.4	1.53%	0.9	1.07%	10	2.28%	4.8	26	1.71%	5.45	6	4.55%	16	11.8%	11	8	0.38%	0.7
δ-5-apa	2.6	1.17%	1	1.19%	1.8	0.41%	1.8	0.01	0.00%	0.01	1.8	1.37%	2.2	1.62%	2.0	0	0.00%	0.0
γ-D,L-4-apa	2.1	0.94%	0.8	0.95%	0.7	0.16%	1.2	0.01	0.00%	0.01	2.9	2.20%	0.9	0.66%	1.9	0	0.00%	0.0
γ-D,L-4-a-2-mba	2.1	0.94%	1	1.19%	1.1	0.25%	1.4	0.01	0.00%	0.01	2.1	1.59%	1.56	1.15%	1.8	0	0.00%	0.0
D,L-α-amino-n-butyric acid	1.8	0.81%	1.4	1.66%	2.9	0.66%	2.0	4	0.26%	1.97	2	1.52%	2.4	1.76%	2.2	0.7	0.03%	0.3
β-3-a-3-mba	1.3	0.58%	0.47	0.56%	1	0.23%	0.9	0.01	0.00%	0.01	4.76	3.61%	5.2	3.82%	5.0	0	0.00%	0.0
α-norvaline (L-2-apa)	1.01	0.45%	1	1.19%	0.31	0.07%	0.8	0.25	0.02%	0.32	0.15	0.11%	0.5	0.37%	0.3	0	0.00%	0.0
β-amino-n-butyric acid	0.59	0.26%	0.38	0.45%	0.64	0.15%	0.5	1.08	0.07%	2.01	3.4	2.58%	2.4	1.76%	2.9	6	0.29%	2.1
β-3-a-2,2-dmpa	0.47	0.21%	0.18	0.21%	0.17	0.04%	0.3	1	0.07%	3.66	1.9	1.44%	1.73	1.27%	1.8	0	0.00%	0.0
ε-amino-n-caproic acid (EACA)	0.4	0.18%	0.7	0.83%	1.8	0.41%	1.0	1.4	0.09%	1.45	2.2	1.67%	2.2	1.62%	2.2	0	0.00%	0.0
γ-D,L-4-a-3-mba	0.31	0.14%	0.06	0.07%	0.04	0.01%	0.1	0.01	0.00%	0.07	0.42	0.32%	0.07	0.05%	0.2	0	0.00%	0.0
β-D,L-3-apa	0.27	0.12%	0.6	0.71%	0.9	0.21%	0.6	0.5	0.03%	0.85	2.7	2.05%	2.5	1.84%	2.6	0	0.00%	0.0
β-D,L-3-a-2-epa	0.1	0.04%	0.1	0.12%	0.1	0.02%	0.1	0.1	0.01%	1.00	0.3	0.23%	0.3	0.22%	0.3	0	0.00%	0.0
β-D,L- and allo-3-a-2-mba	0.04	0.02%	0.8	0.95%	1.4	0.32%	0.7	0.01	0.00%	0.01	0.29	0.22%	0.3	0.22%	0.3	0	0.00%	0.0
Non-Proteinogenic:	34.0	15.3%	22.7	26.9%	41.0	9.3%	32.5	60.8	4.0%		70.0	50.5%	73.0	52.6%	69.1	19.8	0.95%	
Total:	223	100%	84.3	100%	438	100%	248	1,523	100%		132	100%	136	100%	134	2,079	100%	

contamination from soil but not from collection, storage, and/or handling of the samples.

As a rule, much or most AA identified in meteorites were not present as such but created through hydrolysis of carboxylic acid amides, hydroxy acid amides, lactams, carboxylactams, N-acetylamino acids, substituted hydantoins, and other chemicals from the meteorites.[1]

The laboratory processes of grinding the samples to a powder followed by high-temperature extraction with very acidic water would not have occurred naturally, but presumably hydrolysis may have occurred given enough time.

The data in table 1 often shows considerable variation for the same AA across the samples. Therefore, we

Table 3. Comparison of % L-enantiomer for amino acids obtained from Aguas Zarcas meteorite fragments (average value) and the nearby soil. Data were calculated from entries in table 1.

	UA 2741, 0.08 g			UA 2741, 0.5 g			UA 2746, 0.52 g				UA soil			Mur. 0.08			Mur. 1 g				Mur. soil		
Proteinogenic AA	L	D	% L	L	D	% L	L	D	% L	Aver. L	L	D	% L	L	D	% L	L	D	% L	Aver. L	L	D	% L
alanine	18.4	3.7	83.3%	3.5	1.6	68.6%	38	17	69.1%	73.7%	213	74.3	74.1%	3	2.2	57.7%	8.2	8.3	49.7%	53.7%	356	47	88.3%
glutamic acid	19.7	2.2	90.0%	3.7	0.59	86.2%	36	10.3	77.8%	84.7%	119	28	81.0%	6.3	1.03	85.9%	7.6	2.7	73.8%	79.9%	269	19	93.4%
valine	20.1	0.92	95.6%	1.2	0.35	77.4%	27	3.6	88.2%	87.1%	204	10	95.3%	2.8	0.55	83.6%	0.93	0.62	60.0%	71.8%	97	4	96.0%
serine	18	3.4	84.1%	1.5	0.3	83.3%	6.6	1.9	77.6%	81.7%	91.3	16.9	84.4%	3.5	0.13	96.4%	0.6	0.4	60.0%	78.2%	199	15	93.0%
threonine	14.8	0.01	99.9%	28	0.2	99.3%	56	0.7	98.8%	99.3%	107	4.2	96.2%	2.21	0.02	99.1%	0.32	0.17	65.3%	82.2%	0	0	–
aspartic	10.1	2.4	80.8%	0.5	0.16	75.8%	27	15.1	64.1%	73.6%	120	50	70.6%	3	0.59	83.6%	1.7	0.95	64.2%	73.9%	314	72	81.3%
Non-proteinogenic AA																							
α-isovaline	5	4	55.6%	3.5	2.8	55.6%	3.9	2.9	57.4%	56.2%	0.1	0.1	50.0%	11.8	10	54.1%	11.5	9.5	54.8%	54.4%	0	0.1	–
α-norvaline (L-2-apa)	0.56	0.45	55.4%	0.5	0.5	50.0%	0.16	0.15	51.6%	52.4%	0.17	0.08	68.0%	0.05	0.1	33.3%	0.25	0.25	50.0%	41.7%	0	0	–
β-amino-n-butyric acid	0.26	0.33	44.1%	0.19	0.19	50.0%	0.3	0.34	46.9%	47.0%	0.6	0.48	55.6%	1.6	1.8	47.1%	1.2	1.2	50.0%	48.5%	0	6	–

combined the L- and D-enantiomer concentrations to facilitate a comparison of relative concentrations, leading to the data shown in table 2.

The data in table 2 suggested to us a correlation between [proteinogenic AA] from soil and the fragments. We focused on the Aguas Zarcas data, since all the analyses had been performed by the same team and under very similar conditions. $[\text{AA}]_{\text{soil}}$ vs average $[\text{AA}]_{\text{meteorite}}$ for all cases where $[\text{AA}]_{\text{soil}} > [\text{AA}]_{\text{meteorite}}$ was plotted as shown in figure 1. A convincing correlation was found ($R^2 = 0.81$). Noteworthy from the regression equation is that the Y-intercept ≈ 0; i.e., when AAs were absent in the soil,

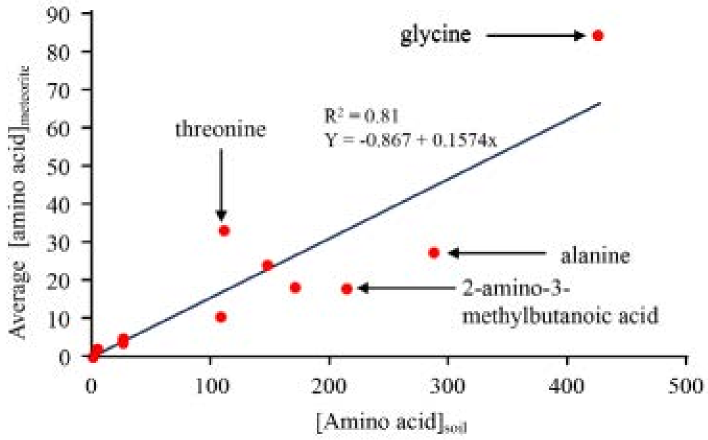


Figure 1. Concentration of AA (in nmol/g sample) in soil vs the average of three fragments from the Aguas Zarcas meteorite. Data from table 2.

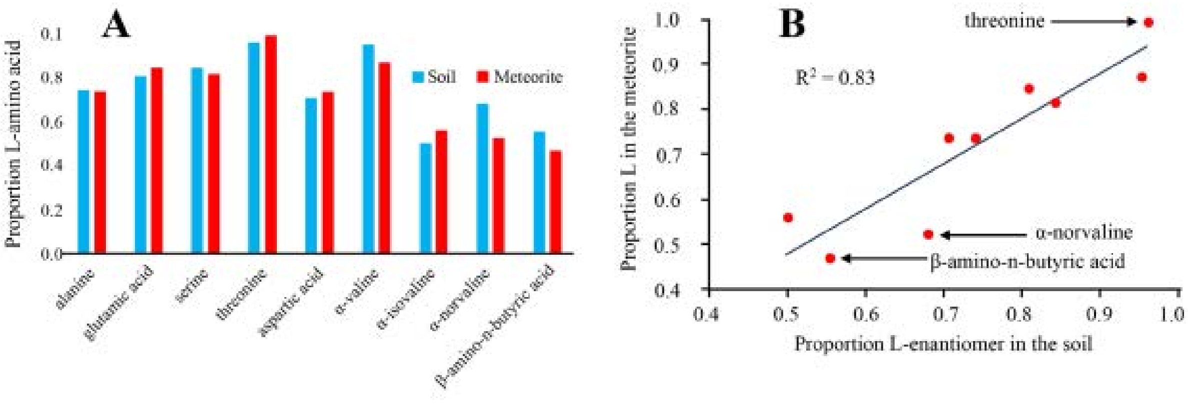


Figure 2. Comparison of proportion L-amino acid in Aguas Zarcas meteorite fragments (average value) vs from nearby soil. Data from table 3.

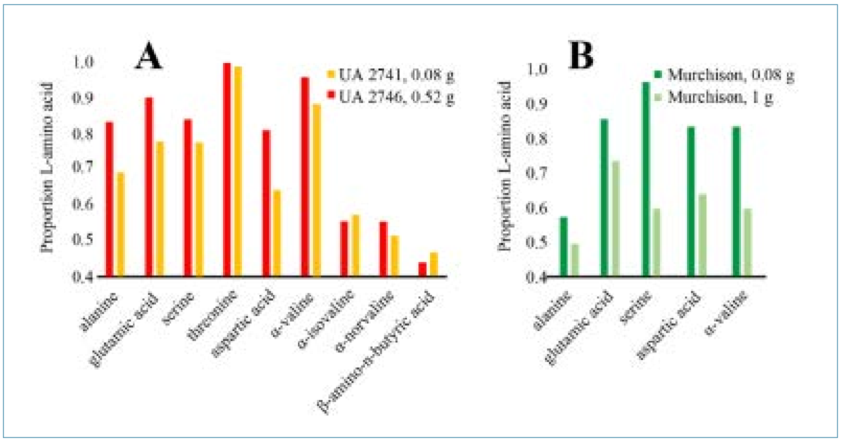


Figure 3. Comparison of A: % L-amino acids from two fragments from the Aguas Zarcas meteorite and B: both aliquots from the Murchison meteorite. Data taken from table 3.

almost none would have been found in the meteorite sample! *This suggested that very little AA would have been indigenous to the meteorite.*

Glycine, threonine, alanine and 2-amino-3-methylbutanoic acid were fairly distant from the correlation line but also had more than a 10-fold discrepancy in [AA] across the three samples.

The correlation might improve considerably if the average of several soil samples could be used, all *adjacent to the meteorite fragment analyzed*.

According to the data in table 2, the soil sample from the Murchison site contained about 33% more proteinogenic AA than the soil from the Aquas Zarcas site, whereas, on average, the Aquas Zargaes meteorite fragments contained >3 times more proteinogenic AA. Also noteworthy is that the two Murchison aliquots contained about the same total concentration of proteinogenic AA (62 vs 62.9 nmol/g), whereas for the Aguas Zarcas, they ranged from 60–367 nmol/g (columns 2, 4, and 6).

Major contamination could explain these observations: Aquas Zarcas in Costa Rica is a very humid region (unlike Murchison, Australia); much more AA could have dissolved and transferred to the meteorite fragments; for example, from morning dew. This would also explain why 4 of the 6 proteinogenic AA from the two Murchison aliquots had only 1.4–8.8 nmol/g on average, compared to 10.6–24.2 for the same AA for the three Aquas Zarcas fragments.

The concentrations of non-proteinogenic AA are very low in the meteorite and soil samples; usually ≤1 nmol/g in soil samples, as shown in table 1. β-alanine was the non-proteinogenic AA found in highest concentration in both soil samples (β-alanine is produced naturally by many organisms). Were the three UA meteorite samples contaminated? Perhaps, and to different degrees, since the concentrations measured varied from 0.9 to 10 nmol/g.

One way to test the plausibility that most of the AA was contamination from soil would be to compare % L-enantiomer from the fragments and soil. The data is shown in table 3 and plotted in figure 2.

A convincing correlation is apparent in figure 2-A and 2-B ($R^2 = 0.83$). Absent contamination, there is no apparent reason why excess L-AA manufactured biosynthetically would correlate so well with L-AA produced abiotically in space. Considerable contamination is the most parsimonious explanation. For example, the L-enantiomer for β-amino-n-butyric acid had a low mean value of 47% but a high mean value of >99.3% for threonine in the meteorite samples. The values measured in the soil sample (55.6% and 96.2%, respectively) matched these within experimental error.

In figure 3, the proportions of L-amino acids were compared for different fragments and aliquots. Systematic trends can be observed, where the L-enantiomer was almost always more abundant in the same sample. This could be explained by different amounts of contamination and also emphasizes a concern that the proportion of L-enantiomers could differ significantly between even nearby soil samples.

Analysis of $^{13}C/^{12}C$ isotope ratios

The proportion of ^{13}C and ^{12}C isotopes tends to be very different for terrestrial vs extra-terrestrial organic material, expressed as $\delta^{13}C$ values:

where

$\delta^{13}C$ is the reported value (e.g., –5‰ or –20‰; ‰ means parts per thousand),

R_{sample} is the $^{13}C/^{12}C$ ratio in the sample,

$R_{standard}$ is the $^{13}C/^{12}C$ ratio in the standard reference material, usually traceable to Vienna Pee Dee Belemnite (VPDB) for carbon isotopes.[2]

Typically, terrestrial organic carbon has a range of about –6‰ to –40‰ (Bowen 1988).[3]

Table 2 shows that about 6 times more proteinogenic AA was measured in UA 2746 than in the UA 2741 0.5 gm aliquot. Significantly, according to table 3 in reference 1, the $\delta^{13}C$ values of the proteinogenic AA examined in UA 2746 and nearby soil matched significantly, implying that most was due to contamination. However, the same proteinogenic AA from UA 2741 (which contained far less AA than in UA 2746) typically had high $\delta^{13}C$ values outside the range usually found on the earth, but their *L-enantiomers had lower $\delta^{13}C$ values*. Recalling that the concentration of L-enantiomers for these AA had been much higher than the D-enantiomers (table 2), and that very high L proportions had been found (table 3), all these facts strongly imply that much less (but still a significant amount of) contamination had occurred for the UA 2746 sample.

Take home messages

Glavin *et al.* also concluded that a considerable amount of contamination had occurred, especially for the Aguas Zarcas fragments, but did not provide an estimate of how much. In fact, plant material could clearly be seen attached to one of the fragments analyzed.

Very little terrestrial contamination from any sources would be necessary to account for a major fraction of the AA measured in meteorite samples. Using the data in table 2 and assuming a molecular weight of ≈ 100 for the proteinogenic AA shows that, on average, the Aguas Zarcas fragments contained only ≈ 20 ppm AA, and the Murchison fragments ≈ 6 ppm, by weight.

Soil samples include soluble racemizing peptide segments from dead organisms in addition to potentially very different living local biota. Proper quantification of contamination would require multiple soil samples to be collected as close as possible to each meteorite fragment. The average absolute and relative proportions of AA from the soils, their isotope ratios, and relative solubilities would need to be determined.

Although the Aguas Zarcas samples had been collected within days of landing and before rainfall, the data suggests that perhaps ≈ ⅒ of the moles of biological chemicals found (primarily proteinogenic AA) were extra-terrestrial. Alternatively, nonproteinogenic AA, like α-AIB and isovaline, were probably entirely extra-terrestrial. Since virtually all the literature reports AA from old meteorite landings, correcting for considerable amounts of contamination would:

- Eliminate all or most claims of extra-terrestrial excess of L-enantiomers.
- Decrease, significantly, the amount of proteinogenic AA delivered by meteorites.
- Raise, significantly, *the proportion of non-proteinogenic AA* delivered. Furthermore, hundreds of non-proteinogenic AA detected in Murchison samples have not been characterized yet[1] and would also have interfered with forming biological-like peptides.

References

1. Glavin, D.P., Elsila, J.E., McLain, H.L., Aponte, J.C., Parker, E.T., Dworking J.P., Hill, D.H., Connolly Jr, H.C., and Lauretta, D.S., Extraterrestrial amino acids and L-enantiomeric excesses in the CM2 carbonaceous chondrites Aguas Zarcas and Murchison, *Meteoritics & Planetary Science* **56**(1):148–173, 2021.
2. Fleisher, A.J., Yi, H., Srivastava, A., Polyansky, O.L., Zobov, N.F., and Hodges, J.T., Absolute 13C/12C isotope amount ratio for Vienna Pee Dee Belemnite from infrared absorption spectroscopy, *Nature Physics* **17**:10.1038/s41567-021-01226-y, 2021.
3. Bowen R., Isotopes in the biosphere; in: Bowen, R. (Ed.), *Isotopes in the Earth Sciences*, Kluwer, New York, pp. 452–469, 1988.

Unusual accumulation of dinosaurs in Italy better explained by Noah's Flood

Michael J. Oard

A herd of seven, and possibly up to eleven, dinosaurs has been discovered at a quarry in northeast Italy. The herd is believed to have been overwhelmed, buried, and fossilized together.[1] At least seven skeletons are articulated, the bones being connected or nearly so. This is one of the few locations where nearly complete hadrosaur skeletons have been found outside of North America. The dinosaurs were assigned to an existing genus and species previously named in 2009, *Tethyshadros insularis*.

Original uniformitarian interpretations

The hadrosaur species was once thought to have lived 67 Ma ago on an island, when Europe was believed to be a series of islands in the northwest Tethys Sea.[2] The species is believed to have come from Asia by island hopping. The date is based on foraminifera biostratigraphy, the stratigraphic framework of the karst plateau, and an alligatoroid fossil. The limestone is interpreted to be marine in origin.

The first individual of *Tethyshadros insularis* analyzed was considered fully grown with no juvenile features, but small for a hadrosaur, only 3.6 m long. Therefore, because it was believed to have lived on an island, researcher Dalla Vecchia thought it to be dwarfed. It is typical of the 'island rule' that large animals on islands become dwarfed, but small animals become larger.[3]

The dinosaurs were found in a lens of high-organic black limestone, 10 m thick and 70 m long. It was originally believed to have been deposited over a period of less than 10,000 years. Other organisms and organism products were fossilized at the same time as the dinosaurs and foraminifera: fish, small crocodilians, a flying reptile, several crustacean taxa, rare coprolites, pollen, and algae.[4]

Tethyshadros insularis has several peculiar features.[2] It was said to have anatomical features adapted to a cursorial (running) lifestyle, and, although judged a 'primitive' hadrosaur, it had a mix of 'primitive' and 'derived' (advanced) features; in other words, it is a mosaic.

To uniformitarian scientists, such articulated skeletons buried together suggest herding of dinosaurs and gregarious behaviour. Parallel dinosaur trackways suggest the same. Such an interpretation is simply based on the idea that evidence for past behaviour should be assumed to have occurred under normal conditions of life.

New research suggests different uniformitarian interpretations

New research has turned much of their earlier interpretation on its head. First, the researchers redated the dinosaur fossils to 80.5–81.5 Ma, 14 million years earlier, based again on foraminifera biostratigraphy. The other methods of dating must have been flawed as well. This was enough for the new paleoenvironment to be a continent and not a series of islands in Europe.

Second, researchers discovered that at least one of the seven new hadrosaurs was of normal size, so the species was no longer considered dwarfed. Despite the earlier analysis, the first small hadrosaur found earlier[2] was reinterpreted to be a young, immature dinosaur. Dalla Vecchia originally assumed the *Tethyshadros* specimen he described was an adult because some of the bones showed fusion. However, he did not cut open any bones to look at growth rings. Chiarenza *et al.*,[1] however, did exactly that and realized that the smaller specimens were not full-grown. Dalla Vecchia did use methods appropriate for 2009 to analyze a dinosaur skeleton's maturity. While he *could* have cut open the bones, that was impracticable for two reasons. First, it is a type specimen, which researchers prefer not to damage. Second, it was believed at the time that assessing skeletal fusion was a valid way to determine ontogenetic state in dinosaurs. Nonetheless, Della Vecchia was biased to think it was an island dwarf, since he assumed it was of Maastrichtian age (72.1 to 66 Ma ago) and that these were island environments. Therefore, he assumed insular dwarfism, in part because of his paleoenvironmental interpretation. This illustrates an important lesson: scientists must constantly keep in mind how much their paradigm shapes how they see the data.

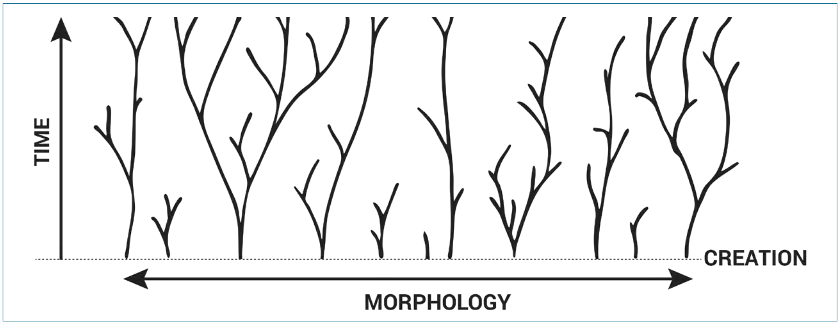


Figure 1. The Creation Orchard of Life

Flood burial—a better interpretation

The data is better interpreted as the burial of dinosaurs in the Genesis Flood. These terrestrial animals were buried in a marine carbonate, which would be predicted by the Genesis Flood. The fact that the dinosaurs were pristinely buried together points to rapid burial, another prediction of the Flood.

These dinosaurs could have herded together because it was their normal behaviour, but it is also possible that this aggregation was due to the looming catastrophe,[5] similar to elk in Montana that herd as winter approaches. It is also possible that they herded together on BEDS (Briefly Exposed Diluvian Sediment) during a temporary local drop in the Flood level,[6] and then were buried when waves of sediment-filled water overwhelmed them.

Although the age of the 10 m of rhythmites is said to be a few thousand years, the researchers now believe it is an intermixture of several rhythmites and slumps.[1] Rhythmites are normally interpreted as the result of slow deposition in periodically changing paleoenvironments. Many researchers now suggest that such rhythmites in the rock record are varves; i.e., each couplet deposited in a single year.[7] But the fact that 10 m of finely laminated rhythmites had the same species of dinosaurs throughout would plausibly suggest such layering happened rapidly, possibly automatically by mass flow. This would be a good hypothesis for a creationist sedimentologist to test.

As for the mosaic nature of the species' anatomical features, they can be explained in the Creation Model, where each kind has variable characteristics. Primitive and derived features are subjective evolutionary concepts. They arbitrarily assign age designations according to what they deem are primitive features or more evolved features. In this case the same hadrosaur had both primitive and advanced features. The Creation Orchard of Life expects variation within a Genesis kind (figure 1). Each kind has tremendous variability built in at the creation, and this variability can be expressed by different 'species', 'genera', and possibly 'families' depending on the boundaries of the kind. Indeed, previous creationist research has found evidence for multiple hadrosaur species belonging to the same kind.[8] In this case, it is not unusual for a dinosaur to display both 'primitive' and 'advanced' features, or even cursorial (running) features, while other members of its kind do not.

References

1. Chiarenza, A.A., Fabbri, M., Consorti, L., Muscioni, M., Evans, D.C., Cantalapiedra, J.L., and Fanti, F., An Italian dinosaur Lagerstätte reveals the tempo and mode of hadrosauriform body size evolution, *Scientific Reports* **11**(23295), 2021.
2. Dalla Vecchia, F.M., *Tethyshadros insularis*, a new hadrosauroid dinosaur (Ornithischia) from the Upper Cretaceous of Italy, *J. Vertebrate Paleontology* **29**(4):1100–1116, 2009.
3. Baechens, S. and Van Damme, R., The island syndrome, *Current Biology* **30**:R338–R339, 2020.
4. Anonymous, Fossils from a herd of 11 dinosaurs have been found in Italy, *Newsround*, bbc.co.uk, 3 Dec 2021.
5. Tuinstra, L., *T. rex* dinosaur relatives found buried together: were these Tyranosauridae social creatures? creation.com, 3 Aug 2021.
6. 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.
7. Oard, M.J., *Ancient Ice Ages or Gigantic Submarine Landslides?* Creation Research Society Books, Chino Valley, AZ, 1997.
8. Doran, N., McLain, M.A., Young, N., and Sanderson, A., The Dinosauria: baraminological and multivariate patterns, *Proceedings of the International Conference on Creationism* **8**:404–457, 2018.

Phosphite oxidizing bacteria: support for evolutionary origin-of-life theory?

Andrew J. Fabich

One of the key stumbling blocks to evolutionary theory is the origin of life. Many explanations have been suggested, such as life coming into existence multiple times and at different locations.[1–3] Perhaps the most notable location for an origin of life has been at deep-sea thermal vents (figure 1).[4] It is believed that the chemical and thermal dynamics in hydrothermal vents makes such environments highly suitable thermodynamically for chemical evolution processes to have taken place about 3.8 Myr ago in evolutionary time.[5]

The primary appeal of deep-sea thermal vents for the origin of life is the numerous species of extremophiles (organisms able to live in extreme conditions of temperature, pressure, salinity, pH, etc.) and other organisms currently living immediately around deep-sea vents. Also, the way in which this type of ecosystem relies on a form of chemoautotrophy (the ability to create its own energy and biological materials from inorganic chemicals) using the reduction of hydrogen sulfide as an electron donor in the absence of sunlight. It is also hoped that a study of these environments may give insights into how life may have originally arise in the hostile environments of other planets and then came to Earth (panspermia). However, this hypothesis simply pushes the evolutionary problem of the origin of life elsewhere.

A novel type of energy metabolism

Recently, two chemoautotrophic microorganisms have been identified in

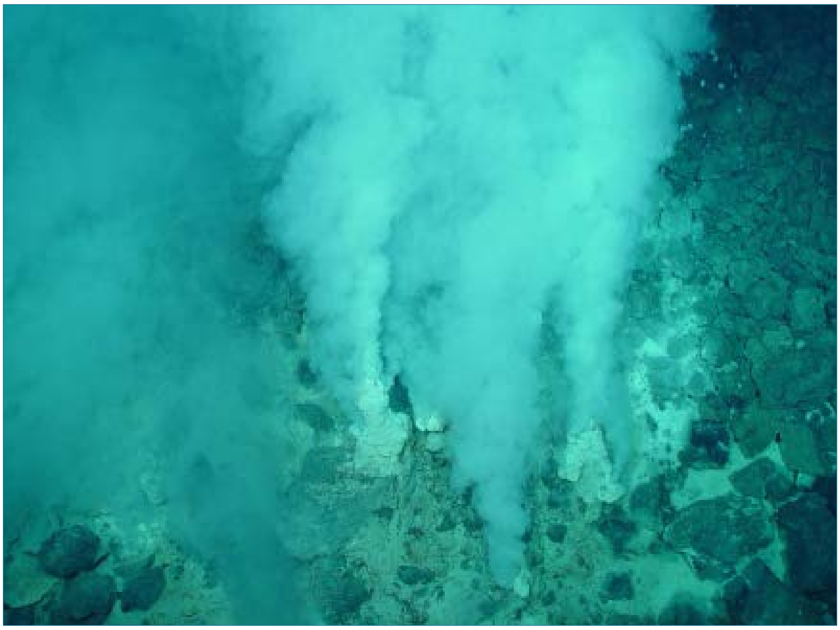


Image: NOAA, Wikimedia / Public Domain

Figure 1. Deep-sea thermal vent. White flocculent mats in and around the extremely gassy, high-temperature (>100°C, 212°F) white smokers at Champagne Vent.

less extreme environments with a new type of energy metabolism believed to be an evolutionary "remnant from around 2.5 billion years ago" within the evolutionary/uniformitarian timescale.[6] These bacteria use phosphite as an electron donor:

> "A first dissimilatory phosphite-oxidizing bacterium, the strictly anaerobic *Desulfotignum phosphitoxidans* FiPS-3T was isolated from marine sediment … and oxidizes phosphite to phosphate with simultaneous reduction of sulfate to sulfide, or with homoacetogenic reduction of CO_2 to acetate."[7,8]
>
> "A further strictly anaerobic dissimilarity phosphite-oxidizing bacterium "*Phosphitispora fastidiosa* DYL19T, was isolated recently from anaerobic sludge of a sewage treatment plant … ."[7,9]

Identification of both organisms is significant because it means that there are additional ways chemoautotrophic life exists besides utilizing hydrogen sulfide at deep-sea thermal vents. Overall mechanisms for phosphite oxidation involve a coupling with carbon dioxide, sulfate, or nitrate for it to be energetically favourable (see table 1).

Although there is only a small fraction of phosphites in today's phosphorus minerals, they are believed to have been "more abundant in the Archean period when the Earth's crust was less oxidized than today and played perhaps a key role in the early evolution of life."[7,10]

But how novel is this biochemistry and what does it imply for life's origin?

Phosphite oxidizing enzymes

The enzyme primarily responsible for phosphite oxidation in *D. phosphitoxidans* and *P. fastidiosa* is the AMP-dependent phosphite dehydrogenase (AdpA). AdpA shows approximately 35 to 60% amino acid sequence identity within the enzyme family of the large, short-chain dehydrogenases/reductases (SDR).[7]

Table 1. Phosphite energetics (after Figueroa and Coates, ref. 10)

Reactions	**ΔG^{o} (kJ/mol HPO_3^{2-})**
$4HPO_3^{2-} + SO_4^{2-} + H^+ \rightarrow 4HPO_4^{2-} + HS^-$	−91
$4HPO_3^{2-} + 2CO_2 + 2H_2O \rightarrow 4HPO_4^{2-} + CH_3COO^- + H^+$	−77
$4HPO_3^{2-} + NO_3^- + H_2O + H^+ \rightarrow 4HPO_4^{2-} + NH_3$	−89
$HSO_3^- + 3H_2 \rightarrow SH^- + 3H_2O$	−172
$HSO_3^- + 3NADH + 3H^+ \rightarrow SH^- + 3NAD^+ + 3H_2O$	−118
$HSO_3^{2-} + NAD^+ + ADP^{3-} \rightarrow NADH + ATP^{4-}$	−14

There are currently three known mechanisms for phosphite oxidation, involving coupling phosphite oxidation with either (1) carbon dioxide, (2) sulfate, or (3) nitrate for the reactions to be energetically favourable (see table 1).[10] But these organisms demonstrate

> "… an unusual substrate-level phosphorylation with phosphite as an inorganic electron donor. … The enzyme oxidizes phosphite with concomitant phosphorylation of AMP (adenosine monophosphate) to ADP (adenosine diphosphate), and reduction of NAD^+ (oxidized nicotinamide adenine dinucleotide)."[7]

The clear difference of these enzymes from those in metabolic pathways discovered to date is remarkable. But the degree to which they are different also carries the burden of proof for finding some evolutionary mechanism for these to evolve from nothing. These enzymes share no significant homology to provide for an evolutionary story for their origin, which is a hallmark of intelligent design. Not only do these enzymes showcase design, but they also confuse the possibilities for evolutionary origin-of-life scenarios.

The evolutionary origin of life now more problematic

According to Darwin's original view (figure 2), descent with modification produced a tree of life. From the 1970s through today, however, deep sequencing across many forms of life has turned the tree of life into a bush of life (figure 3).[11] One major caveat to this bush of life is that life originated multiple times. Even as unscientific as it is to suggest multiple origins of life, one common assumption was that central metabolism always had carbon as the electron donor (i.e., glycolysis). The reason glycolysis is suggested as being ancient is because glycolysis is widespread across living things.[12,13] It was an initial surprise, then, having to suggest hydrogen sulfide as a possible electron donor that funnels into central metabolism because very few forms of life have these pathways. So finding phosphite-based life only adds confusion to the bush of life because none of these three pathways share any homology with each other, as required from an evolutionary worldview.

It is not scientific to say that carbon-based metabolism is ancient because many life forms have it, while now suggesting that phosphite-based metabolism is ancient, since only two dissimilatory phosphite oxidizers have been discovered to date. While

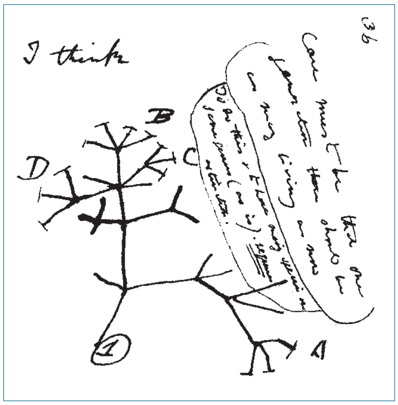


Image: Charles Darwin, Wikimedia / Public Domain

Figure 2. Charles Darwin's original idea of a tree of life published in his First Notebook on Transmutation of Species (1837)

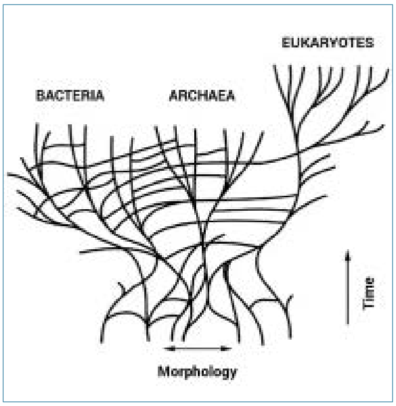


Figure 3. Revised phylogenetic tree of life representing the 3 domains of life (after Doolittle, ref. 11)

it is possible they are suggesting both scenarios happened, the issue is that evolutionists are drawing conclusions about the early Earth without any empirical observations supporting either view—metabolic pathways do not come with birth certificates or expiration dates. The style of thinking that life originated based on either carbon, hydrogen sulfide, or phosphite metabolism instead of being part of a range in God's created order is closed-minded and a science-stopper.

Discussion

The major findings of this study highlight a novel

> "… type of phosphorylation [that] covers the major part of energy conservation in these bacteria and *might represent* a remnant of early biochemical evolution when phosphite was more abundant in the biosphere than it is today [emphasis added]."[7]

The authors continue by stating that this particular form of phosphite oxidation for energy production 'most probably' was preserved from a time in the early earth that no longer exists. While there is no disputing their major finding of a mechanism from two novel bacteria for phosphite oxidation and energy production, their assertion that this mechanism may have been "preserved from the primeval times of our planet" is simply a statement of faith that lacks empirical support and is a result of an evolutionary worldview, as highlighted by Denner:

> "If you are to believe many of the theories of chemical evolution at all, you simply have to believe the earth's atmosphere was once radically different from its composition today, and then look for evidence and experiments to support your belief."[14]

The relatively low overall sequence similarity of these novel enzymes within the large family of SDR enzymes likely represents the unique role these microbes serve in creation. The identification of these new enzymes is, in some ways, reminiscent of the surprise discovery of microbes capable of breaking down man-made nylon.[15]

There are probably even more forms of life based on alternative electron donors ready to be discovered. Instead of suggesting that life randomly came into existence multiple times, we must remind ourselves of God's wisdom. He created microorganisms, about 6,000 years ago, to handle all the different environments and chemicals found on the planet. In this sense, it represents much of what Joseph Francis has described with microbes being called 'organosubstrate' to make life on Earth possible.[16]

References

1. Martin W., Baross J., Kelley D., and Russell, M.J., Hydrothermal vents and the origin of life, *Nature Reviews Microbiology* **6**(11):805–814, 2008.
2. Damer B. and Deamer D., The Hot Spring hypothesis for an origin of life, *Astrobiology* **20**(4):429–452, 2020.
3. Wickramasinghe, N.C., Wickramasinghe, D.T., and Steele, E.J., Cometary panspermia and origin of life? *Advances in Genetics* **106**:5–20, 2020.
4. Dodd, M., Papineau, D., Grenne, T. *et al.* Evidence for early life in Earth's oldest hydrothermal vent precipitates, *Nature* **543**:60–64, 2017.
5. Colin-Garcia, M., Heredia, A., Cordero, G., Camprubi, A., Negron-Mendoza, A., Ortega-Gutierrez, F., Beraldi, H., and Ramos-Bernal, S., Hydrothermal vents and prebiotic chemistry: a review, *Boletin de la Sociedad Geológica Mexicana* **68**(3):599–620, 2016.
6. University Of Konstanz, Ancient power unlocked: scientists discover 2.5 billion-year-old bacterial energy source, scitechdaily.com, 20 Jan 2024.
7. Mao, Z., Fleming, J.R., Mayans, O., Frey, J., Schleheck, D., Schink, B., and Müller, N., AMP-dependent phosphite dehydrogenase, a phosphorylating enzyme in dissimilatory phosphite oxidation, PNAS **120**(45):e2309743120, 2023.
8. Schink, B., Thiemann, V., Laue, H., and Friedrich, M.W., *Desulfotignum phosphitoxidans* sp. nov., a new marine sulfate reducer that oxidizes phosphite to phosphate, *Archives in Microbiology* **177**:381–391, 2002.
9. Mao, Z. *et al.*, *Phosphitispora fastidiosa* gen. nov. sp. nov., a new dissimilatory phosphite-oxidizing anaerobic bacterium isolated from anaerobic sewage sludge, *International J. of Systematic Evolutionary Microbiology* **71**:1–7, 2021.
10. Figueroa, I.A. and Coates J.D., microbial phosphite oxidation and its potential role in the global phosphorus and carbon cycles, *Advances in Applied Microbiology* **98**:93–117, 2017.
11. Doolittle, W.F., Uprooting the tree of life, *Scientific American* **282**(2):72–77, 2000; p. 77.
12. Ronimus R.S. and Morgan, H.W., Distribution and phylogenies of enzymes of the Embden-Meyerhof-Parnas pathway from archaea and hyperthermophilic bacteria support a gluconeogenic origin of metabolism, *Archaea* **1**(3):199–221, 2003.
13. Doolittle, W.F., Phylogenetic classification and the universal tree, *Science* **284**(5423):2124–2129, 1999.
14. Denner D., The primitive atmosphere, *Creation* **3**(3):23–27, 1980.
15. Batten, D., Nylon-degrading bacteria: update, creation.com, 19 May 2017.
16. Francis, J.W., The organosubstrate of life: a creationist perspective of microbes and viruses, *Proceedings of the International Conference on Creationism* **5**:433–444, 2003.

Have scientists solved the dolomite problem?

Michael J. Oard

Dolomite, $CaMg(CO_3)_2$, is a major mineral in sedimentary rocks with some layers being over 1,000 m thick over areas of 500,000 km².[1] Its origin is a major mystery for uniformitarian earth science that has remained unsolved for over 200 years.[2,3] Xu *et al*. claim, "Rarely is there a geological challenge that has endured as long a search for answers as the 'dolomite problem' has."[4] A similar difficulty exists with magnesite, $MgCO_3$, which is frequently found in sedimentary rocks.[4] So, it stands to reason that conventional scientists are working hard trying to solve it. Just recently, it was claimed that uniformitarian scientists have a solution.[5] But before we can understand the solution, first we need to understand the dolomite problem.

The dolomite problem

The dolomite problem is the remarkable abundance of dolomite in 'ancient' sedimentary rocks, contrasted with its strange rarity in modern environments, despite conditions that favour its formation.[6] Dolomite must have a stoichiometry of 50% magnesium and 50% calcium, but it can deviate a little from this ratio and still be called 'dolomite'. Even more problematic, the crystal structure of dolomite is ordered. Ordered dolomite is a remarkable, special arrangement of alternating layers of calcium ions and magnesium ions separated by layers of carbonate ions (figure 1).[7] This has a lower energy, thus greater stability. However, when crystallizing, the ions tend to find the first available vacancy at random. Thus, most attempts to make dolomite make a random arrangement instead. The right way is to use more intense conditions for longer times, so that there is enough energy and time to dislodge the randomly settled ions, and allow them to settle into the lower-energy alternating state. Chemists call this *kinetic vs thermodynamic* reaction control, where the random arrangement is the kinetic product, while the alternating layers are the thermodynamic product.[8] Dolomite does form today in hypersaline water bodies, especially by microorganisms that overcome the kinetic barriers.[9,10]

The current ocean is supersaturated in magnesium and calcium, but dolomite does not precipitate at ambient temperatures. One problem is that each magnesium ion is surrounded by six water molecules that need to be dislodged first. This is called the *hydration barrier* and is believed to be the critical kinetic inhibiting factor.[11]

However, there are other kinetic barriers,[4] and Kim *et al*. think that growth inhibition is a stronger barrier.[5] It has been discovered that certain catalysts, especially dissolved silica, can aid the formation of disordered 'dolomite' at room temperature.[8] Disordered dolomite is also called Ca-Mg disordered dolomite. One recent discovery is that ethanol can be used to partially replace the water surrounding magnesium at low temperatures to overcome the hydration barrier.[8] One main problem with the ethanol solution mechanism is that "high-ethanol-percentage solutions do not exist in natural environments."[12] The large-scale application of these catalysts is very unlikely, and the 'dolomite' is still unordered.

Abundant Precambrian dolomite likely primary

The abundance of dolomite has been variably estimated at 50% of all carbonate rocks[4] to 30% of all carbonate rocks.[5] Since carbonate rocks make up 20–25% of all sedimentary rocks,[13] then dolomite would make up around 10%. Dolomite is most common in Precambrian sedimentary rocks, making up around 80% of the carbonate.[14] It drops off sharply in the Phanerozoic. Moreover, it is likely that Precambrian dolomites are primary, i.e., they *precipitated* directly from solution.[12] This clearly indicates that conditions were much different in the Precambrian than in the Phanerozoic.

The researchers also discovered that precipitated non-biogenic laminae can sometimes look like stromatolites:

> "Precipitated stromatolites can form with or without the templating influence of microbial mats, and precipitated structures in

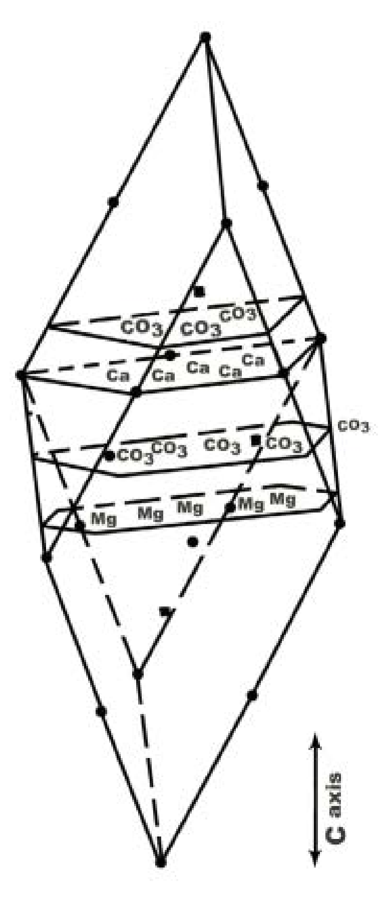


Figure 1. Ordered dolomite crystal (from Morrow, ref. 7, p. 6; redrawn by Melanie Richard)

> Precambrian succession have provoked debate about biogenicity for decades.”[15]

Primary dolomite is formed at temperatures over 100°C.[16] This is also why most conventional scientists believe that dolomite was formed by replacement, since they believe that the surface temperature has been about the same as today, when not glaciated.[17] There is evidence for replacement, but its significance is limited, and it, too, requires hot temperatures.[18]

The new ‘solution’

The recent ‘solution’ to the dolomite problem claims that dolomite can form with innumerable cycles of supersaturation and undersaturation. Researchers suggest that if non-ordered dolomite (protodolomite) first forms, it becomes more ordered with geological time.[19] They conclude this mainly because the older dolomite formations are ordered. The new solution claims that even in disordered dolomite, there are a few stable ordered regions. The disordered regions dissolve faster during undersaturation. Reprecipitation from a supersaturated solution again produces more disordered dolomite that has a little more local ordered regions. Thus, after countless dissolution/reprecipitation cycles, the order gradually increases.[6]

Problems with the new solutions

The ‘solution’ has numerous problems. First, it is a controlled lab experiment with the simulations starting on an *ordered* 3-micron dolomite seed crystal.[6] Second, they varied the saturation state by a pulsed electron beam. When the beam was turned on, dissolution occurred. When it was turned off, supersaturation came back. They had to go through 3,840 dissolution cycles to get a total growth of 200 nanometers on the seed crystal, which took 128 minutes. Third, and most significantly, the researchers had to increase the temperature to 80°C to accelerate the dissolution and growth processes, reinforcing the need for hot water during dolomite deposition. Fourth, the researchers could not run the experiment longer than 128 minutes because undetectable evaporation of the solution in the tiny fluid cell would invalidate the experiment. Fifth, such an undersaturation/saturation process is unrealistic in a natural environment, especially on a grand scale with such huge dolomite formations in the rock record:

> “New questions emerge regarding how these atomistic mechanisms extend from microscopic to geological length scales. Do supersaturation fluctuations in nature occur on a daily, seasonal, or annual cycle?”[20]

Hot water, especially early in the Flood, can explain dolomite

Stoichiometric ordered dolomite is abundant in the Precambrian and even occurs in some lower Phanerozoic rocks. Assuming that many, if not all, Precambrian sedimentary rocks are from the Flood,[21] the abundance of dolomite would suggest that the floodwaters during the Precambrian were often hot. The dolomite must also be primary, since creation scientists have very little time for massive dolomite deposition by any other mechanism. This suggests a unique Precambrian environment early in the Flood. And we should look for a mechanism to cause hot water. Eruption of the fountains of the great deep, lava flows, vulcanism, and meteorite or comet impacts would cause hot water. Moreover, abundant carbonate must first end up in the flood waters from some source. Perhaps the origin of so much carbonate is from the fountains of the great deep?

References

1. Ning, M., Lang, X., Huang, K., Li, C., Huang, T., Yuan, H., Xing, C., Yang, R., and Shen, B., Towards understanding the origin of massive dolostone, *Earth and Planetary Science Letters* **545**(16403):1–8, 2020.
2. Oard, M.J., The “dolomite problem” solved by the Flood, CRSQ **59**(1):21–28, 2022.
3. Oard, M.J., A more likely origin of massive dolomite deposits, *J. Creation* **36**(1):4–6, 2022.
4. Xu, J., Yan, C, Zhang, F., Konishi, H., Xu, H., and Teng, H.H., Testing the cation-hydration effects on the crystallization of Ca–Mg–CO_3 systems, PNAS **110**(44):17750, 2013.
5. Kim, J., Kimura, Y., Puchala, B., Yamazaki, T., Becker, U., and Sun, W., Dissolution enables dolomite crystal growth near ambient conditions, *Science* **382**:915–920, 2023.
6. Garcia-Ruiz, J.M., A fluctuating solution to the dolomite: episodes of dissolution and crystal growth stoke the formation of a common carbonate mineral, *Science* **382**:883–884, 2023.
7. Morrow, D.W., Diagenesis 1. Dolomite—part 1: the chemistry of dolomitization and dolomite precipitation, *Geoscience Canada* **9**(1):5–13, 1982.
8. Jonathan Sarfati, personal communication.
9. Petrash, D.A., Biale, O.M., Bontognali, T.R.R., Vasconcelos, C., Roberts, J.A., McKenzie, J.A., and Konhauser, K.O., Microbially catalyzed dolomite formation: from near-surface to burial, *Earth-Science Reviews* **171**:558–582, 2017.
10. Fang, Y., Hobbs, F., Yang, Y., and Xu, H., Dissolved silica-driven dolomite precipitation in the Great Salt Lake, Utah, and its implications for dolomite formation environments, *Sedimentology* **70**:1328–1347, 2023.
11. Fang, Y., Zhang, F., Farfan, G.A., and Xu, H., Low-temperature synthesis of disordered dolomite and high-magnesium calcite in ethanol–water solutions: the solvation effect and implications, *ACS Omega* **7**:281–292, 2022.
12. Fang *et al*., ref. 10, p. 290.
13. Boggs, Jr, S., *Principles of Sedimentology and Stratigraphy*, 5th edn, Prentice Hall, New York, p. 135, 2012.
14. Cantine, J.D., Knoll, A.H., and Bergmann, K.D., Carbonates before skeletons: a database approach, *Earth-Science Reviews* **201**(103065):1–37, 2020.
15. Cantine *et al*., ref. 13, p. 27.
16. Burns, S.J., McKenzie, J.A., and Vasconcelos, C., Dolomite formation and biogeochemical cycles in the Phanerozoic, *Sedimentology* **47**(Suppl. 1):49–61, 2000.
17. Kaczmarek, S.E. and Sibley, D.F., A comparison of nanometer-scale growth and dissolution features on natural and synthetic dolomite crystals: Implications for the origin of dolomite, *J. Sedimentary Research* **77**(5):424–432, 2007.
18. Mueller, M. *et al*., Testing the preservation potential of early diagenetic dolomites as geochemical archives, *Sedimentology* **67**(2):849–888, 2020.
19. Manche, C.J. and Kaczmarek, S.E., A global study of dolomite stoichiometry and cation ordering through the Phanerozoic, *J. Sedimentary Research* **91**:520–546, 2021.
20. Kim *et al*., ref. 5, p. 918.
21. Oard, M.J., Reed, J.K., and Klevberg, P., Suggested strategies for fitting Precambrian rocks into biblical earth history, CRSQ **60**(2):97–111, 2023.

Petroleum systems do not require millions of years

By virtue of working in the upstream petroleum industry for over 30 years, I am interested in the origin of petroleum. When training for this career I was subjected to uniformitarian teaching and thinking in all matters geological. That suited me because I was then a theistic evolutionist, and it provided me with a way to beat creationists. But after a few years I was deeply aware that all was not right with uniformitarianism. There were too many unjustified assumptions. Eventually I became a young-earth creationist, though the process was slow.[1] May I therefore comment respectfully on Dickens' perspective?[2]

Now, Froede and Akridge[3] explain that there are two significantly different philosophical approaches creationists use to develop geological models of the Flood. The first group start with uniformitarian interpretations of geological observations (naturalism) and try to compress these interpretations (with perhaps some other, smaller, adjustments) into short timescales to align with the biblical story of the one-year Flood. For example, plate tectonics is 'rushed' into Catastrophic Plate Tectonics even though uniformitarians already find many significant difficulties with this theory.[4] Putting a biblical timescale on plate tectonics causes further difficulties in providing good explanations for observations.[5]

Also, the geological column is often used by creationists with a simply very much shortened timescale. But that ignores some crippling problems with the uniformitarian geological column.[6,7] As far as the origin of petroleum products is concerned, most of the attempts to explain such hydrocarbons on a shortened biblical-Flood timescale take uniformitarian ideas of kitchen/source rocks and migration and offer evidence that they can be speeded up. But in these three examples of contrasting approaches, the data and inferences used by them have already been through the uniformitarian mill, which specifically excludes the possibility of a recent global Flood. In other words, 'data' are pretainted with an antibiblical agenda.

If, instead of this 'naturalistic approach', creationists proceed with the other philosophy identified by Froede and Akridge (which they call the 'Bible-based outline'), then no uniformitarian concept or explanation is used as a starting point to develop a Flood model. In particular, there are six statements in the Bible which, though not couched in modern geological terminology, nevertheless are geological pointers which must be the foundation of any credible Flood model.[8]

Where I am left disappointed is that Dickens' perspective[2] starts with a uniformitarian assumption: "A petroleum system is characterized by a genetic relationship connecting a source rock to all the oil and gas it has generated." Fifteen years ago, in a major article I identified seven fundamental flaws with this assumption.[9] While I understand that the author is starting in this basic framework of naturalism, the fact that a 'Bible-based outline' has been in the literature since 2008 and is not acknowledged leaves me expressing this disappointment.

More recently, Klevberg[10] discussed oil in the Williston Basin and referred to my 2008 paper. We did have a brief discussion with letters to the editor where Klevberg[11] suggested that because it was not easy from his perspective to accept my 'theobaric' model of oil, he, Richard Bruce (see Klevberg's double reference to his work which Dickens also uses) and I should team together with others who have offered contributions openly or privately on the subject, sharing data that they have that have not currently been published on hydrocarbon characterization and pyrolysis. We would also need to see international contributions on the hypothesis that faults can be channels of migration and impediments to flow rather than relying solely on examples for the Danish, Norwegian, and UK sectors of the North Sea data as I did. These are relevant because only such information could challenge another key point in my thesis; that is that we cannot get oil into sediment deposits *unless the oil existed* before such sediments formed.

As yet, we have not heard from Bruce, but we could, in the meantime, include Dickens (as there seems to be an overlap in their approaches) either as an alternative or supplement if Bruce should now decide to join. Can it be done so that the subject can be moved forward, please? For too long anxious creationists have noted that it is easier to "talk past one another"[12] than open up on difficult issues.

John Matthews
Wareham, Dorset
UNITED KINGDOM

References

1. Cox, G., Gentleman geologist leads Jurassic journeys: Gavin Cox talks to geologist John D. Matthews, *Creation* **43**(3):44–46, 2021.
2. Dickens, H., Petroleum systems do not require millions of years, *J. Creation* **33**(3):18–21, 2023.
3. Froede, C.R. and Akridge, A.K., A developing schism in Flood geology, *J. Creation* **27**(2): 49–54, 2013.
4. Ollier, C. and Pain., C., *The Origin of Mountains*, Routledge, London, p. 298, 2000.
5. McGuire, M., Catastrophic Plate Tectonics and Plate Tectonics—a comparison of two theories, *J. Creation* **29**(3):104–112, 2015.
6. Matthews, J.D., The stratigraphic geological column—a dead end, *J. Creation* **25**(1):98–103, 2011.
7. Reed, J. and Oard, M.J. (Eds.), *The Geologic Column—Perspectives within diluvial geology,* Creation Research Society Books, Chino Valley, AZ, 2006.

8. Matthews. J.D., Why was the UK once totally under water? *J. Creation* **27**(10):107–113, 2013.
9. Matthews, J.D., The origin of oil—a creationist answer, ARJ **1**:145–168, 2013.
10. Klevberg, P., Petrified Ideas of the Williston Basin Part III: Coal and Oil, CRSQ **59**(1):39–50, 2022.
11. Klevberg, P., Klevberg reply to Matthews—Letters to the Editor, CRSQ **59**(3):190, 2023.
12. Reed and Oard, ref. 7, p. v.

» Harry Dickens responds:

Most of my professional background is in petroleum exploration. I commenced employment in this area in 1977, and currently work in a petroleum basin studies team. I have worked at petroleum wellsites in the North Sea, around Asia, and around Australia, and have delivered petroleum exploration presentations in North America, UK, Asia, and Australia.

Usefulness of petroleum systems

Exxon geologist Peter Vail and others pioneered seismic stratigraphy, using interpretation of seismic sections to determine the extent of coastal onlap evident from strata in sedimentary basins around the world, and so estimate sea level changes.[1,2] Ross[3] and others use the geologic column as a reference tool. Unfortunately, Matthews seems to continue to deny the geologic column. As far as I am aware, Matthews has yet to make any attempt to provide an alternative explanation for how these mappable sequences may be understood within a young-earth creationist framework. To deny the usefulness of the geologic column as a tool in stratigraphic studies would be a giant step backwards in our global creationist research.

Clarey and co-workers have done commendable work mapping megasequences around the world. Correlation of basal megasequence units, and other unique lithologies (i.e., salt and chert layers) within the megasequences, confirms the validity of the geologic column on a global scale.

> "The observable pattern in the fossil record further confirms these findings. Indeed, a global Flood could produce globally extensive, stacked lithologic units on an intercontinental scale. Creationists should not be critical of the geologic column, but embrace it as evidence of a global Flood event."[4]

A significant and basic point of disagreement between Matthews's two 'camps' is whether long-distance correlations (based on biostratigraphy, physical stratigraphy, radioisotopic data, etc.) are valid, for it is on these correlations that the geological column is established.[5]

Genetic relationship connecting a source rock to an oil accumulation

Oil companies consider the chemistry of specific source rocks and that of specific oil deposits. When there is great similarity between the two it may be inferred that the oil was derived from the source rock. This is like a fingerprinting exercise for particular crudes. Thus, inferences can be made on the migration path from source kitchen to an oil accumulation, and so give clues to where other accumulations may be found. This is not uniformitarianism or antibiblical. It can be done by a YEC scientist. It is just good predictive science.

In laboratory experiments today, land plants can be heated under reducing conditions to form a type of hydrocarbon. Similar experiments on algae produce another type of hydrocarbon. This does not require deep time!

Hydraulic fracture stimulation (fracking) of petroleum source rocks to liberate hydrocarbons has been so successful that the US has become a major exporter of hydrocarbons in recent years.

Theobaric idea lacks both explanatory and predictive power

Matthews' 'theobaric oil' idea is that the oil existed in pristine state before the Flood, and it moved during the Flood into the (huge petroleum) reservoirs where we now find it. This is not consistent with the vast amount of literature on the formation and occurrence[4] of various petroleum types and the practical application in finding petroleum deposits used by oil companies around the world.

I don't know how the theobaric idea can have any useful predictive value for petroleum explorationists. This is unlike petroleum system elements, seismic stratigraphy, well post-mortems and hydraulic fracturing used by oil exploration companies.

I wish John Matthews all the best for his future endeavours.

Harry Dickens
Willetton, WA
AUSTRALIA

References

1. Vail, P.R., Mitchum, R.M., Todd, R.G., Widmier, J.M., Thompson, S. III, Sangree, J.B., Bubb, J.N., and Hatelid, W.G., Seismic stratigraphy and global changes of sea level; in: Payton, C.E. (Ed.), *Seismic Stratigraphy—Application to hydrocarbon exploration*, American Association of Petroleum Geologists, Memoir 26, pp. 49–212, 1977.
2. Clarey, T.L. and Werner, D.J., Global stratigraphy and the fossil record validate a Flood origin for the geologic column; in: Whitmore, J.H. (Ed.), *Proceedings of the Eighth International Conference on Creationism*, Creation Science Fellowship, Pittsburgh, PA, pp. 327–350, 2018.
3. Ross, M., A developing schism in Flood geology (Letter to the Editor), *J. Creation* **27**(3):46–47, 2013.
4. An example is Tissot, B.P. and Welte, D.H., *Petroleum Formation and Occurrence*, 2nd edn, Springer-Verlag, Berlin, 1984.

The end of 'New Atheism'?

Coming to Faith Through Dawkins: 12 Essays on the pathway from new atheism to Christianity

Denis Alexander and Alister McGrath (Eds.)

Kregel Publications, Grand Rapids, MI, 2023

Peter Smartt

Has the New Atheism[1] movement failed? The agenda of the 'four Horsemen' (Richard Dawkins, Sam Harris, Christopher Hichens, Daniel Dennett) has been to try to demonstrate that religion in general, and Christianity in particular, is not just wrong, but is positively dangerous and needs to be neutralized. So, has this aggressive slogan-driven project been a success, or have the New Atheists scored an own goal?

According to Alistair McGrath and Denis Alexander (figure 1), New Atheism is definitely on its way out. In an interview about the newly released book *Coming to Faith Through Dawkins,* McGrath says:

> "The reality is, an awful lot of people are coming to faith because of their reaction against the overstatements, the misrepresentations, and the existential inadequacy of the 'New Atheism'."[2]

He goes on to point out that a lot of the younger generations, if they have heard of it at all, just see New Atheism as an exclusive, irrelevant group of predominantly old white men (the same demographic as Alistair McGrath). Many have never even heard of Richard Dawkins.

Against that backdrop, McGrath and Alexander noticed that a lot of people were telling them of how they became Christians *through* Dawkins. Intrigued by this, they managed to get 12 of them to write down their stories, in some detail, and this book is the result (see table 1).

Most of the stories are quite encouraging, but a couple are extremely disappointing. Some are very emotional, others more cerebral (with little about their own testimonies, just the arguments themselves). There are some delightfully humorous incidents recounted.[3] The writers come from many different countries and backgrounds, but all are well educated—several scientists, a historian, a drama graduate, an artist, an engineer, a philosophy lecturer, a high-level public servant, among others.

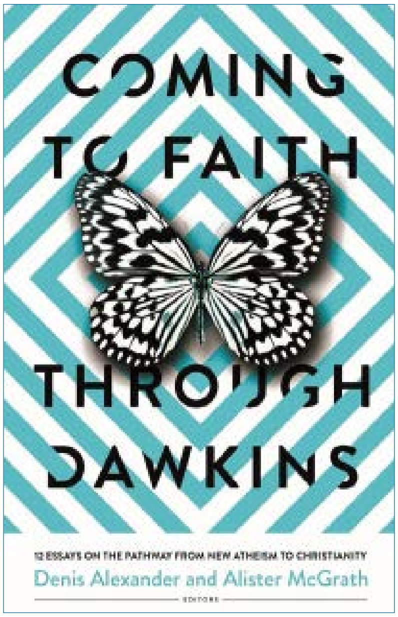
But, sadly, both editors are committed theistic evolutionists, as, it seems, are many of the contributors. The book does a great job of deconstructing many of the arguments and assumptions of the New Atheists. In many places it shows the power of the Gospel of Jesus Christ to transform lives. But, for the most part, it does very little to instil confidence in the truth of the Bible (that is not its aim), and in some cases, undermines it.

It is also worth pointing out a few minor anomalies, despite the title. A couple of the essayists were already Christians when they came across the New Atheists, but they claim that their faith was really cemented by these encounters. A couple of others were not as strongly influenced by Dawkins as by other New Atheists, specifically Peter Singer and Christopher Hitchens.

Common themes

Given the wide range of backgrounds of the authors, we should not be surprised that there is also a wide range of perspectives, ways of approaching the task of writing the essays, and, frankly, the quality and usefulness of the contributions.

Nevertheless, there is a common pattern among most of these testimonies. Contributors are typically introduced to New Atheism and become quite enamoured, motivating them to study it in more detail. Some events or realisations leave them unsettled, questioning or disillusioned, marking a turning point in their journey. They then sometimes follow some other pathway (e.g., Buddhism, New Age), or at least a process of some sort, before finally embracing the good news of Jesus Christ.



Within these near-universal themes, there are also some common patterns. One of these is the frequent determined refusal of many New Atheists (especially Richard Dawkins) to debate Christian apologists of any stature[4] (particularly William Lane Craig[5]). We should not be surprised about this at all—not only would they struggle to make a convincing case, but agreeing to such a debate would also undermine the central narrative that Christian apologists (and creationists in particular) are not worthy of debate, only of contempt. It is no surprise that so many are coming to faith in Jesus Christ *because of* such polemics; this condescending attitude is childish—hardly a persuasive, compelling case for atheism.

Another is the weakness of Dawkins' central argument—essentially that the universe we observe is so complex


Image: Deryck Chan, Wikimedia / CC BY SA 3.0

Image: Alister McGrath, Wikimedia / CC BY SA 2.0

Figure 1. Denis Alexander (left) and Alister E. McGrath (right), editors of *Coming to Faith Through Dawkins*

(and thus its existence is so improbable), any being that created it must be even more complex, and less probable. Of course, this logic fails at many levels; it only makes sense to talk about probabilities where the outcome is unknown. Since the universe exists, its existence has a probability of 100%, so Dawkins' premise is wrong.[6]

Sadly, theistic evolution is also a very common theme—not in the sense of having helped anyone come to faith, but just the fact that it is just assumed, without question, through a lot of the text. Anything to do with biblical creation is treated dismissively, almost in a mocking way[7]—some of the contributors have the same approach to biblical creation as they see in the New Atheist approach to any belief in a deity.

A deeper look at a few of the essays

Due to the number of essays and the length of the book, I have picked out a couple of the best and the worst, to go through in more detail. Thankfully, most of the others veer towards the better end of the spectrum.

Wrestling with life's biggest questions, by Sarah Irving-Stonebraker

This testimony is arguably the most encouraging one in the book. Sydney-born Sarah Irving-Stonebraker, while starting her career as a history professor at Oxford and Cambridge, in the interests of academic integrity, set out to determine whether the atheism she had been born and raised in was true.

During her doctoral dissertation, she realized that Dawkins' claim that science and faith were fundamentally in conflict was simply untrue. Scientists she was studying, such as chemist Robert Boyle and microscope inventor Robert Hooke, routinely referred to the Bible (and biblical creation)—indeed depended on its presuppositions. To them, it provided the rationale, motivation, and methodology for doing science.

> "One of Boyle's chief interests was how to develop a method of establishing reliable and verifiable knowledge about the natural world. How do we minimize the error that arises from human fallibility? Can we rely upon our senses to gain knowledge of nature, and if we can, to what extent and under what conditions?
>
> "These were questions that also concerned Boyle's colleague and laboratory assistant Robert Hooke. Hooke's work *Micrographia* (1665) is one of the most important pioneering works on the microscope and the methodology of experiment to which instruments like the microscope are central. In his introduction, Hooke turns straight to the Bible. He believes that, in the garden of Eden, before Adam and Eve rebelled against God in an episode known as the 'fall' from grace, these two original humans possessed perfect senses and a perfect knowledge of nature. This interpretation of Genesis was commonplace among Protestants in the seventeenth century.[8] Adam's ability to give names to all the creatures, described in Genesis 2, reveals his state of perfect knowledge of and authority over the creation. Through the fall, however, when Adam and Eve rebelled against God, disobeying his command, not only did they lose their dominion over the creation, but their once-perfect senses were damaged by the effects of sin. Our vision, for example, is now merely a poor reckoning of the perfect sight Adam and Eve had before they turned away from God. In fact, precisely this idea is the driving force behind the creation of scientific instruments. Here is an excerpt from Hooke's introduction: 'By the addition of such artificial Instruments and methods, there may be, in some manner, a reparation made for the mischiefs, and imperfection, mankind has drawn upon itself … resulting from a corruption, innate and born with him'" (p. 49).

She became very unsettled by the ethical implications of her atheism as presented by Peter Singer. While she had assumed every sensible person believed in the inherent dignity of all, she was confronted by Singers' clear way of demonstrating the logical ethical implications of atheism.

Table 1. List of essays covered in *Coming to Faith Through Dawkins*

Section no.	Title	Author
Introduction	The ambiguity of Richard Dawkins	Alister McGrath
1	A new Christian meets new atheism	Sy Garte
2	Wrestling with Life's Biggest Questions	Sarah Irving-Stonebraker
3	From Dawkins to Christ via William Lane Craig	Peter Byrom
4	A winding path through new atheism to faith	Anikó Albert
5	Hearing God through an enchantment with nature	Andrew G. Gosler
6	An Afrikaner's faith pilgrimage	Johan Erasmus
7	Coming to faith via *The God Delusion*	Nick Berryman
8	*The God Delusion* and probability	Louise Mabille
9	My Egyptian journey to faith	Rafik Samuel
10	From lukewarm theism to committed faith	Judith R. Babarsky
11	From religion to agnosticism to faith in Christ via Dawkins	Waldo Swart
12	Seeking the truth via new atheism and psychedelic drugs	Ashley Lande

> "Singer's belief that not all human beings are of equal moral worth alarmed me, but soon I began to question why I was alarmed. As Singer had explained, this position follows necessarily from an atheist view of human life. So on what basis could I disagree, other than simple emotivism? Just because I feel something is wrong does not make it wrong. Another aspect of the logical consistency of Singer's ethics with atheism was that I could not think of these arguments as held only by an extremist fringe of atheist philosophers. Far from it. Singer sits in the company of [other academics]. The second option available to us [is that] … all reasonable and sensible people agree that all people are valuable and entitled to the same basic rights, and that is all there is to it. I must admit, until attending Singer's lectures, this was my position, which I had thought was unremarkable and not up for serious debate. But reading the work of Singer and his colleagues made me realize the naivete of my position, which is simply an ungrounded assertion … . The equality of all human beings is not a self-evident truth, as Singer and other world-class secular philosophers are more than happy to remind us" (pp. 53–54).

She was also troubled by blatant inconsistencies in Dawkins' position:

> "It's perfectly consistent to say this is the way it is—natural selection is out there and it is a very unpleasant process. Nature is red in tooth and claw. But I don't want to live in that kind of a world. I want to change the world in which I live in such a way that natural selection no longer applies" (p. 56).[9]

She realized, with some angst, she could not rely on Richard Dawkins' answers to theistic challenges, but needed to confront the issues for herself. She reluctantly realized that the ethical principles she held so dearly did not arise from atheism at all, and that atheistic ethics would be completely unliveable.

> "Would not such a life lack integrity? If I believed that there was no God, and consequently no objective morality or inherent value to human life, then surely I ought to have the integrity to actually live in accordance with my belief. To invent an ethic of care for the marginalized and weak would actually deny my atheist naturalism; it would be a blatant slap in the face—to both my atheism and my integrity. As I thought this through, I had an awkward sinking feeling. Care for the marginalized and the equality of all human life—principles to which I clung so dearly—did not stem from atheism at all. They were actually (I cringed) Judeo-Christian principles" (pp. 56–57).

She ended up reading the Bible, and asked herself the following compelling question:

> "If God created all humanity in his image, then all people were inherently and equally precious. What a beautiful idea. But could it be true?" (p. 59).

Thankfully she ended up embracing the Gospel, and is quite open about it:

> "Rather, my intention is to give you a vignette—a window of entry, as it were—into how an atheist historian, grappling with some of the most

> profound questions in life, realized that the God revealed in the Bible is real, that he loves us, and that Jesus Christ is his Son who died for you and for me so that we may have a relationship with God." (p. 49)

The God Delusion and probability, by Louise Mabille

South African philosophy lecturer Louise Mabille has done a masterful (although somewhat hard-to-read) job of deconstructing the primary argument put forth in *The God Delusion*. She says very little about her own journey except that she had a thoroughly secular upbringing and was already a philosophy lecturer (with a particular interest in Nietzsche) when *The God Delusion* was published. She had great expectations about new arguments the author might raise. But, as a philosopher with an interest in the sciences, she was extremely disappointed, leading to her eventually coming to faith in Jesus Christ.

The remainder of the essay outlines Dawkins' primary argument (that because the universe is so complex it is highly improbable, and that if there was a creator, it (He) must have been even more complex, and thus more improbable), but here Mabille also spends time destroying it.

A lot of it is quite difficult to follow, but as she herself says:

> "I believe when one places The God Delusion in relation to the other sciences, its arguments go nowhere. If anything, they point right back at God. However, this will mean some serious engagement with other fields of science, such as probability theory. Kindly bear with me—it will be rewarding, I promise!" (p. 173).

Mabille shows how Dawkins confuses randomness and causation, misapplies the Law of Large Numbers (LLN), and makes a category mistake, treating probability as a property of an object in the same sense that mass, colour, and even complexity are properties.

She provides a thoughtful (though sometimes hard-to-follow) critique of Dawkins' understanding and use of randomness in his arguments against design, highlighting his misunderstandings. Randomness is no more than a description of our inability to detect a pattern or predict an outcome. Mabille describes it as "a lack of order, purpose, cause, or predictability." Yet, to Dawkins, randomness, when combined with natural selection has almost divine power to generate complexity.

In claiming that life and the universe being improbable entails whatever/whoever caused it to also be improbable, Dawkins is in effect saying that the random activity that caused it is improbable. He admits as much, and invokes natural selection, a non-random process, to rescue his position. He thinks that by breaking the process down to a set of simpler steps (hierarchical reductionism) it becomes more probable. While this sounds reasonable on the surface, the simpler, smaller steps are actually of no help:

> "The hierarchical reductionist … attempts to explain something complex on a particular level in terms of the next, more essential level of complexity until the explanatory possibilities of that level is [*sic*] exhausted. Obeying Occam's razor, he continues down the line until he finds the simplest explanation possible. Naturally, it goes without saying that the kinds of explanations that are suitable at high levels in the hierarchy are quite different from the kinds of explanations that are suitable at lower levels. It depends on the context, of course: 'This was the point of explaining cars in terms of carburettors rather than quarks.' However, when one makes ultimate, fundamental claims about the nature of reality, one has to go all the way down. After all, 'reductionism, in this sense, is just another name for an honest desire to understand how things work.' What makes our attempt so significant is that we are prepared to go down the organizational hierarchy to a point where explanations in concrete terms no longer work, where the obvious and tangible become abstract and counter-instinctual" (pp. 177–178).[10]

Dawkins completely ignores all this, treating biology as a fundamental 'first-cause' science.

