GENOMICS

Acorn worms in a nutshell

The genome sequences of two members of the hemichordate group of marine invertebrates bring the evolution of their relatives, including vertebrates, into sharper focus. SEE ARTICLE P.459

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By examining the similarities and differences among the genomes of living organisms, we can reconstruct features of the genomes of long-dead ancestors. Such reconstructions provide insight into patterns of genome diversity and how organisms evolved through the gain, loss and modification of genomic features. The greater the number of sequenced genomes from living organisms, and the broader their distribution across the tree of life, the better is our view of these ancestral genomes. However, although hundreds of animal genomes have been published in recent decades, the vast majority are from only two groups: vertebrates and arthropods. Simakov and colleagues' publication[1] in this issue (page 459) of genome sequences for two species from a group of invertebrates known as hemichordates takes the sampling of animal genomes an important step forward.

Hemichordates are exclusively marine animals. The adults live on the ocean bottom, whereas the larvae are free-swimming. There are about 130 described species[2], which are divided into 2 groups. The pterobranchs, of which there are around 20 species, are small animals (up to about 5 millimetres long) that form colonies of asexually produced clones attached to a central disk by fleshy tethers[3]. The animals live in a tube network that they secrete. Just as birds were found to be 'living dinosaurs' — a group that had been thought extinct — pterobranchs are living graptolites, animals that are abundant in the fossil record[4]. In contrast to pterobranchs, the other group of hemichordates, called enteropneusts, are solitary animals that range in length from less than a millimetre[5] to more than 2 metres (Fig. 1). Known as acorn worms, enteropneust adults burrow in soft sediments.

Simakov and colleagues present the genome sequences of two enteropneusts — *Saccoglossus kowalevskii* and *Ptychodera flava*. The authors used these sequences, together with additional DNA sequence data on pterobranchs and several other animals, to build a phylogenetic tree that finds pterobranchs and enteropneusts to be sister groups (Fig. 2). This finding is in agreement with another analysis[6] in rejecting the previously suggested placement of pterobranchs within enteropneusts.

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Figure 1 | Pharyngeal gill slits. Enteropneusts, better known as acorn worms, use internal gill slits in the pharynx region of their trunk to move water through their mouth to obtain oxygen and, in some species, for filter feeding. The gill slits connect to external gill pores. This specimen is several centimetres long.

As interesting as hemichordates are in their own right[2], much of the motivation for taking a closer look at them comes from a desire to understand their relatives. This is because hemichordates fall within Deuterostomia, the group of animals that also includes echinoderms (radially symmetrical organisms such as sea stars and sea urchins) and chordates. Chordates are of particular interest because they include humans and our vertebrate kin. Although many chordate genome sequences are available, there are few genome resources for other deuterostomes. A draft genome for a sea urchin is available[7], but until now there were no published genomes for hemichordates.

The most recent common ancestor of deuterostomes lived more than 500 million years ago, and there is great diversity in the anatomy of adults of this group. However, many features of deuterostome embryology, including the formation of the anus from the blastopore and the creation of coelomic cavities by pinching off from the gut, are highly evolutionarily conserved. The main finding of Simakov and colleagues' study is that deuterostome genomes, like their embryology, show extensive conservation across great evolutionary timescales. The hemichordate sequences share many features with other deuterostome genomes, including gene composition, exon–intron structure and small- and large-scale gene order. This means that many well-characterized features of chordate genomes are not chordate-specific, but arose earlier in animal evolution.

One of the most conspicuous deuterostome-specific traits is the pharyngeal gill slits. These openings allow water to pass through the mouth without entering the digestive tract, and they are involved in feeding and respiration in these animals. Gill slits arose in the stem lineage that gave rise to deuterostomes, and are not found in non-deuterostome animals, nor in echinoderms, in which they were secondarily lost (Fig. 2). A detailed understanding of the evolutionary origin of this feature is key

