

make micrometre-sized structures, and to scale up the amounts that can be produced.

Tikhomirov *et al.*² (page 67) used square DNA origami decorated with surface patterns (formed by DNA strands that extend from the origami surface) as building units to create 2D DNA origami arrays up to about half a micrometre across (Fig. 1a). The square origami join together through the formation of short DNA duplexes at their interfaces. To program the interactions between the square origami, the authors developed a fractal method in which local assembly rules were used recursively in a hierarchical, multi-step process that assembles increasingly large arrays of the square origami. Tikhomirov and colleagues also produced design software called FracTile Compiler, which will enable non-experts to devise DNA sequences and experimental procedures to make large DNA patterns. The authors validated this automated design process by using it to make several DNA 'pictures', including the *Mona Lisa*, a rooster and a chess-game pattern (see Fig. 3 of the paper²).

Wagenbauer *et al.*³ (page 78) have made 3D DNA origami structures at sizes up to the micrometre scale, using another hierarchical self-assembly approach (Fig. 1b). They used a V-shaped DNA origami object as the basic building block, in which the angle of the V could be altered. By controlling the geometry and interactions between the building blocks, higher-order assemblies can be constructed. The authors demonstrated the capabilities of their method by constructing micrometre-long tubes (similar in size to some bacteria) out of stacked planar rings up to 350 nm in diameter, and three types of polyhedron up to 450 nm in diameter.

Ong *et al.*⁴ (page 72) report a method that allows 3D SST DNA constructs to be made at the micrometre scale (Fig. 1c). By extending the principles of first-generation SST systems, the authors designed a brick-shaped DNA building block composed of 52 nucleotides, which contains four 13-nucleotide binding domains. These domains enable the bricks to assemble into larger constructions. Compared with the first-generation bricks (which contained four binding domains, each composed of eight nucleotides), the longer binding domains of the DNA bricks provide better yields and stabilities for large assembled structures. The authors developed software called Nanobricks to design the brick strands needed to make target 3D objects, and used it to plan the synthesis of a set of different complex architectures (see Fig. 3 of the paper⁴).

Praetorius *et al.*⁵ (who belong to the same research group as Wagenbauer and colleagues; page 84) report biotechnology that should greatly reduce the cost of the hundreds of staple strands that are usually used to make DNA origami. They use viruses known as bacteriophages to produce single-stranded precursor DNA that contains hundreds of staple-strand

sequences. These sequences are separated by a 'DNAzyme' sequence that cleaves itself; the cleavage products then self-assemble into designed DNA origami shapes. Remarkably, the authors' method reduces the cost of the folded DNA origami structures from about US\$200 per milligram to around 20 cents. This strategy will enable scalable and efficient mass production of DNA origami and SST structures, thus enabling large-scale applications, such as therapeutics, drug-delivery systems and nanoelectronic devices.

The papers also offer solutions for long-standing challenges in the field of biomolecular engineering, providing low-cost methods for fabricating self-assembled structures from smaller building blocks, at sizes that can be integrated into objects made using complementary 'top-down' techniques (those that carve structures out of bulk material). Furthermore, the reported DNA structures are large enough to enable the production of devices that interact with cells for therapeutic applications, or to make sophisticated molecular machines and assembly lines that

make synthetic polymers or program cell-cell interactions. Such self-assembled structures might even be used in synthetic organelles to create systems that sense, monitor and regulate biological processes in living cells. ■

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- Whitesides, G. M. & Grzybowski, B. *Science* **295**, 2418–2421 (2002).
- Tikhomirov, G. *et al. Nature* **552**, 67–71 (2017).
- Wagenbauer, K. F. *et al. Nature* **552**, 78–83 (2017).
- Ong, L. L. *et al. Nature* **552**, 72–77 (2017).
- Praetorius, F. *et al. Nature* **552**, 84–87 (2017).
- Chen, Y.-J., Groves, B., Muscat, R. A. & Seelig, G. *Nature Nanotechnol.* **10**, 748–760 (2015).
- Li, J., Green, A. A., Yan, H. & Fan, C. *Nature Chem.* **9**, 1056–1067 (2017).
- Zheng, J. *et al. Nature* **461**, 74–77 (2009).
- Rothmund, P. W. K. *Nature* **440**, 297–302 (2006).
- Douglas, S. M. *et al. Nature* **459**, 414–418 (2009).
- Wei, B., Dai, M. & Yin, P. *Nature* **485**, 623–626 (2012).
- Ke, Y., Ong, L. L., Shih, W. M. & Yin, P. *Science* **338**, 1177–1183 (2012).