Speaking about Dawkins' appeal to LLN to imply that abiogenesis will eventually happen if there are enough 'experiments' on enough planets, Mabille states:

> "And if we are to take Dawkins at his word and apply the law of large numbers to the universe in general, we may just as well say that not only will life pitch up sooner or later but so will the Flying Spaghetti Monster, Batman, E.T., and Darth Vader. If the law of large numbers as Dawkins understands it is consistently applied, it means in effect that sooner or later, given the infinity of time and space, *everything* will turn up [emphasis in original]. *This implies that, sooner or later, a redeemer will be born from a virgin* [emphasis added]. Who says you need Stephen Jay Gould's non-overlapping magisteria to reconcile science and religion? Apparently, according to the law of large numbers, anything is quite literally possible" (p. 181).

Hearing God Through an Enchantment with Nature, by Andrew G. Gosler (the most disappointing essay)

I will not say too much about this essay, except to alert the readers, highlight the variation in the quality of the essays covered in this book, and assure them that it doesn't get any worse. Andrew Gosler, an ornithology professor and minister (of what must be a very liberal denomination), writes at length about the greater honeyguide, an African bird that has developed a symbiotic relationship with the local tribal people. It has a stomach that can digest beeswax, and it is rather impervious to bee stings. It guides humans to wherever it finds a hive, the humans can smoke out the hive, collect honeycomb, extract some of the honey, and give the wax to the honeyguides. Evolution is assumed and referred to repeatedly throughout the essay.

His primary argument against Darwin and Dawkins is that they promote evolution as a competitive, unpleasant process, whereas to him it is a cooperative, joyous process. I doubt that the less fit creatures destroyed in the process would agree. Any biblical creationist will find it painful to read.

A new Christian meets new atheism, by Sy Garte

Slightly better than Andrew G. Gosler's contribution is that of Sy (Seymour) Garte, a biochemistry professor. He gives a good account of having grown up in a committed Marxist, militantly atheistic family, discovering that communist and atheist propaganda presented a very distorted view of religion's involvement in world conflict. So, after a long period, he became a very new and quiet Christian, just before the New Atheists burst onto the scene. He was actually relieved to find that they did not have anything new and challenging to add to the conversation. So his faith and confidence in the Bible was strengthened, and he became more outspoken.

But he unfortunately assumes theistic evolution, and believes he can successfully marry it with his Christian faith:

> "When, after becoming a Christian, I learned that it was not necessary for me to immediately denounce evolution as a plot of the devil or reject any part of my long-held scientific worldview, I was quite relieved. But I also came to understand that, due to my acceptance of evolution, I was considered by both atheists and some Christians to be a 'moderate Christian'. I thought that being in that camp would allow me to be able to dialog effectively with more conservative, fundamentalist Christians as well as with atheist scientists, since I shared so many viewpoints with each group. I even made a comment or two on Jerry Coyne's blog, Why Evolution Is True.
>
> "How naive I was! One of Coyne's followers let me know that 'moderate Christians', including those who accept evolution, are actually the worst kind of enemy, for while they have learned 'the truth', they continue to indulge and support the great lie of theism. It turned out that this attitude was a common New Atheist trope, and that making common cause to promote good scientific education was harder than I thought" (pp. 40–41).

Does he realize he is in an untenable position? The only "more conservative, fundamentalist Christian" he has ever debated is Kent Hovind, and it shows.[11] This would not surprise any biblical creationist.[12]

Conclusion

As Christians and biblical creationists, we should be pleased that the influence of the New Atheists seems to be waning, and alert to where the next battle fronts are. One thing this book achieves is to highlight how deeply theistic evolution is entrenched within large swathes of the Christian community (especially among intellectuals) and is seldom challenged.

It contains a lot of useful material, but the tacit support for theistic evolution can undo a lot of the good.

References

1. 'New Atheism' refers to a cultural movement that began around 2006, with the publication of *The God Delusion*, among several similar titles, which captured the imagination of large sections of the liberal media and academia. It seeks to paint science as the only way we can know anything, and any sort of belief in a deity as so bizarre as to not even be worthy of debate, only of contempt.
2. (2280) How Richard Dawkins ACCIDENTALLY Led People TO GOD, youtube.com.
3. For instance, Peter Byrom talks about the incredible frustration with Richard Dawkins' absolute refusal to debate William Lane Craig. He recounts: "Then the idea hit us! Dawkins had been behind the launch of the British Humanist Association's 'atheist bus campaign' back in 2009. We could turn this upside down, putting banners on Oxford buses that, instead of reading 'There's probably no God. Now stop worrying and enjoy your life', read 'There's probably no Dawkins. Now stop worrying and enjoy Oct. 25th at the Sheldonian Theatre' (i.e., expect a no-show from Dawkins and enjoy a substantial critique of *The God Delusion*)."

   In another incident, Johan Erasmus, an Afrikaner raised in the Reformed Church, describes the following incident that occurred in the middle of his enchantment with his new-found New Atheism: "I was visiting family friends, and the eldest daughter of that family was home from the United States, where she was studying theology. I asked her a little about her studies and whether she knew anything about the likes of Dawkins, Hitchens and Harris. Those names seldom meant anything to most of the Christians I interacted with, and those brave enough to venture a guess thought they were sports stars. Her answer, however, caught me completely off guard. In a disappointed tone she said, 'You seriously need to get yourself some better atheists.'"
4. See: Wieland, C., World atheist convention rejects Australian creationist debate challenge, creation.com, for an example of the New Atheist's response to a challenge to debate scientists from *Creation Ministries International*.
5. Unfortunately, while William Lane Craig has been a very capable and effective apologist for Christian belief in the past, he is now publicly expressing doubts about some of the fundamental truths of the Christian faith, including the virgin birth of Jesus Christ—see: Sander, L., Price, P., and Carter, R., William Lane Craig on creation and anthropology, creation.com.
6. See: Kastelein, N., The probability of God: a response to Dawkins, *J. Creation* **32**(3):63–69, 2018.
7. For instance, in *From Dawkins to Christ via William Lane Craig*, Peter Byrom writes: "Religious people, by contrast, were those simplistic, backward folks who saw everything in black and white, believed the world was only six thousand years old, and got easily offended."

   In *From Religion to Agnosticism to Faith in Christ via Dawkins*, Waldo Swartz writes: "The conflicts between what I read in the Bible and what I knew about science became much more apparent. The order of the creation days in Genesis was wrong; it didn't fit with what we now know about the world, what I learned from science books and documentaries."
8. See also Weinberger, L., The Fall and the inspiration for science: A review of *The Fall of Man and the Foundations of Science* by Peter Harrison (2007), *J. Creation* **24**(3):18–21, 2010.
9. This was part of an answer he gave during an interview in *Skeptic*. Miele, F., Darwin's dangerous disciple: an interview with Richard Dawkins, *Skeptic* **3**(4):80–85, 1995.
10. See: Catchpoole, D., Sarfati, J., and Batten, D., Natural selection cannot explain the origin of life, creation.com.
11. See: Wieland, C., Ham, K., and Sarfati, J., Maintaining creationist integrity: a response to Kent Hovind, creation.com.
12. See Richard Dawkins: "Theistic evolutionists are deluded", creation.com.

How Darwin evaded the lack of evidence for his theory

Darwin's Bluff: The mystery of the book Darwin never finished

Robert F. Shedinger

Discovery Institute Press, Seattle, WA, 2022

John Woodmorappe

Author Robert F. Shedinger is a professor of religion at Luther College in Decorah, Iowa. He specializes in the religion/science relationship.

This book is about Darwin's promised sequel to The *Origin of Species* (figure 1), in which Darwin promised to supply the proofs that were lacking in his 'outline' *Origin of Species*, but which was never published. No-one called Darwin out on his broken promise, much less questioned any aspect of evolution. Instead, Darwin got much 'hero worship', much like the fabled emperor that has no clothes, yet everyone affirms and blindly cheers his clothes.

This book also discusses recent members of the Intelligent Design (ID) movement, and the discrimination that they face because of their views. It makes for chilling reading.

Author Shedinger does some discerning. He asks why textbooks continue to use Ernst Haeckel's doctored drawings of embryos, when modern technology allows for digital photographs. He discerns that the latter would not be as convincing of evolution (p. 227).

Did uniformitarian geology inspire Darwin's organic evolution?

In the past, creationists have pointed to a connection between uniformitarianism and evolution. Both attacked biblical orthodoxy: the former disavowed the Flood and the young earth, while the latter disavowed the special creation of living things. Both advocated that changes on Earth and to its living things happen naturalistically and slowly (on average) and over long periods of time. So-called old-earth creationists, on the other hand, wanting to have a foot in both camps, have tended to view the two as completely separate developments.

Shedinger sheds some light on this question. He elaborates on Darwin's early geologic field work and his fascination with Lyellian uniformitarianism. While not going into detail, he affirms a connection between geologic uniformitarianism and organic evolution, at least in Darwin's thinking.

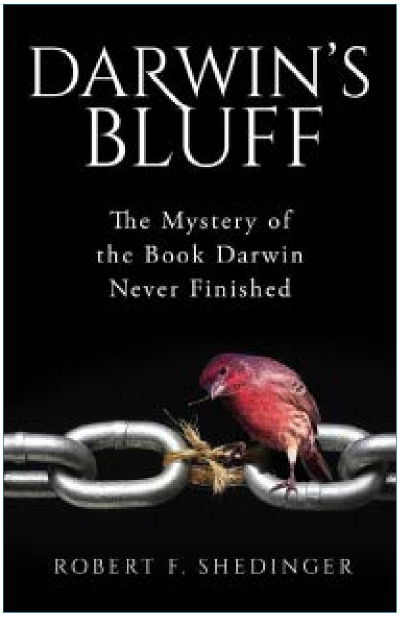
Thus, Shedinger writes:

> "Even before returning to England, Darwin was laying plans to make his mark in geology despite his lack of professional training in the discipline. *Lyellian uniformitarianism was becoming his new religion, a religion that would form the foundation of his species work* [emphasis added]" (p. 53).

Uniformitarianism a religion—good choice of words.

Darwin's disingenuous advocacy of evolution

The author does a thorough analysis of Darwin's thinking. He finds some



frankly deceptive argumentation on the part of Darwin. He comments:

> "He (Darwin) admits that the issue is indeed perplexing, but then passes off valid and substantive criticism as just 'two or three puzzles'. But most importantly, he bases his continued confidence in his theory on the grounds that it 'explains so well many facts'. Philosophers of science have long recognized that the same set of facts can be explained by more than one theory; this is the problem of underdetermination. If one starts with a theory; then interprets the facts through the lens of that theory, then of course it may look like the facts prove the theory" (p. 57).

Elsewhere, Shedinger points out Darwin's shoddy scientific reasoning. He writes:

> "Darwin's instincts, alas, often proved unreliable. Following the publication of the *Origin*, he was particularly stung by criticisms that he had not followed the inductive method. But such criticisms should not have come as a surprise for someone so guided by instinct. *Darwin did not accumulate data and then reason from the data to general principles*. He rather

> developed general principles by instinct and then tried to find data to support them, frequently becoming frustrated when perverse nature defied his will [emphasis added]" (p. 90).

Darwin also deflected legitimate questions about his theory by engaging in what today is called gaslighting. The author writes, "As we saw earlier, Darwin's favorite line of response to his critics was to accuse them of not understanding his theory" (p. 155). How convenient!

Darwin performed a bait and switch

Shedinger writes:

> "Darwin downplayed expectations by informing his readers that the *Origin* was a mere abstract of a larger work on species that he hoped to publish shortly after the *Origin*. But when criticisms of the abstract came in and Darwin realized his big book would not effectively address these criticisms, he abandoned the idea of publishing the big book and turned instead to orchids" (p. 199).

How could this happen? Darwin could get away with never publishing his promised second book, because most people just came to accept Darwin's ideas and never held Darwin's broken promise against him.

The author suggests that the evolutionary establishment did a bit of a cover up about Darwin's promised second book, and that is why so few people ever heard of it. I agree. I have been studying evolution for some decades, and had never before heard of this second book.

Adaptationist just-so stories are not evidence

Storytelling about how a feature in an organism may have evolved is a characteristic of both Darwin and of modern evolutionary theory. Shedinger comments:

> "In any case, Darwin was never going to be able to satisfy his readers with mere imaginary scenarios about how natural selection might work in hypothetical situations. His readers were expecting hard evidence. But despite his many earlier comments building up expectations, the big book was sorely lacking in this regard" (p. 182).

Note that this consideration parallels that used against creationism: an organism has a particular feature because God made it that way. Only now the organism has a particular feature because natural selection made it that way.

In the end, Darwin never proved his case

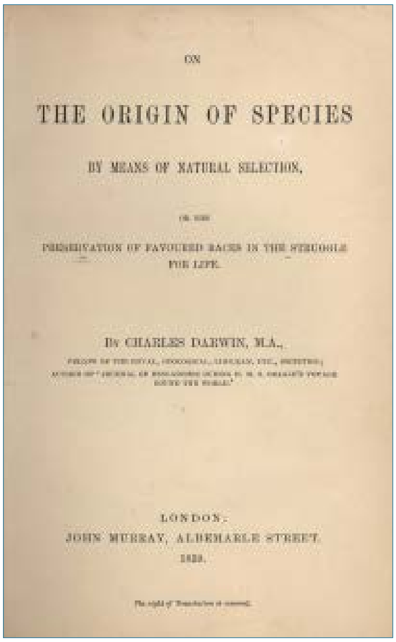
The problem with Darwinism went beyond just-so stories. The author is rather harsh on Darwin as he concludes:

> "Where cogent confirming evidence for the creative powers of natural selection were called for, there was instead only talk of geographic distribution, microevolution of domesticated breeds via artificial selection, and imaginative just-so stories about bears evolving into whales and such" (pp. 199–200).

Darwin a racist? Darwin a sexist? Leftist hypocrisy

The author brings up the question of Darwin's attitudes regarding slavery, racism, and gender issues. Rather than wading through these questions yet again, as has been done by creationists in the past, I look at deeper and more contemporary matters that Shedinger does not discuss.

Nowadays, so-called 'progressive' pseudo-intellectuals are prone to pontificate and do virtue signalling about the racism and sexism of 'dead white males'. In the United States, for example, this has policy issues. Statues to Columbus have been torn down via mob action, and there have been serious calls to take down the statues of American historical figures such as George Washington and Thomas Jefferson—all because of their alleged 'racism'. I know, from personal experience, that bird-watching organizations such as local chapters of the Audubon Society have been renamed because of Audubon's alleged racist leanings. As an educator, I know a school district where schools long named after the explorer Boone and after the biologist Agassiz have been renamed for the same reason.


ON

THE ORIGIN OF SPECIES

BY MEANS OF NATURAL SELECTION,

OR THE

PRESERVATION OF FAVOURED RACES IN THE STRUGGLE
FOR LIFE.

BY CHARLES DARWIN, M.A.,

LONDON:
JOHN MURRAY, ALBEMARLE STREET.
1859.

Image: John Murray (Publisher), Wikimedia / Public Domain

Figure 1. Darwin's *Origin of Species* was supposed to be followed up by a more evidence-based book. This never materialized.

The foregoing also happens in other western nations.

Enter Darwin. I have yet to hear of a single instance of an institution bearing the name of Darwin getting renamed because of any racism or colonialism that Darwin may once have held! Instead, we usually hear the exculpatory line, 'Darwin was a product of his time'. Exactly right. Yet this common-sense consideration is applied selectively, and Darwin gets excused, while various other "dead white males" do not.

This also touches on the matter of unequal rights. Evidently, 'progressives' have discovered some sort of right to cancel historical figures not to their liking, in public policy matters, while Christians never have a right to cancel Darwin should they be so inclined.

Why the hypocrisy and double standards? Could it be that Darwin is exempt from cancel culture's wrath because of his iconic status as the one that has 'discredited' Christian orthodoxy and as the one who has fostered evolutionistic thinking in our collective minds?

Ongoing discrimination against creationists and proponents of ID

Shedinger discusses the blatant flouting of the critical inquiry that is supposed to characterize science. Consider these incidents:

Eric Hedin, a onetime physics professor at Ball State University, taught a popular course that introduced students to the evidence of design in biochemistry and cosmology. Pressure from America's atheistic Freedom from Religion Foundation pressured the university to cancel the course.

Gunter Bechly is a paleontologist and internationally recognized expert on fossil insects. He long accepted evolution, but began to question it and to entertain the possibility of Intelligent Design. He was fired as the curator at the State Museum of Natural History in Stuttgart, Germany.

Cuban-American Guillermo Gonzales was an astronomer with an extensive publication record. He was forced out of the astronomy department of Iowa State University because he coauthored a book, *The Privileged Planet*, which pointed to evidence of intelligent design.

Let us keep these odious events in perspective. Imagine any professor subject to such treatment for attacking God or Christianity. It would make front page headlines, and we would not hear the end of it.

'Creationists do not publish'—the exception that proves the rule

Two Scandinavian scientists, Steinar Thorvaldsen and Ola Hossjer, got a mathematically based study of intelligent design approved by the referees, and published in the prestigious *Journal of Theoretical Biology*. It explicitly endorsed the works of ID scientists such as Michael Behe, William Dembski, and Douglas Axe.

The reaction of evolutionists was beyond hysterical! As Shedinger comments:

> "The editors clearly thought the paper made a significant contribution to biology and sent it out for peer review. The peer reviewers must have agreed, and so the paper was published. This touched off a firestorm of criticism toward the journal for publishing a paper so favorable to intelligent design, an idea derided as religiously motivated pseudo-science by establishment biologists. How, critics wanted to know, could the editors and peer reviewers have possibly let such a worthless piece of research into the journal, a move that would only serve to embolden these pseudo-scientific quacks? The backlash was so severe that the editors published a disclaimer several months later … . This disclaimer, of course, does not pass the smell test. First, the professors listed their university affiliations because they were in fact professors at those universities. Also, as noted, the paper is so shot through with intelligent design thinking and references to leading intelligent design thinkers that no one reading the paper could miss it. Clearly, the editors and peer reviewers thought that scientific evidence for intelligence [sic] design in biology *was* an appropriate topic for the journal, the editors making an about-face only after the angry backlash [emphasis in original]" (p. 230).

Let us analyze this 'shocking' development. For the longest time, evolutionists have asserted that creationists do no science, as demonstrated by the fact that scientific journals do not contain any creationist studies. Then, when faced with the fact that scientific journals will not publish creationist studies, they change their argument. They say that creationists do not do any research that would merit publication in a scientific journal. The experience of Thorvaldsen and Hossjer graphically exposes the complete dishonesty of this long-repeated evolutionistic argument.

We clearly see that the evolutionary establishment is not merely prejudiced against creationists. Their comically hysterical reaction to this ID paper, published in a top journal, speaks volumes about the vehemence of their antipathy to anything that challenges evolutionary orthodoxy. So much for objective science!

Conclusions

Darwinism was mostly speculation from the beginning, and thus it continues today. Darwin was never held accountable for not producing his second book because most people let it slide, accepting Darwin without the hard evidence that his theory required. And so it continues today.

The absolute fury with which the evolutionary establishment deals with any creationist and Intelligent Design challenges to their theory itself is telling about their insecurity and their deep realization that their evolutionary theory, far from proven fact, is inadequate.

Combining Adam and evolution: an exercise in futility

The Origin of Humanity and Evolution—Science and Scripture in conversation

Andrew Ter Ern Loke

T&T Clark, London, UK, 2022

Keaton Halley

Andrew Loke is a philosopher at Hong Kong Baptist University, and an influential advocate of theistic evolution (figure 1). His overpriced book on human origins at least covers a lot of ground in a short space of less than 200 pages.

Loke proposes "a new model of human origins" which purports to reconcile the historicity of the biblical Adam and Eve with the standard theory of human evolution (p. 2). Unfortunately, Loke's unworkable compromise leads him into bizarre and dangerous territory regarding the definition of human beings and fails in the end because it contradicts the Bible's clear meaning. This is the kind of scholarship that makes Christian laypeople mistrust academia, because it eagerly sacrifices orthodoxy at the altar of vain, worldly speculations that were designed to avoid the Creator. It's a shame that Loke has wasted so much of his time and brilliant mind on developing ideas so plainly unfaithful to Scripture.

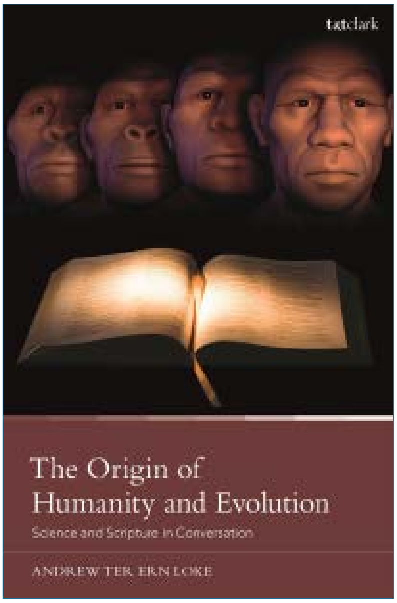
Building on Swamidass

Loke's view is a variation of Joshua Swamidass's genealogical Adam and Eve (GAE) model.[1] He even dedicated this book to Swamidass. But Loke has added slight modifications of his own and supplements borrowed from biblical scholars like John H. Walton and C. John Collins.

According to Swamidass's GAE concept, a group of beings with anatomically human bodies evolved from ape-like creatures just as textbook narratives say, placing the origin of the genus *Homo* over 2 million years ago. Adam and Eve did not give rise to all these individuals, but existed some time later, when this large population was already established. Adam and Eve could have been individuals chosen from this wider population or created separately and supernaturally. Because the descendants of Adam and Eve then intermarried with the wider population, and they happened (providentially?) to thoroughly mix with every tribe throughout the world, eventually all living members of the genus *Homo* could trace their genealogical ancestry back to Adam and Eve.

There are several questions Swamidass's bare GAE proposal leaves undecided. It leaves open whether Adam and Eve lived as recently as 6,000 years ago, or in the more distant past—perhaps hundreds of thousands of years ago, prior to standard dates for the advent of Neanderthals. It leaves open whether Adam and Eve themselves evolved or were created *de novo*. It leaves open whether the wider population of *Homo*, not descended from Adam and Eve, were bearers of God's image.

In Loke's version of GAE, he insists that only Adam and Eve and their descendants are image-bearers, and therefore only they are true humans. Loke differentiates between those genealogically descended from Adam and Eve, who are in God's image, and mere anatomical *Homo*, who are not in God's image. In Loke's mind, this distinction allows his model to satisfy the biblical requirements that Adam is the first man and that all of humanity descended from him. But, as will be shown, Loke's strategy promotes an unhealthy view of mankind and fails to do justice to Scripture.



Points of affirmation

Loke is conversant with a wide range of relevant literature. He seems more familiar with young-earth creationist (YEC) and Intelligent Design (ID) material than is typical of our ideological opponents.

He also seems to be relatively theologically conservative in comparison to his fellow theistic evolutionists. Though he does not reveal his hand about whether he is committed to inerrancy, he does push back against those quick to abandon it. While promoting the idea that God's revelation in Scripture accommodates the limitations of mankind, Loke says accommodation need not entail scientific errors in the Bible. He takes issue with Denis Lamoureux, for example, who claims that Scripture affirms a three-tiered universe with a flat Earth and a solid firmament (pp. 23–28).

Loke also critiques the idea that alleged parallels between Genesis and other ancient Near Eastern literature show that it is simply ahistorical myth (pp. 44–51). He contends that the arguments against the historicity of Genesis are unsuccessful, though he is noncommittal about whether Genesis could combine myth and history, as William Lane Craig has argued (p. 49).

Criticisms that hit the target

Loke's critics would do well to make the same careful distinctions he makes, when he differentiates between: "Task (A) 'interpreting the Bible', Task (B) 'showing that the biblical account is true' and Task (C) 'showing that there is no incompatibility between evolution and the Bible'" (p. 3). His project is to propose a model that satisfies Task (C). Thus, Loke points out that he doesn't need to show that the Bible *teaches* various aspects of his model, only that the Bible doesn't clearly *contradict* it. So it would be misguided to critique him by saying merely that the biblical authors nowhere affirm evolution or GAE (p. 14).

On the other hand, it would be legitimate to say that there is a conspicuous absence in Scripture of various concepts proposed by Loke, if they would reasonably be expected. Also, a proper exegesis of Scripture does contradict Loke's model. Loke offers alternative interpretations of biblical passages to avoid the contradictions, but since his interpretations are faulty, he has not sustained his burden of proof. He must distort Scripture to make it compatible with evolution.

Scientific evidence for deep time and evolution

When Loke presents evidences for evolution and an ancient universe, his treatments are brief and only scratch the surface of the discussion. He appeals to the "consistent results" of radiometric dating, for example (p. 34), but doesn't address the problems posed by carbon-14 in allegedly ancient samples, dinosaur soft tissue, and other young-age indicators. As evidence for evolution, Loke points to "genetic scars", which he presumes are "functionally unimportant" (pp. 71–72).

But that supposition, e.g., 'junk DNA', has a long history of being overturned. Loke also appeals to the disputed idea that human chromosome 2 resulted from an end-to-end fusion of previously separated chromosomes. Even if this were true, it would not supply compelling evidence for ape ancestry.[2]

He naively appeals to 'fossil intermediates' like *Archaeopteryx*, *Tiktaalik*, and "several species between land mammals and whales" (p. 72). This blithely overlooks the massive problems with the evolution of birds, tetrapods, and whales, documented by creationists. Even some evolutionists acknowledge these enormous hurdles, which Loke heedlessly bypasses. He mentions biogeography and other arguments as well, but it is all too brief and fails to interact with substantive criticisms. The human evolution 'evidence' he presents (pp. 85–88) is likewise superficial and ignores creationist critiques.

Weak attempts to squeeze long ages into Scripture

Loke suggests the Genesis genealogies have gaps, but he neglects the differences between the genealogies of Christ in the Gospels and the Genesis chronogenealogies.[3] He appeals to the extra Cainan in Luke 3:36, ignoring the fact that this is a copyist error; i.e., not in the original manuscripts.[4]

Loke tries in vain to get around Jesus' statement that humans were present "from the beginning of creation" (Mark 10:6), not billions of years later. He says this phrase "may well be referring to the creation and beginning of humans with the image of God, rather than the creation and beginning of time or of the cosmos or of the earth or of all other living things" (pp. 39–40). However, Loke misconstrues the meaning of the term 'creation' as a *creative act* (creation of …), when the context demands it is a *created object* (creation that God created, as in Mark 13:19).[5]

Loke's fallback position regarding Mark 10:6 is to say that, if John Walton's 'functional creation' view of Genesis 1 is correct, then Jesus could have been saying Adam and Eve were present from the time the heavens and earth began to exist in a functional sense, not from the time they materially began to exist. But Walton's eccentric interpretation has been exposed as fallacious.[6]

Loke doesn't commit himself to any particular interpretation of Genesis 1 and its creation days. He thinks a view similar to John Walton's is plausible, that these could be six literal calendar days extolling the *functions* of creation, while the *material* creation took place long before. But, he is also open to John Collins's view that the days of creation are God's cyclical periods of work and rest—merely analogous to the days of an ordinary seven-day week, not themselves 24 hours long. But it is unfounded to treat these as 'God's days' of undefined length, when the creation account begins with God establishing the light/dark cycle, each day contains an evening and a morning, and God designates the last day as a holy day of rest—clearly establishing the pattern for the Sabbath (Exodus 20:11). If language means anything, these are Earth days.

Image: FifthSparrow, Wikimedia / CC BY SA 4.0

Figure 1. Andrew Loke at Hong Kong Baptist University

Loke also views Noah's Flood as a local affair, which allows him to have it wipe out all of Adam's descendants save those aboard the Ark, while anatomical *Homo* survived in large numbers outside the flood zone. But Loke's arguments for a geographically restricted flood are not convincing (pp. 130–133). For example, he says the Hebrew term *kasah* (to cover) in Genesis 7:19 may only indicate that the waters drenched the mountains, rather than covering them (p. 131). This might be a reasonable translation of the term when water falls to cover or drench what is below it (Job 38:34; Malachi 2:13). But, in context, Genesis 7 is talking about waters *rising* to cover the mountains. This isn't falling water that merely soaked them.

Death and the Fall

Loke is aware of the problem that a deep-time interpretation of the fossil record presents for the Bible's teaching that death, disease, and carnivory began after the Fall. To get around this, he performs interpretive gymnastics. His main strategy is to restrict all references to pre-Fall, paradisiacal conditions to the Garden of Eden rather than the whole world. So, when God sees His creation is "very good", this may have referred only to Eden (p. 76). Never mind that God applied this assessment to "everything that he had made" (Genesis 1:31) before Eden was ever mentioned. Loke says animal predation could have been occurring throughout the world while the herbivory of Genesis 1 could have been limited to Eden too (p. 74–75). Never mind that the context speaks about all animals throughout the world: "everything that has the breath of life" (Genesis 1:30). According to Loke, even God's Curse on the ground applied only to Eden (p. 127). Never mind that Genesis 5:29 and Revelation 22:3 demonstrate the broader extent of the Curse.

Creationists naturally associate Romans 8 with the Fall, when it says that creation is in "bondage to corruption" and longing to be "set free" (v. 21). But Loke maintains that God subjected creation to futility before the Fall, based on the fact that Genesis 1:2 describes the earth as "without form and void", and because the Second Law of Thermodynamics was operating before the Fall (p. 77). Loke is clutching at straws. These concepts have nothing to do with 'corruption'. Most creationists today agree that the Second Law predates the Fall, but that is irrelevant to Romans 8.

Loke gets around the problem of human death before Adam by his arbitrary division of anatomical *Homo* into two groups. All those fossils that exhibited human behaviours and look indistinguishable from humans—they aren't; problem solved! But this is *ad hoc* and poses further problems.

Tampering with humanity

Loke's model has three disturbing implications for those traditionally understood as mankind, since he understands a significant portion of us to be non–image-bearers.

1) Loke's model regards many ancient people as non-humans.

Who is and who isn't human depends on where Adam is placed chronologically. If Adam lived as recently as 6,000 years ago, many people groups living then, and even millennia afterward, were not human. Loke quotes Dennis Venema's objection to this scenario:

> "Humans are widely dispersed on the planet at 6,000 years ago—in the Americas, in Australia and Tasmania, and so on. Do we really want a theology that names them all as subhuman animals until their lineage happens to encounter and interbreed with Adam's … offspring? God forbid."[7]

Also, even if a more ancient Adam was instead posited around 1 Ma, so that he was the forefather of all *H. sapiens* and even Neanderthals, this difficulty is not solved. There are manifestly human skeletons 'dated' earlier than this, including *H. erectus* individuals like Turkana Boy, who supposedly lived around 1.8 Ma. *H. erectus* had skeletal anatomy resembling living humans, made sophisticated tools, operated watercraft, and displayed many other evidences of being human. Venema-style discomfort could apply to these people being labelled 'non-human' as well.

To answer Venema, Loke says his "use of the term 'human' … begs the question because this is the point being disputed", and he complains that Venema's judgment "is just an emotional response" (p. 137). But it is not just emotional. The above anatomical *Homo* groups check the boxes of reasonable empirical criteria to detect humanness, Loke's sophistry notwithstanding.

Loke spends many pages discussing the image of God and how to define it (pp. 95–106). He does not think the image of God primarily has to do with our capacities to reason, perform moral actions, or connect with God. It has more to do with representing God functionally, though Loke says this does require some of the above capacities. In the end, though, part of Loke's definition of God's image includes being specially chosen by God to be His royal representatives (p. 127).

There is no way to empirically detect this, so it makes the *imago dei* impossible to identify in the anthropological fossil record. No matter how human someone appears, he might not be chosen, and would therefore lack God's image. Using this criterion, Loke can arbitrarily place the dividing line between human and non-human anywhere he likes. But given how much like us these other anatomical *Homo* are (p. 99), it is unreasonable to dismiss their humanity.

2) Loke's model has no compelling reason to deny the possibility that some living *Homo* could be non-human.

Loke's model does affirm that all living anatomical *Homo* are image-bearing humans (p. 117), but he doesn't supply adequate reasons to insist on this. His only Scriptural warrant is Acts 17:26: "And he made from one man every nation of mankind to live on all the face of the earth". But, for the sake of the argument, if one grants Loke's invented category of mere anatomical *Homo* who do not qualify as humans, yet lived alongside them, Acts 17 would say nothing about these beings one way or another. Using Loke's interpretive methodology, verse 26 could simply mean that Adam gave rise to nations of his image-bearing offspring. It doesn't say the world is now completely devoid of non–image-bearing *Homo*. They could exist in pockets within those nations or they could compose separate groups in far-flung places of the world that would not be defined as 'every nation of mankind'.

Loke ardently believes all *Homo* today are image-bearers, but once he created the idea of non-humans who are very hard to distinguish from us, it is not so easy for him to get rid of them. These beings would be invisible to Acts 17:26, so Loke has no biblical basis for saying they are gone. He can stipulate that this is the case, but his stipulation is arbitrary.

3) Loke's model requires that living people descended from human/non-human pairings.

In Loke's version of GAE, only Adam's offspring are human, but they don't reproduce solely within their group. They mate with those from the non-human group to produce human offspring as well.

Loke has a short section addressing the question of whether this should be understood as bestiality (pp. 117–120). He allows for a yes or no answer. If this was a case of bestiality, Loke says Adam's descendants were disobedient to God by marrying outside their community. But, Loke says this may not have been considered bestiality, since the two groups were *biologically* the 'same flesh'. Although not technically human, the non-image-bearers were similar enough that the two groups could intermarry.

Loke even suggests that Cain might have married a non-human woman, rather than a relative. This just goes to show how bizarre and outlandish Loke's proposals are. To be married and raise children, this non-human woman must have operated a lot like a human. Loke even acknowledges that these non-humans could have been persons, creative, religious, and sinful (p. 138). They just didn't have God's image or the dominion mandate.

It also seems that mere anatomical *Homo* would have been less valuable than true humans. Loke assures us that "denying other hominids the status of God's-image-bearing human beings does not mean that they are not loved or valued by God" (pp. 101, 139). But Genesis 9:6 connects the unique value it places on human life with our status as image-bearers.

The mating of humans with non-humans raises all sorts of concerns about Loke's model, and these show just how foreign Loke's ideas are to the Bible. They aren't merely absent from Scripture; they require outrageous scenarios that fly in the face of Scripture.

Conclusion

Loke says his model removes all conflict between evolution and the biblical teaching about Adam. But his view denies humanity to many who do not deserve such discrimination, and he distorts Scripture to arrive at his conclusions, so he is mistaken.

References

1. Carter, R. and Sanford, J., Review of *The Genealogical Adam and Eve: The surprising science of universal ancestry* by S. Joshua Swamidass, creation.com, 25 Feb 2020.
2. Luskin, C., Chromosomal fusion without common ancestry; in: Gauger, A., Axe, D., and Luskin, C., *Science and Human Origins*, Discovery Institute Press, Seattle, WA, pp. 92–96, 2012.
3. Sarfati, J., Biblical chronogenealogies, *J. Creation* **17**(3):14–18, 2003.
4. Sarfati, J., Cainan: how do you explain the difference between Luke 3:36 and Genesis 11:12?, creation.com.
5. Halley, K., 'From the beginning of creation'—what did Jesus mean?, creation.com, Nov 2014.
6. Halley, K., Is Genesis 1 only about functional creation? Analyzing the claims of Old Testament professor John H. Walton, creation.com, May 2020.
7. Venema, D., as quoted in Loke, p. 137.

A deficient and defective doctrine of creation

The Doctrine of Creation: A constructive Kuyperian approach

Bruce Riley Ashford and Craig G. Bartholomew

IVP Academic, Downers Grove, IL, 2020

Martin Duboisée de Ricquebourg

Methodological complications

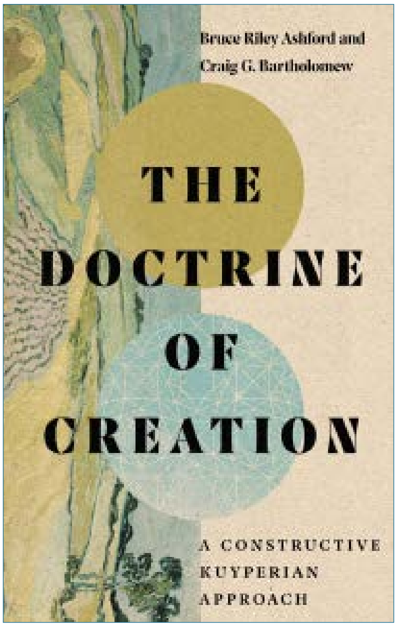
The Doctrine of Creation is an attempt by Ashford and Bartholomew to provide a 'robust' theological treatment of the Doctrine of Creation from the Kuyperian tradition in dialogue with Karl Barth (1886–1968; figure 1) (pp. x–xi). To anyone familiar with Barth's writings on creation, it is hard to conceive how any 'robust' doctrine of creation is obtainable on these grounds when so severely hamstrung at the outset. This is because Barth views Genesis as 'non-historical history', a 'pure saga' probably derived from older Babylonian myths.[1] He is also convinced that the first two chapters of Scripture are irreconcilably contradictory, having arisen from "different sources, originating at different times, against different backgrounds, and from a different intellectual approach."[2] Barth, like many other German scholars from his time, had been captured by the zeitgeist of evolutionary dogma.[3] Abraham Kuyper (1837–1920), on the other hand, is not crippled to the same extent by Barth's naturalistic myopia. Kuyper is wary of the "hypnosis of the dogma of evolution".[4] But he is still not ready to dismiss Darwin completely.[5] Kuyper endorses a theistic version of evolution or 'evolutionistic creation'.[6]

Put simply, both Barth and Kuyper are critically compromised when they engage with Genesis theologically. The pervasive secular scepticism of creation noticeably shapes their understanding of Scripture. For this reason, while Ashford and Bartholomew maintain that Scripture is their final authority, their theological conclusions betray an alternative allegiance (p. x). Their "great respect" for Barth, while tempered by their disagreements,[7] critically undermines this entire project. And although they claim to make a concerted effort to avoid engaging explicitly with contemporary science on matters of creation, the spectre of naturalistic science overshadows their project.

The goodness of a cursed world

That Ashford and Bartholomew want to provide a novel approach to the Doctrine of Creation is evident from the first paragraph of this book. They begin their discussion of creation with Peter's betrayal of Jesus in Mark 14:66–72 (p. 1). Their goal, following Erich Auerbach (1892–1957), is to "defamiliarize us with the doctrine of creation" (p. 3). It is hoped that this "fresh perspective" will lead to a renewed reverence for creation and help us escape from any "sub-Christian sacred-secular dualism" (p. 4).

Their first chapter goes on to explore creation from the standpoint of the early Christian creeds; namely, the Apostle's Creed and the Nicene-Constantinopolitan Creed. From the opening clause in both creeds, they discuss the relationship between God and creation, arguing for *creatio ex nihilo*[8] and the contingency of creation upon its creator (pp. 1–11). Ashford and Bartholomew then argue that the Doctrine of Creation has doxological and eschatological ramifications (p. 14). They assert, following Gottfried Leibniz (1646–1716), that this world is the best of all possible worlds (p. 38). What they mean by this is that the proclamation in Genesis 1:31, that God said it was very good, is still true of creation today. Put simply, they believe that the Fall has not altered or compromised the ontological goodness of creation (p. 51).



We are told that any denial of the goodness of creation marks the re-emergence of Neoplatonism (pp. 37, 39). They complain that the church has often failed to "articulate and embrace a full-orbed doctrine of creation" (p. 41). By 'full-orbed' they mean a doctrine of creation that affirms the triune creator, the goodness of creation, the *imago Dei*, and the future restoration and glorification of creation "in the eschaton" (p. 42). But their biggest concern is how theologians have failed to preserve an understanding of the "ontological goodness of creation" (p. 71). And their concern here is not merely for the state of creation *before sin came into the world*, but after it.

Thus, to argue for the goodness of creation, post-Fall, Ashford and Bartholomew try to make their case from Hebrews 11:1–3 (pp. 14–15). According to their reading of the text, "The effect of what has gone wrong in God's 'very good' (Gen 1:31) creation is that … we do not now naturally see that the world was created by the word of God" (p. 14). In other words, the Fall means that we now need faith to believe in the goodness of God's creation. But, as most commentaries on Hebrews will corroborate, the faith spoken of in Hebrews 11:1–3 is restricted to the fact that God created the universe by his Word. The goodness of creation is not in view here. And, even if it was, the act of creation spoken of in these verses is pre-Fall. To state the obvious, God did not create the world after the Fall, but before it.

But Ashford and Bartholomew persist with their conviction about the goodness of creation post-Fall. Appealing to Kuyper's distinction between *structure* and *direction*, they argue that structurally, creation is good; but directionally, it is 'twisted' (pp. 21, 102, 231, 254, 259). These categories are useless, however, unless explained with concrete examples. Is cancer not a structural change? How does animal cruelty or death feature within this framework? Ashford and Bartholomew do not explore this any further. Neither is the Curse of Genesis 3 discussed in any detail. But most importantly, the concept of 'goodness' is insufficiently clarified. We are told that God's creation is ontologically good but not perfect (pp. 100–101). What does this mean? What are the principal theological distinctions between a good creation and a perfect creation? This becomes even more problematic when discussing the new creation. Apparently, the future restoration of creation will be an "elevation and enhancement of creation in its original form" (p. 102). But what about pain, sickness, suffering, and death? If the Fall has not affected the intrinsic goodness of creation, how are we to respond to Darwin, who once asked:

> "...what advantage can there be in the sufferings of millions of the lower animals throughout almost endless time? This very old argument from the existence of suffering against the existence of an intelligent first cause seems to me a strong one".[9]

The so-called 'goodness' of creation becomes a hollow concept detached from reality. As we will see later, Ashford and Bartholomew believe that pain, suffering, sickness, and death were typical of that world which God once called 'very good'. This is why Christians who embrace theistic evolution or interpret the fossil record on naturalistic terms severely compromise any effort to provide a robust theodicy to address the obvious problem of evil.

To try and bolster their argument from history, Ashford and Bartholomew summon Irenaeus, Tertullian, Athanasius, Basil, Augustine, Maximus, and Aquinas as witnesses to the fact that God's creation, *contra* Gnosticism, should be viewed as good (pp. 48–63). Even the Reformation is restricted to this narrow viewpoint as a movement that "sought to recover the goodness of creation" (p. 63). Thus, Calvin, Luther, and the Puritans all endeavoured to "recover the goodness of material creation" (p. 64). The Anabaptists, however, are labelled regressive and neo-gnostic for failing to "distinguish between the structures of creation and the moral direction of creation" (pp. 66–67). In the same way, "American fundamentalists" are blamed for undermining the goodness of creation by misinterpreting 2 Peter 3:12–13 (pp. 98–99).

But what Ashford and Bartholomew fail to provide from their brief survey of early church history is a single instance of someone arguing for the ontological goodness of creation *post-Fall*. Did the early church fathers really believe that the Fall had no effect on the goodness of creation? This is not evident from the citations provided.


Image: Unknown author, Wikimedia / Public Domain (colorised)

Figure 1. Karl Barth (1886–1968) was one of the most influential theologians of the 20th century.

Hermeneutical baggage from the Ancient Near East

I first encountered Bartholomew's views on creation in an undergrad course at Bible college where we were assigned readings from his book, *The Drama of Scripture* (2004). Even back then, Bartholomew was arguing that Genesis 1–2 is an ancient polemic in competition with other ANE (Ancient Near East) creation stories and should not be consulted for information about "how God made the world".[10] Two decades later, and hardly anything has changed.

Thus, while Ashford and Bartholomew stress the critical importance of creation to the entire drama of Scripture, it is disconcerting to see how they recast the creation story as a polemic against ANE views of the world with deference to the documentary hypothesis (pp. 23, 24, 26, 28–29, 40, 176, 181, 186).[11] But if creation is to function as a necessary "presupposition of the entire drama of Scripture", any tampering with Genesis can only compromise the integrity of the whole theological structure which is built upon these foundations (p. 25).

In the fourth chapter, Ashford and Bartholomew explore the power of the creator, looking at four different Psalms. Once again, their interpretation of Scripture is hindered by unnecessary external factors. We are told that Psalm 29 and 82 must be interpreted in light of the Canaanite gods Baal and El along with their corresponding mythologies (pp. 113–114). Attention to the practices and beliefs of the ANE forms an integral part of the hermeneutical toolbox required to correctly decipher the Old Testament (pp. 115, 126, 134–135). The discussion eventually turns to the subject of theodicy, where Ashford and Bartholomew insist that "The Bible is profoundly in touch with the brokenness of the world and the reality of evil", rightly pointing out the critical importance of the Cross of Jesus Christ (p. 131). But even here, the discussion suffers from a lack of engagement with Genesis 3.

Chapter 5 begins with a renewed emphasis on the foundational importance of the Doctrine of Creation to the rest of redemptive history (p. 142). Ashford and Bartholomew rightly observe that Genesis 1:1–2:3 establishes the "forming and ordering" of creation (p. 143). But, because the creation account is a "sui generis event", they also insist that the genre of Genesis is essentially inscrutable. Thus, although the authors acknowledge the narratival structure of the text—even to the point of calling Genesis 1 historical—it still cannot be understood apart from the context of other ANE stories (pp. 145, 150, 158, 162, 286, 294). This is reminiscent of Barth's unhistorical history. The historical details in Genesis are not taken seriously.

We are then told that Genesis places the creation of light before the sun and moon in order to challenge the beliefs of ancient Egyptians (p. 160). There may be some truth in this, but if God did not literally create the light before the sun and moon, how does this polemic carry any weight? Without a literal ordering of days within a fixed timeframe, the argument that Genesis presents to a pagan ANE world falls flat. Similarly, Ashford and Bartholomew accept the portrayal of animals and humans as herbivores in Genesis 1:29–30, calling the text 'evocative', when it is evident that they also believe, on naturalistic grounds, that this state of affairs never actually happened (pp. 163–164). This leads to a discussion on cruelty of animals, but without any acknowledgment of how evolution makes this a feature instead of a bug (pp. 164, 345). Once again, the goodness and completeness of creation is accepted from Genesis 2:1–4, but without any appreciation for what this would necessarily preclude (p. 170).

Using the wrong framework

We are led to believe that the timeframe of creation is a matter for modern science, not Scripture. This leads to a brief discussion of 'modern evangelical issues' concerning how to read Genesis, specifically the days of creation (p. 96). There are six views presented: (1) six-day creation, (2) the gap theory, (3) revelatory-day theory, (4) day-age theory, (5) analogical-day theory, and (6) the framework hypothesis. Ashford and Bartholomew express their preference for the framework hypothesis (p. 98). Thus, they insist that Genesis can only inform us that God created time without providing any further details as to how or when he did so (pp. 154–155). Not surprisingly, Ashford and Bartholomew are sympathetic to Augustine's emphasis on the simultaneity of creation where "the days are not time periods but categories for teaching purposes" (pp. 144–145).

Ashford and Bartholomew admit that without revelation we would not know that God had created the world *ex nihilo* and made man in his image (p. 225). But what they fail to appreciate is that the efficacy of this revelation is severely compromised when its literal historicity is denied. A non-historical Genesis is incapable of revealing the true history of how God created everything. Ashford and Bartholomew cannot pick and choose what to retain as factual and what to reject from Genesis. The creation account stands or falls *in toto*.

This type of problem persists with their exposition of Genesis 3. Here, we are encouraged to regard the text as historical and paradigmatic (p. 226). Ashford and Bartholomew reject the allegorizing that typifies how many scholars interpret the two trees of Eden (p. 227). But, at the same time, they never go so far as to assert that these trees literally existed. Following Wenham, the account is deemed 'protohistorical' (p. 231). Likewise, the serpent merely "symbolizes sin, death, and the power of evil", and the Fall is all about how human beings chose 'moral autonomy' or forbidden wisdom (p. 255). Whether or not this involved a literal Adam and Eve is carefully avoided.

Eschatologically implausible

Ashford and Bartholomew return to the subject of cruelty to animals, lamenting the "abysmal record of the exploitation" in history, but with no recognition of how theistic evolution makes this category of evil a complete misnomer (p. 178). Their emphasis on environmentalism brings mystic sentimentalism to bear upon an over-realized eschatology. We are told to "make place for birds in our lives" so that "they will call us back into place" (p. 196). There is an expectation for humans to live peaceably with wild animals.

In general, Ashford and Bartholomew see great continuity between the old creation and the new. In fact, it is their conviction that this world will not be destroyed but restored (pp. 306–311). Put simply, "The new heaven and earth is *this* universe" (p. 315). Following the text preserved in Codex Sinaiticus and Codex Vaticanus, they argue that the fire spoken of in 2 Peter 3:10 is a purifying fire, not a destroying one (pp. 317–322). They emphasize this because they want to retain an eschatological purpose for the care of creation. A creation destined for obliteration means that all environmental efforts will ultimately amount to nothing.

What Ashford and Bartholomew want to establish is a 'cultural continuity' between this present life and the next (p. 328). In other words, the physical or material effects of man's efforts in this world will carry over to the next. The example they offer is of ships built in this world that are restored in the next. They anticipate "such developments" to "find their way into the new heaven and new earth" (p. 329). Whether or not the reader finds this compelling, we are encouraged to think of the new creation as a "future cosmic resurrection" akin to the resurrection of the body (p. 321, 325). But this analogy fails to consider the fact that the human body is literally destroyed by death before being raised to life. Annihilation of the flesh does not negate continuity between the old creation and the new creation. These are eschatological realities which Ashford and Bartholomew need to examine more closely. And, once again, while they have no problem appealing to texts like Isaiah 65 to describe what the new creation might be like, they give little thought to why there would be a cessation of carnivory in this world (pp. 314–315). If suffering and death can exist in a "very good" world, why not in the new creation also? Their doctrine of creation is deficient. Consequently, they allow for the possibility of death even in the new creation. They state, "It remains an open question as to whether humans will be vegetarians in the new heavens and the new earth" (p. 342). This is hard to stomach given their insistence that our "practices of eating and drinking" be informed by a "robust doctrine of creation" (p. 346).

Philosophically flawed

In the first chapter of this book, Ashford and Bartholomew point out how Maimonides failed to correctly understand God and creation because his interpretation was heavily influenced by Greek philosophy instead of Scripture (pp. 36–37). This line of thinking is developed further in the next chapter as they look in more detail at the influence of Plato, Plotinus, and Philo on the early church fathers (pp. 44–47). Origen is singled out as a theologian who regretfully "reinterprets Scripture to fit the philosophical system he prefers" (p. 55). For similar reasons, they also acknowledge that "Augustine's writings are not an entirely trustworthy guide to the biblical teaching on creation" (p. 60). They state that his Neoplatonic convictions "kept Augustine from ever reading the Genesis account on its own terms" (p. 61). This is true. But what Ashford and Bartholomew fail to see is how *their* endeavour to derive a doctrine of creation suffers from its own philosophical baggage.

For example, Johann Georg Hamann (1730–1788) is praised for not capitulating to the Radical Enlightenment, being lauded as "the most profound Christian thinker of the eighteenth century" (pp. 72–76). Apart from his influence upon Barth, he is also famous for introducing Hume's writings to Kant (pp. 76–77). We are told that Hamann considered Scripture "the key to our understanding of the world" (p. 78). What Ashford and Bartholomew do not mention is the fact that Hamann treats Genesis more like a dramatic poem or 'rhapsody' than as narrative history.[12] He had a significant influence on Gottfried von Herder (1744–1803) (figure 2), who was one of the first to call the creation story a 'child-like fable'.[13]


Image: Franz Gerhard von Kügelgen, Wikimedia / Public Domain

Figure 2. Portrait of Gottfried von Herder (1744–1803) by Gerhard von Kügelgen (1772–1820)

In fact, this book is filled with the opinions of men who do not take Scripture as the infallible Word of God. The reader is repeatedly encumbered by lengthy discussions in dialogue with liberally minded scholars like Gerhard von Rad (1901–1971), Ernst Käsemann (1906–1998), Emil Brunner (1889–1966), Friedrich Schleiermacher (1768–1834), Michel Henry (1922–2002), Claus Westermann (1909–2000), Søren Kierkegaard (1813–1855), Jürgen Moltmann (1926–) *et al.*.

Accompanying them are prominent secular philosophers like Arthur Schopenhauer (1788–1860), Immanuel Kant (1724–1804), Paul Ricoeur (1913–2005), Ludwig Wittgenstein (1889–1951), Alfred North Whitehead (1861–1947), Philip Rieff (1922–2006), and Jacques Derrida (1930–2004). It is hard to conceive how Ashford and Bartholomew had any hopes to derive a robust doctrine of creation from such a milieu.

When Ashford and Bartholomew discuss the French phenomenologists, we are told that they "provide the reader with a feast" when it comes to delineating the Doctrine of Creation (p. 93). All the examples provided, however, are painfully esoteric and philosophically burdensome to parse. Thus, Jean-Louis Chrétien (1952–2019) is praised for developing a "remarkable philosophy of language" in which he uses Noah's Ark as a metaphor for the language man must "inhabit" (p. 91). Michel Henry (1922–2002) is celebrated for his 'trinitarian anthropology', which describes the "reciprocal phenomenological interiority" of the "common Spirit" of the Self and the Word (p. 93). Emmanuel Falque extends Chrétien's metaphor of the "ark of speech" to the "ark of flesh" by which it is apparently "evocative to think of creation as 'the first ark'" (p. 93). None of the so-called greater thinkers in this chapter treat Genesis as history.

So while Ashford and Bartholomew correctly maintain that the fear of the Lord is foundational to any attempt to understand creation, it is disappointing to notice how much space is allocated in this book to the opinions of men who do not fear the Lord (p. 337). Indeed, only a few paragraphs after mentioning the fear of the Lord, they praise Oliver O'Donovan's theological epistemology as "most profound" (p. 338). We are informed that O'Donovan's epistemological stance "operates between Barth and Brunner" (p. 338). But neither Barth nor Brunner serve as admirable examples of what it means to begin with the fear of the Lord in philosophy. One can only think that O'Donovan's position must likewise be compromised. And, indeed, if we explore O'Donovan's writings further, especially his views on homosexuality, this is sadly the case.[14]

Following Kuyper, the authors assert that all cultural spheres, including science and education, operate under the sovereignty of Christ (p. 267). But what does this look like? How should we do science and education to the glory of God? What are we to make of the naturalistic framework which continues to exclude God's Word from science and education? What does it mean to actually fear the Lord in practice (p. 269)? Barth is praised for not capitulating to Nazism, but to what extent do Christians in the public square capitulate to the secular agenda today (p. 270)? Ashford and Bartholomew rightly acknowledge that the "roots of modern science" can be traced back to the "Christian culture of medieval Europe", but they should also remember why this was the case (p. 272). At the heart of this scientific renaissance was a reinvigorated interest in the literal interpretation of the creation story.[15]

Ashford and Bartholomew argue that our doctrine of creation should inform our view of time and history (p. 347). They even concede that "Genesis 1 establishes the day and the week as constituent elements of time". But they never go so far as to actually treat the first week of the world as seven days or, from the fact, make any inferences concerning the actual chronology of history. And while they point out that scientific theories cannot be "proven true or even probably true", they refuse to let Scripture challenge the edicts of modern science, fallible as they are (pp. 351–353). Instead, we are to take the "strong scientific support" for an old earth as hermeneutically formative for how we read Scripture (p. 355). This is despite their admission that "Modern science is not religiously neutral" (p. 358).

Ashford and Bartholomew, following Plantinga, express some scepticism of evolution (pp. 355–357). But they deliberately leave room for theistic evolution, which they claim is "compatible with theism and theistic religion" (p. 357). This stance is not merely erroneous; it also critically compromises the robustness of their doctrine of creation. This becomes apparent a few pages later, where they go on to identify transgenderism as "deeply incoherent" (p. 360). They even make their case, to some extent, from Genesis 1:27 (p. 361). Evidently, some details in Genesis 1 retain their literal value—but their lack of attention to the rest of Genesis 1 undermines their overall case. In particular, they fail to recognize how transgenderism finds its logical roots in evolutionism. If, by ignoring how God created his creatures in Genesis 1, we accept the possibility of ape-like creatures becoming humans, how will we rule out the much easier transformation of male to female *within the same species*? If we can swallow the camel, why not the gnat?

Final thoughts

Ashford and Bartholomew set out to provide a robust doctrine of creation. But the end result is less than satisfying. It is philosophically flawed, theologically compromised and exegetically weak. This book reads more like a historical survey of secular and liberal views—often barely tangential to the intended subject—than a coherent case for the Doctrine of Creation. Thankfully, there are many other excellent works on the Doctrine of Creation that do not suffer from these failings.[16]

References

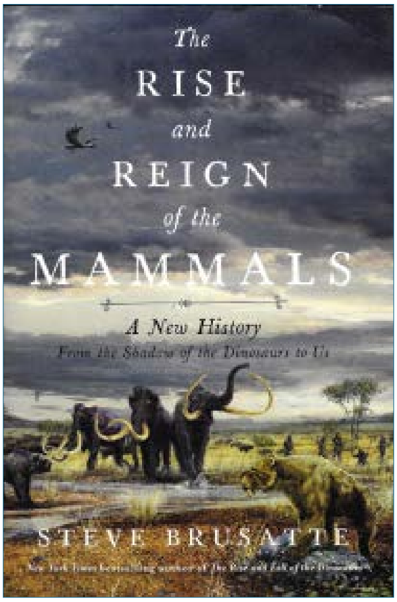
1. Barth, K., The doctrine of creation: the work of creation; in: Bromiley, G.W. and Torrance, T.F. (Eds.), *Church Dogmatics*, vol. 3.1, §40–42, T&T Clark, London, pp. 78–81, 87, 2009.
2. Barth, ref. 1, pp. 79–80.
3. Barth, K., *Letters 1961–1968*, William B. Eerdmans, Grand Rapids, MI, p. 184, 1981.
4. Kuyper, A., Evolution (1899): the deleterious philosophy and consequences of evolutionary naturalism, in: Bratt, J.D. (Ed.), *Abraham Kuyper: A centennial reader*, William B. Eerdmans, Grand Rapids, MI, p. 405, 1999.
5. Kuyper praises Darwin for "paying his respects to the mystery of religion". Bratt, ref. 4, pp. 405–420, 1999.
6. Bratt, ref. 4, pp. 436–437, 1999.
7. See pages 159, 162, 164, 167, 181, 213, 218–219, 287, and 300.
8. At this point, Ashford and Bartholomew claim that Justin Martyr denies *creatio ex nihilo*, but they have misread him. Justin explicitly states that the universe had a beginning. His comments in the first Apology (10.2) that God created "all things out of unformed matter" relate to Genesis 1:2ff, not Genesis 1:1. Martyr, J., Writings of Saint Justin Martyr; in: Falls, T.B. (Ed.), *The Fathers of the Church*, Christian Heritage, New York, p. 156, 1948.
9. Darwin, C.R., *The Autobiography of Charles Darwin 1809–1882: With the original omissions restored*, Collins, London, p. 90, 1958. Darwin, C.R., *The Life and Letters of Charles Darwin, Including an Autobiographical Chapter*, Darwin, F. (Ed.), vol. 2, John Murray, London, p. 312, 1887.
10. Bartholomew, C.G. and M.W. Goheen, *The Drama of Scripture: Finding our place in the biblical story*, Baker Academic, MI, p. 32, 2007.
11. In the few places where Ashford and Bartholomew do question the documentary hypothesis, they are conspicuously cautious (pp. 26, 157).
12. Hamann, J.G., *Writings on Philosophy and Language*, Cambridge University Press, Cambridge, pp. 67–68, 70, 2007.
13. Herder, J.G., *The Spirit of Hebrew Poetry*, vol. 1, Edward Smith, Burlington, pp. 49, 124, 131–132, 1833.
14. O'Donovan, O., *Church in Crisis: The gay controversy and the Anglican communion*, Cascade Books, OR, pp. 102–118, 2008. O'Donovan, O., Homosexuality in the church: can there be a fruitful theological debate?; in: Bradshaw, T. (Ed.), *The Way Forward? Christian voices on homosexuality and the church*, Hodder and Stoughton, London, p. 35, 1997.
15. Harrison, P., The Bible and the emergence of modern science, *Science and Christian Belief* **18**:115–132, 2006; p. 130. Snobelen, S.D., *Isaac Newton and Apocalypse Now: A response to Tom Harpur's "Newton's strange bedfellows"*, University of King's College, Canada, p. 2, 2004.
16. For example, Berkhof, L., *Systematic Theology*, The Banner of Truth Trust, Edinburgh, 1976.

Entertaining storytelling about the presumed evolution of mammals

The Rise and Reign of the Mammals: A new history from the shadow of the dinosaurs to us

Steve Brusatte

Mariner Press, New York, 2022



John Woodmorappe

Author Steve Brusatte (b. 1984) is an American paleontologist. He is currently Reader (second-highest academic rank) in Vertebrate Paleontology at the University of Edinburgh.

This book is delightful, sometimes entertaining, reading. The author is clearly a storyteller, not only in terms of the presumed evolutionary origin of mammals, but also in terms of the adventures of the leading personalities in mammalian paleontology.

As an example of the latter, Brusatte discusses Leigh Van Valen (1935–2010), a very brilliant and creative evolutionary biologist at the University of Chicago, with his personal library of 30,000 books. I can relate. While I never went to that school, I often met informally with Van Valen and had long discussions with him on various details of evolutionary theory.

Author Brusatte's writing is not pushy; it is rather low-key. He avoids the usual evolutionistic triumphalism and the bashing of those who dissent from evolution (creationists and proponents of Intelligent Design). However, he presents really nothing new, just the same old shibboleths of evolutionistic orthodoxy. His gentle storytelling style may evoke childhood memories of bedtime fairy tales, and thus make the reader more prone to be receptive to his evolutionistic claims (fairy tales?).

Mammal-like reptiles or stem mammals?

By way of introduction, the author rejects the term 'mammal-like reptiles' as outdated (p. 20), as it seems to imply some kind of correspondence with modern 'crown' reptiles, such as snakes, lizards, and turtles. In addition, Brusatte considers the 'reptilian' traits in mammal-like reptiles to be 'primitive' features shared with many other organisms in the fossil record, and not features that are specifically reptilian. He uses the term 'stem mammals' instead of 'mammal-like reptiles'.

This new term is a bit Orwellian, in that it, by itself, implies the validity of organic evolution and cladistics. For this reason, I reject it in favour of the old term. In addition, 'mammal-like reptiles' is a long-standing term, and has never before seemed to bother anyone.

Mammal-like reptiles are not a prediction of evolutionary theory!

Author Brusatte brings up T.H. Huxley's belief that certain salamanders, and not the mammal-like reptiles, were ancestral to mammals. Unfortunately, he caricatures and scorns this position as some kind of a personal spat between Huxley and Owen (a fellow evolutionist), and does not mention any specific evidence that Huxley used to arrive at his conclusions.

Huxley was clearly a thoughtful and doctrinaire evolutionist. After all, they did not call Huxley 'Darwin's Bulldog' for nothing! Was Huxley's personal grudge against Owen the *only* reason for Huxley accepting evolutionary mammalian origins from salamander-type amphibians instead of from mammal-like reptiles? (p. 27). Hardly.

In fact, Brusatte inadvertently destroys his 'personal grudge' argument as he admits that the salamander-as-ancestors position had persisted for several decades, long after the deaths of Darwin, Huxley, and Owen. In fact, it was not finally laid to rest until paleontologist Robert Broom (1866–1951, figure 1) did his extensive work in the early 20th century (pp. 27–28).

Let us take a closer look at all this. Evolutionists commonly refer to mammal-like reptiles as being a prediction of evolutionary theory. This evolutionary triumphalist assertion is nothing of the sort. T.H. Huxley, who was about as evolutionistic as one can get, had no problem rejecting mammal-like reptiles as ancestors of mammals and still fully believing in evolution.

What if we extend this reasoning? If mammal-like reptiles had never existed, would evolutionary theory be discredited or falsified? Absolutely not. Evolutionists would just pick out some other fossil organism and invoke it as an ancestral state of mammals. And evolutionists would live happily ever after.

In other words, evolution is endlessly plastic. No matter what turns up in the fossil record, it will not only be explained in terms of evolution, but can even be proclaimed a 'prediction' of evolutionary theory.

No special explanatory power of evolutionary theory

The author makes these candid comments on the presumed evolutionary 'chain' of Permian therapsids into eventual mammals:

> "Many things were changing in harmony, and *it's difficult to untangle what was driving what*. Perhaps small size necessitated higher body temperatures to buffer against sudden climate shifts or demanded more efficient ways of gathering and processing smaller parcels of food. Maybe warm-bloodedness mandated that these cynodonts ate bigger meals to fuel themselves, or possibly it was the other way around: changes to the jaws and muscles came first, allowing them to eat more, and thus provided more energy for warm-blooded physiology to develop. *We don't really know the answer*. What we do know, though, is that small size, warm-blooded metabolism, and stronger and more efficient bites developed together as part of a package deal [emphases added]" (p. 57).

We see that the 'chain' of mammal-like reptiles 'becomes more and more mammalian' only in a rather forced and confused sense. Also, based on the foregoing quoted statements, evolutionary theory has rather limited explanatory power. It does not predict the evidence: It *follows* the evidence. In addition, evolutionary theory is not read out of the evidence: Evolutionary theory is read *into* the evidence. And all this is supposed to pass for 'absolutely factual' evolutionistic science!

The bewildering assortment of 'reptilian' and 'mammalian' traits does not require an evolutionistic explanation. It can readily be explained by the larger morphospace enjoyed by fossil organisms in comparison with that of the relatively narrow set of extant mammals.

A closer look at the 'chain' of mammal-like reptiles, as customarily assembled, bears the hallmarks of an artificial set of disparate organisms that had been cobbled together. At best, it shows only a contrived 'progression' to 'mammal-ness'—one that is full of internal inconsistencies, major discontinuities, and trait reversals.[1]

Potential problems of a transitional mammalian-reptilian masticatory-auditory system

According to standard evolutionary orthodoxy, a mammal-like reptile having a quadrate-articular jaw joint evolved into an organism with a dentary-squamosal jaw joint, and the remaining bones evolved into the three tiny bones in the inner ear. Decades ago, the immortal creationist debater Dr Duane Gish (1921–2013), objected to this scenario, questioning the workability of the proposed transitional system.[2]

While not going as far as Gish, Brusatte, in his discussion of *Origolestes*, alludes to the potential handicap that is inherent in the believed transitional system:

> "Because these two former jaw bones are not fully detached from the jaw, we can call them by their new names: the hammer and the ring. This small step was revolutionary. Now the jaws could go their own way, and become more efficient at biting and chewing, *without worrying about interfering with hearing function*. The ears could go their own way, too, and become even better at hearing high-frequency sounds *without being*

> *disturbed by the jaws* [emphases added]" (p. 111).

Taking Brusatte further, one must keep in mind that unless the transitional system gives the organism immediate selective advantage, or at least does not diminish its fitness even slightly, it will be removed by natural selection. This reinforces the fact that evolution does not have foresight and is not teleological: an organism cannot have a transitional system merely in 'anticipation' of a later evolutionary development—wherein some of the jaw bones become 'free' to become the bones in the inner ear for better hearing. It must fully work immediately, or it will not work at all.

Based on what Brusatte has written, it does not sound as though evolutionists have solved the problem of the adequate fitness of their suggested transitional masticatory-auditory system.

Ontogeny recapitulates phylogeny—special pleading?

Brusatte falls back on embryonic recapitulation, wherein the ontological development of the mammalian jaw and ear is supposed to recapitulate the presumed evolution of the reptilian jaw into the mammalian jaw and ear. He presents no independent evidence demonstrating that embryonic development ever became a 'movie' of presumed evolutionary history.

In addition, use of embryological evidence is another evolutionistic pick-and-choose exercise: If embryonic development happens to recapitulate phylogeny as it is currently understood, then it 'counts'. If it does not, then this fact is disregarded. This reeks of special pleading. In conclusion, any correspondence of embryological development and presumed evolutionary history appears to be little more than a coincidence.

Mammaliaformes and mammals

Many decades ago, Duane Gish was berated by his evolutionist opponents for 'refusing to recognize' that the 'first mammal', *Morganucodon*, was indeed a mammal. Let us look closer at this.

Evolutionists themselves have different definitions of 'mammal'! Brusatte comments:

> "The definition of mammals that I use throughout the book—any descendant of the first cynodont to develop a robust dentary-squamosal jaw joint [and includes *Morganucodon:* p. 72]—is prevalent in the historical literature… . This group—what I call 'mammals'—is referred to as Mammaliaformes by those researchers who prefer a 'crown group' definition for mammals, *which limits the name 'mammals' to the group on the family tree including the modern mammals* (monotremes, marsupials, placentals) and all descendants of their most recent common ancestor [emphasis added]" (p. 419).

Clearly, it is 'permissible' to deny that *Morganucodon* is a mammal, even within the confines of evolutionistic reasoning. The evolutionists owe Gish a posthumous apology.

By the way, the ability of the term 'mammal' to have different shades of meaning is unremarkable, and does not necessarily imply evolution. As noted earlier, fossil organisms had utilized a broader morphospace than do the animals that we are familiar with. So it is hardly surprising that traits we consider mammalian, because they only appear in mammals today, had a broader deployment in the fossil record. The term 'Mammaliaformes' appears to be a good one, if it is divested of its evolutionary baggage.

Image: Author unknown, Wikimedia / Public Domain (colourized)

Figure 1. Robert Broom, the South African paleontologist who officially 'promoted' mammal-like reptiles, over salamanders, as the putative evolutionary ancestors of mammals.

Nor is this playing with definitions confined to academic matters. Words can have different shades of meaning in an everyday sense. Consider the word *meat*. It usually means the flesh of common farm animals, such as that of cows and pigs. It can also be broadened to include game animals, and even insect-based food. Finally, the term meat can refer to *any* solid food, whether it is of animal or plant origin—e.g., "I have given every green herb for meat" (Genesis 1:30, KJV).

The molecular 'clock' conflicts with fossil-based evolutionary scenarios

I now shift the discussion to more modern-looking mammals. With reference to the DNA molecular 'clock', Brusatte comments:

> "When Springer's team applied this rationale to their DNA trees, *they were in for another shock*: many of the modern placental lineages—not only the fundamental groups like Afrotheria and Laurasiatheria, but also individual lines like primates and rodents—must have originated back in the Cretaceous or the earliest Paleocene. *In many cases, this is long before their fossils first*

> *appear*, hinting at a vast unrecorded history [emphasis added]" (p. 210).

Most definitely, this was not a prediction of evolutionary theory! For those who are 'keeping score' about the wonderful predictive powers of evolutionary theory, here is another example of the contrary.

Evolutionary 'natural groupings' and nested hierarchies blown away

One of the pillars of evolutionary theory is the premise that living things can be sorted in accordance with a hierarchy of shared similarities, and that the very ability of such a hierarchy to be constructed proves evolution. Decades ago, George Gaylord Simpson (1902–1984) had all the mammals sorted and classified in accordance with such an evolutionistic methodology.

With reference to him, Steve Brusatte comments:

> "When the first DNA-based genealogies of mammals were published in the late 1990s and early 2000s, by molecular biologist Mark Springer and his network of collaborators, *paleontologists were shocked. Many of the relationships among placentals championed by Simpson disintegrated*, revealed as illusions of anatomical convergence. Genes showed that pangolins are not closely related to anteaters and sloths, but group with dogs and cats. Bats are not next-of-kin to primates, but part of a larger assemblage with dogs, cats, and pangolins, plus the perissodactyls with an odd number of toes (like horses) or even-toad artiodactyls (like cattle). These latter two groups both have hooves, but there are other hoofed mammals dispersed around the family tree—like the cute little hyraxes, which group with elephants. Hooves, therefore, really did evolve multiple times [emphasis added]" (pp. 208–209).

Brusatte then turns the knife as he continues:

> "But that is nothing compared to the madness of the insect-eaters. Once thought by Simpson and Novacek to compose a single group, they were scattered all across the DNA tree. Some, like the golden moles and tenrecs, are closely related to the hyraxes and elephants—*a most unusual union that nobody had ever predicted from anatomy*. Insectivory, and the distinctive molars that enabled it, was thus reinvented numerous times by numerous different mammal lineages [emphasis added]" (p. 209).

