ISSUE HIGHLIGHTS

Ploidy and the evolution of endosperm of flowering plants, pp. 439–453
Aurélie Cailleau, Pierre-Olivier Cheptou and Thomas Lenormand
Double fertilization is an eccentricity of flowering plants: Both the embryo and the nutritive tissue result from fertilization. In addition, the maternal contribution is often doubled in the nutritive tissue. Double fertilization and maternal contribution doubling are currently hypothesized to result from a male/female conflict over resource allocation. The authors explore theoretically the hypothesis that double fertilization and maternal contribution doubling evolved as a way to mask deleterious mutations. A new type of male/female conflict emerges from their model.

Transient genotype-by-environment interactions following environmental shock provide a source of expression variation for essential genes, pp. 587–593
Kevin H. Eng, Daniel J. Kvitek, Sündüz Keles and Audrey P. Gasch
Selection acts on phenotypic variation to remove deleterious mutations or select advantageous alleles. But some traits show little variation, raising questions as to how they evolve. The authors of this article show that hidden variation in yeast gene expression is unmasked by environmental transitions. Of genes subject to genotype-by-environment interactions, half show transient variation in their expression, specifically during environmental acclimation, and they are enriched for essential genes, whose steady-state expression is under strong purifying selection. Thus, transient variation during environmental shifts reveals a source of previously unrecognized transcript variation, an important prerequisite for the evolution of gene expression.

Experimentally increased codon bias in the Drosophila Adh gene leads to an increase in larval, but not adult, alcohol dehydrogenase activity, pp. 547–555
Winfried Hense, Nathan Anderson, Stephan Hutter, Wolfgang Stephan, John Parsch and David B. Carlini
Codon usage bias is a nearly universal feature of genomes. Is it a result of the fact that optimal codons are translated more accurately and efficiently than suboptimal codons? These investigators address this question by replacing seven suboptimal leucine codons in the Drosophila Adh gene with optimal leucine codons. The preferred substitutions result in a decrease in ADH activity in adults but lead to an increase in ADH activity in larvae. These results are consistent with stronger translational selection in the larval stage and suggest that there may be a selective conflict over optimal codon usage between different life-history stages.

Rate of adaptation in large sexual populations, pp. 467–481
R. A. Neher, B. I. Shraiman and D. S. Fisher
The idea that recombination speeds up adaptation by combining beneficial variants goes back to Fisher and Muller, but a quantitative analysis of adaptation in sexual populations is still lacking. Here, the authors calculate the rate of adaptation in large sexual populations and arrive at surprising results: In large populations, the rate of adaptation increases only logarithmically with the population size, but it increases rapidly with the rate of recombination.

Gene genealogies strongly distorted by weakly interfering mutations in constant environments, pp. 529–545
Jon Seger, Wendy A. Smith, Jarom J. Perry, Jessalynn Hunn, Zofia A. Kaliszewska, Luciano La Sala, Luciana Pozzi, Victoria J. Ravintrea and Frederick R. Adler
Mutations with very small effects on fitness are hard to study, but if they are abundant, they can collectively generate much of theheritable phenotypic variation within populations. These investigators show that the accumulation of small-effect mutations in nonrecombining chromosomes such as mitochondria can distort gene trees in three different ways, all of which could be detected easily under suitable circumstances. The amphipod crustacean ectoparasites of right whales (“whale lice”) appear to meet the assumptions of this model, and their mitochondrial genome genealogies appear to be “warped,” as expected.

The genetics of postmating, prezygotic reproductive isolation in Drosophila, pp. 401–410
Andrea L. Sweigart
To understand the process of speciation, it is critical to identify the genetic basis of reproductive isolation. The author describes a strong postmating barrier that prevents fertilization between two species of Drosophila, D. simulans and D. americana. This interspecific fertilization incompatibility is caused by an interaction among autosomal, recessive loci, and maps to only four genetic regions. The author argues that male-female coevolution within D. americana has given rise to reproductive isolation between species.

The genetic signature of conditional expression, pp. 557–570
J. David Van Dyken and Michael J. Wade
In an ideal world, organisms could maintain a vast reserve of environment-specific genes, ready to be deployed whenever the need arises. While that would be marvelously adaptive, the genetic mechanisms underlying such conditional gene use carry the seeds of their own evolutionary limitation. When a gene is silent, it escapes the shaping hand of natural selection and becomes a target for the disruptive force of mutation. The authors determine the genetic signature of conditional selection and quantify its fitness consequences. They conclude that in the real world, natural selection might allow a species to become a jack-of-all-trades, but mutation ensures that it is master of none.

The evolution of control and distribution of adaptive mutations in a metabolic pathway, pp. 483–502
Kevin M. Wright and Mark D. Rausher
Because most proteins are parts of larger biological systems, their evolution is driven by the effect of each protein on system output. This article describes a model of metabolic pathways with the purpose of understanding if position in a pathway influences enzyme evolution. Metabolic control theory and saturation kinetics are used to determine the effects of mutations on pathway output. The results reveal that control of pathway output evolves to be unequal among enzymes, with upstream enzymes evolving the greatest control and accumulating more adaptive substitutions.