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GENOMICS

# Stickleback is the catch of the day

**Whole-genome sequences from a marine fish that has adjusted to life in fresh water give hints about general genetic mechanisms that drive the evolution of adaptations to new environmental niches.** SEE ARTICLE P.55

HOPI E. HOEKSTRA

The traditional recipe for publication of a genome sequence goes something like this: one part 'biology' (an often flowery description of the distinctive aspects of the organism whose genome has been sequenced); two parts 'assembly and annotation' (how the latest DNA sequencing and computational technologies were used to produce a high-quality sequence); and three parts 'comparative analyses' (for example, observations of rapidly evolving genes, or expansion or loss of gene families). All this is followed by a dash of 'fun speculation' on how these distinctive genomic characteristics might yield insight into the biology of the creature under study.

Although each genome paper has its own twist, such as filling in a critical gap in the tree of life[1], a novel sequencing and assembly strategy[2], or proof that an entire genome can be sequenced by a single laboratory[3], the main contribution of such work is usually the sequence itself — as a tool to delve deeper into biological questions. But there are new cooks in the kitchen, and some of them are following a different recipe. On page 55 of this issue, Jones *et al.*[4] report the first whole-genome sequence of the threespine stickleback fish, and at the same time reel in answers to some big questions in evolutionary biology.

The ancestral form of the threespine stickleback (*Gasterosteus aculeatus*) was a marine fish with protective bony 'armour' that repeatedly colonized lakes and streams around the world following the retreat of glaciers at the end of the last ice age some 10,000 years ago. In their new freshwater habitats, these fish repeatedly evolved new morphological and physiological adaptations, such as loss of the bony plating and spines and a change in salinity tolerance, and this evolutionary pattern has elevated the threespine stickleback to 'supermodel' status[5] in studies of adaptation and speciation. The one missing piece has been the complete genome sequence. Jones and colleagues[4] provide just this, with a high-quality sequence of a freshwater Alaskan stickleback.

But the authors don't stop there. They also report sequence information from another 20 sticklebacks sampled around the globe (Fig. 1) that form 10 geographically linked pairs of marine and freshwater fish. And they develop two complementary approaches — one based on phylogenetic relationships and a second on pairwise genetic distance — to scan the genomes for regions that are substantially different between marine and freshwater sticklebacks but similar within marine, or freshwater, populations from different geographical locations. Such genetic regions are likely to have contributed to shared adaptations.

This novel approach allowed the researchers to tackle long-standing questions surrounding adaptation from a genomic perspective. First, they identified genomic regions that share similar patterns of sequence variation (characteristic of parallel evolution), as opposed to different patterns of sequence variation (characteristic of convergent evolution), in ecologically similar but geographically separate populations. They conclude that the same gene regions are "often" involved in parallel adaptation — at a conservative estimate, approximately 150 genomic regions are shared among freshwater populations, covering 0.2% of the genome. However, the exact proportion of parallel changes relative to convergent changes cannot be estimated, because the methods the authors used to identify genomic regions of interest rely on their repeated occurrence across populations, such that some regions contributing to convergent adaptation (via different or novel mutations) go unnoticed. So this specific question remains open.

A second, related, question in the study of rapid adaptation is the relative reliance on pre-existing genetic variation compared with new mutations[6]. To address this, Jones *et al.*[4] focused on a single stream in Scotland where marine and freshwater sticklebacks meet and interbreed. They estimate that around 35% of the genomic regions that differ between this population pair (sampled from opposite ends of the hybrid zone in the river) overlap with regions that show an ancient shared origin in the worldwide population samples. The remaining regions of high genetic divergence may be attributable to local adaptations specific to this location or to evolution from different novel mutations. Thus, it seems that repeated evolution of traits may often, but not always, arise from genetic variation that already existed in an ancestral population.

The third question tackled by the authors may be considered a contentious one: that of the relative role of mutations in regulatory versus coding sequences in adaptive change. Whereas some researchers have argued for the predominance of regulatory mutations[7,8],

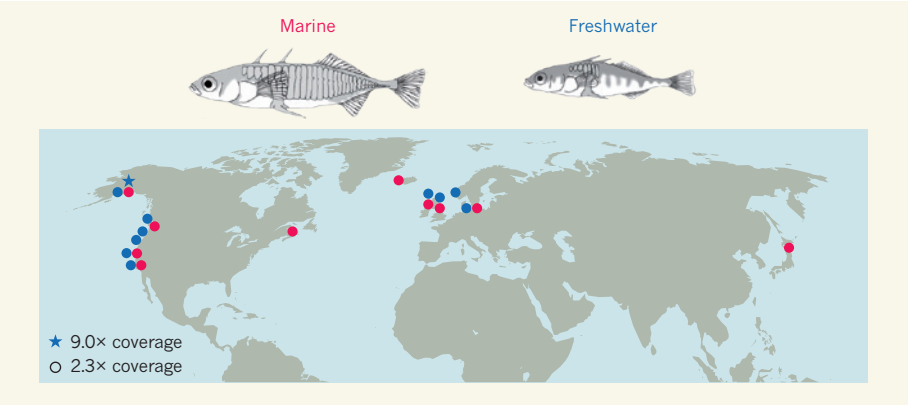


**Figure 1 | Adapting to new surroundings.** Jones *et al.*[4] provide a high-quality whole-genome sequence of a freshwater threespine stickleback from Alaska (location indicated by the blue star). This sequence is at 9× coverage, which means that each DNA nucleotide is represented, on average, nine times in the sequence reads used to construct the genome sequence. The authors also generated lower-coverage (2.3×) sequences of stickleback fish from 20 additional populations around the globe — 10 in freshwater (blue circles) and 10 in marine environments (red circles). Their sequence comparisons allow an analysis of how similar genetic adaptations can arise repeatedly in isolated populations.

others caution that the role of coding changes may not be negligible[9]. Although these conclusions are not mutually exclusive, data to support either of these claims have previously come predominantly from case studies (of variable quality), rather than from a systematic empirical survey (although see ref. 10 for a review of the latter approach).

