ISSUE HIGHLIGHTS

Molecular population genetics and evolution of Drosophila meiosis genes, pp. 177–185

Jennifer A. Anderson, William D. Gilliland and Charles H. Langley

Even though meiosis is virtually universal in eukaryotes, a significant fraction of genes involved in the process are lineage-specific. These investigators survey polymorphism and divergence of 33 meiosis-related genes in *Drosophila melanogaster* and *Drosophila simulans*. A number of intriguing differences in patterns of polymorphism and divergence between the two species are evident, affording an opportunity to investigate phenotypic effects associated with polymorphisms and recently fixed sibling–species differences.

Pds1p is required for meiotic recombination and prophase I progression in *Saccharomyces cerevisiae*, pp. 65–79

Katrina F. Cooper, Michael J. Mallory, Vincent Guacci, Katherine Lowe and Randy Strich

The metaphase–anaphase transition of mitosis is triggered by the destruction of Pds1, which leads to the removal of the cohesin that holds replicated sister chromatids together. Cells without Pds1 survive, but they are sick and often aneuploid. These authors find, to their surprise, that Pds1 is required for meiosis, where its role is to protect Mcd1p from degradation.

LINE-like retrotransposition in *Saccharomyces cerevisiae*, pp. 301–311

Chun Dong, Russell T. Poulter and Jeffrey S. Han

How was a third of the human genome made? Much of the DNA in our genome is the result of LINE element retrotransposition. This process is poorly understood, in part due to the difficulty studying these highly repetitive DNA elements. These authors reengineer a LINE element and introduce it into the LINE-free model organism *Saccharomyces cerevisiae*, where it appears to faithfully transpose. The vast experimental resources provided by budding yeast are sure to advance our understanding of LINE retrotransposition.

Drosophila and vertebrate casein kinase Iδ exhibits evolutionary conservation of circadian function, pp. 139–152

Jin-Yuan Fan, Fabian Preuss, Michael J. Muskus, Edward S. Bjes and Jeffrey L. Price

Casein kinase Iδ plays many roles in many different cellular processes in many organisms. It is essential for circadian rhythms such as the sleep/wake cycle. This article reports that the properties of the fly and vertebrate casein kinases Iδ are similar. Remarkably, alterations in mammalian CKIs that lead to shortening of the circadian period have the same effect when expressed in flies. This is due to an alteration of the frequency of cycling of phosphorylation of its substrate protein PER, a central regulator of circadian rhythms. Thus, the mechanism of the sleep/wake cycle is remarkably similar in flies and mammals.

Population genetic inference from resequencing data, pp. 187–197

Rong Jiang, Simon Tavaré and Paul Marjoram

Ultralow-cost sequencing technologies are increasingly available. They generate a large number of quite short sequence reads that often incompletely cover the genomic region of interest. These authors modeled data produced by these technologies and describe the degree of genome coverage required for successful population genetic inference from such data.

Drosophila PCH2 is required for a pachytene checkpoint that monitors double-strand-break-independent events leading to meiotic crossover formation, pp. 39–51

Eric F. Joyce and Kim S. McKim

The proper repair of DNA double-strand breaks during meiotic prophase generates crossovers that ensure proper meiotic segregation. This is controlled at two checkpoints: one monitors repair of the double-strand breaks, the other—the PCH2-dependent pathway—has been thought to respond to a defect in synaptonemal complex (SC) formation. These investigators find that the PCH2-dependent checkpoint in Drosophila is activated in the absence of defects in SC formation. They propose that there is a "crossover checkpoint" that detects problems in the process of forming crossovers.

The classical nuclear localization signal receptor, importin-α, is required for efficient transition through the G_1/S stage of the cell cycle in *Saccharomyces cerevisiae*, pp. 105–118

Kanika F. Pulliam, Milo B. Fasken, Laura M. McLane, John V. Pulliam and Anita H. Corbett

Eukaryotic cells use their compartments to great effect. In the case described in this article, eukaryotic cells regulate steps in the cell cycle by regulating import of proteins into the nucleus. The authors find that the protein import pathway is required for yeast cells to replicate their DNA: when it is blocked, progress through the cell cycle stops. The researchers identify three import factors that are mislocalized to the cytoplasm when that happens, identifying some targets of this mode of regulation.

Simple telomeres in a simple animal: Absence of subtelomeric repeat regions in the placozoan *Trichoplax adhaerens*, pp. 323–325

Hugh M. Robertson

The subtelomeric DNA sequences of most animal chromosomes are similar between chromosomes, presumably reflecting their concerted evolution. The roles of subtelomeric sequences are unclear. Robertson reports that *Trichoplax adhaerens*, the sole named species of the animal phylum Placozoa, has an extremely simple body plan and also extremely simple telomeres: each of eleven telomeres has 1.5–13 kb of unique sequence between the simple telomeric repeats and the first gene.

Formation and longevity of chimeric and duplicate genes in *Drosophila melanogaster*, pp. 313–322

Rebekah L. Rogers, Trevor Bedford and Daniel L. Hartl

Duplicate genes are well known to be a major source of novel genetic material, but the contribution of chimeric genes to evolutionary novelty has been largely overlooked. These authors identify 14 chimeric genes in *Drosophila melanogaster* and explain how they formed. They also model duplicate and chimeric gene dynamics, assessing rates of their formation, loss, and preservation. An appreciable number of chimeric genes are preserved 1 every 6.3 million years, indicating that chimeras contribute significantly to genome content.

Curing of yeast [*URE3*] prion by the Hsp40 cochaperone Ydj1p is mediated by Hsp70, pp. 129–137

Deepak Sharma, Robert F. Stanley and Daniel C. Masison

Yeast prions are highly ordered protein aggregates that propagate by purloining the soluble form of the same protein, prodding it to misfold similarly as it joins the aggregate. Hsp40 chaperones promote protein folding and prevent protein aggregation by regulating Hsp70. Overexpressing Hsp40 "cures" yeast of [*URE3*] prions. This article presents the surprising finding that Hsp40 dimerization, substrate binding, membrane localization, and ability to transfer substrate to Hsp70 are dispensable for its curing function. Only the domain required for regulating Hsp70 activity is sufficient for curing. Thus, Hsp40 cures prion disease indirectly by regulating Hsp70.

Loss of the mitochondrial nucleoid protein, Abf2p, destabilizes repetitive DNA in the yeast mitochondrial genome, pp. 331–334

Rey A. Sia, Stephanie Carrol, Lidza Kalifa, Christine Hochmuth and Elaine A. Sia

Deletions of repetitive DNA of the mitochondria are associated with human cancer and aging. This article describes the role of the Abf2p, an abundant mitochondrial nucleoid-associated protein of yeast that has been called the "mitochondrial histone," in avoiding this fate. Loss of Abf2p, the ortholog of human mTFA, results in increased rates of frameshift mutations and recombination between direct repeats in the mitochondrial genome, but does not affect point mutation rates.