Meeting report

Trends in genomic 'evo-devo'

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A report on the joint Spring meeting of the British Society of Developmental Biology and the Genetics Society, York, UK, 20-23 March 2002.

Evolutionary biologists look at an organism and want to understand its history: how it evolved, where it came from, and who its closest relatives are. Developmental biologists want to understand how a single fertilized egg grows into an adult organism. In the 1980s new molecular techniques allowed developmental geneticists to manipulate development, at least in a few model organisms, in order to explore the molecular and genetic bases of developmental processes. At the same time the discovery that the Hox transcription factors are fundamentally important during development and occur in most or all animals demonstrated that many aspects of development are shared across taxa. The two fields overlapped when biologists began to manipulate different species and compare the results of those manipulations to make hypotheses about relationships and evolutionary processes. A new discipline, evolutionary developmental biology or 'evo-devo', grew from this work and today encompasses a wide range of research from genome comparisons to studies of single genes. All aspects of the field were discussed during the recent conference in York; a few highlights are described here.

Jonathan Hodgkin (Oxford University, UK) compared the sequenced genomes of the fruit fly *Drosophila melanogaster* and the nematode *Caenorhabditis elegans*. Both genomes contain far more genes than was originally thought: an estimated 19,000 for *C. elegans* and 14,000 for *D. melanogaster*. Of these, around 3,000 are shared by all eukaryotes whose genomes have been sequenced and another 2,000 by all metazoans. Many aspects of chromosomal organization are completely different between the two taxa, however, and some gene families have expanded massively in one taxon when compared to the other. For example, in *C. elegans* there are 270 genes encoding nuclear hormone receptors, but in *Drosophila* there are only 21. By contrast, there are only 7 trypsin-like peptidases in the worm but 200 in the fly. In both species most gene knockouts lack a phenotype, which means that it can be quite difficult to determine the function of a single gene. Developmental biologists should note that the Hedgehog signaling pathway, much studied by *Drosophila* developmental geneticists because of its importance in embryonic patterning, has in *C. elegans* apparently lost its developmental role and been co-opted into the process of sex determination.

Paul Nurse (Cancer Research UK, London, UK) compared the recently completed genome of the fission yeast (*Schizosaccharomyces pombe*) with those of the budding yeast (*Saccharomyces cerevisiae*) and other sequenced eukaryotes. With only 4,824 genes *S. pombe* has the smallest eukaryotic genome sequenced to date. Some 3,000 of these genes are shared in all of the sequenced eukaryotes, including a set of highly conserved genes for various aspects of cell organization and around 50 that are homologous to human disease-related genes. Nevertheless, *S. cerevisiae* has about 1,000 more genes than *S. pombe*. Given that both species occupy ecologically similar habitats, an immediate question must be what *S. cerevisiae* does with its extra genes. The talks of Hodgkin and Nurse demonstrated that it is now possible to ask which genes are conserved in a given taxon (such as all metazoans, a phylum, a class, or a genus), and which of those are involved in development, and then to attempt to determine what those genes are doing in a particular organism.

John Postlethwait (University of Oregon at Eugene, USA) asked what genetic changes could facilitate major episodes of morphological innovation and, specifically, what genetic events in the evolution of chordates could have given rise to

'fierce' predators with complex behaviors from 'meek' sessile filter feeders. One likely answer to this question is genome duplication. The evolutionary history of the chordates is characterized by two major episodes of morphological innovation, and these two events are correlated with probable genome duplications. Studies of Hox genes suggest that cephalochordates and urochordates have only one cluster of Hox genes and, by inference, an unduplicated genome. The origin of vertebrates is associated with an expanded diversity of chordate forms, and Postlethwait noted that a representative basal vertebrate, the lamprey, has three or four Hox clusters. These are seen as evidence for at least one, and probably two, genome duplications at the origin of vertebrates. A second major increase in morphological diversity is associated with the evolution of the teleost fishes, which have seven or perhaps eight Hox clusters, presumably the result of yet another genome duplication in the fish lineage. How does a duplication event lead to morphogical innovation? After a duplication, whether of a whole genome or an individual gene, one copy of any given gene may take on an entirely new function while the other retains the original function, or both may diverge to share different aspects of the original function. In either case the duplication provides an opportunity for new function to arise. Work from Postlethwait and others suggests that the redundant gene copies in the duplicated genome are free to diverge, and that this functional divergence, when it occurs over a whole genome, fuels the evolution of morphological diversity.

Genome duplications are important evolutionary events, but they must be quite rare. Most evolution occurs through the accumulation of small changes, and new molecular techniques now allow dissection of the genetic or regulatory changes that control very small morphological differences in closely related organisms. New molecular methodologies have led to much greater insight into how these incremental changes occur. For example, David Stern (Princeton University, USA) reported work in *Drosophila* species that demonstrates morphological change caused by changes in gene regulation. Various species of *Drosophila* have differences in patterning of the cuticle in larval segments and adult legs. Stern and his colleagues have shown that these differences are caused by differential regulation of two genes, *ovo* (larval cuticle), and *Ubx* (adult legs). They suggest that the evolution of *cis*-regulatory regions are the dominant cause of microevolutionary phenotypic evolution.

Three-spine sticklebacks are a group of fishes that have undergone a huge morphological radiation in postglacial freshwater streams and lakes in western North America. Different 'morphs' are segregated by geography or behavior in the wild but are interfertile. David Kingsley (Stanford University, USA) and his colleagues have artificially crossed various morphs and used microsatellite typing to create a genome-wide linkage map of skeletal traits. Their results show that many important morphological changes are controlled by quantitative trait loci (QTLs) that map to single linkage groups on specific chromosomes.

It is clear from the reports of genome-level research that whole-genome comparisons and other genome-scale studies will provide much new information for biologists of all types over the next few years. But this 'big biology' work can, it seems to us, only provide half the story. Even if we know which genes are shared between organisms and when they are expressed, we can understand gene function properly only by experimental manipulation of one or a few genes in well-understood organismal systems. Such work complements whole-genome studies, and it is clear that both types of work are important if we are to understand how development evolved in the organisms we see today.