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The dynamics of *Drosophila* development

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In the September 27 Science, Arbeitman *et al.* report extensive transcriptional profiling of a third of the genes in the Drosophila melanogaster genome at stages from fertilization through to aging adults (*Science*, **297:**2270-2275, September 27, 2002). Arbeitman *et al.* used cDNA microarrays to follow the fate of over 4000 genes over 66 sequential time periods during the fly life cycle; they found that the vast majority of genes changed significantly (many over four-fold) over the 40-day test period. Around 36% of genes showed a single major expression peak, 40% showed two peaks, and the rest showed three or more peaks. About half the genes changed during embryogenesis, whereas only 118 changed during adult life. They found that genes with related biochemical functions (defined by gene ontology annotations) tend to be expressed at similar times. Hierarchical analysis identified clusters of genes co-expressed in particular tissues or at distinct developmental stages.

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