PALAEOONTOLOGY

A tip of the hat to evolutionary change

The relative roles of biological and environmental factors in driving evolutionary change have been unclear. Now fossil analysis shows that their action depends on where an animal group is in its evolutionary trajectory. SEE LETTER P.92

CHARLES R. MARSHALL

Assessing the relative importance of biological interactions (biotic factors) and changes in the physical environment (abiotic factors) in driving evolution has proved difficult, partly owing to the lack of high-quality data sets that combine both fossil remains and associated ancient environmental data. The few studies that have quantified the relative contributions of these two drivers describe a complex relationship¹. However, on page 92, Žliobaitė *et al.*² report an unexpectedly simple pattern of driver action in peak evolutionary success.

Between a species originating and becoming extinct, its evolutionary success can be measured in a number of ways, such as the extent of its geographical range. Such metrics often form a 'hat-shaped' curve, with a rise towards a central peak, followed by a decline to extinction. Why this pattern occurs so often and the degree to which biotic and abiotic factors influence this trajectory is a matter of debate.

To assess the relative role of biotic factors,

such as competition between organisms, and abiotic factors in evolutionary trajectories, Žliobaitė and colleagues analysed the fossil record of large herbivorous mammals. This grouping offers several advantages for this type of analysis. For instance, the authors could solve the problem of finding consistent regional ancient environmental data because the height of these mammals' teeth correlates strongly with characteristics of their environment, including precipitation levels³ and the amount of plant material in the ecosystem⁴. Without this measure, the authors would have had to rely on standard global measurements of environmental change, an approach that can mask substantial regional-level variation.

Another advantage is that these animals all share a similar ecological niche, so the authors could use the average number of genera (groups of closely related species) per locality to measure competition intensity, a biotic factor that is otherwise difficult to quantify. In addition, the fossil record of large mammalian herbivores is sufficiently rich that the proportion of localities in which

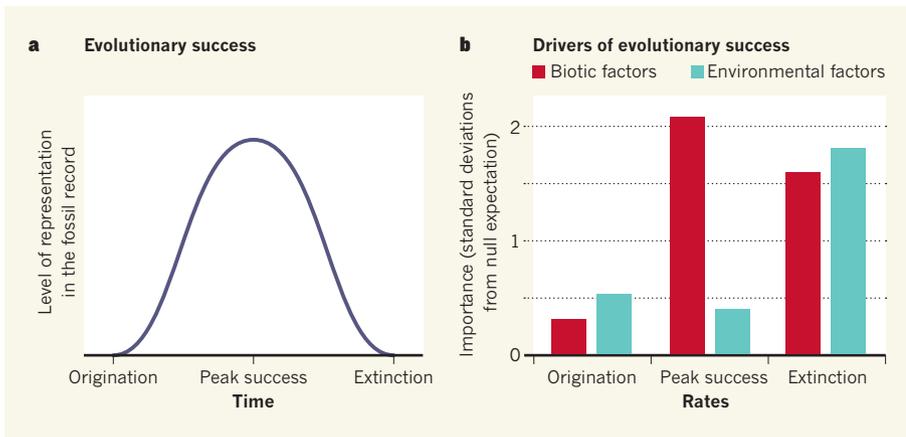


Figure 1 | Factors driving the evolutionary trajectory of large herbivorous mammals. Žliobaitė *et al.*² analysed the fossil record of groups (genera) of large herbivorous mammals over the animals' evolutionary trajectories from origination to peak success (the highest representation in the fossil record) to extinction. **a**, Hat-shaped trajectories of evolutionary success and failure are frequently observed in the fossil record for many groups of organisms. **b**, In North America and Europe, at the time of peak success rates, the biotic factor of competition with other large herbivores was the dominant evolutionary driver. Both competition and environmental factors were important at the time of extinction, whereas neither was key for driving species origination. Graph generated from data in Table 1 of ref. 2, which reports computer simulations to test correlations between evolutionary measures (such as peak success rates) and the role of potential drivers. Importance was calculated as the number of standard deviations of the data from the null expectation of random evolutionary trajectories.

each genus was found is a good measure of the evolutionary success of each genus.

