**Genetic architecture of tameness in a rat model of animal domestication,** pp. 541–554

*Frank W. Albert, Örjan Carlborg, Irina Z. Plyusnina, Francois Besnier, Daniela Hedwig, Susann Lautenschläger, Doreen Lorenz, Jenny McIntosh, Christof Neumann, Henning Richter, Claudia Zeising, Rimma Kozhemyakina, Olesya Shchepina, Jürgen Kratzsch, Lyudmila Trut, Daniel Teupser, Joachim Thiery, Torsten Schöneberg, Leif Andersson and Svante Pääbo*

Using two lines of rats bred for tameness and aggression towards humans, these investigators map the genetic basis of those traits. They identify a network of five interacting genomic regions underlying tameness and aggression. They also find other regions of the genome that influence behavioral, anatomical and physiological traits. These regions provide starting points for identifying genes underlying tameness.

**Segmental duplications contribute to gene expression differences between humans and chimpanzees,** pp. 627–630

*Ran Blekhman, Alicia Oshlack and Yoav Gilad*

These investigators find that species-specific segmental duplications are enriched with genes that are differentially expressed between humans and chimpanzees. Their observations suggest that the expression level of genes lying within species-specific segmental duplications is affected by different proximal *cis*-regulatory elements compared to the orthologous genes in their original genomic location.

**Reciprocal silencing, transcriptional bias and functional divergence of homeologs in polyploid cotton (Gossypium),** pp. 503–517

*Bhupendra Chaudhary, Lex Flagel, Robert M. Stupar, Joshua A. Udall, Neetu Verma, Nathan M. Springer and Jonathan F. Wendel*

These investigators seek to understand how genome merger and doubling (polyploidy) have impacted evolution of gene expression in natural and synthetic cotton allopolyploids and in an $F_1$ hybrid. These plants contain two genomes that evolved in isolation for millions of years but are now reunited in a common nucleus. The pace of expression evolution is estimated by measuring the relative contributions of the two genomes to the transcriptome. This reveals tissue-specific, biased expression patterns, gene silencing, and significant expression perturbation caused by hybridization and allopolyploidization. Notably, silencing and biased expression of some gene pairs is suggestive of transcriptional subfunctionalization and neofunctionalization.

**Coordinated regulation of heterochromatic genes in *Drosophila melanogaster* males,** pp. 481–491

*Xinxian Deng, S. Kiran Koya, Ying Kong and Victoria H. Meller*

Highly differentiated sex chromosomes pose some tricky problems. One is the difference in gene copy number in males and females. Male flies address this problem using a complex of proteins and RNA that modifies the X chromosome to increase its transcription. Unexpectedly, some (but not all) members of this complex also influence expression of heterochromatic regions in male flies. The authors propose that this reveals a system that accommodates the large, heterochromatic Y chromosome. While the differentiated Y chromosome is known to influence other heterochromatic regions, this is the first indication of a system to counteract its effect.

**Selection for chaperone-like mediated genetic robustness at low mutation rate: Impact of drift, epistasis and complexity,** pp. 555–564

*Pierre-Alexis Gros and Olivier Tenaillon*

How can we explain that most organisms are unaffected by most mutations? Current theory predicts that such genetic robustness can be selected only in organisms having high mutation rate and population size, such as RNA virus. The authors show that genetic drift, *i.e.,* stochastic variations of reproductive success, can be a sufficient force for robustness selection, even when the mutation rate becomes vanishingly small. This process, enhanced by phenotypic complexity and small population size, should be universal, as illustrated by computer simulations and endosymbionts evolution.

**Evolution of new disease specificity at a simple resistance locus in a crop–weed complex: Reconstitution of the *Lr21* gene in wheat,** pp. 595–602

*Li Huang, Steven Brooks, Wanlong Li, John Fellers, James C. Nelson and Bikram Gill*

The genetic treasures of native agricultural ecosystems have been exploited for bountiful crop harvests to feed the world. The authors of this article show that a potent leaf rust gene, *Lr21*, arose from a rare intragenic recombination in a diploid relative of wheat in Iran, in association with bread wheat evolution 8,000 years ago. Haplotype analysis provided clues to the origin and enabled reconstitution of the gene in the laboratory. Thus, plants can reuse "dead" alleles to generate new disease-resistance specificities, which leads to a "death–recycle" model of plant-resistance gene evolution at simple loci.

**Minimal effect of ectopic gene conversion among recent duplicates in four mammalian genomes,** pp. 615–622

*Casey L. McGrath, Claudio Casola and Matthew W. Hahn*

This article reports genomewide rates of ectopic ("nonallelic") gene conversion in mammals. The authors demonstrate that gene conversion has not had a large effect on the evolution of duplicated genes in the four species they studied.

**Novel nucleotide sequence motifs that produce hotspots of meiotic recombination in *Schizosaccharomyces pombe*,** pp. 459–469

*Walter W. Steiner, Estelle M. Steiner, Angela R. Girvin and Lauren E. Plewik*

Hotspots of meiotic gene conversion and crossing over have been observed in species as diverse as yeast and humans, but the chromosomal determinants of hotspots have been elusive. Using a clever screen, the authors identify dozens of simple sequence motifs that produce hotspots of gene conversion in the fission yeast *Schizosaccharomyces pombe*. At least two of these families of motifs are targets for specific transcription factors, which are required for the high levels of recombination at those hotspots. This suggests that simple sequence motifs may underlie the complex pattern of recombination seen in other species.

**Precise gene-dose alleles for chemical genetics,** pp. 623–626

*Zhun Yan, Nicolas M. Berbenetz, Guri Giaever and Corey Nislow*

Chemicals (*i.e.,* small molecule probes) can be employed as proxies for conditional mutations. For this study, the authors devise a strategy to combine chemical and other perturbations to turn yeast cells into phenotypic potentiometers. Specifically, they create sets of alleles of budding yeast and dialed-down gene dose to show that the gene-dose response of these alleles behaves exactly as one would expect for a drug-dose response.