GENETICS, Vol. 195, SEPTEMBER 2013, Copyright © 2013

Correlation between mutation rate and genome size in riboviruses: mutation rate of bacteriophage Qβ, pp. 243–251

Katie Bradwell, Marine Combe, Pilar Domingo-Calap, and Rafael Sanjuán

Mutation rates have been shown to depend on genome size in many viruses and eukaryotes. RNA viruses mutate quickly, but their mutation rates vary considerably. These investigators found that mutation rates of RNA viruses correlate negatively with genome size. This explains why RNA viruses with small genomes tend to have faster rates of molecular evolution, and has implications for antiviral therapy.

A DNA damage checkpoint pathway coordinates the division of dikaryotic cells in the ink cap mushroom *Coprinopsis cinerea*, pp. 47–57

Carmen de Sena-Tomás, Mónica Navarro-González, Ursula Kües, and José Pérez-Martín

Having two non-identical nuclei share the same cytoplasm presents a challenge to the dikaryotic cell: both nuclei must enter mitosis at the same time to ensure each daughter cell inherits both genomes. These authors identified the DNA damage checkpoint as a major contributor to maintenance of the dikaryotic state in the ink cap mushroom *Coprinopsis cinerea*.

Robust identification of local adaptation from allele frequencies, pp. 205–220

Torsten Günther and Graham Coop

This article describes a powerful tool to robustly identify loci involved in local adaptation. By comparing multiple populations from different environments, loci important for adaptation to local environments can be identified. But such comparisons should acknowledge the shared history of populations and uncertainties involved in allele frequency estimates due to sampling. The new tool accounts for these potential sources of spurious results, and its utility is shown through simulations and the analysis of empirical data from humans and Atlantic herring.

Cloning and characterization of a critical regulator for pre-harvest sprouting in wheat, pp. 263–273

Shubing Liu, Sunish K. Sehgal, Jiarui Li, Meng Lin, Harold N. Trick, Jianming Yu, Bikram S. Gill, and Guihua Bai

Consumers prefer white wheat, but it is prone to pre-harvest sprouting (PHS), which causes crop losses of $1 billion annually. Cultivars resistant to PHS exist, but the mechanism of resistance is unknown. This article reveals that a MOTHER OF FLOWERING TIME-like gene plays a role in PHS resistance. Two mutations in the coding region of the gene lead to mis-splicing and a truncated protein. A DNA marker in the gene will facilitate deployment of these mutations to protect grain yield and quality and extend the range of white wheat production.

The FACT histone chaperone guides histone H4 into its nucleosomal conformation in *Saccharomyces cerevisiae*, pp. 101–113

Laura McCullough, Bryan Poe, Zaily Connell, Hua Xin, and Tim Formosa

FACT is a histone chaperone that can destabilize nucleosomes and can also tether nucleosome components together to promote their efficient reassembly. This article describes a FACT mutation that can cause FACT:nucleosome complexes to become permanently stuck together. Histone mutations that prevent these dead ends from forming reveal hinges that allow the histones to adopt their nucleosomal conformations. Thus, FACT has the previously unknown function of guiding histones into the shapes they need for nucleosome assembly.

Learning natural selection from the site frequency spectrum, pp. 181–193

Roy Ronen, Nitin Udpa, Eran Halperin, and Vineet Bafna

This article presents a novel method for identifying signatures of selective sweeps. Using supervised learning, the authors trained models of the Site Frequency Spectrum that best separate genomic regions evolving neutrally from those affected by a wide range of selective sweeps. The resulting test can be used without knowledge of the sweep parameters, and can easily be applied to WGS data from large populations.

The RNA-binding protein Whi3 is a key regulator of developmental signaling and ploidy in *Saccharomyces cerevisiae*, pp. 73–86

Sarah Schladebeck and Hans-Ulrich Mösch

RNA-binding proteins are well known to govern cell growth and development, but the number and nature of their targets are mostly unknown. These authors show that budding yeast Whi3 protein, which carries an RNA-binding motif, is a post-transcriptional regulator of several key components of signaling pathways that control cell division and biofilm development. They also found that Whi3 regulates ploidy by controlling expression of genes involved in chromosome segregation.

Maintenance of interphase chromosome compaction and homolog pairing in *Drosophila* is regulated by the condensin Cap-H2 and its partner Mrg15, pp. 127–146

Helen F. Smith, Meredith A. Roberts, Huy Q. Nguyen, Maureen Peterson, Tom A. Hartl, Xiao-Jun Wang, Joseph E. Klebba, Gregory C. Rogers, and Giovanni Bosco

Condensins are structural components of chromosomes that modulate compaction and pairing of homologs. How do condensins find their way onto chromosomes? Smith and Bosco and colleagues identified the Mrg15 chromodomain protein as an adaptor for the Cap-H2 subunit of condensin. They demonstrate that Mrg15 cooperates with condensins to antagonize somatic homolog pairing and maintain proper interphase compaction levels. This new condensin adaptor points to histone modifications as possible chromatin landing pads for condensin on interphase chromosomes.

This Month's Perspectives

Wilhelm Weinberg's early contribution to segregation analysis

Alan Stark and Eugene Seneta

Most geneticists will recognize the name Weinberg if it is paired with Hardy, but few geneticists know Weinberg's solo contributions to the field. This Perspectives article describes Weinberg's signal contribution—the demonstration that Mendel's laws apply to human heredity—and the controversy it stimulated.

This Month in the American Journal of Human Genetics

Whole genome sequencing uncovers the genetic basis of chronic mountain sickness in Andean highlanders, Am. J. Hum. Genet. 93(3)

Dan Zhou, Nitin Udpa, Roy Ronen, Tsering Stobdan, Junbin Liang, Otto Appenzeller, Huiwen W. Zhao, Yi Yin, Yuanping Du, Lixia Guo, Rui Cao, Yu Wang, Xin Jin, Chen Huang, Wenlong Jia, Dandan Cao, Guangwu Guo, Jorge L. Gamboa, Francisco Villafuerte , David Callacondo, Jin Xue, Siqi Liu, Kelly A. Frazer, Yingrui Li, Vineet Bafna, and Gabriel G. Haddad

Most high-altitude dwelling populations are well-adapted to hypoxic conditions, but some individuals suffer from chronic mountain sickness (CMS). Zhou *et al.* utilized whole-genome sequencing to identify the genetic basis of CMS in Andean highlanders. They found that the tumor suppressor *ANP32D* and the SUMO deconjugator *SENP1* are involved in the cellular response to hypoxia. These findings could provide key insights into other pathological conditions, such as ischemia and cancer, in which hypoxia plays a contributing role.