The presumed predictive powers of evolutionary theory have just taken another nosedive. Note also that 'convergent evolution', or 'things evolving multiple times', is another form of evolutionistic special pleading. It allows for shared, detailed anatomical similarities to remain proofs of evolution—except, conveniently, when they don't.

No transitions in the alleged evolution of bats

Brusatte candidly writes:

> "It goes without saying, but a bat looks nothing like a horse or a dog, so there must have been a transitional sequence of extinct species that morphed from a ground-dwelling mammal with walking limbs to a hand-winged flier. The problem is, we don't have many fossils depicting this evolutionary transformation. The first bat skeletons that turn up in the Eocene, like Nancy Simmons's *Onchonycteris*, *already look like bats* [emphasis added]" (p. 261).

Conclusions

Special creation is often dismissed, based on the claim that 'God can do anything and everything', and especially that 'it explains too much' in that any possibility can be fitted to it. As shown in this review, this criticism backfires. Much the same (if not more) can be said about evolutionary theory.

The more that is learned about alleged evolution, the more plastic and *ad hoc* it becomes. Just about any observation, from living things or from the fossil record, can be fitted to it. All this further erodes evolutionistic claims of the explanatory power of evolution over special creation.

The mammal-like reptiles, nowadays touted as the self-evident ancestors of mammals, were, for a long time, challenged as mammalian ancestors in favor of certain salamanders. Were mammal-like reptiles never discovered, evolutionists would just have nominated some other organism as the ancestor of mammals, and evolutionary theory would just have continued on its merry way.

Does detailed anatomical similarity self-evidently imply a close common evolutionary relationship? Hardly, and certainly not self-consistently. Certain evolutionary relationships, deduced from careful studies of comparative anatomy, have been shown to be impossible based on analysis of DNA.

References

1. Woodmorappe, J., Mammal-like reptiles: trait reversals and discontinuities, *J. Creation* **15**(1):44–52, 2001.
2. Cserháti, M., Did the ear bones of mammals really evolve from the jawbones of reptiles? Eardrum is an obstacle for evolution of middle ear bones in mammals, 2 Jul 2019, creation.com.

Where can the speed of light change?

Richard Ward

The wave theory of light is firmly established, and consequently the path of light will usually bend where its speed changes because of its location. This restricts models of the universe to those in which the bending is so small that it cannot be observed from the earth.

Refraction

One hypothesis, among many, to solve the Distant Starlight Problem is that the speed of light is much higher in parts of the universe distant from the earth.[1] To test this hypothesis, we need to apply the wave theory of light, which was first propounded in the 17th century, but not widely accepted until two hundred years later.

Refraction had been observed and measured in the ancient world, but the relationship between the angles (figure 1) had not been found. In the figure, the dotted line is called the normal, and the angles are measured from it. The earliest known document stating the correct relationship is dated AD 985,[2] but this was not widely known, and several men independently rediscovered it over the following centuries. In the English-speaking world it is commonly known as Snell's Law (Willebrord Snell 1621).[3]

In general,

$$n_1 \sin i = n_2 \sin r$$

where n_1 is the refractive index of the first medium and n_2 is the refractive index of the second medium. The refractive index of a vacuum is defined to be 1.

Competing hypotheses

In the 17th century there were two hypotheses for the nature of light. Isaac Newton suggested that it was a stream of particles (or corpuscles),[4] but Christiaan Huygens thought it was a series of waves.[5]

Isaac Newton thought that the medium of higher refractive index attracted the corpuscles, so increasing their velocity perpendicular to the surface, and bending their path. Let u be their speed in medium 1, and v their speed in medium 2. The component of their velocities parallel to the surface does not change:

$$u \sin i = v \sin r$$

This matches Snell's Law if the ratio of the speeds is the same as the ratio of the refractive indices.

Huygens' model is shown in figure 2. In time t the wave travels from C to B at speed u, but a shorter distance from A to D at speed v.

$$\text{CB} = u\,t = \text{AB} \sin i$$
$$\text{AD} = v\,t = \text{AB} \sin r$$

Therefore

$$v\,t = \text{AB} \sin r$$
$$u\,t\ \text{AB} \sin i$$

So

$$v \sin i = u \sin r$$

This also matches Snell's Law, but the speed ratio is the inverse of the refractive indices.

Both hypotheses agree with the experimental observations, but Newton's requires a faster speed in the medium of higher refractive index, and Huygens' a slower speed. Both men were glad that Ole Roemer confirmed, in 1674, that the speed of light in the vacuum of space was finite, but there was no way to compare it with the speed in a dense medium. Because of Isaac Newton's brilliance in mechanics, most scientists supported his corpuscular hypothesis.

At the start of the 19th century Thomas Young performed an experiment using two slits very close to each other in which he observed *interference* which is characteristic of waves.[6] He published this is 1807, but many supporters of the corpuscular hypothesis remained sceptical.

The French Academy arranged a competition in 1818 which was won by a paper on *diffraction* by Augustin Fresnel, a strong supporter of the wave model. The eminent mathematician Siméon Poisson, one of the judges, used the argument in Fresnel's paper to show that there would be a bright spot in the centre of the shadow of a circular obstacle.[7] He thought this was ridiculous and concluded that Fresnel's treatment was absurd. Somewhat to his chagrin, the bright spot was verified by the astronomer François Arago. Figure 3 shows the bright spot in the centre of the shadow of a steel ball of diameter 0.66 mm.

As the corpuscular hypothesis could not explain this, it received its death wound. From that date onwards all physicists accepted that the wave model was the correct

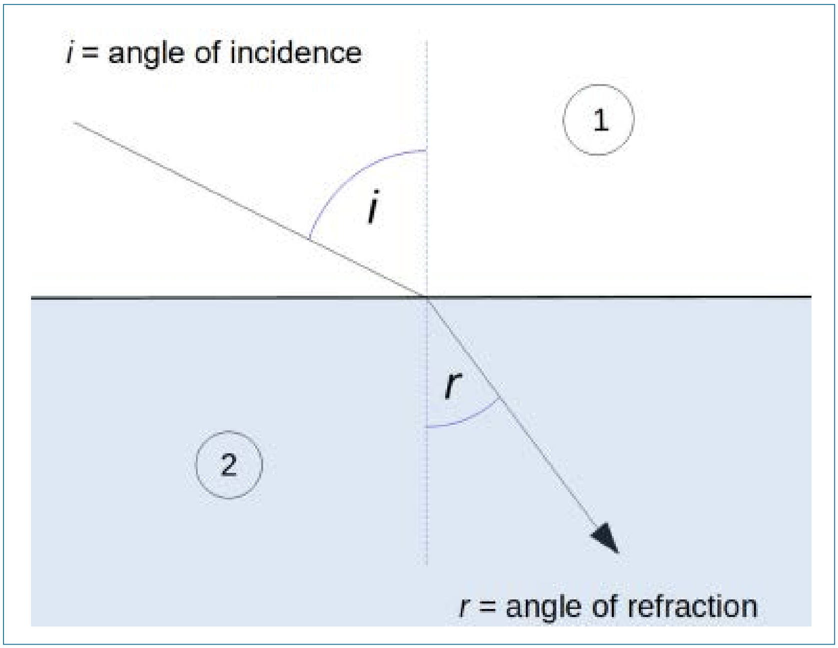


Figure 1. Angles

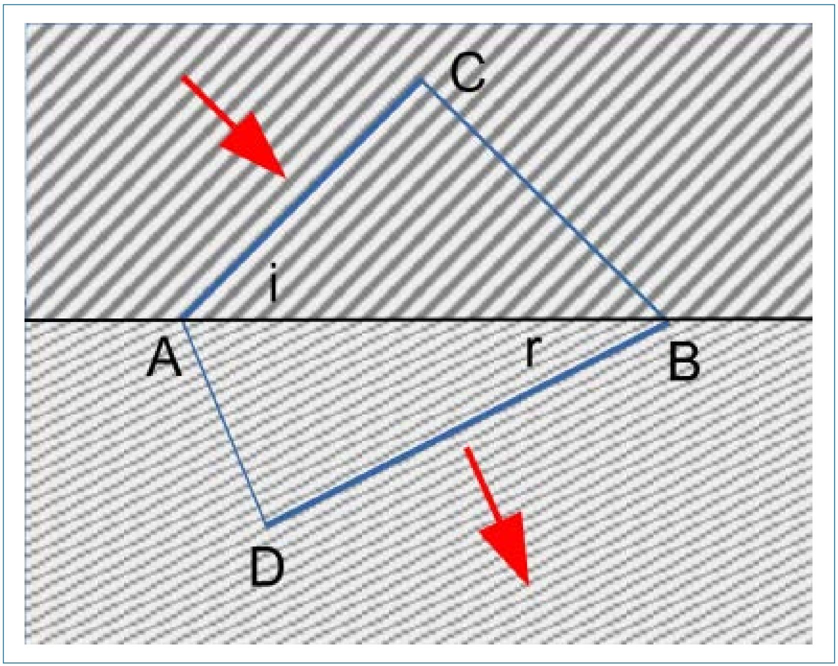


Figure 2. Refraction of waves

theory. It explains several other phenomena, such as how the iridescent colours of many birds, butterflies,[8] and soap bubbles are produced without using any pigments.

The wave theory requires that the higher the refractive index, the slower the light travels. Arago, in 1836, designed a method for measuring this directly, but practical difficulties and failing eyesight prevented him from achieving it.[9] A direct measurement was eventually made by Armand Fizeau and Léon Foucault in 1850, which agreed with the refractive indices.

Based on 19th-century experimental work by others, in 1862 the godly James Clerk Maxwell wrote: “We can scarcely avoid the conclusion that light consists in the transverse undulations of the same medium which is the cause of electric and magnetic phenomena.”[10] This led Heinrich Hertz to perform experiments which produced radio waves. Having a much longer wavelength, it is possible to demonstrate their reduction in speed on entering a transparent medium, with little experimental difficulty.

There can be no doubt that changing the speed of light causes refraction.

Critical angle

One issue of practical importance is illustrated in figure 4. The speed of light in medium 1 is 2.5 times that in medium 2. The light from any object in medium 1 will strike the boundary with an angle of incidence up to 90°. After passing through the boundary, the maximum angle of refraction, called the ‘critical angle’, is, in this instance, 24°. An observer in medium 2, looking directly upwards would see everything in medium 1 within 24° of the normal. There would appear to be a circular hole at the boundary, sometimes called ‘Snell’s Window’. No light from medium 1 would be seen around the window, but some objects in medium 2 would be visible.

If light from medium 2 is travelling upwards at an angle of incidence less than the critical angle, it refracts as in figure 2 with the arrows reversed. Note that the waves are continuous across the boundary. If the angle of incidence exceeds the critical angle, the crests of the waves in medium 2 are too far apart at the boundary to match those in medium 1. Instead of refracting, the waves are reflected back into medium 2. This is called ‘total internal reflection’.[11] Referring to figure 2, for refraction:

$$\mathrm{CB} < \mathrm{AB}$$
$$u\,t < v\,t / \sin r$$
$$\sin r < v / u$$

So

$$\sin c = v / u = n_1 / n_2, \text{ where } c \text{ is the critical angle.}$$

In figure 5, the brown line indicates the path of light that is totally internally reflected. The diagram has been simplified by omitting the light that has been partially reflected.

Multimedia

If there are more than two media, the final angle of refraction is determined only by the initial and final refractive indices and the angle of incidence, if all the boundaries are parallel and total internal reflection does not occur. This follows from Snell's law.

At the first boundary,

$$n_1 \sin i_{12} = n_2 \sin r_{12}$$

At the second,

$$n_2 \sin i_{23} = n_3 \sin r_{23}$$

The angle of refraction at the first boundary, r_{12}, equals the angle of incidence at the second, i_{23}:

$$\sin r_{12} = \sin i_{23}$$

Therefore .

$$n_1 \sin i_{12} = n_3 \sin r_{23}$$

and in general

$$n \sin i \text{ is constant in all the media.}$$

In 1820, shortly after the corpuscular hypothesis had been rejected, Augustin Fresnel used the wave theory to derive formulas for how much light was partially reflected at the boundary between two layers at different angles of incidence[12]. These were confirmed by experiment and are somewhat cumbersome, but for light travelling along the normal the formula is simply:

Fraction of incident light reflected,

$$\mathrm{R} = (n_2 - n_1)^2 / (n_2 + n_1)^2$$

Or in terms of the speeds,

$$\mathrm{R} = (u - v)^2 / (u + v)^2$$

With a 2.5:1 ratio of speeds, as in figure 5, for a ray travelling up or down, the normal 18.4% of the energy would

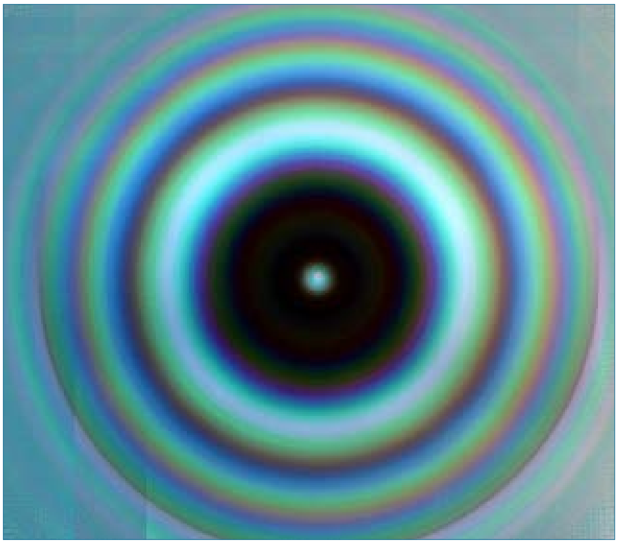


Figure 3. Poisson's bright spot

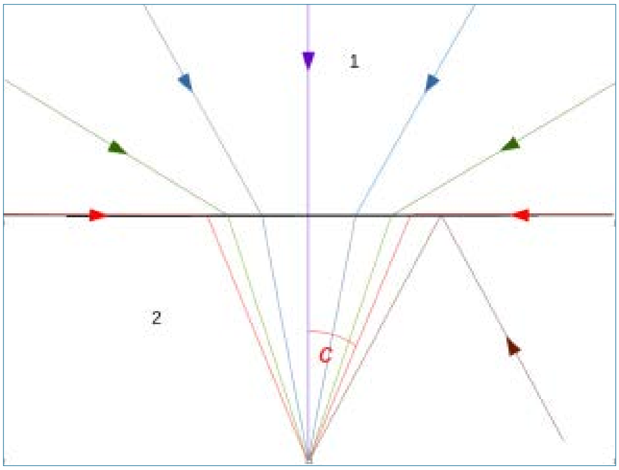


Figure 4. The Critical angle is labelled *c*.

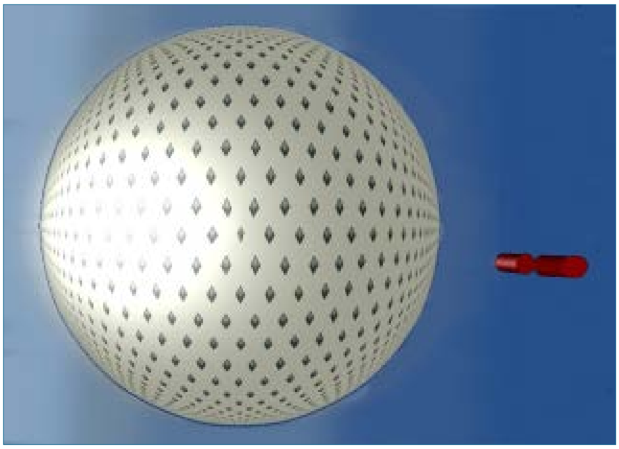


Figure 5. Flat boundary

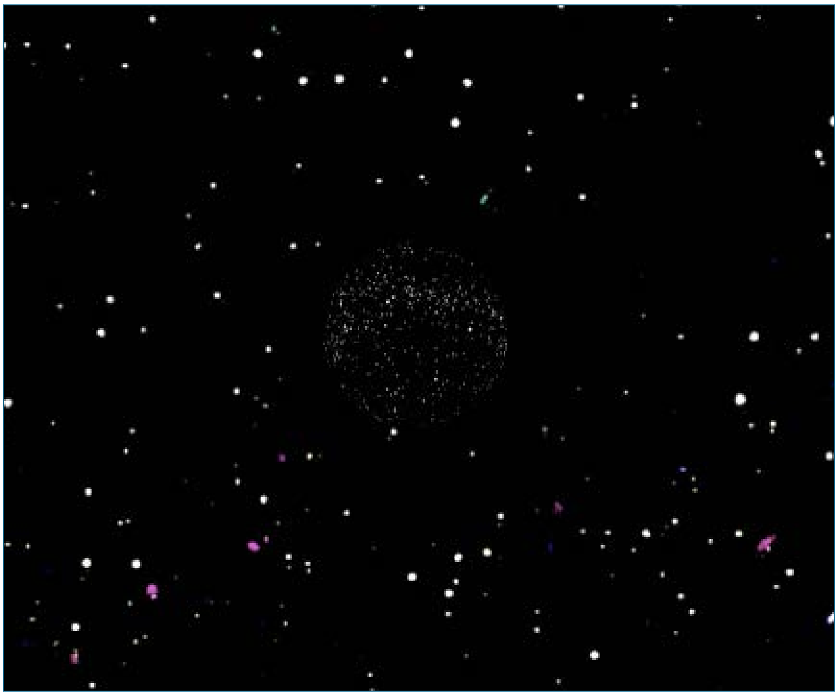


Figure 6. Southern view

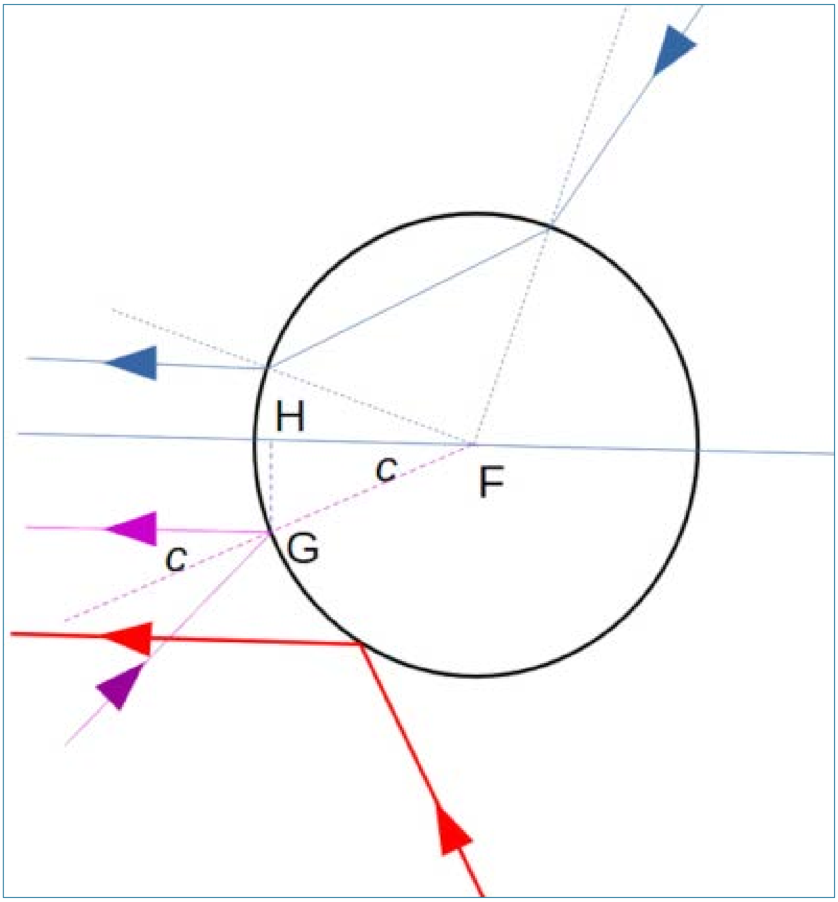


Figure 7. Rays across sphere

be reflected, and 81.6% transmitted. As the angle is increased, the proportion reflected increases and that transmitted decreases until at, and above, the critical angle, 100% is reflected and none transmitted.

Putting another medium between medium 1 and medium 2 will reduce the energy reflected if its thickness exceeds two micrometres (for white light). This is most effective if its index n is the geometric mean of the media either side of it. In this example, $n = 1.58n_1$, 9.6% would be reflected. For more than two boundaries, the exact calculation requires very advanced maths, but R is almost inversely proportional to the number of boundaries (the more boundaries, the closer the approximation).

In the limit as the number of boundaries tends to infinity, R tends to zero. The speed changes smoothly and no light is reflected. Many moths' eyes have a surface with a structure on the nanometre scale, which slows down the incoming light gradually so that none is reflected.[13] This was designed so that predators are not attracted by light reflected from the moths' eyes.

The speed of light at the surface of the earth at 0°C is about 0.03% slower than in a vacuum, and gradually increases with increasing altitude. This very small change is sufficient to refract light travelling almost horizontally by about 0.5° downwards, causing objects in space to appear higher than they are. This enables the setting (or rising) sun to be seen when it is actually below the horizon.

Incidentally, the critical angle at the surface of the earth is 88.6°, so if the earth were a flat disk, the edge of Snell's Window would be 1.4° above the horizon. In that 1.4° we would see inverted images of distant parts of the earth by total internal reflection!

The mirages seen on hot sand and roads occur because the air that is heated by contact with the hot surface is less dense than at eye level, so the speed of light is slightly higher, and light from the sky is totally internally reflected up to the eye.

Astronomy

I will now examine three hypothetical boundary shapes where the speed of light increases, on an astronomical scale.

A flat boundary beyond which the speed is considerably higher than on the observer's side

This is essentially that drawn in figure 4. All objects beyond the boundary would be seen at smaller angles from the normal, through a circular window. Figure 5 is a computer simulation[15] looking at a regular wallpaper pattern across a boundary with speed ratio 2.5:1. Note that the motifs on the wallpaper appear closer to each other as one looks further from the centre. Straight rows, except those which pass through the centre, appear as curves. Photographers call this *barrel distortion*. Outside the window, total internal reflection produces an image of the red rod which is just this side of the boundary, and an image of the blue background behind the observer.

Partial reflection will not occur if the speed reduces gradually across the boundary. The larger the speed ratio, the smaller the window. The refracted image, resembling a sphere, will shrink. The boundary will look like a mirror with a small hole in it. Counter-intuitively, the increase in speed is hindering vision.

Figure 6 shows the view, from the southern hemisphere looking parallel to the axis of the earth, if there were an 8:1 speed ratio across a boundary between the earth and the nearest stars. Most of the picture shows an inverted image of the northern sky with the Plough (aka Great Dipper) upper centre. In the centre is the window with a diminished and distorted view of all the stars beyond the boundary.

I am not aware that astronomers have observed anything like this.

A sphere where the speed inside is greater than outside

Figure 7 shows three rays, again with a speed ratio of 2.5:1. The blue one indicates the path typical of those that come from beyond the sphere and are refracted—away from the normal on entering and towards the normal on leaving. The purple line represents reflection at the critical angle c, and the red line shows how objects beyond the sphere can be seen by total reflection.

As

$$\sin c = v / u$$

and

$$GH = FG \sin c$$
$$GH = FG\, v / u$$

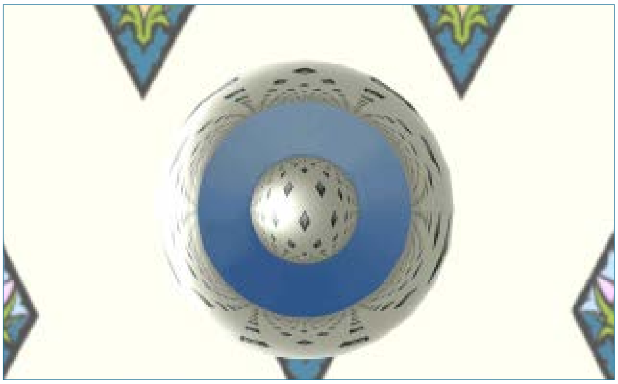


Figure 8. View of sphere

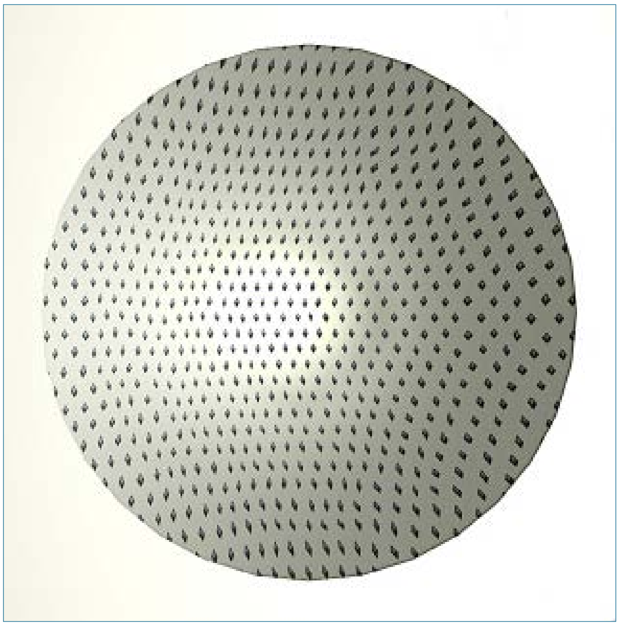


Figure 9. View from right of centre

In this case, $v / u = 1/2.5 = 0.4$. The refracted rays all come through a circular window, the radius of which is 0.4 of the radius of the sphere.

Figure 8 gives the appearance of the sphere as seen by a distant observer. The refracted rays form an image which looks like a ball; the outermost reflected rays show the true size of the sphere; the blue ring is light from the observer's side which has been reflected. Some of the motifs can be seen three times: by refraction, by reflection, and directly with correct size and spacing. Nothing which matches this, replacing the motifs with stars, has been observed.

An observer near the centre of a sphere where the speed inside is less than outside

If an observer is at the exact centre of a transparent sphere, all the light coming to him from outside will be at right angles

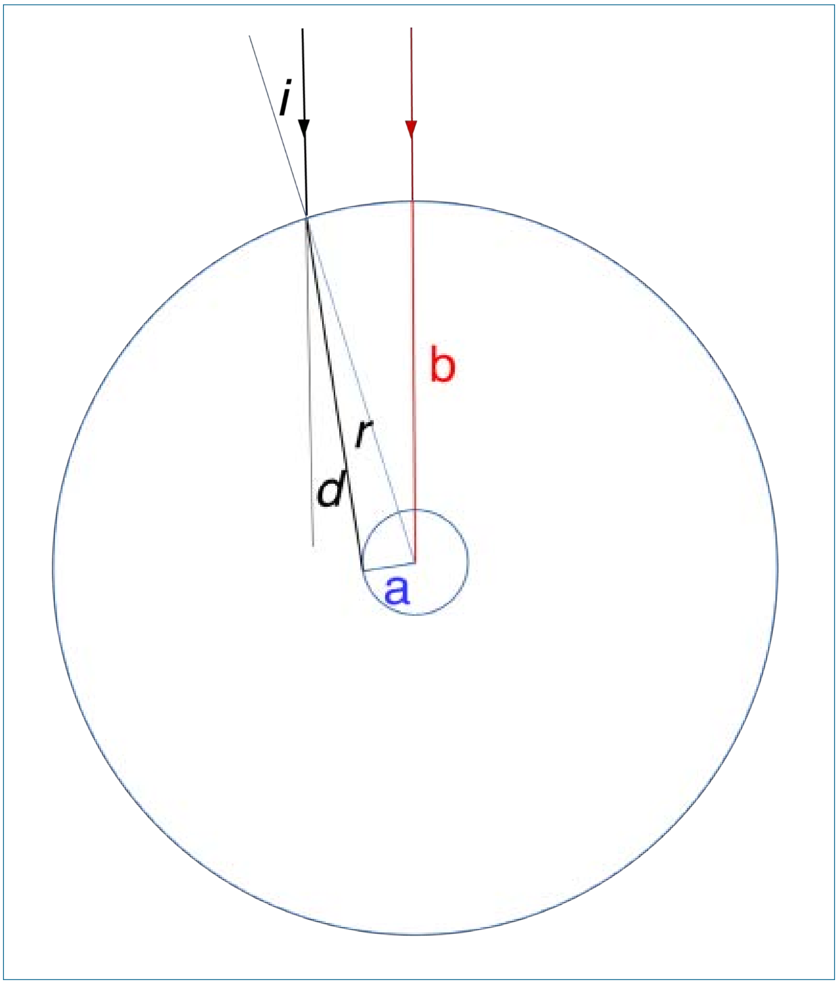


Figure 10. Sphere centred on the sun

to the boundary, so will not be refracted. He will have an undistorted view.

If the observer moves away from the centre, he will see a distorted image. Figure 9 is the image as seen from the right of the centre. The straight rows appear curved and further apart on the right.

Suppose the sun to be in the centre of such a sphere with radius b, larger than the orbit of Neptune, and the radius of the earth's orbit to be a, as shown in figure 10. Let the speed of light outside the sphere be u and the speed inside be v.

When the earth is directly above the sun, light from a distant star will be seen in its true direction as shown by the red ray; but, when left of the sun, the light's path is shown by the black ray, which has been deviated by the angle d. During the year it will appear to change its direction by $D = 2d$.

James Bradley looked for such a change, from a different cause and in the opposite direction[16] (c. 1728) and found that if there was a change it was less than one second of arc (or 5×10^{-6} radians). I will calculate how large b needs to be to make D so small.

$$i = d + r$$

From Snell's Law,

$$v \sin i = u \sin r$$

For very small angles,

$$v\, i = u\, r$$
$$v\,(d + r) = u\, r$$

Measuring the angles in radians,

$$r = a \,/\, b$$

Therefore

$$v\,(d + a \,/\, b) = u\, a \,/\, b$$

From which

$$b = a(u/v - 1)/d = 2a(u/v - 1)/D \text{ and the speed ratio } u/v = 1 + db/a = 1 + Db/2a$$

Where could such a spherical boundary be?

After it had completed its mission in the solar system, *Voyager 1* continued measuring the Solar Wind of very energetic charged particles emitted by the sun. In August 2012 a rapid forty-fold increase in the density of the plasma was observed, marking the edge of the Heliosphere.[17] This was at a distance of 120 Astronomical Units (au) from the sun. 1 au is the mean distance from the earth to the sun. Measured in Astronomical Units $a = 1$.

At this distance, $b/a = 120$. So

$$u/v = 1 + 5 \times 10^{-6} \times 120 \,/\, 2 = 1 + 3 \times 10^{-4} = 1.0003$$

Clearly 120 au is far too small.

The nearest star to the sun is Proxima Centauri, at a distance of 4.2 light-years (ly). Halfway there the gravitational attraction of the sun is no more than that from other nearby stars.

1 ly = 63,240au[18]

At 2 ly,

$$b/a = 2 \times 63{,}240$$
$$u/v = 1 + 5 \times 10^{-6} \times 2 \times 63{,}2400 \,/\, 2 = 1.32$$

To allow a speed ratio of 1,000,

$$b = 2a(u/v - 1)/D = 2a(1{,}000 - 1)/5 \times 10^{-6} =$$
$$4.00 \times 10^{8}\ a = 4.00 \times 10^{8}\ \text{au} = 6{,}325\ \text{ly}$$

This is about 9% of the radius of our galaxy (70,000 ly).

Finally, consider a boundary of radius 100,000 ly, which would give $D = 0.061$ seconds of arc. This looks possible if it is centred on the sun, but if its centre is the centre of mass of the galaxy some 20,000 ly from us, our view would be severely limited. The critical angle is 1/1,000 radians.

Geometry shows that multiplying by 100,000/20,000 yields the radius of Snell's window. This is 1/200 radians = 0.29 degrees, just over the angular radius of the moon as seen from Earth. Directly opposite to the galactic centre would be a window about the size of the moon through which other galaxies would be seen at 1/300 of true angular size. In all other directions we would see either stars or dust in our galaxy or images of them by total internal reflection.

The only observations which are anything like refraction are those attributed to *gravitational lensing*. These deviations from a straight line are typically a few seconds of arc.[19] If they are not due to gravity but to a change in the speed of light, a change of the order of 0.1% would be sufficient.

Conclusion

It is difficult to find any way in which the refraction caused by the current speed of light changing from one place to another would go unobserved. Where it changes, whatever its cause, the waves must be continuous across the region where it changes. This places severe limitations on any model in which the speed in different parts of the universe differs enough to solve the distant starlight problem.

Changing the speed with time rather than position, such as the cosmology posited in 2022 by Dr Russell Humphreys,[20] would not cause refraction if the speed changed simultaneously throughout the universe. He starts that article by stating that a rigorous creationist cosmology must

- have a firm biblical basis
- explain the increasing red shift of light with increasing distance
- explain the Cosmic Microwave Background Radiation
- explain the seemingly great age of the distant cosmos.

I would add to that list:

- avoid detectable refraction and other effects contrary to observations.

Ideally, it should permit straightforward explanations of currently puzzling discoveries such as the second large scale structure found recently by Alexia Lopez studying at the University of Central Lancashire,[21] and predict features which can be tested.

Acknowledgment

I thank William Worraker for reviewing a draft of this article and making comments for improving it.

References

1. Denton, C., The passage of light in the universe, *J. Creation* **37**(2):68–71, 2023; p.71.
2. Zghal, M., Bouali, H.-E., Lakhdar, Z.B., and Hamam, H., The first steps for learning optics: Ibn Sahl's, Al-Haytham's and Young's works on refraction as typical examples, etop07fundamentalsII, spie.org, 2007.
3. Willebrord Snell, britannica.com, accessed 19 Jan 2024.
4. Corpuscular theory of light, britannica.com, accessed 19 Jan 2024.
5. Christiaan Huygens: Dutch scientist and mathematician, britannica.com, 10 Dec 2023.
6. Thomas Young: British physician and physicist, britannica.com, accessed 19 Jan 2024.
7. Poisson's spot: diffraction, britannica.com, accessed 19 Jan 2024.
8. Sarfati, J., Beautiful black and blue butterflies, *J. Creation* **19**(1):9–10, 2005.
9. François Arago: French physicist, britannica.com, 2023.
10. James Clerk Maxwell, Molecular expressions: science, optics and you, fsu.edu, 2015.
11. An excellent animation of this can be seen at Total internal reflection, britannica.com, accessed 19 Jan 2024.
12. Lecture13, Fresnel's equations for reflection and transmission, brown.edu, accessed 19 Jan 2024.
13. Peck, M., Learning from nature: moth eyes inspire nonreflective screen coating, scientificamerican.com, 26 Jul 2017.
14. Thomas, M.E. and Joseph, R.I., Astronomical refraction, *Johns Hopkins Apl. Tech. Digest* **17**(3):279–284, 1996.
15. Using Cobalt™ 3D Modeling, 2024.
16. Bradley, J., Rev., On the motion of the fixed stars, *The Monist* **22**, reprinted from the Philosophical Transactions of 1727.
17. The ringing of interstellar space, voyager.jpl.nasa.gov, accessed Jan 2024.
18. What is an astronomical unit? earthsky.org, 31 Jul 2022.
19. Gravitational lens, wikipedia.org, 2023.
20. Humphreys, D.R., A more biblical cosmology, *J. Creation* **36**(3):114–122, 2022.
21. A big cosmological mystery, uclan.ac.uk, 11 Jan 2024.

Richard Ward *received his B.A. (1969) and M.A. from the University of Cambridge, England, where he studied mathematics and primarily physics. He also has a certificate in education from the University of Leicester, England. He spent most of his life teaching boys physics, or supporting physics teachers in Salisbury. The Institute of Physics has published five of his articles in* Physics Education.

Design without a designer?—the unsolved problem of coordination

Richard W. Toosey

The essential nature of design can be defined as the generation of organized functional systems. Central to this process must be the active coordination of independent variables, these being principally the form and materials of each component part, and the relationship of components. Coordination is required at all levels of design—whether of individual elements, systems of parts, or the integration of whole systems. Natural selection theory, however, must assume coordinated improvements as already given. This is illustrated here with particular reference to the classic vertebrate eye sequence. At each stage this can be shown to fail Darwin's own test of full functional gradualism, the basic premise of evolution. Both empirical design experience and analysis show that only some basic design properties are continuously variable; even these require coordination for function. An equal number, however, are inherently systemic; i.e., inherently incompatible with evolution. It is also explained why functional systems cannot ever be generated by scientific laws of regularity.

Coordination is both the process and result of design

All design necessarily consists of matter coordinated in both form and appropriate material properties, and the relationship between parts (structure in its more general sense). Timing or sequence of construction also requires coordination. The same form can be made in different materials, though, and form and materials are themselves effectively infinitely variable. There is no physically necessary relationship between the two. Living systems are composed of up to trillions of cells, which could each be of thousands of different material specifications. The need for active coordination will be immediately apparent, as will the impossibility of achieving it by fully random variations.

As one example, in the knee joint the form of the end of the femur with its two condyles must be coordinated with the form of corresponding depressions in the upper tibia. The bones must be consistently of one material, separated by a different cartilage material to avoid friction. The connecting cruciate ligaments must be accurately placed and composed of another material specified for tensile strength (collagen/elastin). If any of these correspondences were missing, the knee would not function, making it inaccessible by a series of gradual steps.[1] Continuity of function is essential not only in Darwinian theory, but in life itself. Richard Dawkins includes the knee among the "living wonders that Darwinism uniquely does solve ... by breaking the improbability up into small, manageable parts";[2] but, oddly, he omits to expand on this claim.

Coordination and irreducible complexity

The term 'irreducibly complex' (ic) was introduced by microbiologist Michael Behe as describing "a single system composed of several well-matched, interacting parts that contribute to the basic function, wherein the removal of any one of the parts causes the system to effectively cease functioning."[3] 'Well-matched' here is synonymous with coordinated, but his focus was on dimensional/geometrical coordination (as also in his mousetrap illustration), and on the irreducible number of parts. In larger scale anatomy the matching of numerous different material specifications with functional requirement is a further aspect of coordination, which I would wish to highlight here.

He also limits the definition to a single system, which at this smallest of biological scales (the nano-scale motor) is valid. The knee though is not a single system. Its function is dependent on the thigh muscles, their blood supply and nervous control by the brain, and indeed cellular functions down to those nano-scale 'machines'. Life thus requires the coordination not only of the parts within systems, but of systems with other systems. There are eleven such major systems in the body; respiratory, cardiovascular, nervous, muscular, skeletal, gastrointestinal (digestive), renal/urinary, integumentary (skin), immune/lymphatic, endocrine (hormonal) and reproductive. This total coordination argues *a fortiori* against evolutionary gradualism.

In a far simpler human design this principle can be seen in the motor car (which, significantly, appeared at a defined time in history). It needed *simultaneously* coordinated but individually ic systems. The ic combustion engine, the ic steering system, the ic transmission system (and wheels), the ic braking system, the ic chassis: all must be coordinated dimensionally and spatially. Here, the removal of any one of the *systems* causes the whole to effectively cease functioning; although some subsequently added sub-systems could be lost and are therefore 'reducible'—(instrumentation, say). Here, though, one may suspect that analogies must not be pushed

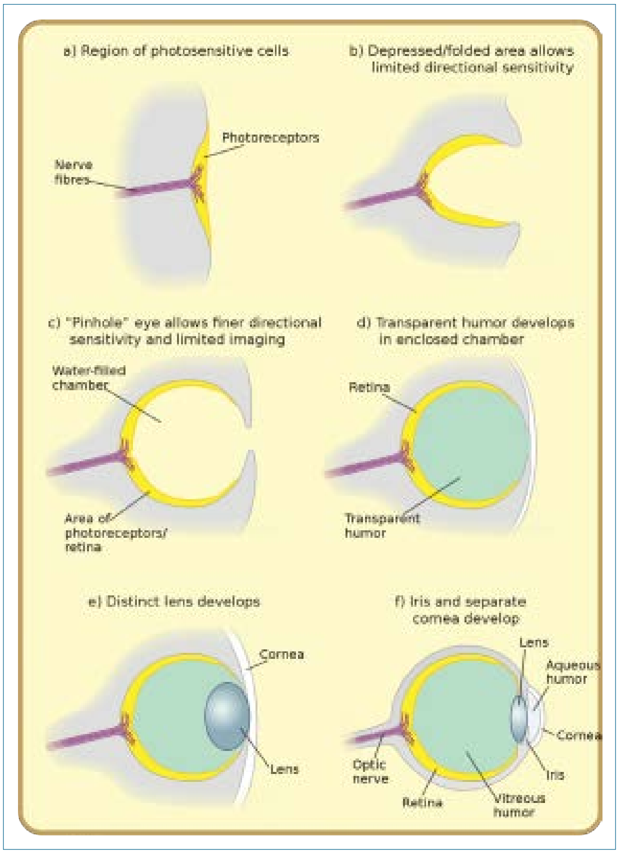


Image: Matticus78, Wikimedia / CC BY SA 3.0

Figure 1. The evolutionary vertebrate eye sequences

too far; it does not follow that creation, too, followed any additive path over time.

A biological example is that of vision. This is an irreducibly complex system, even with only a few photoreceptor cells (themselves ic). That is because its usefulness is dependent also on a central information receiving and decision-making centre, controlling a further mechanism enabling the organism to react accordingly. However, we can theorize the progressive addition of further photoreceptors—providing they are correctly located and integrated with the brain. There can clearly be degrees of visual acuity—degrees of complexity—but the *sine qua non* of design is coordination. The problems besetting gradual eye evolution (discussed below) are in any case so extensive that there is no reason to suppose that it occurred at all.

Our own design experience illuminates the considerable challenge of integrating different systems. A building's structure for instance must be integrated with various services (heating, ventilation, plumbing, electrical) while avoiding clashes between them. This requires an overall design strategy or awareness of the irreducible requirements of each system. It is certainly seen in anatomy; as in the way the spinal cord nerves are accommodated by holes in the structural vertebrae, branching laterally to the rest of the body, while the vertebrae have extensions to link with the muscular system. It is this overall coordinating role that is central to design.

Reducible complexity

The problem for general evolution is to explain the origin of systems—'uphill' development, with continuity of function. Creation in total contrast, starts from an initial fully functional point, or rather points (kinds), which include the availability of variations in form and colour. These *already existing* traits can be 'selected' from, which is essentially a reductive process.

It is such processes that turn out to underlie what is commonly termed evolution—as Michael Behe himself further illuminates in his book *Darwin Devolves*.[4]

Another form of reduction involves the slow loss of genetic information by small reproductive errors which accumulate in the genome, described by geneticist John Sanford in *Genetic Entropy*.[5] He compares it to small losses by corrosion, again commencing from a perfect starting point.

The need for a design safety factor or initial 'overdesign' may be in view here. In any case if irreducibility disproves Darwinism, it does not follow that *every* useful feature must be indispensable.

Self organization'?

Evolutionary theorists sometimes seek an alternative to creation in ideas of 'self organization'. On the face of it, this is logically incoherent, equivalent to 'self creation'. The examples proposed do little to dispel that conclusion. One such is the ripple patterns 'emergent' in sand grains following the action of wind and waves. It is quite illogical to describe the sand grains themselves as *self* organizing though. Another is the coordinated *movement* in shoals of fish or flocks of birds, resulting from each intelligently or instinctively following a 'rule' relative to its neighbour without requiring any external coordinating agent. But patterns are not analogous to functional systems.

Why would the same cell type (bone generating, for example) self organize into many radically *different* bone morphologies, each specifically adapted to its particular location? The application of rules can certainly generate some kinds of regularity, or patterns, but a universal feature of functional design is that it is always highly specific and, at some point, *irregular* (though often within an overall general symmetry). This differs from the coordinated but non-functional regularity of a crystal lattice, for example. No rule could specify the highly varying and irregular but functional shape of each bone. *No functional design can be generated by rules alone.*

In truth it must be admitted that the actual process of morphogenesis and the way it is coded are still not well

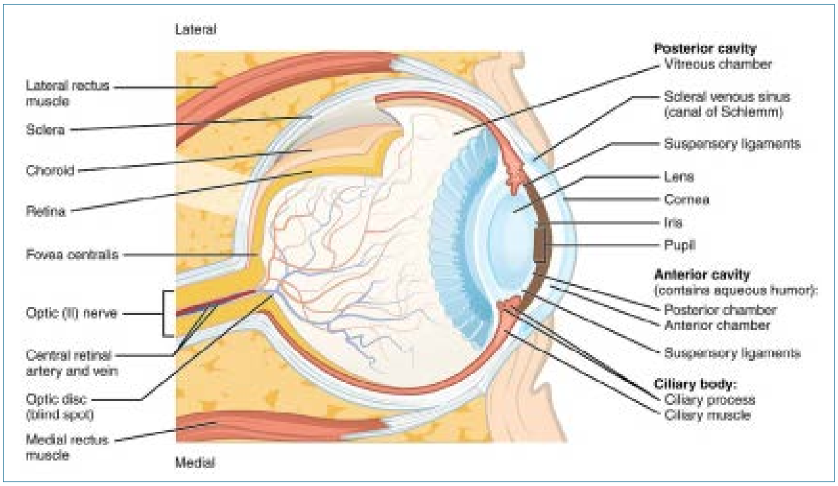


Figure 2. The eye in section

Image: OpenStax College, Wikimedia / CC BY 3.0

understood;[6] although the information must clearly be present to enable reproduction. It must also be very remarkable to extend even to the small details and precise shapes of anatomy. Wherever the information resides, it must yet again be closely coordinated with the coding for material specification. We do know that under 2% of the genome codes for proteins.

The denial of intelligence

Darwin's hope was to provide a fully naturalistic or materialist theory of evolution, precluding any intelligent input. As he wrote in a letter to Charles Lyell dated 11 October 1859:

> "I would give absolutely nothing for theory of nat. selection, if it require miraculous additions at any one stage of descent."[7]

This was in reply to a letter from Lyell (a deist) of 4 October 1859, whose comments on the soon to be published *Origin* included the suggestion that:

> "… it would be better to put more broadly and fairly how little it explains, and how much of the mysterious intervention of some other & higher & what we call creative power is required … ."[8]

It seems that even Lyell (uniformitarian as a geologist) appreciated better than Darwin the inadequacy of natural selection alone to account for true origins. Genetics would eventually prove him right.

Darwin's assumption that selection theory provides a radical alternative to design has for long been uncritically bought into. Even in 2007, biologist Francisco Ayala wrote that Darwin's 'discovery' was 'design without a designer'.[9] Yet Darwin himself admitted repeatedly in the *Origin of Species* that he had no idea where the variations he studied actually came from,[10] and that natural selection could 'do' nothing without them. (Here he did acknowledge the doubt expressed by Lyell). In reality though, because natural selection is not an 'agent', differential survival is built in to his key assumption of beneficial 'uphill' or constructive advances. He was ultimately taking for granted the same gradual evolution with common descent as had various philosophers writing decades earlier.[11]

The development of genetics left no obvious alternative for naturalistic theory but to appeal to chance alone as the true origin of variation. Mathematician Sir Fred Hoyle described this as "the real plunge into a logical abyss ... taken by his followers rather than by Darwin himself."[12] Chance has no power to coordinate widely different materials according to function; or even to generate the lengths of protein coding required to specify those materials in the first place, as Hoyle showed mathematically.

Darwin's own stated test of what he called "my theory", meaning specifically natural selection following "successive, slight modifications", was that every such modification must be *selectable*. This requires improved function at *every* stage; i.e., function itself must be very gradually graded for all required aspects of design. This means that to test his theory as one of *design*, necessarily involves testing it against specific design problems. This requires a design analytic approach, not an abstractly theoretical one.

So what are the essential elements or properties of design?

The elements of design

Whatever their level of complexity, biological or not, functional systems share the following elemental properties:

1. material specification
2. form
3. structure (both as support, and relationship of parts) [S]
4. mechanism (moving parts) [S]
5. control and regulation systems [S]
6. colour.

To these may be added the means of specification itself, to carry the information required; i.e., coded or written information in some form, which is translated into production. Some simpler designs may not feature every one of the above properties, but they are all present in life.

The properties not labelled 'S' are in principle fully variable on a gradual basis (but still require coordination for function, being independent of each other). These may seem the most initially promising areas for gradualist theory. The remaining three, however, are intrinsically systemic (S) and thus highly problematic for evolutionists. A system, after

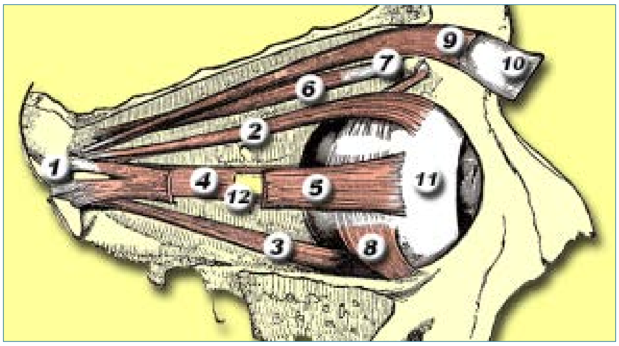


Image: Edelhart Kempeneers, Wikimedia / PD-self

Figure 3. Lateral view of the right human eye showing muscles and related structures: 1) sphenoid bone, 2) superior rectus, 3) inferior rectus, 4) medial rectus, 5) lateral rectus, 6) superior oblique, 7) trochlea, 8) inferior oblique, 9) levator palpebrae superior, 10) tendon, 11) sclera, 12) optic nerve.

Image: Peter L. Higgs, Wikimedia | CC BY SA 4.0

Figure 4. A cable stay bridge under construction

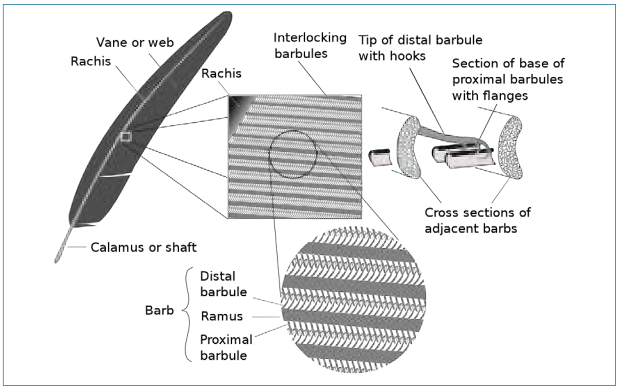


Image: Shyamal, Wikimedia / Public Domain

Figure 5. Flight feather interlocking structure

all, by definition, is "a group or combination of *interrelated, interdependent or interacting elements forming a collective entity* [emphasis added]" (Collins).

The above properties may now be looked at briefly in turn, with initial examples being taken from the classic vertebrate eye sequence (figures 1 and 2).

Material specification

The eye lens has a unique cellular architecture comprising a single layer of cuboidal cells, the transparent lens capsule which differentiates into lens fibre cells. These are tightly packed, very elongated cells, their structure somewhat resembling the rings of an onion and producing high levels of the crystallins essential for transparency. The eye contains the only tissue in the body which is truly transparent and colourless, located exactly where it is essential for function.

The overall form, of course, is a biconvex lens shape. A different material specification would be functionally useless, as would indeed a different form, orientation, size, or placement in the body. Thus, the result cannot be approached by way of the right form in any of the numerous opaque possibilities, or the right material in the wrong shape, orientation, size or overall location. The lens, seemingly but a single 'element' of the system, itself requires much coordination. It also has to be a little flexible to allow focussing by the ciliary muscle, which holds it in place. If 'evolved', it would just have to stay in position while awaiting the supposedly unplanned arrival of its supporting ligaments, ciliary muscle and nerves.

Material specification is important even at the base of biological organization. Its molecular building blocks (amino acids) are almost exclusively 'left handed' (they occur in mirror images), while their synthesis always produces an undifferentiated mixture. This again represents an apparently 'artificial' selection or purification of materials, as frequently required in known design.

Form

This can be considered in relative isolation in the context of the curvature of the retina, which is theorized to have given a gain of function over a primitive flat surface by improved sideways perception. This reaches a maximum at the half sphere point (180°). Beyond this, as it moves towards circular enclosure, sideways vision becomes *worse* while still almost as far as possible from the 'pinhole' stage. By the same logic of sideways vision, it should therefore be deselected. Thus the tight correspondence between change and gain of function, required by Darwin, as above, does not actually exist.

However, form is one of the genetic variables which is selectable within a created genome (birds' beaks being a classic example). Overall somatic form is also variable, but this must remain coherent, never truly random variation.

Structure

The evolution of the structural wall of the eyeball (sclera) is another problem for gradualism. This, too, is just added to the sequence, appearing as an outline in the final cross section. What functional advantage could this provide, without its three pairs of controlling muscles? (figure 3). To repeat, Darwinian selection requires *continuity* of function.

By Darwin's own admission, "A nascent organ, though little developed, must be useful in every stage of development.”[13] This is often impossible to visualize in the adult form, as against embryonic development which is free of functional demands. For example, what functional use could apply to small bone nodules developing adjacent to the lumbar vertebrae in the adult stage? They are only useful as ribs when substantially developed.

Our own experience of design shows that structures are only useful when complete. This is simply demonstrated by looking at any bridge under construction (figure 4). How is it to be crossed? Note though that the cable stay bridge is not ‘absolutely’ irreducible. It includes redundancy, in fact one advantage of the type is that individual stays can be replaced. It is, however, fully coordinated.

A further example of structure is the flight feather and contour feather (figure 5) which are only functional when all the many hundreds of lateral barbs and their connecting, paired (complementary) ‘barbules’ are in place and coordinated *in the same plane* when each could vary randomly about their origin point. Function requires them to provide a plane surface resistant to wind or water (in the latter case, completed with oil from a preening gland), repairable by preening when overstressed.

The underlying downy feathers perfectly serve a quite different function—insulation. Again there is no *functional* advantage in any halfway point. Optimal design is always specific to function. This is the fatal flaw in the idea of ‘co-opting’ one function for another.

Mechanism

The muscles controlling the eyeball (figure 3) constitute a mechanism. Muscles are often arranged in complementary pairs; in this case, three pairs to provide a full range of directional control. It hardly needs saying that they must be correctly positioned and complete between their insertions, including integration with the nervous system. Thus evolution theorists can only say something like ‘enervated muscles arise’, as with the ciliary muscle.

Consider, especially, the superior oblique muscle attachment (labelled ‘6’ in figure 3). Its origin is behind the eye; its anterior attachment to the eyeball is via an elongated tendon which passes through a small U-shaped piece of cartilage attached to bone over the eye (trochlea; labelled ‘7’ in figure 3). It thus constitutes a pulley mechanism, enabling reversal of the pulling force (from the front in other words). This represents, if it were possible, an even more severe challenge to imagining a gradual functional evolutionary pathway.

Stephen J. Gould admitted:

> “… our inability, even in our imagination, to construct functional intermediates in many cases has been a persistent and nagging problem for gradualistic accounts of evolution.”[14]

One has to ask, what would be recognized as an insoluble problem?

Image: AlexDuarte, Wikimedia / PD-self

Figure 6. Coloured patterns in feathers

Image: TAPAS KUMAR HALDER, Wikimedia / CC BY SA 4.0

Figure 7. Colour attracts the bee to pollinate flowers.

The same failure has attended all attempts over a quarter of a century to counter Michael Behe’s demonstration of irreducible complexity in the bacterial flagellum (a miniature motor). After reviewing them at length in *A Mousetrap for Darwin*, he concludes:

> “At this point in science’s investigation of life it seems like just a cruel taunt to challenge Darwinian biologists to experimentally justify the ability of random mutation and natural selection to make an irreducibly complex molecular machine.”[15]

Systems of control and regulation

In life, these are governed by the nervous system, all under the control of the brain as the central coordinator and regulator of the body’s interdependent systems. Each control system requires *three* essential parts—one to detect what needs to be controlled, a second to apply decision logic, and a third to change the thing being controlled. This is required for many life-critical physiological parameters which must be kept within a narrow range, such as respiratory and heart rates, blood pressure, and core temperature.[16]

An example is the response of the eye pupil, which contracts or expands in response to the level of light available. This is also a protective reflex that prevents damage. The detection is by the photoreceptor cells, the decision logic by the brain, and the active control by the two different muscles operating the iris. Similar control systems apply to the lens focussing and eyelid muscles.

Colour

In the eye, detection of colour is concentrated at the centre of the eye, each eye having about six million cone cells. Each of these makes one of three light sensitive molecules which react to specific wavelengths of visible light—either red, green, or blue. Since each cone reacts to just a single colour, this requires a fairly even distribution of each type. The photoreceptor cells pre-process the sensory information before sending the results along the optic nerve to the brain. This alone is a hugely complex biochemical process and a critical requirement for vision.

Colour in nature can be both functional and a source of added beauty. Its organization in specific locations, such as feathers or flower petals (figures 6 and 7) comprising numerous cells, poses similar problems to those already discussed. Why should colourful bird plumage be subdivided into well-defined areas, seemingly independent of function? And where such concentration does provide function, as in the flowers which attract pollinators, how would only faint colours be of help? Of course this would require that bees, etc. already had excellent colour vision, making 'co-evolution' meaningless. (Both being weak would be worse). Thus, even above the level of individual organisms, we find a functional interdependence between them which is hard to make sense of in terms of sequential development.

Conclusion

Natural selection enables variation based on already existent genetic information but does not enable *increases* in complexity.

Darwin's criterion for falsification has been repeatedly met. Systemic properties are inherently only present when the system is complete, and extended time is therefore of no help.

Input of functional information must *always* be coordinated, regardless of complexity.

Functional systems are inherently irregular (aperiodic), and so cannot be generated by natural laws, which can only deal with regularities. Like art, design will always lie beyond the important realm of pure science.

Glossary
(from *Collins Dictionary*)

Coordinate: "1) to integrate diverse elements in a harmonious operation" ("*integrate*: make into a whole"). Because diverse elements are not yet integrated, they must be so *at the same time* under some means of external control.

Information: a basically immaterial, or supra-material concept of knowledge that can be transmitted in different material ways. In a design context, though, it is essentially the same as "3) *specification*: a detailed description of the criteria for the constituents, construction, appearance, performance etc., of a material, apparatus, etc.". This must of course be a fully sufficient description. In design work this stage is referred to as 'production information'.

Structure: "1) a complex construction or entity" is the sense generally used here, especially in load bearing. "2) the arrangement and interrelationship of parts" is a secondary definition.

Mechanism: "1) a system or structure of moving parts that performs some function".

Irreducibly complex: anything which cannot be made in small steps, each with function.

References

1. The critical nature of geometrical characteristics here is demonstrated in Burgess, S., *Hallmarks of Design*, Day One, chap.1, 2000.
2. Dawkins, R., *Climbing Mount Improbable*, Penguin Books, p. 68, 2006.
3. Behe, M.J., *Darwin's Black Box*, The Free Press, p. 39, 1996.
4. Behe, M.J., *Darwin Devolves*, Harper One, 2019.
5. Sanford, J.C. *Genetic Entropy* FMS Publications 2005.
6. Sean B. Carroll states that "constellations of switches distributed all over the genome" specify 3-dimensional coordinates in the process of embryonic development. Carroll, S.B., *Endless Forms Most Beautiful*, W.W. Norton, p. 111, 2005.
7. Darwin Correspondence Project, Letter 2503, accessed 1 Mar 2024.
8. Darwin Correspondence Project, letter 3132, accessed 1 Mar 2024.
9. Ayala, F.J., Darwin's greatest discovery: design without designer, PNAS **104**(suppl. 1):8567–8573, 2007.
10. Darwin, C., Laws of variation; in: *On The Origin of Species: By means of natural selection, or the preservation of favoured races in the struggle for life*, London, John Murray, 5th edn, chap. v and elsewhere, 1869.
11. In 1815 Coleridge wrote to Wordsworth referring to "the absurd notion of Pope's Essay on Man, [Erasmus] Darwin, and all the countless believers—even (strange to say) among Christians—of man's having progressed from an Ouran Outan state ... ." Quoted in Holmes, R., *The Age of Wonder*, HarperCollins, p. 322, 2008. In 1815 Darwin was aged 6.
12. Hoyle, F., *The Intelligent Universe*, Michael Joseph, Holt Rinehart & Winston, p. 32, 1983.
13. Letter to Charles Lyell, dated 11 Oct 1859 (see ref. 7).
14. Gould, S.J., writing in 1980, quoted by Burgess, ref. 1, p. 19.
15. Behe, M.J., *A Mousetrap for Darwin*, Discovery Institute Press, p. 507, 2020.
16. A summary drawn from Laufmann S. and Glicksman H., *Your Designed Body*, Discovery Institute Press, p. 83, 2022.

Richard W. Toosey *B.A., Dip.Arch., RIBA (retired) is an English architect/artist whose professional life was in design practice. He has published* Design and Natural Selection: A comparative study, *Michael Terence Publishing, Amazon, 2022.*

The design of bacterial flagella: part 2—flagellar diversity across bacterial species

David Thomas

As expected from a design perspective, bacterial flagella show significant diversity in their design across the bacterial domain. Flagella differ between species in five main ways: (1) the number and arrangement of flagella per cell, (2) the presence of sheaths surrounding flagellar filaments, (3) the structure of the parts found in all flagella, (4) the structure of additional parts found in the flagella of only some species, and (5) their function (what flagella are used for). This paper is the second in a seven-part review on the design of bacterial flagella and their associated systems. The structural design of the flagella of the model organisms *Escherichia coli* and *Salmonella enterica* was discussed in part 1. In this paper, the flagellar designs observed in other bacterial species are shown to differ significantly from those found in the model organisms.

Pioneering research on the structure of bacterial flagella, from various species, used purification techniques that removed many flagellar parts from the flagellar structure when isolating them from cells. The parts that remained (such as the MS-ring, rod, hook, and filament) appeared very similar among species.[1] This gave the false impression that flagella have a very similar structural design across the bacterial domain.[1] In reality, flagellar structural design is diverse with most flagella containing additional parts not found in the flagella of the model organisms discussed in part 1 (*E. coli* and *S. enterica*)[2] (figure 1).

Over 80% of bacterial species have flagella.[3] The distribution of flagella across the domain Bacteria does not match what would be expected from a Darwinian tree of common descent (see part 7).[4] Evolutionists have argued that the diversity of flagellar designs across the domain Bacteria is evidence against design because, from their perspective, a Designer would not make diverse designs.[5,6] However, this is a theological argument, not a scientific one, and breaks down when human design approaches are considered.[4] Humans frequently design things with considerable diversity, especially when product variants need to be optimally designed to satisfy various constrains (e.g., a city car vs an off-road car vs a race car). Flagellated bacteria live in diverse environments and have different lifestyles, both of which impose design constraints in order to optimize flagellum function. With these things in mind, we *would* expect to see much diversity in the design of bacterial flagella. And indeed we do. The design of flagella differ among species in five main ways:

1. the number and arrangement of flagella per cell
2. the presence of sheaths surrounding flagellar filaments
3. the structure of the parts common to all flagella
4. the structure of additional parts found in the flagella of only some species
5. the function of flagella.

Each of these areas of diversity is discussed below.

1. The number and arrangement of flagella per cell

The clearest difference in flagella systems among bacterial species is the number and arrangement of flagella. There are at least nine different bacterial flagellar arrangements (table 1, figure 2) and these can significantly affect swimming behaviour, as will be discussed in part 3.

Flagella can be organized broadly into three systems—polar (at the cell pole(s)), lateral (along the side of the cell body), and peritrichous (evenly covering the cell body).[7] Polar is likely the most common flagellar system, especially in marine environments, where 90% of motile bacteria have a single polar flagellum (monotrichous).[8,9] The flagella of different systems have distinct morphologies suited to different environments and swimming behaviours (see part 3).[7] Polar flagella typically have a pitch and diameter half that of peritrichous flagella.[7]

Several examples of flagellar arrangements in various bacterial species will be mentioned, commencing with two examples of bacteria with polar flagella. *Spirillum volutans* has a bundle of about 75 external flagella at each pole.[10] In contrast, *Campylobacter jejuni* has just one flagellum at each pole.[11] Both *S. volutans* and *C. jejuni* have helical cell bodies like spirochetes, which allows them to produce some thrust from rotation of their bodies.[10]

Vibrio species possess two flagellar systems. They have a lateral flagellar system (used for swarming motility on surfaces) and a polar flagellar system (used for swimming

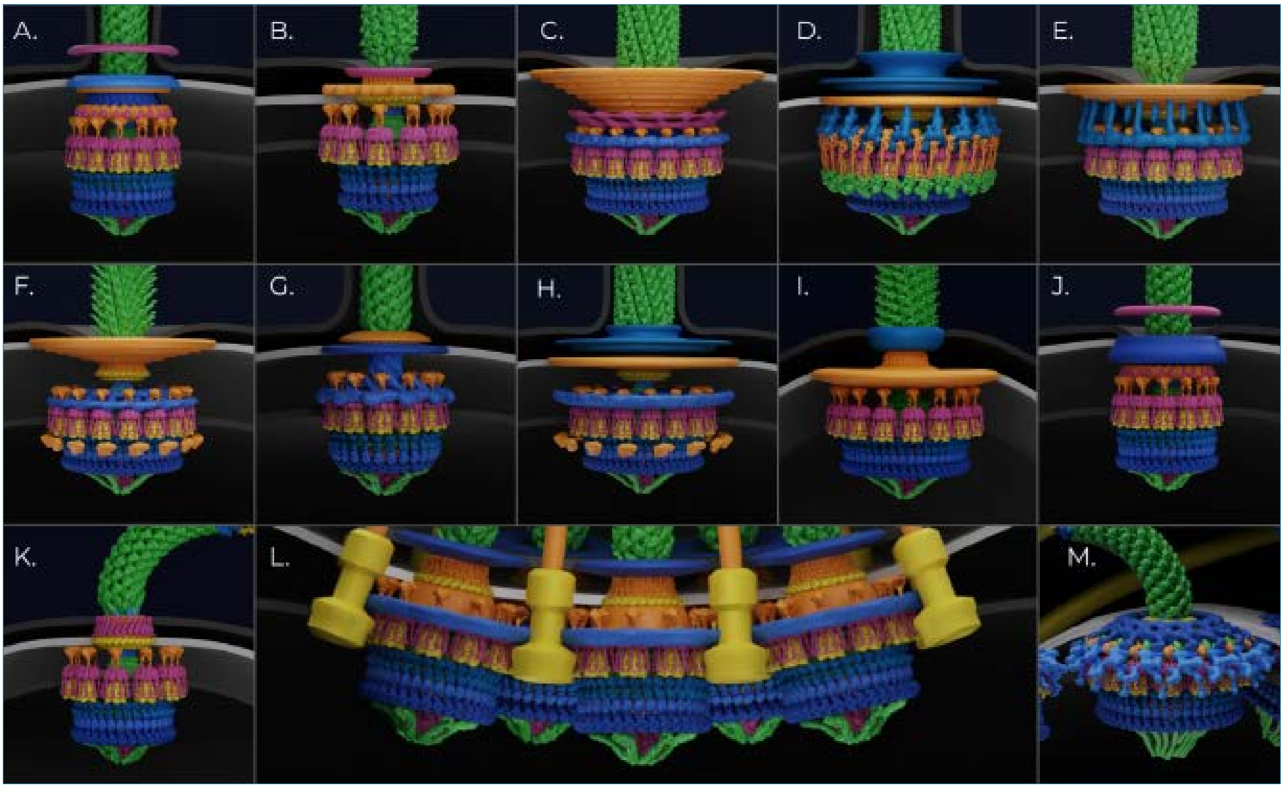


Figure 1. Computer models of a selection of diverse flagellar motor designs, based, in part, on Cryo-EM data, RCSB Protein Data Bank files,[59] and AlphaFold predictions.[60,61] (A) *V. alginolyticus*, (B) *C. crescentus*, (C) *C. jejuni*, (D) *H. pylori*, (E) *W. succinogenes*, (F) *A. butzeri*, (G) *B. bacteriovorus*, (H) *H. hepaticus*, (I) *H. gracilis*, (J) *Shewanella oneidensis* (based, in part, on EMD-0467[62]), (K) *E. coli*, (L) *Magnetococcus massalia* strain MO-1, with two motors from the array removed, (M) *B. burgdorferi*.
Note: The central gears of *C. jejuni* and *H. pylori* contain a protein called 'FliY', which is not shown in these illustrations. Images not at same scale. Unless stated otherwise, computer models in figures were made in Blender 3.5 (blender.org) with the Molecular Nodes add-on (bradyajohnston.github.io/MolecularNodes).

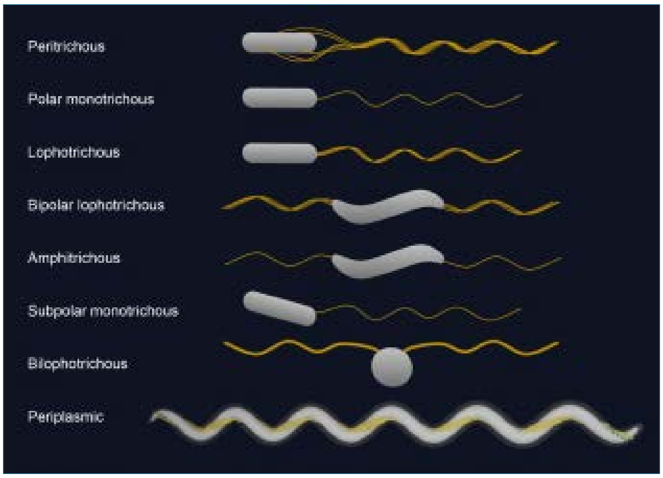


Figure 2. Flagellar arrangements. 'Periplasmic flagella', while not typically described as a flagellar arrangement, is included for comparison. Flagella shown in yellow. Cell bodies shown in grey (except for the spirochete cell body, where the PG-layer is shown in grey and the membranes are shown in transparent dark grey). The thick yellow lines of the bilophotrichous coccus cell represent bundles of seven or more flagella which are encased in a sheath.

motility in liquids).[12,13] The polar flagella are always expressed, but the lateral flagella are only expressed in viscous environments or on surfaces (see part 5 for how this is controlled).[12]

The spirochetes are bacteria characterized by a distinct flat-wave or corkscrew cell morphology—caused by unique subpolar intracellular flagella within the periplasm (figure 3).[14,15] Spirochetes have one or more periplasmic flagella (sometimes called 'endoflagella'), which extend from the cell poles in a parallel, ribbon-like arrangement and spiral around the cell body towards the cell centre (figure 3).[14,16,17] In the figure, it is evident that the motors at each polar location are arranged in a row that spirals away from the cell tip. Unlike species with external flagella that swim by pushing on the surrounding fluid with their flagella, spirochetes swim by the rolling or the undulation of the cell body as controlled by its endoflagella.[14,18] The genera of spirochetes vary widely in cell morphology, the number of flagella and whether their flagella overlap in the centre.[19] For example,

Table 1. Various flagellar arrangements observed in bacterial species

Name	Description	Example species
Peritrichous	Multiple flagella located uniformly across the cell body	*Escherichia coli, Salmonella enterica, Bacillus subtilis*
Polar monotrichous	A single flagellum at one pole	*Pseudomonas aeruginosa, Vibrio parahaemolyticus, Caulobacter crescentus, Bdellovibrio bacteriovorus, Shewanella oneidensis*
Lophotrichous	Multiple flagella located at one pole	*Helicobacter pylori, Pseudomonas fluorescens, Vibrio fischeri, Aquaspirillum serpens*
Bipolar lophotrichous	Multiple flagella located at both poles	*Spirillum volutans, Helicobacter suis*
Amphitrichous	A single flagellum at each pole	*Campylobacter jejuni, Magnetospirillum magneticum, Rhodospirillum rubrum*
Bilophotrichous	Two bundles of flagella on one cell hemisphere	*Magnetococcus massalia* strain MO-1, *Magnetococcus marinus* strain MC-1
Subpolar/medial monotrichous	A single flagellum near one pole or located mid-cell	*Cereibacter sphaeroides*
Lateral*	Multiple flagella along the sides of the cell body	*Vibrio parahaemolyticus, Azospirillum brasilense*
Periplasmic**	One or more periplasmic flagella extending from each pole and remaining within the periplasmic space	All spirochete species including *Borrelia burgdorferi, Leptospira biflexa, Treponema pallidum*

*Lateral flagella can exist in combination with other arrangements (e.g., polar monotrichous)

**Typically not described as a flagellar arrangement since it can fit under bipolar lophotrichous/amphitrichous

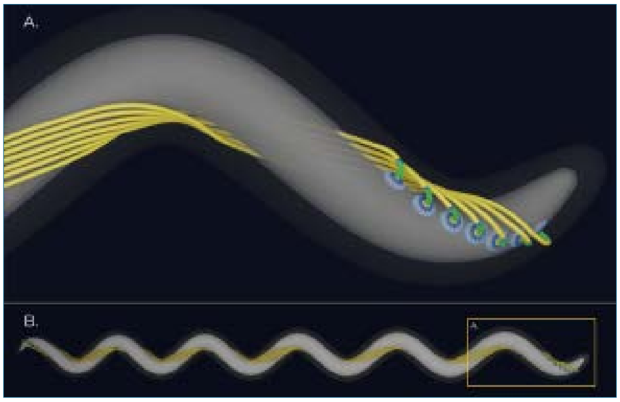


Figure 3. Periplasmic flagella of *B. burgdorferi* (membranes in transparent dark grey, peptidoglycan layer in transparent light grey). (A) Close-up of cell tip, showing motors spiralling around the cell body in a row and filaments forming a 'ribbon' that wraps around the cell body. (B) View showing whole cell body.

