

Ghost locus appears

The sequences of two sponge genomes provide evidence that the ParaHox developmental genes are older than previously thought. This has implications for animal taxonomy and for developmental and evolutionary biology. [SEE LETTER P.620](#)

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An array of transcription factors controls development in animals¹. Transcription-factor-encoding genes belonging to one class — Antennapedia (ANTP) — are present throughout the animal kingdom and usually have a key role in development. The ANTP group includes the Hox, ParaHox and NK genes, all of which are paralogues, meaning that they have arisen in different animals from a shared ancestor as a result of gene-duplication events. However, the origins, evolution and, in particular, the timing of these duplication events have been unclear. On page 620 of this issue, Fortunato *et al.*² report the analysis of two new genomes from sponges of the class Calcarea (the calcisponges) that substantially clarifies the evolutionary history of the ANTP genes and provides insight into tissue structures that are shared across the animal kingdom.

A substantial puzzle has arisen concerning the repertoire of ParaHox and Hox genes in animals. The first sponge genome to be sequenced was that of the demosponge (class Demospongiae) *Amphimedon queenslandica*³. Although there seem to be no Hox or ParaHox genes in this genome, the evolutionary conservation of clusters of genes known to be neighbours of Hox and ParaHox genes in other organisms led to the proposal that Hox and ParaHox genes were present in the common ancestor of all animals but had been lost in sponges. The researchers called their idea the 'ghost locus' hypothesis³. However, this evidence, although intriguing, was indirect, because it was based on an inference of ancestral gene content.

Despite their simple morphologies, sponges from different classes are thought to be quite divergent and indeed it is not certain that they all form a monophyletic (natural) group^{4,5}. If they are monophyletic⁴, then their last common ancestor dates to approximately 600 million years ago; if they are a paraphyletic group, then the time at which the Calcarea and the Demospongiae diverged, for instance, might be as much as 800 million years ago⁵. Either way, the antiquity of their divergence means that the genomes of a demosponge

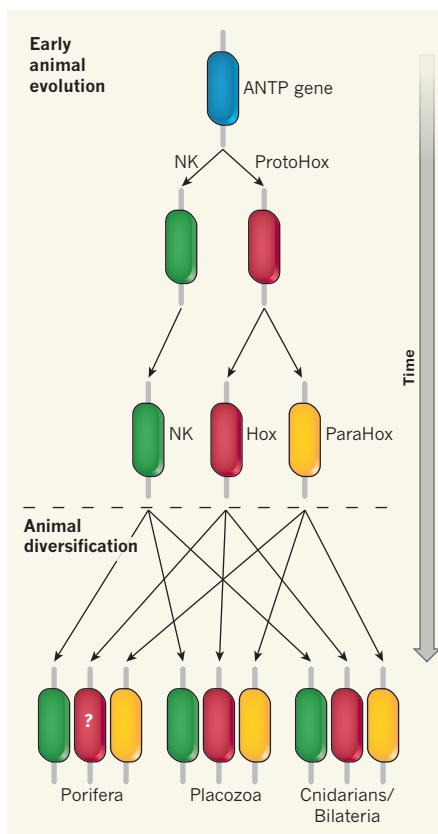


Figure 1 | Evolution of Hox, ParaHox and NK genes in animals. Fortunato and colleagues' comparison² of two calcisponge genomes (phylum Porifera) with genome data from other animals, including placozoans, cnidarians and bilaterians, suggests that an ancestral Antennapedia (ANTP) gene duplicated to give rise to the ancestor of NK genes and a 'ProtoHox' gene. The ProtoHox gene subsequently duplicated to give rise to the existing Hox and ParaHox gene families. Animal diversification occurred after these gene-duplication events, but gene losses have complicated the picture, explaining, for example, the seeming lack of Hox genes in calcisponges and of both Hox and ParaHox genes in demosponges.

and a calcisponge might be expected to differ from one another more than is usual for two animals from the same phylum, such that a single representative of the sponges can never be emblematic of the sponges — the phylum Porifera — as a whole. Sampling these divergent taxa is therefore crucial if we are

to understand the evolution of the genetic circuitry that effects animal development.

A 'superphylum' called the ParaHoxozoa⁶ has been defined on the basis of the presumed shared presence of Hox or ParaHox genes. This group includes the Bilateria (comprising all animals with bilateral symmetry), the Placozoa (simple, flat animals that live on the ocean floor) and the Cnidaria (radially symmetrical aquatic animals, such as jellyfish). The animals excluded from the ParaHoxozoa are the sponges and the Ctenophora (comb jellies), because of their presumed lack of these genes.

Fortunato *et al.* provide direct support for the ghost locus hypothesis, at least for the ParaHox genes. By combining data from their sponge genomes with existing data for phylogenetic, gene-neighbourhood and gene-expression analyses, they suggest that developmental-gene evolution has not only been very different in sponges compared with most other animals, but that early animals did indeed contain a repertoire of ANTP genes that included the NK and ParaHox genes at least (Fig. 1).

The authors first constructed a phylogenetic tree of a large family of ANTP genes. Given the great phylogenetic breadth that is spanned by the tree, it is unsurprising that high statistical support for relationships is not achieved. Nonetheless, the tree topology does indicate the presence of NK and ParaHox genes in the genomes of the calcisponges.

Next, the researchers demonstrated that there is some conservation in the gene neighbourhoods between these putative ParaHox genes in sponges and their presumed equivalents in bilaterians. Conservation of gene neighbourhoods is a hallmark of the evolution of ANTP genes, but the authors find that the strong conservation observed in most animals is not found in sponges. This implies that conservation of ParaHox gene neighbourhoods is not a universal rule as was once thought.

Finally, the authors show that the expression patterns of the calcisponge ParaHox genes are remarkably similar to those of other animals. For example, the choanoderm cell layer in sponges has a similar pattern of ParaHox expression to the endoderm in bilaterian animals, and the pattern in the sponges' cross cells is like that of sensory cells in other

animals. This opens up the possibility that certain tissue types in sponges might have a common ancestry with other tissue types in bilaterian animals. However, it should be kept in mind that homology in developmental genes does not always equate to homology of organs⁷.

One implication of Fortunato and colleagues' findings is that, although the ParaHoxozoan superphylum may still be a useful taxonomic group, it can no longer be defined by the possession of ParaHox or Hox genes. In addition, the results suggest that the origin of the ParaHox genes is earlier than was previously thought and that the first animals probably had a ParaHox gene repertoire (Fig. 1). This idea leads to the intriguing question of whether the common ancestor of all animals was in fact more developmentally complex than present-day sponges, cnidarians and placozoans, and

that these groups have lost complexity, rather than that complexity has been gained in other animal lineages.

Our existing sample of animal genomes has heavily influenced our current ideas about ANTP gene evolution. There are two other classes of sponge, the Homoscleromorpha⁸ and the Hexactinellida⁹, and a draft genome sequence for the homoscleromorph *Oscarella carmela* is available¹⁰. Investigating its ANTP gene repertoire should shed further light on the evolution of ParaHox and Hox genes. More generally, the sequencing of additional genomes from organisms at the sparsely sampled base of the animal phylogenetic tree will be key to refining our understanding of the changing complexity of animals over the course of evolution. ■

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