

**Genetic Analysis of Desiccation Tolerance in *Saccharomyces cerevisiae*, pp. 507–519***Dean Calahan, Maitreya Dunham, Chris DeSevo, and Douglas E. Koshland*

The study of desiccation tolerance exhibited by species like budding yeast is likely to provide important insights into the stresses induced by dehydration and the cellular responses to those stresses. This article provides novel insights into desiccation tolerance in budding yeast that establish it as a powerful genetic system to understand the molecular basis of desiccation tolerance.

**Joint Inference of Population Assignment and Demographic History, pp. 561–577***Sang Chul Choi and Jody Hey*

Although genetic data can be used to determine which population individuals come from, and which individuals in a sample are from the same population, existing methods for assignment do not take into account how populations have diverged. This article describes a new method for assignment that simultaneously estimates a model of population divergence.

**Coalescence-Time Distributions in a Serial Founder Model of Human Evolutionary History, pp. 579–593***Michael DeGiorgio, James H. Degnan, and Noah A. Rosenberg*

Worldwide patterns of human genetic variation are well-described by the serial founder model, a nonequilibrium model of human evolutionary history. This study provides a general formulation of the model and derives coalescence-time distributions under the model. The authors show that the model reproduces trends in genetic diversity observed from human population-genetic data and is capable of describing worldwide trends in both within- and between-population summary statistics.

**Distribution of Parental Genome Blocks in Recombinant Inbred Lines, pp. 645–654***Olivier C. Martin and Frédéric Hospital*

Multi-locus genetic analyses are the rule in many linkage, association, and population genetics studies. In the past few years, high throughput technologies have revealed the existence of haplotype blocks, forcing one towards an infinite-locus or continuous genome picture. Early work in this framework began with Donnelly for identical-by-descent relations, and was further developed for special pedigree cases. These investigators solve the longstanding problem of the statistics of genome blocks in the case of recombinant inbred lines using a continuous-time random walk framework and Markov chain theory.

**Organization of the Synaptonemal Complex During Meiosis in *Caenorhabditis elegans*, pp. 411–421***Kristina Schild-Prüfert, Takamune T. Saito, Sarit Smolikov, Yanjie Gu, Marina Hincapie, David E. Hill, Marc Vidal, Kent McDonald, and Monica P. Colaiácovo*

The synaptonemal complex (SC) is a zipper-like structure observed between homologous chromosomes during meiosis

from yeast to humans that promotes stable association between homologs and interhomolog recombination. Despite its importance for sexually reproducing organisms, its assembly and organization remain poorly understood. The authors use several approaches to produce the first model for the organization of the SC in the nematode *Caenorhabditis elegans*.

**A Conserved Long Noncoding RNA Affects Sleep Behavior in *Drosophila*, pp. 455–468***Alexey A. Soshnev, Hiroshi Ishimoto, Bryant F. McAllister, Xingguo Li, Misty D. Wehling, Toshihiro Kitamoto, and Pamela K. Geyer*

Here is another example of the functional diversity of noncoding RNAs. This study shows that loss of the long noncoding (lnc) yellow-achaete intergenic RNA (yar), a lncRNA gene conserved among drosophilids, reduces and fragments nighttime sleep and diminishes sleep rebound following deprivation. As yar is a cytoplasmic RNA, its regulatory effects are likely to depend upon stabilization or translational regulation of target RNA.

**A Boundary Element Between *Tsix* and *Xist* Binds the Chromatin Insulator *Ctcf* and Contributes to Initiation of X-Chromosome Inactivation, pp. 441–454***Rebecca J. Spencer, Brian C. del Rosario, Stefan F. Pinter, Derek Lessing, Ruslan I. Sadreyev, and Jeannie T. Lee*

X-chromosome inactivation in mammals balances male and female X-chromosome dosages. This process is regulated by two long noncoding RNAs: *Xist* RNA spreads across the X-chromosome to initiate silencing; the antisense *Tsix* RNA blocks the ability of *Xist* to do so. Previous work demonstrated the existence of a chromatin transitional zone between these two genes. This article shows that this chromosomal zone binds the chromatin insulator, *Ctcf*, and that it is required to achieve *Xist* expression for initiation of X-chromosome inactivation.

**This Month in the American Journal of Human Genetics****Denisova admixture and the first modern human dispersals into southeast Asia and Oceania, *Am. J. Hum. Genet.* 89/4***David Reich, Nick Patterson, Martin Kircher, Frederick Delfin, Madhusudan R. Nandineni, Irina Pugach, Albert Min-Shan Ko, Ying-Chin Ko, Timothy A. Jinam, Maude E. Phipps, Naruya Saitou, Andreas Wollstein, Manfred Kayser, Svante Pääbo, and Mark Stoneking*

This article addresses the history of arrival of modern humans in southeast Asia and Oceania. It is known that ancestors of New Guineans and Bougainville Islanders inherited a portion of their genomes from Denisovans, an archaic hominin group from Siberia, but the authors report that descendants of the earliest inhabitants of southeast Asia do not all harbor Denisova admixture. This suggests that southeast Asia was settled by modern humans in multiple waves.