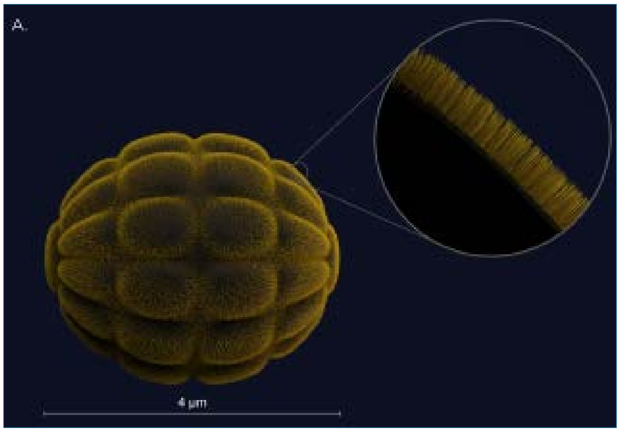


Figure 4. A model of an ellipsoidal bundle of multicellular magnetotactic prokaryotes (MMPs). Thousands of flagella form a fur-like coating over the surface of the bundle, similar to cilia. Inset shows close-up of flagella on cell surface.

Borrelia burgdorferi has a flat-wave morphology and has seven to eleven flagella at each pole that overlap in the centre (figure 3). In contrast, *Leptospira illini* has a corkscrew morphology and one flagellum at each pole, which do not overlap.[12,14,20] There are also some large spirochetes with hundreds of endoflagella,[21] which undoubtedly means added complexity is involved.

In ovoid bacteria that orientate along magnetic field lines (magnetotactic), a more refined classification version of flagellar arrangements (table 1) is more helpful than the three systems highlighted above. For example, in the marine ovoid species *Magnetococcus massalia* strain MO-1 and *Magnetococcus marinus* strain MC-1, flagella assemble into two clusters on one hemisphere of the cell. The seven

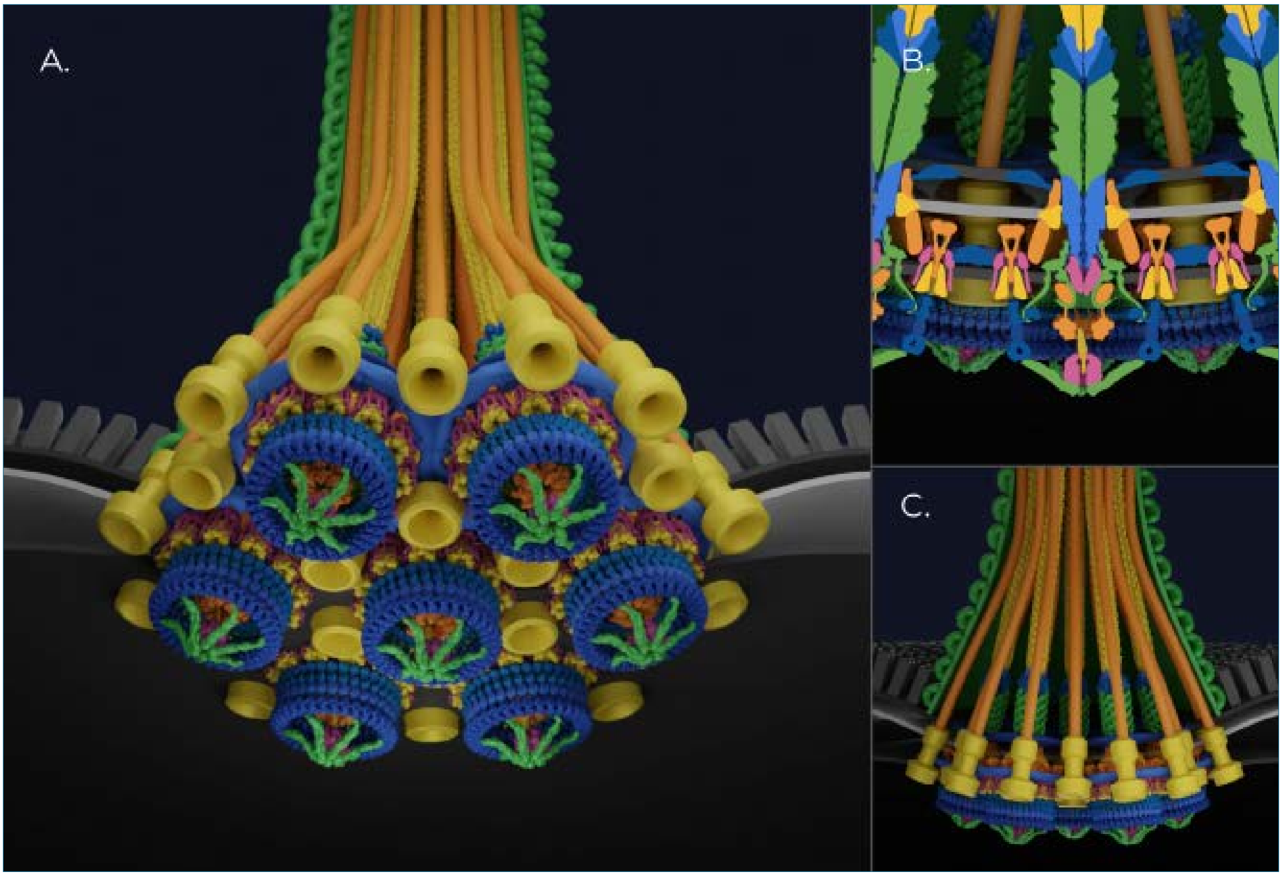


Figure 5. MO-1 hexagonal hepta-motor array (based, in part, on figures 1–6 of ref. 30, and AlphaFold predictions). (A) Low view, (B) cross-section diagram, (C) front view. Note the shorter universal joints compared to other species. MO-1 has two of these arrays located on one hemisphere of their ovoid cell body (see the bilophotrichous arrangement in figure 2).

motors at the base of each cluster form a hexagonally arrayed hepta-motor complex with a 2:3:2 arrangement (figure 5). Several other marine cocci that are magnetotactic have bilophotrichous flagella in a similar motor array architecture.[22,23] A 2017 study found novel magnetotactic cocci that possess an even more complex flagellar motor array with 19 motors arranged in a 3:4:5:4:3 arrangement.[24]

The magnetotactic bacteria represent a diverse group and some can cluster together into spherical or ellipsoidal bundles of 40 to 80 cells.[25] These bundles (called ‘multicellular magnetotactic prokaryotes’, MMPs) are coated in thousands of flagella, similar to the arrangement of cilia over the surface of single-celled eukaryotic ciliates (figure 4). Through some unknown mechanism, these cells coordinate all their flagella, which is necessary for efficient motility and navigation.[25]

The large ovoid species *Ovobacter propellens* displays a large unsheathed tuft of about 400 flagella, mostly rooted in a depression, and spaced about 100 nm apart at one end of its cell body.[26] This flagellar arrangement does not fit readily into the classification system proposed in table 1.

2. The presence of sheaths surrounding flagellar filaments

The polar flagella of several genera of Gram-negative bacteria are surrounded by a sheath, which is a membranous tube around the filament and is continuous with the cell membrane (figure 1a, d, g, h).[27] (Interestingly, there is one reported case of sheathed peritrichous flagella.[28]) Some membrane proteins and lipopolysaccharides localize to these sheaths, though the exact mechanisms of this localization remain unknown.[27] It is worth noting that when multiple flagella are present on a cell pole, each is surrounded with its own sheath. In contrast, whole bundles of flagella in *Magnetococcus massalia* MO-1 and *Magnetococcus marinus* MC-1 are surrounded with a stretchable sheath made of glycoproteins arranged in a helical array (figure 5).[29,30]

Many functions have been proposed for membranous sheaths, including protecting the filament from the gastric environment, hiding flagellins from the host’s immune systems, altering the mechanical properties of flagellar filaments, and improving adhesion to surfaces.[27,31]

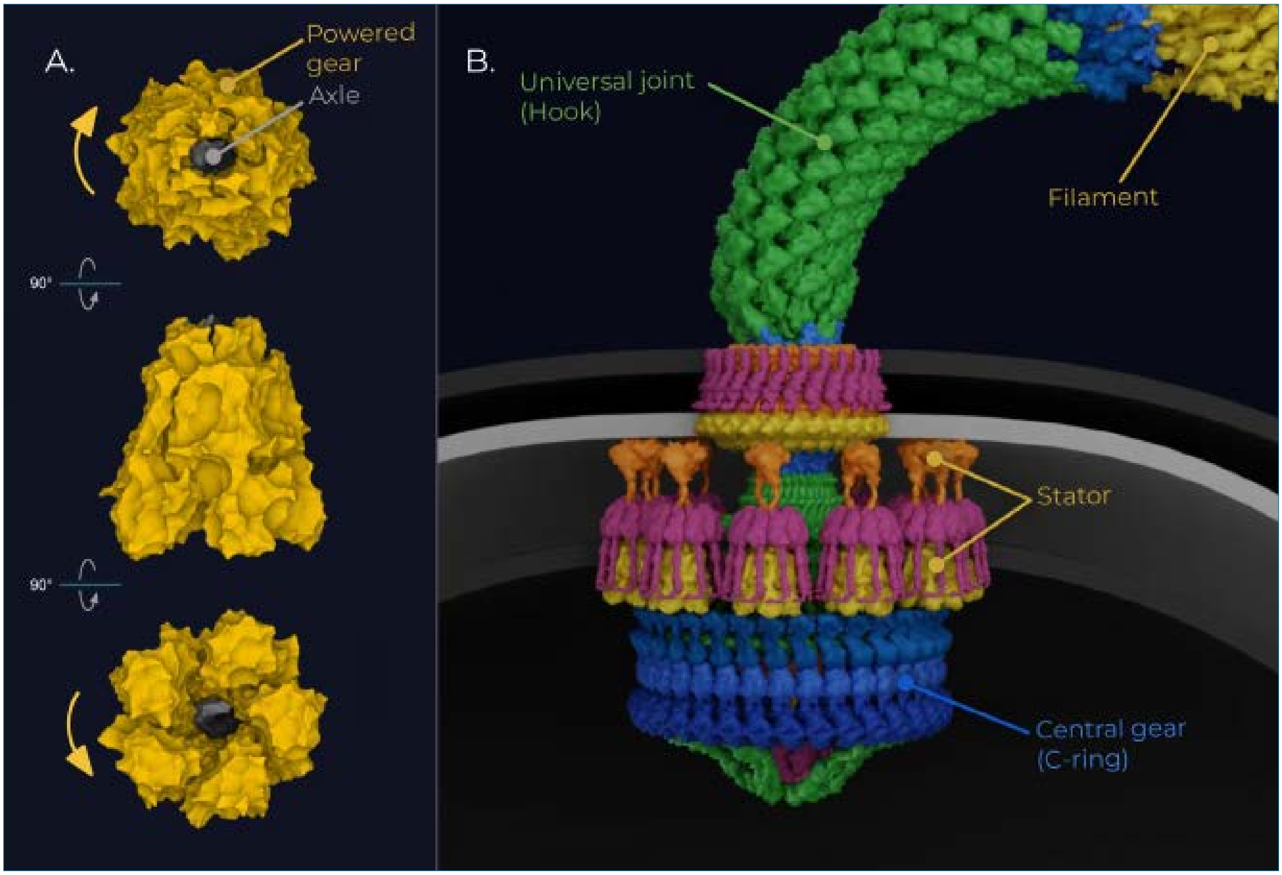


Figure 6. (A) The lower portion of a stator unit (PDB[58] ID: 6YSL, molecular surface representation made in Mol*[62]). The powered gear is shown in yellow and axle is shown in black and grey. The upper portion of the MotB proteins that make the axle are not shown (but are shown in orange in b) (B) The flagellar motor of *E. coli* with the central gear, stators, universal joint and filament labelled.

3. The structure of the parts common to all flagella

With the exception of the L- and P-rings (which are absent in Gram-positive species), the parts discussed in part 1 are found in the flagella of all flagellated bacterial species.[17] This list of parts includes the stators, FliL rings, central gear (C-ring), export apparatus, hub (MS-ring), driveshaft (rod), universal joint (hook), universal joint–filament junction, and propeller filament.[17] It is worth highlighting the spirochete family, as *L. interrogans* has both the L- and P-rings; *B. burgdorferi* has only the P-ring; and *T. pallidum* has neither.[17]

While these parts are present across flagellated species, there is some diversity in their designs. This designed diversity is most clearly seen in the stators, central gear, universal joint, and filament. Below is a brief summary of the diversity of these parts. For more detail, see appendix 1.

Stators

Flagellar stators are units consisting of an axle and a rotating gear which drives the central gear of flagellar motors (see part 1) (figure 6). Stators differ in a number of ways, including the ion their rotation is powered by, the torque they produce, and how they are regulated.[17,32] The most common ion used is H^+ but Na^+ is also used by the stators of some species, especially marine species.[17] For example, H^+-driven MotAB is used by *E. coli* and *S. enterica*, while Na^+-driven PomAB is used by *Vibrio* species.[17]

At least 65 bacterial species use more than one type of stator.[33] For example, *Shewanella oneidensis* MR-1 has a single polar flagellum (figure 1j) driven by both MotAB and PomAB.[34] Likewise, *Bacillus subtilis* uses a mix of MotAB and Na^+-driven MotPS to drive each of its flagella.[35] *S. oneidensis* and *B. subtilis* can regulate what proportion of each type of stator is engaged in their motor(s) to adjust the proportion of each ion used (see part 3).[34,35]

Central gear

The diameter of the central gear (commonly called the 'C-ring', figure 6b) varies considerably between species.[36] This larger central gear allows more stators to be engaged and positions the stators further away from the central axis of the motor, allowing for greater torque to be produced (compare

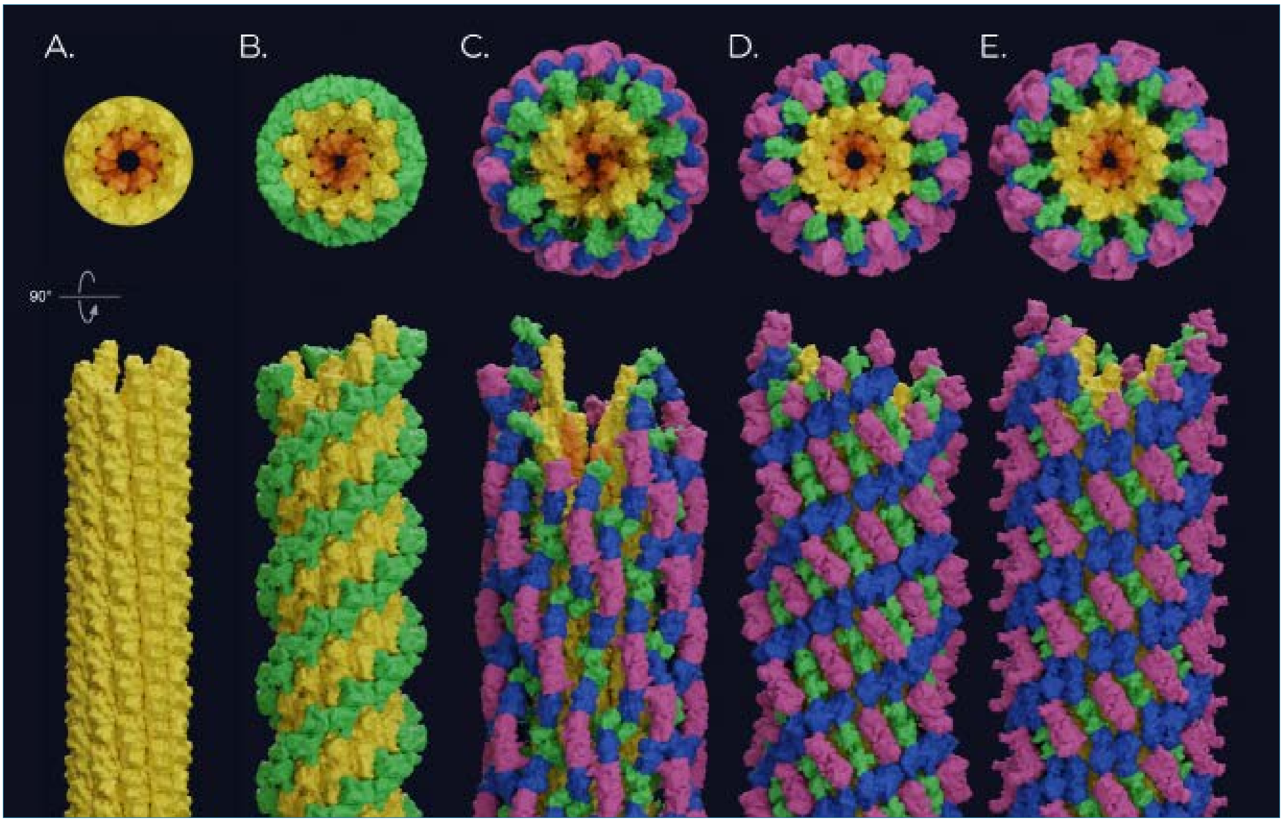


Figure 7. Molecular surface representations of diverse flagellar filament structures coloured by domains (orange = domain 1; yellow = domain 2; green = domain 3; blue = domain 4; pink = domain 5). (A) *C. crescentus* filament (PDB ID: 6XKY) with no outer domains, (B) *Sinorhizobium meliloti* filament with outer domains in a screw formation (PDB ID: 7SN9), (C) *E. coli* O127:H6 filament with outer domains forming tetramers to form a sheath (PDB ID: 7SN7), (D) *Achromobacter sp.* filament with outer domains forming tetramers to form a sheath (PDB ID:7SQD), (E) *E. coli* O157:H7 filament with outer domains forming dimers to form a sheath (PDB ID:7SN4)

figure 1b with 1c). There is also diversity in the proteins that make up the central gear, including the presence of a protein called FliY, which is used in place of or alongside FliN.[34]

Universal joint

The universal joint (sometimes called the 'hook') transmits the rotation of the flagellar motor to the propeller filament and, in polar flagella, facilitates turning manoeuvres (see part 3). The universal joint differs in its structure, leading to differences in its rigidity, stability, and robustness between species.[37–39]

Filament

The flagellin proteins that make up flagellar filaments differ considerably in the structure of their outer domains.[40,41] Flagellin outer domains can also form dimers or tetramers between subunits to form complex outer-domain sheaths or screw-like structures (figure 7). Glycosylation of flagellins is common in gram-negative species and some gram-positive species.[42] In some species, flagellins are also methylated or phosphorylated.[43,44] Around 45% of bacterial species contain two or more flagellin genes.[45] Typically, in species with multiple flagellin genes, the abundance of specific flagellins is different in the proximal end of the filament from that in the middle and distal end of the filament.[46,47] In spirochetes, proteins bind to the outside of the filament.[48] The filaments of some species (e.g., *E. coli*) switch between a left- and right-handed helix upon a switch in rotational direction. The filaments of other species maintain a constant morphology, either always left-handed (e.g., *V. alginolyticus*) or always right-handed (e.g., *C. crescentus*).[49]

4. The structure of additional parts found in the flagella of only some species

Along with differences in the design of the core parts, the flagella of many species contain many additional parts. This is especially true of high-torque polar and periplasmic flagellar motors which have cage, ring, and/or disk structures around them for structural support (figures 1a–j, m).[50,51] These structures are sometimes referred to as 'stator scaffolds' and can be essential for flagella to function in these species (see part 7).[52] These structures likely serve other functions as well, which future research will uncover. For more detail on these structures in various species see appendix 2.

5. The function of flagella

Flagellum researcher Dr Scott Minnich predicted, from an intelligent design perspective, that flagella would serve more functions than that of just a propulsion device.[53] This is now known to be the case. Flagella are also used for biofilm formation, adhesion, mechanoreception, secretion of virulence factors and/or cleaving peptides.[38,43,54,55] In fact, some non-motile bacteria, such as those of selected species in the genus *Brucella*, use flagella solely for purposes other than motility.[56] However, this lack of motility may be a defect, as other strains of *Brucella* do use flagella for motility.[57]

Conclusion

Bacterial flagella show immense diversity in their design across the bacterial domain, from the number and arrangement of flagella to the presence of additional specialized components like cages and disks. Flagellar designs are optimized for the lifestyles and environmental conditions of a wide array of species. Further research into diverse flagellar designs will surely continue to unveil the brilliance of our Creator.

The next paper in this review series, part 3, will show how flagellar motors change gears and how differences in flagellar arrangement affect the swimming behaviour of bacterial species.

Acknowledgments

I would like to thank Dr Andrew Fabich for looking over drafts of this paper and providing many helpful suggestions and comments.

References and notes

1. DePamphilis, M.L. and Adler, J., Fine structure and isolation of the hook-basal body complex of flagella from *Escherichia coli* and *Bacillus subtilis*, *J. Bacteriology* **105**(1):384–395, 1971.
2. Thomas, D., The design of bacterial flagella: part 1—flagellar design in model organisms, *J. Creation* **37**(2):83–95, 2023.
3. De Maayer, P., Pillay, T., and Coutinho, T.A., Flagella by numbers: comparative genomic analysis of the supernumerary flagellar systems among the Enterobacterales, *BMC Genomics* **21**(1):670, 2020.
4. Luskin, C., Flagellar diversity challenges Darwinian evolution, not intelligent design, *EvolutionNews*, 2015.
5. Pallen, M.J., and Matzke, N.J., From the origin of species to the origin of bacterial flagella, *Nature Reviews, Microbiology* **4**(10):784–790, 2006.
6. Baker, M. The bacterial flagellar motor: brilliant evolution or intelligent design? *ABC Science In Depth*, 2015.
7. Fujii, M., Shibata, S., and Aizawa, S., Polar, peritrichous, and lateral flagella belong to three distinguishable flagellar families, *J. Molecular Biology* **379**(2):273–283, 2008.
8. Thormann, K.M., Beta, C., and Kühn, M.J., Wrapped up: the motility of polarly flagellated bacteria, *Annual Review of Microbiology* **76**:349–367, 2022.
9. Leifson, E., Cosenza, B.J., Murchelano, R., and Cleverdon, R.C., Motile marine bacteria, I. Techniques, ecology, and general characteristics, *J. Bacteriology* **87**(3):652–666, 1964.
10. Wadhwa, N. and Berg, H.C., Bacterial motility: machinery and mechanisms, *Nature Reviews Microbiology* **20**(3):161–173, 2022.
11. Cohen, E.J., Nakane, D., Kabata, Y., Hendrixson, D.R., Nishizaka, T., and Beeby, M., *Campylobacter jejuni* motility integrates specialized cell shape, flagellar filament, and motor, to coordinate action of its opposed flagella, *PLoS Pathogens* **16**(7):e1008620, 2020.
12. Merino, S., Shaw, J. G., and Tomás, J. M., Bacterial lateral flagella: an inducible flagella system. *FEMS Microbiology Letters* **263**(2):127–135, 2006.
13. Kim, Y.K. and McCarter, L.L., Analysis of the polar flagellar gene system of *Vibrio parahaemolyticus*, *J. Bacteriology* **182**(13):3693–3704, 2000.
14. Nakamura. S., Spirochete flagella and motility, *Biomolecules* **10**(4):550, 2020.
15. Liu, J., Howell, J.K., Bradley, S.D., Zheng, Y, Zhou, Z.H., and Norris, S.J., Cellular architecture of *Treponema pallidum*: novel flagellum, periplasmic cone, and cell envelope as revealed by cryo electron tomography, *J. Molecular Biology* **403**(4):546–561, 2010.
16. Carroll, B.L. and Liu, J., Structural conservation and adaptation of the bacterial flagella motor, *Biomolecules* **10**:1492, 2020.
17. Terashima, H., Kawamoto, A., Morimoto, Y.V., Imada, K., and Minamino, T., Structural differences in the bacterial flagellar motor among bacterial species, *Biophysics and Physicobiology* **14**:191–198, 2017.
18. Wolgemuth C.W., Flagellar motility of the pathogenic spirochetes, *Seminars in Cell and Developmental Biology* **46**:104–112, 2015.
19. Chang, Y., Xu, H., Motaleb, M.A., and Liu, J., Characterization of the flagellar collar reveals structural plasticity essential for spirochete motility, *mBio* **12**(6):e0249421, 2021.
20. Motaleb, M.A., Pitzer, J. E., Sultan, S.Z., and Liu, J., A novel gene inactivation system reveals altered periplasmic flagellar orientation in a *Borrelia burgdorferi* fliL mutant, *J. Bacteriology* **193**(13):3324–3331, 2011.
21. Margulis, L. and Hinkle, G., Large symbiotic spirochetes: *Clevelandina, Cristispira, Diplocalyx, Hollandina and Pillotina*; in: Dworkin, M., Falkow, S., Rosenberg, E., Schleifer, KH., Stackebrandt, E. (Eds.), *The Prokaryotes*, *Springer* New York, 2006.
22. Zhang, W.J. and Wu, L.F., Flagella and swimming behavior of marine magnetotactic bacteria, *Biomolecules* **10**(3):60, 2020.
23. Zhou, K., Pan, H., Yue, H., Xiao, T., and Wu, L.F., Architecture of flagellar apparatus of marine magnetotactic cocci from Qingdao, *Marine Science* **34**(12):88–92, 2010.
24. Liu, J., Zhang, W., Li, X., Li, X., Chen, X., Li, J. H., Teng, Z., Xu, C., Santini, C. L., Zhao, L., Zhao, Y., Zhang, H., Zhang, W. J., Xu, K., Li, C., Pan, Y., Xiao, T., Pan, H., and Wu, L.F., Bacterial community structure and novel species of magnetotactic bacteria in sediments from a seamount in the Mariana volcanic arc, *Scientific Reports* **7**(1):17964, 2017.
25. Qian, X.X., Santini, C.L., Kosta, A., Menguy, N., Le Guenno, H., Zhang, W., Li, J., Chen, Y.R., Liu, J., Alberto, F., Espinosa, L., Xiao, T., and Wu, L.F., Juxtaposed membranes underpin cellular adhesion and display unilateral cell division of multicellular magnetotactic prokaryotes, *Environmental Microbiology* **22**(4):1481–1494, 2020.
26. Fenchel, T., and Thar, R., ‘Candidatus *Ovobacter propellens*’: a large conspicuous prokaryote with an unusual motility behaviour, *FEMS Microbiology Ecology* **48**(2):231–238, 2004.
27. Chu, J., Liu, J., and Hoover, T.R., Phylogenetic distribution, ultrastructure, and function of bacterial flagellar sheaths, *Biomolecules* **10**(3):363, 2020.
28. Busse, H.-J., Auling, G., Achromobacter; in: Whitman, W., Rainey, F., Kampfer, P., Trujillo, M., Chun, J., DeVos, P. (Eds.), *Bergy’s Manual of Systematics of Archaea and Bacteria*, *John Wiley and Sons*, Hoboken, NJ, 2015.
29. Lefèvre, C.T., Santini, C.L., Bernadac, A., Zhang, W.J., Li, Y., and Wu, L.F., Calcium ion-mediated assembly and function of glycosylated flagellar sheath of marine magnetotactic bacterium, *Molecular Microbiology* **78**(5):1304–1312, 2010.
30. Ruan, J., Kato, T., Santini, C. L., Miyata, T., Kawamoto, A., Zhang, W.J., Bernadac, A., Wu, L.F., and Namba, K., Architecture of a flagellar apparatus in the fast-swimming magnetotactic bacterium MO-1, PNAS **109**(50):20643–20648, 2012.

31. Kreutzberger, M., Sobe, R.C., Sauder, A.B., Chatterjee, S., Peña, A., Wang, F., Giron, J.A., Kiessling, V., Costa, T., Conticello, V.P., Frankel, G., Kendall, M. M., Scharf, B. E., and Egelman, E.H., Flagellin outer domain dimerization modulates motility in pathogenic and soil bacteria from viscous environments, *Nature Communications* **13**, article 1422, 2022.
32. Wu, Z., Tian, M., Zhang, R., and Yuan, J., Dynamics of the two stator systems in the flagellar motor of *Pseudomonas aeruginosa* studied by a bead assay, *Applied and Environmental Microbiology* **87**(23):e0167421, 2021.
33. Thormann, K.M., and Paulick, A., Tuning the flagellar motor, *Microbiology (Reading, England)* **156**(5):1275–1283, 2010.
34. Paulick, A., Koerdt, A., Lassak, J., Huntley, S., Wilms, I., Narberhaus, F., and Thormann, K. M., Two different stator systems drive a single polar flagellum in *Shewanella oneidensis* MR-1, *Molecular microbiology* **71**(4), 836–850, 2009.
35. Terahara, N., Noguchi, Y., Nakamura, S., Kami-Ike, N., Ito, M., Namba, K., and Minamino, T., Load- and polysaccharide-dependent activation of the Na+-type MotPS stator in the *Bacillus subtilis* flagellar motor, *Scientific reports* **7**:46081, 2017.
36. Chen, S., Beeby, M., Murphy, G.E., Leadbetter, J.R., Hendrixson, D.R., Briegel, A., Li, Z., Shi, J., Tocheva, E.I., and Müller, A., Structural diversity of bacterial flagellar motors, *The EMBO J.* **30**:2972–2981, 2011.
37. Kato, T., Makino, F., Miyata, T., Horváth, P., and Namba, K., Structure of the native supercoiled flagellar hook as a universal joint, *Nature Communications* **10**(1):5295, 2019.
38. Matsunami, H., Barker, C.S., Yoon, Y.H., Wolf, M., and Samatey, F.A., Complete structure of the bacterial flagellar hook reveals extensive set of stabilizing interactions, *Nature Communications* **7**:13425, 2016.
39. Miller, M.R., Miller, K.A., Bian, J., James, M.E., Zhang, S., Lynch, M.J., Callery, P.S., Hettick, J.M., Cockburn, A., Liu, J., Li, C., Crane, B.R., and Charon, N.W., Spirochaete flagella hook proteins self-catalyse a lysinoalanine covalent crosslink for motility, *Nature Microbiology* **1**(10):16134, 2016.
40. Eckhard, U., Bandukwala, H., Mansfield, M.J., Marino, G., Cheng, J., Wallace, I., Holyoak, T., Charles, T. C., Austin, J., Overall, C.M., and Doxey, A.C., Discovery of a proteolytic flagellin family in diverse bacterial phyla that assembles enzymatically active flagella, *Nature Communications* **8**(1):521, 2017.
41. Hu, D. and Reeves, P.R., The remarkable dual-level diversity of prokaryotic flagellins, *mSystems* **5**(1), e00705-19, 2020.
42. For a detailed overview on flagllar glycosylation, see Hayakawa, J. and Ishizuka, M., Flagellar Glycosylation: Current Advances, *Glycosylation,* Petrescu, S., (Ed.), 2012.
43. Horstmann, J.A., Lunelli, M., Cazzola, H., Heidemann, J., Kühne, C., Steffen, P., Szefs, S., Rossi, C., Lokareddy, R.K., Wang, C., Lemaire, L., Hughes, K.T., Uetrecht, C., Schlüter, H., Grassl, G.A., Stradal, T.E.B, Rossez, Y., Kolbe, M., and Erhardt, M., Methylation of *Salmonella typhimurium* flagella promotes bacterial adhesion and host cell invasion, *Nature Communications* **11**, 2020.
44. Kelly-Wintenberg, K., South, S.L., and Montie, T.C., Tyrosine phosphate in a- and b-type flagellins of *Pseudomonas aeruginosa*, *J. Bacteriology* **175**(8):2458–2461, 1993.
45. Nedeljković, M., Sastre, D.E., and Sundberg, E.J., Bacterial flagellar filament: a supramolecular multifunctional nanostructure, *International J. Molecular Sciences* **22**(14):7521, 2021.
46. Kühn, M.J., Schmidt, F.K., Farthing, N.E., Rossmann, F.M., Helm, B., Wilson, L.G., Eckhardt, B., and Thormann, K.M., Spatial arrangement of several flagellins within bacterial flagella improves motility in different environments, *Nature Communications* **9**(1):5369, 2018.
47. Kostrzynska, M., Betts, J.D., Austin, J.W., and Trust, T.J., Identification, characterization, and spatial localization of two flagellin species in *Helicobacter pylori* flagella, *J. Bacteriology* **173**(3), 937–946, 1991.
48. Kurniyati, K., Chang, Y., Liu, J., and Li, C., Transcriptional and functional characterizations of multiple flagellin genes in spirochetes, *Molecular Microbiology* **118**(3):175–190, 2022.
49. Thormann, K.M., Beta, C., and Kühn, M.J., Wrapped up: the motility of polarly flagellated bacteria, *Annual Review of Microbiology* **76**:349–367, 2022.
50. Rossmann, F.M. and Beeby, M., Insights into the evolution of bacterial flagellar motors from high-throughput in situ electron cryotomography and subtomogram averaging, *Acta Crystallographica, Section D, Structural Biology* **74**(6):585–594, 2018.
51. Chaban, B., Coleman, I. and Beeby, M., Evolution of higher torque in *Campylobacter*-type bacterial flagellar motors, *Scientific Reports* **8**:97, 2018.
52. Zhou, X. and Roujeinikova, A., The structure, composition, and role of periplasmic stator scaffolds in polar bacterial flagellar motors, *Frontiers in Microbiology* **12**:639490, 2021.
53. Gillen, A., Bacterial flagella—icon of the intelligent design movement; in: Gillen, A. (ED.), *The Genesis of Germs*, chap. 1, 2007.
54. Chaban, B., Hughes, H.V., and Beeby, M., The flagellum in bacterial pathogens: for motility and a whole lot more, *Seminars in Cell and Developmental Biology* **46**:91–103, 2015.
55. Barrero-Tobon, A.M. and Hendrixson, D.R., Flagellar biosynthesis exerts temporal regulation of secretion of specific *Campylobacter jejuni* colonization and virulence determinants, *Molecular Microbiology* **93**(5):957–974, 2014.
56. Coloma-Rivero, R.F., Flores-Concha, M., Molina, R.E., Soto-Shara, R., Cartes, Á., and Oñate, Á.A., *Brucella* and its hidden flagellar system, *Microorganisms* **10**(1):83, 2021.
57. Soler-Lloréns, P F., Quance, C.R., Lawhon, S.D., Stuber, T.P., Edwards, J.F., Ficht, T.A., Robbe-Austerman, S., O'Callaghan, D., and Keriel, A., A *Brucella* spp. Isolate from a Pac-Man frog (*Ceratophrys ornata*) reveals characteristics departing from classical brucellae, *Frontiers in Cellular and Infection Microbiology* **6**:116, 2016.
58. Berman, H.M., Westbrook, J., Feng, Z., Gilliland, G., Bhat, T.N., Weissig, H., Shindyalov, I.N., and Bourne, P.E., The protein data bank, *Nucleic Acids Research* **28**:235–242, 2000 | rcsb.org.
59. Jumper, J., Evans, R., Pritzel, A., Green, T., Figurnov, M., Ronneberger, O., Tunyasuvunakool, K., Bates, R., Žídek, A., Potapenko, A., Bridgland, A., Meyer, C., Kohl, S.A.A., Ballard, A.J., Cowie, A., Romera-Paredes, B., Nikolov, S., Jain, R., Adler, J., Back, T., Petersen, S., Reiman, D., Clancy, E., Zielinski, M., Steinegger, M., Pacholska, M., Berghammer, T., Bodenstein, S., Silver, D., Vinyals, O., Senior, A.W., Kavukcuoglu, K., Kohli, P., and Hassabis, D., Highly accurate protein structure prediction with alphafold, *Nature* **596**(7873):583–589, 15 Jul 2021.
60. Varadi, M., Anyango, S., Deshpande, M., Nair, S., Natassia, C., Yordanova, G., Yuan, D., Stroe, O., Wood, G., Laydon, A., Žídek, A., Green, T., Tunyasuvunakool, K., Petersen, S., Jumper, J., Clancy, E., Green, R., Vora, A., Lutfi, M., Figurnov, M., Cowie, A., Hobbs, N., Kohli, P., Kleywegt, G., Birney, E., Hassabis, D., and Velankar, S., AlphaFold protein structure database: massively expanding the structural coverage of protein-sequence space with high-accuracy models, *Nucleic Acids Research* **50**(D1):D439–D444, 17 Nov 2021.
61. Kaplan, M., Ghosal, D., Subramanian, P., Oikonomou, C.M., Kjaer, A., Pirbadian, S., Ortega, D.R., Briegel, A., El-Naggar, M.Y., and Jensen, G.J., The presence and absence of periplasmic rings in bacterial flagellar motors correlates with stator type, *eLife* **8**:e43487, 2019.
62. Sehnal, D., Bittrich, S., Deshpande, M., Svobodová, R., Berka, K., Bazgier, V., Velankar, S., Burley, S. K., Koča, J., and Rose, A.S., Mol* Viewer: modern web app for 3D visualization and analysis of large biomolecular structures, *Nucleic Acids Research* **49**:W431–W437, 6 May 2021.
63. Maki-Yonekura, S., Yonekura, K., and Namba, K., Conformational change of flagellin for polymorphic supercoiling of the flagellar filament, *Nature Structural and Molecular Biology* **17**(4):417–422, 2010.
64. Yamaguchi, T., Toma, S., Terahara, N., Miyata, T., Ashihara, M., Minamino, T., Namba, K., and Kato, T., Structural and functional comparison of *Salmonella* flagellar filaments composed of FljB and FliC, *Biomolecules* **10**(2):246, 2020.
65. Maruyama, Y., Momma, M., Mikami, B., Hashimoto, W., and Murata, K., Crystal structure of N- and C-terminal regions of flagellin, *to be published.*
66. Zhu, S., Nishikino, T., Takekawa, N., Terashima, H., Kojima, S., Imada, K., Homma. M, Liu, J., *In situ* structure of the *Vibrio* polar flagellum reveals a distinct outer membrane complex and its specific interaction with the stator, *J. Bacteriology* **202**(4):e00592-19, 2020.
67. Zhao, X., Norris, S.J., and Liu, J., Molecular architecture of the bacterial flagellar motor in cells, *Biochemistry* **53**(27):4323–4333, 2014.

David Thomas *(a pen name), B.Sc., is currently studying biological sciences at university. He was introduced to CMI materials through his parents, both in science fields. David is actively involved in creation apologetics.*

Enantiomeric amplification of amino acids: part 9—enantiomeric separation via crystallization

Royal Truman, Chris Basel, and Stephen Grocott

For some amino acids (AAs), DL racemic crystals are more soluble than pure D or L crystals, and vice versa for other AAs. Experiments to amplify small initial excesses of L enantiomers are critiqued here for lacking realism under natural conditions:

- Excessively high concentrations of pure AAs would have been required.
- Solution temperature would have to be kept fixed as water slowly evaporated.
- At just the right time the two phases would need to have separated whereas evaporation would more likely have completely desiccated the mixtures.
- Enriched AAs would have redissolved after rainfall, tidal incursion, or other sources of water in addition to mixing with racemic AAs from the environment.
- L-AAs solidified into crystals would have been unable to participate in the putative prebiotic origin of life chemistry.

Experiments wherein depleted D-enantiomers in a solution phase were replenished by adding complex catalysts to enhance racemization overlook that such catalysts would have racemized all kinds of AA indiscriminately. Rapid stirring while continually grinding crystals with glass beads does not reflect natural processes either.

We continue here, in part 9, a series of papers that evaluate the main proposals from the Origin of Life (OoL) community on how a small enantiomeric excess (e.e.) of D- or L-amino acids (AA) could have been naturally amplified. All the proposals have been found to be irrelevant or inadequate to explain how proteins based on only L enantiomers could have arisen through natural processes.

Amino acid conglomerates vs racemic compounds

When both enantiomers of an amino acid (AA) are present in solution, crystallization produces either DL enantiomer mixtures within each crystal or the crystals are composed of only D and L enantiomers. When the mixed enantiomers are combined 1:1 within the same crystal, the result is called a *racemic compound* (e.g., see figure 1, right panel). Alternatively, mixtures of individually pure D and L crystals are known as *conglomerates* (figure 1, left panel). Pasteur was able to separate D from L crystals of tartaric acid using tweezers and a microscope.[1]

The difference in the two types of crystals is determined by whether the stronger interaction in the solid phase is between heterochiral (racemic) or homochiral (conglomerate) enantiomers. Racemic compounds are formed by ~90% of all known chiral compounds, and around 17 of the proteinogenic amino acids,[2] although in many of the AA cases the ΔG is <2 kJ/mole.[3]

Physical separation of AA enantiomers is possible if they form racemic crystals (DL) having different solubility than their enantiopure compounds.[4,5] This occurs when the free energy of formation for the mixed DL crystal is sufficiently different than for the pure crystals.[6] Solubility differences could be affected by temperature, pH, ionic strength, or other factors.

Enantiomeric enrichment using the liquid phase

Consider the case in which the racemic compound of an AA is *less soluble* than its homochiral crystals. Suppose that solutions are prepared with one enantiomer in excess. As the racemic material preferentially crystallizes, the e.e. (of the more soluble isomer) would increase in the solution phase, see figure 2.[2] This separation can occur as the temperature is lowered or the concentration increased through evaporation. This provides the potential to separate solvent which is enriched with one enantiomer from the racemic solid phase.

Amplification of phenylalanine and tryptophan

For most AAs found in proteins, the *racemic crystals are less soluble* than crystals composed of a single enantiomer. Breslow and Levine reported in 2006 that they prepared an aqueous solution containing ~500 mg *of phenylalanine* with a 1% excess of the L component and allowed it to slowly

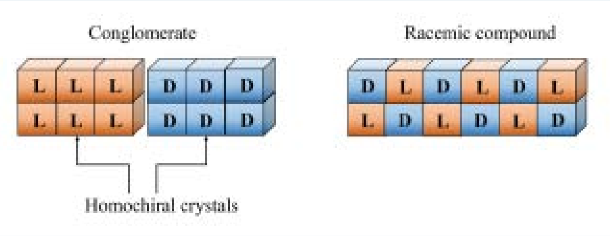


Figure 1. Left: conglomerates consist of pure D- and pure L-enantiomer crystals since homochiral interactions dominate. Right: Racemic compounds include D and L enantiomers in the same amount within each crystal, since the heterochiral interactions are stronger than homochiral ones. (Figure based on a diagram in ref. 2.)

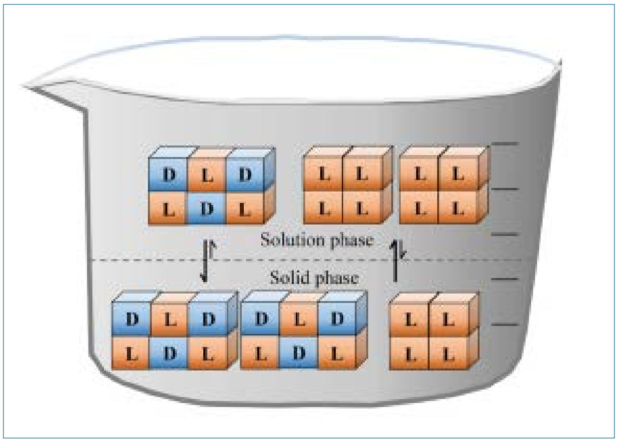


Figure 2. By adjusting temperature or concentration, enantiomeric excesses can be amplified in the solution phase when racemic compounds are *less soluble* than the homochiral crystals. (Figure based on a diagram in ref. 2.)

evaporate until the majority of the material (>400 mg) had crystallized.[7] Surprisingly, the experimental details were not provided, such as temperature, the volume of water, duration or rate of evaporation, and whether stirring was used. The crystals were racemic, and the solution now contained phenylalanine having a 40% e.e.$_L$. They then prepared a new aqueous solution with 500 mg of a 40% L e.e. and again slowly evaporated the water. Racemic crystals (racemate) again crystallized and were again separated. The supernatant solution now contained ~100 mg of phenylalanine having a ~90% e.e.$_L$. This represented an L/D ratio of 95/5.[8] The mirror results were obtained when they began with an excess of D-phenylalanine.[6]

Experiments were also performed beginning with aqueous solutions having 1%, 5%, or 10% e.e., which also led to an e.e. of up to 90% for phenylalanine. Similar experiments were conducted using tryptophan[9], and the results from both papers are summarized in table 1.

The scenario resembles a process carefully designed by chemical engineers, and would not have occurred without expert guidance for the reasons discussed next.

The use of pure AA solutions

Prebiotically very rare phenylalanine and tryptophan would have been present in ppb concentrations, based on thermodynamic, Miller-type experiments, and meteorite composition studies.[10–12] Concentrated aqueous solutions could not have existed since contaminants (such as NaCl from seawater) would have been present in concentrations many orders of magnitude greater. Realistically, evaporation would have produced a dense slurry of chemicals containing virtually none of these AA.

Ideally controlled crystal separation conditions

Slow evaporation under carefully controlled conditions was used. Under natural conditions there would have been temperature fluctuations; e.g., between day and night or seasons, forming and dissolving LL, DD, and DL crystals. At any time, it would have been very rare for a solution to have contained predominantly pure DL-precipitated crystals.

Perfect timing for crystal separation

The researchers watched until >80% of the AA had crystallized and then measured the e.e.$_L$ of the liquid. Levine *et al.* speculated that

> "Amplification via evaporation of water could have occurred on prebiotic earth in a drying lake bed near a site of meteorite landing. Preferential dissolution may have occurred when river or rainwater passed over an amino acid mixture, dissolving the single enantiomer with enriched enantiopurity and carrying it downstream."[9]

Creating a measurable e.e.$_L$ from chemicals provided from a meteorite is far fetched. The lake would have initially contained racemic AA, and it is not plausible that meteorites would have provided the necessary e.e.$_L$.[13] Furthermore, the proportion of AA to other chemicals from a meteorite would have been negligible. In any event, the authors visualized rivers and rainwater waiting until much DL crystallization occurred and then extracting some of the supernatant, instead of diluting the lake water and redissolving the crystals, as would have occurred naturally. This is further discussed under 'Optimization of all details'.

Remixing prevented

The fortuitous separation of racemic crystals and L-enriched liquid is contrived. Rainfall or extraneous water incursions would have simply remixed everything. For example, with temperature changes and addition of water,

Table 1. Enantiomeric concentration in % of phenylalanine and tryptophan after two consecutive partial crystallizations from water. Phenylalanine data were taken from ref. (6), and tryptophan data were from ref. (8).

	Phenylalanine [a]			
Initial (%) e.e.$_{D}$	Final (%) e.e.$_{D}$	Initial (%) e.e.$_{L}$	Final (%) e.e.$_{L}$	Final (%) e.e.$_{D}$–e.e.$_{L}$
1	87.2	1	88.3	-1.1
5	91.7	5	88.6	3.1
10	90.0	10	90.9	-0.9
Aver.:	89.6		89.3	0.4

	Tryptophan [b]			
Initial (%) e.e.$_{D}$	Final (%) e.e.$_{D}$	Initial (%) e.e.$_{L}$	Final (%) e.e.$_{L}$	Final (%) e.e.$_{D}$ - e.e.$_{L}$
1	86.0	1	81.1	4.9
5	86.7	5	86.9	-0.2
10	89.0	10	84.6	4.4
Aver.:	87.2		84.2	3.0

Average of duplicate experiments

[a] From ref. 6

[b] From ref. 8

the DL crystals in the lake would have redissolved and mixed with previously separated L-enriched water. In addition, homogenous L crystals evaporated near the shore from L-enriched water would have easily redissolved back into the lake.

Evolutionary dead end

LL crystals precipitated from highly L-enriched water would not have served any purpose for OoL models.

Optimization of all details was necessary

The scenario requires e.e.$_{L}$ to increase faster than would be lost through racemization and mixing with racemic AA. However, what might a realistic scenario resemble? Consider a lake containing a miniscule proportion of dissolved phenylalanine with 1% e.e.$_{L}$, mixed with many other chemicals. It is subject to random rainfall or contact with rivers, evaporation, and temperature fluctuations. Making the questionable assumption that some DL crystals did precipitate (despite the insignificant concentration of AA), what might the e.e.$_{L}$ of the separating L-enriched water be? The extracted water would have been diluted and contaminated with racemic AA by the new water transporting it, so >1% is not reasonable. L-enriched water could have desiccated near the lake, but what would have prevented rainfall from remixing everything later? Importantly, note that the excess L enantiomer being slowly removed would have automatically decreased the amount of excess L remaining behind in the lake.

Of course, water extracted from a drying lake after a considerable amount of LL crystals had also precipitated would have been even less enriched after mixing.

Nevertheless, assume some L-enantiomer–enriched water had separated. It would need to then undergo multiple additional cycles of amplification. However, the amount of AA now present would decrease with each cycle since, by assumption, crystals of DL had been removed. The resulting low concentration of AA would soon no longer be able to form crystals. Separating enriched water by first adding water and then evaporating it would also have continually increased the proportion of contaminants.

The researchers were only able to obtain e.e.$_{L}$ incrementally because every cycle was initiated with a pure sample of 500 mg AA having about the maximum theoretical e.e.$_{L}$ achievable during the preceding cycle.[7]

It is interesting that OoL researchers draw much attention to cases of e.e.$_{L}$ which are 1% or less, whether from meteorite samples or laboratory experiments. There is a high probability that these could be laboratory artifacts. But according to the duplicate experiments summarized in table 1, an average e.e.$_{D}$ of 87.2% was found for tryptophan, but only an average e.e.$_{L}$ of 84.2% for the L enantiomer. This is a considerable difference and in the *wrong* direction, since an excess of the L form is needed.

Suppose the goal of an experiment had been to show that an e.e.$_{D}$ could have arisen naturally (instead of the L form). It is very likely that this 3% average net difference, based on repeated experiments, would have been presented as supporting the wished-for hypothesis. Anomalous results are often interpreted as flawed and unlikely to be followed up on than results congruent with a favoured theory. This behaviour leads to a statistical distortion whereby more evidence will be collected to support the researcher's view than to potentially refute it.[14]

Enantiomer enrichment using the solid phase

We will now switch to the case in which the racemic compound of an AA is *more soluble* than its homochiral crystals. In this case, beginning with an excess of one enantiomer in solution could produce homochiral crystals under the right conditions.[2] This would lead to an e.e. in the solid phase.

Among the proteinogenic AAs, racemic *asparagine* (Asn) and *threonine* (Thr) can crystallize from aqueous solutions as conglomerates under the right conditions.[15,16] Albrecht

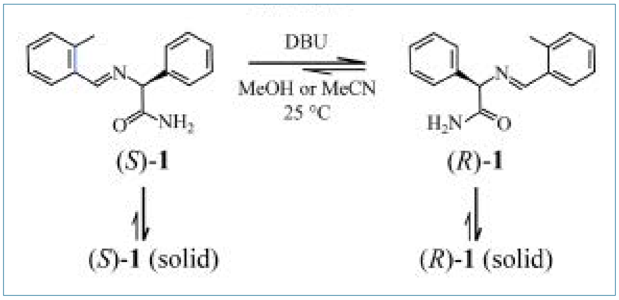


Figure 3. Chemical and physical equilibria in the racemization and crystallization/dissolution processes for the product of 2-methyl-benzaldehyde and phenylglycinamide, designated here as '1'.[19] (Redrawn from a figure in ref. 19.)

claimed, in 1943, that *methionine* also forms crystalline conglomerates, but this does not seem consistent with a detailed eutectic study, published in 2009 by Polenske, for temperatures between 1–60°C.[17,18]

For preferential crystallization to work for conglomerating crystals, the homochiral interactions must be stronger than heterochiral interactions at the crystal–aqueous interface. Since the solubilities of both enantiomers are identical, saturated solutions will contain an equal number of D and L molecules regardless of how great the overall difference between the amount of D and L in the conglomerate. This results in the potential for enantioenrichment in the solid phase.[2]

Critique of these studies

The same critiques apply here as above for those racemic compounds which were *less soluble* than the homochiral crystals; for example:

- For some AAs, enrichment required processing the solution phase, and for others the solid phase. A single natural process does not apply to all biological AAs.
- Nature would not have conveniently evaporated enough water until the L enantiomer in excess began to solidify and then quickly separated the enriched (in D enantiomer) liquid phase. Realistically, if enough water had evaporated to achieve a high concentration of the L crystals, then a little more evaporation would have caused the pure D and DL crystals to also crystallize from solution.
- The initial AAs would have been mixed with many other substances—instead of being highly pure and concentrated.
- Upon removing the L enantiomer, the solution phase would have become depleted in L compared to nearby water and would have decreased its e.e.$_L$.
- One heavy rainfall or tide would have dissolved all the L-enriched crystals, racemizing the solution.
- Crystals containing a high e.e.$_L$ would have served no purpose for OoL purposes unless they first redissolved in water, interacted with other AAs, and formed peptides. But as soon as they dissolved, they would have begun to racemize and been contaminated with water less enriched (if at all) in L enantiomer.

Enrichment by forming larger pure D or L crystals

Under special laboratory conditions, some AAs can be enriched if one enantiomer is present in sufficient excess, permitting it to form larger crystals than the other enantiomer would. This occurs because the larger pure D or L crystals are less soluble than smaller ones. The solution phase will eventually become depleted in the formerly major enantiomer. However, this would be counteracted if the 'wrong' enantiomer had enough time to racemize in the solution phase.

For this enrichment process to work, the larger homochiral crystals must attract more of the same enantiomer faster than DL crystals form, and the DL crystals must be more soluble than the homochiral ones.[19–22] The left- and right-handed crystals will grow and dissolve at the same rate unless there is a greater amount of one chiral form since secondary nucleation can amplify the difference.[23]

In 2008 Noorduin *et al.* showed that a crystalline enantiomer of a chiral non-AA molecule could be produced, starting from a nearly racemic mixture using *attrition enhancement*.[19] This was accomplished using the imine of 2-methyl-benzaldehyde and phenylglycinamide shown as '**1**' in figure 3. This molecule exists as two enantiomers that form separate *R* and *S* solid-phase crystals (i.e., a conglomerate). It also racemized rapidly in methanol or acetonitrile solution phase in the presence of the special organic-base DBU (1,8-diazabicyclo[5.4.0]undec-7-ene).[19]

The experiments were initiated with solution-solid mixtures of (RS)-**1** with various e.e. of (R)-**1** or (S)-**1** and magnetically stirred (1,250 rpm) at ambient temperature in the presence of 2.5 mm glass beads. Crystals of the majority enantiomer began to form first. This led automatically to enrichment in the solution phase of the other enantiomer.[19] After solution-solid equilibrium was reached, the researchers forced solution-phase racemization by adding DBU as a catalyst, thereby replenishing the enantiomer lost through crystallization. With the help of the glass beads, which provided mechanical energy and continuous attrition of the crystals, the e.e. of the solid phase increased over time. This eventually led to a single enantiomer in the solid phase.[19]

The process seemed to rely on the fact that crystals having larger sizes grow faster than smaller crystals (called Ostwald ripening). This was initiated by the small e.e. of one of the enantiomers under continual attrition caused by agitation in the presence of glass beads.

Once enough of the solid crystals of a single enantiomer had formed, the system was ‘committed’, since competing nucleation to form crystals of the opposite enantiomer would be very difficult in the racemizing solution.[19]

Critique of these studies

- Large homochiral crystals based on only an L AA would need to grow rapidly and crystallize accompanied by the very rapid conversion of resulting excess D → L. Biogenetic AAs don’t have these properties. For most AAs, racemizing most of a ~1% excess of D under cold, crystallizing temperatures would have required hundreds of thousands or millions of years.[24] During this time, any homochiral crystals already produced would have had countless opportunities to redissolve in rainwater or tides and to mix with racemic AAs.
- The racemization experiments did not involve AAs but molecules in special laboratory solvents like methanol or acetonitrile which are irrelevant for OoL purposes.
- Special organic bases like 1,8-diazabicyclo[5.4.0]undec-7-ene are irrelevant for OoL purposes. Racemizing catalysts on a primordial Earth would have been devastating since the last thing OoL scientists would want are substances *able to racemize all AAs*. The opposite is needed, that is a means to generate only L enantiomers for 19 biogenetic AAs. (Glycine does not possess a chiral carbon and therefore cannot exist as separate D and L enantiomers).
- The initial conditions required not just an e.e.$_L$ to permit the enrichment process to initiate, but a racemizing base, which was added at just the right time. Why would such a racemizing catalyst (which was soluble in the solvent used) not have already eliminated the initial e.e.?
- The necessary conditions have no natural analogue: rapid stirring at ~1,250 rpm, super-concentrated solutions of AAs, the presence of 2.5 mm glass beads for attrition, and a controlled ambient temperature.
- Random temperature changes, such as day and night transitions could have caused the entire AA content to freeze and contaminate any large homochiral crystals.

Deracemization by crushing crystals through mechanical stirring

Viedma performed studies beginning with a supersaturated aqueous solution of 50:50 L and D $NaClO_3$ chiral crystals, stirred in the presence of glass balls with 3 mm diameter, usually stirred at 600 rpm using a magnetic bar.[25] Sodium chlorate’s ions Na^+ and ClO_3^- are not chiral, but the crystals they form are, typically produced in equal amounts of left- and right-handed crystals. The very first crystal formed could be based on either enantiomer.[2]

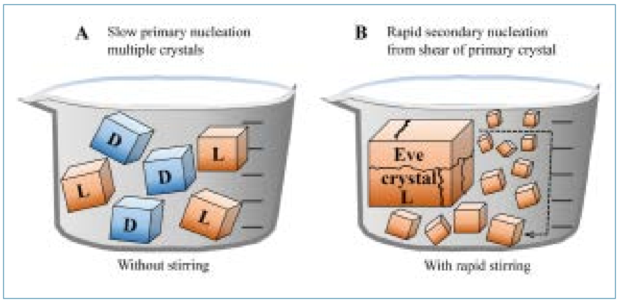


Figure 4. ‘Eve crystal’ model of conglomerate forming $NaClO_3$. (A) Primary nucleation can be followed by (B) degradation of an ‘Eve’ crystal through vigorous stirring to produce secondary nucleation. (Figure based on a diagram in ref. 2.)

Under rapid stirring, this ‘Eve’ crystal was broken into thousands of smaller crystals by impact with the stirring bar. All the ‘daughter’ crystals had the same chiral form and grew by secondary nucleation which attracted ions from solution. If secondary nucleation occurred fast enough, a single chiral solid state was obtained, as shown in figure 4.[2]

This effect was believed to be due to so-called Ostwald ripening, which was highly enhanced by the continuous abrasion-grinding process.[20,26]

Crushed between the glass balls, crystals were repeatedly broken down while others formed. After grinding for several hours, one chiral form of crystal predominated. Viedma reported that the dominant form which crystallized was random when the original mixture was racemic.[20]

In the absence of crystal attrition by glass balls, no excess of crystals was obtained, even with rapid stirring. Tests demonstrated that enantiomeric crystal formation depended on the concentration of the glass balls and rate of stirring.[20]

Viedma showed, in 2008, that under special conditions, this effect could be set up for one proteinogenic amino acid, namely *aspartic acid*.[15]

Critique of these studies

- Importantly, the experiments using $NaClO_3$ produced D or L crystals with equal probability. If such processes could have occurred naturally, no e.e.$_L$ would have resulted.
- The unusual conditions necessary produced a laboratory artifact not expected to occur in nature. Rapid stirring was not enough; crystal attrition by glass balls was also necessary.
- Only the AA aspartic acid has been shown to produce these conglomerates.

References

1. Kauffman, G.B. and Myers, R.D., Pasteur's resolution of racemic acid: a sesquicentennial retrospect and a new translation, *The Chemical Educator* **3**(6):1–18, 1998.
2. Blackmond, D.G., The origin of biological homochirality, *Cold Spring Harb Perspectives in Biology* **11(3)**:a032540, 2019.
3. Huang, J. and Yu, L., Effect of molecular chirality on racemate stability: α-amino acids with nonpolar r groups, *J. American Chemical Society* **128**(6):1873–1878, 2006.
4. 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.
5. Klussmann, M, White, A.J.P., Armstrong, A., and Blackmond, D.G., Rationalization and prediction of solution enantiomeric excess in ternary phase systems, *Angewandte Chemie, International Edition* **47**:7985–7989, 2006.
6. Morowitz, H.J., A mechanism for the amplification of fluctuations in racemic mixtures, *J. Theoretical Biology* **25**:491–494, 1969.
7. Breslow, R. and Levine, M., Amplification of enantiomeric concentrations under credible prebiotic conditions, PNAS **103**:12979–12980, 2006.
8. $e.e._{L}$ = (L – D)/ (L + D) = 0.9; replacing D by= (1 – L) leads to 2L – 1 = 0.9. Therefore, L = 0.95 and D = 0.05.
9. Levine, M., Kenesky, C.S., Mazori, D., and Breslow, R., Enantioselective synthesis and enantiomeric amplification of amino acids under prebiotic conditions, *Organic Letters* **10**:2433–2436, 2008.
10. Higgs, P.G., and Pudritz, R.E., A thermodynamic basis for prebiotic amino acid synthesis and the nature of the first genetic code, *Astrobiology* **9**(5):483–490, 2009.
11. Parker, E.T., Cleaves, H.J., Dworkin, J.P., Glavin, D.P., Callahan, M., Aubrey, A., Lazcano, A., and Bada, J.L., Primordial synthesis of amines and amino acids in a 1958 Miller H2S-rich spark discharge experiment, PNAS **108**:5526–5531, 2011.
12. Burton, A.S., Stern, J.C., Elsila, J.E., Glavin, D.P., and Dworkin, J.P., Understanding prebiotic chemistry through the analysis of extraterrestrial amino acids and nucleobases in meteorites, *Chemical Society Reviews* **41**:5459–5472, 2012.
13. Breslow and Levine reported that reactions using L-α-methylvaline (presumably from a meteorite) produced the *wrong* D-phenylalanine in their chemical transformations![7] To revert this disastrous outcome, the reaction conditions (temperature, duration, etc.) were optimized, using ideal 4 equiv of 100% L-α-methylvaline (presumably from a meteorite) mixed with 1 equiv of sodium phenylpyruvate (of unknown origin) and 1 equiv cupric sulfate (of unknown origin).[9] Such mixtures have no prebiotic plausibility. A maximum of 37% e.e. L-phenylalanine was obtained, based on 100% L-α-methylvaline. Of course, pure L-α-methylvaline would not have been available, and decreasing the proportion of cupric sulfate would have led to the incorrect D-phenylalanine.
14. Truman, R., Clean-up and analysis of small data sets can distort conclusions, *J. Creation* **36**(2):66–71, 2022.
15. Bernal, I., Conglomerate crystallization and chiral discrimination phenomena: in vivo and in vitro, *J. Chemical Education* **69**:468–469, 1992.
16. 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, *Origins of Life and Evolution of Biospheres* **43**:129–135, 2013.
17. Albrecht, G., Schnakenberg, G.W., Dunn, M.S., and McCullough, J.D., Quantitative investigations of amino acids and peptides. xii. structural characteristics of some amino acids, *J. Physical Chemistry* **47**:24, 1943.
18. Polenske, P. and Lorenz, H., Solubility and metastable zone width of the methionine enantiomers and their mixtures in water, *J. Chemical Engineering Data* **54**:2277–2280, 2009.
19. Noorduin, W. L., Izumi, T., Millemaggi, A., Leeman, M., Meekes, H., Van Enckevort, W.J., Kellogg, R.M., Kaptein, B., Vlieg, E., and Blackmond, D.G., Emergence of a single solid chiral state from a nearly racemic amino acid derivative, *J. American Chemical Society* **130**:1158−1159, 2008.
20. Viedma, C., Ortiz, J.E., de Torres, T., Izumi, T., and Blackmond, D.G., Evolution of solid phase homochirality for a proteinogenic amino acid, Evolution of solid phase homochirality for a proteinogenic amino acid, *J. American Chemical Society* **130**:15274–15275, 2008.
21. Viedma, C., Verkuijl, B.J.V., Ortiz, J.E., de Torres, T., Kellogg, R.M. and Blackmond, D.G., Solution-Phase Racemization in the Presence of an Enantiopure Solid Phase 2010, *Chemistry–a European J.* **16**:4932−4937, 2010.
22. Blackmond, D.G., The Origin of Biological Homochirality, *Cold Spring Harb Perspectives in Biology* **2**:a002147, 2010.
23. Day, C., Crushing a solution of left-handed and right-handed crystals breaks its chiral symmetry, *Physics Today* **58**(4):21–22, 2005.
24. Truman, R., Racemization of amino acids under natural conditions: part 2—kinetic and thermodynamic data, *J. Creation* **36**(2):72–80, 2022.
25. Viedma, C., Chiral symmetry breaking during crystallization: complete chiral purity induced by nonlinear autocatalysis and recycling, *Physical Review Letters* **94**:065504, 2005.
26. Noorduin, W.L., van Enckevort, W.J. P., Meekes, H., Kaptein, B., Kellogg, R.M., Tully, J.C., McBride, J.M., and Vlieg, E., The driving mechanism behind attrition-enhanced deracemization, *Angewandte Chemie International Edition* **49**:8435–8438, 2010.

__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.

__Stephen Grocott__ has 1st Class Honours and Ph.D. degrees in organometallic chemistry (chiral metal complexes). Currently, he is managing director with an advanced chemicals manufacturing business. Before that, he was the lead processing technology expert for some of the world's largest resource companies. He is an adjunct professor with a large Australian university and was the chair of the board of the world's largest non-profit minerals R&D organisation. He has also served on the board of Youth for Christ Australia.

Enantiomeric amplification of amino acids: part 10—extraction of homochiral crystals accompanied by catalytic racemization

Royal Truman, Chris Basel, and Stephen Grocott

For abiogenesis to be possible, a natural process must separate proteinogenic L-amino acid enantiomers from racemic mixtures. It was shown that laboratory methods that separate L- and D-amino acid enantiomers based on differential solubility are impossible under unguided natural conditions. Preferential enrichment was used to separate these enantiomers in the solution phase. Crystallization-Induced Asymmetric Transformation was used to separate enantiomers in the solid phase. The separated L-amino acid must be replenished to continue the asymmetric transformation method. The remaining D-amino acids must therefore be racemized. This was accomplished in the laboratory using a racemizing agent in organic solvents at high temperatures. These methods cannot explain the origin of pure L-amino acids for several reasons. Organic solvents would not have existed in sufficient concentrations at high temperatures. High-quality catalysts would not have been available in high concentrations. Initial enantiomeric excesses in hot organic solvents to seed the formation of the first homochiral crystals would not be present. An unrealistically high amino acid concentration having an enantiomeric excess was necessary. Rapid stirring and glass beads in a contained volume to generate new, small seeds is not a realistic prebiotic environment. Finally, hot solvents and catalysts would have racemized any enantiomeric excess present.

We continue here our series of papers which critique possible natural explanations offered by origin of life (OoL) researchers for the origin of pure L-amino acids (AAs), necessary to produce proteins. In Part 9 of this series, we mentioned that most AAs preferentially form crystals that are 1:1 DL enantiomers, termed racemates or racemic compounds. Asparagine (Asn) and threonine (Thr) are exceptions, since homochiral DD and LL crystals (known as conglomerates) are formed preferentially.

In all cases the energy difference in crystal stability is very small, and a mixture is produced. Nevertheless, under careful laboratory conditions an enantiomeric excess (e.e.) can sometimes be obtained with careful timing by separating the solidified crystals from the solution phase after partial crystallization.

In Part 9 we discussed the example of an initial e.e. of an *(S)*-enantiomer imine being used to produce *(S)*-only crystals.[1] This required the resulting excess in *(R)*-form in solution to be reduced through rapid racemization with a special organic base, thereby replenishing the extracted S enantiomer.[2]

Chemical firms have been optimizing manufacturing processes for many years to selectively extract an enantiomer present in small excess. The key is to partially racemize the remaining mixture to replenish the enantiomer just extracted or the amount of pure enantiomer which could be obtained would be limited. For some substances (rarely proteinogenic AAs) this can ultimately yield 100% pure enantiomer.[3] However, this is not a process that occurs naturally.

Preferential enrichment

In preferential enrichment, the *solution phase* is used to obtain an e.e., taking advantage of the greater solubility of LL or DL crystals compared to DL racemates. Suppose that there is initially a small e.e.$_L$ in a solution. DL will slowly precipitate out, and small LL crystals will form in the solution. It would then be increasingly difficult for a D enantiomer to encounter another D enantiomer and therefore it would attach to a DL crystal. The consequence is an increase in e.e.$_L$ in the solution accompanied by an e.e.$_D$ in the deposited crystals.[2,4] The liquid phase is then removed, and solvent added with heating to redissolve the crystals. Now the solution begins with an excess of D, so after cooling and deposition of DL crystals an e.e.$_D$ remains dissolved accompanied by an e.e.$_L$ in the deposited crystals.

Tamura and his colleagues studied the compounds shown in figure 1, by dissolving them in hot ethanol and cooling to 25°C with stirring to form crystals. Repeating the process of dissolving in solvent, crystallization, and removal of solution phase led to new crystals having the opposite chirality after each cycle as expected, with increasing e.e. yields in the separated solution phase, but rapidly decreasing yields of product.[5–8]

Crystallization-Induced Asymmetric Transformation (CIAT)

In the Crystallization-Induced Asymmetric Transformation (CIAT) process solid crystals are used to obtain an e.e.. Now one takes advantage of the lower solubility of LL or DL crystals of some compounds compared to DL racemates. Assume once again that the L-enantiomer is desired and is provided in slight excess initially in a solution. The special feature of this method is that as the amount of L in solution is decreased as LL crystals form, racemization of D and L enantiomers in solution is deliberately accelerated and carried out continuously. Therefore, as the proportion of D increases, the conversion of D → L will exceed the reverse L → D, thereby preferentially replenishing the L lost.[9,10]

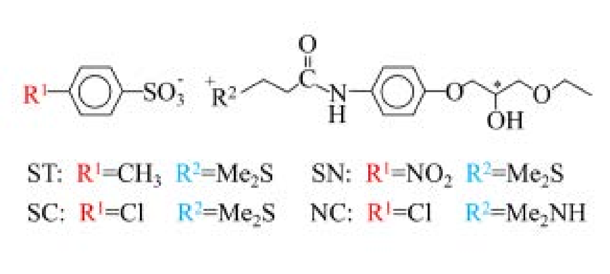


Figure 1. Compounds used to demonstrate preferential enrichment. An enantiomeric excess is amplified in the solution phase and that of the mirror enantiomer in the solid phase. Preparing a fresh solution by dissolving the crystallized material, and repeating the process, now reverses which enantiomer is amplified in the solution and solid phases.[8–11]
ST: ref 8, 9; SC: ref 10; SN: ref 11. (Figure redrawn from ref. 8.)

Almost all other processes proposed by OoL researchers would merely increase the e.e. in one location by decreasing it elsewhere. However, remixing would reverse the local excesses. With methods like CIAT, the e.e. could be deposited as crystals, in which AA racemization would be slower than in solution.

Various aliphatic and aromatic aldehydes catalyze AA racemization; see examples in table 1 using acetic acid as the solvent at 100°C for one hour.[5]

Allegedly the necessary aldehydes could have been provided through an influx from extraterrestrial sources like meteorites.[11]

The mechanism believed to racemize ***α***-AAs under acidic conditions is shown in figure 2.[5] This involves an initial protonation of the imine (Schiff base), followed by proton abstraction from the *α*-carbon atom by an acetate anion.

There do not seem to be restrictions on the type of aldehyde that could be used to induce racemization.

An absurdly high catalyst concentration under abiotic conditions, 0.01 mol of salicylaldehyde/mol of the pure AA, was necessary to completely racemize L-alanine in acetic acid within 1 hour at 100°C. Racemization was shown to increase rapidly with temperature. Rapid racemization also occurred when formic or propionic acid was used instead of acetic acid, as shown in table 2, but was most effective with acetic acid.

