RESEARCH HIGHLIGHTS



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Genomics on the fly

Non-scientists might look at the tiny fruitfly and see an unwelcome guest at the fruitbowl. But for more than 100 years scientists have looked at *Drosophila melanogaster* and seen a powerhouse for studying genetics, development, behaviour, evolution and, more recently, genomics. A wealth of papers detailing the analysis of 12 *Drosophila* genomes now shows that size doesn't matter: these flies are ready to revolutionize evolutionary genomics.

In addition to the two Drosophila genomes that have previously been published, the Drosophila 12 Genomes Consortium now reports, in Nature, the sequence of ten more species, spanning a genetic distance that is equivalent to that from human to lizard. One aspect of their analysis is on positive selection, where changes in protein-coding sequences have been adaptive. Recurrent positive selection seems to have affected roughly one-third of the singlecopy genes. The 12 species have roughly the same number of genes - although 44 lineage-specific genes were found — but there seem to have been abundant genome rearrangements, some of which might have contributed to speciation events.

A companion paper from Stark *et al.* focuses on negative selection or cases in which the genome has not accrued any base changes, suggesting pressure over time for sequences to stay the same. Looking at bases that are conserved among all 12 genomes, the group identified 'evolutionary signatures', such as protein-coding exons, regulatory motifs and novel microRNA

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genes. These genomic predictions were compared to chromatin immunoprecipitation data to demonstrate their effectiveness, and a regulatory network for *D. melanogaster* with 60% confidence is presented in the supplementary information.

Geneticists aren't waiting around to use these data. For example, Brian Oliver's group has used these genome sequences to generate species-specific microarrays to address long-standing questions of sex chromosome evolution in *Drosophila*. They found that genes with male-biased expression differ among species, and that X-chromosome gene expression is not compatible with a simple model of X-chromosome inactivation. The *Nature* issue that contains these papers also has two Reviews and two Progress pieces on the latest *Drosophila* research from other fields in biology, from physiology and cell biology to neural circuits and gene expression. At the same time, more than forty companion papers, including nine in *Genome Research*, are being published in several journals, using the genome sequences to ask evolutionary and genetic questions. As a scientist, you now might think that flies are taking over the world!

Chris Gunter, Senior Editor, Nature

ORIGINAL RESEARCH PAPERS Drosophila 12 Genomes Consortium. Evolution of genes and genomes on the Drosophila phylogeny. Nature 450, 203-218 (2007) | Stark, A. et al. Discovery of functional elements in 12 Drosophila genomes using evolutionary signatures. Nature **450**, 219–232 (2007) FURTHER READING Birney, E. Come fly with us. Nature 450, 184-185 (2007) | Zhang, Y et al. Constraint and turnover in sex-biased expression in the genus Drosophila, Nature 450, 233-237 (2007) | Sturgill, D. et al. Demasculinization of X chromosome genes in the Drosophila genus. Nature 450, 238-241 (2007) | Leopold, P. & Perrimon, N. Drosophila and the genetics of the internal milieu. Nature 450, 186-188 (2007) | Lecuit, T. & Le Goff, L. Orchestrating size and shape during morphogenesis. Nature 450, 189–192 (2007) | Vosshall, L. B. Into the mind of a fly, Nature 450, 193–197 (2007) | Lis, J. T. Imaging Drosophila gene activation and polymerase pausing in vivo, Nature 450, 198-202 (2007) Sackton, T. B. et al. Dynamic evolution of the innate immune system in Drosophila. Nature Genet. 7 November 2007 (doi:10.1038/ na.2007.60)

WEB SITE

Web focus on Drosophila: http://www.nature. com/nature/focus/drosophila

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