A fundamental innovation in Žliobaitė and colleagues' study was their analysis of not only rates of origination and extinction, but also the rates at which genera reached peak evolutionary success. Their decision to do this was partly motivated by a wish to investigate the apparent inconsistency between the law of constant extinction proposed⁵ by the evolutionary biologist Leigh Van Valen, and the observed prevalence of hat-shaped evolutionary trajectories. The contradiction arises because, for such trajectories, the probability of extinction increases with time⁶, whereas the law of constant extinction states that the extinction probability is independent of how old a species is.

Van Valen put forward the Red Queen hypothesis⁵ to explain the law of constant extinction. The hypothesis is named after the character in Lewis Carroll's book *Through the Looking-Glass*, who states that "it takes all the running you can do, to keep in the same place". The law of constant extinction fits with this model, in which species must continually evolve to maintain their existence in the face of changing biotic interactions with other organisms, because the probability of extinction does not change with time for species able to keep up with this evolutionary race.

The key finding made by Žliobaitė *et al.* is that the rate at which the number of genera reached their peak representation in the fossil record (and thus their peak success) strongly correlates with just the biotic competition intensity (Fig. 1). For extinction, the situation is more complex, with biotic competition and

abiotic environmental drivers both correlating with extinction rate, although competition has less effect than it does for peak success. Notably, neither competition nor environmental change correlates strongly with the rates at which species first appeared in the fossil record. Other studies^{1,6} have found similar patterns associated with origination and extinction rates, but none of these earlier studies analysed peak success. The dominance of competition during the peak expansion of genera found by Žliobaitė and colleagues is an unexpectedly simple result, given the anticipated complexity of the ecological and evolutionary dynamics of species and species richness.

As anticipated for hat-shaped trajectories, Žliobaitė *et al.* show that extinction events in the history of large mammalian herbivorous genera do violate the law of constant extinction; the probability of extinction increases the older the genus is. However, the probability of when a genus will stop expanding, that is, when it will reach its peak evolutionary success, was found to be independent of the age of the genus. Thus, Žliobaitė and colleagues have discovered a phenomenon that is equivalent to the law of constant extinction in the way that it describes an evolutionary-trajectory pattern that is time independent, but that pertains to when genera reach peak success, and which they call the law of constant peaking.

This key discovery resonates with another of Van Valen's ideas: that only the expansion phase of an evolutionary trajectory, which equates to the acquisition of more resources, should be viewed as evolutionary success⁷. From this viewpoint, evolutionary failure begins at the inception of decline after the peak, well before

the time of actual extinction. Thus, the authors argue that we must, at least conceptually, tip our hats to the law of constant extinction because the time at which a genus reaches its peak and starts the decline to extinction is independent of how old the genus is.

Žliobaitė and colleagues' study was conducted at the level of genera, which is one taxonomic level above species, and both species and genera commonly exhibit hat-shaped evolutionary trajectories⁸. Yet such simple patterns are rare at the higher taxonomic levels that Van Valen studied to develop the law of constant extinction. At those levels, evolutionary trajectories of species richness (a measure of evolutionary success) often have multiple peaks instead, and sometimes have long-lasting, persistent 'tails' of reduced diversity that show no signs of extinction⁹. At lower taxonomic levels, complete ecological replacement of one species or genus with another is common — at higher taxonomic levels it is not.