Now, however, because their novel mapping approach results in the identification of narrow genomic regions (of the order of only 5 kilobases), Jones and colleagues[4] were able to simply assess whether or not a region implicated in an adaptation contains a coding sequence. If not, then the causal mutation was considered 'regulatory', as they found for 41% of cases. If the region contains both coding and non-coding regions but there is no consistent amino-acid difference between marine and freshwater populations, this was considered 'likely to be regulatory' (43% of cases), but if they do have consistent amino-acid differences the authors classed them as 'coding' (17% of cases). Although some researchers may not be convinced of these allocations until precise mutations are identified and functionally verified, this large-scale analysis suggests that both amino-acid and regulatory mutations contribute to adaptation, and that most are regulatory in nature.

This genome-wide view of the evolutionary processes acting in sticklebacks has provided us with many clues — that rapid adaptation is often caused by parallel genetic changes, often evolves from pre-existing genetic variation, and often involves regulatory mutations.

Although these results do not provide simple yes or no answers to such concepts, that was not to be expected, as evolution doesn't follow strict rules. Our focus must now shift to 'why' questions. Why are the same genes sometimes used repeatedly in adaptation but at other times involve different genes? Why, in some cases, does evolution take advantage of pre-existing variation and other times new mutations? Why are regulatory mutations sometimes preferred over amino-acid changes and vice versa? Such enquiry will further improve our understanding of the evolutionary process, and increase our ability to predict evolutionary outcomes. So, for evolutionary geneticists, there are still big fish to fry. ■

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QUANTUM OPTICS

# An entangled walk of photons

**By harnessing the quantum nature of light and guiding the light through a network of circuits integrated in a glass chip, it is possible to mimic fundamental particles undergoing a quantum walk.**

JONATHAN C. F. MATTHEWS & MARK G. THOMPSON

Quantum mechanics is the most successful model of nature that we have, accurately describing fundamental physical processes. Although quantum effects such as entanglement and superposition are counterintuitive and often described as 'spooky', they are being observed and characterized in laboratories worldwide. Writing in *Physical Review Letters*, Sansoni *et al.*[1] describe how they have designed and built an optical network, integrated in a glass chip, that manipulates photons to simulate a process known as a discrete-time quantum walk. Furthermore, using a particular kind of entanglement, the authors simulated different classes of fundamental particles undergoing the quantum-walk process[2]. The results are a step towards the development of quantum-mechanical machines that promise to outperform conventional supercomputers, which operate according to the laws of classical physics*.

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Perhaps the most far-reaching applications of quantum technologies will be based on the American physicist Richard Feynman's proposal that an efficient way to simulate one quantum system is to use another. Such simulators could be used to study complex quantum systems that are computationally hard to simulate or difficult to physically control. We are currently witnessing initial demonstrations of these simulators in the form of purpose-built quantum devices that mimic other, less readily accessible quantum systems.

Developments in quantum simulation are still at the stage of mimicking systems simple enough to be handled with classical computers. However, photonics is an attractive candidate for reaching the point at which quantum machines could outperform state-of-the-art supercomputers for particular tasks. This is partly thanks to the complexity and stability of quantum networks realized with integrated optics, and to the nature of multiple identical photons interfering in a sufficiently complicated optical network[3].

In classical physics, the analogue of Sansoni and colleagues' discrete-time quantum walk would be a form of random walk, a tool already used in a broad range of fields from animal behaviour to economics, for example in modelling the path of a foraging animal or fluctuating prices in the stock market. The simplest random walk is on a line, and is conducted by repeatedly flipping a coin and walking left if

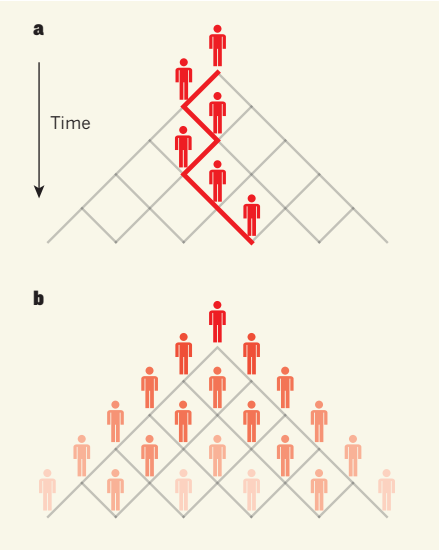


**Figure 1 | Classical and quantum walks. a**, In a classical random walk, a walker must make a choice (randomly) of moving either left or right at each step. After many trials of a fixed number of steps, the walker is most probably found close to its initial starting point. **b**, In a quantum walk, the walker uses a 'quantum coin' mechanism that allows it to move in a superposition of both left and right. The probability distribution of its position after many steps is therefore starkly different from that of a classical random walk, with the walker most likely to be found far from its initial starting point.