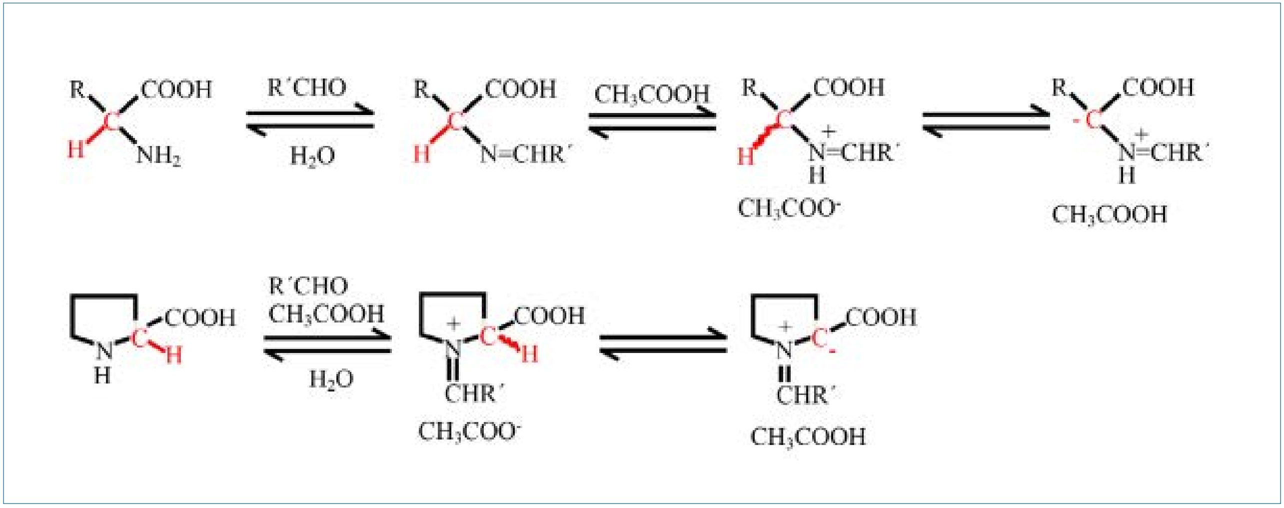


Figure 2. Racemization mechanism of amino acids under acidic conditions.[4]
The chiral C which racemizes is shown in red. (After scheme 1 on p. 91 of ref. 4.)

Table 1. Ability of various aldehydes to racemize some amino acids. A mixture of L-amino acid (1.5 mmol), aldehyde (0.3 mmol), and acetic acid (6 ml) was heated in a sealed tube in an oil bath at 100°C for 1 hour. Data is from table 2 of ref. 5.

		Degree Racemization, %			
Aldehyde	**Reaction Temp, °C**	**L-Ala**	**L-Met**	**L-Phe**	**L-Pro**
None	80	7	0	35	0
None	100	13	24	35	3
Formaldehyde	100	83	95	100	63
Acetaldehyde	100	97	100	100	98
Propionaldehyde	100	78	100	100[a]	87
n-butyraldehyde	80	97	95[a]	100[a]	99
n-heptylaldehyde	80	100	100[b]	100[b]	100
Benzaldehyde	100	72	100	100	72
Salicylaldehyde	80	100	100	100	91

[a] A ninhydrin test revealed degradation products containing an amino group.

[b] Considerable decomposition was found.

Table 2. Comparison of kinds of aliphatic acid solvent on the racemization of amino acids. A mixture of L-amino acid (1.5 mmol), aldehyde (0.3 mmol), and acetic acid (6 ml) was heated in a sealed tube in an oil bath at 100°C for 1 hour. Data is from table 4 of ref. 5.

Aliphatic acid	**L-Ala**	**L-Lys**	**L-Met**	**L-Phe**
Formic acid	81	43[a]	49	100
Without salicylaldehyde	53	19[a]	18	95
Propionic acid	9[b]	99[a]	96[a]	100[a]
Without salicylaldehyde	2[b]	15[a]	19[a]	100[a]
Acetic acid	100	100	100	100
Without salicylaldehyde	13	9	24	35

[a] A ninhydrin test revealed degradation products containing an amino group.

[b] Low solubility of the amino acid in the aliphatic acid.

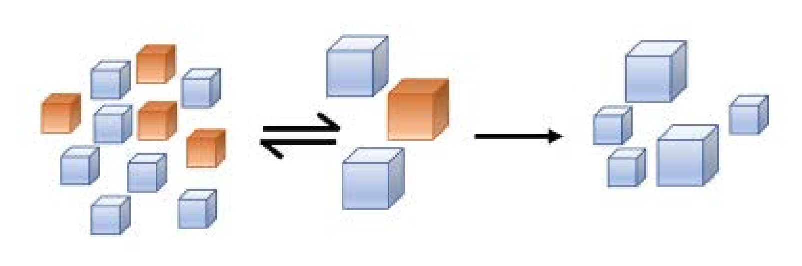


Figure 3. Without attrition by rapid stirring with glass balls, larger crystals are favoured due to the decrease in surface area per volume. An enantiomeric excess can be used to form one crystal form preferentially in solution. Racemization using a catalyst can be used to replenish the now-depleted enantiomer still dissolved.[13] (After scheme 2 from ref. 13.)

Other racemization procedures use an aldehyde and a metal ion which forms a chelate compound with the initially formed Schiff base, and the reactions are carried out under neutral or weakly alkaline conditions instead of pure organic acid.[5] This highlights the fact that metal cations would have been ubiquitous in primordial oceans. Why is this important? Loss of a proton at the α-carbon of an AA produces a planar carbanion intermediate, and re-protonation could occur at either plane, leading to either D- or L-enantiomers. Bada calculated that chelation by dissolved Cu^{2+} in oceans would have facilitated the removal of these protons, increasing the rate constant for racemization of for example alanine by about a hundred-fold (at pH 7.6 and 0°C).[12] However, *indiscriminate and unavoidable racemization would have resulted for all amino acids in the solution; not the outcome wished for by OoL researchers*.

Aspartic acid in acetic acid with catalytic salicylaldehyde

Heating promotes the preferential dissolution of smaller crystals, as illustrated in figure 3.

This is related to the Gibbs–Thomson effect, whereby small crystals are observed to be in equilibrium with their liquid melt at a lower temperature than large crystals.[14] The observation that small crystals dissolve and redeposit onto larger crystals leading to preferential growth of larger crystals is known as 'Ostwald ripening'.[13,15] This effect was described by Wilhelm Ostwald in 1896.[16,17]

OoL researcher Viedma *et al.* studied aspartic acid with an initial e.e. of each of the enantiomers under racemizing conditions in acetic acid at 90–160°C, using salicylaldehyde as the catalyst even though it does not form abiotically.[13] Asp was selected

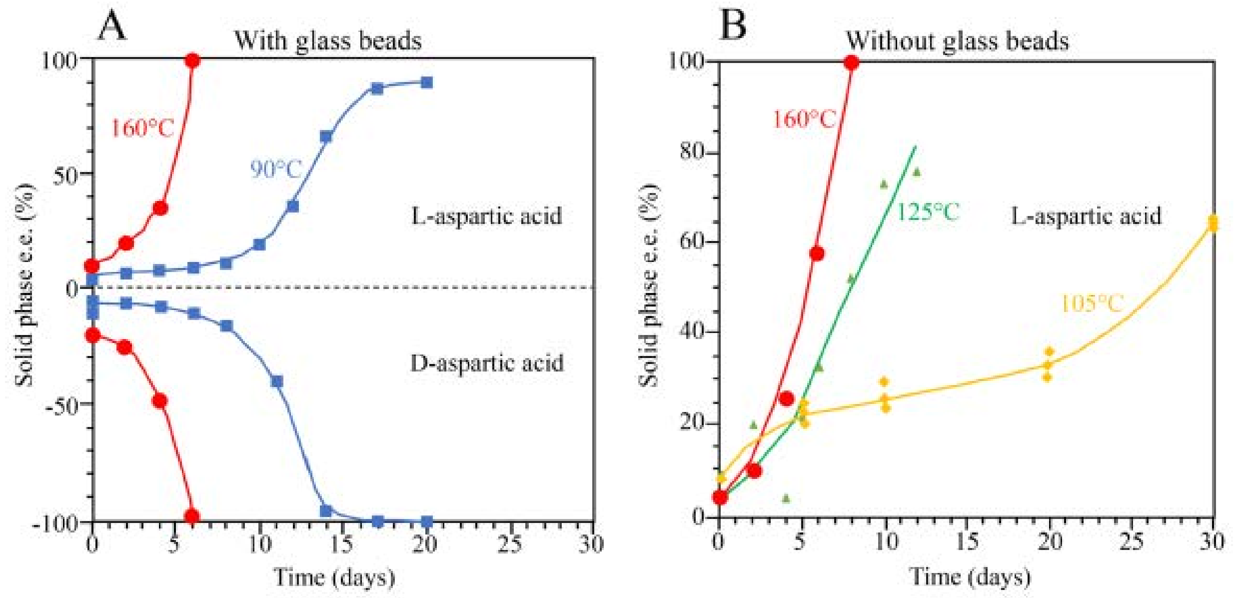


Figure 4. Progress of solid phase e.e. for D- and L-aspartic acid while racemizing.[13] A: Using attrition-enhancement. Red: gradient heating to 160°C. Blue: isothermal at 90°C. Positive e.e. values refer to the biological L-asp. B: Stirring only, without attrition enhancement. Red: gradient heating to 160°C. Green: under reflux at 125°C. Yellow: isothermal heating to 105°C. (After figure in ref. 13.)

Table 3. Data from the open circles in figure 4 at 90°C[13]

Day	e.e. (d), %	e.e. (l), %
0	5	5
11	40	28
15	100	75
20	100	90

knowing that of the 20 biogenetic AAs aspartic acid is one of only two that form separate crystallize D and L crystals under ambient conditions. Salicylaldehyde was known from industrial experience to be an unusually effective racemizing agent and, as mentioned above, acetic acid was the best choice to accelerate this racemization. Experiments were carried out both in the presence and absence of 2.5 mm glass beads (which, when stirred rapidly, lead to continuous crystal attrition).[13] In part 9 of this series, we documented how attrition caused by stirring glass beads can sometimes cause homochiral crystals to form before the more stable racemic ones.[1]

For the attrition-enhanced experiments (i.e., glass beads were added) summarized in figure 4 A, temperatures of 90°C and 160°C were used with 0.5 g total Asp, 5 ml acetic acid and 0.3 ml salicylaldehyde placed in a screw-capped bottle. The initial e.e. and rpm of rotation were not identical (for reasons not explained).[13]

For the three experiments summarized in figure 4 B, which did not use attrition enhancement, surprisingly the proportion of Asp to acetic acid and Asp to salicylaldehyde used by the researchers all differed considerably. The reason for this decision was not explained in the paper and was only apparent upon examining the separate Supporting Information document. The solid phase enrichment was found to occur about three times faster at 125°C than at 105°C, and even faster at 160°C. In the absence of glass beads, the e.e. only reached 58% after 30 days. For comparison purposes, one must also consider that the proportion of Asp to acetic acid used at 105 °C was much higher than that used at 125°C and 160°C. It is noteworthy that the experiments were not continued for extended periods, since this would have resulted in the thermal destruction of aspartic acid under these conditions.

The experiments at 105°C were repeated three times with results that agreed with each other quite well. Unfortunately, the counterpart experiments using D-Asp were not performed at this temperature, as is discussed below.

Reporting bias of results

Notice in figure 4 that e.e.$_D$ increased considerably faster over time than e.e.$_L$. In addition, the L-form attained a maximum of ~90% but the D-form reached an e.e. of ~100%. The results for both enantiomers are summarized in table 3.

Why was this difference not mentioned by the authors? This seems to be an example of reporting bias, which occurs all too frequently in science. The results which support the desired outcome are reported and discussed extensively, whereas those which don't are often downplayed, ignored, or attributed to experimental error. This does not necessarily reflect dishonesty but rather a prior conviction as to what the correct results should be and a desire not to confuse with flawed data.[18]

According to figure 4 B, the e.e.$_D$ also increased more rapidly than e.e.$_L$ at 160°C. But this is inconclusive since, according to the Experimental section, an initial e.e.$_L$ of only 9% was used vs. an initial e.e.$_D$ of 20% e.e., hindering a comparison. Additional experiments should have been performed and the e.e.s documented at identical time intervals. What we see instead is an example of another kind of bias that can occur in research. Experiments that offer the potential to support a favoured theory are often performed, rather than those offering the potential to discredit the theory.[18] For events from the distant past that are impossible to prove in a laboratory, statements like "the bulk of the evidence indicates" may well be an artifact of bias in deciding what kinds of research to perform.

The OoL community rejoices over all examples of AAs producing an e.e.$_L$, no matter how small. However, some small differences in D/L could simply reflect measurement errors. The same effort is not devoted to finding, communicating, or justifying examples of e.e.$_D$. Taking all the data into account would emphasize how, under natural conditions, maximum entropy is the expected outcome over time, in which the concentration of D- and L-AAs is equal.

Critique of these studies

Two centuries of experimentation and careful thought by physical chemists have produced a deep understanding of phase changes between solids, liquids, and gases and the circumstances which permit an e.e. to be distributed across them. Researchers like Viedma, who have devoted their careers to OoL topics, design their experiments based on deep chemical knowledge, benefiting from a plethora of techniques and special equipment to drive chemical changes in the manner they wish. Chemists are trained to guide chemical processes to attain a predetermined goal, and this has produced many valuable products. The non-chemist rarely understands why specific details were necessary and can be misled to think that with enough time the same outcomes might have occurred naturally. Someone with a comparably low level of understanding of how art is produced, using the same logic, might also be led to believe that natural processes could have produced all the works of art in the Louvre Museum.

In the experiments described above, several important design principles were indispensable. The researchers needed to cause rapid racemization of the mixture to replenish the desired enantiomer being extracted, but avoid racemization of the initial mixture which contained an e.e. of the desired enantiomer (necessary to produce the first homochiral crystal seeds). Being competent chemists who have mastered many 'tricks of the trade', they skilfully did this. They knew that crystallization required the interaction of two or more molecules of the enantiomer in initial excess. Therefore, the rate is a higher order in concentration; see eqn (1). Loss of e.e., however, is first order with respect to the concentration of the e.e., see eqn (2).

$$\text{Rate of formation of initial homochiral seeds} \sim k_1 \times [\text{e.e.}]^n, n \geq 2 \tag{1}$$

$$\text{Rate of loss of enantiomer excess} \sim k_2 \times [\text{e.e.}] \tag{2}$$

The initial homochiral seeds can be caused to form as fast as possible by beginning with a high concentration of Asp already having an e.e. Additional enhancement by stirring, and especially through adding glass beads to break the crystals formed causes the rate of formation to be greater than the rate of loss.

The researchers also knew that Asp would be one of the two AAs likely to produce homochiral crystals.[19,20] To optimize equilibration and high concentrations, the reactions were carried out in equipment that constrained the volume. Acetic acid boils at 118°C, but most of the experiments were carried out in screw-capped bottles so that temperatures above the boiling point could be used, giving the best results.[21] Racemization had to be perfectly timed and balanced to replenish the depleted enantiomer. This required a special solvent instead of water. Acetic acid was typically used since it was known to provide the best results among all the carboxylic acids tested.

One might think that the ideal conditions used were only for researcher convenience and that more time might have adequately compensated for less ideal conditions. Let us extrapolate to provide some insight into this possibility. Instead of an initial absurd concentration ≥0.5 g Asp in 5 ml acetic acid (i.e., 0.1 kg/l), what concentration might have been more realistic? After all, this is about three times

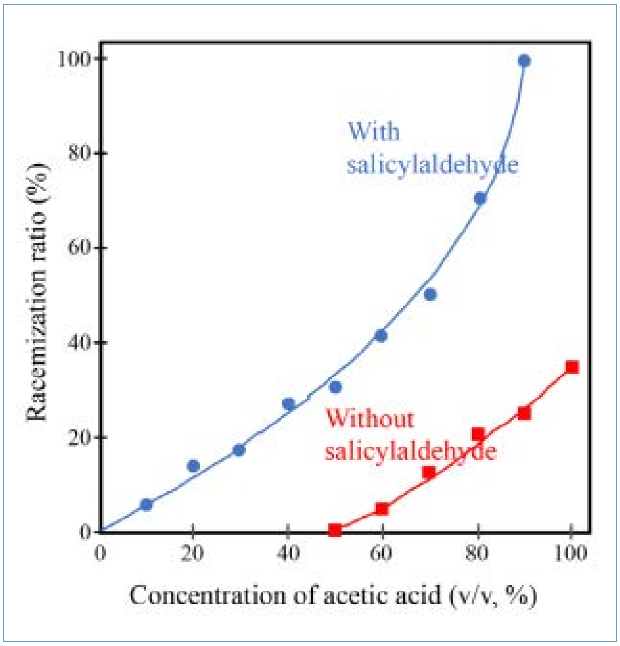


Figure 5. Racemization of L-phenylalanine (0.1 g) at 100°C in a sealed tube of aqueous acetic acid (3 ml) for 1 hour. Blue: With 0.2 molar equivalent salicylaldehyde racemizing agent. Red: Without salicylaldehyde. (Redrawn from figure 3 of ref. 5.)

more Asp than the weight of all salts currently found in a litre of ocean water![22] Leading OoL researcher Professor Bada estimated that the maximum concentration of AAs in ancient oceans would have been only about 10^{-8} g/l water, a staggering difference of a factor of 10^{10}.[23] Worse, the specific sample of Asp would have required an e.e.$_L$. of at least 5% and be present in a suitable highly concentrated organic solvent at a temperature of 100°C or higher. Under those conditions, Asp as an amino acid, and any e.e.$_L$ could only have survived a few hours. Even without a racemizing agent AAs would racemize rapidly in the hot organic acid at various levels of aqueous concentration, as shown in the example in figure 5 for after only 1 hour.

A naturally occurring location and chemical environment would also have had to be hermetically enclosed to force equilibration and production of racemic Asp. Suppose, by miraculous good fortune, a sample satisfied all these constraints, which we'll endow with an Asp concentration ~10^{-6} M. This is significantly lower than used in the above reports but still far too concentrated to be plausible for pure Asp created abiotically.

Using $n = 2$ in eqn (1) reveals that the first homochiral seeds would form at a rate ~10^{12} times lower than reported in the laboratory experiments. Some additional corrections would be needed to permit realistic extrapolations. Rapid stirring (600–1,200 rpm) and the presence of ideally sized glass beads or anything analogous in a clean, closed environment would not have existed, decreasing the rate given by eqn (1) by many more orders of magnitude. Comparing the laboratory data which is expressed in hours with the fact that a year consists of <10^4 hours demonstrates that billions of years would not have compensated for the guiding expertise provided by the chemists.

The unavoidable conclusion is that once again OoL researchers have spent decades exploring how L-only AAs might arise naturally, using deep knowledge. This has led to expertly designed experiments that could not possibly have any natural relevance—even in the most wildly conceived optimistic scenarios. Here are some specific objections to the above reports:

- Without intelligent guidance, racemizing chemicals like salicylaldehyde would have eliminated any initial e.e. needed to act as seeds.
- The presence of racemizing agents in an appropriate solvent at high temperature would have indiscriminately racemized *all* proteinogenic AAs present in nature.
- There is no natural analogy for an enclosed high-temperature volume containing a pure suitable organic acid. How would Asp have been placed there?
- All the concentrations were carefully selected and are unrealistic for OoL purposes. Pure, highly concentrated Asp with an e.e.$_L$ could not arise naturally. Even the concentration of the racemizing agent was carefully selected. If racemization occurred randomly, there would have been no initial e.e.
- The e.e. required a very hot, pure organic solvent. Lowering the temperature of acetic acid from 125°C to 105°C in the absence of glass beads decreased the maximum e.e. obtained dramatically and increased the time needed for e.e. to build up. At acetic acid temperatures under 50°C, no measurable amount of enantiopure crystals would likely have formed.
- Loss of e.e. occurs at a kinetic rate which is first order with respect to its concentration but at a higher order to form homochiral crystals. For the initial e.e. to form the first seed crystals instead of racemizing, a very high initial concentration of the A.A. had to be quickly mixed in a hot solvent. Realistically, the initial e.e. would not have been available.
- An e.e.$_L$ which remained in a solid crystalline state would have been irrelevant for OoL purposes. It would have to eventually dissolve in water, where racemization would then occur, plus contamination with already racemized dissolved AAs. Truman and Schmidtgall showed that for both kinetic and thermodynamic reasons, the rate of racemization will always be faster than the formation of peptides under any known natural aqueous conditions.[24]

References

1. Truman, R., Enantiomeric amplification of amino acids: part 9—enantiomeric separation via crystallization, *J. Creation* **38**(2):62–67, 2024.
2. Noorduin, W.L., Izumi, T., Millemaggi, A., Leeman, M., Meekes, H., Van Enckevort, W.J., Kellogg, R.M., Kaptein, B., Vlieg, E., and Blackmond, D.G., Emergence of a single solid chiral state from a nearly racemic amino acid derivative, *J. American Chemical Society* **130**:1158−1159, 2008.
3. Sakai, K., Hirayama, N., and Tamura, R. (Eds.), Novel Optical Resolution Technologies, *Topics in Current Chemistry* **269**:1–313, Springer, 2007. See in particular the section, "Features of Preferential Enrichment" starting on page 58. This chapter was also published as Tamura, R., Takahashi, H., Fujimoto, D., and Ushio, T., Mechanism and scope of preferential enrichment, a symmetry-breaking enantiomeric resolution phenomenon, *Topics in Current Chemistry* **269**:53–82, 2007.
4. Tamura, R., Takahashi, H., Hirotsu, K., Nakajima, Y., Ushio, T., and Toda, F., Unusual disordered crystal structure of a racemate exhibiting a novel enantiomeric resolution: preferential enrichment, *Angewandte Chemie, International Edition* **37**:2876, 1998.
5. Ushio, T., Tamura, R., Takahashi, H., Azuma, N., and Yamamoto, K., Unusual enantiomeric resolution phenomenon observed upon recrystallization of a racemic compound, *Angewandte Chemie* **108**:2544–2546, 1996; *Angewandte Chemie, International Edition* **35**:2372–2374, 1996.
6. Ushio, T., Tamura, R., Azuma, N., Nakamura, K., Toda, F., and Kobayashi, K., Polymorphism of compound existing as both racemic compound crystals and mixed crystals of enantiomers, *Molecular Crystals and Liquid Crystals* **276**:245–252, 1996.
7. Takahashi, H., Tamura, R., Ushio, T., Nakajima, Y., and Hirotsu, K., Ideal enantiomeric resolution (preferential enrichment) by recrystallization of a racemic compound. V: Relationship between preferential enrichment and crystal structures, *Chirality* **10**(7):705–710, 1998.
8. Tamura, R., Ushio, T., Takahashi, H., Nakamura, K., Azuma, N., Toda, F., and Endo, K., Ideal enantiomeric resolution by recrystallization of a racemic compound (part 4): relationship between enantiomeric resolution phenomenon and crystal properties, *Chirality* **9(3)**:220–224, 1997.
9. Anderson, N.G., Developing processes for crystallization-induced asymmetric transformation, *Organic Process Research & Development* **9**(6):800–813, 2005.
10. Yoshioka, R., Racemization, optical resolution and crystallization-induced asymmetric transformation of amino acids and pharmaceutical intermediates, *Topics in Current Chemistry* **269**:83–132, 2007.
11. Pizzarello, S., The chemistry of life's origin: a carbonaceous meteorite perspective, *Accounts Chemical Research* **39**(4):231–237, 2006.
12. Bada, J.L., Kinetics of the nonbiological decomposition and racemization of amino acids in natural waters, Nonequilibrium Systems in Natural Water Chemistry, *Advances in Chemistry* vol. 106, chap. 13, pp. 309–331, 1971, American Chemical Socierty.
13. Viedma, C., Ortiz, J.E., de Torres, T., Izumi, T., and Blackmond, D.G., Evolution of solid phase homochirality for a proteinogenic amino acid, *J. American Chemical Society* **130**:15274–15275, 2008.
14. Perez, M., Gibbs–Thomson effects in phase transformations, *Scripta Materialia* **52**(8):709–712, 2005.
15. IUPAC, Compendium of Chemical Terminology, 2nd edn (the 'Gold Book').
16. Ostwald, W., *Lehrbuch der allgemeinen Chemie*, vol. 2, part 1, Leipzig, Germany, 1896.
17. Ostwald, W., Studien über die Bildung und Umwandlung fester Körper, *Zeitschrift für Physikalische Chemie* **22**:289–330, 1897.
18. Truman, R., Clean-up and analysis of small datasets can distort conclusions, *J. Creation* **36**(2):66–71, 2022.
19. Jacques, J., Collet, A., Wilen, S.H., *Enantiomers, Racemates, and Resolutions*, Krieger, Malabar, FL, 1994.
20. Eliel, E., Wilen, S.H., and Mander, L.N., *Stereochemistry of Organic Compounds*, Wiley, New York, p 297, 1994.
21. Pravasi, S.D., Acetic acid; in: *Encyclopedia of Toxicology*, 3rd edn, 2014.
22. Why is the ocean salty? USGS, Science for a changing world.
23. Bada, J.L., Amino acid cosmogeochemistry, *Philosophical Transactions Royal Society London B* **333**:349–358, 1991.
24. 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.

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.*

Stephen Grocott *has 1st Class Honours and Ph.D. degrees in organometallic chemistry (chiral metal complexes). Currently, he is managing director with an advanced chemicals manufacturing business. Before that, he was the lead processing technology expert for some of the world's largest resource companies. He is an adjunct professor with a large Australian university and was the chair of the board of the world's largest non-profit minerals R&D organisation. He has also served on the board of Youth for Christ Australia.*

Enantiomeric amplification of amino acids: part 11—spontaneous resolution in a porous environment

Royal Truman, Chris Basel, and Stephen Grocott

Spatial separation of D- and L-amino acid (AA) enantiomers would be easier if homochiral crystals formed than when in solution. Experiments using capillary motion of aspartic acid (Asp) and glutamic acid (Glu) solutions through porous brick produced a mixture of D and L crystals. These were intimately mixed and thus could not explain how only L-AAs would have been used to form proteins prebiotically. Furthermore, the experiments used: 1) pure water instead of a saline solvent; 2) AA concentrations many orders of magnitude higher than realistic; 3) excluded contaminants; and used 4) a clean brick having suitable cavity sizes. A natural brine environment would have had none of these characteristics. Trapped in solid form, Asp and Glu could not have formed peptides, but redissolution would have regenerated the racemic solution.

We continue here with part 11 of a series of papers that critique proposed natural explanations for the abiogenetic origin of pure L-amino acids (AAs). Bonner championed the theory that spontaneous resolution of D and L crystals would offer the best natural terrestrial mechanism for separating D- and L-AAs.[1] Only L-AA enantiomers must be used to form biological proteins. However, about 90% of AAs form racemic crystals at moderate temperatures, which therefore never spontaneously resolve.[2–6]

In several experiments discussed below, origin of life (OoL) researcher Viedma examined solutions of aspartic acid and glutamic acid, arguing that these AAs have been identified in samples from the Murchison meteorite. These two AAs were each found at concentrations of only ~1 ppm, though, of which the amount of terrestrial contribution was unknown.[7] Furthermore, AAs found on some meteorites are usually bound within larger complex molecules which must be extracted through vigorous acid hydrolysis.[8]

Viedma also mentioned that these two AAs are among the most abundant formed in experiments simulating the primitive earth.[3] However, he overlooked that, in the paper he referenced, Sidney Fox correctly disparaged the notion of lightning acting in the atmosphere under necessarily but geologically implausible hydrogen-rich conditions and the experimental use of electric discharges in closed containers.[9]

Enantiomer enrichment in porous solid environments

Viedma reported, in 2001, that racemic mixtures of aspartic acid and of glutamic acid can be caused to form homochiral crystals mixed in equal proportions (i.e., *conglomerates*) at ambient temperature.[3] However, their usual behaviour is to form *racemic compounds* (which consist of D and L enantiomers intimately combined within each crystal) to first crystallize from solution.

Forming the homogenous crystals was not easy. In the first series of experiments, 10 g of either racemic aspartic acid or glutamic acid was dissolved in 1 litre of water, constantly stirred, and heated to 80°C for 30 min to ensure complete dissolution. 50 mL samples were extracted and allowed to cool to permit crystals to grow. The initial concentration was too low, and crystals were not produced. Therefore, the solution was concentrated by evaporation.[3] When aspartic and glutamic AAs were crystallized from free aqueous solutions, however, only racemic DL-aspartic and DL-glutamic AA crystals were produced.

Remarkable crystallization processes were known to occur in porous media.[10] Therefore, Viedma carried out another set of experiments using a porous insulating fire brick, partially immersed in the 10 g / L of each AA to cause capillary rise, as illustrated in figure 1.

Water was evaporated and aspartic or glutamic acid crystals were found in a narrow upper zone inside the porous brick. *Contra* the results from simply evaporating solutions, these crystals formed conglomerates; i.e.,

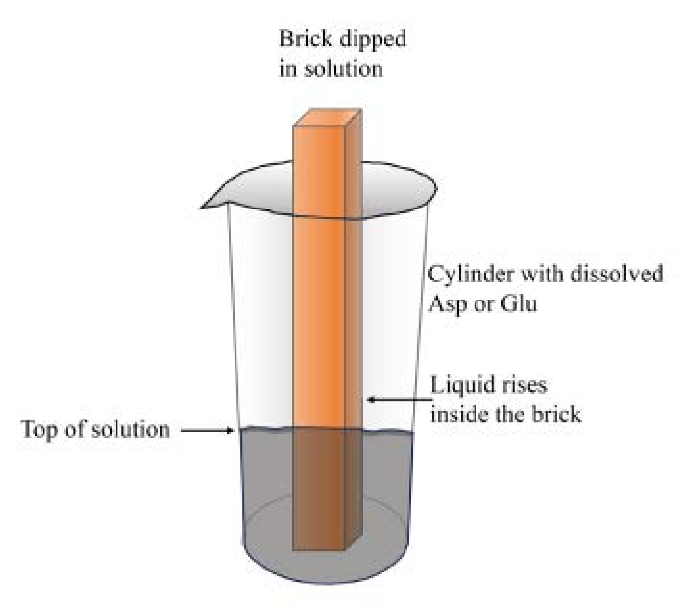


Figure 1. A fire brick was dipped into aqueous solutions of aspartic acid or glutamic acid. Homochiral crystals were formed after capillary rise inside the brick.[3] Original figure created by Royal Truman.

the individual crystals consisted of only D or only L enantiomers, mixed in identical amounts.[3]

This is a case of polymorphism, involving two phases ($D_{crystal} + L_{crystal}$) and $DL_{crystal}$. Because the racemic crystals were more stable than enantiomeric conglomerates, the free energy change for the transformation:

$$(D_{crystal} + L_{crystal}) \rightarrow \text{Racemic compound} \qquad (1)$$

is negative. Therefore, the D-only and L-only crystals obtained were metastable with respect to racemic DL crystals.[3]

Why did separate D and L crystals form in porous media, resulting in a far-from-equilibrium outcome? It is well known that crystals resulting from high supersaturation can behave abnormally, giving rise to metastable (i.e., kinetically stable) phases, for several possible reasons.[3,11,12] This seems to be an example of Ostwald's Rule, which expresses that often the first solid formed upon crystallization of a solution or a melt is the least stable polymorph, which is kinetically favoured, rather than the thermodynamically favoured form(s) that are created later.[13–15] Maximum supersaturation depends on factors such as temperature, stirring and mechanical shock, thermal history, and total mass of solution. The limited particle mobility in a porous media provided a range of high supersaturation levels, as compared to the crystallization in free solutions.[3]

Since, in the most probable natural environments, evaporation of water containing an AA did not yield the results wished for, a new naturalist narrative had to be invented. The conditions of the latter experiments were claimed to mimic a sedimentary environment such as a dry lakebed where capillary rise of saline ground water might occur.

Viedma does admit the obvious, that this spontaneous resolution mechanism over time will produce an equal number of opposing AA resolutions. Therefore, no net increase in enantiomeric excess could have occurred.

Critique of these studies

- The evaporation experiments allegedly "mimic a sedimentary environment such as a playa where one may expect capillary rise of saline ground water". However, in contrast to this, pure Asp or Glu was dissolved in doubly *distilled water* instead of a saline solution.
- Proteins require many additional kinds of L-AAs whose enantiomers didn't resolve under these conditions.
- 10 g / L solutions of Asp and Glu are many orders of magnitude more concentrated than putative prebiotic conditions would have been. Leading OoL researcher Professor Bada estimated that the maximum concentration of AAs in ancient oceans would have been only ~10^{-8} g / L water.[16] Viedma's solutions were a billion times more concentrated than this. Asp and Glu crystals could not have formed from concentrations many orders of magnitude lower. Evaporation of extremely dilute solutions would have distributed any

Asp or Glu contained over vast distances, so redissolving them would have produced very dilute solutions of Asp and Glu.[17]

- Ocean water currently contains, on average, about 35 g of salts / L.[18] Asp and Glu produced today or on a primordial earth through natural chemical processes could only represent an insignificant proportion of the highly contaminated saline ground water. Pristine bricks having suitable cavities for crystallization to occur were placed into solutions of an AA. A continuous flow due to capillary action and a source of extremely concentrated Asp or Glu was ensured. The clean laboratory glass vessel prevented dilution and contamination. These factors cannot be compared to a primordial slurry of innumerable substances.
- Furthermore, even if Asp and Glu crystals had formed, they would have been encased in a solid cement-like environment. They could not have formed peptides unless the crystals redissolved in water, where they would have regenerated a racemic solution. Any temporary periods of warming, due to volcanic action, meteorite impacts, etc. would have facilitated extraction and dissolution of the crystals.
- Any L and D crystals formed would be in identical proportion and intimately mixed spatially. This would not have led to peptides of only L enantiomers.

References

1. Bonner, W.A., Origins of molecular chirality? in: Ponnamperuna C., (Ed.), *Exobiology*, North-Holland, Amsterdam, pp. 170–234, 1972.
2. Bernal, I., Conglomerate crystallization and chiral discrimination phenomena: in vivo and in vitro, *J. Chemical Education* **69**:468–469, 1992.
3. Viedma, C., Enantiomeric crystallization from dl-aspartic and dl-glutamic acids: implications for biomolecular chirality in the origin of life, *Origins of Life and Evolution of Biospheres* **31**:501−509, 2001.
4. 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, *Origins of Life and Evolution of Biospheres* **43**:129–135, 2013.
5. Jacques, J. and Collet, A., Wilen, S.H., *Enantiomers, Racemates, and Resolutions*, Krieger, Malabar, FL, 1994.
6. Eliel, E., Wilen, S.H., and Mander, L.N., *Stereochemistry of Organic Compounds*, Wiley, New York, p. 297, 1994.
7. Koga, T. and Naraoka, H., A new family of extraterrestrial amino acids in the Murchison meteorite, *Scientific Reports* **7**(636):1–8, 2017.
8. Kvenvolden, K.A., Lawless, J.G., and Ponnamperuma, C., Nonprotein amino acids in the Murchison meteorite, PNAS **68**:486–490, 1971.
9. Fox, S.W., Thermal synthesis of amino acids and the origin of life, *Geochimica et Cosmochimica Acta* **59**:1213–1214, 1995.
10. Lopez-Acevedo, V., Viedrna, C., Gonzalez, V., and La Iglesia, A., Salt crystallization in porous construction materials II. Mass transport and crystallization processes, *J. Crystal Growth* **182**:103–110, 1997.
11. Kondepucli, D.K. and Nelson, G.W., Weak neutral currents and the origin of biomolecular chirality, *Nature* **314**:438–441, 1985.
12. Avetisov, V.A., Goldanskii, V.I. and Kuz'rnin, V.V., Handedness, origin of life and evolution, *Physics Today* **44**:33–41, 1991.
13. Van Stanten, R.A., The Ostwald step rule, *J. Physical Chemistry* **88**(24):5768–6769, 1984.
14. Threlfall, T., Structural and thermodynamic explanations of Ostwald's rule, *Organic Process Research & Development* **7**(6):1017–1027, 2003.
15. Putnis, A. and McConnell, J.D.C., *Principles of Mineral Behaviour*, Blackwell Scientific Publications, Oxford, p. 257, 1980.
16. Bada, J.L., Amino acid cosmogeochemistry, *Philosophical Transactions of the Royal Society of London B* **333**:349–358, 1991.
17. Bada's estimate of <10^{-8} g/l AA in water is equivalent to 1 g in a water volume 1 km × 100 m × 1 m. Therefore, any dissolved Asp or Glu would have been widely distributed upon evaporation of the water.
18. According to Wikipedia and the United States Geological Survey, one litre of ocean water contains, on average, about 35 g of salts. Why is the ocean salty? usgs.gov, accessed 14 Nov 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.*

Stephen Grocott *has 1st Class Honours and Ph.D. degrees in organometallic chemistry (chiral metal complexes). Currently, he is managing director with an advanced chemicals manufacturing business. Before that, he was the lead processing technology expert for some of the world's largest resource companies. He is an adjunct professor with a large Australian university and was the chair of the board of the world's largest non-profit minerals R&D organisation. He has also served on the board of Youth for Christ Australia.*

Evidence of a seven-day week in the Ancient Near East—part 1

Andrew Sibley

This paper will discuss evidence for use of a seven-day week in the Ancient Near East. These cultures were utilizing an approximate seven-day week, what has been termed a *quasi*-week, prior to the giving of the Law of Moses. The evidence is that the month, of 29- or 30- days duration, was divided into four parts according to the moon's orbit; that is the new moon, full moon, and the two intermediate half moons. The proposal here is that these cultures were following a tradition that could have been passed down through the patriarchs; from Adam to Noah, and to the people living in the immediate post-Flood period. Later this was codified in the Mosaic Law for the Israelites. The paper also briefly outlines how the week we use today was developed by the Romans, with influence from Egypt, Babylon, the early Christians, and Jews. Knowledge of a *quasi*-week spread as far as the Pacific Islands.

An interesting question is the origin of the week, in terms of it being a period of seven days, and how it was incorporated into the practices of cultures from the Ancient Near East. Is there any astronomical feature that dictates the seven-day week, or was it determined *solely* by the order of creation in Genesis 1 and 2? There are a couple of biblical passages of relevance to this discussion; that God put the sun and moon in place to help mankind determine the 'seasons', 'days', and 'years,' and that He declared the seventh day holy.

> "And God said, 'Let there be lights in the expanse of the heavens to separate the day from the night. And let them be for signs and for seasons, and for days and years, and let them be lights in the expanse of the heavens to give light upon the earth.' And it was so. And God made the two great lights—the greater light to rule the day and the lesser light to rule the night—and the stars" (Genesis 1:14–16).
>
> "So God blessed the seventh day and made it holy, because on it God rested from all his work that he had done in creation" (Genesis 2:2).

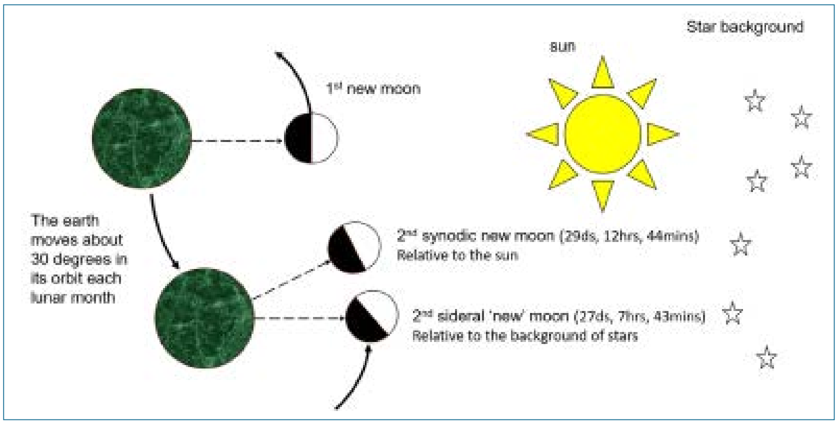
However, these Scriptures were given later to Moses. The historical evidence for the existence of a seven-day week will be considered from extra-biblical records among non-Hebraic cultures in this paper; particularly that of the Sumerian, Babylonian, Egyptian, and Roman cultures. A second paper will discuss this in relation to the Hebrew nation and the Mosaic Law.

A number of different calendars were used by these ancient cultures, but one involving an approximate seven-day week was notably also in use, and this was prior to the giving of the Mosaic Law to the Israelites. This calendar was particularly used for religious purposes based on the cycles of the sun and moon; i.e., they can be said to be *luni-solar*. These beliefs even spread across Asia, likely through the influence of Hinduism and Buddhism, with recognizable pollination of ideas extending to east Asia and even the Pacific Islands.

However, some commentators have stated that the week is not associated with any astronomical feature,[1,2] which suggests it is derived solely from religious texts and observance. Zerubavel also denied that the seven-day week is connected directly to a physical cycle, although he does acknowledge the existence of a *quasi*-week that is related to the quarter phases of the lunar orbit. The reason for this *quasi*-week is that the quarter phase of the moon's orbit only approximates seven days (it is about 7.4 days), and a lunation (a monthly period of the moon's orbit) is either 29 or 30 days in duration.[3] Copeland has proposed that the week was initially determined either by the phases of the moon or by the seven clearly-visible stars in Pleiades, or those in Ursa Major, or by the 'planets' moving through the Zodiac. However, he favoured the former explanation relating to the orbital period of the moon.[4] Box 1 and figure 1 explains the difference between the sideral and synodic month. The following sections are a brief overview of the evidence, which highlights the existence of seven-day periods in antiquity related to the phases of the moon.

Sumerian calendar

The early Ur III Sumerian civilization influenced the later Babylonian and Egyptian calendars, with evidence showing them to be based upon the cycles of the sun and moon; the moon being the god Nanna (figure 2). This luni-solar calendar was followed in Mesopotamia from the 3rd to 1st millennium BC for sacrificial purposes.[5,6] The Sumerian (Ur III) year was



Box 1 and Figure 1. The sidereal month versus the synodic month. In many ancient calendars the orbit of the moon around the earth marks out the period of each month. In terms of definitions, the sidereal month is the time it takes for the moon to return to the same place relative to the background of stars; which is, on average, 27 days 7 hours and 43 minutes. But because the earth is moving around the sun in its orbit, it takes longer for the moon to return to the same place relative to the sun—about two days longer each month. This is referred to as the 'synodic month', and is, on average, a period of 29 days 12 hours and 44 minutes. In terms of the number of whole days, it implies that the synodic lunar month must be either 29 or 30 days long. A lunar quarter-phase is then approximately 7.4 days long, or seven or eight whole days. However, we may note that the moon is invisible for about a day and a half at the end of the lunar orbit as it approaches the sun's relative position, occasionally through a lunar eclipse. This leads to a monthly period of *visibility* of close to 28 days. Another way of measuring the length of the month is the observance of the passage of the sun through the astrological signs of the Zodiac, until the sun returns to its original position. There are twelve in all, approximately between 29 and 31 days in length.
The phases of the moon still influence the Western Julian/Gregorian calendar in terms of approximate length, although the monthly cycle is out of sync with the lunar cycle in the West. Typically, Western months now retain periods of 30 or 31 days, which are slightly longer than that of the moon's cycle. Each year covers a period of nearly 365.25 days. When we seek to fit the cycles of the moon into the solar year, there is a discrepancy—there are approximately twelve and one third lunar cycles in a year. Different cultures have used occasional leap, or intercalary days, or months to keep the count of months and the beginning of the year aligned.

established upon 12 lunar monthly cycles of 29 or 30 days each, together with an additional intercalary month every few years. Each month appears suggestively to have been divided into four periods according to the phases of the moon, with certain days of the month ascribed designations (as denoted below by the Cuneiform Digital Library Initiative):[7]

u$_4$-sakar gu-la ("great crescent")

u$_4$-sakar u$_4$ 1(u)-5(diš) ("crescent of day 15")

e$_2$-u$_4$-1(u)-5(diš) ("house of day 15")

e$_2$-u$_4$-7(diš) ("house of day 7").

The major division was between the new moon and the full moon, with intermediate divisions of seven or eight days. Like the Hebrews, the Sumerians saw significance in the number seven.[8,9] The Enuma Elish (or Enūma Eliš) myth probably dates to around the second dynasty of Isin (12th century BC),[10] although it relays an earlier account (the earliest tablet probably dates to the 9th century BC). In Tablet V (table 1) there is a division of the month into four periods, which are related to the phases of the moon. The moon is described as waxing to half brightness at day 7 and full at day 15 when it is in opposition to the sun. The moon is said to wane at the same pace as its prior waxing, before disappearing and completing its cycle by day 30. The moon is inferred to have completed its orbit within 30 days.[11] We see, then, that there is some evidence for the existence of an approximate seven-day week in the earliest cultures, and this evidence extended to Assyria and Babylon.

Assyrian and Babylonian calendars

The city of Kültepe, or ancient Kaneš, in Central Anatolia (modern Turkey) has yielded thousands of Old Assyrian cuneiform tablets, most of which are loan contracts from merchant houses. They are dated to as early as the 19th century BC, and give glimpses of the structure of the Old Assyrian calendar. In these, there were 12 months of 29 or 30 days, with an occasional intercalary month. The weekly period was denoted by the word *hamuštum,* although scholars disagree on its length, with possible periods given of 5, 6, 7, or 10 days.[14] However, the period of 7 days is considered more likely because of a complete list of 50 or 52 *hamuštum* in one almanac (Kt g/k 118), representing that of a full year.[15] These documents record the first day of the month as the appearance of the moon god (*nāmarti ilim*), the end of the month when the moon god disappears (*ilum ūbilma*), and the *Šapattum* in the middle of the month, day 15, when the moon is full.[7]

Some of the calendar texts from Assyria and Babylon date from the 12th century BC (for example, one calendar was produced for the Kassite king, Nazimaruttash), but the bulk have been attributed to a period later than the 8th century BC, a timeframe which covered the Israelite exile in Assyria and Babylon. Some texts included knowledge of an economic or administrative calendar with 12 months of 30 days each.[16] However, George Smith found a particular tablet at Warka (Erech) which recorded monthly sacred sacrificial days on the 7th, 14th, 21st, and 28th day of each month (and also the

Table 1. Enuma Elish Tablet V

Enuma Elish, Tablet V (Heinrich)	Enuma Elish, Tablet V (King)
12 He made the Moon [nannāra] appear, entrusted (to him) the night. 13 He assigned to him the crown jewel of nighttime to mark the days (of the month), 14 Every month, without ceasing, he exalted him with a crown. 15 “At the beginning of the month, waxing over the land, 16 “You shine with two horns to mark the naming of six days, 17 ““At the seventh day, the crown is [ha]lf. 18 “At the fifteenth day, you shall be in opposition, at the midpoint of each [month]. 19 “When the Sun can see you on the horizon, 20 “Wane at the same pace and form in reverse. 21 “At the day of di[sappeara]nce, approach the Sun’s course, 22 “On the thirtieth day, you shall be in conjunction with the Sun as a double.	12. The Moon-god he caused to shine forth, the night he entrusted to him. 13. He appointed him, a being of the night, to determine the days; 14. Every month without ceasing with the crown he covered(?) him, (saying): 15. “At the beginning of the month, when thou shinest upon the land, 16. “Thou commandest the horns to determine six days, 17. “And on the seventh day to [divide] the crown. 18. “On the fourteenth day thou shalt stand opposite, the half [...]. 19. “When the Sun-god on the foundation of heaven [...] thee, 20. “The [...] thou shalt cause to ..., and thou shalt make his [...]. 21. “[...] ... unto the path of the Sun-god shalt thou cause to draw nigh, 22. “[And on the ... day] thou shalt stand opposite, and the Sun-god shall ... [...]
18, “A (sabbath) [sa]pattu shall thou then encounter mid-[month?]ly” (Pinches).[11] The word [sa]ppatu (sabbath) possibly appears in line 18, but is not clear due to a broken letter—it is inferred from the context.	

19th, which is 49 days from the beginning of the previous month—although sometimes occurring a day early depending upon the length of the lunar month).[16] Whether these days were properly considered days of rest in Babylon has not been firmly established.[17]

As noted, the Babylonian calendar was influenced by the Sumerian, and Assyrian examples, with the lunar phases tracing out the week. The ‘sabbath’ (it’s uncertain and unclear whether the Hebrew term is related to the Akkadian *sapattu* or *sabattu* meaning heart rest or mid rest) was ascribed to the 15th day of the month, when the moon reached its peak brightness, thus ‘resting,’ before waning towards the second half of the month. The moon was said to rest at peak brightness.[6] The Babylonians, possibly following the Assyrians, ascribed a specific meaning to the weekly day of rest, which they termed ‘evil days’; essentially days of bad omens when work was discouraged. Instead, it was necessary to sacrifice to appease the gods. The month then could be divided into four weeks: which included three seven-day weeks, and a fourth week adjusted by a day to complete the lunar month of 29 or 30 days. The requirement to know the beginning of each month was initially determined by observations of the new moon, but due to occasional inclement weather, there was a greater desire to predict the length of each month in the neo-Babylonian and Achaemenid period of the 1st millennium BC. The luni-solar calendar continued into the Seleucid and Parthian periods.[5] In terms of the necessity for the insertion of an intercalary month, use was later made of the Metonic Cycle.[18,19]

Incidentally, we ought to note two further points. An idealized calendar of 30 days per month, over a 12-month period, or 360 days, arose in Babylon for administrative purposes. It was later used for Hebraic prophetic purposes; e.g., see Daniel 7:25, 11:3. There is another calendar known from the Near East. This was the *Pentecontad* calendar used by the Amorites and Canaanites. This divided time into periods of fifty days, with seven seven-day weeks, and an extra day; the *atzeret*.

Egyptian calendar

The Egyptians used both a solar calendar of twelve 30-day months, and a ceremonial/religious one that was luni-solar. Scholars generally agree that the lunar calendar preceded the civil one, although it is believed that for centuries they ran side-by-side.[20,21] Based on an annual 360-day year, the civil calendar added five extra days to the end of the year, and each month was divided into three-weekly periods of 10 days each. There were three seasons of four months each, based upon the flood cycle of the Nile, and the year began with the rising of the star Sirius (Sopdet). However, because the Egyptians did not intercalate for the additional quarter day, the seasons gradually moved out of sync with the civil calendar.

Each month of the luni-solar calendar, of 29-or 30-days duration, began with the new moon. The months were divided into four equal weeks, based upon the quarter lunar phases. Twelve months completed the year, with an additional intercalary month added every second or third

Image: Steve Harris, Wikimedia / CC BY SA 2.0 (cropped)

Figure 2. Ur III cylinder seal impression, possibly of King Ur-Nammu, seated on an elaborate throne beneath the crescent moon—the moon was considered a god, Nanna-Suen. Located in the British Museum.

year to maintain synchronicity with earth's solar orbit. The new month is thought to have begun on the morning on which the waning crescent moon disappeared from view, and reappeared on the 2nd day of the month, although with some disagreement over the known detail.[4] According to a New Kingdom text from the Temple of Karnak, the moon became visible on the 2nd of each month, reaching its fullness on the 15th of the month.[22] Centuries earlier, as recorded in the Coffin Texts of the Middle Kingdom, a further reference to the cycles of the moon stated: "I know, O souls of Hermopolis, what is small in the 2nd day and what is great on the 15th day; it is Thoth [god of the moon]" (figure 3).[11] This seems to mirror the Sumerian example described above, again evidently arising before the giving of the Mosaic Law.

Roman observance

The Roman Republic's (c. 509–27 BC) calendar was originally luni-solar, at least in part, being developed from an earlier Greek system (which was itself influenced by the Babylonian and Egyptian luni-solar examples described above). However, the early Roman calendar seems to have amalgamated more than one tradition, evidenced by its complexity, before gradually changing into the Western solar one we have today. The semi-legendary account of the development of the earlier Roman Kingdom's calendar is that it was established by Romulus (possibly born 771 BC). Originally the organization of the year consisted of 10 months (March to December) of 30 or 31 days length beginning and ending with the new moon; 304 days in total, divided into 38 'weeks' of eight days each.[23] There were four 'long' or 'full' months, and six 'short' or 'hollow' months, which corresponded, to some extent, with that of the Alban state (although Plutarch suggested the lengths of the months were more irregular at this time). The 51-day winter period was considered unimportant for the harvest, and not counted in the year. Livy and Plutarch point to the second king, Numa Pompilius (753–672 BC), as the one who introduced a 12-month year, adding January and February to the calendar, being 29 and 28 days respectively.[24,25] The six short months each lost a day; the six days were then added to the 51-day period of January and February (even numbers were considered unlucky, and so the preference was for months (except February) to be either 31 or 29 days in length). This led to a year of 355 days length, which is longer than the lunar year by one day. Every other year, an intercalary month of 22 days was added to adjust the lunar to the solar cycle (355 + (22/2) = 366), but there was a gradual disjunction between the cycles, and the Roman civil calendar moved out of phase with those calculated from the natural cycles.[26]

Later, in 153 BC, the beginning of the year was moved to January.[27] This is why the numerical names of some of the months are out of sequence with the beginning of the solar year. For example, September, October, November, and December are now the ninth to twelfth months, and not the seventh to tenth as their names suggest. July and August were originally called Quintilis and Sextilis, later being named after Caesars Julius and Augustus. However, for decades the priests, or pontiffs, controlled the calendar, and kept March as the first month for offerings to their idols. And without a consistent intercalary scheme the passage of the months moved out of sequence with the solar year. Sometimes this was due to political reasons.[28]

The Roman calendar fixed special days (*Kalends*, *Nones*, *Eides*) in each month approximately to the phases of the moon: for the new moon at the beginning of the month, the *Kalends*; to the time of the first phase of the moon, the *Nones*; and to the full moon, the *Eides* (figure 4). The Nones, which were once set aside for official notices and markets, were either 5 or 7 days after the beginning of the month, the Eides 13 or 15 days after. Days in the month were identified in relationship to the next special day; e.g., three days before Eides.

But the calendar also ran with an eight-day period, or ‘week’, which progressed from month to month without readjustment to the moon’s cycle. This was known as the *Nundinae or Nundinal Cycle* (not to be confused with the *Nones* as described above). The eighth day was essentially a market day, when farmers would sell their goods and wares in the towns and cities, and other official business was set aside. Children were also free from school. The eight days of the week were ascribed letters A to H (although the noun *nundinae* is based on the number nine because the Romans counted the start and end days inclusively for an eight-day week).[29–31]

There were ongoing problems with the complexity of the Roman system, especially through synchronization with the solar cycle, and it was open to abuse for political reasons. Various adjustments were made, particularly by such figures as Julius Caesar in 46 BC, who tied the calendar more closely with the solar cycle. Ten days were added to the calendar to bring it in line with the 365-day solar year, together with an extra day every four years to account for the quarter-day. Effectively, this broke the connection to the cycle of the moon, but retained the *nundinal* system that determined the market days.

Influence from Babylonian and Egyptian astrological sources was imported into the Roman calendar in the first or second century AD, more specifically in terms of the development of a seven-day week, and the pagan names given to each day. This development, probably cultural as opposed to formal at first, was certainly simpler than the traditional Roman calendar. The emerging seven-day calendar was based upon the number of the ascribed wandering ‘planets’ (which depended upon their distance from Earth in the Ptolemaic system; the order being Saturn, Jupiter, Mars, Sun, Venus, Mercury, and the moon). For complex mathematical and astrological reasons, as discussed by Dio Cassius, the days of the sun and moon actually fell upon days two and three, with Saturn’s day the first of the week.[32] There is also some suggestion that Jewish and Christian migration influenced the development of the seven-day week in Rome (although early Christians resisted the astrological names for the days at first).[33,34]

In the fourth century (AD 321) Constantine formally adopted the seven-day week, with Sunday promoted to the first day, and named as an official Christian holiday and day of rest. So, the Roman Saturday or Saturn’s day, essentially the Jewish sabbath in exile, was moved to the last day of the week, which also suited the Rabbis.[35] Combined, these developments effectively broke the link between the new moon and the start of the month in Roman thinking. This forms the basis for our Western calendar today, with the only major adjustment being that made by Pope Gregory in the

Image: Diego Delso, delso.photo / CC-BY-SA 4.0

Figure 3. The moon god Thoth, depicted with the moon-disk resting on his head. Located in the Tomb of Ramses V and Ramses VI, Valley of the Kings, Luxor, Egypt.

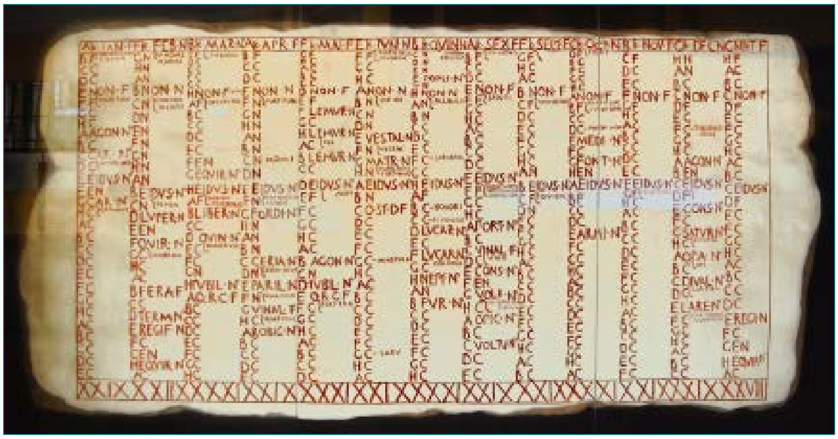


Image: Bauglir, Wikimedia / CC BY SA 4.0 International

Figure 4. Reproduction of the Anzio Calendar (*Fasti Antiates Maiores*) dated to between 84 and 55 BC, prior to Julius Ceasar's reforms. It is located in the *Museo del Teatro de Caesaraugusta,* Zaragoza, Spain. The original is in the Museo Nazionale Romano, Baths of Diocletian. It was painted on a plaster wall, with about 300 fragments found in 1915.

16th century, who moved the calendar forward ten days, and added a small correction to keep the beginning of the year near to the winter solstice.

Hindu, Buddhist and Islamic calendars

Observance of an approximate seven-day week, linked to the cycles of the moon, spread more widely than the Middle East, although with the Babylonian commitment to a seven-day 'week' gradually attenuated through time and distance. Hinduism, with its influence from the ancient Babylonian religious system, relies upon a luni-solar calendar, which also passed to Buddhism. Within Buddhist' culture, holy or *Uposatha* days are set aside each month for worship; these days are related to the lunar phases, although different branches of Buddhism have slightly different practices. For Theravada Buddhists, the new and full moons are considered the most sacred days, but the more devout also commemorate the quarter periods, ascribed to the 8th and 23rd days of the month.[36] Buddhist culture may have influenced other parts of the Far East with regard to the luni-solar calendar before the spread of Islam. For the majority of Muslims, a lunar calendar is followed; one without an intercalary month to adjust to the solar year. Thus, the year is 354 or 355 days long, and the months, such as Ramadan, move relative to the solar year.

Polynesian calendars

Many Polynesian cultures historically observed special days, with prohibition of work on those dates; these are referred to as *Tabu*. For the Hawaiians this was closely linked to the cycle of the moon, observing tabu at the new and full moons with worship to their gods. Intermediate days were also observed in the month, but offset somewhat from the half-moon period. The Bontoc community of Northern Luzon (Philippines) observed days of rest approximately every 10 days when work was discouraged, with worship directed towards their supreme deity, Lumawig.[37]

Discussion and summary

So, there is evidence from the earliest times, specifically in Sumer and Egypt, that early post-Flood cultures held to an approximate seven-day *quasi*-week, and one linked to the phases of the moon. However, some modification was necessary to fit to the lunar cycle, which is slightly longer than 28 days, by the addition of one or two extra days each month. These ancient calendars evidently pre-date the giving of the Mosaic Law. How do we account for this? As noted, we read in Genesis 1:14–16 that God gave the sun and moon as a means of determining times and seasons for humanity.

We also see in Genesis the creation taking place over the period of seven days, and the number 7 was considered to possess special symbolism by the people of Ur, as it was for the later Hebrews. We can conceive that such knowledge, that the sun and moon may be used to determine the calendar to observe a sabbath rest, may feasibly have been passed down from Adam to later generations via the prophet Noah, and been retained in the developing Egyptian and Sumerian cultures.

Knowledge of the *quasi-week* has also passed around the world through religious sources, with the idea that some days are to be treated as more holy than others, or *tabu* in some of the Pacific Islands. However, adherence to a seven-day week was weakened due to loss of knowledge with greater distance from the Ancient Near East, with *quasi*-weeks evidently being between five and ten days long.

Although some commentators have, in the past, suggested that the seven-day week is not related to any astronomical feature, the evidence does seem to indicate that it is related to the phases of the moon. Of course, a seven-day week was ordained by God according to the order of creation in Genesis 1 and 2—and this is also consistent with Genesis 1:14–16. The way in which the modern week developed in Roman culture has also been outlined, with influence from the Hebrew Scriptures possibly being one component through Jewish exile, and the growth of Christianity. How the Hebrew people understood and operated the seven-day week will be discussed in a second part.

References

1. Week, britannica.com, 25 May 2023.
2. Malcolm D., Calendars more than just days and months, creation.com, 26 Jun 2014; Hughes, J., The Seven-Day Week: where did the seven-day week come from? creation.com, 5 May 2022.
3. Zerubavel, E., *The Seven Day Circle: The history and meaning of the week*, University of Chicago Press, Chicago, pp. 5–11, 1985. Although, for consistency, this argument also ought to be applied to the month and year, because neither can be stated as being equal to an exact number of days.
4. Copeland, L.S., Sources of the Seven-Day Week, *Popular Astronomy* **XLVII**:4, Apr 1939; pp. 175–182
5. Steele, J.M., The length of the month in Mesopotamian calendars of the first millennium BC; in: Steele, J.M., (Ed.), *Calendars and Years: Astronomy and time in the Ancient Near East*, Oxbow Books, Oxford, pp. 133–48, 2007.
6. Brack-Bernsen, L., The 360-day year in Mesopotamia; in: Steele, J.M., (Ed.), *Calendars and Years: Astronomy and time in the Ancient Near East*, Oxbow Books, Oxford, pp. 83–100, 2007.
7. Cuneiform Digital Library Initiative (CDLI), Ur III Calendars, ox.ac.uk, 25 Apr 2017.
8. Muroi, K., The origin of the mystical number seven in Mesopotamian culture: division by seven in the sexagesimal number system, arxiv.org, 2014.
9. Zerubavel, ref. 3, p. 8.
10. Frahm, E., Counter-texts, commentaries, and adaptations: politically motivated responses to the Babylonian epic of creation in Mesopotamia, the Biblical world, and elsewhere, *Orient* **45**:3–33, 2010.
11. Pinches, T.G., Sabbath: Babylonian; in: Hastings, J., Selbie, J.A. and Gray L.H. (Eds.), *Encyclopaedia of Religion and Ethics*, Edinburgh, vol. X., T&T Clark, C. Scribner's Sons, New York, pp. 889–891, 1919.
12. Heinrich, A. C., Poem of Creation (Enūma eliš), chap. v, with contributions by Földi, Z.J., Hätinen, A., Jiménez E., and Mitto, T.D.N., translated by Foster, B.R., electronic Babylonian Library, lines 12–22, 2021.
13. King, L.W., The Seven Tablets of Creation, translation of Enuma Elish, Tablet V, lines 12–22, Luzac and Co. London, 1902.
14. Cuneiform Digital Library Initiative (CDLI), The computation of time in the old Assyrian period, ox.ac.uk, 20 Oct 2015.
15. Michel, C., The day unit within the Old Assyrian Calendar; in: Dönmez S., (Ed.), *Studies Presented in Honour of Veysel Donbaz*, Ege Yayinlari, Istanbul, pp. 217–224, 2010.
16. van Wyk, K., Seventh day cycles and seventh-day sabbath in cuneiform texts, *Korean J. Christian Studies* **84**:25–48, 2012.
17. Johns, C.H.W., Statistics of sabbath keeping in Babylonia, *The Expositor*, 7th series, 2.5, Butler & Tanner, Frome & London, pp. 433–440, Nov 1906.
18. Denotes a 19-year period in which there are 235 synodic months. The phases of the moon then repeat on the same solar days in the subsequent 19-year period. Discovered by the Greek astronomer Meton around 432 BC. See Metonic cycle, britannica.com, 23 Oct 2016.
19. Britton, J.P., Calendars, intercalations and year-lengths in Mesopotamian astronomy; in: Steele, J.M. (Ed.), *Calendars and Years: Astronomy and time in the Ancient Near East*, Oxbow Books, Oxford, pp. 115–32, 2007.
20. Kamrin, J., Telling Time in Ancient Egypt; in: *Heilbrunn Timeline of Art History*, The Metropolitan Museum of Art, New York, metmuseum.org, 2000.
21. Clagett, M., Ancient Egyptian science: a source book, vol. II, *Calendars, Clocks, And Astronomy*, *Memoirs of the APS*, no. 214, American Philosophical Society, Philadelphia, pp. 3–4, 1995.
22. The Temple of Karnak was built by Ramesses III (1186–1155 BC) at the end of the New Kingdom. In Parker, R.A., *The Calendars of Ancient Egypt: Studies in ancient oriental civilisation*, no. 26, University of Chicago Press, Chicago, p. 12, 1950.
23. Macrobius, *Saturnalia*, Book 1, chap. 12, v. 3.
24. Livy, *The History of Rome*, Book 1, chap.19.
25. Plutarch, Life of Noma; in: *Parallel Lives*, chaps. 18 and 19.
26. Censorinus, De Die Natali, XX, (ad 238), transl. Maude, W., *The Natal Day*, The Cambridge Encyclopedia Co., New York, pp. 27–40, 1900.
27. Livy, *The History of Rome, Periochae*, Book 47:13–14.
28. Fowler, W.W., *The Roman Festivals of the Period of the Republic*, Macmillan & Co., New York, p. 5, 1899.
29. Mommsen, T., *The History of Rome, vol. I: The period anterior to the abolition of the monarchy*, Dickson, W.P. trans. and ed., 2nd edn, Richard Bentley, London, pp. 216–220, 1864.
30. Beck, C., Syntax of the Latin, Chiefly from the German of C.G. Zumpt, 2nd edn, Charles C. Little & James Brown, Boston, pp. 175–178, 1844.
31. This inclusivity in counting days may also have a bearing upon our understanding of the 'three' days between Jesus' death and Resurrection; assuming the period covered one whole day, and two parts-of-days, thus ascribed as three days.
32. Falk, M., Astronomical names for the days of the week, *J. Royal Astronomical Society of Canada* **93**:122–133, Mar 1999.
33. O'Neil, W.M., *Time and the Calendars*, Manchester University Press, Manchester, p. 36, 1976.
34. Dio Cassius., *Roman History*, Book 37, E. Cary transl., vol. 3, Heinemann, London, chap, 16–19, 1974. According to Dio Cassius, each hour of the day was given a 'planetary' name as listed, and the names progressed through the week. The name of the first hour of each day became identified with that day. See also Malcolm D., The seven-day cycle, *Creation* **9**(2):32–35, 1987.
35. O'Neil, ref. 33, pp. 36–39.
36. Kariyawasam, A.G.S., Buddhist ceremonies and rituals of Sri Lanka, *The Wheel Publication* no. 402/404, Buddhist Publication Society, Kandy, Sri Lanka, 1995.
37. Zerubavel, ref. 3, p. 10.

Andrew Sibley *is a Chartered Meteorologist, based in the UK, and has published a number of papers in the field. He has a B.Sc. (Hons) and completed an M.Sc. in Environmental Decision Making in 2003 with the Open University. He also has an M.Phil. in theology from Exeter University (UK); his dissertation was* Intelligent Design: Scientific and Theological Perspectives. *He is the author of several books, including* Restoring the Ethics of Creation and Cracking the Darwin Code: Exploring the non-scientific foundations of deep-time and evolution. *Already a frequent contributor to CMI's publications, he joined the staff of CMI-UK/Europe as a speaker and writer in August 2021.*

Life did not originate from amyloids and ATP

Royal Truman, Alan White, and Chris Basel

Recent proposals for how life might have begun from ordinary, simple chemicals on the early earth do not withstand scientific scrutiny. One proposal is the amyloid world hypothesis, coupled with the idea that ATP could form prebiotically. Both ideas have little hard scientific evidence. ATP does not form readily in or near hydrothermal vents. All three phosphate group additions to a nucleoside are very endothermic, ensuring that the steady-state concentration of the nucleoside triphosphate, such as ATP, would have to be vanishingly low. ATP would have a very short lifetime near hydrothermal vents. The proposed pH gradients to accomplish ATP synthesis would have required ~1-nm-thin mineral membranes, which would not have been strong enough to form stable, hermetical regions separating oceanic and vent water having very different temperatures and pHs. The theoretical embedded inorganic nanomachines needed to extract useful energy remain pure speculation. Amyloids do not possess true ATPase properties, being unable to position ATP and target substrates in transition-state-like orientations. Furthermore, the concept of a LUCA (Last Universal Common Ancestor) that 'bubbled off' overlooks that the alkaline interior would have soon neutralized the proton gradient that drove the hypothetical energy-producing machines.

Dr Maury, Emeritus Professor from the Department of Medicine, University of Helsinki, Finland, has had a long and distinguished career centred around amyloids, amyloidosis, and fibrillogenesis research from a medical perspective.[1] He has since chosen to become a leading proponent of the amyloid world hypothesis. This is a shift away from his expertise in medicinal chemistry.

In an influential review article on the amyloid world theory, Maury claimed that prebiotic amyloids produced a series of biology-like new functions including self-replication, catalytic activities, information transfer, chiroselective addition of amino acids, and error-correcting information-processing system.[2]

Other amyloid world proponents such as Rout *et al.* have observed correctly that forming highly ordered amyloid aggregates is a simple physical process analogous to crystallization.[3]

None of the OoL experiments associated with the amyloid world hypothesis have any resemblance to realistic prebiotic conditions.[4–6] Critically, the high concentration of single-sequence peptides would not have been present in aqueous conditions.[7,8]

There is a current trend for the mass media, including YouTubers, to provide simplistic and severely flawed versions of the chemistry involved. Technical publications are skimmed over, exaggerated claims extracted (especially from the abstracts), and then a plausible-sounding narrative is offered with some technical terms to provide a veneer of credibility.

For example, one supporter of the amyloid world theory is a YouTuber who reviewed Maury's paper.[2] Remarkably, six commonly circulated errors were presented in a single paragraph.

> "[1] And ATP is another naturally occurring energy source near hydrothermal vents. [2] So, we know that amyloids have ATPase activity they can utilize the energy of ATP to do work. [3] 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. [4] The stringing of ATP and different triphosphate nucleotides together into DNA and RNA, [5] the incorporation of lipids which are again found naturally at hydrothermal vents and which spontaneously formed bilayer membranes; [6] as well as the creation of protein enzymes to do specific functions [labels 1–6 added]."[9]

These claims, labelled 1 to 6, have been encountered before and will now be examined. We will not address the many other chemical errors in the above lecture.[10–12]

The most serious misconception is that just a "matter of time" explains what materialists cannot explain using sound scientific principles—the source of new information.

Error 1—ATP does not form naturally near hydrothermal vents

Although the claim is often encountered that ATP is produced under prebiotic conditions, Chu and Zhang pointed out, in 2023, that

> "Although the de novo synthesis of ATP has not been reported, the origin of its components, including ribose, adenine, and the triphosphate group has been extensively studied."[13]

Later in this paper, Chu and Zhang speculate about prebiotic conditions that might produce ATP. Most of the experimental conditions proposed are not realistic in terms of temperatures, concentrations of reactants, or the need for purification. Not even one experiment was reported. This type of speculation in the literature is far from supporting a claim that "ATP is another naturally occurring energy source near hydrothermal vents."[9]

Fictitious pH gradient and machines in hydrothermal vents

Allegedly, ATP was readily created in pH gradients in hydrothermal vents.

> "But back at the prebiotic Earth proton gradients were formed naturally at hydrothermal vents which are key and integral in forming ATP in the first place."[14]

This claim, presented as a self-evident fact, was based on someone else's unfounded speculations. In the early 1990s, Russell *et al.* proposed a clever source of energy to drive chemical reactions to produce ATP, which is an endothermic (i.e., thermodynamically unfavourable) reaction. This required a *hypothetical* pH gradient separating extremely hot alkaline fluid generated in hydrothermal vents from colder acidic oceanic water.[15]

Meanwhile, three groups, headed by M.J. Russell, W. Martin, and N. Lane, have integrated this notion in their hypothesis of a non-organic, mineral autotrophy origin of life. The key papers have been referenced and discussed in a decidedly unflattering review article by Jackson, who observed:[16]

> "… these have been extensively cited but not critically reviewed in the literature."

Nevertheless, these vacuous speculations evolved into 'scientifically proven facts' in the mass media.

The highest proton motive force would result from the greatest difference in pH. These are usually optimistically assumed to be pH = 6 in the ocean and pH = 10 in the hydrothermal vent side.[16] If the entire ΔpH of 4 could be used effectively, this would provide a maximum energy of $24\ kJ\ mol^{-1}$.[16] This energy is claimed to have driven the reduction of CO_2 by H_2 to form $HCOO^-$ (which could generally unhelpfully decompose to form carbon monoxide, CO).

