IN BRIEF

EVO–DEVO

Evolution of *yellow* gene regulation and pigmentation in *Drosophila*.

Wittkopp, P. J. *et al. Curr. Biol.* **12**, 1547–1556 (2002)

One goal of evolutionary developmental biology is to understand the molecular-genetic basis of phenotypic evolution. A useful system for such studies is the evolution of the pigmentation pattern in the *Drosophila* lineage. By using transgenic flies that carry a heterologous *yellow* (melanin-encoding) gene, the authors show that changes in *yellow* expression in closely related species have resulted from changes in both *cis*-regulatory regions and *trans*-acting factors. The different *yellow* expression patterns can also be attributed to evolutionary changes in other genes.

DEVELOPMENTAL BIOLOGY

Hedgehog-mediated patterning of the mammalian embryo requires transporter-like function of Dispatched.

Ma, Y. *et al. Cell* **111**, 63–75 (2002)

Mouse *Dispatched homolog1* is required for long-range, but not juxtacrine, Hh signaling.

Caspary, T. *et al. Curr. Biol.* **12**, 1628–1632 (2002)

Signalling by the Hedgehog (Hh) family of proteins is required to pattern many vertebrate and invertebrate tissues in a concentration-dependent manner. In flies, the long-range action of Hh proteins is thought to occur through the ability of Dispatched (Disp), a transmembrane protein, to release Hh from the outer membrane of Hh-producing cells. Ma and colleagues show that this function is conserved in mouse and that *DispA*, a mouse *disp* homologue, is required for all mouse Hh patterning functions. In a screen for genes required for the ventral patterning of the neural tube, Caspary *et al.* identified *Disp1*, a second mouse *disp* homologue, and have shown that it is required for long-, but not short-, range Hh signalling.

FUNCTIONAL GENOMICS

Gene expression during the life cycle of *Drosophila melanogaster*.

Arbeitman, M. N. *et al. Science* **297**, 2270–2275 (2002)

This paper reports the microarray-based transcriptional profiling of 4,028 wild-type *Drosophila* genes, assayed at 66 sequential time points during the organism's life cycle. Expression was also assayed in mutant flies that lack germline and eye tissue to refine expression data for these tissues. Many dynamic gene-expression changes are reported that correlate with *Drosophila*'s development, maturation and sex. Hierarchical clustering analyses also provide new information on gene function and on the components of pathways and complexes, as these analyses clustered many genes of unknown function with genes of known or predicted function.

EVO–DEVO

A question of control

Although sequence similarity between genes is a good indicator of their evolutionary relatedness, you wouldn't necessarily expect their encoded proteins to have similar activities — particularly if they belong to different species. But Wang *et al.* recently found an interesting exception: complete functional overlap between the fruitfly *atonal* (*ato*) gene and its mouse homologue, *Math1*. Although these two transcription factor genes have only partial sequence similarity and have different functions in the two species, they substitute for each other seamlessly. This work is the first to find an invertebrate gene sequence that can completely rescue the mutant phenotype of its vertebrate counterpart.

The *Drosophila* gene *atonal* has a well-characterized function in specifying cell fates in the peripheral nervous system (PNS) and is required for axonal branching in the central nervous system (CNS). By contrast, the mouse homologue *Math1* specifies cell identities in both the PNS and the CNS and, oddly enough, in certain gut cell lineages. But just how different are these two genes? Not at all, it seems. The expression of the *Math1* coding sequence under the control of the *ato* enhancer rescues the *ato*$^{-/-}$ fly embryonic phenotype, which includes missing photoreceptors and stretch receptors. The reciprocal experiment gave an equally clear-cut result: *Math1*$^{-/-}$ mice that expressed only one copy of *ato* were indistiguishable from their wild-type littermates. What is surprising about this work is that Ato and Math1, although similar enough to be considered homologous, are only 68% identical in a crucial domain and not at all similar elsewhere.

The differences between Ato and Math1 probably do not arise from new protein domains but from *cis*-regulatory changes that cause the two genes to be expressed in different tissues. Ato is not expressed in the fly gut, for example, but it substitutes perfectly for Math1 in this tissue in the mouse. Full functional conservation is commonplace between paralogous genes — those derived from gene duplication (see the review on p827 of this issue) — but has never before been documented in genes such as *Math1* and *ato* that are related through speciation.

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References and links

ORIGINAL RESEARCH PAPER Wang, V. Y. *et al.* *Drosophila atonal* fully rescues the phenotype of *Math1* null mice: new functions evolve in new cellular contexts. *Curr. Biol.* **12**, 1611–1616 (2002)

FURTHER READING Prince, V. E. & Pickett, F. B. Splitting pairs: the diverging fates of duplicated genes. *Nature Rev. Genet.* **3**, 827–837 (2002)

WEB SITES

Huda Zoghbi's lab: http://www.hhmi.org/research/investigators/zoghbi.html

Hugo Bellen's lab: http://www.hhmi.org/research/investigators/bellen.html