

Polymorphism and divergence of novel gene expression patterns in *Drosophila melanogaster*, pp. 79–93

Julie M. Cridland, Alex C. Majane, Hayley K. Sheehy, and David J. Begun

One mechanism by which transcriptomes evolve is through tissue-specific gene expression. Cridland *et al.* measured gene expression in *Drosophila melanogaster* in five tissues: accessory gland, testis, larval salivary gland, head, and first instar larvae. Data from *D. melanogaster* were combined with comparable data from two outgroups, allowing the authors to identify tissue-specific gains and losses of gene expression. They observed changes in expression phenotypes, both fixed and polymorphic, tissue specific differences in gain and loss patterns, potential *cis*-regulatory variants, as well as genes that show quantitative differences in expression.

Extensive recombination suppression and epistatic selection causes chromosome-wide differentiation of a selfish sex chromosome in *Drosophila pseudoobscura*, pp. 205–226

Zachary L. Fuller, Spencer A. Koury, Christopher J. Leonard, Randee E. Young, Kobe Ikegami, Jonathan Westlake, Stephen Richards, Stephen W. Schaeffer, and Nitin Phadnis

The *Drosophila pseudoobscura* Sex-Ratio (SR) chromosome was one of the first-discovered segregation distorter chromosomes. Despite being a historically significant and well-studied segregation distortion system, the mechanisms allowing for the long-term association of the *Drosophila pseudoobscura* SR chromosome with multiple nonoverlapping inversions remain unclear. Fuller *et al.* perform a comparative genomic analysis between SR and uninverted standard X-chromosomes in *D. pseudoobscura* to study the evolutionary

history and dynamics of SR chromosomes. Combining the genomics analysis, direct recombination experiments, and population genetic modelling, they demonstrate that SR chromosomes are maintained through a combination of suppressed recombination and epistatic selection.

Punctuated aneuploidization of the budding yeast genome, pp. 43–50

Lydia R. Heasley, Ruth A. Watson, and Juan Lucas Argueso

Heasley, Watson, and Argueso present findings demonstrating that transient and punctuated destabilizing events can promote the rapid formation of extraordinarily reconfigured karyotypes.

New aspects of invasive growth regulation identified by functional profiling of MAPK pathway targets in *Saccharomyces cerevisiae*, pp. 95–116

Matthew D. Vandermeulen and Paul J. Cullen

MAPK pathways are universal regulators of morphogenesis and stress responses in eukaryotes. In this study, Vandermeulen and Cullen identified the function of transcriptional targets of a MAPK pathway in yeast that positively regulates filamentous growth. This led to the discovery of new positive and negative regulators of filamentous growth. They also found that the pathway negatively regulates filamentous growth under some conditions and discovered new positive roles for the pathway in controlling cell adhesion and the cell cycle. The study suggests characterizing the genetic targets of other signaling pathways could lead to important advances in understanding signal transduction regulation.