To prevent water having different pH values from mixing, a stable inorganic membrane was proposed. Various very complex precipitate membranes have been hypothesized, consisting of partly composed of iron sulphides doped with Ni, Co, and Mo, as well as ferrous/ferric oxyhydroxides, dosed with Ni and Mo.[17] Russell *et al.* also proposed metal-layered hydroxides such as the hydrotalcite pyroaurite $[\sim Mg_6Fe_2(CO_3)(OH)_{16}\cdot 4(H_2O)]$ and fougèrite variants like $\sim[(Fe^{II},Mg)_2Fe^{III}(OH^-)_5\cdot CO_3^{2-}]$.[17] Other candidate precipitates include montmorillonites, smectites, and other cationic clays.

There is no evidence that any of the kinds of membrane systems did, or could have, existed, possessing steep pH gradients, neither at the extensively studied Lost City hydrothermal field, located 20 km west of the Mid-Atlantic Ridge nor anywhere else.[16]

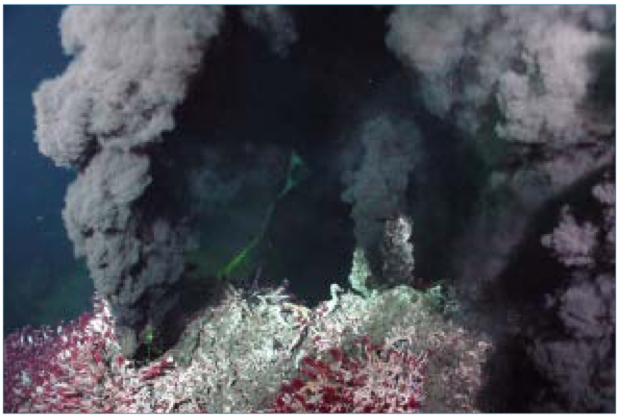


Image: National Oceanic and Atmospheric Administration (NOAA) NOAA

Figure 1. Black smoker at Sully Vent in the Main Endeavour Vent Field in the northeast Pacific Ocean

Russell *et al.* pointed out that a *simple* inorganic proton electrochemical gradient machine would have been needed to replace an extraordinarily sophisticated rotary mechanism such as ATP synthetase.[17] This machine must traverse the membrane, being in contact in some manner with both the source of protons (the cold acidic ocean at lower pH) and the hot alkaline hydrothermal vent side. The hypothetical machine must play the role of cellular H^+-ATP synthase (which is about 10 nm in diameter) and the H^+-pyrophosphate synthase. The inner membranes of mitochondria in which the huge ATP synthase complexes are embedded are only about 5–6 nanometres (nm) thick.

Since the hypothetical much simpler embedded prebiotic machine would have had to be very small, the membrane must not have been much thicker at the location of proton influx. Otherwise no H^+ transfer would have been possible. Consequently, the required membrane would have had to be exceedingly thin, no wider than about 1 nm, and therefore very fragile.

Photographs (like figure 1) and YouTube videos illustrate the explosive force of high-pressure hydrothermal vents at around 400°C, offering a reality check for how plausible it would be to form delicate 1-nm-thick layers of soluble minerals hermetically sealed from the surrounding ocean water. Random precipitates would not have been conveniently limited to 1 nm layers, possessing some kind of mineral machine.

Thicker membranes would have been conceptually possible if there were channels through which protons could flow, and the machines would be fortuitously placed along the open paths. However, this would have decreased the electrical potential difference, realistically even entirely.

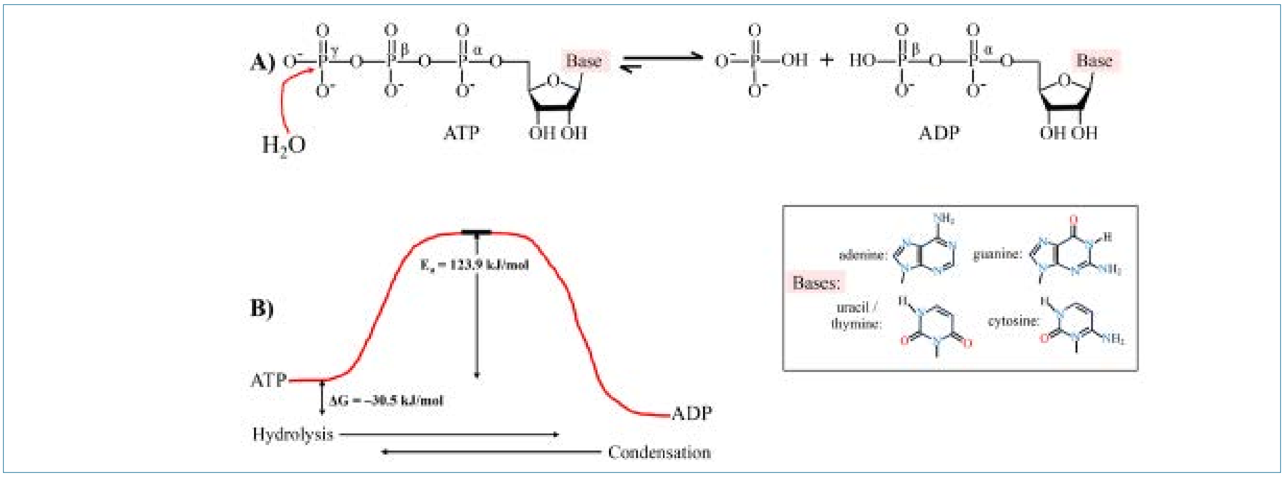


Figure 2. Triphosphate nucleotides hydrolyze when dissolved in water. A) Hydrolysis of the γ-phosphate group. Adenine in the inset is the base used by ATP. The four bases shown are used by RNA. B) Energy of activation, E_a, is high for both hydrolysis and formation of ATP, but the hydrolysis reaction is very exothermic. ΔG values are reported under standard conditions (25°C, 1 bar, 1 mol/L, pH = 7). ATP = adenosine triphosphate, ADP = adenosine diphosphate.

Note that the theoretical maximum energy extractable by a perfect machine, 24 kJ mol^{-1}, is already near the minimum to be of any chemical value.[16]

Speculations on the composition of the theoretical machines have centred recently on Fe(Ni)S and silicate structures. However, vents at Lost City are dominated by forms of calcium carbonate and magnesium hydroxide, unsuitable as membranes. Furthermore, silicate was present as only a trace component within the chimney materials at Lost City, with no sulphide whatsoever.[16]

Jackson accurately described the narratives on how these fictitious proton transporters were claimed could have worked as

> "… splendidly imaginative, but not in the least supported by observations in the laboratory."[16]

In all the decades since these kinds of fictitious inorganic membranes were first proposed, no details of their hypothetical properties and functioning have been put forward.[16]

Instead of ATP being a "naturally occurring energy source near hydrothermal vents", we see instead that production of ATP from non-biotic sources near hydrothermal vents has not been demonstrated at all; only speculative models exist; and no evidence for a mineral membrane exists. Worse, Jackson has pointed out that *not even a laboratory proof-of-concept* has been offered. To deserve any scientific credibility:

> "A direct demonstration that a model, laboratory-synthesized, non-protein, molecular machine can utilize a ΔpH established across a laboratory-synthesized, inorganic membrane is needed."[16]

The possibility of a steady supply of concentrated ATP forming near hydrovents to support pre-RNA life will be disproven next, based on chemical principles.

ATP does not form in high concentrations near hydrothermal vents.

ATP is a high-energy molecule used to fuel countless cellular processes. Hydrolysis of each phosphate is very exothermic. In the case of the end phosphate, –28.0 to –33.5 kJ/mol would be released under standard conditions, as shown in figure 2.[18–21]

Increasing the temperature to overcome the high energy of activation barriers shown in figure 2B would accelerate addition of each of the three phosphate groups to adenosine. This is because providing reactants like ADP and inorganic phosphate (P_i) with a higher kinetic energy would increase their frequency of collision and the proportion able to overcome the activation energy barrier.

However, the three condensation/hydrolyzation processes are reversible, so that increasing temperatures would accelerate both the forward and reverse reactions:

$$\text{Adenosine} \xrightleftharpoons[H_2O]{P_i} \text{AMP} \xrightleftharpoons[H_2O]{P_i} \text{ADP} \xrightleftharpoons[H_2O]{P_i} \text{ATP} \qquad (1)$$

where ATP means adenosine triphosphate, ADP adenosine diphosphate, AMP adenosine monophosphate, and P_i represents the inorganic phosphate group. Once ATP forms, the energy of activation of hydrolysis is high enough for it to remain intact for some time *at low temperatures*.

During a sequential addition of phosphate groups under prebiotic conditions, as shown in scheme (1), AMP would first need to build up, then ADP, and finally ATP. At equilibrium,

$$k_{con}[ADP]_{eq}[P_i]_{eq} = k_{hyd}[ATP]_{eq} \qquad (2)$$

where k_{con} is the rate constant of condensation, and k_{hyd} of hydrolysis. As usual in chemistry, the concentration of H_2O (55.5 M) will be considered unchanged and k_{hyd} already incorporates this.

The highest concentration of ATP beginning with adenosine according to scheme (1) would result at the system's equilibrium point. It cannot be higher according to the definition of equilibrium expressed by eqn (2). The equilibrium concentration of [ATP] is what matters, not how fast the equilibrating forward and reverse reactions occur.

Finding the equilibration concentration of ATP at 350°C (623 K)

Assume that all the ATP present at equilibrium would be equilibrating with only ADP; i.e.,

$[ADP]_{eq} + [P_i]_{eq} \leftrightarrows [ATP]_{eq}$. The rationale for this approximation being reasonable is given in Appendix 1. The equilibrium constant is

$$K_1 = [ATP]_{eq} / [ADP]_{eq}[P_i]_{eq} \tag{3}$$

K_1 can be found using the van 't Hoff equation

$$\Delta G° = –RT \times \ln(K_1) \tag{4}$$

where ΔG° is the Gibbs free energy change under standard conditions, R is the gas constant (8.314 J/mol·K), and T is the temperature in Kelvin. Fortunately, ΔG° values are available from literature sources and eqn (4) can be expressed as

$$K_{eq} = e^{(–\Delta G°/(RT))} \tag{5}$$

Using ΔG = –30,500 J/mol[19,20,21] leads to

$$K_1 = \approx 2.8 \text{ x } 10^{–3} \tag{6}$$

at 350°C, since $K_1 = e^{(–(30{,}500 \text{ J/mol}) / (8.314 \text{ J/(mol·K) x } 623 \text{ K}))}$. The units of the equilibrium constants were excluded in this paper to simplify the notation.

Rearranging (3) leads to

$$[ATP]_{eq} = K_1 \times [ADP]_{eq} [P_i]_{eq} \tag{7}$$

Hence, the values for $[P_i]_{eq}$ and $[ADP]_{eq}$ are needed to solve this equation.

Concentration of prebiotic inorganic phosphate

The average phosphate concentration in oceans is approximately 70–72 µg/L.[22] Not all these phosphates are in the P_i form which is needed to form ATP, so setting $[P_i]$ = 70 µg/L is generous. Using a molecular weight of P_i = 94.97 g/mol leads to an average molarity in ocean water of

$$[P_i] \approx 7.4 \times 10^{–7} \text{ M.} \tag{8}$$

The current concentration of phosphates measured is higher than would have been present billions of years ago, since they are being transported off continents mostly via river runoff. Near hydrothermal vents phosphates are adsorbed onto iron oxyhydroxides, removing them from solution, and remobilization within the sediments is limited afterwards.[23] These considerations imply that the effective prebiotic $[P_i]$ would not have been higher than given in (8).[23]

Concentration of prebiotic [ADP]

Prebiotic ADP would have formed via the very unfavourable equilibrium AMP + $P_i \leftrightarrows$ ADP + H_2O. The equilibrium constant is

$$K_2 = [ADP]_{eq} / [AMP]_{eq}[P_i]_{eq} \tag{9}$$

Using ΔG = +30.5 kJ/mol[24] in (5) leads to

$$K_2 \approx 2.8 \times 10^{–3} \tag{10}$$

$$[ADP]_{eq} = K_2[AMP]_{eq}[P_i]_{eq} \tag{11}$$

The concentration of $[AMP]_{eq}$ is now needed to solve this equation.

Concentration of prebiotic [AMP]

Prebiotic AMP would have formed via the very unfavourable equilibrium adenosine + $P_i \leftrightarrows$ AMP + H_2O. The equilibrium constant is

$$K_3 = [AMP]_{eq} / [adenosine]_{eq}[P_i]_{eq} \tag{12}$$

Using ΔG = +14.2 kJ/mol[24] in (5) leads to

$$K_3 \approx 6.5 \times 10^{–2} \tag{13}$$

at 350°C. Rearranging (12) leads to

$$[AMP]_{eq} = K_3[adenosine]_{eq}[P_i]_{eq} \tag{14}$$

The $[ATP]_{eq}$ in eqn (7) can now be expressed using $[ADP]_{eq}$ from eqn (11) and $[AMP]_{eq}$ from (14):

$$[ATP]_{eq} = K_1 \times K_2 \times K_3[adenosine]_{eq}[P_i]^3{}_{eq} \tag{15}$$

Since $K_1 = 2.8 \text{ x } 10^{–3}$ from (6), $K_2 = 2.8 \times 10^{–3}$ from (10), $K_3 = 6.5 \times 10^{–2}$ from (13), and $[P_i] = 7.4 \times 10^{–7}$ M from (8), this leads to

$$[ATP]_{eq} \approx 2.1 \text{ x } 10^{–25} \text{ x } [adenosine]_{eq} \tag{16}$$

at 350°C. The equilibrium constant of [adenosine] will determine how much [ATP] would be produced. But key life-relevant chemicals like adenosine are rapidly destroyed at such high temperatures. As Levy and Miller pointed out:[25]

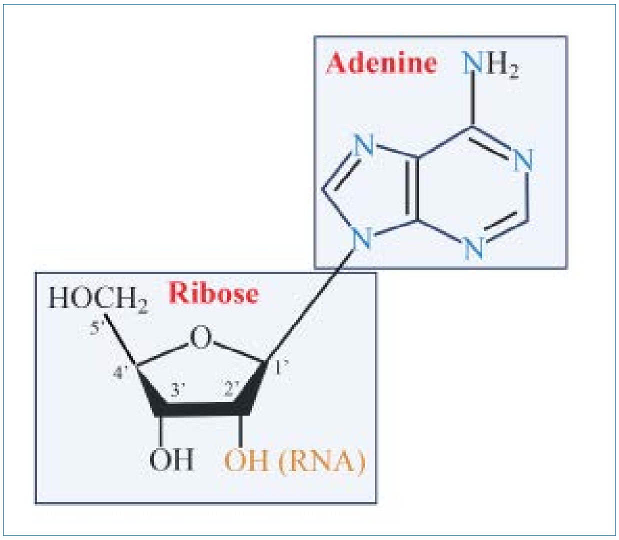


Figure 3. Chemical structure of adenosine. When a hydroxyl group is attached at the 2'-position, this is a ribose, used by RNA. When the 2'- group is absent, this is a deoxyribose, used by DNA.

> "Previous studies have shown that a major problem with an origin of life between 250°–350°C is the stability of the presumed components of the first organisms, where the half-lives for decomposition are at most a few minutes."

One of these components is ribose, a precursor of adenosine, which has a half-life of only 73 min at pH 7.0 and 100°C and 44 years at pH 7.0 and 0°C.[26] At higher pH, the half-lives are shortened significantly.

In fact, the half-life of adenosine, shown in figure 3, is less than 15 seconds at 350°C,[25] assuming any could have been formed. Shapiro pointed out that adenine synthesis requires unrealistically high HCN concentrations of at least 0.01 M to obtain any at all. However, HCN forms many other similar chemicals, and isomers instead of adenine.[27]

From eqn (16), the molar $[ATP]_{eq}$ is the product of $[adenosine]_{eq} \approx 0 \times 2.1 \times 10^{-25}$. Clearly, no relevant amount of ATP would have formed at hydrothermal temperatures of around 350°C.

Lower temperature scenarios to form ATP

Since adenosine is thermally unstable, perhaps ATP may have formed somewhere *near* a prebiotic hydrothermal vent but at much less than 350°C. Lower temperatures, though, would *decrease* the values of K_1, K_2, and K_3, as summarized in table 1.

To illustrate, eqn (15) was solved using equilibrium constants at other temperatures summarized in table 1. Since at 350°C the half-life of adenosine is less than 15 seconds, the temperature range 25–100°C would be worth considering. Using the K_1, K_2, and K_3, and $[P_i] = 7.4 \times 10^{-7}$ M, we can predict:

$$[ATP]_{eq} \text{ (at 25°C)} = 2.7 \times 10^{-32} \, [adenosine]_{eq} \qquad (17)$$

$$[ATP]_{eq} \text{ (at 100°C)} = 1.2 \times 10^{-29} \, [adenosine]_{eq} \qquad (18)$$

Suppose a high $[adenosine]_{eq} = 10^{-3}$ M could have been produced prebiotically at 25°C, and a factor 1,000 less at

Table 1. Half-life of adenosine and equilibrium constants for ATP precursors at different temperatures. Equilibrium constants calculated using $K = e^{(-(\Delta G \text{ J/mol}) / (8.314 \text{ J/(mol·K)} \times T \text{ (K)})}$.

		Equilibrium constants				
°C	Half-life Adenosine [a]	ADP + P_i ⇆ ATP + H_2O (ΔG ≈ +30.5) [b] K_1	AMP + P_i ⇆ ADP + H_2O (ΔG ≈ +30.5) [c] K_2	Adenosine + P_i ⇆ AMP + H_2O (ΔG ≈ +14.2) [d] K_3	AMP + PP_i ⇆ ATP + H_2O (ΔG ≈ +46) [e] K_4	2 P_i ⇆ PP_i + H_2 (ΔG ≈ +29.3) [f] K_5
25	10,000 yr.	4.50×10^{-6}	4.50×10^{-6}	3.24×10^{-3}	8.64×10^{-9}	7.31×10^{-6}
100	1 yr.	5.35×10^{-5}	5.35×10^{-5}	1.03×10^{-2}	3.61×10^{-7}	7.88×10^{-5}
250	< 35 min.	8.99×10^{-4}	8.99×10^{-4}	3.82×10^{-2}	2.54×10^{-5}	1.18×10^{-3}
350	<15 sec.	2.77×10^{-3}	2.77×10^{-3}	6.45×10^{-2}	1.39×10^{-4}	3.49×10^{-3}

[a] From Levy and Miller[25]
[b] +30.5 kJ/mol from several refs.[19–21] 32 kJ/mol according to Wimmer *et al.*[28]
[c] +30.5 kJ/mol from vrchemistry[24]
[d] +14.2 kJ/mol from vrchemistry[24]
[e] +46 kJ/mol from Wimmer *et al*[28]
[f] +29.3 kJ/mol from Kotter and Nair[29]

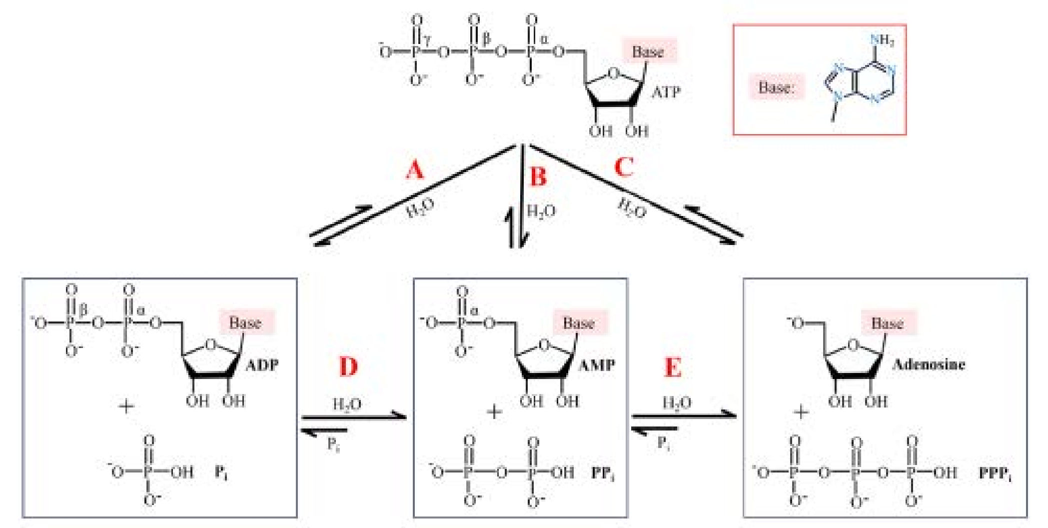


Figure 4. Equilibrium reactions involved in the formation and hydrolysis of ATP

100°C. Then in this temperature range $[ATP]_{eq}$ would have been $< 1 \times 10^{-35}$ M. From Avogradro's number a $[ATP]_{eq}$ = 1 M would have contained about 6×10^{23} ATP molecules. Therefore, based on the collection of optimistic assumptions made, in the temperature range 25–100°C, less than 1 ATP molecule would have been present per 10^{11} litres of water.

Other potential pathways to form ATP

Figure 4 shows the various equilibrating chemicals which are involved in forming and hydrolyzing ATP. It is important to understand that the pathways A, B, and C which connect ATP all strongly favour hydrolysis of ATP thermodynamically. The overall *synergetic outcome* of having multiple hydrolysis options is to increase the concentration of P_i and the hydrolyzed precursors to ATP at equilibrium.

Pathway A $\leftrightarrows$ D $\leftrightarrows$ E was analyzed in the discussion above. Would an alternative involving already condensed P_i be more feasible? No, since the reaction 2 $P_i \leftrightarrows PP_i$ also has $\Delta G \approx +29.3$ kJ, as shown in the last column of table 1;[28] the same as for addition of a P_i to a phosphate which was already bonded to an ATP precursor.[19–21,25] Furthermore, column 6 of table 1 shows that the reaction between AMP + PPi to form ATP has the most unfavourable ΔG (+46 kJ/mol) of all the equilibria options.

ATP could not have accumulated in a concentration of any relevance for OoL speculations, since it can readily hydrolyze, as could its precursors. This is elaborated on in Appendix 2, which considers the scenario of ATP forming elsewhere through unknown processes, which then migrates to the vicinity of a hydrothermal vent. The final equilibrium state is the same whether the reaction is initiated with an excess of reactants or products.

A prebiotic catalyst would not change the equilibrium constants. So the conclusion is inescapable that ATP concentrations of any relevance for OoL purposes would not have existed in the vicinity of hydrothermal vents.

Prebiotic pH gradient membranes won't form

A large difference in pH between alkaline vent fluids and acidic ocean water has been proposed to power addition of three phosphate groups to adenosine. This would have required a hypothetical membrane to separate the high from lower proton-containing water. We will now revisit this second mistake.

What would have prevented mixing of very high-pressure-and-temperature hydrothermal vent water with icy ocean water? The membrane would have been less than 1 nm thick to permit the conceptual molecular motor to traverse it. For water with a high pH difference to have formed, a *hermetical membrane* would have had to form virtually *instantaneously before any mixing occurred.*

A membrane, formed through slow precipitation in less turbulent lower temperature alkaline water, would also have provided sufficient time for the protons to mix.

The region impermeable to sea water would have had to replenish ATP, which has a half-life on the order of minutes or days, depending on the temperature. That implies that the complex adenosine molecule, which is also unstable (in addition to its precursor ribose; see figure 3), would have had to be replenished continuously. Recall that the concentration of adenosine would have had to be much higher than that of ATP due to the unfavourable equilibrium constants. A high concentration of phosphate would also have been indispensable. Clearly, these requirements would not have been fulfilled and maintained for millions of years naturally.

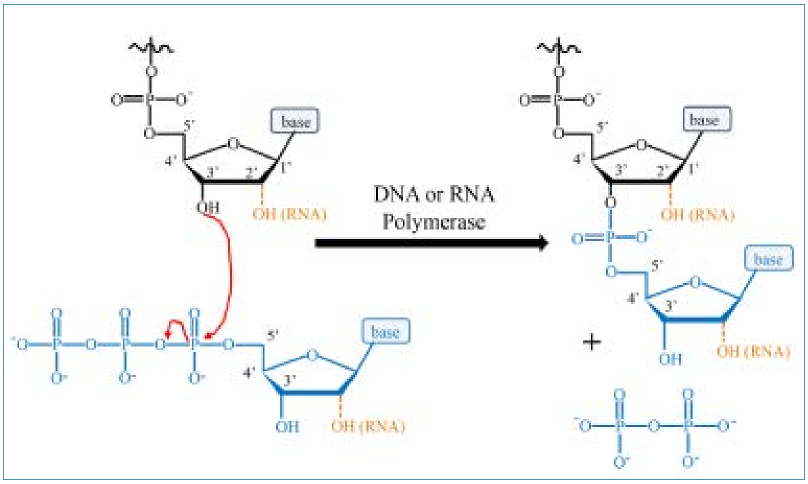


Figure 5. DNA and RNA polymerases, which consist of multiple enzymes, are indispensable to form long DNA and RNA chains. The –OH group on the 3' carbon of ribose or deoxyribose displaces PP_i in an exothermic (thermodynamically favourable) reaction.

We explored the mathematical aspects of ATP hydrolysis and formation further in Appendix 1.

Error 2—Random ATP hydrolysis won't produce useful work

We saw, above, that hydrolysis of ATP would have prevented ATP from building up. The claim that amyloids act as ATPases (i.e., accelerators of hydrolysis) would have only made matters worse. Many substances could have catalyzed hydrolysis of ATP, but this does not make them enzymes known as ATPases!

Enzymes function by structuring reactants to achieve an energetically favourable transition site. By definition, highly customized ATPase enzymes must do much more than merely hydrolyze ATP. They must form distinct three-dimensional structures able to position ATP and reactant together to achieve the geometry of the transition state. This lowers the E_a necessary to hydrolyze a useful chemical reaction at the right time.

Motors don't work by dousing them with a high-energy fuel and setting them on fire. Useful work is not produced by random dissipation of energy. If anything, hydrolysis of multiple ATPs might even occasionally break the amino acid bonds that form amyloids.

Error 3—Time does not automatically refine information-storing systems

We have addressed the relevant meaning of *information* in the context of biology elsewhere.[30,31] An important example of information is the language encoded in DNA which specifies the sequence of proteins, usually many thousands of them in the same organism.

Maury misused the multiple meanings of the word information to create a 'play on words', claiming that

> "Information transfer on the early Earth for about 4,000 million years ago 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]

'Environmentally derived information', like any deterministic response to environmental influences (e.g., expansion of a gas upon heating), is not how instructions are 'encrypted' by genomes and has no relevance to the topic of biological information. The fundamental characteristic of coded information systems is that the symbols must be freely arrangeable in order to provide a variety of unrelated instructions.[32,33]

An important reason that time does not automatically generate goal-oriented information is based on the Second Law of Thermodynamics: there is a natural tendency in nature toward maximum entropy, which would corrupt the physical carriers on which information is encoded.

DNA cannot 'self-replicate' by physical interactions with another strand. Furthermore, this would leave unanswered where the extra identical copies, which were then moulded by the pre-existing ones, came from. This is a critical consideration that also applies to amyloids, which require a large number of identical copies to be physically templated by pre-existing ones in an alleged form of 'self-replication'.

Different β-sheet zipper structures found in amyloids could form and unform under the influence of temperature fluctuations and hydrolysis. But this has no more relevance to how biological information is coded than random changes during the manufacture of silicon chips would determine what is encoded on them using computer programs.

Maury's misuse of the fundamental entity of biological information allowed free reign to mental imagery by others. One explained online that Maury's paper demonstrated that then "*refinements of the RNA and DNA information storing system is inevitable*".[9] Reviewing the online video confirmed that coded information in the form of instructions based on nucleotide sequences was meant, and that these instructions had been self-created. No explanation was offered as to why such refinement would be inevitable. Under cold conditions, amyloids would freeze solid; under very hot conditions, they would disintegrate. This is irrelevant to refining the DNA and RNA information-storing system. Such physical-chemical behaviour does not address the source of biological information in any manner.

Error 4—Triphosphate nucleotides don't produce DNA and RNA in water

As mentioned above, bonding two P_i groups has an unfavourable $\Delta G \approx + 29.3$ kJ, and linking triphosphates would require two such reactions. An insignificant amount could have been produced. But more importantly, DNA and RNA are not produced by mixing triphosphate nucleotides, neither in free nature nor in cells. The relevant part of the reaction, which involves the 3'–OH group, is shown in figure 5 and occurs with the help of the DNA polymerase enzymes.[34] DNA and RNA are not produced in water by "stringing of ATP and different triphosphate nucleotides together".[9]

Error 5— Amyloids do not spontaneously form bilayer membranes

Research on designing organic amphipathic molecules to form liposomes, micelles, and bilayer sheets has been going on for about a century. OoL chemists use well-known principles to design long hydrocarbon chains with polar ionic ends which they know will form bilayers. The claim in OoL literature that these carefully designed laboratory experiments represent "plausible prebiotic conditions" is not reasonable, though.[35,36]

Typically, dyes are added to the surfactant solutions, and researchers show that for a few hours they are separated between the two layers. This has virtually nothing to do with any life-relevant membrane requirements, which must selectively pump the correct substance inside and selectively pump out the waste products and deleterious substances.

In the above quote, supposedly after amyloids and ATP interact, there follows:

> "… the incorporation of lipids which are again found naturally at hydrothermal vents and which spontaneously formed bilayer membranes."[9]

This is a non-sequitur. What lipids are incorporated into what? Jackson had something to say about hypothetical membranes. In his review articles, Jackson critiqued the notion that mineral membranes preceded biological membranes.[16,37] Some amyloid world hypothesis proponents have suggested that following the phase of hydrothermal vent chemistry a LUCA (Last Universal Common Ancestor) transferred to a new environment. The vague evolutionist imagery involves a LUCA-engulfed membrane that 'bubbled off'.[38] No mention is even made of an amphipathic bilayer.

Jackson explained the dilemma. The alkaline solution in a tiny bubbled-off volume would become increasingly pH-neutral as protons continued to flow in. Therefore, the ΔpH-dependent molecular machines in the new organism would have quickly fizzled out.[36]

A potential solution would have required a second, new kind of proton pump to *remove* protons to re-establish a proton gradient. To operate, it would have needed to be linked to a new energy source, such as some kind of internal inorganic redox reactions. In the immense volume of the hydrothermal vent, this second machine would not have been needed, so how and why should this now suddenly become available?[16] Natural processes know no teleology. Complex new chemical equipment does not arise naturally for the convenience of a future biological life.

Error 6—Protein enzymes performing specific functions don't automatically arise

In the lecture above, the claim, "it's only a matter of time" included several allegedly inevitable processes, including "the creation of protein enzymes to do specific functions".[9]

Protein enzymes having the necessary amino acid sequences to perform specific functions aren't created simply because amyloids are present. It is well known that the vast majority of random sequence peptides won't lead to reliably folded proteins having useful functions.[39,40]

These six are serious errors (several more will not be addressed here but some are mentioned in the endnotes).[10–12,14]

The intention here is not so much to draw attention to technical errors being disseminated[9] but to discourage ***the speculation rampant in much of OoL research****. Perhaps the origin of life can be explained by* ***experimental*** *results using simple chemicals that might have been present on the early earth under conditions that could have reasonably existed then and there. But this will only be accomplished by* ***disciplined scientific work rather than pure speculation or an appeal to the passage of time****.* Today, a great many are not convinced that a reasonable alternative to a supernatural creation has been provided.

Appendix 1. Concentration of ATP precursors when multiple equilibria exist

The equilibrium concentration of ATP was calculated above at different temperatures using equilibrium constants derived from the Gibbs free energy of the various reactions under standard conditions. A complication arises when the same chemical partakes in multiple equilibrating reactions, such as AMP in this example:

$$\textbf{Adenosine}\ \underset{H_2O}{\overset{P_i}{\rightleftharpoons}}\ \textbf{AMP}\ \underset{H_2O}{\overset{P_i}{\rightleftharpoons}}\ \textbf{ADP}$$

For the condensation of AMP and adenosine, the equilibrium constant is $[AMP]_{eq}$ / $[adenosine]_{eq}[P_i]_{eq}$, which is K_3 in eqn (12). At equilibrium

$$k_{con1}[adenosine]_{eq}[P_i]_{eq} = k_{hyd1}[AMP]_{eq} \quad (19)$$

However, at equilibrium, AMP must also satisfy the second equilibrium step:

$$k_{con2}[AMP]_{eq}[P_i]_{eq} = k_{hyd2}[ADP]_{e} \quad (20)$$

What is the shared $[AMP]_{eq}$ for the last two equations? This can be understood by considering how the equilibrium state was reached. Initially, some initial concentration of $[adenosine]_i$ would have been slowly consumed as it condensed with P_i to form AMP. Absent any other reactions, AMP and adenosine would have reached equilibrium concentrations, where $[adenosine]_i - [AMP]_{eq} = [adenosine]_{eq}$. Since ΔG^0 is so high, $[adenosine]_i >> [AMP]_{eq}$ and therefore to a close approximation $[adenosine]_i \approx [adenosine]_{eq}$. In addition to the thermodynamic aspects, eqn (19) shows that condensation requires adenosine to react with P_i, which has a very low concentration, whereas AMP reacts with water, which has a concentration of about 55.5 M.

As [AMP] begins to build up before equilibrium is reached, some now reacts with P_i to form ADP. Condensation is once again thermodynamically unfavourable; in addition, the reaction depends on P_i, which is found in very low concentration, compared to water for the reverse hydrolysis process (20). As a consequence, very little of the available [AMP] is consumed, and $[AMP]_{eq} >> [ADP]_{eq}$. Therefore, it is acceptable to treat this second equilibrium involvement of AMP as hardly affecting the concentration compared to what would have existed had only AMP ⇆ adenonine + P_i been present.

The slight decrease in AMP is replenished by a corresponding amount of adenosine → AMP. Ultimately, any ADP formed followed by ATP must decrease adenosine by the same amount.

In conclusion, K_3 can be used, as shown in eqn (14), to estimate the 'true' $[AMP]_{eq}$ to a very close approximation; K_2 to find $[ADP]_{eq}$, as shown in eqn (11); and K_1 to find $[ATP]_{eq}$, as shown in eqn (7).

Appendix 2. Inability of ATP to build up during exponential hydrolysis

In the main text, the prebiotic scenario to produce ATP was that it built up slowly by adding individual P_i groups. Since ATP hydrolyzes relentlessly over time, especially at high temperatures, in a relatively short time the equilibrium concentration will have been reached *no matter how it was formed*. This must be taken into account when evaluating experiments where ATP was synthesized under prebiotically irrelevant conditions. For OoL purposes, this ATP would at some point need to be in an aqueous solution to have any relevance.

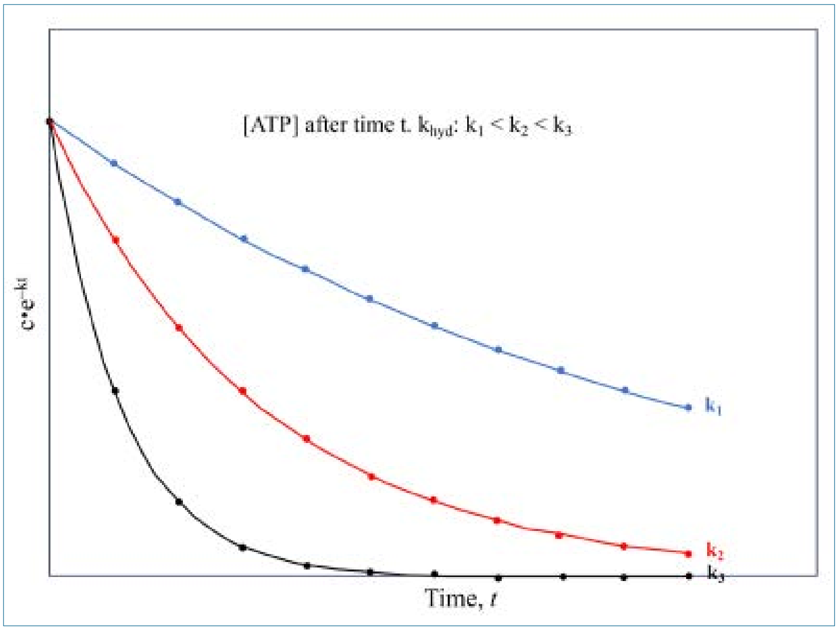


Figure 6. ATP remaining after decomposition by hydrolysis decreases at an exponential rate. Higher values for k_{hyd} result in faster disappearance of ATP. Here a constant influx of new ATP is assumed at a constant rate, ***c***, and $k_1 = 0.1$; $k_2 = 0.3$; $k_3 = 0.9$ for illustration purposes.

An example is the experiments reported by Cheng *et al.*, using pre-synthesized sodium trimetaphosphate salt mixed in high concentration with adenosine and a catalyzing ion under multiple rounds of wet–dry cycles.[41]

The hydrolysis of ATP's triphosphate nucleotides is a first-order reaction when ATP is surrounded by water molecules and follows an exponential decay rate law:

$$[\mathrm{ATP}]_t = [\mathrm{ATP}]_0 e^{-kt} \qquad (21)$$

which can be expressed as

$$\ln([\mathrm{ATP}]_t \,/\, [\mathrm{ATP}]_0) = -kt \qquad (22)$$

where $[\mathrm{ATP}]_0$ is the concentration at a point in time; $[\mathrm{ATP}]_t$ is the concentration after an interval of duration *t*; and k can be solved as the slope of a linear fit of ATP concentrations taken over a range of time intervals.

Hydrolysis of ATP has been studied in unbuffered solutions of 0.1 mol/L of ATP with pH values of 3, 5, and 7.[42] Rate constants of hydrolysis were found to increase about an order of magnitude per 20°C increase in temperature. The rate constants for hydrolysis at 120°C were 4.34×10^{-3} s^{-1} at pH 3 and 2.91×10^{-3} s^{-1} at pH 7. These correspond to ATP *half-lives of only a few minutes*.

Studies of ATP hydrolysis using pure and tap water with a pH of 7 led to a half-life of 4–5 days at 24°C, and 8–10 days at 4°C.[43] Impurities accelerated the rate of hydrolysis; i.e., it was slower in pure milli-Q water.

As mentioned above, forming triphosphate nucleotides is strongly disfavoured both kinetically and thermodynamically. The Gibb's free energy, ΔG for the hydrolysis of one mole of ATP into ADP and P_i is about −30.5 kJ/mol, (−7.3 kcal/mol) under standard conditions. In addition, the energy of activation for the phosphate groups are each about $E_a = 123.9$ kJ/mol (29.6 kcal/mol). It is worth recalling that according to Jackson the theoretically maximum energy extractable by a *perfect pH gradient machine* would have been only 24 kJ mol^{-1}, based on an electromotive force caused by $\Delta\mathrm{pH} = 4$.[16]

Suppose that in a contained area around a hydrothermal vent ATP was being produced at a constant rate, *c*, per time unit. After a short interval, *t*, the amount produced would have been be $c{\cdot}dt$. But simultaneously the ATP just produced would also be hydrolyzing at a rate of $(c{\cdot}dt)e^{-k\cdot t}$. The next interval of duration, *t*, a fresh amount of ATP would have formed, $(c{\cdot}dt)e^{-kt}$, during which time the formerly produced ATP would have continued to hydrolyze, with $(c{\cdot}dt)e^{-k\cdot 2t}$ of it remaining after 2 intervals of duration *dt*. This is repeated for as many dt intervals as we wish. The total amount remaining after many intervals is the area under the integral, as shown in figure 6, where the rightmost region was recently produced, and in the longer period region, the ATP which was produced long before which has not yet hydrolyzed. The integral can be expressed as:

$$\int_{t=0}^{t=t} ce^{-kt}dt = -\frac{c}{k}\,e^{-kt} \qquad (23)$$

Evaluation between t = t and t = 0, using large values of t leads to

$$-\frac{c}{k}\left(e^{-kt} - e^{0}\right) = -\frac{c}{k}(0-1) = \frac{c}{k} \qquad (24)$$

Slower hydrolysis rate constants (such as found at lower temperatures) lead to longer survival of ATP, as shown in the top curve in figure 6.

Any value for k can be used in (24), depending on the temperature, pH, etc. Assuming as an example that $t_{½} = 1$ day leads to a steady state of [ATP] which converges to $1.4{\cdot}c$.

All three phosphate groups can hydrolyze, and the analysis here indicates that the concentration of ATP which could have accumulated would have been slightly above the constant rate of daily production of ATP. It was shown above that the addition of each of the P_i is thermodynamically unfavourable, and $[P_i]$ would have been very low. The daily rate of production of new ATP, $c{\cdot}dt$, would be very small.

Should, at some point, an influx of ATP have occurred, it would have temporarily increased the concentration generated by $c{\cdot}dt$ during that time period. However, the exponential rate of hydrolysis would apply to the new combined concentration, reducing half of it during the same half-life as before. Concurrently, fresh ATP would be added at the rate of $c{\cdot}dt$. Therefore, after a few half-lives, the effect of the original influx of ATP would have no discernible effect on [ATP].

References

1. Peter Maury, Prof. emer., Clinicum, University of Helsinki.
2. Maury, C.P.J., Amyloid and the origin of life: self-replicating catalytic amyloids as prebiotic informational and protometabolic entities, *Cellular and Molecular Life Sciences* **75**:1499–1507, 2018.
3. Rout, S.K., Friedmann, M.P., Riek, R., and Greenwald, J., A prebiotic template-directed peptide synthesis based on amyloids, *Nature Communications* **9**:234–242, 2018.
4. Truman, R., Non-existence of error correction in plausible prebiotic amyloids, *J. Creation* **38**(2):127–130, 2024.
5. Truman, R. and Basel, C., Prebiotically plausible peptides don't self-assemble to produce useful catalytic amyloids, *J. Creation* **37**(3):135–140, 2023.
6. Truman, R., Amyloids having sequence-, regio-, and stereoselective properties don't form under plausible prebiotic conditions, *J. Creation* **37**(3):128–134, 2023.
7. Truman, R. and McCombs, C., Insignificant concentrations of peptides form in water: part 1—using hot temperatures or high pH, *J. Creation* **38**(1):126–135, 2024.
8. Truman, R., Tan, C., and McCombs, C., Insignificant concentrations of peptides form in water: part 2—using moderate temperatures, *J. Creation* **38**(1):136–149, 2024.
9. Amyloid world hypothesis: the origin of life, youtube.com, uploaded 12 May 2023; starting at 15:30.
10. Ref. 9, starting at 14:00: "As that happens the amyloids that are more stable will stick around for longer than the ones that are less stable and will continue to incorporate new amino acids and elongate themselves". Actually, the more stable amyloid fibrils become insoluble. And the way the experiments were designed, only as many a*rtificially activated* amino acids could be added so as to match the longer templating peptide (i.e., one to three amino acids); they don't just "continue to incorporate new amino acids".

11. Ref. 9, starting at 13:20: "All of the building blocks that go into the formation of amyloids have all been shown to be naturally occurring". This is not true. The key building blocks were homochiral peptide templates, which do not form naturally. In addition, these were almost always built from amino acids not believed to have been available prebiotically.
12. Ref. 9, starting at 13:20: "amyloids being formed with essentially random sequences". This is incorrect. β sheets require precise combinations of amino acids which are also homochiral. And a vast number of the *same* sequences is needed to form amyloid fibrils.
13. Chu, X.-Y. and Zhang, H.-Y., prebiotic synthesis of atp: a terrestrial volcanism-dependent pathway, *Life* **13**:731, 2023.
14. Ref. 9 starting at 13:20: the presence of pH gradients in hydrothermal vents in hydrothermal vents is presented as established fact instead of mere imagery.
15. Russell, M.J., Daniel, R.M., and Hall, A.J., On the emergence of life via catalytic iron-sulphide membranes, *Terra Nova* **5**:343–347, 1993.
16. Jackson, J.B., Natural pH gradients in hydrothermal alkali vents were unlikely to have played a role in the Origin of Life, *J. Molecular Evolution* **83**(1–2):1–11, 2016.
17. Russell, M.J. *et al.*, The drive to life on wet and icy worlds, *Astrobiology* **14**(4)308–343, 2014.
18. The ΔG value depends on the concentration of Mg^{2+} cations, which stabilize the ATP molecule.
19. Standard Gibbs free energy of ATP hydrolysis, bionumbers.hms.harvard.edu,
20. Rosing, J. and Slater, E.C., The value of ΔG° degrees for the hydrolysis of ATP, *Biochimica et Biophysica Acta* **267**(2):275–290, 1972.
21. Cooper, G.M., Metabolic energy—the cell; in: *The Cell: A molecular approach*, 2nd edn, Sinauer Associates, Sunderland, MA, 2000.
22. Azam, H.M., Alam, S.T., Hasan, M. *et al.*, Phosphorous in the environment: characteristics with distribution and effects, removal mechanisms, treatment technologies, and factors affecting recovery as minerals in natural and engineered systems, *Environmental Science Pollution Research* **26**:20183–20207, 2019.
23. Linsy, P. *et al.*, Distribution and diagenesis of phosphorus in the deep-sea sediments of the Central Indian Basin, *J. Geophysical Research: Oceans* **123**(11):7963–7982, 2018.
24. Proteins and nucleic acids: information carriers, ox.ac.uk, 20 Feb 2024.
25. Levy, M., and Miller, S.L., The stability of the RNA bases: implications for the origin of life, PNAS **95**(14):7933–7938, 1998.
26. Larralde, R., Robertson, M.P., and Miller, S.L., Rates of decomposition of ribose and other sugars: Implications for chemical evolution, PNAS **92**:8158–8160, 1995.
27. Shapiro, R., The prebiotic role of adenine: a critical analysis, *Origins of Life and Evolution of Biospheres* **25**:83–98, 1995.
28. Wimmer, J.L.E., Kleinermanns, K., and Martin, W.F., Pyrophosphate and irreversibility in evolution, or why ppi is not an energy currency and why nature chose triphosphates, *Frontiers in Microbiology: Microbial Physiology and Metabolism* **12**, 2021.
29. Kottur, J. and Nair, D.T., Pyrophosphate hydrolysis is an intrinsic and critical step of the DNA synthesis reaction, *Nucleic Acids Research* **46**(12):5875–5885, 2018.
30. Truman, R. *et al.*, Trivializing information, a cornerstone of reality (in press).
31. Truman, R., Amyloids are not sources of information, *J. Creation* **38**(1):15–18, 2024.
32. Gitt, W., Scientific laws of information and their implications—part 1, *J. Creation* **23**(2):96–102, 2009.
33. Gitt, W., Implications of the scientific laws of information—part 2, *J. Creation* **23**(2):103–109, 2009
34. Kazlauskas, D., Krupovic, M., Guglielmini, J., Forterre, P., and Venclovas, Č., Diversity and evolution of B-family DNA polymerases, *Nucleic Acids Research* **48**(18):10142–10156 2020.
35. Jordan, S.F., van Zuilen, M.A., Rouillard, J., Martins, Z., and Nick Lane, Prebiotic membrane structures mimic the morphology of purported early traces of life on Earth, *bioRxiv* 2023.11.03.565097.
36. Thomas, J.A. and Rana, F.R., The influence of environmental conditions, lipid composition, and phase behavior on the origin of cell membranes, *Origins of Life and Evolution of Biospheres* **37**:267–285, 2007.
37. Jackson, J.B., Ancient living organisms escaping from, or imprisoned in, the vents? *Life (Basel)* **7**(3):36, 2017.
38. Lane, N. and Martin, W.F., The origin of membrane bioenergetics, *Cell* **151**:1406–1416, 2012.
39. Axe, D.D., Estimating the prevalence of protein sequences adopting functional enzyme folds, *J. Molecular Biology* **341**(5):1295–1315, 2004.
40. Axe, D.D., The case against a Darwinian origin of protein folds, *BIO-Complexity* **1**:1–12, 2010.
41. Cheng, C., Fan, C., Wan, R., Tong, C., Miao, Z., Chen, J., and Zhao, Y., Phosphorylation of adenosine with trimetaphosphate under simulated prebiotic conditions, *Origins of Life and Evolution of Biospheres* **32**:219–224, 2002.
42. Moeller, C., Schmidt, C., Guyot, F., and Wilke, M., Hydrolysis rate constants of ATP determined in situ at elevated temperatures, *Biophysical Chemistry* **290**:106878, 2022. See also EGU21-3419_presentation-h318776.pdf, copernicus.org.
43. Ochromowicz, K. and Hoekstra, E.J., ATP as an indicator of microbiological activity in tap water, European Commission Directorate-General, Joint Research Centre, EUR 22157 EN, 2005.

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.*

Alan White *has a bachelor of science degree in chemistry from the University of Tennessee, and a Ph.D. in synthetic organic chemistry from Harvard University. Alan worked in an industrial setting for 30 years in the fields of organic chemistry, biochemistry and polymer chemistry during which time he was granted 45 US patents and coauthored 18 publications. He is currently retired, but continues to speak and write on creation science*

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.*

Mendelian speciation: part 3—fixation and reproductive isolation

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

Mendel's law of exponential trait combinations reveals how pre-existing genetic information, both expressed and latent, can produce a large number of phenotypic variants. Heterozygous individuals freely mate among themselves, and highly variable species arise. This meiotic process of global genomic change, however, also leads to loss of heterozygosity, and gene fixation, and is an efficient mechanism of speciation. Reproductive isolation accompanies fixation, and progeny are constrained in groups of separated, less variable, individuals that produce unique species. Mendelian speciation gradually gives rise to genetic families of related species. It is clearly consistent with plants and animals being created after their kind.

Mendel's Law of Exponential Trait Combinations (he called it *das Gesetzt der Combinirung der differirenden Merkmale*[1]) reveals how the phenotypic diversity of species within a genetic family can arise within relatively few generations based on pre-existing genetic programs. Meiosis causes the profuse recombination. But how does reproductive isolation contribute to the emergence of species?

In the first two parts of this series[2,3] it was shown that living organisms have an enormous latent (hidden) reservoir of genetic information and that the processes created to produce variation can result in their expression within relatively few generations. This potential for variation provides for an exponentially large number of trait combinations within each genetic family (basic type/baramin), see figure 1. But how do new species arise from this diversity? How does reproductive isolation and thus speciation occur? Are there examples in nature that demonstrate dynamic speciation and reproductive isolation?

This third paper looks at the consequence of Mendelian speciation over a series of generations. It looks at the mathematics of heterozygosity loss and of homozygosity fixation. It examines the role of reproductive isolation and how this plays a crucial role both in the production of new species and in their persistence. The difference between genetic families and derivative species is discussed and how these natural processes can be understood in terms of the biblical claims about organisms and their kinds.

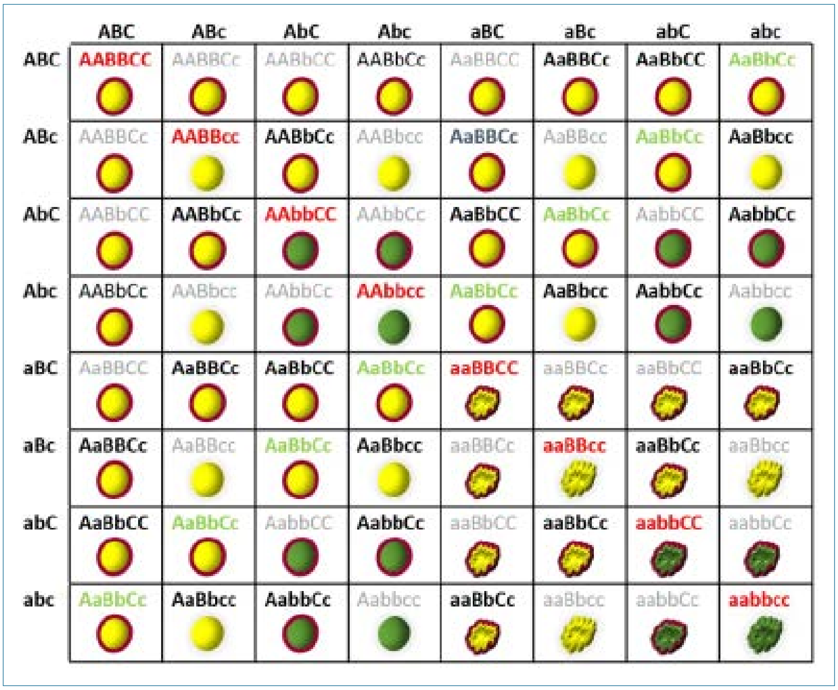
Fixation and global genotypic change

Figure 1 displays a Punnett square of a triple-heterozygous self-cross that obeys Mendelian rules. The lagging diagonal (top right to bottom left, green text) displays the genotype and phenotype of the triple heterozygote. As shown, this triple heterozygote can give rise to eight different phenotypes, all eight of which are displayed down the leading diagonal (top left to bottom right, red text) of the figure, together with all eight unique triple-homozygous genotypes. The other phenotypes have reduced variability: double-heterozygote genotypes (dark grey text) and single-heterozygote genotypes (light grey text). Self-crosses between triple heterozygotes give rise to any of the phenotypes and genotypes. Self-crosses between triple homozygotes, however, only give rise to the same triple homozygotes. Homozygosity permanently fixes genes. This fixing of homozygosity, or loss of heterozygosity (Mendel referred to the process as *das Entwicklungsgesetzt*, the law of population development) relentlessly drives populations to become entirely homozygous. However, which one of the various possible pan-homozygous alternatives arises is entirely arbitrary. The process, called 'random genetic drift', resulting in complete loss of heterozygosity, is central to the field of population genetics.[4]

These Punnett squares are very simplified examples. Characters and traits are typically encoded by a number of genes, each of which is regulated by a variety of genetic processes. The proteins and protein interactions that eventually give rise to the traits can be complex. This all enhances the potential for genetic variation. However, such extensive details detract from the simple take-home message.

We use the generic term *gene* to refer to a unit of heredity which gives rise to the alternative traits of a character. A gene in this sense can be composed of multiple genetic elements. Mendel referred to these units of heredity, A, a, B, b, *etc.* as elements[4]. He did not know their material composition but deduced that they came in pairs, one from each parent. We refer to each variant gene as an *allele* (each located on a different homologous chromosome).

The differences between the alleles can be caused by a plethora of possible sequence differences in the protein coding regions of the gene, or the regulatory regions of the gene, or differences in regulatory RNAs (e.g., miRNA and lncRNA), or differences in regulatory proteins (e.g.,



	ABC	ABc	AbC	Abc	aBC	aBc	abC	abc
ABC	AABBCC	AABBCc	AABbCC	AABbCc	AaBBCC	AaBBCc	AaBbCC	AaBbCc
ABc	AABBCc	AABBcc	AABbCc	AABbcc	AaBBCc	AaBBcc	AaBbCc	AaBbcc
AbC	AABbCC	AABbCc	AAbbCC	AAbbCc	AaBbCC	AaBbCc	AabbCC	AabbCc
Abc	AABbCc	AABbcc	AAbbCc	AAbbcc	AaBbCc	AaBbcc	AabbCc	Aabbcc
aBC	AaBBCC	AaBBCc	AaBbCC	AaBbCc	aaBBCC	aaBBCc	aaBbCC	aaBbCc
aBc	AaBBCc	AaBBcc	AaBbCc	AaBbcc	aaBBCc	aaBBcc	aaBbCc	aaBbcc
abC	AaBbCC	AaBbCc	AabbCC	AabbCc	aaBbCC	aaBbCc	aabbCC	aabbCc
abc	AaBbCc	AaBbcc	AabbCc	Aabbcc	aaBbCc	aaBbcc	aabbCc	aabbcc

Figure 1. A Mendelian triple-heterozygous self-cross displaying the phenotypic ratio 27:9:9:3:9:3:3:1. All eight phenotypes are displayed along the Punnett square's leading diagonal. Mendel conducted most of his experiments on garden peas, *Pisum sativum* (now *Lathyrum oleraceus*[5]). Three characters are displayed: A, seed shape; B, seed (endosperm) colour; and C, seed-coat colour (also causes purple and white flowers). Smooth, yellow seeds with purple seed-coats are dominant traits; wrinkled, green seeds with white coats are recessive traits. Mendel also studied three characters in hybrids of the Common Bean, *Phaseolus vulgaris*, with corresponding results.

transcription factors). They can be caused by transposons, or regions of DNA possessing alternative epigenetic regulatory methylation patterns. Each phenotypic character comprises a minimum number of molecular parts and is irreducibly complex. Many of their parts, however, can be modified and so give rise to alternative traits. Such characters would require far too many beneficial mutations to simply have arisen by chance. Such irreducible complexity can only realistically be explained as the product of design. Furthermore, only intensive research will eventually reveal how all the many parts and their interactions give rise to each of the various characters.

If four genes had been included in the Punnett square, it would be four times larger and display 16 different phenotypes. The number of possible phenotypes increases exponentially with the number of genes. Mendel described meiosis. He studied seven characters representing seven genes, and he observed all 128 different phenotypes.[1] Meiosis automatically gives rise to a great number of fixed phenotype alternatives (because of the homologous chromosome disjunction that occurs during anaphase I), resulting in a great number of potential species. Of fundamental significance to speciation is the fact that the resulting phenotypes vary in numerous different characters, from numerous different genes (because of the recombination that occurs during both prophase I and metaphase I). Meiosis is a genomically global mechanism; it is a polygenic process.

As discussed in part 2 of this series, Mendel recognized that well-defined species differ in many characters.[3] Mendelian speciation inexorably gives rise to a plethora of multi-character species. It is important to understand that although mechanisms of genetic change, such as mutation, transposition, and epigenetics, give rise to new traits (phenotypes), by modifying pre-existing characters, these are only very rarely granted the status of new species. This fact is most readily appreciated in humans, *Homo sapiens*, where many heritable diseases and phenotypic differences resulting from such genetic change have been observed, but never any species other than human, *Homo sapiens*.

Reproductive isolation

Mendelian speciation requires latent phenotypic information, loss of heterozygosity, but also reproductive isolation. The latter prevents mating between select individuals, which would otherwise result in hybridization, re-establishing heterozygosity and disappearance of recessive phenotypes.

For multiple species to arise through loss of heterozygosity, reproductive isolation must be a stable process. *Allopatric (geographic) speciation*, caused by spatial separation on islands or due to mountain ranges, is a single event that separates two subpopulations and which maintains isolation. As a result, two distinct phenotypes (or species) can arise due to random loss of heterozygosity, giving rise to alternative combinations of homozygous dominant and recessive traits.

Figure 2 illustrates how initially genetically heterozygous populations, which become reproductively isolated, can become more homozygous, leading to new species (smaller circles in figure 2. Hybridization can reverse the trend towards loss of heterozygosity. If natural selection (vertical arrows) occurs (in the third and fourth generations), the populations with the most favourable constellation of traits (darker shading in figure 2) are best adapted, fittest, and survive best.

The importance of reproductive isolation is easily overlooked, despite being fundamental to speciation. Mendel included a table describing how it works.[1,6] He illustrated the single two-trait character (or gene) situation. Organisms are typically diploid, their traits encoded twice, once in the paternally derived chromosomes, and once in the maternally derived chromosomes. Therefore, single-character organisms possess one of three possible genotypes: AA, Aa, or aa (which Mendel wrote as A, Aa, and a).

To begin with (generation P), all his plants were heterozygous; Aa. Table 1 shows what happens at each subsequent generation, F1–F4, (assuming each plant produces 4 viable seeds). Homozygous organisms have all homozygous traits. Here, there are two possible types: AA or aa. Heterozygous organisms have non-identical traits; i.e., Aa. If they self-cross, which Mendel's peas did, homozygous organisms will give rise to 4/4 offspring with identical homozygous genotypes; heterozygous organisms will give rise to all three genotypes in a 1:2:1 ratio. *With each successive generation, the homozygous organisms (highlighted in bold) overwhelm the growing population at an exponential rate. If reproductive isolation is maintained, the two homozygous phenotypes become two unique, separate species.*

The two gene, or double two-trait character situation gets quickly (exponentially) more complex. Such double-character organisms possess one of nine possible genotypes: AABB, AABb, AAbb, AaBB, AaBb, Aabb, aaBB, aaBb, or aabb. Table 2 shows what happens at each generation. Doubly homozygous organisms have two homozygous traits. There are four here: AABB, AAbb, aaBB, and aabb. Heterozygous organisms can be singly or doubly heterozygous: AABb, AaBB, Aabb, aaBb, or AaBb. If they can self-fertilize (which Mendel's peas could) doubly homozygous organisms will give rise to offspring with identical homozygous genotypes. Singly heterozygous organisms give rise to three genotypes in a 1:2:1 ratio, and doubly heterozygous organisms give rise to all nine genotypes in a 1:2:1:2:4:2:1:2:1 ratio.

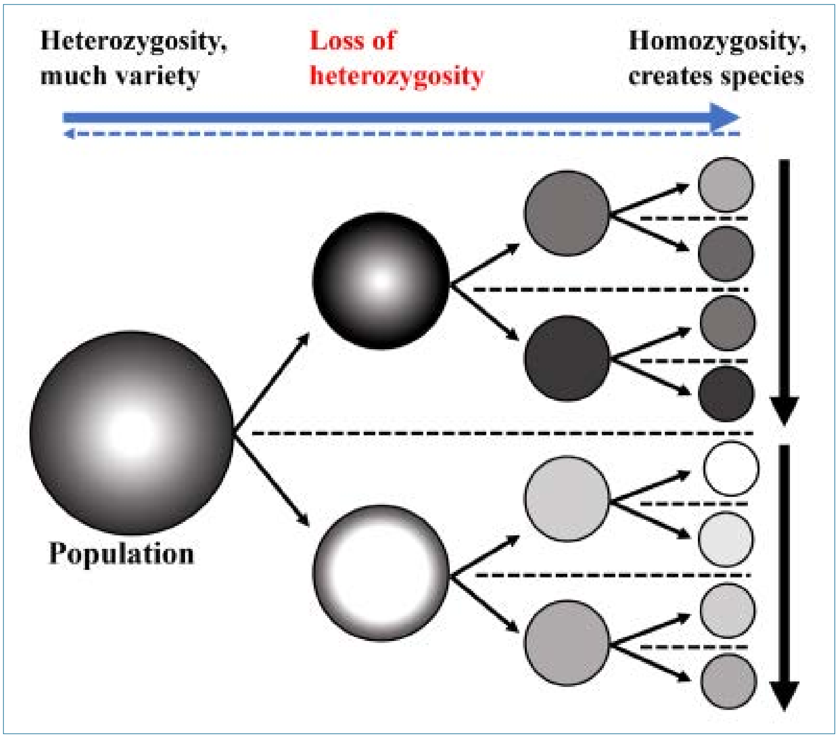


Figure 2. Loss of heterozygosity, reproductive isolation, and speciation. Populations are shown as circles. Each column of circles represents a consecutive generation. Over time, populations become reproductively isolated (dashed lines). Initially, the populations are genetically heterozygous (highly graded shading). However, with each successive generation they lose more and more heterozygosity, due to genetic drift, and eventually become homozygous, or fixed. At this point they form genetically distinct groups (uniform shading).

Table 1. Generational expectation of offspring number and genotype ratios for self-crossing (reproductively isolated) single-character organisms. The single character has two traits: one, A, is dominant; the other, a, is recessive. Offspring can be AA, Aa, or aa.

	Offspring number			Pop. size	Genotype ratios		
Generation	**AA**	**Aa**	**aa**		**AA**	**Aa**	**aa**
F1	**1**	2	**1**	4	**1**	2	**1**
F2	**6**	4	**6**	16	**3**	2	**3**
F3	**28**	8	**28**	64	**7**	2	**7**
F4	**120**	16	**120**	256	**15**	2	**15**
F(n)				4^n	$\mathbf{2^n-1}$	2	$\mathbf{2^n-1}$

Table 2. Generational expectation of genotype ratios for self-crossing (reproductively isolated) two-character organisms. Both characters display two traits: dominant A or B, recessive a or b.

Generation	**AABB**	AABb	**AAbb**	AaBB	AaBb	Aabb	**aaBB**	**aaBb**	**aabb**
F2	1	2	1	2	4	2	1	2	1
F3	9	6	9	6	4	6	9	6	9
F4	49	14	49	14	4	14	49	14	49
F5	225	30	225	30	4	30	225	30	225
F(n)	$(2^n-1)^2$				4	$2\bullet(2^n-1)$			

To find out what happens to a population of such plants over time, the simplifying assumption is made that each plant produces exactly 16 viable seeds. *With each successive generation the doubly homozygous organisms (highlighted in bold) overwhelm the growing population at an 'exponential-squared' rate. As long as reproductive isolation is maintained, the doubly homozygous offspring quickly become four unique, separate species.* (In table 2, for reasons of space and clarity, only offspring ratios are given; and general formulas for the genotype ratios (for the *double* and single homozygotes) are given only once).

Although the double-heterozygote ratios stay a constant four, *the doubly homozygote ratios* exponentially increase. (These ratios are conveniently simplified in this example; in reality, at each generation the fraction of double or pan-heterozygotes decreases at the rate $1/2^{ng}$; and *the total fraction of all pan-homozygotes increases at the rate* $[(2^n-1)/2^n]^g$, where n is the number of generations and g is the number of genes—here g is 2.)

This rapid increase in pan-homozygous phenotypes, which represents the origin of four separate species, only takes place in the presence of reproductive isolation. If reproductive isolation is not in place, all plants can cross with all plants (the pan-cross situation) and the genotype ratios remain identical at each generation; e.g., with one two-trait character = 1:2:1; with two two-trait characters = 1:2:1:2:4:2:1:2:1. When no reproductive isolation is in place heterozygosity stays high [$= 1 - (0.5)^g$], and no speciation occurs. Theoretically, however, this would require a population of infinite size.

Actual populations are always finite in size, and the smaller the population, the faster it loses heterozygosity. This relentless fixation, a process called random genetic drift,[4] occurs quickly in Mendel's pea plants because they are self-fertilizing. It is more typical, however, for species to reproduce sexually. This requires at least two individuals, and under these circumstances heterozygosity is lost, but more slowly. In small groups of organisms (demes) heterozygosity is lost even more slowly, and in large populations heterozygosity is lost but can be maintained for numerous generations. Eventually, random genetic drift always leads to fixation, but this can take many generations. In large populations, considerable genetic variation can definitely be present. A fifth paper discussing random genetic drift as it relates to Mendelian speciation is currently in preparation.

The chronology of speciation and speciation exhaustion

It has been suggested that fixation would lead to an apparent paradox, because no further speciation should be possible: speciation exhaustion. When Mendelian speciation occurred in the past, at first there would have been rapid production of species, but gradually, as more and more heterozygosity was lost and species became fixed, speciation would have come to an end. Today, certainly, much speciation appears to have run its course, and many species are stable. Yet new species sometimes arise. How is this possible?

At least three mechanisms are known. First, speciation occurs as a result of interspecies hybridizations, when reproductive isolation is lifted and heterozygosity is partially restored, as discussed in part 1 of this series.[2] Second, speciation could be considered to have occurred if sufficient latent genetic variation were activated or traits were modified (e.g., by epistatic, epigenetic, or transpositional mechanisms, as discussed in part 2 of this series[4]). Third, speciation could also occur in the presence of reproductive isolation. In large populations with significant residual heterozygosity, if a deme (small group) undergoes a bottle-neck event, becoming reproductively isolated via physical isolation or expression of a veritable plethora of pre-zygotic and post-zygotic barriers,[7] loss of heterozygosity and speciation would proceed quickly and independently in the deme. This process has been observed on islands and in large lakes.[7]

When strict reproductive isolation is in place, as tables I and II confirm, at each generation heterozygosity decreases (is lost). Homozygosity, however, increases, and all the more so as the number of characters (genes) increases. *This is speciation in a nutshell. Reproductively isolated organisms with unique combinations of homozygous dominant and recessive traits (involving multiple genes) are typically considered separate species.*

A notable example of speciation is observed in the six abalone species found along the Pacific coast of California. They share the same marine environment, they freely release their gametes into the sea, and they are able to produce hybrids. Nevertheless, they remain reproductively isolated because of sympatric speciation.[8] This is a genetic process caused by gradual but progressive alteration of the interaction site between a ligand from the sperm cell and its receptor on the oocyte. In eukaryotes, sperm must locate, attach to, and fuse with the egg. The structures of the egg envelope are highly variable and taxon-specific, as shown in figure 3.[9] Egg–sperm interaction serves both for reproductive isolation and to assess the reproductive compatibility of the two parents. It is a major cause of sympatric speciation.

As in allopatric speciation, in sympatric speciation subpopulations are separated, and altered phenotypes (or species) emerge through the resulting loss of heterogeneity. The changes occur continuously and result in the continuous generation of subpopulations with unique phenotypes, which have the potential to become separate species.[10]

Buri demonstrated that loss of heterozygosity occurs randomly when subpopulations remain reproductively isolated.[11] A closer look at nature reveals a wealth of behavioural, morphological, or genetic mechanisms, which maintain reproductive isolation between species, thereby preserving their unique combinations of traits. If not, hybrids arise, and sometimes small species can even go extinct, merging into other species through hybridization.[12,13]

A species' current reproductive isolation may have been caused just once in the past by a single mechanism. However, the ancestors of an emerging species may have experienced the effects of various mechanisms of reproductive isolation. Some may have arisen through allopatric speciation, others through sympatric speciation.

Isolation mechanisms can be genetic, encoded in the genome of a species. These can affect a species' phenotype, structure, behaviour, or other features. The nature of previous isolation mechanisms determines to what extent genetic variability is still present. Loss of heterozygosity can be minor or significant, as mentioned in part 2 of this series. Considerable potential for variation, and thereby adaptability to environmental factors, remains in the case of the grove snail, *Cepaea nemoralis*, shown in figure 4, and in the wood tiger moth, *Arctia plantaginis*.

