ISSUE HIGHLIGHTS

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Detecting structure of haplotypes and local ancestry, pp. 625–642
Yongtao Guan
As units of inheritance, haplotypes are more informative than single nucleotide polymorphism in many statistical genetics applications. Haplotypes are structured in human populations: those sampled in one ethnic group are more similar to each other than those sampled from different ethnic groups. This article reports development of a flexible statistical model for detecting structure of local haplotypes and inferring local ancestries of admixed individuals. The high resolution of the method leads to surprising discoveries of significant deviation in local ancestry in HapMap admixed samples.

DNA replication error-induced extinction of diploid yeast, pp. 677–691
Alan J. Herr, Scott R. Kennedy, Gary M. Knowels, Eric M. Schultz, and Bradley D. Preston
Mutators accelerate evolution in the natural world and during tumorigenesis by generating genetic diversity. But accumulation of deleterious mutations compromises long-term fitness and can drive extinction of mutator populations. Herr et al. show that the maximal mutation rate in diploid yeast is 10 times higher than in haploids and likely determined by the probability of homzygous inactivation of essential genes. Replicative fitness rapidly declines once mutation rates are within an order of magnitude of the maximum, suggesting extinction is inevitable. These findings are highly relevant to the ability of mutator-driven tumors to withstand mutation accumulation during cancer progression.

A novel CaM kinase II pathway controls the location of neuropeptide release from Caenorhabditis elegans motor neurons, pp. 745–765
Christopher M. Hoover, Stacey L. Edwards, Sai-chieh Yu, Maike Kittelmann, Janet E. Richmond, Stefan Einse, Rosalina M. Yorks, and Kenneth G. Miller

Dense core vesicle release: controlling the where as well as the when, pp. 601–604
Stephen Nurrish
Neurons release neuropeptides to evoke or modulate behaviors by exocytosis of neuropeptide storage compartments known as dense core vesicles (DCVs). Hoover et al., report the unexpected discovery of a novel pathway that controls the location of DCV exocytosis within neurons. (Commentary in this issue by Steve Nurrish.) The pathway acts via CaM Kinase II, which, despite many studies, has never been implicated in neuropeptide release.

Epigenetic variation, inheritance, and parent-of-origin effects of cytosine methylation in maize (Zea mays), pp. 653–666
Massimiliano Lauria, Sara Piccinini, Raul Pirina, Gertrud Lund, Angelo Viotti, and Mario Moro

Inheritance patterns and stability of DNA methylation variation in maize near-isogenic lines, pp. 667–676
Qing Li, Steven R. Eichten, Peter J. Hermanson, and Nathan M. Springer
DNA methylation is heritable epigenetic information. These two articles describe variation, inheritance and stability of DNA methylation in maize. Lauria et al. demonstrate developmentally stable differences in DNA methylation patterns between plants of an inbred maize line. The variation they found was primarily within genes and is fairly constant between plants grown in different years, suggesting little influence of environmental cues on epigenetic inheritance. Li et al. documented inheritance patterns and trans-generational stability for DNA methylation variants in seventy near-isogenic lines and found that inheritance of DNA methylation across generations is quite robust, with almost no examples of unstable inheritance.

The anaphase promoting complex regulates yeast lifespan and rDNA stability by targeting Fob1 for degradation, pp. 693–709
Johannes Menzel, Mackenzie E. Malo, Cynthia Chan, Martin Przuntekiewicz, Terra G. Arnason, and Troy A. A. Harkness
This article describes a molecular network that monitors stress, cell cycle progression, protein degradation, genomic stability and longevity in yeast. Fob1 is a protein that drives aging by stalling rDNA replication, which is linked to increased rDNA recombination, genomic instability, and reduced lifespan. The authors show that degradation of Fob1 via the Anaphase Promoting Complex increases genomic stability, thereby promoting longevity.

The impact of accelerating, faster than exponential population growth on genetic variation, pp. 819–828
Mark Reppell, Michael Boehnke, and Sebastian Zöllner
High throughput sequencing and genotyping technologies provide large amounts of information on population genetic diversity that contains signatures of natural or artificial selection. Vitalis et al. developed a method for identifying those signatures, which explicitly measures the strength of selection targeting single nucleotide polymorphisms.

Sequencing and assembly of the 22-Gb loblolly pine genome, pp. 875–890

Unique features of the loblolly pine (Pinus taeda L.) megagename revealed through sequence annotation, pp. 891–909
These two articles describe the sequencing and annotation of the largest genome yet to be tackled: that of the Loblolly Pine. Assembly of this large and complex genome required several approaches, including the use of DNA sequence data obtained from haploid tissue. The annotation represents 20.1 Gb of sequence, of which about 82% is repetitive. About 50,000 genes are predicted, and their average intron length is longer than that of any previously-sequenced angiosperm. Of the approximately 20,000 gene families, about 1500 are unique to conifers, and around 10% of those are found exclusively in loblolly pine.

This Month’s Perspective

Genetics of sexual development: an evolutionary playground for fish, pp. 579–591
Corina Heute, Walter Salzburger, and Astrid Böhme
Reproductive strategies and mechanisms of sex determination are especially diverse in fish. This review of recent advances in understanding genetic sex determination focuses on how new master sex-determining genes evolve. The case of newly discovered master regulators in teleost fish might change perceptions of the genetics of sex determination, moving away from the view of a hierarchical cascade towards a network perspective that implicates new pathways and rewiring of downstream components.