

ISSUE HIGHLIGHTS

Population structure with localized haplotype clusters, pp. 1337–1344

Sharon R. Browning and Bruce S. Weir

F_{ST} is a useful measure of population divergence that measures variation between populations versus the variation within populations. This article presents a new multi-locus version of F_{ST} based on localized haplotype clusters that has the appealing property of providing estimates of population structure expected from existing models of human population origins. In particular, it shows African populations to have the lowest divergence from the ancestral population, East Asian populations to have highest divergence, with other populations (European, Indian, and Mexican) having intermediate levels of divergence.

Estimating the parameters of selection on nonsynonymous mutations in *Drosophila pseudoobscura* and *D. miranda*, pp. 1381–1396

Penelope R. Haddrill, Laurence Loewe and Brian Charlesworth

Two outstanding issues in evolutionary genetics concern the strength of natural selection against new deleterious mutations that cause changes in the amino-acid sequence of a protein, and the proportion of amino-acid sequence differences between related species that have been fixed by selection favoring new advantageous mutations. These investigators compare several different methods for estimating these parameters in two closely related species of *Drosophila*. They find that, on average, deleterious mutations segregating in the populations are subject to only very weak negative selection, but the majority of new amino-acid mutations are under such strong negative selection that they are extremely unlikely to become fixed in the population. In addition, they find that a large fraction of amino acid sequence differences between species results from positive selection.

The consequences of regulation of *desat1* expression for pheromone emission and detection in *Drosophila melanogaster*, pp. 1297–1309

Benjamin Houot, François Bousquet and Jean-François Ferveur

Mate recognition requires exchange of sensory signals and precise matching between the transmission and the perception of those signals. *desat1* determines both of these aspects of mate recognition since it controls the production and discrimination of sex pheromones in *Drosophila*. This gene produces different transcripts, each yielding a unique protein. These authors find that they can separately affect signal transmission and perception by selectively manipulating different regulatory regions of *desat1*. Thus, the dual roles of *desat1* on pheromonal communication depends on regulation of its transcriptional activity.

Meiotic regulators Ndt80 and Ime2 have different roles in *Saccharomyces* and *Neurospora*, pp. 1271–1282

Elizabeth A. Hutchison and N. Louise Glass

While meiosis is a highly conserved process, the manner in which the steps of meiosis are controlled is not conserved, even among fungi. These authors find that homologs of regulators of meiosis in yeast regulate other aspects of sexual development in the filamentous fungus *Neurospora crassa*. Although interactions between these regulators may be conserved, the biological program they control can evolve rapidly.

***Phantom*, a new subclass of *Mutator* DNA transposons found in insect viruses and widely distributed in animals,** pp. 1507–1517

Claudia P. Marquez and Ellen J. Pritham

Mutator transposons, which play a critical role in the evolution of plant genomes, are rare in other eukaryotes. This article describes a previously uncharacterized group of DNA transposons, designated *Phantom*, found in the genomes of a wide range of eukaryotes, and provides evidence that they are *Mutator* transposons. Interestingly, *Phantom* proteins were identified in two insect viruses, and they seem to move horizontally from insect to virus, providing a new line of evidence for the role of viruses in the horizontal transfer of DNA transposons in animals.

The antidepressant sertraline targets intracellular vesiculogenic membranes in yeast, pp. 1221–1233

Meredith M. Rainey, Daniel Korostyshevsky, Sean Lee and Ethan O. Perlstein

Can a unicellular model organism like yeast, which lacks neurons and neurotransmitters, teach us anything about mechanisms of action of psychoactive drugs in people? This article addresses this question by exploiting the cytotoxicity of the selective serotonin reuptake inhibitor sertraline (Zoloft) in a simple drug-resistance selection. The results demonstrate that sertraline targets intracellular membranes of the vesicle transport system. The two pathways that shape drug response in yeast are conserved throughout evolution and play important roles in the function of synapses in multicellular organisms.

Extensive loss of RNA editing sites in rapidly evolving *Silene* mitochondrial genomes: Selection vs. retroprocessing as the driving force, pp. 1369–1380

Daniel B. Sloan, Alice H. MacQueen, Andrew J. Alverson, Jeffrey D. Palmer and Douglas R. Taylor

The evolutionary origin and maintenance of RNA editing have been proposed to determine the frequency of editing. These authors sequenced whole mitochondrial genomes of closely related angiosperm species with highly divergent mutation rates, and found that recent mutational accelerations are associated with rapid loss of editing sites. Based on the pattern of editing site loss, the authors develop a model of gene conversion and RNA editing evolution that may apply throughout the angiosperms.