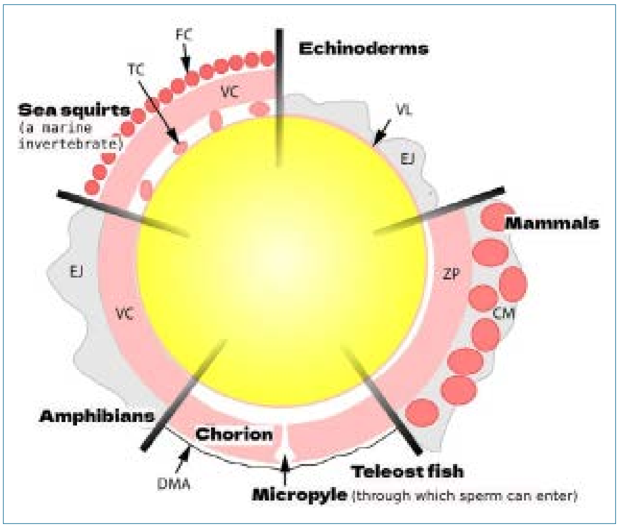


Figure 3. The structures of the outer layers of the egg complex in different groups of animals. The egg is displayed in yellow. Its outer extracellular layer, the egg envelope, shown in pink and grey, varies between animal taxa and forms one of various selective barriers preventing fertilization by incompatible sperm. Abbreviations: CM Cumulus protective layer (*corona radiata*); DMA aqueous slime zone; EJ egg jelly; FC follicular cells; TC test cells; VC vitelline shell; VL vitelline layer; ZP zona pellucida.[9]

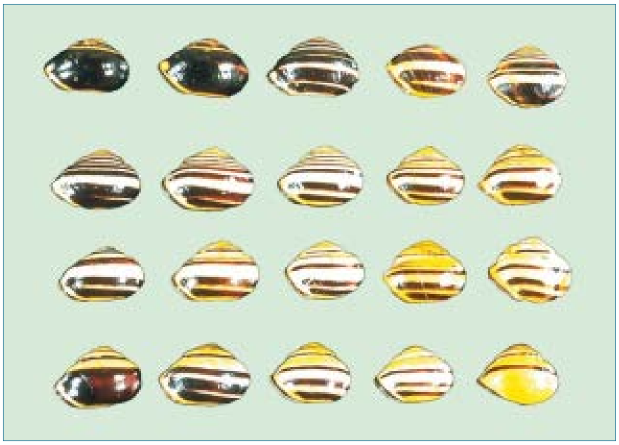


Figure 4. The grove snail, *Cepaea nemoralis*, is an example of a species which has retained much genetic potential for variability. (From Junker & Scherer 2013, with permission).[14]

Extreme reproductive isolation can lead to significant loss of heterozygosity, preventing the resulting genetically homogeneous species from being able to adapt to new, potentially challenging, environments. Examples of this are known in the cheetah, *Acinonyx jubatus*, and the northern elephant seal, *Mirounga angustirostris*.[15,16]

Difference between family and species

How do Mendel's experiments with plant hybrids help clarify what a species is, and what a family is? Let's assume that an ancestral species had 20 heterozygous genes. This

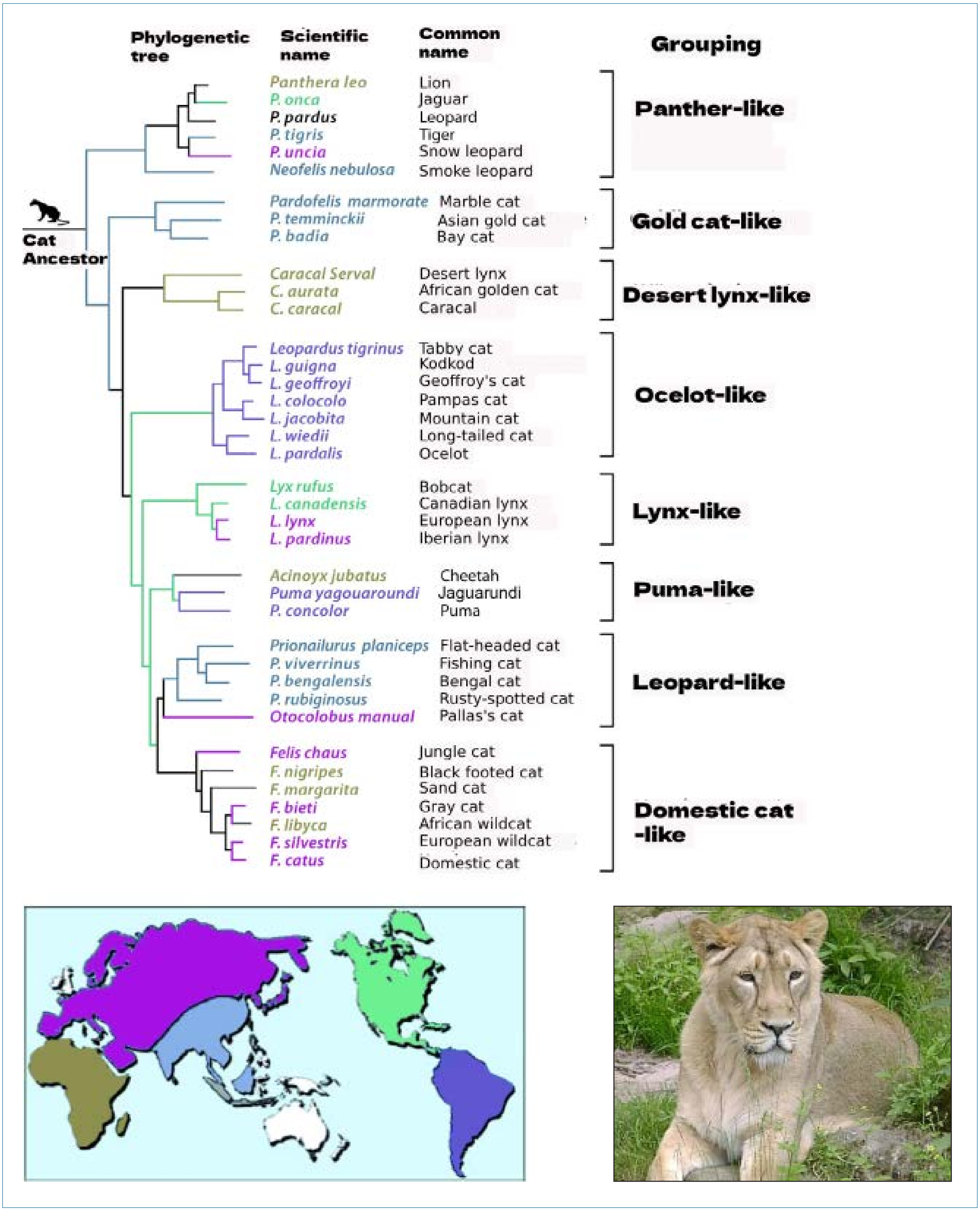


Figure 5. Dendrogram of the cat groups. The end points correspond to a species. The colours link them to the continent(s) they live on. Of all cats, the leopard has the widest geographic distribution, from Africa through southern Eurasia to East Asia. Redrawn from Johnson *et al.*[18] (where additional information such as genetic distance etc. is also available). Inset picture: Female Asiatic lion (*Panthera leo perisca*). (Photo: Edradour, CC BY-SA 3.0; translated and modified by R. Truman using Photopea; photopea.com).

species could theoretically produce more than a million (2^{20} = 1,048,576) unique homozygous trait combinations (phenotypes). Many of these descendants would be assigned to separate species, and even separate genera, because of extensive phenotypic differences.

In this limiting case of just 20 heterozygous genes, these million different phenotypes represent a basic limit to the potential phenotypic diversity of the ancestral species. In theory, all the descendants belong to the same species, the pan-heterozygous ancestor. However, for practical reasons, due to their significant phenotypic differences and reproductive isolation, they are often classified into separate species and genera within a single overarching genetic family. When reference is made in the Bible to plants and animals being made "after their kind", it is reasonable to equate this reference with the ancestral pan-heterozygous organisms, which are capable of giving rise to a plethora of related descendant species; i.e., after their kind. These differ significantly, but still within genetically defined limits, from their ancestral origin. As such, the Genesis kinds (also called 'baramins') are considered to be these genetic families.

For example, lions, tigers, servals, cheetahs, lynxes, leopards, pumas, and domestic cats are all members of the Felidae family. They likely share a single common pan-hybrid ancestor. Based on the criterion of being able to interbreed, most cat species belong to a single basic type.[17] They share the same characters and the same genes, and form a genetic family as shown in figure 5.

The combinations of constant traits (combinations of homozygous dominant and recessive alleles) are the basis for their classification into unique species and genera.

Similarly, the Birds of Paradise display a spectacular array of amazing phenotypes. DNA sequence studies show that they are all members of the family Paradisaeidae. The ability of most species to hybridize confirms they belong to a single basic type.[19] The fact that the various intergeneric hybrids show similar phenotypes strongly indicates they all descend from a common pan-heterozygous ancestor.[20] The Birds of Paradise are a genetic family.

Conclusions

Mendelian speciation is based on his law of exponential trait combinations. It is an efficient genetic mechanism for the emergence of biological diversity. It is a meiotic process of global genomic change, and because of loss of heterozygosity it leads to polygenic fixation of unique phenotypes. It is a highly effective mechanism of speciation. It is accompanied by reproductive isolation, and the progeny are constrained in groups of separate, less variable, populations. Mendelian speciation eventually gives rise to whole genetic families of related species, completely consistent with plants and animals being created after their kind. Mendelian speciation readily occurs because the genetic information required for speciation is already present in the genomes of ancestral organisms, though usually unseen; i.e., present in a latent state.

A fourth accompanying paper[21] describes fascinating examples of rapid and extensive speciation episodes, 'microevolution on steroids', referred to as 'adaptive radiations'. It examines how Mendelian speciation readily accounts for these extraordinarily impressive examples of natural diversity; attended by, though certainly not requiring any, mutation events.

Glossary

Adaptive radiation: Emergence of many differently adapted species from one ancestral form.

Allele: Variant of the same gene, having a unique nucleotide sequence. When a gene is sequenced; what is almost always meant is that a single allele of the gene was sequenced.

Allopatric speciation: Speciation caused by physical (geographical) separation.

Epistasis: Gene interaction. The action of one gene, called 'epistatic', masks the effects otherwise caused by another gene, called 'hypostatic'.

Gene: The functional unit of heredity. Usually, restricted to a single site in the genome that may then be called its 'locus'. Its variants are referred to as 'alleles'. In his classic paper,[1] Mendel referred to these units of heredity as 'elements'.

Genetic family: A family whose species are characterized by common genetic ancestry. It is similar in concept to a Genesis kind or a baramin. It results from Mendelian speciation.

Genome: An organism's chromosome complement.

Heterozygous: When information for more than one trait of a gene is present in the genome; also, when a gene has two different alleles.

Homozygous: When information for only one trait of a gene is present in the genome; also, when a gene has two identical alleles.

Karyotype: The number and visual appearance of the chromosomes.

Meiosis: Formation of four (usually unique) genomes from a single parental genome when the sex cells develop.

Pan-heterozygous: When all genes are heterozygous.

Pan-homozygous: When all genes are homozygous.

Recessive allele: An allele, the expression of which is suppressed by the effect of a dominant allele.

Recombination: The mixing of portions of homologous chromosomes and the mixing of chromosome sets, during meiosis when the sperm and egg are formed.

Reproductive isolation: Separation of sub-populations, and suppression of gene exchange.

Speciation: When a species splits into two daughter species.

Sympatric speciation: Evolution of new species from an ancestral species when both continue to inhabit the same geographic location.

Translocation: Rearrangement of chromosome segments.

Zygote: A fertilized egg cell resulting from the fusion of a sperm and an egg cell.

References

1. Mendel, G., Versuche über Pflanzenhybriden, *Verh. Naturforschung Vereins Brünn* **4**:3–47, 1866. Republished by Vieweg+Teubner Publishers (Springer Vieweg Verlag), Wiesbaden, 1970. The quote is correct, although the spelling would be different in modern German.
2. Crompton, N.E.A., Sprague, T., Truman, R., and Junker, R., Mendelian speciation: part 1— what is the abundant source of significant biodiversity, *J. Creation* **37**(3):110–120, 2023.
3. Crompton, N.E.A., Sprague, T., Truman, R., and Junker, R., Mendelian speciation: part 2—latent genetic information, *J. Creation* **38**(1):77–86, 2024.
4. Hedrick, P.W., *Genetics of Populations*, 4th edn, Jones and Bartlett Publishers, 2011.
5. Schaefer, H., Hechenleitner, P., Santos-Guerra, A., Menezes de Sequeira, M., Pennington, R.T., Kenicer, G., and Carine, M.A., Systematics, biogeography, and character evolution of the legume tribe Fabeae with special focus on the middle-Atlantic island lineages, *BMC Evolutionary Biology* **12**, article 250, 2012.
6. Mendel, ref. 1, p. 18.
7. Futuyma, D.J., *Evolution*, 3rd edn, Sinauer Associates, 2013.
8. Crompton, N.E.A., Die genetische Familie der Halotidiae—Hybridisierung, Fortpflanzungsisolation und sympatrische Artbildung, *Wort-und-Wissen Special Paper* **B-18-2**:1–24, 2018.
9. Mengerink, K.J. and Vacquier, V.D., Glycobiology of sperm–egg interactions, *Glycobiology* **11**(4):37R–43R, 2001.
10. Swanson, W.J. and Vacquier, V.D., The rapid evolution of proteins, *Nature Reviews Genetics* **3**:137–144, 2002.
11. Buri, P., Gene frequency drift in small populations of mutant Drosophila, *Evolution* **10**:367–402, 1956.
12. Wolfe, D.E., Takebayashi, N., and Rieseberg, L.H., Predicting the risk of extinction though hybridization, *Conservation Biology* **15**:1039–1053, 2001.
13. Todesco, M., Pascual, M.A., Owens, G.L., Ostevik, K.L., Moyers, B.T., Hübner, S., Heredia, S.M., Hahn, M.A., Caseys, C., Bock, D.G., and Rieseberg, L.H., Hybridization and extinction, *Evolutionary Applications* **9**:892–908, 2016.
14. Junker, R. and Scherer, S., *Evolution—ein kritisches Lehrbuch*, Wevel Biologie, Gießen, 7th edn, 2013.
15. Dobrynin, P., Liu, S., Tamazian, G., Xiong, Z., Yurchenko, A.A., Krasheninnikova, K., Kliver, S., Schmidt-Küntzel, A., Koepfli, K.-P., Johnson, W., Kuderna, L.F.K., García-Pérez, R., de Manuel, M., Godinez, R., Komissarov, A., Makunin, A., Brukhin, V., Qiu, W., Zhou, L., Li, F., Yi, J., Driscoll, C., Antunes, A., Oleksyk, T.K., Eizirik, E., Perelman, P., Roelke, M., Wildt, D., Diekhans, M., Marques-Bonet, T., Marker, L., Bhak, J., Wang, J., Zhang, G., and O'Brien, S.J., Genomic legacy of the African cheetah, Acinonyx jubatus, *Genome Biology* **16**, article 277, 2015.
16. Abadia-Cardoso, A., Friemer, N.B. Deiner, K., and Garza, J.C., Molecular population genetics of the Northern Elephant Seal *Mirounga angustirostris*, *J. Heredity* **108**:618–627, 2017.
17. Pendragon, B. and Winkler, N., The family of cats: delineation of the feline basic type, *J. Creation* **25**(2):118–124, 2011.
18. Johnson, W.E., Eizirik, E., Pecon-Slattery, J., Murphy, W.J., Antunes, A., Teeling, E., and O'Brien, S.J., The Late Miocene radiation of modern Felidae: a genetic assessment, *Science* **311**:73–77, 2006.
19. Scherer, S., Basic types of life; in: Scherer, S. (Ed.), *Typen des Lebens*, Pascal Verl., Berlin, pp. 11–30, 1993.
20. Crompton, N.E.A., Die Paradiesvögel, ihre Hybriden und die Rolle der sexuellen Selektion, Wort-und-Wissen, 2020.
21. Crompton, N.E.A., Sprague, T., Truman, R., and Junker, R., Mendelian speciation: part 4— Adaptive radiations, *J. Creation* **38**(2):104–111, 2024.

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.*

Mendelian speciation: part 4—adaptive radiations and *cis*-evolution

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

When an abundance of new species arises in a restricted geographical location, a logical consequence of Mendelian speciation, the process is referred to as an 'adaptive radiation'. A number of well-researched examples confirms that adaptive radiations occur far more quickly than can be explained by random mutations. All the various species that arise over time and in various geographic locations via Mendelian speciation, including any and all adaptive radiations, give rise to a single genetic family. The range of variation possible, from all potential combinations of pre-existing genetic information, defines phenotypic limits to such genetic families. Biodiversity observed within these genetically constrained, yet modifiable, limits is called, here, '*cis*-evolution'. These genetic families are considered equivalent to Genesis kinds or baramins. Mendelian speciation is consistent with straightforward reading of Genesis. It provides an eminently reasonable and entirely satisfactory solution to rapid speciation as required by a young-earth understanding of origins.

This fourth paper looks at the consequence of Mendelian speciation over a series of generations. It describes adaptive radiations observed in nature and how these result from poly-heterozygous ancestors. They are a natural consequence of Mendelian speciation. The paper also clarifies the difference between *cis*-evolution, speciation radiations observed to occur within genetic families (baramin) based on pre-existing genetic programs, and *trans*-evolution, speciation radiations claimed to occur between genetic families (baramin) but for which no realistic genetic mechanisms are currently known.

Adaptive radiations rely on pre-existing genetic programs

Why is loss of heterogeneity so important for speciation? If only complete heterogeneity were present, only the pan-dominant phenotype would be seen, as discussed in part 2 of this series.[1] All those potential phenotypes, resulting from combinations of recessive and hypostatic trait expression, would be invisible. Loss of heterozygosity must occur so that the enormous wealth of phenotypic potential that otherwise lies latent in a genome can be revealed.

Mendelian speciation gives rise to many new phenotypes (potential species). As few as 10 two-trait characters allow for the emergence of a thousand ($2^{10} = 1,024$) distinct phenotypes. Very few vertebrate families show so much variation (or species). Most mammalian families have fewer than 100 distinct species. Furthermore, Mendelian speciation can give rise to all these new species within relatively few generations. If these are maintained in populations, separated by reproductive isolation, the result is a sudden burst of species referred to as an 'adaptive radiation'.

Would all the possible variations ever be observed in nature? That is very unlikely. Nevertheless, dramatic examples of extensive variability and speciation are seen in adaptive radiations. In molecular sequencing studies, these have been confirmed to arise from existing genetic information, as will be described below. Remarkable examples include:

- the picture-wing Drosophilas (sometimes called the birds of paradise of the insect world) on Hawaii
- the silversword plant group also on Hawaii
- the cichlids in the Great East African Lakes, and
- the finches on the Galápagos islands, and also on Hawaii.

A question that immediately comes to mind when studying adaptive radiations is, why do some plants and animals display prominent adaptive radiations, whereas others, in similar situations, display little or no speciation? In Hawaii the finches (honeycreepers) underwent a significant diversification, producing 20 genera and 51 species, but the thrushes and owls produced very few; four species and one subspecies, respectively. Adaptive radiations result from Mendelian speciation; therefore, an immediate answer is found in the degree of heterozygosity carried by any founder species. Those species with significant numbers of heterozygous genes can give rise to many new species, but those with few heterozygous genes can only give rise to a few.

Radiation of *Drosophila*

The nearly 1,000 *Drosophila* species native to Hawaii are believed to have arisen from a single ancestral species. Carson analyzed all the chromosome structures (karyotypes)

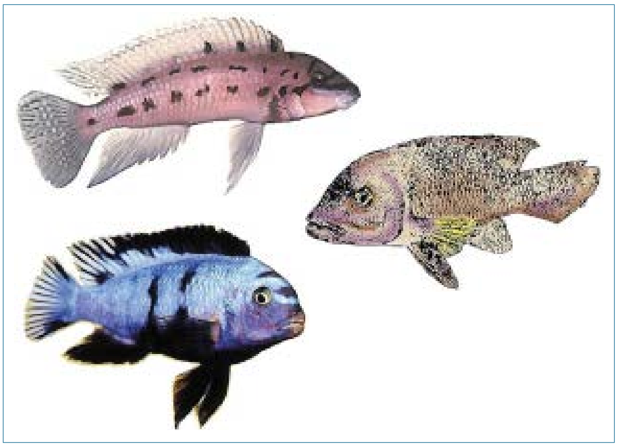


Figure 1. Examples of the diversity of cichlids in East African lakes. From above: *Pseudotropheus saulosi, Lamprologus* spec. and *Chalinochromus ndobhoi*.

of the existing species in the picture-winged Drosophila group.[2] Recognizing that chromosome inversions had occurred allowed him to trace the speciation events back to the original founder karyotype—possibly from South America.

The inversions *per se* do not explain how the phenotypic changes came about.[3] It is known that the radiation of the ~112 species in the picture-winged group proceeded with relatively few changes in DNA sequence.[4] If this radiation resulted from the loss of heterozygosity, as we propose, then few DNA sequence changes would have been required, merely recombination and homozygosity in new combinations of already existing alleles.

Radiation of silverswords

The silversword plants of Hawaii include trees, shrubs, subshrubs, semi-woody rosette plants, carpet plants, cushion plants, and lianas. This group includes three genera: *Argyroxiphium*, *Dubautia* and *Wilkesia*, and 33 species. Despite the great variety of forms, most can be interbred, and molecular phylogenetic analysis indicates it is a monophyletic species group that arose from a single founder event.

The plants are allopolyploid (their usual chromosome number $n = 14$) and are believed to have arisen from a cross between *Anisocarpus scabridus* ($n = 7$) and *Carlquistia muirii* ($n = 8$), two species of California tarweeds, followed by chromosome number reduction to $n = 14$. Studies of their homeotic flower genes, *ASAP1* and *ASAP 3*, provide strong experimental confirmation for the hybrid origin of these plants.[5]

Detecting translocation events in the different genera allowed researchers to trace back lineages, similar to *Drosophila*.[6] However, these translocation events were not the mechanism responsible for the different morphological forms but only important markers of the divergences that took place.

It is loss of heterozygosity that offers an explanation for the extensive phenotypic diversity observed in this group of plants and for their potential to adapt so extensively and to segregate into a large number of forms. The tetraploid state of the original tarweed cross might have unmasked various genes in the resultant silversword genome, potentially altering the dosage of regulatory proteins, which could have led to the rich phenotypic diversity. Because silverswords derive from tarweeds, they are only a part of a larger family. Their radiation has given rise to a whole taxonomic clade, with either tribe or subfamily status.[7,8]

Radiation of cichlids

Cichlids found in the large East African lakes display significant morphological differences, as illustrated in figure 1. Species vary in length from a few centimetres to about 30 centimetres.

There are many trait reiterations between species in the cichlid radiations in these three lakes, which are understood to arise from pre-existing genetic programs and common ancestry. There is a consensus that dramatically rapid adaptive radiations occurred in these cichlids, serving as examples of sympatric speciation.[9]

The cichlids display a wide variety of specialized anatomical features related to feeding. The range of alternatives includes: feeding on other fish or on their eggs and larvae, chewing off fins, scraping algae, tearing off scales, or crushing molluscs. A multitude of other anatomical features are also observed in these fish in the three lakes: Tanganyika, Victoria, and Malawi.[10]

In Lake Victoria there are >500 cichlid species based on only two lineages.[11] However, in spite of these enormous phenotypic differences, DNA analysis has revealed that the large majority of cichlids in Lake Victoria are descended almost entirely from a single lineage of mouth brooders. Since all the different phenotypes are found in multiple lakes, the obvious explanation is that almost identical species evolved many times independently.[10]

Detailed analysis has led to the conclusion that algae scrapers in Lake Victoria and Lake Malawi diverged independently from an ancestor from Lake Tanganyika, which had more generalized feeding capabilities. The >500 species of cichlids in Lake Malawi were shown to be descended from only a single ancestor.[12]

Significantly, it was shown that the huge variety of cichlids in Lake Victoria must have developed extremely rapidly from a conventional evolutionary point of view. The >500 species contained less genetic variation than the single species *Homo sapiens*. Since palaeoclimatological data is believed to show that Lake Victoria dried out almost completely less than 14,000 radiometric years ago, killing all or virtually all, the fish living there, the huge morphological variety must have arisen since then from a small founder or surviving population.

A similar explosive radiation of cichlids, occurring during a short window of ecological opportunity, appears to have occurred in the dried-up prehistoric Makgadikgadi Paleo Lake and appears to have seeded various river systems in southern Africa.[13]

Recombination and loss of heterozygosity

Given the time constraints, the cause for these very different genotypes could not have been multiple beneficial mutations. But recombining large numbers of alleles (traits) through meiosis provides a very reasonable solution, especially if the alleles had been designed to compatibly work together to generate new biologically relevant features.

Stiassny and Meyer claimed that "The genetic studies thus show that evolution repeatedly discovers the same solutions to the same ecological challenges."[10] However, they found significant divergence in genotypes *within* species but *conservation* of genotypes when comparing more distantly related species. This demonstrated that DNA differences *per se* are not a sufficient explanation for speciation.

Of course, the best way to quickly generate a functional biological response to an environmental challenge is to already have genetic programs available, latent in the genome. This would also provide an elegant explanation for the evolutionary observation of 'convergent evolution' at, and below, the family taxonomic level.

Loss of heterozygosity offers a reasonable explanation for the enormous diversity observed. Sequencing studies were performed on five cichlid fish by Brawand *et al.*, one from each of the larger cichlid lineages, to investigate the origin of diversity.[14] The 75 authors of this paper came to the collective conclusion that pre-existing variation (i.e., pre-existing genetic programs) was important for evolutionary diversification. Commenting on the decisive study, Jiggins confirmed that the data on cichlids complemented work "ranging from sticklebacks to butterflies", demonstrating that adaptive radiations arise "from ancient common variations".

This prediction by Jiggins, based on numerous field studies of species emergence in adaptive radiations, was critically reviewed by Berner and Salzburger. They concluded that

> "… the genomes of these species contain adaptive allelic variants that originated long before the actual species or populations have [sic] formed."[15]

This corresponds exactly to what Mendelian speciation predicts concerning pre-existing genetic programs.

Stiassny and Meyer and others have suggested a very reasonable mechanism for the speciation of cichlids, once variants have arisen. That is, repeated isolation during which new species could form, exquisitely adapted to their local feeding requirements; followed by subsequent contact with other species with which they now could no longer interbreed.[10,16]

Seehausen and his colleagues sequenced 450 whole cichlid genomes, representing 150 species from African lakes.[17] They conclude that the fish in the various major lakes had experienced reproductive isolation and, on rare occasions, were reunited with their ancestral cousins and then separated again, a process they called 'fission-fusion-fission', and a mechanism of hybridization they referred to as "the most powerful engine for the formation of new species and new adaptations".

Their results were presented at an Origins of Adaptive Radiation conference in Honolulu, Hawaii.[18] Pennisi summarized what all the genetic data had revealed:

> "Genomic studies have shown they arose from a few ancestral species in just 15,000 years, a pace that has left researchers baffled about how so much genetic variation could have evolved so quickly. Now, extensive sequencing of cichlids from around Lake Victoria suggests much of it was there at the start, in the cichlids' ancestors."[18]

Evolutionary biologist Dolph Schluter also commented on the results: "It's mind-blowing. All the variation required for speciation is already there in the hybrids."[18]

These researchers clearly acknowledge the existence of pre-existing genetic programs. Latent phenotypic information, expressed through cycles of hybridization and through loss of heterozygosity, explains the origin of the species observed in these adaptive radiations; and clearly confirms the importance of Mendelian speciation.

Past adaptive radiations and family limits to speciation

Darwin's finches (tanager species), the Hawaiian honeycreepers (finch species), and other organisms, e.g., Caribbean Dewlap lizards, have all undergone adaptive radiation. Similar adaptive radiations are observed in the fossil record. These, too, can be readily understood to represent different combinations of constant dominant and recessive homozygous traits and to have arisen by Mendelian speciation within a genetic family. The sauropods are an excellent example (see figure 2).

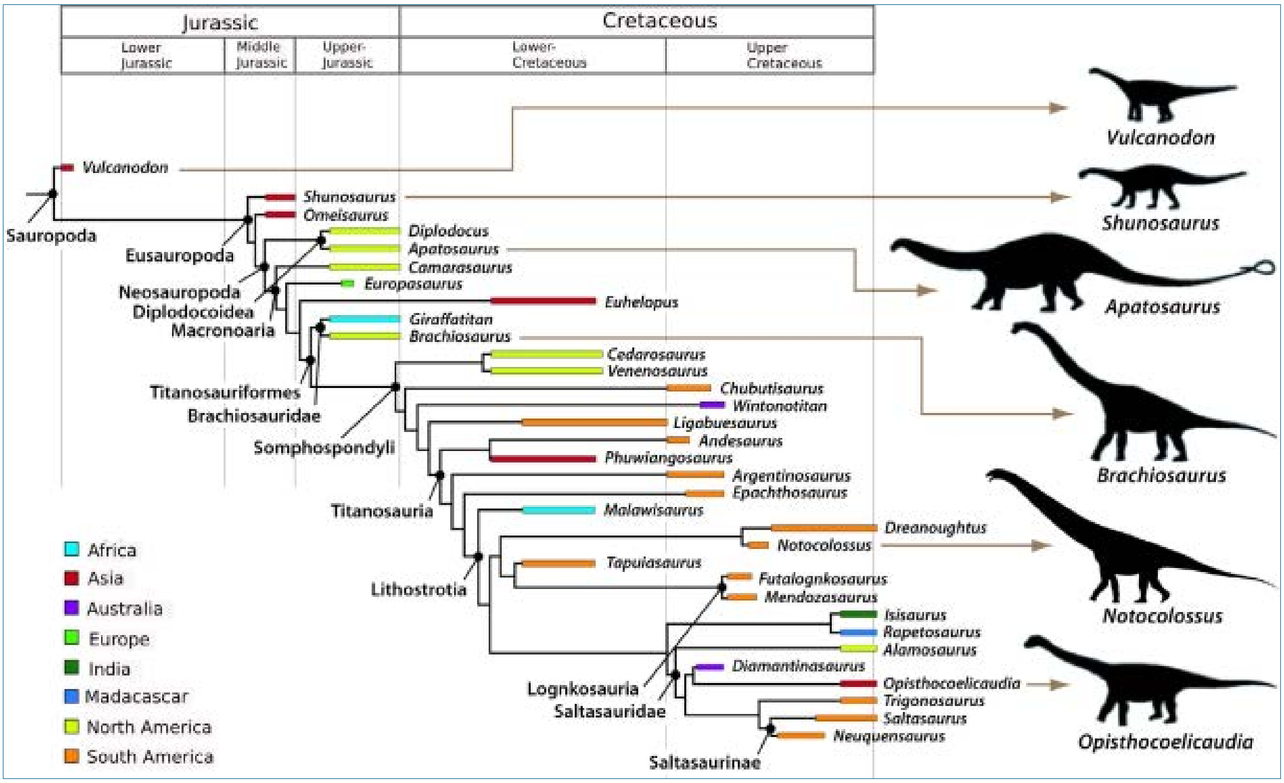


Figure 2. Dendrogram of the Sauropoda. The endpoints correspond to genera. The colours identify the continent(s) where the fossils were discovered. The stratigraphic stages in which the respective groups were found are also shown.

The Sauropoda appear to form a morphogenetic unified family. They certainly appear to have arisen as an adaptive radiation. Their latent pre-existing genetic programs would have segregated according to Mendelian rules, producing this limited but diverse family. Fossils often lack important features necessary for accurate taxonomic classification, and it is possible that the Sauropoda constitute more than one genetic family. However, they certainly appear to reflect a single radiation. Such adaptive radiations can occur quickly, within relatively few generations. There is no genetic reason why vast numbers of generations over tens of millions of years would have been necessary for dinosaur radiations.

Because Mendelian speciation gives rise to significant numbers of species, but fewer with each successive generation, adaptive radiations were originally frequent and extensive, as described in part three of this series.[19] Even in the recent past, however, spectacular adaptive radiations have effortlessly spawned hundreds of new species within plant and animal families based on the expression of genetic information already present in their DNA.

Phenotypic variation and sub-threshold speciation

Towards the end of his scientific treatise,[4] Mendel reflected on how far speciation could vary. If speciation has no boundaries, life could theoretically have originated from a single cell. If speciation has limits, however, not one, but many independent genetic families would exist, and life on Earth can be compared not to one tree, but a forest of many trees. This would be elegant confirmation of what Scripture says about plants and animals being created after their kinds.

Mendel's findings led him to believe there were limits to phenotypic change. He drew attention to experiments by Professor Gärtner, who argued that one species could transform into another, but that there were fixed limits beyond which no further change was possible.[20,21] Mendel was cautious, referring to Gärtner's experiments as confirmation of limited change. However, at the end of his paper, Mendel listed the various species studied by Gärtner, all of which supported this interpretation, and which demonstrated that such an understanding extended well beyond Mendel's own experiments with peas and beans.

Gärtner's argument was correct. Speciation can be shown to result largely from Mendel's Law of Exponential Trait Combinations, and, as this is the case, genetic families have intrinsic phenotypic limits defined by the modifiable potential of their phenotype-defining traits (or pre-existing genetic programs). There are limits to phenotypic change. This all strongly supports a classification of organisms based on a large forest of many separate trees of life, a sylvan taxonomy, with organisms created after their kind.

Because epigenetics and genetic variation is enjoying a prominent position in contemporary genetics, a question often asked is, how does this relate to Mendelian speciation? Epigenetics including structural variants, DNA methylation, and transposable elements, are all important factors in Mendelian speciation. These issues were addressed at a more general level in the second part of this series under the section Transposons and Mendelian speciation.[22]

More than 165 years ago, the importance of genetic variation was emphasized by Darwin in the first chapter, "Variation under domestication", of his famous book.[28] He was familiar with many breeds of pigeon (rock dove), some of them displaying prominent phenotypic differences. Nevertheless, the breeds were, and are, all classified as the same species, *Columba livia*. Similarly, there are many breeds of dog, many of them displaying prominent phenotypic differences, but they are all classified as the same species, *Canis familiaris*. What is observed here is significant genetic variation, but no new species.

A similar observation is made, based on genetic change in humans, which, though extensive, have resulted in no accompanying speciation. Yet another familiar example is seen in the peppered moth, *Biston bistularia*, with its light (typica) and dark (carbonaria) forms. In this case, the genetic change is known to be caused by a retrotransposon,[23] and once again there is no accompanying speciation.

Of very great interest in this respect are the *Brassica oleracea* vegetable crops; such as cauliflower, broccoli, cabbage, kale, Brussels sprouts, kohlrabi, *etc*. Very significant phenotypic differences in these common crop varieties, referred to as 'morphotypes', are immediately apparent. A recent paper[24] examining the genetic basis for these phenotypic differences in more than 18 different crop varieties revealed they result from mostly genomic structural variation, predominantly transposition events. However, when the authors referred to the phenotypic morphological changes, they described them as "the role of intra-specific variation … associated with variation in important traits". They, too, acknowledge that these morphotypes are not separate species. It strongly confirms the general principle: there can be significant phenotypic change resulting from significant genetic variation, yet no accompanying speciation.

Without a doubt, epigenetics, DNA methylation, structural variations, and transposable elements are all important agents of genetic change that give rise to significant phenotypic variation. However, the reason the different dog breeds and the different *Brassica* vegetables are not classified as separate species is that they are caused by a limited number of trait or gene differences. Species, however, differ across the whole genome, and such global genomic change requires mechanisms involving very many genes, not just one or a few.

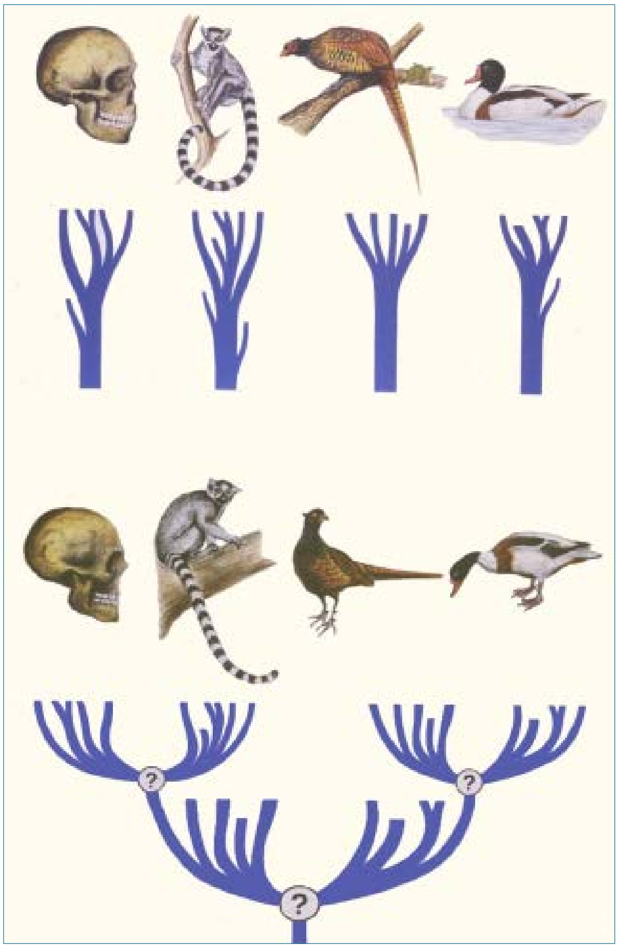


Figure 3. *Cis*-evolution vs *trans*-evolution. In *cis*-evolution (top half) speciation in each genetic family is shown as a separate tree, with the branches being formed by reproductive isolation (though they may sometimes be reunited through hybridization). In *trans*-evolution (bottom half), all genetic families are assumed to have been derived from a common ancestor through random mutations and selection. (From Junker and Scherer, with permission.[25])

Mendelian speciation gives rise to adaptive radiations by employing meiosis and recombination that simultaneously impact the whole genome and not just one or a few select sites. Mutations, transposition, and epigenetics all play a role in Mendelian speciation. On their own, however, they do not give rise to the kind of global phenotypic change needed to warrant classification of organisms as new species. With respect to speciation, they are sub-threshold. The phenotypic changes achieved are insufficient to produce new species. They are also insufficient to produce new characters, which would involve far too many proteins and protein interactions. They are sufficient to produce new traits, and new phenotypic change, and they do this by modifying pre-existing genetic programs.[23] Mendelian speciation is polygenic and is able to account for the characteristically distinctive species observed within genetic families.

Cis-evolution and *trans*-evolution

Worldviews concerning origins collide here. To understand why, one must recognize the difference between evolution *within* genetic families (*cis*-evolution) and evolution *across* genetic families (*trans*-evolution). Only *cis*-evolution is observed in practice, both in the field and in laboratory studies. The difference between *cis*-evolution and *trans*-evolution was discussed in part 2 of this series[1] and is illustrated in figure 3.

Cis-evolution includes examples such as:

- the changes in the light and dark morphs of the peppered moth
- the changes described in Darwin's finches (e.g., in the shape of the beak, body size, or plumage colouration), and
- the diversity observed in the various adaptive radiations listed in the text above.

Cis-evolution occurs because the information required for these changes is already latent in the genome in the form of pre-existing genetic programs. Normally, this information is expressed when meiotic recombination causes loss of heterozygosity. Dominance, epistasis, and also mechanisms associated with transposon activity play a role here.

Pre-existing genetic programs are referred to as 'standing variation' by Brawand *et al*., and as 'ancient genetic variants' by Jiggins[14,26] All three terms express the idea that information for variation that drives adaptive radiations is already present in the genome. The full set of allele pairs of a diploid organism could potentially give rise to an enormous range of phenotypes, one which defines a modifiable but phenotypic limit for a family. The required number of pre-existing genetic programs can be modest. Just 20 biologically important characters, each having two traits (i.e., 40 programs), can generate around 1,000,000 species. If species were defined, on average, by only 10 distinctive trait-pairs (i.e., just 20 programs), families of 1,000 species could theoretically still be produced.

The counterpart to *cis*-evolution, *trans*-evolution, represents unknown, speculative mechanisms that would allow families to transform beyond their phenotypic limits, into other families. Evolutionists believe this type of evolution gave rise to all the separate genetic families, starting from a single common ancestor. A primordial carnivore produced both cats and dogs; and a primordial perissodactyl produced horses, rhinos, and tapirs.

Limits of the genetic family

What kind of mechanism could account for *trans*-evolution? Mendel did not believe that such a mechanism existed. Describing the adaptation of plants to new environments, he wrote:

> "... nothing warrants us to suppose that the tendency to produce varieties is so greatly increased that the species soon lose all independence, and their descendants in an endless series of highly variable forms diverge [our translation.]."[27]

Wallace[28] and Darwin[29] thought otherwise, although neither could provide a feasible mechanism for *trans*-evolution.

Mendelian speciation explains *cis*-evolution but not *trans*-evolution. The only speculated mechanism of *trans*-evolution, mutation/selection, can lead to some *cis*-evolutionary variation, which principally results in loss or impairment or dysregulation of biological function. However, mutations do not explain speciation events, for which extensive phenotypic change is validly necessary. Instead, countless experiments with mutagens confirm the predictably deleterious changes caused by mutations.

Wallace and Darwin recognized that species could give rise to varieties, which, in turn, could give rise to new species. However, they erred in over-extending these findings and assuming that biological change has no limits, which would be a necessary condition if *trans*-evolution is to account for all of life arising from a single tree.

Mendel showed that new biodiversity emerges from latent trait information based on a repertoire of pre-existing traits, and that evolutionary change is essentially confined to this. By all accounts, life is a forest of many trees. This explains why textbooks on evolution give many good examples of *cis*-evolution, but only mere speculation about mechanisms of *trans*-evolution.

Since *cis*-evolution is based on the recombination of alternative traits (pre-existing genetic programs), the logical expectation is that numerous fully functional alternative species will eventually emerge. The same cannot be said for *trans*-evolution as it is based on multiple mutational events that are not designed to produce useful novelty. The logical outcome of multiple mutation events would be a general background of dysfunctional phenotypes.

In contrast, pre-existing genetic programs provide a logical basis for creating the rich diversity of life we see today. Pre-existing genetic programs that give rise to a plethora of healthy and vigorous species is strong evidence that they arose in the mind of an omniscient creator.

Many good examples of *cis*-evolution are known, but only speculation about mechanisms of *trans*-evolution

Mendel's findings open a door onto the enormous phenotypic potential of organisms. This potential is hinted at by several examples:

- In the past, humans tamed the grey wolf, *Canis lupus*, and selected them to produce hundreds of dog breeds with their vast spectrum of phenotypes.

Figure 4. A number of often bizarre forms have been bred from the rock pigeon (far left). (From Junker & Scherer, ref. 25, with permission).

- Man took the common field mustard, *Brassica oleracea*, and, by artificial selection, produced cauliflower, cabbage, broccoli, kale, Brussels sprouts, collards, and kohlrabi.
- Darwin bred the rock pigeon, *Columbia livia*, to produce a number of new breeds, as shown in figure 4. But he clearly over-reached his conclusion after writing: "Under domestication, it may be truly said that the whole organisation becomes in some degree plastic."[30]
- Rose finches appeared in Hawaii and gave birth to the extraordinarily diverse honeycreeper radiation.
- Two precursors (small herbaceous daisy family members, so-called 'tarweeds') of the Hawaiian silversword alliance came from California to the Hawaiian Islands and produced many extremely diverse forms.
- Cichlids entered the great lakes of Africa, and hundreds of new fish species emerged.
- Marine sticklebacks adapted quickly to living in freshwater thanks to a crucial gene variant already present in low percentages in the fishes' marine ancestors.[18]
- Standing variation enabled long-winged beetles to evolve into short-winged ones on the Galápagos Islands.[18]

Mendel's findings provide us with a much better understanding of what species and genetic families are, and also why defining species always proves extraordinarily difficult. Species in a family share a common genetic basis but possess different combinations of dominant and recessive alleles. It sanctions hybridization between different species within families—despite the many mechanisms in place that promote reproductive isolation—and makes defining species somewhat arbitrary.

Reproductive isolation is critical because it allows fixation of recessive or hypostatic allele combinations. This maintains phenotypic diversity that would otherwise be lost through hybridization and subsequent restoration of heterogeneity. The alternate alleles of shared genes offer great potential for phenotypic diversity. They allow a genetic family to evolve into a superabundance of healthy, vibrant species through adaptive radiation.

This non-mutational form of speciation is Mendel's legacy, the fruit of his Law of Exponential Trait Combinations. His experiments on plant hybrids led to extensive and significant ground-breaking insights into genetics and, in particular, into 'the origin of species'.

Conclusions

Mendelian speciation is based on his Law of Exponential Trait Combinations. It provides a powerful explanation for the emergence of biological diversity. It readily explains the most spectacular examples of adaptive radiations within families. Mendelian speciation occurs because the information required for speciation and variability is already present in the genome of organisms, held in a latent state. Mendelian speciation gives rise to extensive, wholesome evolution within a family; *cis*-evolution. It can occur within relatively few generations and provides eminently reasonable and entirely satisfactory solutions to many of the questions that arise when attempting to bring the extensive biodiversity observed in nature and a scriptural understanding of origins into meaningful alignment.

Appendix 1—*cis*-evolution and microevolution

In debates about evolution, the terms 'microevolution' and 'macroevolution' are often used. These two terms are defined differently, and often vaguely, by different groups. Some say macroevolution is evolution within a species; others, within a family. For yet others, both terms only differ quantitatively (i.e., very little or much evolution).

For this reason, the terms '*cis*-evolution' and '*trans*-evolution' are introduced here. It was to express a qualitative and essential difference between these two types of change (cf. figure 3). One can define 'microevolution' and 'macroevolution' as done in Junker and Scherer,[25] which are essentially identical to '*cis*-evolution' and '*trans*-evolution', respectively.[31] According to these two authors, microevolution deals with the question of how existing (latent) information is expressed, whereas macroevolution is about where pre-existing genetic programs and new characters come from.

A glossary of terms is to be found in the accompanying third paper of this series.[19]

References

1. Crompton, N.E.A., Sprague, T., Truman, R., and Junker, R., Mendelian speciation: part 2— latent genetic information, *J. Creation* **38**(1):77–86, 2024.
2. Carson, H.L., Chromosomal sequences and inter-island colonizations in Hawaiian Drosophila, *Genetics* **103**:465–482, 1983.
3. Noor, M.A.F., Grams, K.L., Bertucci, L.A., and Reiland, J., Chromosomal inversions and the reproductive isolation of species, PNAS **98**:12084–12088, 2001.
4. Edwards, K.A., Doescher, L.T., Kaneshiro, K.Y., and Yamamotol, D., A database of wing diversity in the Hawaiian Drosophila, *PloS ONE* **2**:e487, 2007.
5. Barrier, M., Baldwin, B.G., Robichaux, R.H., and Purugganan, M.D., Interspecific hybrid ancestry of a plant adaptive radiation: allopolyploidy of the Hawaiian silversword alliance (Asteraceae) inferred from floral homeotic gene duplication, *Mol. Biol. Evol.* **16**:1105–1113, 1999.
6. Carlquist, S., Baldwin, B.G., and Carr, G.D., *Tarweeds and Silverswords*, Missouri Botanical Garden Press, St. Louis, 2003.
7. Crompton, N.E.A., Die Radiation der Silberschwert Gruppe 1. Indizien für präexistente genetische Programme, *Studium Integrale J.* **29**:80–89, 2022.
8. Crompton, N.E.A., Die Radiation der Silberschwert Gruppe 2. Hybriden und die Geschichte der Silberschwerter, *Studium Integrale J.* **30**:13–21, 2023.
9. Seehausen, O. and van Alphen, J.J.M., The effect of male coloration on female mate choice in closely related Lake Victoria cichlids (*Haplochromis nyererei* complex), *Behavioral Ecology and Sociobiology* **42**:1–8, 1998.
10. Stiassny, M.L.J. and Meyer, A., Cichlids of the Rift Lakes, *Scientific American* **280**:64–69, 1999.
11. Verheyen, E., Salzburger, W., Snoeks, J., and Meyer, A., Origin of the Superflock of cichlid fishes from Lake Victoria, East Africa, *Science* **300**:325–329, 2003.
12. Albertson, R.C., Markert, J.A., Danley, P.D., and Kocher, T.D., Phylogeny of a rapidly evolving clade: the cichlid fishes of Lake Malawi, East Africa, PNAS **96**:5107–5110, 1999.
13. Joyce, D.A., Lunt, D.H., Bills, R., Turner, G.F., Katongo, C., Duftner, N., Sturmbauer, C., and Seehausen, O., An extant cichlid fish radiation emerged in an extinct Pleistocene lake, *Nature* **435**:90–94, 2005.
14. Brawand, D., Wagner, C.E., *et al.*, The genomic substrate for adaptive radiation in African cichlid fish, *Nature* **513**:375–381, 2014.
15. Berner, D., and Salzburger, W., The genomics of organismal diversification illuminated by adaptive radiations, *Trends in Genetics* **31**:491–499, 2015.
16. Salzburger, W. and Meyer, A., The species flocks of East African cichlid fishes: recent advances in molecular phylogenetics and population genetics, *Naturwissenschaften* **91**:277–290, 2004.
17. 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 Communicatuons* **8**:14363, 2017.
18. Pennisi, E., Hybrids spawned Lake Victoria's rich fish diversity, *Science* **361**:539, 2018.
19. Crompton, N.E.A., Sprague, T., Truman, R., and Junker, R., Mendelian speciation: part 3—fixation and reproductive isolation, *J. Creation* **38**(2):96–103, 2024.
20. Mendel, G., Versuche über Pflanzenhybriden, *Verh. Naturforschung Vereins Brünn* **4**:3–47, 1866. Republished by Vieweg+Teubner (now Springer Vieweg Verlag) Publishers, Wiesbaden, 1970.
21. Mendel, ref. 20, p. 46.
22. Crompton, N.E.A., Sprague, T., Truman, R., and Junker, R., Mendelian speciation part 2—latent genetic information, *J. Creation* **38**(1):77–86, 2024.
23. 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.
24. Li, X., Wang, Y., Cai, C., Ji, J., Han, F., Zhang, L., Chen, S., Zhang, L., Yang, Y., Tang, Q., Bucher, J., Wang, X., Yng, L., Zhuang, M., Zhang, K., Lv, H., Bonnema, G., Zhang, Y., and Chang, F., Large-scale gene expression alterations introduced by structural variation drive morphotype diversification in *Brassica oleracea*, *Nature Genetics* **56**:517–529, 2024.
25. Junker, R. and Scherer, S., *Evolution—ein kritisches Lehrbuch*, Wevel Biologie, Gießen, 7th edn, 2013.
26. Jiggins, C.G., Radiating genomes, *Nature* **513**:318–319, 2014.
27. Mendel, ref. 20, p. 36.
28. Wallace, A.R., On the tendency of varieties to depart indefinitely from the original type, The Ternate Essay, *J. Proceedings of the Linnean Society* **3**:53–62, 1858.
29. 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.
30. Darwin, ref. 29, p. 80.
31. Junker and Scherer, ref. 25, pp. 44 and 48.

__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.*

Quartzarenites violate the uniformitarian principle

Michael J. Oard

Many unusual sedimentary rocks occur on Earth. One of these is quartzarenite, a type of cemented sandstone. The sand that makes up quartzarenite does not appear to be forming today, while an enormous amount of quartzarenite is found in the sedimentary rock record, especially in the Precambrian and Paleozoic. Quartzarenites convey important information for creation scientists working on a Flood model.

The four main types of sandstone

Cemented sandstone makes up 20 to 25% of all sedimentary rocks.[1] Sandstone has classically been divided into four main types that would categorize practically all sandstones.[2] They are: (1) quartzarenite, (2) lithic arenite, (3) arkose, and (4) graywacke.[3] A quartzarenite is a 'mature' or 'supermature' cemented sandstone in which the individual grains are 90–95% quartz and rounded to well rounded.[4,5] If a sandstone has a fair percentage of rock fragments, usually greater than 50%, with a lesser percentage of feldspar, it is termed a 'lithic arenite'. Sands with 25% or more feldspar with a smaller percentage of rock fragments are identified as an arkose. Graywacke is defined by a fine-grained matrix greater than 15% between the sand particles. This classification does not include the cements (e.g., silica and sometimes carbonate and other cements) that bind the individual sand grains into sandstone.

The classification of sandstones has always been difficult, probably because each sandstone has a variable amount of the three main framework grains: quartz, feldspar, and lithics (figure 1). Sedimentologist Eduardo Garzanti has devised a new classification for sandstones incorporating some of the older terminology and subdividing it.[6] One of the reasons for the new classification is that he believes the older classification systems use

> "… cumbersome petrographic descriptions based on obsolete classification schemes or awkward terms such as arkose or greywacke, the use of which has been contested since their early introduction two centuries ago."[7]

Garzanti's classification is intuitive, but would require extensive analysis of the sixteen individual types of sandstone to determine its proper abundance or origin. Despite the terms 'arkose' and 'greywacke' being vague, this paper and a companion paper will examine the four classical descriptions of sandstone to question how well they can be accounted for by uniformitarianism, simply stated as 'the present is the key to the past'.

What is a quartzarenite?

Quartzarenites are common sandstones and are believed to make up about 33% of all sandstones according to Boggs,[8] a percentage he obtained from Pettijohn. Then quartzarenites make up about 7–8% of all sedimentary rocks, a not insignificant volume.

However, the definition of quartzarenite is not straightforward.[9] The precise definition likely has caused confusion about whether the sand that makes up quartzarenite is forming today or not, and how prevalent it is in the rock record. A few researchers think that the amount of cemented quartz grains needs to be greater than 90% while most believe it needs to be greater than 95%.[10,11] This is called mineralogical or compositional 'maturity'. Textural maturity consists of the quartz grains being rounded to well-rounded. Some researchers assume that mineralogical maturity is all that is needed to call the cemented sand a quartzarenite.[12] However, most researchers consider that a quartzarenite needs both mineralogical and textural maturity,[13] which is the definition used in this paper.

Quartzarenite is sometimes metamorphosed to metaquartzite or simply quartzite (figure 2). There is another type of quartzite, not discussed in this paper, that is not metamorphosed and is called 'orthoquartzite', a hard cemented sandstone. Metaquartzite is commonly associated with continental cratons and has few interbeds of fine-grained sedimentary rocks.[14] Quartzarenites and metaquartzite are predominantly cemented by silica.[15]

Quartzarenite must first start as individual quartz sand grains in which most of the other lithologies disappear. It is likely that the quartz comes from the weathering or disintegration of igneous and metamorphic rocks that contain much quartz, such as granite. However, it is difficult to

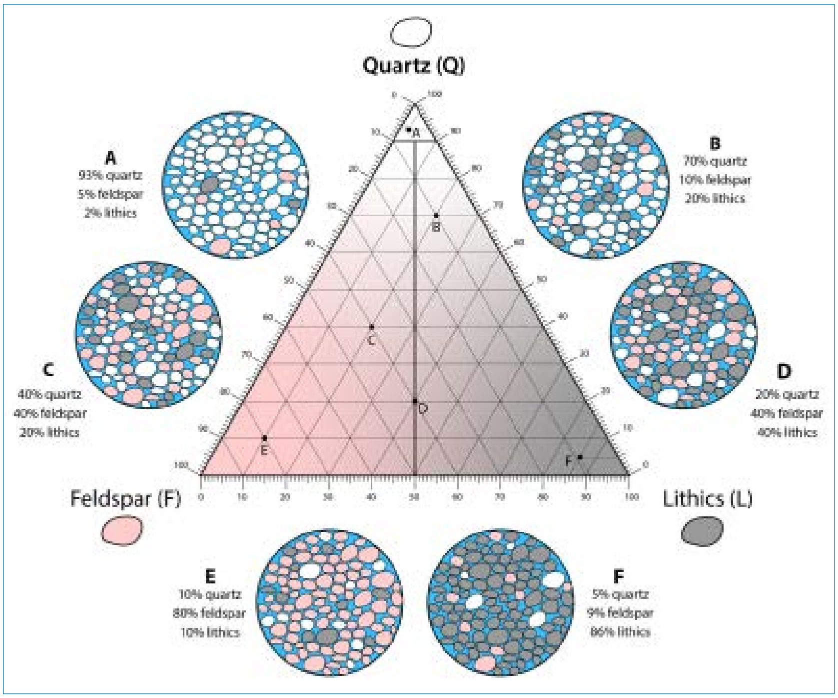


Image: Michael C. Rygel, Wikimedia / CC BY SA 4.0

Figure 1. Classic sandstone ternary diagram showing the relative abundance of quartz, feldspar, and lithics (rock particles) in a sandstone with six thin sections colour-coded, showing what those abundances would look like.

Figure 2. Well-rounded quartzite boulder transported from the southwest over 100 km and found on top of the Gravelly Mountains, southwest Montana, USA. Note the vitreous texture in the lower left from the metamorphism. The boulder has numerous percussion marks, not forming today on quartzite and indicating torrential water flow.

envisage a geological process that can account for it: "How can we explain the complete disposal [weathering] of at least 75% of any ultimate parent igneous or metamorphic rock to yield a residue that is at least 95% quartz sand?"[16] The sand that makes up quartzarenites is considered 'first-cycle' if it formed *directly* by chemical and/or mechanical weathering processes from mainly igneous or metamorphic rocks and then became well-rounded. But if the sand grains originate from a *pre-existing* quartzarenite, then the sand is considered a 'multi-cycle' quartz sand. When it is cemented, it would be a multi-cycle quartzarenite.

From that sedimentary base, somehow the quartz grains then become well rounded by the action of water. Then they are deeply buried and subject to migrating silica-rich fluids that cement the sand grains into a quartzarenite. Then the quartzarenite must be uplifted with overburden eroded, when the quartzarenite is found at the surface.

Quartzarenites are sometimes enormous

The sedimentary rock record includes enormous volumes of quartzarenite, such as the 1,000 m thick Precambrian Athabaska Formation of northern Saskatchewan, Canada, which covers 104,000 km^2.[17] The Thelon Formation in the northwest Territories of Canada is of similar extent.[17] The Cambrian/Ordovician Jura Quartzite, a metamorphosed quartzarenite, is an impressive 5,300 m thick![18]

Quartzarenite can sometimes be deposited as a thin widespread sheet of sandstone, especially in the early Paleozoic, such as the Ordovician St. Peter Sandstone, which thinly outcrops over much of the middle USA over an area of 582,750 km^2.[19] A vast sheet of quartzarenite with a volume of 15 million km^3 was laid down in northern Africa from the Atlantic coast to the Persian Gulf in Cambrian/Ordovician times by paleocurrents flowing toward the north.[20]

The sensational Roraima quartzarenite

The Paleoproterozoic Roraima Formation (or Supergroup), which outcrops mostly in Venezuela (figure 3) is mostly a quartzarenite that is greater than 2,500 m thick. It once covered a huge area of about 250,000 km^2, but has been 90% eroded into erosional remnants in the form of high mesas and plateaus, called 'tepuis'.[21,22] The sandstone is only slightly metamorphosed and forms local quartzite. The area is mysteriously riddled with large caves and deep sink holes on top of some tepuis. The world's largest waterfall, Angel Falls, is in this region. However, if far outliers are included, the sand would have been deposited over an area of 2.4 × 10^6 km^2, an area four times that of France.[21] There are over 100 of these mesas and plateaus. The tepuis can be up to 1,000 m above the forest floor (figure 4)![23] The top of the tepuis is considered an eroded planation surface with the amount of erosion believed to be about 3,000 m![23] The deposition and erosion of the Roraima Formation indicates powerful catastrophic action during the Paleoproterozoic.

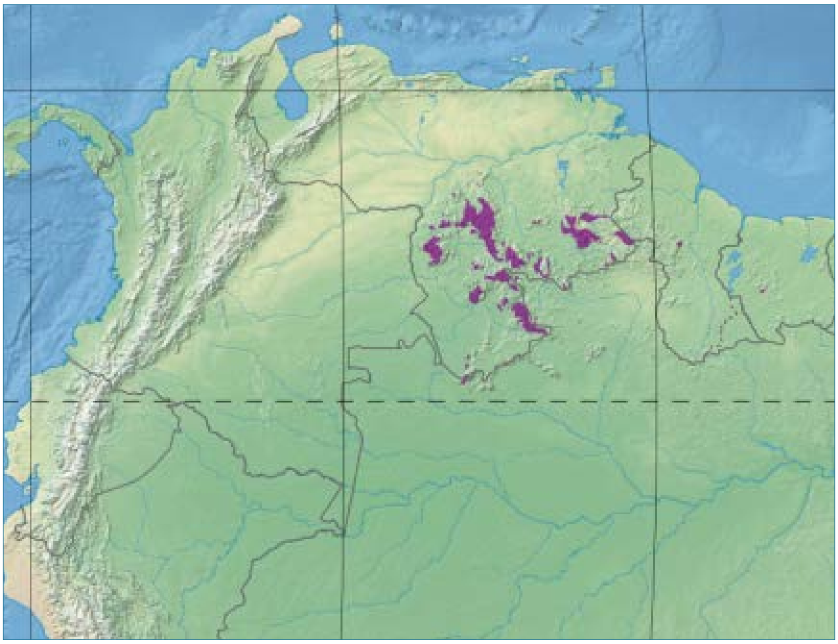


Image: Every-leaf-that-trembles, Wikimedia / CC BY SA 4.0

Figure 3. Location of tepuis mostly in southeastern Venezuela


Image: Paolo Costa Baldi, Wikimedia / CC BY SA 3.0

Figure 4. Kukenan Tepuy in Gran Sabana National Park, Venezuela, that is 2,700–2,800 m asl

The temporal distribution of quartzarenites

What is the temporal occurrence of quartzarenites, assuming the geological column, and what is the significance? Much more quartzarenite occurs in the Precambrian, decreasing upward in the Phanerozoic. Dott states:

> "In reality, there are far greater volumes of pure quartz arenites in the Precambrian than in the Phanerozoic record. They occur on most continents, and many are hardly sheetlike, being hundreds to thousands of meters thick."[24]

Quartzarenite is even found in the early and late Archean.[18]

Moreover, Precambrian and lower Paleozoic quartzarenites are commonly medium to coarse grained with very few shale interbeds compared to other sandstones. For instance, quartzarenites are globally distributed on top of the Precambrian/Cambrian Great Unconformity, as Lorentzen *et al.* state: "Lower Cambrian quartz arenite deposits have a world-wide occurrence".[25]

Are first-cycle well-rounded, nearly pure quartz sands forming today?

Before we even consider the formation of a cemented quartzarenite, an important question to consider is whether first-cycle well-rounded, nearly pure quartz sand is being produced today anywhere on the earth? This is important in considering whether the sand that forms quartzarenite violates the uniformitarian principle or not. Conventional scientists believe that there are two locations on Earth where high quartz sand is forming today. These are areas of intense chemical weathering in a hot, humid climate with leaching by acidic rainwater or by organic acids in the soil. A stable, generally flat terrane ensures a long residence time for weathering to reach completion. Such an environment would cause the more stable grains, mainly quartz and ZTR (zircon, tourmaline, rutile] minerals to become more concentrated. Such an environment can be found in the rain belts of northern South America and the Congo drainage basin of Central Africa.

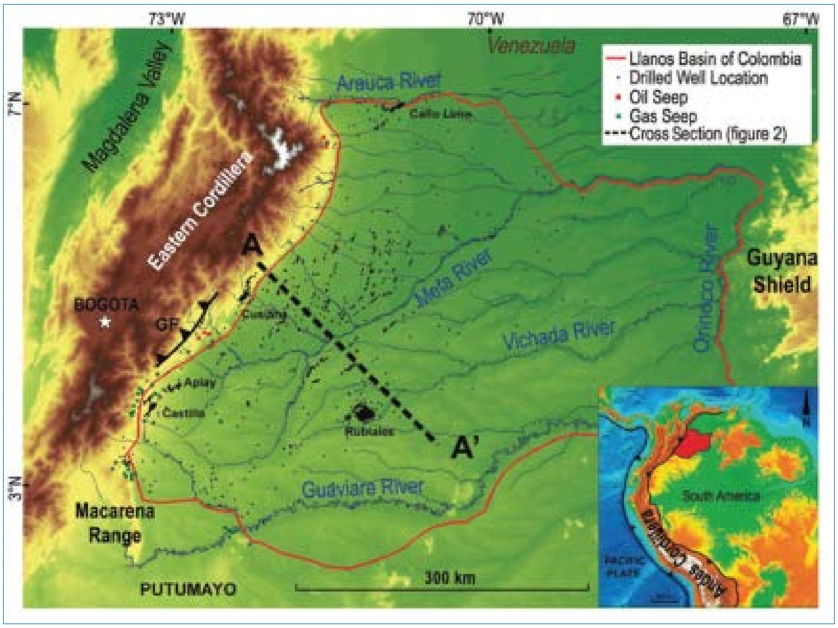


Figure 5. The bottom right inset presents the eastern forelands of the northern Andes, west of the Guyana Shield in Colombia (from Gonzalez-Penagos *et al*., ref. 30). The Llanos Basin is outlined in red near the top of the figure. The main map shows the topography colour coded by altitude with reddish-brown indicating high altitude and green, low altitude. Also shown are the fluvial system, the oil and gas seep occurrence, and the drilled well locations.

South America

Johnsson *et al*. claim first-cycle quartz sand can form by intense chemical weathering over extended periods of time. They believe it has been forming on top of granite in the eastern Llanos Basin, east of the Andes in Columbia and southern Venezuela and on low-relief surfaces of the western Guyana Shield (figures 5 and 6).[26,27] The climate is warm and humid, and drainage is by the Orinoco River of northern South America (figure 7). The intense chemical weathering leaves behind the quartz from the weathered granite, and, over an extended period, time supposedly allows multiple passes through the 'fluvial system' to reach textural maturity: "But what of the textural criteria? It seems reasonable that multiple passes through a fluvial system should result in increased roundness."[28] However, this is contrary to the experimental work of Keunen, who showed that water does not round sand grains.[29] Garzanti also disagrees with the conclusions of Johnsson *et al.* and considers it a myth that physical processes, such as fluvial, littoral, and even wind transport, can result in a mature or supermature sandstone.[4]

There is another problem with the idea that first-order quartz sand is forming in the tropical jungles of South America. East of the Orinoco River and part of the Guyana Shield is the Roraima Formation, which is predominantly quartzarenite. The formation has been highly eroded (see above), so that much of the claimed quartzarenite would be erosional detritus. However, Johnsson *et al.* disagree that their high quartz sand came from sand eroded from the Roraima Formation. Their evidence is that the lowland, granitic Guyana Shield sand is more rounded than the quartz eroded from the Roraima Formation. However, this is because the quartz eroded from the Roraima Formation still has rough cement overgrowths that cap the well-rounded grains of the Roraima quartzarenite. Johnsson *et al*. do admit more study is needed on textural maturity: "The discrimination between first- and multi-cycle quartz arenites is exceedingly difficult."[28]

Potter examined sand in many rivers of South America besides the Orinoco drainage basin.[31] He discovered that quartz sand occurs in all rivers draining cratons, especially the Guyana and Brazilian Shields, which have several widespread erosional surfaces. This represents 62% of South America. Potter does postulate that Johnsson and colleagues' Orinoco River sands have been contaminated by the erosion of quartzarenite from the shields, i.e., the Roraima Formation. Although the river sands have compositional maturity, Potter identified the sand on low-relief shield areas as *subangular*; it is not texturally mature. Dott also recognizes that the sands of the Orinoco drainage basin are texturally immature.[24] In summary, the quartz sand analyzed by Johnsson and colleagues is mineralogically mature, but it is not texturally mature, unlike practically all lithified quartzarenites in the rock record.

The Congo Basin

Another hot, humid, and stable environment is the Congo Basin of Central Africa (figure 8), where first-cycle quartz sand could be forming. Indeed, the Congo River is delivering high-quartz sand that is mostly rounded to well-rounded to its mouth.[32,33] However, Garzanti and colleagues show that the mature quartz sand is probably not from intense chemical weathering, although this is occurring in Central Africa. This is because numerous ancient ultra-pure quartzarenite sandstones also occur in the Congo River Basin. Thus, it is difficult to prove whether the quartz sand from the Congo Basin is first- or multi-cycled.[32,34] In fact, Garzanti *et al.* believe the quartz sand of the Congo Basin is multi-cycled: "Quartz abundance thus chiefly reflects the abundance of quartzose sandstone in the catchment and recycling, rather than weathering intensity."[35] They state: "Pure quartzose sand occurs only in catchments where cover strata including thick upper Proterozoic quartzarenite is exposed."[9]

Quartzarenites violate the uniformitarianism principle

Despite the claims of some researchers, such as Johnsson and colleagues, first-cycle well-rounded clean quartz sands apparently are not forming today.

> "A never solved problem in sedimentary petrology is the origin of sandstone consisting exclusively of quartz and most durable heavy minerals."[36]

Because of the difficulty today of forming such sand, the researchers in the Congo River drainage claim that most, if not all, ancient quartzarenite sandstones must also be multi-cycled. But this begs the question of how do the first-cycle mineralogically and texturally mature quartz sands originate in the first place, especially considering the enormous sizes of the formations that contain quartzarenite (see above)? Chemical weathering in a warm, wet environment with little relief is not enough.

> "Moreover, the abundance of pure quartzarenite in the rock record can hardly be explained by chemical weathering or physical recycling alone."[36]
>
> "… first-cycle sand consisting of quartz and ZTR minerals exclusively cannot be generated by chemical weathering alone in the atmospheric and climatic conditions of the modern Earth".[37]

As a result, sedimentologists have been debating the origin of quartzarenites for well over 100 years. The very existence of such sandstones presents a challenge to the uniformitarian principle, the assumption which undergirds their research.

> "Another seeming 'non-uniformitarian' kind of sandstone is the extremely thick quartz arenite that seems to be widespread in the upper Precambrian. Quartzites [mainly orthoquartzite or hard cemented sandstone] such as the Lorrain of Ontario, the Baraboo of Wisconsin, the Athabaska of Saskatchewan, and the Uinta of Utah are all very pure and well over 1000 m thick whereas Phanerozoic quartz arenites tend to be very thin, rarely over a few tens of meters thick."[38]

It is interesting to note the difference between Precambrian and Phanerozoic quartzarenites, but, regardless, the formation of the original well-rounded, nearly pure quartz sand, as well as quartzarenites, violates the uniformitarian or actualistic principle, as also reinforced by Dott:

> "A century-long debate over the origin of these remarkably pure sandstones has remained unresolved, largely because they seem nonactualistic."[39]

In a more recent article, Konstantinou *et al.* declare, "Despite numerous studies, the century-long debate on how these arenites formed is still unresolved, primarily because

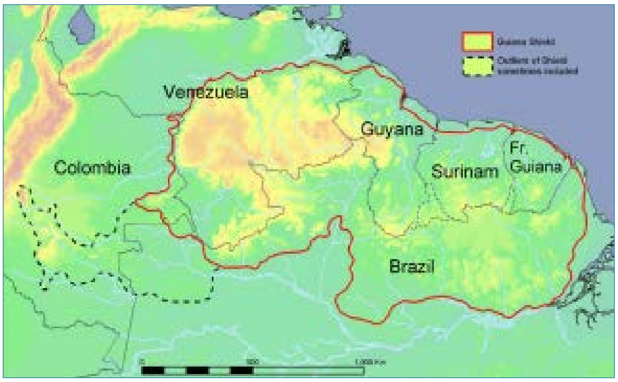


Figure 6. The Guyana Shield of northern South America colour-coded by altitude, with brown colours showing high altitude, and green colours, low altitude

Image: Suriname Central, Wikimedia / CC BY SA 4.0

Figure 7. Orinoco drainage basin

Image: Mileniocura, Wikimedia / CC BY SA 4.0

Figure 8. The Congo River drainage basin

Image: Kmusser, Wikimedia / CC BY SA 4.0

of the compositional and textural purity of the deposits."[40] Pastore *et al*. support this conclusion:

> "The debate on the existence of first-cycle quartzarenites went on for long [sic]… , until the modern-sand lesson indicated unambiguously that sand consisting virtually entirely of quartz and ZTR minerals cannot be the result of mechanical or weathering processes even in the most aggressive climatic conditions met in modern Earth, but that the final cleansing of less stable minerals requires extensive intrastratal dissolution, i.e., inheritance from previous sedimentary cycles of weathering and diagenesis … . Pure quartzose composition thus implies that sand originated from homogenization of detritus chiefly produced by physical disaggregation of quartz-rich parent sandstones, possibly derived in turn from older granparent [sic] sandstones, along a line of ancestry rooted in the deep past."[41]

Quartzarenites violate the uniformitarian principle in other ways, as do most sandstones. Most modern-day sands are small scale, and usually long, narrow, and thin, while sandstones in the rock record are large three-dimensional sheets.

> "It is noteworthy that most common modern sites of sand accumulation—the beaches and rivers—are linear features and the sand associated with them is confined to a narrow zone. Yet the sands of the past commonly occur in areally extensive stratiform sheets."[42]

Creation science explanations

Although uniformitarian scientists cannot explain the origin of mineralogically and texturally mature quartzarenites, nor their sometimes widespread and/or thick accumulations, creation scientists can potentially explain them by the Flood. The large volume of quartzarenite in the sedimentary rocks correlates well with the expectations of the global Flood and the massive size of the many formations.

Well-rounded, nearly pure quartz sand not from wind

Whitmore and colleagues have shown that the eolian claim for many sandstones on Earth is a mistaken uniformitarian interpretation (figure 9).[43–46] The Coconino Sandstone does not qualify as a quartzarenite since it contains too much feldspar, and the grains are not well-rounded. It was discovered that a detailed petrological analysis of the sandstone had never been made by uniformitarian scientists. Instead, researchers have cherry picked their facts to support an eolian origin. The Coconino Sandstone is, on average, only moderately sorted and only locally well sorted, with sub-angular to sub-rounded sand grains. Mica, angular K-feldspars, dolomite ooids, dolomite clasts, bedded dolomite, and dolomite cements occur within the formation. Mica would be rapidly destroyed by eolian action but not necessarily by water.[47] None of these characteristics is typical of modern eolian sands.

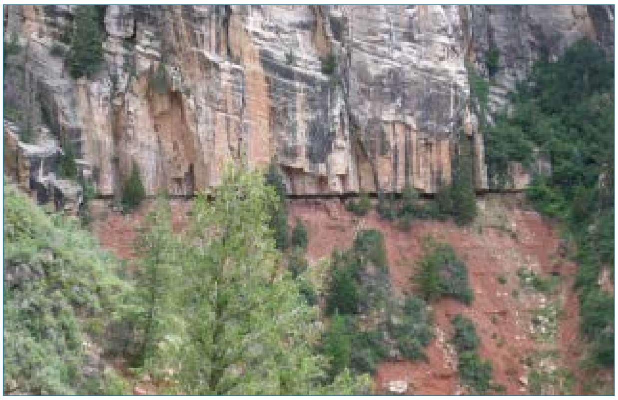


Figure 9. Cross-bedding within the Coconino Sandstone, a formation that lies like a knife edge on the Hermit Formation. Conventional scientists claim this contact has 5 to 10 Myr of missing rock record.

Grain frosting not necessarily by wind

The frosting of quartz sand grains is often considered a sign of rounding by wind.[48] However, frosting is more often caused by chemical weathering: "Surface textures such as frosting and rounding may be caused by different processes, including chemical dissolution and eolian abrasion."[49]

Well-rounded, nearly pure quartz sand points to powerful turbulence with chemical weathering.

