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ISSUE HIGHLIGHTS

Mendel’s genes: Toward a full molecular characterization, pp. 3–10
James B. Reid and John J. Ross
Modern genetics is founded on the studies performed by Gregor Mendel on the inheritance of seven “factors” in the pea. Yet, until fairly recently, the actual genes involved were unknown. In this Perspectives article, the authors review work that has identified four of the seven genes and given insights into the probable molecular nature of their recessive variants. The status of current work on the other three genes is also discussed.

Massive changes in genome architecture accompany the transition to self-fertility in the filamentous fungus Neurospora tetrasperma, pp. 55–69
Christopher E. Ellison, Jason E. Stajich, David J. Jacobson, Donald O. Natvig, Alla Lapidus, Brian Foster, Andrea Aerts, Robert Riley, Erika A. Lindquist, Igor V. Grigoriev, and John W. Taylor
These authors use a comparative genomics approach to solve a decades-old genetics question concerning possible structural rearrangements and the origin of a large region of suppressed recombination in the fungus Neurospora tetrasperma. They discover a series of three inversions within the nonrecombining region, formulate a model for its evolution, and examine the consequences of suppressed recombination for the genes residing within it.

Quantification of inbreeding due to distant ancestors and its detection using dense single nucleotide polymorphism data, pp. 237–249
Matthew C. Keller, Peter M. Visscher, and Michael E. Goddard
Inbreeding depression, the reduced fitness among offspring of related parents, has traditionally been studied in pedigrees. The use of SNP data to estimate inbreeding arising from distant common ancestors in “outbred” human populations is a promising approach, but it is unclear which estimate of inbreeding is optimal for detecting inbreeding depression. The authors of this study use theory, simulated genetic data, and real genetic data to show that inbreeding estimated from runs of homozygosity retains variation even in large populations and is likely to be the most powerful method of detecting inbreeding effects.

Genetic evidence that synaptonemal complex axial elements govern recombination pathway choice in mice, pp. 71–82
Xin Chenglin Li, Ewelina Bolcun-Filas, and John C. Schimenti
Crossing over between homologous chromosomes is critical for proper chromosome segregation in meiosis. Recombination is driven by programmed double strand break (DSB) repair, which in meiosis occurs primarily by interhomolog recombination rather than the inter-sister recombination that repairs DSBs in somatic cells. This article describes experiments on mice that suggest that components of the synaptonemal complex direct recombination proteins to promote interhomolog, rather than inter-sister recombinational repair of DSBs.

The genetic basis of rapidly evolving male genital morphology in Drosophila, pp. 357–374
John P. Masly, Justin E. Dalton, Sudeep Srivastava, Liang Chen, and Michelle N. Arbeitman
The morphology of external genitalia of insects evolves rapidly. These authors dissect the genetic basis of this trait using two closely related species of Drosophila. They identify several small genomic regions that have large effects on species-specific morphology, and they show that the size and shape of some rapidly evolving genital structures are specified, in part, by separate loci. Transcriptome analysis of the larval tissue that gives rise to the adult genitalia suggests that the insulin signaling pathway may be an engine of morphological change.

Effect of growth under selection on appearance of chromosomal mutations in Salmonella enterica, pp. 37–53
Semarhy Quiñones-Soto and John R. Roth
Rapid adaption seen in many bacteria has been attributed to “stress-induced” mutagenesis. In contrast, this article describes a selection system in which adaptation results from serial accumulation of chromosomal mutations of small effect, with no increase in general mutation rate. The behavior of this selection system supports a general model that may explain rapid adaptation in both laboratory and natural populations.

Genetic dissection of a key reproductive barrier between nascent species of house mice, pp. 289–304
Michael A. White, Brian Steffy, Tim Wiltshire, and Bret A. Payseur
Reproductive barriers between species often arise through hybrid sterility. House mice are an excellent system for exploring the genetics underlying hybrid sterility, but attention so far has only focused on F1 hybrids and the sex chromosomes. These authors report a genome-wide mapping of quantitative trait loci for several male sterility traits in F2 hybrids of mice. They uncover a large number of novel loci associated with sterility among the autosomes and X chromosome, revealing a suite of reproductive barriers important to generations beyond F1 hybrids.

The joint effects of background selection and genetic recombination on local gene genealogies, pp. 251–266
Kai Zeng and Brian Charlesworth
This article describes a structured coalescent model that accurately and efficiently predicts the joint effects of background selection (the continual removal of deleterious mutations by natural selection) and genetic recombination on DNA sequence variability at linked, selectively neutral sites. The model can consider all the neutral sites in a region simultaneously for an arbitrary sample size, so it should be useful for analyzing the genome-wide polymorphism data sets that are now available for many species.