A G_2-phase microtubule-damage response in fission yeast, pp. 2073–2080

Fernando R. Balestra and Juan Jimenez

The importance of microtubule cytoskeleton integrity during interphase cell-cycle progression of mammalian somatic cells is uncertain. This article reports the discovery of a checkpoint mechanism in fission yeasts that delays entry into mitosis in response to interphase microtubule damage. The use of microtubule-damaging agents in certain cancer therapies, together with the lethality of cells deficient in the mitotic inhibitor Wee1, might provide more efficient chemotherapies.

Drosophila *asterless* and vertebrate Cep152 are orthologs essential for centriole duplication, pp. 2081–2094

Stephanie Blachon, Jayachandran Gopalakrishnan, Yoshihiro Omori, Andrey Polyanovsky, Allen Church, Daniela Nicastro, Jarema Malicki and Tomer Avidor-Reiss

The numbers of centrioles, chromosomes, and yeast spindle bodies in the cell are strictly regulated: one copy gives rise to a single new copy. The mechanism of centriole duplication has proven to be a particularly difficult puzzle to solve. This article reports that *asterless* encodes a protein essential early in centriole duplication in Drosophila and that its vertebrate ortholog Cep152 has a similar role. *asterless* is not a part of the centriole, but is localized near the centriole wall, placing it at the right time and place to play a central role in restricting centriole formation.

Ultraconserved elements: Analyses of dosage sensitivity, motifs and boundaries, pp. 2277–2293

Charleston W. K. Chiang, Adnan Derti, Daniel Schwartz, Michael F. Chou, Joel N. Hirschhorn and C.-ting Wu

What could be the evolutionary forces that maintain DNA sequence elements in distantly related species? One explanation for the remarkable conservation of these ultraconserved sequences is that they are involved in important functions, such as gene regulation. These authors report that ultraconserved sequence elements outside of protein-coding sequences are depleted among segmental duplications and copy number variants. This led them to propose that ultraconservation may reflect copy counting and sequence comparison. The authors present observations consistent with the idea that gene dosage plays a role in the origin of ultraconserved sequences.

Surviving the bottleneck: Transmission mutants and the evolution of microbial populations, pp. 2193–2200

Andreas Handel and Matthew R. Bennett

Understanding the evolution of microbes is important for public health. Many microbes enjoy repeated cycles of growth within a host and then suffer through a transmission bottleneck. Previous studies focused on the evolution of mutants with an increased growth rate within the host. These authors turned their attention to the evolution of mutants better able to survive outside the host. They describe situations in which mutants better able to survive a bottleneck are likely to evolve. They also describe how trade-offs between growth in the host and survival outside influence evolving microbial populations.

The temporal program of chromosome replication: Genomewide replication in *clb5*Δ *Saccharomyces cerevisiae*, pp. 1833–1847

Heather J. McCune, Laura S. Danielson, Gina M. Alvino, David Collingwood, Jeffrey J. Delrow, Walton L. Fangman, Bonita J. Brewer and M. K. Raghuraman

It has long been thought that the different replication times of different regions of the genome reflect staggered activation of origins in S phase. A recently proposed alternative hypothesis is that individual origins have different probabilities of activation, and their random activation through S phase generates the apparent temporal pattern observed in the population. The authors of this article deflate that hypothesis with their finding that origins are not activated randomly in a mutant in which that process is limited to early S phase, but remain divided into different temporal categories, consistent with the first hypothesis.

Outcrossing as an explanation of the apparent unconventional genetic behavior of *Arabidopsis thaliana hth* mutants, pp. 2295–2297

Raphael Mercier, Sylvie Jolivet, Julien Vignard, Stéphanie Durand, Jan Drouaud, Georges Pelletier and Fabien Nogué

The reappearance of *HTH* alleles in the offspring of homozygous Arabidopsis *hth* mutants is surprising. An existing hypothesis purports that the *HTH* information in the DNA is restored using as a template RNA stored for several generations. This article presents evidence supporting the idea that the apparent non-Mendelian behavior of *hth* mutants stems from their susceptibility to outcrossing.

The mating-type-related bias of gene conversion in *Schizosaccharomyces pombe*, pp. 1859–1868

Emil Parvanov, Juerg Kohli and Katja Ludin

Remarkably, fission yeasts seem to know one chromosome from the other: the direction of meiotic gene conversion is influenced by mating type. This study demonstrates that this is a general phenomenon that occurs at multiple loci. It depends on proteins that influence chromatin structure and homologous recombination, suggesting an interplay between an imprinting-like process and double-strand break repair.

Complex genetics control natural variation in *Arabidopsis thaliana* resistance to *Botrytis cinerea*, pp. 2237–2250

Heather C. Rowe and Daniel J. Kliebenstein

How is the interaction between two complex and polymorphic organisms affected if a single species is highly polymorphic? It is tempting to reduce the complexity of biological interactions by replacing species × species interactions with interactions between single genotypes. These authors present a cautionary tale in which quantitative trait loci controlling resistance of Arabidopsis to a pathogenic fungus depend upon the pathogen isolates tested. Even loci influencing all tested pathogen genotypes showed complex and variable epistases.

RNA-dependent RNA polymerase is required for enhancer-mediated transcriptional silencing associated with paramutation at the maize *p1* gene, pp. 1983–1993

Lyudmila Sidorenko and Vicki Chandler

This article describes how paramutation—the ability of one gene to heritably silence transcription of another, homologous gene—provides a window into RNA-mediated transcriptional silencing. Mutations in *mop1* (*mediator of paramutation1*), which encodes a RNA-dependent RNA polymerase, prevent establishment of paramutation at the *p1* locus of maize, but did not immediately reactivate a previously silenced allele; several generations in the mutant background are required for that. The *mop1* mutation also releases tissue-specific silencing of a *p1* allele that is not subject to paramutation. These results reveal that RNA-mediated transcriptional silencing affects *p1* paramutation and can influence tissue-specific gene expression.

Telomere loss provokes multiple pathways to apoptosis and produces genomic instability in *Drosophila melanogaster*, pp. 1821–1832

Simon W. A. Titen and Kent G. Golic

Loss of a single telomere in cells of a developing metazoan can generate precancerous phenotypes. The authors describe three pathways to death of cells that have lost a single telomere. But some cells escape apoptosis and divide repeatedly, and telomere loss in them causes genome instability, generating significant aneuploidy, chromosome aberrations, and polyploidy.