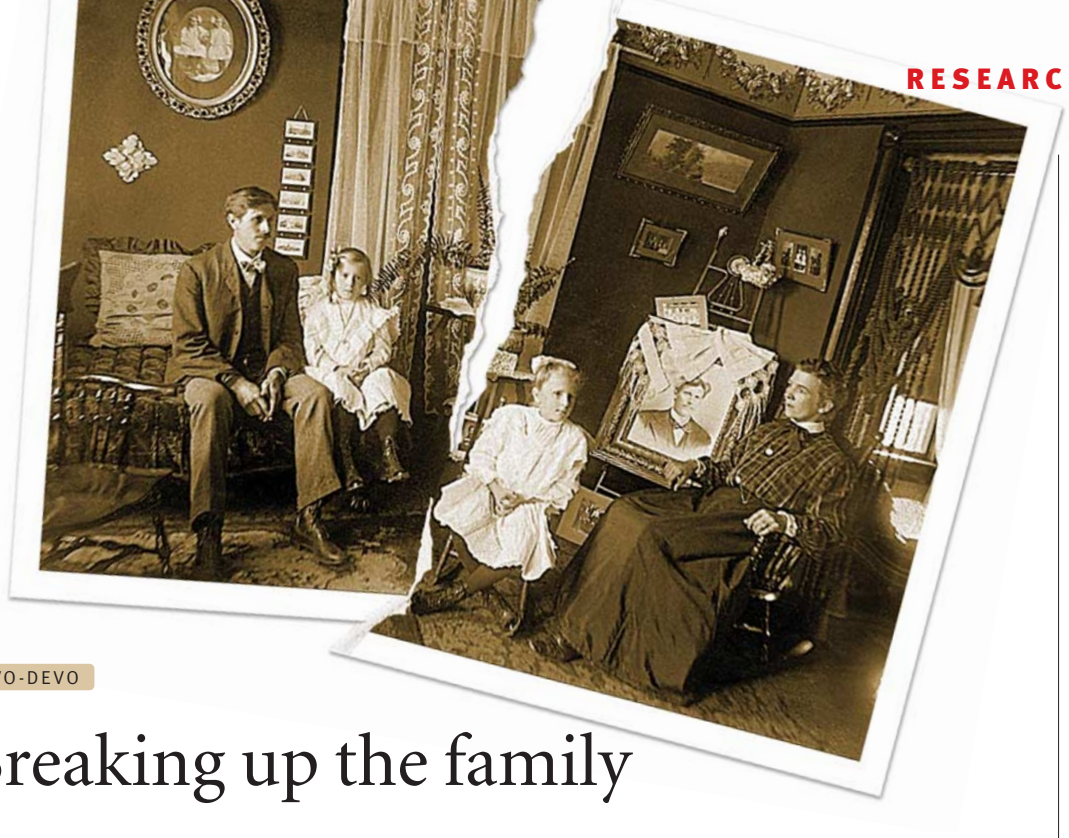

EVO-DEVO

Breaking up the family

A new study that reveals *Hox* genes scattered throughout the genome of the tunicate *Oikopleura dioica* has put to rest the perceived wisdom that the genes in this family need to be clustered.

Hox genes are crucial for specifying differential development along the anteroposterior axis in bilaterally symmetrical animals. These genes have always been found in a genomic cluster, usually ordered in a way that corresponds to the sequential expression of the genes along the anteroposterior axis during development.

Seo and colleagues studied the *Hox* genes of *O. dioica*, a representative of a chordate lineage that diverged at an early stage from the lineage that gave rise to vertebrates. We already knew that the *Hox* genes of tunicates might be slightly unusual after the sequencing of *Ciona intestinalis* revealed a *Hox* cluster with a number of strange features. However, even considering these previous findings, Seo and coworkers' results were unexpected, to say the least.

