

# Evolution: Predictability and the promise of ancient DNA

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**Is evolution predictable? Genomes from thousands-of-years-old stickleback suggest that, despite substantial stochasticity in the course of evolution, our understanding of the recent evolutionary past of this species was generally valid.**

200 years ago, the French scientist Pierre-Simon Laplace conceived what is now known as Laplace's demon — a hypothetical intellect with perfect knowledge of a fully deterministic universe at any particular point in time and of all the laws acting within that universe<sup>1</sup>. Empowered to also make exact calculations, Laplace's demon could flawlessly predict the future. Likewise, the demon could make perfect predictions about the past — technically called retrodictions but hereafter subsumed under 'predictions' in the broader sense of hypothesizing both forward and backward in time. Unlike what is possible for this demon, our ability to predict evolution is currently limited. There are two explanations for this limitation. First, evolutionary change may not be fully deterministic but be subjected to stochasticity. Stochasticity could follow from physical events such as an asteroid impact, chemical events such as the random occurrence of mutations, or be a consequence of biological redundancy of traits or genes. However, striking regularities in our living world make clear that evolutionary change is certainly not fully stochastic and should thus, at least to some degree, be predictable. Second, our current knowledge of the world and how it evolves is imprecise and incomplete. Indeed, even small deviations from perfect knowledge could severely limit our predictive ability, particularly if evolutionary change is chaotic<sup>2</sup>. While chaotic dynamics are in fact deterministic and thus in principle fully predictable<sup>3</sup>, small uncertainties can rapidly grow into large uncertainties, thus making evolutionary predictions in

practice nearly impossible. Be it due to stochasticity or limited knowledge, we are left with the nagging question whether we can make meaningful evolutionary predictions at all. In a new study in this issue of *Current Biology*, Melanie Kirch, Felicity Jones, Andrew Foote and colleagues<sup>4</sup> use ancient genomes from threespine stickleback fish as time capsules to directly glimpse into the past to evaluate long-standing evolutionary predictions about this organism. This exciting work illustrates the power of ancient DNA to provide novel insights into evolution and its predictability. By directly evaluating predictions about the past, ancient DNA may ultimately also guide predictions about the future, overall transforming evolutionary biology from a mainly historical and thus descriptive into a more predictive science.

With the end of the last Pleistocene glaciation 12,000 years ago, a key event in the evolutionary history of threespine stickleback occurred. With the melting of the ice that had covered most parts of the northern hemisphere for 100,000 years, new freshwater habitats formed and became colonized by marine stickleback. Today, there are countless freshwater stickleback populations across the northern hemisphere, and hundreds of studies document marked phenotypic and genetic differences between present-day marine and freshwater stickleback. Despite considerable variation among populations from different freshwater habitats, freshwater stickleback in comparable habitats are remarkably similar. This striking parallelism suggests a high degree of

determinism in the recent evolution of this species.

