Identity-by-descent estimation and mapping of qualitative traits in large, complex pedigrees, pp. 1577–1590
Mark Abney

The multitude and variety of relationships that exist between individuals in very large pedigrees provide a wealth of information for genetic mapping of complex diseases. However, fully mining this information is computationally cumbersome and therefore impractical. This investigator solved this problem with development of a novel and very fast computational method that performs linkage mapping by identity-by-descent sharing in pedigrees of virtually unlimited size, even with hundreds of thousands of markers.

Both costs and benefits of sex correlate with relative frequency of asexual reproduction in cyclically parthenogenetic Daphnia pulexica populations, pp. 1497–1502
Desiree E. Allen and Michael Lynch

Sexual reproduction is generally believed to be beneficial because it expands expressed genetic variation, but sex can actually impede the adaptive progress of a population when gene action is nonadditive. This article takes advantage of the ability of Daphnia pulexia to switch between sexual and asexual reproduction to directly compare the costs and benefits of sex in a series of populations that naturally vary their frequency of sex. Sex was found to result in changes in genotypic mean and genetic variance, and the magnitude of the attendant costs and benefits is inversely proportional to the frequency of sex.

A genetic screen for increased loss of heterozygosity in Saccharomyces cerevisiae, pp. 1179–1195
Marguerite P. Andersen, Zara W. Nelson, Elizabeth D. Hetrick and Daniel E. Gottschling

Loss of heterozygosity (LOH) is a familiar term that provides a conceptual framework for how somatic mutations drive oncogenesis. These investigators identify 61 yeast mutants with increased rates of LOH. Mutations in genes involved in DNA replication and chromatin assembly led to LOH predominantly via reciprocal recombination. In contrast, nonreciprocal LOH events are largely due to mutations in genes implicated in kinetochore function, sister chromatid cohesion, or relatively late steps of DNA recombination.

Meiotic recombination at the ends of chromosomes in Saccharomyces cerevisiae, pp. 1221–1235
Arnold B. Barton, Michael R. Pekosz, Rohini S. Kurvathi and David B. Kaback

This pioneering article on meiotic recombination at the ends of yeast chromosomes reveals recombination at 31 of 32 chromosome ends. The authors observe few crossovers in subtelomeric sequences but surprisingly high rates of recombination in the adjacent sequences. The distribution of crossovers in yeast resembles that seen in many eukaryotes, where distal regions of chromosome arms undergo more recombination than do their internal regions.

Chromosomal rearrangement inferred from comparisons of 12 Drosophila genomes, pp. 1657–1680
Arjun Bhutkar, Stephen W. Schaeffer, Susan M. Russo, Lu Xu, Temple F. Smith and William M. Gelbart

This article describes the relationship of syntetic blocks of genes to the phylogenetic distribution of several Drosophila species. A large number of syntetic stretches of genes are conserved across these species despite the fact that a high rate of chromosomal rearrangements—macro- and micro-inversions—shuffle gene order.

Comparative genetics of hybrid incompatibility: Sterility in two Solanum species crosses, pp. 1437–1453
Leonie C. Moyle and Takuya Nakazato

Why are some hybrids incompatible? Using a set of near-isogenic lines (of two related tomato species), genetic loci influencing hybrid pollen and seed infertility were found. Quantitative trait loci (QTL) for pollen and seed sterility are colocaled, suggesting a shared evolutionary history for these QTL.

Four quantitative trait loci that influence worker sterility in the honeybee (Apis mellifera), pp. 1337–1343
Peter R. Oxley, Graham J. Thompson and Benjamin P. Oldroyd

Worker sterility in social insects is one of the most dramatic examples of genetically determined altruism, yet there are no candidates for genes that control this behavior. Using a line of honeybees with the rare property of highly fecund workers, these authors find evidence for genes that cause selfish cheating behavior in a social animal.

Polytene chromosomal maps of 11 Drosophila species: The order of genomic scaffolds inferred from genetic and physical maps, pp. 1601–1635

Where would genetics be without the polytene chromosomes of Drosophila? This article integrates genetic and physical maps with the cytogenetic maps of polytene chromosomes of 11 Drosophila species. The results corroborate Muller’s conclusion that the majority of genes are syntenic in Drosophila species. Nevertheless, the karyotypes of these species differ due to fusion of chromosomal arms and subsequent rearrangements.

Sequence divergence impedes crossover more than noncrossover events during mitotic gap repair in yeast, pp. 1251–1262
Caroline Welz-Voegele and Sue Jinks-Robertson

Homologous recombination between dispersed repeated sequences is important in shaping eukaryotic genome structure, and such ectopic interactions are affected by repeat size and sequence identity. Gap repair of a plasmid in yeast was used as an assay to examine the genetic control of the crossover/noncrossover (CO/NCO) decision during the mitotic repair of a double-strand break and to determine the effect of sequence divergence on CO and NCO events. The authors find that a small amount of difference in the paired DNA sequences has little effect on NCO events, but strongly inhibits CO events.

Complex network of Wnt signaling regulates neuronal migrations during Caenorhabditis elegans development, pp. 1357–1371
Anna Y. Zinovyeva, Yuko Yamamoto, Hitoshi Sawa and Wayne C. Forrester

This article describes the analysis of the roles of all Wnts and candidate Wnt receptors in directing embryonic and postembryonic neuronal migrations during Caenorhabditis elegans development. The results reveal that specific Wnt ligands and receptors direct the migrations of specific cells. For example, migrations of some cells require all five Wnts whereas others require only a few. Interestingly, simultaneous inactivation of all five Wnts causes defects more severe than mutation of all four frizzled Wnt receptors.

ISSUE HIGHLIGHTS