This difference in the nature of evolutionary trajectories at different taxonomic levels highlights one of the challenges of studying evolution, which is the hierarchical structure of the evolutionary process¹⁰. It is worth noting too that, although hat-shaped trajectories are common at lower taxonomic levels, they are not universal. For example, the North American mammalian fossil record from the Cenozoic era fits the law of constant extinction with remarkable fidelity^{11,12}.

The results of Žliobaitė and colleagues' work also provide insight into the drivers of evolutionary innovation. The authors' data for North America and Europe show that, although both biotic and abiotic factors contribute roughly equally to genus origination rates, neither contribution is statistically significant. As the authors note, this provides evidence that evolutionary innovation is not driven by biotic or abiotic external changes. Instead, the data support the idea that evolutionary innovation is influenced by intrinsic factors — the less-predictable origin of the 'right' variants at the right time, able to exploit either existing or new resources.

It will be necessary to fully scrutinize the approach used by Žliobaitė and colleagues, and especially the theoretical implications of their findings. More data sets need to be analysed using a range of measures of environmental change and competition. Other biotic factors, such as predator interaction, should also be included in future analyses. Nonetheless, this paper represents a next step towards the formulation of general laws and principles in palaeobiology^{13,14}, building on the detailed description of fossil material¹⁴. ■

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1. Ezard, T. H. G., Aze, T., Pearson, P. N. & Purvis, A. *Science* **332**, 349–351 (2011).
2. Zliobaitė, I., Fortelius, M. & Stenseth, N. C. *Nature* **552**, 92–95 (2017).
3. Fortelius, M. *et al. Phil. Trans. R. Soc. B* **371**, 20150232 (2016).
4. Zliobaitė, I. *et al. Proc. Natl Acad. Sci. USA* **113**, 12751–12756 (2016).
5. Van Valen, L. *Evol. Theory* **1**, 1–30 (1973).
6. Quental, T. B. & Marshall, C. R. *Science* **341**, 290–292 (2013).
7. Van Valen, L. *Evol. Theory* **1**, 179–229 (1976).
8. Foote, M. *et al. Science* **318**, 1131–1134 (2007).
9. Sepkoski, J. J. Jr *Paleobiology* **7**, 36–53 (1981).
10. Jablonski, D. *Evol. Biol.* **44**, 427–450 (2017).

11. Alroy, J. *Quantitative Mammalian Biochronology and Biogeography of North America*. PhD thesis (1994).
12. Foote, M. & Miller, A. I. *Principles of Paleontology* 185 (Fig. 7.11) (Freeman, 2006).
13. Marshall, C. R. *Nature Ecol. Evol.* **1**, 0165 (2017).
14. Gould, S. J. *Paleobiology* **6**, 96–118 (1980).

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PLANETARY SCIENCE

A steamy proposal for Martian clays

Martian clays present a conundrum: the models proposed to explain their formation require conditions that are not predicted by computational climate simulations. Experiments now suggest an alternative scenario. SEE LETTER P.88

LAURA SCHAEFER

Clay minerals are found in abundance across the surface of Mars, and many models have been suggested to explain their formation¹. These models often invoke the presence of substantial surface water and a warm climate during Mars's first 500 million to 700 million years. However, computational climate models for early Mars struggle to reproduce such conditions². On page 88, Cannon *et al.*³ present a possible solution to this problem: a model for clay formation during the end stages of Mars's formation that does not require prolonged warm and wet conditions.

During their formation, many planets go through a stage known as a magma ocean, which results from substantial or complete melting of their interiors. Both Earth and Mars went through at least one such phase⁴. The melting of their silicate mantles led to outgassing of volatile components that were originally incorporated in the solid material. This produced atmospheres containing one or

more oceans' worth of water vapour and other volatile compounds such as carbon dioxide⁴. As the planets cooled, processes such as water condensation and the escape of gases to space reduced the size of the atmosphere.

Massive early atmospheres are extremely hot and dense, and generate high pressures at the planet's surface. Under these extreme conditions, water and CO₂ exist as supercritical fluids — neither gas nor liquid. Cannon and colleagues performed experiments to show that supercritical water and CO₂ can react extremely rapidly with minerals typically found in early planetary crusts to make hydrated silicates — clays.