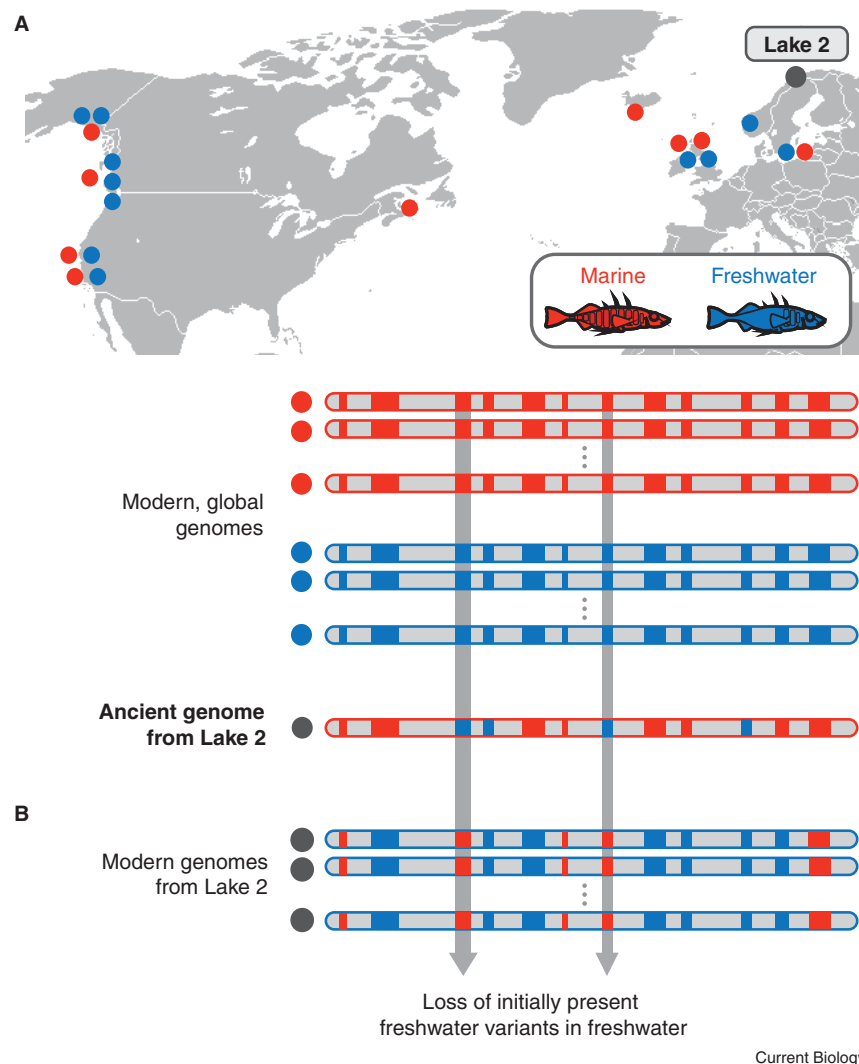
The working hypothesis for why stickleback evolution in freshwater was so parallel and rapid is that freshwater-adaptive variation pre-existed in the marine population and was repeatedly favored by similar selection pressures in independently colonized freshwater habitats. This notion has been supported by the same genetic variants being repeatedly involved in postglacial freshwater adaptation, and their detection in extant marine stickleback<sup>5–7</sup>. Although present-day marine stickleback are morphologically similar to marine stickleback fossils from millions of years ago<sup>8</sup>, it has been questioned whether extant marine stickleback can be taken as 'contemporary ancestors' of the descendant freshwater populations from today<sup>9</sup>. Freshwater variation in extant marine stickleback could also stem from recent and recurrent hybridization of freshwater and marine stickleback<sup>10</sup>, and marine stickleback may not represent a single large, static population, but rather be spatially and temporally variable<sup>9,11,12</sup>. In short, the generally held view that alleles adaptive in freshwater already existed in marine stickleback 12,000 years ago awaits direct testing.

Kirch and colleagues<sup>4</sup> have now directly tested this prediction by taking a paleogenomic approach. They accessed the ancestral gene pool of the marine stickleback that founded modern freshwater populations. For each of two postglacial lakes in Norway, the researchers obtained one partial genome sequence from stickleback

bones recovered from sediment cores of these lakes. Radiocarbon dating revealed these bones to be 12,000 years old, so they should stem from actual marine colonists of the lakes or their early descendants. As predicted by the contemporary ancestor hypothesis, the ancient genomes proved similar to the genomes of present-day marine stickleback from the nearby sea. Backed-up by several genomic analyses, this finding thus indicates that modern marine stickleback are genetically similar to the marine stickleback that founded freshwater populations shortly after the last Pleistocene glaciation.

Although the ancient and modern marine stickleback genomes were similar overall, in-depth analysis of the better-sequenced ancient genome revealed that the ancient genome carried the typical freshwater variant at one quarter of all genome regions with strong differentiation between globally-sampled modern marine and freshwater stickleback<sup>13</sup>. This is in line with the prediction that freshwater variants were already present in the ancestral marine colonists of the freshwater habitats formed after the last Pleistocene glaciation, subsequently enabling rapid and parallel adaptation to freshwater (Figure 1A). Interestingly, however, some of the freshwater variants in the ancient genome were no longer detected in present-day stickleback from the respective lake (Figure 1B). The authors ascribe this loss of freshwater-adaptive variation within freshwater to stochastic drift, which appears to have had substantial impact on both lake populations. The authors thus conclude that, while adaptation of stickleback is a highly deterministic process, stochasticity plays a significant role in the progression of parallel adaptation in this species.