The authors identified, cloned and phylogenetically classified full-length cDNAs for all *O. dioica*'s nine *Hox* genes. Using *in situ* hybridization, they studied the expression patterns of these genes during early development. As for other chordates, expression patterns varied among tissues distributed along the anteroposterior axis, with a subset of the *Hox* gene complement being expressed in each tissue; but in this case, the *Hox* gene expression domains were mostly non-overlapping. However, the order of expression of these genes along the axis was generally correlated with the position in the *Hox* gene cluster of the paralogous genes in other chordates.

So far, so good: the differences that the authors identified between the *Hox* gene complement and expression patterns in *O. dioica* compared with other chordates, although interesting and notable, were not particularly unusual considering the overall variation between bilateral lineages. The unexpected result came when the authors took the next obvious step and looked at the genomic organization of the *O. dioica Hox* genes.

Seo and colleagues screened an *O. dioica* genomic BAC library with their nine *Hox* cDNA probes, no doubt expecting to be able to quickly locate the clone that contained the standard *Hox* cluster. Instead, they found nine separate BAC clones that contained individual *Hox* genes. Follow-up sequencing of the clones confirmed that none of the initial set of nine genes was located anywhere near the others, and indeed many unrelated genes surround each of these at the high density that is expected in this compact genome.

The disintegration of the *Hox* cluster in this tunicate might be most surprising to vertebrate developmental biologists, as the integrity of this cluster has been clearly demonstrated to be essential for temporal coordination of *Hox* gene expression in the mouse. By contrast, partially fragmented *Hox* clusters have already been found in the fly, worm and *C. intestinalis*. The authors raise the intriguing possibility that in the tunicates *C. intestinalis* and *O. dioica*, it is the transition to determinative development, since divergence from their common ancestor with vertebrates, that has allowed the *Hox* gene family to be split apart: a hypothesis that is also consistent with worm data. In determinative development, the destiny of most cell lineages is engaged during the first division of the egg, so the authors postulate that the usual function of *Hox* genes after axis formation might have become superfluous, and with it the genomic clustering of these genes. Regardless of the underlying cause, these striking new results deal the most important blow so far to the pervasive and persistent idea that the *Hox* cluster is ultimately required to build a complex animal.

Nick Campbell,
Nature Publishing Group

References and links

ORIGINAL RESEARCH PAPER Seo, H.-C. *et al.* *Hox* cluster disintegration with persistent anteroposterior order of expression in *Oikopleura dioica*. *Nature* **431**, 67–71 (2004)

WEB SITE
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IN THE NEWS

A barcode for life?

According to two recent studies, a DNA barcode could revolutionize taxonomy, potentially saving hours of peering down microscopes or poring over lists of morphological features to identify species.

The barcode in question is a 648-bp stretch of the mitochondrial gene cytochrome *c* oxidase-I. As mitochondrial genes mutate at a high rate, enough changes should have taken place in this gene to provide a unique sequence for each species, allowing taxonomists to quickly and accurately identify specimens.

A group led by Paul Hebert at the University of Guelph tested the technique in a study of 260 bird species. The barcoding approach proved an accurate way of distinguishing between species, and even identified four potential new species that might have been missed previously. "[Birds are] big, they're coloured differently, and they sing different songs … yet even in that easy to identify group, there are hidden species," commented Hebert (*CBC News Online*).

In a second study, the same technique revealed that the skipper butterfly, *Astrapes fulgerator*, is actually made up of at least ten species that look similar as adults, but have different characteristics as caterpillars. Taxonomist Felix Sperling, who wasn't involved in the study, is enthusiastic, describing this work as "an excellent demonstration of the power of DNA barcoding to make sense of a confusing welter of ecological and color pattern variation" (*The Scientist Online*).

But the method is less popular among some taxonomists, and even those who are in favour are far from suggesting that barcoding is the solution to all taxonomic problems. "There's strong debate about whether one size fits all," stresses ecologist Craig Moritz, "We have to be a little bit cynical about where it works and where it doesn't" (news@nature.com).

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