Radiometric dating⁵ of Martian meteorites suggests that crystallization of the magma ocean on Mars occurred within 20 million to 25 million years of the beginning of the Solar System, and that crustal formation took at most another 15 million years. The steam in the planet's atmosphere would have condensed to form a hot ocean on similar timescales. Cannon and colleagues' findings suggest

that the supercritical atmosphere would have reacted with the crust to form clays during this time (Fig. 1a).

Magma oceans exist for relatively short periods in the context of geological timescales, and so the authors' mechanism for clay formation on Mars halts long before most other proposed mechanisms would have even begun. Numerous models have been proposed for the formation of Martian clays during the later Noachian period (4.1 billion to 3.7 billion years ago), including: the alteration of subsurface material through reactions with groundwater⁶; alteration of crustal material through reactions with water at high temperatures, driven by asteroid impacts⁷; and surface weathering⁸. Cannon and colleagues' proposal does not exclude the possibility of later clay formation, but it does limit the amount of clays that could have formed during the Noachian. Notably, surface-weathering models of clay formation require warm, wet conditions throughout most of the Noachian period — which might have been conducive to life. But the authors' model is consistent with cold, dry Noachian conditions, which would have been unfavourable for life.

For primordial clays still to be present on Mars today, they must have survived the substantial reworking of the Martian crust that occurred as a result of widespread volcanism, disruptions by asteroid impacts and burial by impact ejecta (Fig. 1b). Cannon *et al.* performed computational simulations of the physical evolution of the primordial clay layer during this crustal reworking. The simulations' predictions of the clay content of the Martian regolith (the layer of loose materials, such as dust and

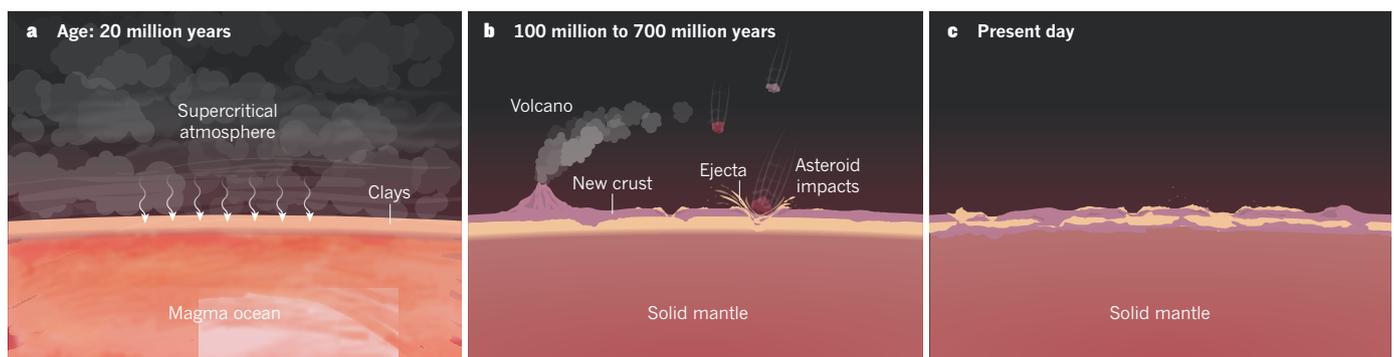


Figure 1 | A model for the formation of primordial clays on Mars. **a**, For about the first 20 million years of its existence, Mars went through a 'magma ocean' phase, during which all, or most, of the planet's interior was molten. The atmosphere was a supercritical fluid (a phase that is neither gas nor liquid) containing water and carbon dioxide. Cannon *et al.*³ show that minerals in Mars's crust could have reacted with steam in the atmosphere (white arrows)

to form a layer of clays. **b**, The magma ocean subsequently solidified, and the atmosphere changed to a gaseous state. During the next few hundred million years, volcanic activity would have generated a fresh layer of material on top of the primordial clays, and asteroid impacts would have churned up the upper crustal layers. **c**, The authors' computational simulations show that this chain of events would have resulted in the observed patterns of partially exposed clay.