So, what could have caused the abundance of well-rounded, nearly pure quartz sand in the Flood? Fast currents with powerful turbulence would explain it. An acidic early Flood environment could produce chemical weathering and leave behind a mostly high-quartz sand.[25] Or the intense mechanical weathering from turbulence could pulverize the softer minerals, leaving behind quartz and some heavy minerals.

But what about Kuenen's fluviatile experiment and Garzanti's conclusion that water cannot produce a well-rounded, nearly pure quartz sand? Both these results assume uniformitarianism. Kuenen's experiment was unnatural in some respects in that the bottom was hard concrete and not loose sand, and the grains were never in suspension because the velocities were too low, 84 cm/sec.[29] All the modern research on sand transport occurs with slow currents and low turbulence, such as Garzanti's research on transport down the Orange River and northwest along the Southwest African coast.[4]

But much greater turbulence and current velocities are capable of rounding medium-coarse sand grains. Some evidence suggests that fast transport of sand in a tidal environment in the Bay of Fundy has resulted in sand grains more rounded than their parent material.[50] Folk suggested that with enough energy, rounded sand could occur.[51,52] Rounding is mainly a matter of the grains hitting harder, which occurs much more efficiently by intense turbulence.

How do we explain its temporal change?

Once a well-rounded, nearly pure quartz sand forms, it must be deeply buried and silica cemented to become a quartzarenite. The temporal distribution shows much greater volume of quartzarenite occurs in the Precambrian, decreasing upward through the geological column. I believe this is because the Precambrian sedimentary rocks were formed in the early Flood and deposited mostly in deep basins and rifts that offered more protection from the turbulent currents. The lack of metazoan fossils in the Precambrian could be due to unique aspects of the Precambrian sedimentary rocks, such as powerful turbulence, acidic water, and hot water.[53,54] The Roraima Formation would represent a Paleoproterozoic deposition in a large basin, resulting in quartzarenite several thousand metres thick over a large area. Then the basin would have inverted with great erosion, leaving the quartzarenite as erosional remnants (tepuis).

Supporting evidence for this tremendous geological activity is derived from large impact features that occurred in both the Proterozoic and Archean.[55,56] Such impacts not only indicate that the pre-Flood/Flood boundary should be below most, if not all, Precambrian sedimentary rocks, but also impacts would cause currents fast enough and turbulence intense enough to form quartzarenites from quartz source rocks, such as the granites and gneisses of the upper crust. Such currents and turbulence would have to have been exceedingly powerful to produce such well-rounded, nearly pure quartz sand over widespread areas and of such enormous thicknesses in the Precambrian. Impact cratering is capable of accomplishing this. The sand grains in the Precambrian and early Paleozoic are coarse[57] and should round much faster. Finer sand grains usually do not round because the force of one grain upon another is not enough to chip off the sharp edges.

The massive thicknesses of many Precambrian quartzarenites would result from deposition into subsiding rifts and basins, covered by thick sediments, and cemented with silica-rich fluids. During the early Flood, the powerful currents and turbulence would have formed planar surfaces such as the Great Unconformity on the upper continental crust and on top of some basins filled with sedimentary rocks. Because of the decrease in the big impacts and the reduction in Flood energy, the Great Deposition followed.[58] This is when the Phanerozoic sediments were laid down and is probably the reason why quartzarenites of especially the lower Paleozoic are rather thin and widespread, such as the St. Peter Sandstone in the Midwest of the United States.

Implications for the pre-Flood/Flood boundary

The fact that quartzarenites are the most abundant cemented sandstone in the Precambrian and lower Paleozoic[23] suggests that there is no major sedimentological break between the Precambrian and the Cambrian, and the pre-Flood/Flood boundary must be located lower in the geological column. Besides, such large Archean and Proterozoic impacts are very unlikely to have taken place during Creation Week or between creation and the Flood. Neither is there any break in occurrence or abundance in carbonates, phosphorites, or black shales across the Precambrian/Cambrian boundary.[59] But there are raindrop imprints in the Proterozoic and late Archean. This suggests the pre-Flood/Flood boundary is much lower than the Precambrian/Cambrian boundary.[60]

Conclusions

The lack of nearly pure quartz sand with grain maturity (i.e., well roundedness) generated in present environments contrasts sharply with the well-rounded, nearly pure quartz sand, lithified to quartzarenite, in the rock record, especially in the late Precambrian and lower Paleozoic. Thus, quartzarenites violate the uniformitarian principle that the present is the key to the past.

The well-rounded, nearly pure quartz sand could have easily formed early in the Flood by powerful turbulence and fast currents, such as would occur with Archean and Proterozoic impacts. The Precambrian well-rounded, nearly pure quartz sand seems to have been deposited in deep rifts and basins formed early in the Flood. The Phanerozoic well-rounded, nearly pure quartz sands, especially in the lower Paleozoic, were deposited as thin formations over wide areas, along with other types of sediments during the Great Deposition.

The other sandstones, especially arkoses and graywackes, also display unique properties that violate the uniformitarian principle that the present is the key to the past. Since sandstones comprise 20–25% of sedimentary rocks, this means that the uniformitarian principle is incapable of explaining a large volume of sedimentary rocks.

References

1. Boggs, Jr, S., *Principles of Sedimentology and Stratigraphy*, 5th edn, Pearson, p. 101, 2012.
2. McBride, E.F., A classification of common sandstones, *J. Sedimentary Petrology* **33**(3):664–669, 1963.
3. Pettijohn, F.J., Potter, P.E., and Siever, R., *Sand and Sandstone*, 2nd edn, Springer-Verlag, New York, 1987.
4. Garzanti, E., The maturity myth in sedimentology and provenance analysis, *J. Sedimentary Research* **87**:353–365, 2017.

5. Oard, M.J., Possible myths in geology, *J. Creation* **38**(1):43–50, 2024.
6. Garzanti, E., Petrographic classification of sand and sandstone, *Earth-Science Reviews* **192**:545–563, 2019.
7. Garzanti, ref. 6, p. 547.
8. Boggs, ref. 1. p. 111.
9. Garzanti, E., Vermeesch, P., Vezzoli, G., Andò, S., Botti, E., Limonta, M., Dinis, P., Hahn, A., Baudet, D., De Grave, J., and Yaya, N.K., Congo River sand and the equatorial quartz factory, *Earth-Science Reviews* **197** (102918):1–23, 2019; p. 16.
10. Pettijohn, F.J., *Sedimentary Rocks*, third edition, Harper and Row, New York, p. 231, 1975.
11. Chandler, F.W., Quartz arenites: review and interpretation, *Sedimentary Geology* **58**:105–126, 1988.
12. Monami, S.J., Uddin, A., and Hames, W.E., Multi-proxy provenance of the Lower Pennsylvanian Pottsville Sandstone of the northern Appalachian Basin in Pennsylvania, U.S.A.: Paleodrainage, sources, and detrital history, *J. Sedimentary Petrology* **92**:304–319, 2022.
13. Folk, R.L., Stages of textural maturity in sedimentary rocks, *J. Sedimentary Petrology* **21**(3):127–130, 1951.
14. Pettijohn *et al*., ref. 3, pp. 184–185.
15. Pettijohn, ref. 10, pp. 231.
16. Dott, Jr, R.H., The importance of eolian abrasion in supermature quartz sandstones and the paradox of weathering on vegetation-free landscapes, *J. Geology* **111**:388, 2003.
17. Pettijohn *et al.*, ref. 3, p. 179.
18. Soegaard, K. and Eriksson, K.A., Origin of thick, first-cycle quartz arenite successions: evidence from the 1.7Ga Ortega Group, northern New Mexico, *Precambrian Research* **43**:129–141, 1989.
19. Hoholick, J.D., Metarko, T., and Potter, P.E., Regional variations of porosity and cement: St. Peter and Mount Simon Sandstones in Illinois Basin, *American Association of Petroleum Geologists Bulletin* **68**:753–763, 1984.
20. Avidgad, D., Sandler, A., Kolodner, K., Stern, R.J., McWilliams, M., Miller, N., and Beyth, M., Mass-production of Cambro-Ordovician quartz-rich sandstone as a consequence of chemical weathering of Pan-African terranes: environmental implications, *Earth and Planetary Science Letters* **240**:818–826, 2005.
21. Santos, J.O.S., Potter, P.E., Reis, N.J., Hartmann, L.A., Fletcher, I.R., and McNaughton, N.J., Age, source, and regional stratigraphy of the Roraima Supergroup and Roraima-like outliers in northern South America based on U-Pb geochronology, *GSA Bulletin* **115**(3):331–348, 2003.
22. Sauro, F., Mecchia, M., Piccini, L., Waele, J.D., Carbone, C., Columbo, A., Pasini, L., and Vergara, F., Genesis of giant sinkholes and caves in the quartz sandstone of Sarisarmama tepui, Venezuela, *Geomorphology* **342**:223–238, 2019.
23. Piccini, L. and Mecchia, M., Solution weathering rate and origin of karst landforms and caves in the quartzite of Auyan-tepui (Gran Sabana, Venezuela), *Geomorphology* **106**:15–25, 2009.
24. Dott, ref. 16, p. 391.
25. Lorentzen, S., Braut, T., Augustsson, C., Nystuen, J.P., Jahren, J., and Schovsbo, N.H., Provenance of Lower Cambrian quartz arenite on southwestern Baltica: weathering versus recycling, *J. Sedimentary Research* **90**:493–512, 2020.
26. Johnsson, M.J., Stallard, R.F., and Meade, R.H., First-cycle quartz arenite in the Orinoco River Basin, Venezuela and Columbia, *J. Geology* **96**:263–277, 1988.
27. Johnsson, M.J., Stallard, R.F., and Lundberg, N., Controls on the composition of fluvial sands from a tropical weathering environment; sands of the Orinoco River drainage basin, Venezuela and Columbia, *GSA Bulletin* **103**:1622–1647, 1991.
28. Johnsson *et al*., ref. 26, p. 275.
29. Kuenen, Ph.H., Experimental abrasion 3: fluvial action on sand, *American J. Science* **257**:172–190, 1959.
30. Gonzalez-Penagos, F., Moretti, I., and Guichet, A., Fluid flow modeling in the Llanos Basin, Columbia, *AAPG Memoir 114*, American Association of Petroleum Geologists, Tulsa, OK, pp. 191–217, 2017.
31. Potter, P.E., Modern sands of South America: composition, provenance and global significance, *Geologische Rundschau* **83**:212–232, 1994.
32. Garzanti *et al*., ref. 9, pp. 1–23.
33. Garzanti, E., Bayon, G., Dennielou, B., Barbarano, M., Limonta, M., and Vezzoli, G., The Congo deep-sea fan: Mineralogical, REE, and Nd-isotope variability in quartzose passive-margin sand, *J. Sedimentary Petrology* **91**:433–450, 2021.
34. Garzanti, E., Dinis, P., Vermeesch, P., Andò, S., Hahn, A., Huvi, J., Limonta, M., Padoan, M., Resentini, A., Rittner, M., and Vezzoli, G., Dynamic uplift, recycling, and climate control on the petrology of passive-margin sand (Angola), *Sedimentary Geology* **375**:86–104, 2018.
35. Garzanti *et al*., ref. 9, p. 14.
36. Garzanti *et al*., ref. 9, p. 1.
37. Garzanti *et al.*, ref. 9, p. 19.
38. Pettijohn *et al*., ref. 3, p. 509.
39. Dott, ref. 16, p. 387.
40. Konstantinou, A., Wirth, C.R., Vervoort, J.D., Malone, D.H., Davidson, C., and Craddock, J.P., Provenance of quartz arenites of the Early Paleozoic midcontinent region, USA, *J. Geology* **122**:201–206, 2014.
41. Pastore, G., Baird, T., Vermeesch, P., Bristow, C., Resentini, A., and Garzanti, E., Provenance and recycling of Sahara Desert sand, *Earth-Science Reviews* **216**:103606, 2021.
42. Pettijohn *et al.*, ref. 3, p. 7.
43. Whitmore, J.H., Strom, R., Cheung, S., and Garner, P.A., The petrology of the Coconino Sandstone (Permian), Arizona, USA, ARJ **7**:499–532, 2014.
44. Whitmore, J.H. and Garner, P.A., The Coconino Sandstone (Permian, Arizona, USA): implications for the origin of ancient cross-bedded sandstones; in: Whitmore, J.H. (Ed.), *Proceedings of the Eighth International Conference on Creationism*, Creation Science Fellowship, Pittsburgh, PA, pp. 581–627, 2018.
45. Whitmore, J.H., Lithostratigraphic correlation of the Coconino Sandstone and a global survey of Permian "Eolian" sandstones: implications for Flood Geology, ARJ **12**:275–328, 2019.
46. Maithel, S.A., Brand, L.R., and Whitmore, J.H., Characterization of hard-to-differentiate dune stratification types in the Permian Coconino Sandstone (Arizona, USA), *Sedimentology* **68**:238–265, 2020.
47. Anderson, C.J., Struble, A., and Whitmore, J.H. (Eds.), Abrasion resistance of muscovite in aeolian and subaqueous transport experiments, *Aeolian Research* **24**:33–37, 2017.
48. Dott, ref. 16, p. 390.
49. Garzanti *et al.*, ref. 9, p. 17.
50. Balazs, R.J. and Klein, G.D., Roundness-mineralogical relations of some intertidal sands, *J. Sedimentary Petrology* **42**(2):425–433, 1972.
51. Folk, R.L., Stages of textural maturity in sedimentary rocks, *J. Sedimentary Petrology* **21**(3):127–130, 1951.
52. Garzanti, ref. 4, p. 358.
53. Oard, M.J., A more likely origin of massive dolomite deposits, *J. Creation* **36**(1):4–6, 2022.
54. Oard, M.J. The 'dolomite problem' solved by the Flood, CRSQ **59**(1):21–28, 2022.
55. Oard, M.J., Precambrian impacts and the Genesis Flood, *J. Creation* **28**(3):99–105, 2014.
56. Oard, M.J., Reed, J.K., and Klevberg, P., Suggested strategies for fitting Precambrian rocks into biblical earth history, CRSQ **60**(2):97–111, 2023
57. Dott, ref. 16, pp. 387–405.
58. Oard, M.J. and Reed, J.K., *How Noah's Flood Shaped Our Earth*, Creation Book Publishers, Powder Springs, GA, 2017.
59. Oard, M.J. and Froede Jr, C., Where is the pre-Flood/Flood boundary? CRSQ **45**(1):24–39, 2008.
60. Oard, M.J., Raindrop imprints and the location of the pre-Flood/Flood boundary, *J. Creation* **27**(2):7–8, 2013.

__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.*

Tracing the sceptre—opposing views on the genealogies of Jesus

Robert Carter

The subject of the genealogy of Jesus is contentious. It raises difficult questions about the descent of the Christ from David, the applicability of the curse on David's descendant Jeconiah, the different number of generations in each genealogy, and biblical inspiration in general. There are also many ways to solve the riddle of why Matthew 1, Luke 3, and 1 Chronicles 3 contain different name lists. For those who accept the historicity of these accounts, one solution posits that Matthew is tracing Joseph's lineage while Luke is tracing Mary's. This is a common view today, though most scholars throughout Christian history appealed to levirate marriages and adoptive relationships to explain the discordant name lists. One rarely explored option is the possibility that Matthew's list is not actually a genealogy but a list of the rightful kings of Judah. In this case, Matthew traces the sceptre and Luke traces the family tree, with the possibility that both converge on Joseph. In fact, the three genealogies can be shown to converge into a single, simple, non-contradictory solution, with Zerubbabel as the pivotal figure. This does not mean that this must be the correct solution, but it is highly likely that, contrary to popular opinion, both Matthew and Luke are tracing different aspects of Joseph's lineage, one kingly and one biological.

The genealogies of Jesus in Matthew 1 and Luke 3 are highly divergent. The parallel information in 1 Chronicles 3 introduces even more difficulties. Skeptics use this to deny the inspiration of Scripture.[1] Scholars have struggled with this for two millennia. Two main views, each with several possible permutations, have been at the forefront of the debate. The 'levirate marriage hypothesis' is probably the most common view espoused throughout church history and can be traced at least as far back as Julius Africanus (c. AD 160–240). Eusebius (c. AD 260–339) also supported this view.[2] A second view, much more popular today, is that Matthew traces Joseph's lineage and Luke traces that of Mary. This can be found in Hilary of Poitiers (c. AD 310–367), who claims this view was common at the time,[2] and John of Damascus (AD 676–749). Being that notable people such as J. Gresham Machen and John Piper held, or hold, to a different interpretation, it is surprising that many Christians are unaware of other possible solutions to the apparent dilemma.

Almost every possible combination of ideas has, at least at one point, been suggested by some scholar of repute. This includes the idea that Matthew and Luke are both tracing the line of Joseph, that both are tracing the line of Mary, and that Matthew is following *Mary's* lineage while Luke is following Joseph's.[3] Consulting historic Bible commentaries, the notes included in various study Bibles, and papers published in various scholarly journals, including sources from all the major publishing houses, will turn up a bewildering array of viewpoints.[4] Among current scholars, the consensus seems to be that the two lists are irreconcilable.[2] Some famous preachers do not even attempt to fix the problem, leaving it up to the scholars.[5] Many teach that Matthew's goal was to emphasize the Davidic kingship. They discuss the theological and symbolic elements in Matthew 1, but often from a literary perspective and not so much from a historical perspective. So they leave the plain reading conundrum unanswered. Many lay people simply throw up their hands, finding a solution neither in the Bible nor coming from their church leadership.

Scholarship is nearly unanimous in believing that Matthew 1 traces the genealogy of Joseph, but they are split on what this means. Some believe that Jeconiah (discussed below) repented and was restored,[6] thus paving the way for him to be in the line of Christ. Others believe that his line was cut off, so Jesus needed another line to David (e.g., through Mary). Among the minority of current scholars who believe that Matthew is tracing the right to the throne of Judah, few have attempted a historical reconstruction of the events that led to the sceptre being passed from the lineage of Solomon to the lineage of his brother Nathan.

For this last position to work, we need a way to incorporate the prophetic, genealogical, and historical information scattered across nearly a dozen biblical books. We need a simple solution that is both faithful to the text and which makes as few assumptions as possible. It also needs to follow Jewish law. This can be done, and one possible solution will be presented below. One can make a strong case that Matthew is indeed tracing the sceptre while Luke is tracing the genealogy, and both converge in Joseph.

No solution answers every possible objection. Since this is an issue of biblical perspicuity, and since this impinges on the deity of Christ, via the accuracy of the Gospels, and since our understanding of biblical genealogies informs us

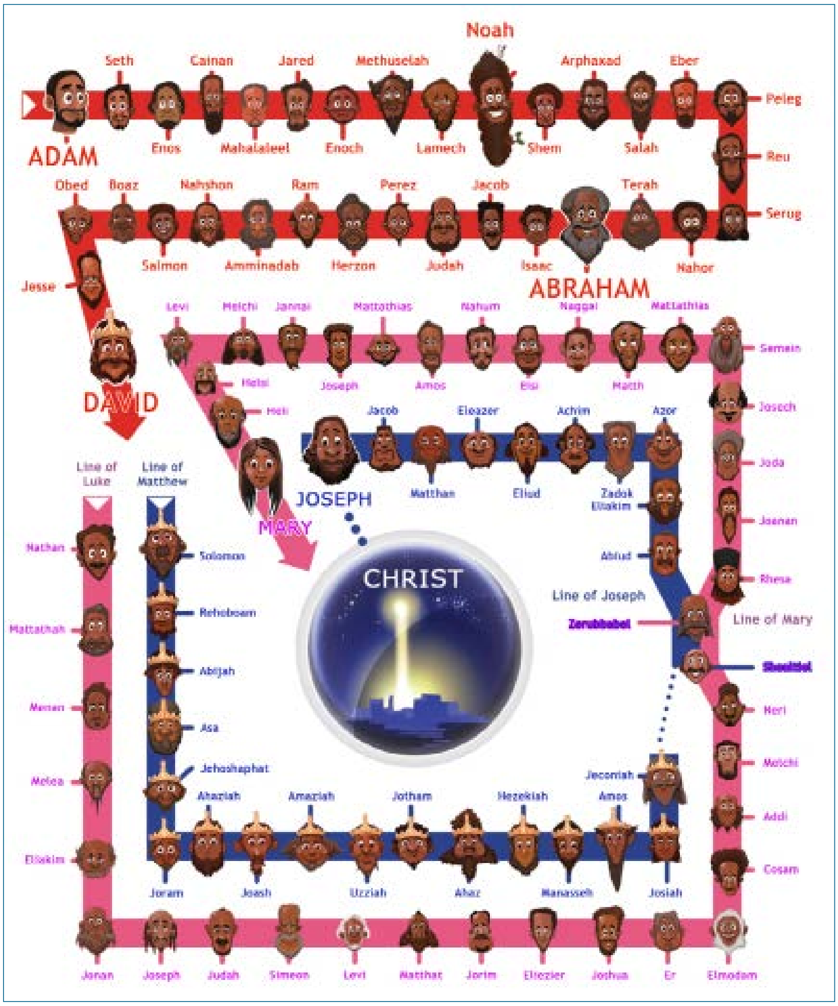


Figure 1. A classic interpretation of the two genealogies of Jesus. Here, the line given in Matthew and Luke splits after David, with Matthew tracing Solomon's line and Luke tracing that of his brother Nathan. Many believe that Matthew is tracing the lineage of Jesus' father, Joseph, while Luke is tracing the lineage of his mother, Mary. An alternative solution is presented in this article.

Illustration by Caleb Salisbury

about other important questions like the age of the earth,[7] we need to carefully parse the relevant data and be circumspect about our conclusions.[8]

Descendants of King David

We know that the 'savior' promised in the Old Testament would be a human male (Genesis 3:15), and a descendant of Abraham (Genesis 22:18), then Judah (Genesis 49:10), then David (Jeremiah 23:5). Yet, the Messiah did not appear prior to the close of the Old Testament canon, and David's descendants had been decimated and scattered via the Babylonian conquest, the return to Judea, and devastating warfare during the Maccabean, Idumean, and early Roman periods.

While the kings of Judah might be expected to have had many children,[9] most of the names of the royal children have been lost to time.[10] The royal family was also constantly embroiled in turmoil and came close to extinction on more than one occasion.[11] Yet, descendants of the house of Solomon and his brother Nathan are known to have survived; Solomon's line continues through all the kings of Judah, of course, and the line of Nathan is mentioned in Zechariah 12:12.

Since David was born over 1,000 years prior, he potentially had millions of descendants by the time of Christ's birth. Yet, there is a difference between a generic descendant of David and a person who could claim to be the *rightful* king. After Solomon, who was not the oldest surviving son of David,[12] the Kingdom of Judah followed strict rules of primogeniture.[13] Only the oldest surviving son of the king could claim the right (e.g., 2 Chronicles 21:3). When a claimant died with no sons of his own, the sceptre would have passed to another line. This is especially important when it comes to tracing the line of David through the Babylonian Captivity.

When the Babylonians destroyed Judah in 586 BC, they set up a crisis in the lineage of David. Three of the four sons of Josiah had sat on the throne, but only one grandson (Jeconiah) had any surviving sons (appendix 1). Yet, the prophecies against this wicked king were direct and severe. Thus, there remains an open question as to whether the Messiah could ever have come from him. The casual reader might insist that Jeconiah's survival (and eventual procreation) does not remove God's curse, citing Jeremiah 22:30. And yet, God did prophesy about forgiveness in this same context (e.g., Jeremiah 36:3). It is possible that God 'repented' of His curse on Jeconiah. Despite the uncategorical nature of the original pronouncement against him, such a reversal is not unwarranted in Scripture. Consider that God proclaimed that Nineveh *would* be overthrown (Jonah 3:4), yet their repentance made Him relent (Jonah 3:6–10). Ezekiel 18 also sets out a path of redemption. Even though God proclaims, "The soul who sins shall die" (v. 20), He also states that He has no "pleasure in the death of the wicked" and wants them to "turn from his way of life and live" (Ezekiel 18:21–23).

The Talmud teaches that Jeconiah repented and was restored,[14] and Christians who believe Jeconiah is in the genealogy of Jesus only have to mention the fact that his descendants are in Matthew's genealogy of the Christ. However, nothing is simple here.

New Testament genealogies

In the New Testament, we are treated to two disparate genealogies of Jesus (figure 1). These follow very different lines and contain a highly divergent number of generations. The Gospel of Matthew includes a list of 44 names in a line that connects Abraham to Jesus.

Luke 3:23–38 includes more names (56 men from Abraham to Jesus) and goes all the way back to Adam. The list from Abraham to David is identical in both accounts, but Matthew has 30 generations from David to Jesus while Luke has 42. Worse, two of the names (Shealtiel and Zerubbabel) are identical in both lists. Thus, either two father/son pairs with identical names just happened to exist in two disparate lines, or the two genealogies come together for unexplained reasons for those two generations, only to split again. But then one line had 11 generations while another had 20, in the same amount of time.

1 Chronicles creates more confusion. Chapter 3 contains a detailed list of the descendants of David. After Jeconiah, none of the names match either those of Matthew or Luke. The exception is that a Shealtiel and a Zerubbabel are listed, but as grandfather/grandson. It is unlikely that all three sources have a *different* Shealtiel/Zerubbabel pair.[15]

Option 1—Luke follows Mary's line; Matthew follows Joseph's line

Matthew's highly stylized list left out multiple generations to arrive at a mathematical formula (three sets of 14 names) that would be easy to memorize. He leaves out Ahaziah, Jehoash, and Amaziah (the kings that ruled between Jehoram and Uzziah) and Jehoiakim (father of Jeconiah). This raises the real possibility that he left additional names out later. Yet, other classic appeals to 'missing generations' (e.g., the lineage of Moses through the Egyptian Sojourn[16] and the detailed chronogenealogies in Genesis 5 and 11[17]) come up short when carefully analyzed. Thus, we should not cavalierly insist that Matthew left out names between Jeconiah and Jesus, even though the shortness of the name list, when compared to that in Luke's list, does suggest it.

Option 1 is supported by the fact that Matthew starts with the words, "The book of the genealogy of Jesus Christ, the son of David, the son of Abraham" (Βίβλος γενέσεως Ἰησοῦ χριστοῦ υἱοῦ Δαυεὶδ υἱοῦ Ἀβραάμ). The word 'genealogy' (γενέσεως) deals with the origin, nature, or existence of something, depending on context. Yet, by starting with the word 'book' (βίβλος), Matthew seems to be laying out a detailed record of Jesus' birth lineage. Even though Jesus was not the literal son of David nor David the literal son of Abraham, he felt free to use the term 'son of' in both cases. This might indicate that there will be missing generations in the subsequent list. Yet, it also means that the names are not always father/son pairs, which will become important later.

Fruchtenbaum believes that the intent of Matthew's genealogy was to show that the Messiah could *not* be a son of Joseph. First, Matthew cites the names of four women, at least two of whom were gentiles and at least three of whom have sordid backgrounds (why did Matthew leave out Sarah, for example?). Matthew then traces the line through Jeconiah, through whom the Messiah could not come. The "seed of the woman" (Genesis 3:15) and "a virgin shall be with child" (Isaiah 7:14) feature heavily in his argument. There is no reference to the male line in either prophecy. He also notes the use of the definite article prior to every name in Luke's list, except for Joseph. He says this would have been a clue to any reader (in the original language) that the genealogy was not that of Joseph. Instead, it was of his unnamed wife. Putting aside his virginal conception, Jesus could not be the son of Joseph, according to Fruchtenbaum, because then Jesus could not be the Messiah.[18]

If Luke is tracing the line of Mary, this would be a unique feature of the Bible. In no other place are the rights of inheritance traced through a woman.[19] Either way, most scholars at least agree that Matthew is tracing Joseph's lineage.

Option 2—Matthew and Luke both trace the line of Joseph

The other common view attempts to blend the genealogies together. Sanders outlined the possibility of the existence of multiple adoptive and levirate relationships among the men listed in Matthew's genealogy, but also left open the possibility of missing generations.[20] She notes that the Greek wording in both genealogical accounts strongly indicates that Joseph is the father of Jesus (see below). One solution to the dilemma is that under Jewish law, when a man died without a son, the man's brother was expected to marry the widow and raise a son for his brother (Deuteronomy 25:5–10). These are called 'levirate marriages' (from the Latin *levir*, 'husband's brother').

As mentioned above, this thinking has a long tradition in Christian scholarship. In the *Letter to Aristides*, Africanus suggested that after Jesus' grandfather Jacob was born, Jacob's father (Matthan) died. The widow then married a man named Helsi and they had Heli. After marrying, Heli died. Being that Jacob was Heli's half-brother, he had a levirate marriage to the widow and together they had Joseph. If you find this confusing, you are not alone. The point is that levirate marriages commingle family lines and provide

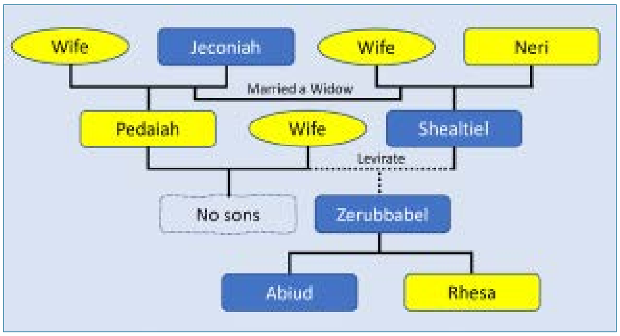


Figure 2. Combining the three genealogies of Shealtiel and Zerubbabel in 1 Chronicles, Matthew, and Luke leads to this possible solution. Names in blue indicate those who held the sceptre. In this schema, 1 Chronicles traces the genealogy of David, through Solomon to Pedaiah, then through Pedaiah to Zerubbabel via a levirate marriage. This would be technically and legally correct. Matthew, on the other hand, traces those who held the sceptre, and so skips over Pedaiah and creates a break in Jeconiah's bloodline. Finally, Luke traces the specific genealogy of Joseph from David, via Nathan, to Neri, Shealtiel, Zerubbabel, and Rhesa.

a possible solution. It is also important to note that levirate marriages can occur at various levels of kinship (e.g., Ruth 4:1–12), not just between brothers.

What if Matthew wrote out a king list, not a genealogy?

One addition to this hypothesis that most have missed is the idea that Matthew's list might be a king list, not a genealogy. This is found in the writings of Machen[21] and John Piper,[22] but neither of them flesh it out much.[23] Machen writes:

> "The most probable answer is that Matthew gives the legal descendants of David—the men who would have been legally the heir to the Davidic throne if that throne had been continued—while Luke gives the descendants of David in that particular line to which, finally, Joseph, the husband of Mary, belonged" (p. 64).
>
> "But on the whole we are inclined to think that the true key to a solution of the problem (however the solution may run in detail) is to be found in the fact that Matthew, in an intentionally incomplete way, gives a list of incumbents (actual or potential) of the kingly Davidic throne, while Luke traces the descent of Joseph, back through Nathan to David" (p. 65).

There are significant differences between a genealogy and a king list. For example, if an outside observer did not know the detailed history of the British monarchy, they might be fooled into thinking these are parent/child relationships, yet fully half of them are not (appendix 2). What might that tell us about Matthew's list?

If Matthew contains a list of eligible kings, it is not a list of *actual* kings, so there are no co-regencies, etc. Any time a man died without a male heir, the birthright would shift to another line. If that sonless man lived to a ripe old age, his brother, nephew, maybe even grandnephew, may have predeceased him. Thus, the sceptre would have passed to a much younger person and the name list would skip several generations. This alone might explain the shortness of Matthew's list.[24]

How can Matthew and Luke both trace *Joseph's* line?

Following Sanders,[13] and contrary to Fruchtenbaum, the Greek seems to indicate that both lines are tracing Joseph's lineage. Matthew 1:15b–16 reads:

> Ματθὰν δὲ ἐγέννησεν τόν Ἰακὼβ Ἰακὼβ δὲ ἐγέννησεν τόν Ἰωσὴφ τὸν ἄνδρα Μαρία
>
> (… Matthan begat Jacob, Jacob begat Joseph, the husband of Mary …).

Luke 3:23–24a reads:

> ὢν υἱος ὡς ἐνομίζετο Ἰωσὴφ τοῦ Ἡλὶ τοῦ Μαθθὰτ τοῦ Λευὶ
>
> (… the son, as was supposed, Joseph, of Heli, of Matthat, of Levi …).

How can both accounts trace the line of Joseph when they are so entirely dissimilar? Was Joseph's father named Jacob or Heli? If Matthew's list is not a genealogy, the mystery might be solvable.

Yet, much has been made of a single missing word in Luke 3:23 (e.g., "the son … Joseph, of Heli …", instead of "the son … of Joseph, of Heli …"). Fruchtenbaum,[7] Robertson,[25] and Sarfati[26] all assert that the omission would indicate to any Greek reader that Joseph was not to be included in the list. Hence, Heli would be Mary's father instead of Joseph's. The Talmud (Hagigah 2:2) also states that Heli was Mary's father. On the other hand, Joseph starts off the list in Luke's genealogy, and writing 'of Joseph' would have indicated that Jesus was Joseph's son, which would be an error. Many have asserted that Mary's reputed father, Heli, may have adopted Joseph if he had no sons of his own. Thus, Joseph *can* be the 'son' of Heli even if Mary is Heli's daughter. This, though, does not address the repetition of Shealtiel/Zerubbabel in the three lists. Unless Mary is also a descendant of Zerubbabel, as some others claim. Yet that proposition does not explain how the names in 'Mary's' genealogy are so different than those of 'Joseph' or how 'Mary's' line could go back to Nathan.

Machen was a contemporary of Robertson and would have been aware of his views, especially since his quotes, above, were printed a full decade after the publication of Robertson's *A Harmony of the Gospels* (1922). One wonders why Machen disagreed with the others. He was certainly competent in the original language (e.g., he wrote an influential NT Greek textbook[27] that was used in many seminaries for decades after he died).

Who was Zerubbabel?

In the first year of Cyrus the Great (ruled 559–530 BC), a group of 42,360 Jews returned to Judah (Ezra 2:1–2, 64; 3:8; 5:2). They were led by two men: Zerubbabel, who was appointed the provincial governor of Judah (Haggai 1:1, 14), and the priest, Joshua son of Jehozadak. Scholarly sources refer to Zerubbabel as the 'Exilarch' (e.g., the head of the exile). Two of his sons, Meshulam and Hananiah, held that title after him, and Hananiah's descendants are detailed in 1 Chronicles (appendix 3). There is another important figure in the account, Sheshbazzar son of Jeconiah. He is referred to as 'the prince of Judah' (Ezra 1:8), and the 'governor' (Ezra 5:14). It can be assumed that the Shenazzar (son of Jeconiah) in 1 Chronicles is the Sheshbazzar (a prince and a governor of Judah) in Ezra. It was to him that the temple treasures were entrusted, although it was Zerubbabel who returned with them to Judah.

Contrast what God said about Jeconiah to what He said about Zerubbabel:

> "… though Coniah … were the signet ring on my right hand, yet I would tear you off …" (Jeremiah 22:24).
>
> "On that day, declares the Lord of hosts, I will take you, O Zerubbabel my servant, the son of Shealtiel, declares the Lord, and make you like a signet ring, for I have chosen you, declares the Lord of hosts" (Haggai 2:23).
>
> See also Zechariah 4:6–10.

Zerubbabel was the son of Shealtiel. Since Zerubbabel was a descendant of David, the remnant (Haggai 1:12) of the Jewish people knew who their leader was, even though the kingly line had nearly died out. Here is an open question: did God restore the line of Jeconiah, or was Zerubbabel from a different line (e.g., that of Nathan)? If the latter, the signet ring had been taken from Solomon's line and transferred to the line of Nathan. If the former, God had retracted His curse.

Sixty or more years after the death of Zerubbabel, one of Nehemiah's opponents claimed:

> "It is reported among the nations, and Geshem also says it, that you and the Jews intend to rebel; that is why you are building the wall. And according to these reports you wish to become their king. And you have also set up prophets to proclaim concerning you in Jerusalem, 'There is a king in Judah'" (Nehemiah 6:6b–7a).

This provides a hint that the Jews were tracking who held the right to the throne, even if they never intended to act on it. And it does not have to be true that this was common knowledge outside the citizens of the village of Bethlehem later on. Even today, there are multiple living people descended from royal families who are alive but will never be in positions of power. This includes individuals from countries like Albania, Burundi, China, Korea, Finland, France, Hawaii, and Mexico. Most people in the world are completely unaware of this, yet the (extended) families certainly have not forgotten.

To resolve the problem of multiple Shealtiel/Zerubbabel pairs, it is possible that men with the same name would appear in different family lines at about the same time.[28] We can see other common names in the biblical account throughout this period.[29] The problem is that the Shealtiel/Zerubbabel combo occurs in three different lines (1 Chronicles, Matthew, and Luke). It is entirely *unlikely* that the name combination happened independently so many times. Two pairs might be a fluke. Three pairs requires a better explanation.

A proposed solution

Marshall claimed, "It is only right therefore to admit that the problem caused by the existence of the two genealogies is insoluble with the evidence presently at our disposal."[30] Was he correct? What if an answer to the dilemma existed? What we would need is a solution that is faithful to Scripture, that incorporates multiple minor details given to us in a dozen biblical books, and that properly handles prophecy, historical narrative, and straight-up genealogy. This solution needs to match Old Testament law and must have as few assumptions built into it as possible. There could be more than one possible solution, but consider figure 2.

Assuming there are no missing generations, we might be dealing with different genealogical tables in 1 Chronicles 3 and Matthew 1. The reason the descendants of Jeconiah don't match might be due to the simple fact that the Chronicler recorded only a subset of the genealogy and Matthew pulled from a different subset. In the world of genealogy, descendant trees are much more complex than ancestor trees. Even though the number of places in the family tree goes up by a factor of '2' for each generation in an ancestor tree, the number of people in a descendant tree is indeterminant and multi-branched and there is no simple way to display multi-generational descendant trees (e.g., the information in Genesis 10). It might also be true that many of the men listed went by more than one name. Thus, there might be no way to combine the two lists, and perhaps we should not expect to be able to do so.

However, there is an elegant and simple solution to the dilemma that incorporates all the relevant information without any contradictions and without any appeals to special pleading. It does, though, involve two steps that are not mentioned in Scripture. Each is probable and each occurred many times in history, so it is not like we must chain together a series of improbable events.

If Jeconiah had several wives, which is not unexpected, and *if* he married a widow who already had a son, that son would have become the son of Jeconiah by adoption. We do not need to know how many wives or how many sons Jeconiah had or by whom. We only need to surmise that he had an older son named Pedaiah by one wife and a younger

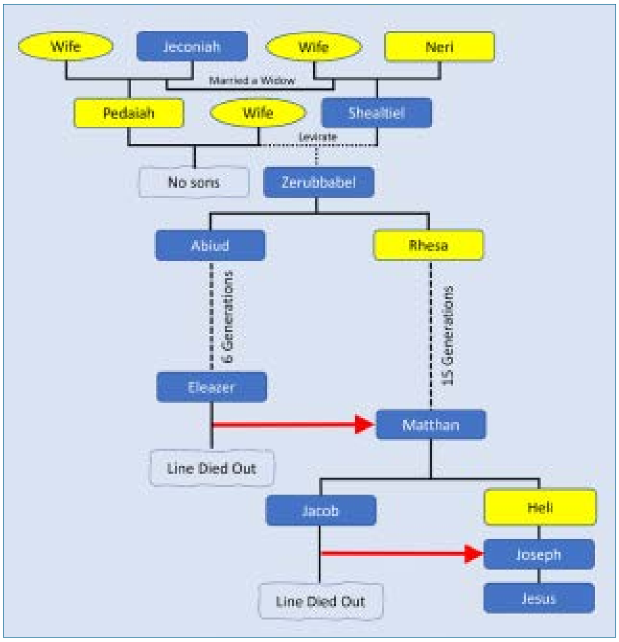


Figure 3. One possible way that the sceptre passed fom Abiud's descendants to a descendant of Rhesa and then from Jacob's line to the son of Heli. As above, the names in blue indicate those who held the sceptre. The red arrows can indicate lineage tracing, marriages to widows who already had a son, adoptions, or levirate marriages, as necessary.

adopted son named Shealtiel by another wife. Pedaiah's being older is an assumption, but it is not critical. It is assumed that it would be unlikely that a former king would marry a woman who already had a son before he had at least one son of his own. The next assumption is that Pedaiah married but died without having any sons. In that case, it was the duty of the stepbrother to marry Pedaiah's widow so he could raise up a son in Pedaiah's name. In fact, had he not done this, he would have been cursed according to the Law (Deuteronomy 25:7–10). The result of this levirate marriage was "Zerubbabel son of Shealtiel". The third assumption is that Pedaiah died before his father.

This putatively solves the puzzle:

- 1 Chronicles 3 traces the levirate line:
  Jeconiah → Pedaiah → Zerubbabel
- Matthew 1 traces the sceptre:
  Jeconiah → Shealtiel → Zerubbabel
- Luke 3 traces the genealogy of Joseph:
  Neri → Shealtiel → Zerubbabel

All three genealogies are correct and true. There is no ambiguity and there are no contradictions in this solution.

Intermarriage among the descendants of David

Consider the final three generations in Matthew and Luke:

- Matthew: Matthan → Jacob → Joseph
- Luke: Matthat → Heli → Joseph

Are Matthan and Matthat the same person? The name similarity is striking. If so, Matthan had two sons, Jacob and Heli. If Jacob was older, and if he died without any sons, the kingship would have transferred to the closet relative. If Heli was already dead, the sceptre would have gone to Joseph (figure 3).[31]

There are many possible ways for the sceptre to have passed from one line to another among the descendants of Zerubbabel. Levirate marriages and adoptions can keep a line going forward, as seen above. But lineage tracing can be used to restore a line that was lost. For example, if the Eleazar in Matthew's list failed to have any sons, a search would have been made for the closest living male relative. Even if they had to go all the way back to the sons of Zerubbabel, this would not have been impossible. In fact, that would mirror the 'Capetian Miracle' that happened in 16th-century France (appendix 2). If that closest relative was Matthan, Matthew would list him as rightful heir and the two New Testament genealogies would be united, briefly. They would have had to be re-united two generations later for Matthew to list Joseph as the rightful heir and for Luke to list him as the (supposed) father of Jesus. In fact, many such events could have happened in the generations between Abiud and Eleazar. All Matthew gave us was a list of the men who held the sceptre, not their genealogical connections.

Fruchtenbaum claimed:

> "Therefore if Jesus were the real son of Joseph, he would have been disqualified from sitting on David's throne. Neither could he claim the right to David's throne by virtue of his adoption by Joseph, since Joseph was not the heir apparent."[7]

Yet, in the construct suggested above, Joseph is not Jeconiah's descendant by blood. Given any number of possible scenarios, the sceptre could have passed from Solomon's line to that of Nathan. Fruchtenbaum also points out that his solution (i.e., Luke traces Mary's line) is only one of several possibilities, linking to an article that asserts that Jeconiah repented and was restored.[32]

Is Matthew's list really a king list?

Option 2 is a real possiblity. We have a realistic explanation that incorporates all the facts and produces a system without any contradictions. *This does not mean that it is true*. However, it does mean that the differences between 1 Chronicles 3, Matthew 1, and Luke 3 do not contradict one another. It also opens up additional theological considerations. For example, did the people around Jesus know that he was the rightful king of Judah (appendix 4)?

Conclusion

If we have a workable solution, biblical skeptics will have to look elsewhere for reasons to reject the Bible. The thought that Matthew is tracing the kingly line does nothing but strengthen the perspecuity of Scripture. This is just one more example of the self-consistency of the text. If the Bible was *not* the Word of God, we would expect to find many errors and contradictions, and we would throw up our hands when approaching difficult challenges like this. If, on the other hand, the Bible is what it claims to be, we would expect to be able to work out solutions to vexing problems like an apparent genealogical discord. And we can.

References

1. E.g., see Genealogy of Jesus, rationalwiki.org.
2. Miller, G.D., Trying to fix the family trees of Jesus, *Scripture Bulletin* 39:17–30, 2009. Miller also states, in *Questiones Evangelicae ad Stephanum*, that Eusebius suggested Luke's account was made up to pacify the Jews who believed the Messiah could not have come through Jeconiah.
3. See, for example, *The IVP New Testament Commentary Series: Luke* (Bock, D.L.), Intervarsity Press, 1994; See The genealogy of Jesus (3:23–38), biblegateway.com.
4. For background research on this article, I consulted: Poole's *A Commentary on the Holy Bible*, 1685, MacDonald Publishing Company, 1985; Matthew Henry's *Concise Commentary on the Whole Bible*, 1706, Thomas Nelson, 1997; John Gill's *Exposition of the Bible* (a multi-volume work published 1746–1763, available online); Robertson's *A Harmony of the Gospels*, Harper, 1922; Machen's *The Virgin Birth of Christ*, Marshall, Morgan, and Scott, 1930; *The Wycliffe Bible Commentary*, Moody Bible Institute, 1962; Busswell's *A Systematic Theology of the Christian Religion*, Zondervan, 1962; Clarke's *Commentary on the Bible*, Baker Book House, 1967; *Unger's Bible Handbook*, Moody Press, 1967; Marshal's *NIGTC Commentary: the Gospel of Luke*, Eerdmans, 1978; Trapp's *A Commentary or Exposition of the New Testament*, Baker Book House, 1981; Nicoll's *The Expositor's Greek New Testament*, Eerdmans, 1983; *The Holman Illustrated Bible Dictionary*, Holman Bible Publishers, 2003; and, *The Dictionary of Jesus and the Gospels*, Intervarsity Press, 2013. I also included various web articles and blog posts in my search, some of which are referenced later in the article. I avoided scholars who followed the trends of higher criticism and focused on a selection of more conservative works that spanned several centuries. Other works that did not add anything new to the discussion were excluded from the list above.
5. E.g., see Sproul, R.C., The genealogy of Jesus, ligonier.org, 11 Mar 2012.
6. This position can be found in, for example, the footnotes in *The Reformation Study Bible*, edited by R.C. Sproul.
7. Hardy, C. and Carter, R., The biblical minimum and maximum age of the earth, *J. Creation* **28**(2):89–96, 2014.
8. In the words of Myles Smith, who wrote the introduction to the first edition of the King James Bible, "It has pleased God in his divine providence, here and there to scatter words and sentences of difficulty and doubtfulness, not in doctrinal points that concern salvation (for in such it has been vouched that the Scriptures are plain), but in matters of less moment, such that fearfulness would better beseem us than confidence." Let us take this admonition to heart as we wrestle with a very difficult topic.
9. For example, David had 20 named children and additional unnamed ones via his several concubines (1 Chronicles 3:1–9).
10. For example, the names of only three of Solomon's children, two of whom were daughters, are known, even though he had 700 wives and 300 concubines (1 Kings 4:11, 4:15, 11:3).
11. For example, Jehoram son of Jehoshaphat killed his seven brothers and multiple princes when he took the throne (2 Chronicles 21:4). Later, Israel's King Jehu slaughtered the relatives of Judah's King Ahaziah (2 Kings 10:12–14), which was followed by the slaughter of the royal family by Athaliah, the mother of Ahaziah. Only one of Ahaziah's sons (Joash), but at least one sister (Jehosheba) survived (1 Kings 11:1–3).
12. Solomon was not the oldest surviving son of David, and, being the fourth son of his mother, was not even the oldest surviving son of David and Bathsheba.
13. From Solomon to Josiah, there was but one exception to the rules of primogeniture (Queen Athalia), but even then, the proper order was restored when Jehoash, the young son of her deceased husband (Jehoram) by another wife (Zibiah), was placed on the throne.
14. The problem of the curse on Jeconiah in relation to the genealogy of Jesus, jewsforjesus.org, 1 Jan 2005.
15. In addition, eight or nine generations are listed after Jeconiah (appendix 1). This is far too many to fit into the timeline of when Chronicles was composed, leading some scholars to postulate a composition date much later than Ezra/Nehemiah.
16. Carter, R. and Sanders, L., How long were the Israelites in Egypt? creation.com, 21 Sep 2021.
17. Sarfati, J., Biblical chronogenealogies, *J. Creation* **17**(3):14–18, 2003.
18. Fruchtenbaum, A.G., The Genealogy of the Messiah: the New Testament traces Jesus lineage through David and Abraham, jewsforjesus.org, 20 Apr 2018.
19. Perhaps with the exception of the Daughters of Zelophehad (Numbers 26:33; 27:1–11; Joshua 17:3–4). But this case is more about property rights and how property was to be distributed and inherited among the clans than about genealogy.
20. Sanders, L., The genealogies of Jesus, *Creation* **37**(1):22–25, 2015.
21. Machen, J.G., *The Virgin Birth of Christ*, Harper & Brothers, New York, chap. 14, 2nd edn, 1932. This work is cited in Sarfati's *The Virginal Conception of Christ* (ref. 21 below), but Machen held to 'Option 2' while Sarfati holds to 'Option 1'. The first edition (1930) is available online; monergism.com/thethreshold/sdg/machen/virginbirth_p.pdf.
22. Piper, J., The baptism and the genealogy of Jesus, desiringgod.org, 23 Feb 1981.
23. According to Miller (ref. 2), Jean Calvin also supported this theory, but without appealing to levirate marriages, so he failed to address the commingling of the names Shealtiel and Zerubbabel in the three lists. He cites Calvin, J., *Commentaries on a Harmony of the Evangelists Matthew, Mark, and Luke*, vol. 1, 1845.
24. Is it also possibile that an unrealized king list might jump from the dead 'king' to the end of the line? This would be akin to Prince George being named 'king', skipping over Charles and William, after the recent death of Queen Elizabeth II.
25. Robertson, A.T., *A Harmony of the Gospels*, Harper, San Francisco, NY, p. 261, 1922.
26. Sarfati, J., The virginal conception of Christ, creation.com, 24 Dec 2014.
27. Machen, A.W., *New Testament Greek for Beginners*, McMillen, Toronto, 1923. Note: I used this in my Greek classes in the 1990s.
28. In my own family, my great-great-grandfather, Henry Augustus Hurlbut, was named after his uncle, a rich financier and philanthropist. But the uncle named his son after himself. A third brother also named his son after the rich brother: three cousins and an uncle all shared the same name!
29. For example, King Josiah had a son named Johanan, but another Johanan (the son of Kareah) featured heavily in the account around this time (c.f., Jeremiah 43:1–7). Also, Jeconiah had a brother named Zedekiah, the same name that Nebuchadnezzar assigned to their uncle Mattaniah.
30. Marshal, I.H., *NIGTC Commentary: The Gospel of Luke*, Eerdmans, Grand Rapids, MI, p. 159, 1978. Quoted in ref. 20.
31. Piper, J., Who Was Jesus' Grandfather? desiringgod.org, 18 Nov 1997.
32. The problem of the Curse on Jeconiah in relation to the genealogy of Jesus, jewsforjesus.org, 1 Jan 2005.

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.*

Non-existence of error correction in plausible prebiotic amyloids

Royal Truman and Chris Basel

Nanda *et al.* have claimed that equilibrating networks of peptides can 'correct errors' by decreasing the proportion of side-chain products and D-amino acid configuration. Their system involved highly concentrated peptides having sequences able to template the reactions by forming β-sheets. The three amino acids used would not have been present prebiotically. Most of the individual experiments led to the wrong results, but a MATLAB simulation indicated that some combinations of chemically modified and activated peptides could favour the linear peptides. *This was not validated experimentally.* The mathematical model had been expertly calibrated for an unrealistically high concentration of peptides (lower concentrations gave the wrong results) and limited to 0–2.5 minutes. Examination of the computed predicted trends confirmed what was already known from the laboratory results: the results (which affected only a single amino acid residue in the final peptide), were *at best a transient artefact* which would have disappeared within minutes, long before the two peptides would have condensed.

In a review article on prebiotic amyloids, key advocate Maury wrote, in 2018:

> "The prebiotic relevance of the β-sheet networks and assemblies was recently highlighted … by Nanda *et al.* [21] who demonstrated error correction within replication networks through the emergence of short polymers exhibiting selective autocatalytic properties."[1]

Error correction is a fundamental property of living cells, and the emergence of *replication networks* under prebiotic conditions would indeed be major news. Selective autocatalytic networks involving processes relevant to life would also be a significant breakthrough.

Therefore, examination of the referred paper titled "Emergence of native peptide sequences in prebiotic replication networks", by Nanda *et al.*, published in the prestigious journal *Nature Communications*, seemed justified.[2] Had significant discoveries been made?

Experiment 1: reaction of peptides E and N alone

This is another study involving synthetic peptides which produced large β-sheet complexes under the right laboratory conditions.[3–5] In the current experiments, two complementary polypeptides were designed, labelled E (Electrophile) and N (Nucleophile).[2] The three amino acids used were phenylalanine(Phe), glutamic acid (Glu), and proline (Pro).

The E isomers contained five residues plus capping groups:

E isomers: ABA-Glu-Phe-Glu-Phe-Glu-COSR

where ABA = 4-acetamidobenzoate, and the end carboxylic acid of glutamic acid had been activated to a thioester, SR = 4-mercaptophenylacetic acid (MPAA).

The N peptide contained seven residues plus a protecting capping group at the end: carboxylic acid:

N peptide: NH_2-Phe-Glu-Phe-Glu-Phe-Glu-Pro-$CONH_2$

E contained a chiral α-carbon and two -COOH positions which the nucleophile could attack, via the reaction:

$$E + N \rightarrow 2,\ 2^D,\ 2_\gamma,\ 2^D_\gamma \qquad (1)$$

where the superscript D referred to the D-enantiomer at the α-position and no superscript to the L-enantiomer. The γ subscript refers to the side-chain position, otherwise the end-position is meant. The four isomers formed are shown in figure 1.

Ligation to form product 2 and 2^D were driven by the highly reactive glutamic acid thioester (-SR) on E, which condensed with the free Phe amino position of nucleophile N. Only a trace amount of the thioester group on E migrated to the γ position on E^D_γ and none to E_γ as shown in figure 6 in their Supplementary file.[2]

Product peptide 2 formed β-sheets as designed, since it possessed alternating hydrophobic and hydrophilic residues and a homochiral backbone. Multiple copies led to amyloid fibril structures consisting of antiparallel peptide bilayers, and, with enough time, large hollow tubes were formed.[2]

An important observation was that the thioester group led to rapid racemization $E \rightleftharpoons E^D$ of the glutamic acid chiral α-carbon. According to figure 6 in their Supplementary file, the L-Glu residue would have only required ≈ 1 month to

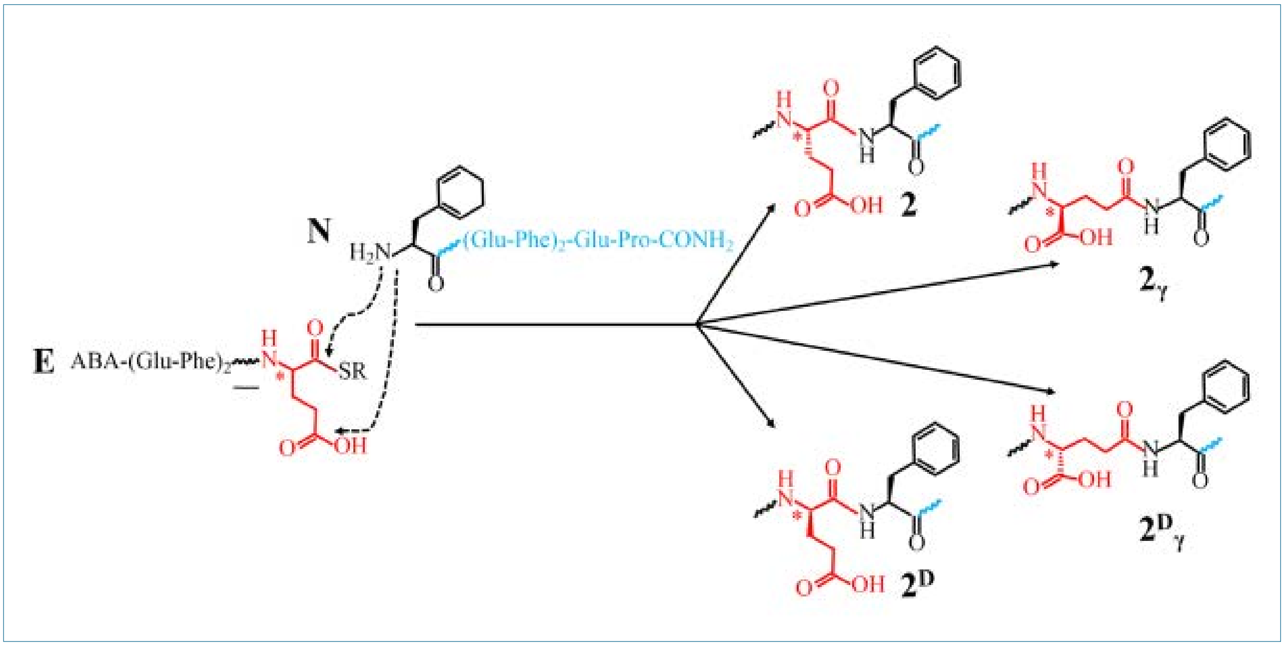


Figure 1. Ligation reaction of peptides **E** (200 μM) and **N** (300 μM) leading to four isomeric products.[2] The glutamic acid involved in the peptide bond is shown in red. ABA = 4-acetamidobenzoate; SR = 4-mercaptophenylacetic acid (MPAA). Artwork by R. Truman based on structures from ref. 2.

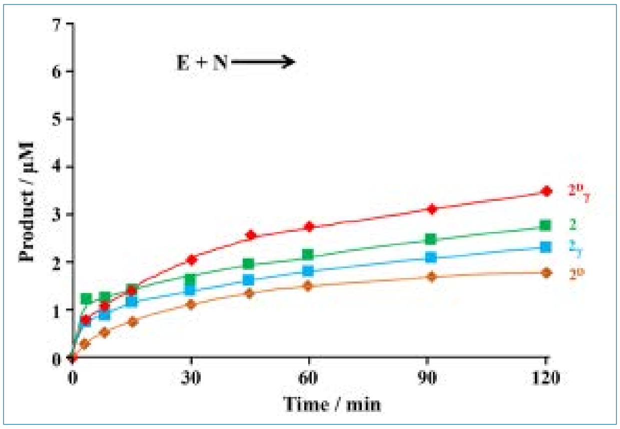


Figure 2. Yield of the four isomers over time from the reaction of peptides E (200 μM) and N (300 μM). Redrawn with slight modification from figure 1a in ref. 2.

become racemic under very mild conditions (75 μM E or E^D in 200 mM MOPS buffer (pH = 7) at room temperature).

Even more startling, examining the reaction E + N → revealed that after 120 hours, the major product was not the hoped-for linear product E having an L-Glu residue, but rather the γ side-chain enantiomer, 2^D_γ having the D-enantiomer as shown in figure 2. Recall that only the end carboxyl group had been activated and not the sidechain one, which nevertheless ended up reacting preferentially.

Figure 2 identifies one critical flaw in this paper: the experiments (and later computer simulation) must be discontinued after about 5 minutes to obtain primarily the desired product 2.

Pure D-enantiomer also led to 2^D_γ preferentially:

$$E^D + N \rightarrow 2^D_\gamma \text{ (major product).} \tag{2}$$

As expected, activated γ-COOH also reacted with N to produce primarily 2^D_γ:

$$E^D_\gamma + N \rightarrow 2^D_\gamma \text{ (major product)} \tag{3}$$

$$E_\gamma + N \rightarrow 2^D_\gamma \text{ (major product).} \tag{4}$$

In all cases (1) – (4), much less linear peptide 2 was produced, whether starting with D-enantiomer (E^D or E^D_γ) or L-enantiomer (E or E_γ)! The details are shown in figure 5 of their Supplementary file.

Experiment 2: reaction of E and N with a template

Close analogues of the four isomer products 2, 2^D, 2_γ, and 2^D_γ, labelled *i*-2, *i*-2^D, *i*-2_γ, and *i*-2^D_γ, were synthesized.[2] All contained the same twelve residue sequences. The isomer structure and chirality matched pairwise (e.g., 2 with *i*-2; 2^D with *i*-2^D). The only difference was the chemical cap added to the N-end amino group: 4-acetamidobenzoate (ABA) for the 2x isomers vs 4-iso-butylamide benzoate (IBA) for the *i*-2x isomers. Both series had their C-end carboxyl -OH replaced by a stabilizing $-NH_2$ cap to stabilize and hinder chemical reactions there.

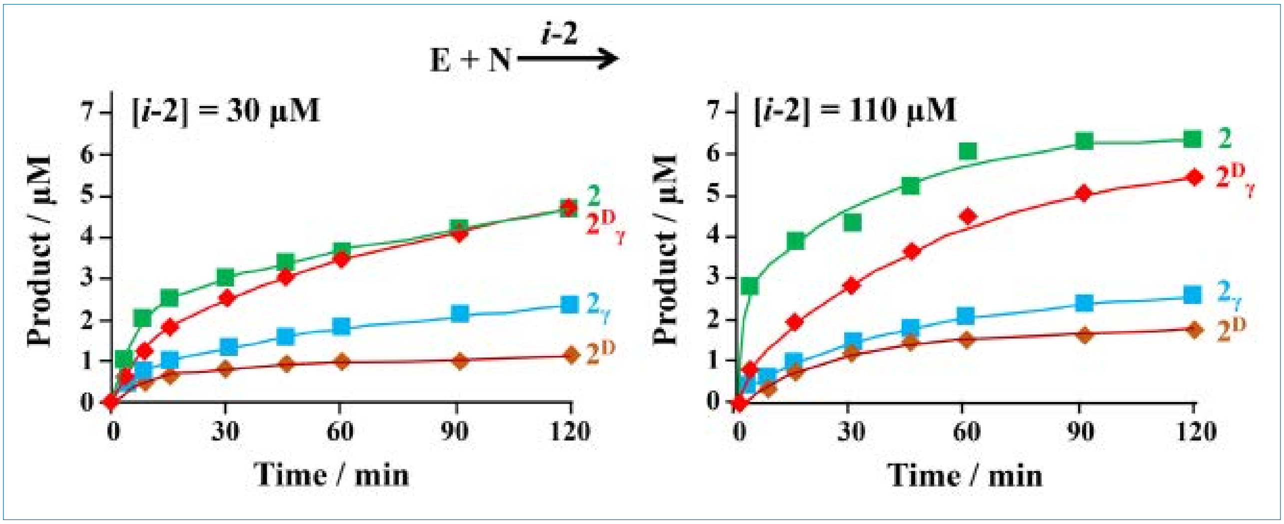


Figure 3. Yield of the four isomers over time from the reaction of E (200 μM) with N (300 μM) in the presence of template *i*-2. Left panel: [*i*-2] = 30 μM. Right panel: [*i*-2] = 110 μM. Redrawn with minor alternations from figures 6a and 6b in ref. 2.

The researchers knew that both 2 and *i*-2 could form amyloid fibrils but did not explain why a different cap was used for the new template peptides nor justify this for origin-of-life purposes.

The E and N peptides were reacted in the presence of template peptide *i*-2, leading to the proportion of four isomers and very low yields shown in figure 3.

Comparing figures 2 and 3 shows that the yield for 2 and 2^D_γ were somewhat higher in the presence of *i*-2, but the template had little effect on the yield of 2^D and 2_γ.

Two important observations from figure 3 were not emphasized by the authors: 1) Yields $[2] > [2^D_\gamma]$ after 120 mins, *only at the higher concentration of template i*-2; 2) After 120 mins*, the yield of 2 had levelled off* whereas 2^D_γ was continuing to increase at both of the concentrations. After only about four hours, the 'undesired' 2^D_γ would have dominated if the concentration of 2^D_γ indeed continued to increase.

The team then examined the effect of using the other three templates *at only the high concentration of 100 μM* and *for no longer than 120 mins*. After 120 mins, in all cases 2^D_γ was the major product; using template i-2^D_λ led to about twice as much 2 as 2^D_γ whereas $[2] \approx [2^D]$ when using templates i-2^D and i-2^D_γ. These results are shown in figure 9 of their Supplementary file.

Experiment 3: reaction of E isomers and N in four templates

The four thioester isomers E, E^D, E_γ, and E^D_γ, were reacted with N mixed with 100 μM of templates i-2^D, i-2_γ, or i-2^D_γ.[2] Only some of the twelve combinations were tested and, of these, not all four 2x isomer products were reported. All except one produced 2^D_γ as the major product after 120 mins (see figures 9 –12 of their Supplementary files). In other words, no *backbone correction* resulted.

A complex *MATLAB* model predicted backbone correction; i.e., $[2] > [2^D_\gamma]$ for some combinations according to their Supplementary figure 14 ($E^D + N$; $E_\gamma + N$; $E + N + 2$; $E + N + 2^D_\gamma$; $E^D + N + 2$; $E^D + N + 2_\gamma$). But also the opposite, $[2^D_\gamma] > [2]$, was found in other cases like $E^D_\gamma + N$, according to figure 8 in their main text. However, the special conditions were *0–2.5 minutes and 250 μM each peptide*. Critically, the observation pointed out above for figure 2 was already apparent for the simulated behavior within 2.5 minutes: the yield of 2 begins to level off but that of 2^D_γ continues to increase linearly.

Discussion and conclusions

Peptide 2 was desired since it conserved an L-glutamic acid and avoided the side-branch reaction.

A *MATLAB* model using more than 40 equations (see Supplementary figure 13) predicted that the backbone correction mechanism could occur for some combination of reactants and templates (but not others) under seriously unrealistic prebiotic conditions. This is another example of an expertly tailored origin-of-life experiment having been designed and interpreted to produce the result desired.[6] Critically, why were the predictions from the incomprehensibly complex *MATLAB* model not simply validated by mixing the components simulated? This should have been an easy experiment, no simulation was necessary.

Conclusion 1. The expertly designed system could have, *at best*, affected the chirality and side-chain reaction of a single artificially activated amino acid within a large peptide, in very low yield.

Reaction not realistic in a pre-life Earth

The detailed 2023 review by Kobayashi *et al.* on the major sources of prebiotic amino acids showed no Phe, Glu, or Pro being formed.[7] Analysis of the Murchison meteorites showed no Phe or Pro, and Glu only in ppb levels.[8] Forming peptide bonds in water is very endothermic, and the five- and seven-residue E and N peptides would not have formed in measurable amounts, far less as amphiphilic sequences co-located in high concentration. Over time, the entire sequences would have racemized, especially after glutamic acid had been converted to thioester, as mentioned above, preventing stable β-sheets from forming.[9]

If the reaction E + N → could have occurred prebiotically in high concentration, the proportion of any template present would have been negligible, and the authors admit that the side-branch D-enantiomer 2^{D}_{γ} would have been the major product. If any template had been present, it would have been 2^{D}_{γ} or *i*-2^{D}_{γ}, resulting in an ever more preferential yield of 2^{D}_{γ}, as shown in figure 9 of their Supplementary file.

Had instead some of the best 'template' *i*-2 been present, it would have been in miniscule proportion. Furthermore, figure 3 shows that after 120 hrs more 2^{D}_{γ} than 2 would have been produced anyway.

> Conclusion 2. Experimental conditions were selected to optimize the desired peptide 2, whereas natural conditions would have produced more product having both the wrong stereochemistry and side-branch reaction.

The term 'error correction' is misleading

The authors wrote that

> "Finally, we note that our results are in line with the old notion that the emergence of a primitive replicator was crucial and potentially sufficient for the origin of life further down the road."

Suppose this replicator had managed to *remove errors*, leading to an identical sequence. How could anything homogeneous, like identical crystals with no 'errors' left, be, or become, living?

The proposed β-sheets responsible for the "correction of the evolutionary drift towards non-functional heterogeneous mixtures" would have led to only insoluble amyloids, not the necessary variety of proteins having a vast range of tertiary structures.

Error only has meaning with reference to a purpose. Flawed biochemicals are *erroneous* if a biological function is hindered, not because they deviate from some templating, homogenous structure. To their credit, the authors did mention that post-replication error correction after DNA polymerization and removal of defective proteins in cells proceed in completely different manners than their equilibrating network. But it confuses matters to talk about error correction, which has no functional meaning.

> Conclusion 3. A mechanism that forces peptides to adopt a homogenous shape has no relevance to error correction in living systems.

References

1. 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.
2. Nanda, J., Rubinov, B., Ivnitski, D. *et al.*, Emergence of native peptide sequences in prebiotic replication networks, *Nat. Commun.* **8**:434, 2017.
3. Rubinov, B., Wagner, N., Rapaport, H., and Ashkenasy, G., Self-replicating amphiphilic β-sheet peptides, *Angew. Chem. Int. Ed.* **48**:6683–6686, 2009.
4. Rubinov, B. *et al.*, Transient fibril structures facilitating non-enzymatic self-replication, *ACS Nano* **6**:7893–7901, 2012.
5. Raz, Y. *et al.*, Effects of mutations in de novo designed synthetic amphiphilic β-sheet peptides on self-assembly of fibrils, *Chem. Commun.* **49**:6561–6563, 2013.
6. Truman, R., Clean-up and analysis of small datasets can distort conclusions, *J. Creation* **36**(2):66–71, 2022.
7. Kobayashi, K., Ise, J.-i., Aoki, R. *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.
8. Koga, T. and Naraoka, H., A new family of extraterrestrial amino acids in the Murchison meteorite, *Sci. Rep.* **7**:636, 2017.
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.

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.*

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.

Authors should:

- check creation.com before submitting an article to ensure their topic has not already been published; this can be a source of good references
- familiarize themselves with the journal, including its position and style
- address previous articles on the topic, and ensure they are properly referenced
- indicate if their manuscript has been submitted elsewhere
- sign our copyright assignment form (see below).

All submissions should be made to journal@creation.com.

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, Research Notes, and Forums: 1,000–2,000 words; Book Reviews (please enquire first): 1,500–3,000 words—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 by the author will usually follow the criticism; Papers, Overviews, Countering the Critics, Viewpoints, and Essays: <5,000 words.

Style: 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 words or superfluous words; e.g., don't use "in spite of the fact that" when "although" would do. Please use first person sparingly, and do not use phrases like "this present writer" instead of "I", which is verbose, ambiguous, and can come across as false modesty. Personal invective and similar comments against others are not acceptable.

Care with spelling is important. *Journal of Creation* uses a (consistent) combination of US and British spelling to suit our multinational readership, though most words with variations between the two take the British spelling as used in the majority of readers' countries. US spellings we use consistently include 'ize' endings instead of 'ise', 'sulfur', not 'sulphur', 'program', not 'programme', 'airplane', not 'aeroplane', and 'hemoglobin'/'anesthetic' etc., not 'haemoglobin/anaesthetic' etc. But it's 'travelled', not 'traveled', and 'favour' not 'favor', litre/centimetre etc., not liter/centimeter etc.

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 be a summary of the key points of the paper, not an introduction, and be comprehensible to readers in and of itself (i.e., without the reader needing to read the paper to aid comprehension).

References: 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. The numbering of endnotes should be in normal (Arabic) numerals. 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 (for consistency, if abbreviating some consider doing so for others which have accepted abbreviations) , 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 (an automated cross reference using that function in Word); do not use 'ibid'. If a citation is to the same source but a different page, a new endnote should be made, but only the author/s name/s with a cross-reference should be given, in this format (do not use 'op. cit.'): Harris and Smith, ref. 11, p. 21. (11 is the automatically linked cross-reference number).

Quotes must be verbatim, with omissions clearly shown by ellipses (…) which should be separated from the text by a space either side of the 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 at the relevant place. Emphases must be in italics, and indicated by adding '[emphasis/es added]' at the end of the quote. 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 accessed 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 to journal@creation.com as *.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 width of 1,300 pixels.

Figures should be numbered according to their sequence in the text. References should be made to each figure in the text. 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 size 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 as granting 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 author's qualifications and experience, and involvement in creationist work.

Please also:

- Send documents in Word (*.doc) or Rich Text (*.rtf) format, not Publisher (*.pub) format. Excel (*.xls) is acceptable for complex tables.
- Type left-justified without hyphenation, except for compound words.
- Use single spaces after each sentence within a paragraph.
- Use Times New Roman 12 font, and use the word processing formatting features to indicate bold, italics, mathematical characters, and superscript and subscript characters.
- Use Unicode for non-English fonts (e.g., Hebrew, Greek)
- Submit complex mathematical formulas or equations using MathType according to the guidelines in our "Equations layout guide", which can be obtained by contacting us.

Copyright: Please note that we require all authors to assign copyright to *Creation Ministries International*. The link below has an online form that allows you do it in a few seconds, and it also explains why we do this (it's not to restrict you from using your own work). We would be grateful if you could tell us after electronically 'signing' this copyright form, as this will save time.

<©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

// 56
PAGES OF FULL
COLOUR
[NO PAID ADVERTISING]

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!

ISSN 1036-2916

Subscribe via CREATION.com, mail or phone (see inside front cover for contact details).