Condensins promote coorientation of sister chromatids during meiosis I in budding yeast, pp. 55–64

Ilana L. Brito, Hong-Guo Yu and Angelika Amon

Sister chromatids segregate away from each other during mitosis, but remain attached during the first division of meiosis. These investigators uncover a novel role for the condensin complex in this process: to create a peri-centromeric scaffold that recruits the kinetochore proteins that clamp sister chromatids together during meiosis I.

Nonallelic gene conversion in the genus Drosophila, pp. 95–103

Claudio Casola, Carrie L. Ganote and Matthew W. Hahn

Nonallelic, or ectopic, gene conversion can change the evolutionary trajectory of gene duplicates by homogenizing their sequences. How common is this process? These authors surveyed more than 17,000 genes in nine Drosophila species and found that many young duplicates were converted, but in general less than 15% of all paralogs—and only 1-2% of all duplicated coding regions—experienced ectopic gene conversion. They also show that the frequency of ectopic gene conversion varies significantly between Drosophila species, which indicates possible differences in the recombination rates or the DNA-repair mechanisms.

Muller's ratchet and the degeneration of the *Drosophila miranda* neo-*Y* chromosome, pp. 339–348

Vera B. Kaiser and Brian Charlesworth

Why do *Y* chromosomes degenerate? The authors of this article show that Muller's ratchet—the accumulation of deleterious mutations in finite populations—can explain much of the observed rate of loss of gene function that is observed in the *Drosophila miranda* neo-*Y* chromosome. In particular, they show that the process is speeded up by the action of selection on minor effect mutations affecting protein sequences.

An auxiliary silencer and a boundary element maintain high levels of silencing proteins at *HMR* in *Saccharomyces cerevisiae*, pp. 113–127

Patrick J. Lynch and Laura N. Rusche

The Sir protein complex mediates gene silencing at multiple locations in the yeast genome. Although the same protein complex acts at all loci, the sequences responsible for recruiting the silencing proteins have a surprising amount of variation. Some silenced regions also have boundary elements that block propagation of silenced chromatin. The authors of this article examine how several silencers and a boundary element contribute to the size of silenced chromatin domains. Interestingly, silencers vary in their ability to influence the propagation of silenced chromatin along the chromosome.

Amplification of the gene for isoleucyl-tRNA synthetase facilitates adaptation to the fitness cost of mupirocin resistance in *Salmonella enterica*, pp. 305–312

Wilhelm Paulander, Dan I. Andersson and Sophie Maisnier-Patin

Mutations that confer antibiotic resistance to bacteria often decrease fitness. Unfortunately, bacteria can rapidly adapt and regain their fitness, often without losing antibiotic resistance. In the case of mupirocin-resistance mutations, which impair isoleucyl-tRNA synthetase, adaptation occurs through mutations that alter the quantity or quality of the defective enzyme. These investigators show how deleterious antibiotic resistance mutations may be compensated for by amplification of the drug target gene, which provides some fitness improvement while also providing more mutational targets, increasing the likelihood of a secondary mutational change.

Aberrant synthesis of indole-3-acetic acid in *Saccharomyces cerevisiae* triggers morphogenic transition, a virulence trait of dimorphic pathogenic fungi, pp. 211–220

Reeta Prusty Rao, Ally Hunter, Olga Kashpur and Jennifer Normanly

This article reports the surprising finding that *Saccharomyces cerevisiae* produces the plant hormone indole-3-acetic acid (IAA). The authors identify two pathways for IAA synthesis and show that loss of one of these pathways alters the dimorphic transition in yeast. They show that IAA induces filamentation in the human pathogen *Candida albicans*, which is linked to its pathogenicity. IAA may function as a secondary metabolite signal that regulates virulence in fungi.

Fast transcriptional responses to domestication in the brook charr *Salvelinus fontinalis*, pp. 105–112

Christopher Sauvage, Nicolas Derôme, Eric Normandeau, Jérôme St.-Cyr, Céline Audet and Louis Bernatchez

What are the genetic changes underlying artificial selection for domestication of species? This article describes the transcriptional responses of brook charr to artificial selection over only four generations. The results show that relatively few generations of selective breeding can produce significant differences in gene expression.

The *Psychedelic* genes of maize redundantly promote carbohydrate export from leaves, pp. 221–232

Thomas L. Slewinski and David M. Braun

Little is known of the mechanisms plants use to control the allocation of sugars between organs. This article describes the *psychedelic* (*psc*) mutant of maize, which hyperaccumulates starch and soluble sugars in distinct leaf regions. Genetic and cytological analyses suggest that the wild-type *Psc* gene functions independently of previously defined pathways regulating carbohydrate partitioning. Interestingly, the *psc* mutant phenotype is inherited as a recessive, duplicate-factor trait in some, but not all, inbred lines. Hence, investigations into the *psc* mutation have uncovered two unknown genes that redundantly function to regulate carbohydrate partitioning in maize.