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# Evolution of gene expression in the *Drosophila melanogaster* subgroup

Scott A. Rifkin, Junhyong Kim, Kevin P. White ·

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Little is known about broad patterns of variation and evolution of gene expression during any developmental process. Here we investigate variation in genome-wide gene expression among *Drosophila simulans*, *Drosophila yakuba* and four strains of *Drosophila melanogaster* during a major developmental transition—the start of metamorphosis. Differences in gene activity between these lineages follow a phylogenetic pattern, and 27% of all of the genes in these genomes differ in their developmental gene expression between at least two strains or species. We identify, on a gene-by-gene basis, the evolutionary forces that shape this variation and show that, both within the transcriptional network that controls metamorphosis and across the whole genome, the expression changes of transcription factor genes are relatively stable, whereas those of their downstream targets are more likely to have evolved. Our results demonstrate extensive evolution of developmental gene expression among closely related species. [LESS](#)

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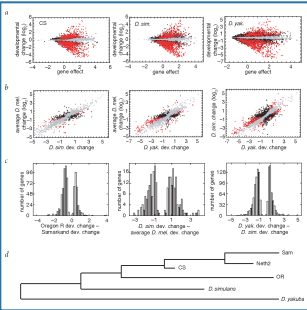


Figure 1

Table 1 - Distances between lineages*				
Lineage	Obscura	Simulans	Obscura	Simulans
Obscura	100	200	100	100
Simulans	200	100	200	100
Obscura	100	200	100	100
Simulans	200	100	200	100

Table 1

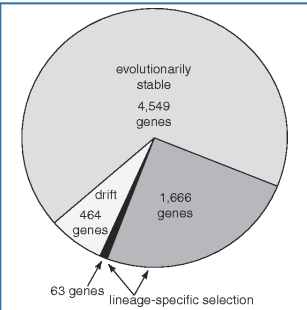


Figure 2

Table 2 - Associations between evolutionary modes and gene function*				
Transcription factor	Obscura	Simulans	Obscura	Simulans
Transcription factor	100	200	100	100
Transcription factor	100	200	100	100
Transcription factor	100	200	100	100

Table 2

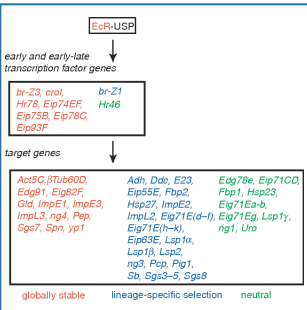


Figure 3

Table 3 - Evolution of upregulated and downregulated genes*				
Lineage	Obscura	Simulans	Obscura	Simulans
Obscura	100	200	100	100
Simulans	200	100	200	100
Obscura	100	200	100	100
Simulans	200	100	200	100

Table 3

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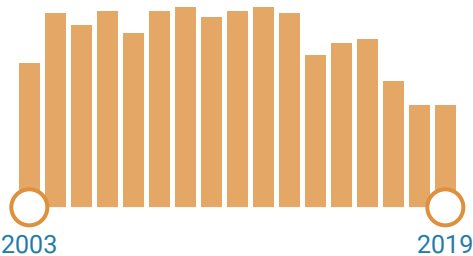
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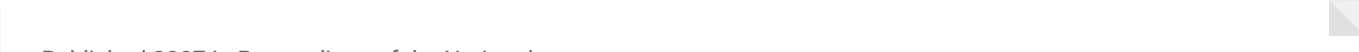
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