ISSUE HIGHLIGHTS

Statistical mechanics and the evolution of polygenic quantitative traits, pp. 997–1011
N. H. Barton and H. P. de Vladar
The evolution of quantitative traits depends on the frequencies of the alleles involved, which can rarely be measured. These authors borrow from statistical mechanics to develop an approximation of the dynamics of observable quantities, such as the mean and variance of a trait. They show that populations evolve to maximize entropy, subject to constraints on the expected values of observable quantities. Their method gives the equilibrium state exactly and is accurate even when there are abrupt changes in directional selection. They outline how their method describes epistatic interactions as, for example, with stabilizing selection.

The control region of maternally and paternally inherited mitochondrial genomes of three species of the sea mussel genus Mytilus, pp. 1045–1056
Liqin Cao, Brian S. Ort, Athanasia Mizi, Grant Pogson, Elen Kenchington, Eleftherios Zouros and George C. Rodakis
The father's mtDNA rebelled 400 million years ago in mussels, clams, and the like. It now coexists with the mother's mtDNA in males, but claims exclusive dominion in the sperm. A study of this doubly uniparental inheritance in three mussel species is described in this article, with the spotlight on the mtDNA's control region, where maternal and paternal genomes are most different. How have they evolved since repeated speciation events? Are there identifiable “feminine” and “masculine” sequences, and what might their role be?

Genomic consequences of background effects on scalloped mutant expressivity in the wing of Drosophila melanogaster, pp. 1065–1076
Ian Dworkin, Erin Kennerly, David Tack, Jennifer Hutchinson, Julie Brown, James Mahaffey and Greg Gibson
A common assumption in genetic analysis is that the observed phenotypic effects of a mutation are a simple consequence of the DNA lesion responsible. However, genetic “background effects” significantly modify the penetrance and expressivity of a mutant phenotype. In this article, the authors introduce a model for the genetic and genomic dissection of genetic background and demonstrate that background effects can extend to the epistatic interactions between mutations.

The evolution and diversification of S-locus haplotypes in the Brassicaceae family, pp. 977–984
Kristina Edh, Björn Widén and Alf Ceplitis
Many members of the Brassicaceae plant family possess a sporophytic self-incompatibility (SI) system, enabling them to avoid self-fertilization. These authors analyze DNA sequence data from wild Arabidopsis and Brassica species along with data from Brassica cultivars to show that extant S-locus alleles trace back to a common Arabidopsis–Brassica ancestor, and that only a small number of these survived in the Brassica lineage after its split from Arabidopsis. Subsequent domestication in Brassica seems not to have affected S-locus diversity in that genus.

The role of protein phosphatase 4 in regulating microtubule severing in the Caenorhabditis elegans embryo, pp. 933–943
Xue Han, José-Eduardo Gomes, Cheryl L. Birmingham, Lionel Pintard, Asako Sugimoto and Paul E. Mains
After fertilization, the embryo switches from the meiotic to the mitotic style of cell division, so meiotic-specific proteins must be eliminated prior to mitosis. This presents a problem for the Caenorhabditis elegans embryo, where the transition takes only 15 min. This article focuses on inactivation of the meiotic-specific microtubule-severing protein MEI-1. Two parallel systems were known to degrade MEI-1 as the embryo moves from meiosis into mitosis; this article describes a third system that relies on phosphorylation. Thus, multiple redundant systems ensure that the embryo makes the transition from meiosis to mitosis.

A mutant plasma membrane protein is stabilized upon loss of Yvh1, a novel ribosome assembly factor, pp. 907–915
Yu Liu and Amy Chang
Putting proteins in the proper place is paramount for the cell. An altered plasma membrane protein, Pma1-10, makes its way to the membrane, but fails to persist at the cell surface. To learn how defective proteins are recognized for removal from the plasma membrane and delivery for vacuolar degradation, these authors identify suppressors of the pma1-10 mutation. Surprisingly, one of these suppressors affects Yvh1, which encodes a ribosome assembly factor. The authors propose that altered ribosome composition and/or function caused by loss of Yvh1 may result in specific changes in protein translation, with consequences for plasma membrane activities.

Nonadditive expression of homoeologous genes is established upon polyploidization in hexaploid wheat, pp. 1147–1157
Michael Pumphrey, Jianfa Bai, Debbie Laudencia-Chingcuanco, Olin Anderson and Bikram S. Gill
The development and domestication of polyploid wheat played a central role in the establishment of modern civilization by providing a stable and readily available source of nutrition, as mankind shifted from migratory clans to stationary societies. How are gene expression dynamics altered by new polyploidization events? This article describes analysis of gene expression in a synthetic hexaploid wheat line, which demonstrates that allopolyploidization, per se, results in rapid initiation of differential expression of homoeologous genes with nonadditive gene expression in wheat.

Rhythmic conidiation in constant light in vivid mutants of Neurospora crassa, pp. 917–931
Kevin Schneider, Sabrina Perrino, Kim Oelhafen, Sanshu Li, Artiom Zatsepin, Patricia Lakin-Thomas and Stuart Brody
The fungus Neurospora crassa is a simple organism, but its circadian clock is complex. Rhythmic conidiation is normally dampened in constant light, and these authors were surprised to find that the vivid mutant’s conidiation rhythm persists in the light. The rhythm’s period (6–23 hr) is influenced by light intensity and temperature and doesn’t require the clock protein FRQ, but it can be reset by dark pulses, in the same way circadian rhythms in animals are reset. The authors propose that vivid reveals a central oscillator that can drive rhythmic conidiation independently of FRQ, with FRQ providing circadian stability.