Concerning the evolution of stickleback, Kirch and colleagues<sup>4</sup> therefore provide direct evidence for the long-standing evolutionary prediction that modern marine stickleback still genetically resemble ancestral marine stickleback, and that genetic variation important for postglacial freshwater adaptation was already present in the marine



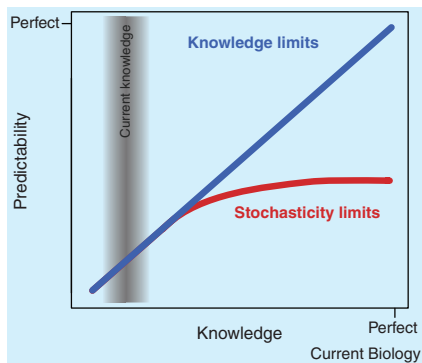
**Figure 1. Predicted and unpredicted patterns of 12,000 years of stickleback evolution.**

(A) As predicted, the ancient genome from Lake 2 is generally marine-like, yet carries some typical freshwater variants at loci of strong marine–freshwater differentiation between extant global stickleback. (B) Although many of the freshwater variants in the ancient genome are currently at high frequency in the Lake 2 population, some of these variants were lost in the course of 12,000 years of stickleback evolution in that lake. Arguably, this would not have been predicted based on the ancient genome.

stickleback founding today's freshwater populations. What remains unclear is the ultimate origin of freshwater-adaptive variation in the sea. The fact that freshwater variants are scattered throughout the generally marine-like ancestral genome suggests that freshwater variation in the sea did not stem from hybridization of freshwater and marine stickleback at the time of colonization. Indeed, there may not have been any marine–freshwater hybridization during the 100,000 years of the last Pleistocene

glaciation at all because, during that time, most current-day freshwater populations either did not exist or existed only in isolation from the sea<sup>14</sup>. The maintenance of freshwater variation in the sea may thus not require recurrent gene flow between marine and freshwater stickleback<sup>10</sup>, but once present, may be preserved in the sea for very long as 'long-standing genetic variation'<sup>15</sup>.

More generally, the study by Kirch and colleagues<sup>4</sup> highlights the potential of ancient DNA as a time capsule for



**Figure 2. Factors limiting our ability to predict evolution.**

Shown are simplified expectations if our ability to predict evolution was limited by knowledge or stochasticity. As long as the predictability of evolution does not saturate with increasing knowledge (i.e., more/better data and models), we are left uncertain whether, or to what extent, true stochasticity inherently limits our ability to predict evolution. Arguably, we are currently in this undecided situation. Note that our ability to predict evolution may be limited, to some degree, by both stochasticity and limited knowledge, and from a practical standpoint will depend on the time scale and the level of biological organization.

evolutionary biologists. Besides uncovering extinct biodiversity<sup>16,17</sup>, ancient DNA enables us to directly evaluate predictions about the evolutionary past of extant species. In stickleback, our prediction was that freshwater variation already existed in the marine founders of today's freshwater populations, and that this variation was maintained and driven to high frequency by positive selection within freshwater. Although generally valid, Kirch and colleagues<sup>4</sup> detected several freshwater variants that were initially present in a lake but are no longer present in today's population in that lake. This implies that adaptation of the modern freshwater population is less 'optimal' than we would have predicted from these initial conditions (Figure 1). It is possible that given the abilities of Laplace's demon — including perfect knowledge of the initial frequencies of all freshwater variants and the type and strength of selection acting upon them — the evolutionary fate of each and every genetic variant would be perfectly predictable. If so, evolutionary change would prove to be fully deterministic.

On the other hand, it is possible that the loss of some freshwater variation in freshwater will always remain unpredictable because no matter how perfect our knowledge and models, true stochasticity will always limit our ability to predict evolution. Arguably, we are currently unable to clearly decide between these two explanations concerning the loss of putative freshwater variants in freshwater, because what appears stochastic now could in fact be deterministic (Figure 2).

Even after many more decades of research and technical advances, we will most likely come to conclude that there will always be limits in predicting evolution. As scientists, our challenge and satisfaction may thus be that the predictions we can make about evolution will more often turn out to be true. As long as we remain uncertain whether predictions fail because of true stochasticity or limited knowledge, there is certainly value in searching and researching. As human beings, we may find comfort in a view of life not being fully predetermined and predictable. And wouldn't it add to the grandeur of the living world if chance was essential for the true uniqueness of the so many forms that have been and are being evolved?

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