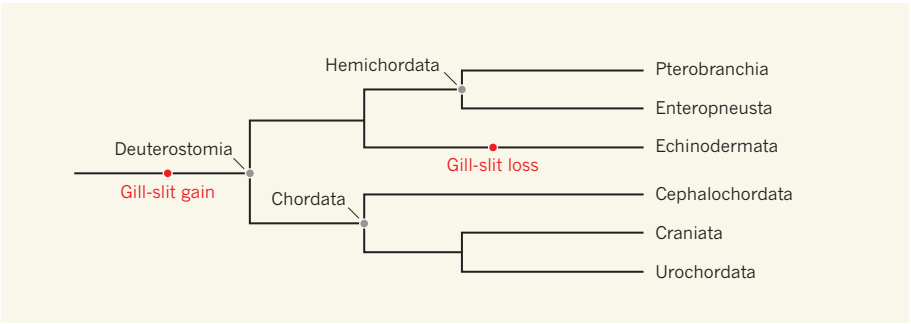

Figure 2 | Deuterostome relationships. The deuterostome group can be divided into three clades: chordates (Cephalochordata, or lancelets; Craniata, which includes all vertebrates; and Urochordata, such as sea squirts); echinoderms (sea stars, sea urchins and relatives); and hemichordates (pterobranchs and enteropneusts). Simakov *et al.*[1] present the first hemichordate genome sequences, from two enteropneust species. The authors' analyses provide new detail on evolutionarily conserved genes that play a part in the development of gill slits. These structures arose along the deuterostome stem, were lost in echinoderms and are reduced in the adults of some chordates (including humans).

to understanding deuterostome, and therefore our own, biology. Simakov *et al.* examine a conserved cluster of six genes that is found only in deuterostomes, and that includes genes known to be involved in patterning gill slits in other deuterostome species. In keeping with the other conserved genome features that they identified, the authors find that these genes are also expressed in the pharyngeal-gill structure of hemichordates.

Simakov and colleagues recognize that there is no 'typical' representative of any animal group; they sequenced two full hemichordate genomes, and collected less-detailed sequence data from a variety of other species to put these genomes in a richer evolutionary context. However, the authors' study still faces the same challenge as all genome investigations — we are far from understanding which evolutionary changes in genomes underlie which evolutionary changes in traits, including development, anatomy and functional biology[8].

There are several reasons for this. First, many evolutionary genome changes are neutral[9] — they have no impact on traits or fitness. This means that we should not assume that any particular genome change affects any traits. Second, on any given phylogenetic branch there will be many changes in both traits and genomes, and there are many possible functional implications for any particular genome change. Third, genome function itself evolves, so the same genome features do not necessarily relate to the same traits in different species.

Our current coarse perspective on genome evolution will improve as more genomes are sequenced, and as functional genomic tools are developed that can be applied to any organism, not just those that can be grown in the laboratory. The conservation of so many features across deuterostome genomes, which is brought into sharp focus with Simakov and colleagues' addition of hemichordate genome sequences, reinforces the fact that radical morphological changes are not necessarily related to radical changes in genomes. This fact will shape the search for which of the variable features of deuterostome genomes are responsible for the great diversity we see across the group. ■

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CIRCADIAN CLOCKS

A receptor for subtle temperature changes

The protein IR25a is best known for its role as an odour receptor in flies, but an analysis reveals that it also acts to synchronize the circadian clock by sensing small temperature fluctuations. SEE LETTER P.516

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Our body's circadian clocks sense the environmental changes that occur over 24 hours, allowing us to adapt our physiology and behaviour to day–night cycles. Light and temperature have by far the greatest influence on the clock that drives rest–activity rhythms, but how the neurons of this clock synchronize to temperature in the brain remains largely unknown. On page 516 of this issue, Chen *et al.*[1] identify a receptor protein in mechanosensory organs in flies that acts as a specialized temperature sensor, synchronizing the circadian clock with low-amplitude temperature cycles.

Small daily fluctuations of just 1–2 °C are enough to synchronize the fly brain's circadian clock with temperature[2] (a process known as temperature entrainment). Experiments using cultures of different fly body parts have revealed that most organs can entrain their clocks with temperature cycles. The exception is the brain, which must thus rely on external sensors[3]. Expression of the *nocte* gene is required both for the normal development of mechanosensory structures called chordotonal organs and for temperature entrainment of the brain clock[3]. This suggests that chordotonal organs, which are present in the antennae and body parts such as legs and wing hinges, are the external sensors. Although the antennae are the major temperature-sensing organ[4,5], they are not essential for entrainment, indicating that the body chordotonal organs can do the job.

To analyse the role of the body chordotonal organs in temperature entrainment of the brain's rest–activity clock, Chen *et al.* looked for proteins that interact with the Nocte protein. Among the putative Nocte-binding partners that they identified was the protein Ionotropic Receptor 25a (IR25a). IR25a is part of the IR family, members of which are found in sensory organs and are involved in detecting chemicals[6]. So far, IR25a has been best known for its role as a component of a multimeric odour receptor in antennae[7]. As expected for a Nocte partner, the authors found that IR25a