

Discovery of lineage-specific genome change in rice through analysis of resequencing data, pp. 617–626

Robert A. Arthur and Jeffrey L. Bennetzen

New mutations are rare, which makes their discovery laborious and time-consuming. Arthur and Bennetzen describe an approach for enriching recent mutations that relies only on a reference genome sequence and resequencing data for other accessions of the species. Testing their strategy with the Nipponbare rice genome, they uncovered thousands of recent mutations. Their approach should be broadly applicable because it is not limited by genome size or generation time.

Linkage disequilibrium estimation in low coverage high-throughput sequencing data, pp. 389–400

Timothy P. Bilton, John C. McEwan, Shannon M. Clarke, Rudiger Brauning, Tracey C. van Stijn, Suzanne J. Rowe, and Ken G. Dodds

High-throughput sequencing methods provide a cost-effective approach for genotyping and are commonly used in population genetics studies. A drawback of these methods, however, is that sequencing and genotyping errors can arise in the form of mis-called bases or missing alleles from low sequencing depth. Bilton *et al.* show that these errors, if not taken into account, lead to underestimation of linkage disequilibrium. They present a new methodology that accounts for these errors and is able to accurately estimate linkage disequilibrium, even in low coverage sequencing scenarios.

Genomic instability promoted by overexpression of mismatch repair factors in yeast: a model for understanding cancer progression, pp. 439–456

Ujani Chakraborty, Timothy A. Dinh, and Eric Alani

Increased expression of mismatch repair proteins often correlates with tumor aggressiveness. Chakraborty, Dinh, and Alani report that co-overexpression of Msh2 and Msh6 in yeast results in genome instability phenotypes that are dependent on interaction with the replication fork component PCNA; this overexpression also alters the cell cycle distribution of exponentially growing cells. These novel observations suggest that overexpression of MSH factors affects the integrity of the DNA replication fork, causing genome instability phenotypes that likely promote cancer progression.

Differential expression of histone H3.3 genes and their role in modulating temperature stress response in *Caenorhabditis elegans*, pp. 551–565

Kamila Delaney, Jonathan Mailer, Joanna M. Wenda, Caroline Gabus, and Florian A. Steiner

Histone H3.3, a major variant of canonical histone H3, is highly conserved and essential for viability or fertility in most lineages. In *Caenorhabditis elegans*, H3.3 is expressed from five genes. Here, Delaney *et al.* find that the five genes show distinct developmental expression patterns but that their nucleosome incorporation depends on the conserved histone chaperone HIRA-1. Surprisingly, H3.3 is dispensable for viability in *C. elegans*; instead, it plays a vital role in the response to stresses such as high temperature.

Efficient expression of genes in the *Drosophila* germline using a UAS promoter free of interference by Hsp70 piRNAs, pp. 381–387

Steven Z. DeLuca and Allan C. Spradling

Using the yeast GAL4 transcription factor to control expression in *Drosophila melanogaster* has long been ineffective in female germ cells during oogenesis. Here, DeLuca and Spradling show that the expression problem of most *Drosophila* molecular tools is caused by their core Hsp70 promoter sequences, which are targeted in female germ cells by Hsp70-directed piRNAs. They create tools to solve this problem, making possible the discovery of novel genes acting during oogenesis that have previously been missed using RNAi tools.

Genetic dissection of a supergene implicates *Tfap2a* in craniofacial evolution of threespine sticklebacks, pp. 591–605

Priscilla A. Erickson, Jiyeon Baek, James C. Hart, Phillip A. Cleves, and Craig T. Miller

Genomic regions that regulate multiple traits, called supergenes, have been found in a range of organisms, including threespine stickleback fish. Here, Erickson *et al.* show that closely linked but genetically separable changes in *Bmp6* and *Tfap2a* contribute to a supergene underlying evolved skeletal gain in multiple freshwater stickleback populations. Close linkage of these skeletal gain alleles in a supergene may facilitate rapid adaptation to freshwater environments.

Regulation of cell-to-cell communication and cell wall integrity by a network of MAP-kinase pathways and transcription factors in *Neurospora crassa*, pp. 489–506

Monika S. Fischer, Vincent W. Wu, Ji E. Lee, Ronan C. O'Malley, and N. Louise Glass

Filamentous fungi depend on asexual cell-to-cell communication and cell fusion to establish and maintain an interconnected mycelial colony. In *Neurospora crassa*, genetically identical asexual spores undergo chemotropic interactions resulting in cell fusion and colony establishment. Fischer *et al.* find that two conserved MAP kinase cascades required for cell fusion regulate two transcription factors that control expression of genes important for growth, communication, fusion, and cell wall stress response.

Evolution of DNaseI hypersensitive sites in MHC regulatory regions of primates, pp. 579–589

Yabin Jin, Rachel M. Gittelman, Yueer Lu, Xiaohui Liu, Ming D. Li, Fei Ling, and Joshua M. Akey

Jin *et al.* report thousands of DNaseI hypersensitive sites in the MHC region that have been gained or lost in primate genomes since their evolutionary divergence, identifying 24 that evolved rapidly in the human lineage. Their results suggest that species-specific motif gains or losses of rapidly-evolving DHSs in primate genomes might play a role in adaptive evolution.