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Patterns of transcriptome divergence in the male accessory gland of two closely related species of field crickets, pp. 501–513

Jose A. Andrés, Erica L. Larson, Steven M. Bogdanowicz, and Richard G. Harrison

What kinds of genetic changes are responsible for the origin of species? What forces drive evolution of "speciation genes"? Answers to these fundamental questions may be found by examining patterns of genomic differentiation between closely related species. The authors have compared transcriptomes of two field crickets to identify candidate gene regions that contribute to reproductive isolation and to assess the role of selection in divergence of genes encoding seminal fluid proteins.

Captured segment exchange: A strategy for custom engineering large genomic regions in *Drosophila melanogaster*, pp. 421–430

Jack R. Bateman, Michael F. Palopoli, Sarah T. Dale, Jennifer E. Stauffer, Anita L. Shah, Justine E. Johnson, Conor W. Walsh, Hanna Flaten, and Christine M. Parsons

and

Long-range targeted manipulation of the *Drosophila* genome by site-specific integration and recombinational resolution, pp. 411–419

Natalia Wesolowska and Yikang S. Rong

This issue of *GENETICS* features two articles that describe significant improvements in the *Drosophila* genetic toolbox (see *Commentary* by Crown and Sekelsky). Wesolowska and Rong describe an approach for targeted manipulation of the genome that promises to render all *Drosophila* genes amenable to systematic targeted mutagenesis. Bateman *et al*. offer a novel approach for swapping large segments of the genome with engineered DNA, permitting custom alterations to any genomic region. And last month Staller and Perrimon and colleagues presented a powerful, simple method for depleting gene function in early embryos with short hairpin RNAs.

Evolutionary rate covariation in meiotic proteins results from fluctuating evolutionary pressure in yeasts and mammals, pp. 529–538

Nathan L. Clark, Eric Alani, and Charles F. Aquadro

Genes leave records of their relationships in their DNA: functionally related genes tend to experience parallel changes in evolutionary rate. What causes this coevolutionary signature? These authors suggest that such a signature in meiotic genes results from a reduction in selective constraint after certain species switched to clonal reproduction. Similar changes in coevolutionary signatures across the genome can be exploited to uncover functional relationships.

The effect of nonindependent mate pairing on the effective population size, pp. 545–556

Ben J. Evans and Brian Charlesworth

This study illuminates how real-world social systems impinge on genome evolution. The effect of overlapping generations on effective population size is generally inferred by assuming that mate pairing occurs independently each breeding season—an assumption violated by many species, including humans. Evans and Charlesworth show that nonindependent mate pairing has no effect if all adults mate pair each breeding season, a small effect if females store sperm, and a large effect with a harem social system.

The relationship between F_{ST} and the frequency of the most frequent allele, pp. 515–528

Mattias Jakobsson, Michael D. Edge, and Noah A. Rosenberg

F_{ST} has long been used as a summary of genetic differentiation among groups, but remarkably, its relationship to locus allele frequencies has been unclear. This article provides a conceptual basis for understanding the dependence of F_{ST} on allele frequencies and genetic diversity. It shows that many unusual properties of F_{ST}, including its relatively low values in high-diversity human populations in Africa, derive from the intrinsic mathematical dependence of F_{ST} on features of allele frequency distributions.

Minimal effect of gene clustering on expression in *Escherichia coli*, pp. 453–466

Lusha W. Liang, Razika Hussein, Dena H. S. Block, and Han N. Lim

Genes that interact or function together are often clustered in bacterial genomes. Does this affect their expression? Surprisingly, no: the authors found that gene clustering in *Escherichia coli* has limited impact on levels or correlation of expression, or on stochastic fluctuations in expression. Their results rule out gene clustering as a general modulator of gene expression.

The relationship between long-range chromatin occupancy and polymerization of the *Drosophila* ETS family transcriptional repressor Yan, pp. 633–649

Jemma L. Webber, Jie Zhang, Lauren Cote, Pavithra Vivekanand, Xiaochun Ni, Jie Zhou, Nicolas Nègre, Richard W. Carthew, Kevin P. White, and Ilaria Rebay

Spreading of repressive complexes along chromatin has been proposed to be driven by the polymerization of transcriptional repressors, but this study of the *Drosophila* repressor Yan suggests oligomerization does not promote chromatin spreading. These results challenge the accepted model of polymerization-mediated chromatin spreading.

This Month's Perspectives

The genetics of canine skull shape variation, pp. 317–325

Jeffrey J. Schoenebeck and Elaine A. Ostrander

The dog as a model organism is young in human years, but insights gleaned in the eight years since its genome's public debut have made it a prodigy. This species' symbiosis with man makes it uniquely suited to address questions of the genetic basis of domestication, evolution, morphology, and disease. This article makes clear that the pertinence of answers awaiting canine geneticists extends beyond the dog.

This Month in the American Journal of Human Genetics

Genetic basis of Y-linked hearing impairment. Am. J. Hum. Genet. 92(2)

Qiuju Wang, Yali Xue, Yujun Zhang, Quan Long; Asan, Fengtang Yang, Daniel J. Turner, Tomas Fitzgerald, Bee Ling Ng, Yali Zhao, Yuan Chen, Qingjie Liu, Weiyan Yang, Dongyi Han, Micheal A Quail, Harold Swerdlow, John Burton, Ciara Fahey, Zemin Ning, Matthew E. Hurles, Nigel P. Carter, Huanming Yang, and Chris Tyler-Smith

The dearth of genes on the Y-chromosome makes Mendelian disorders mapped to it rare: only one—hearing impairment associated with the DFNY1 locus—is known. Wang *et al.* identified the causal mutation as an insertion of DNA in the Y-chromosome. Interestingly, the inserted DNA includes a region of chromosome 1 associated with hearing impairment. The authors suggest that this extra copy of one or more genes from chromosome 1 is responsible for the hearing loss phenotype.