Comprehensive scanning mutagenesis of human retrotransposon LINE-1 identifies motifs essential for function, pp. 1401–1414

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Adney *et al.* describe the complete and comprehensive codon substitution mutagenesis of human retrotransposon LINE-1 using a synthetic DNA approach. This experiment is the first of its kind for any transposon. The data show that the transposon is particularly sensitive to mutation, supporting the notion that it is evolutionarily streamlined, and identifies a number of new motifs important for retrotransposition.

Fine-mapping complex inversion breakpoints and investigating somatic pairing in the *Anopheles gambiae* species complex using proximity-ligation sequencing, pp. 1495–1511

Russell B. Corbett-Detig, Iskander Said, Maria Calzetta, Max Genetti, Jakob Mcbroome, Nicholas W. Maurer, Vincenzo Petrarca, Alessandra della Torre, and Nora J. Besansky

In this work, Corbett-Detig *et al.* use proximity-ligation sequencing (Hi-C) of several *Anopheles gambiae* and *A. coluzzii* inversion-bearing individuals to detect and map inversion breakpoints. They show that inversion breakpoints can be mapped precisely using Hi-C data and that the approach is amenable to extremely light sequencing depths. They found that each breakpoint of 2Rb, 2Rc and 2Rd is situated in a large block of repetitive sequence. Strikingly, two breakpoints were reused twice; this potential indicates that natural selection favors inversions whose breakpoints intersect these genomic regions in this species complex. Finally, they use Hi-C to investigate the impacts of somatic pairing in inversion heterokaryotypic individuals.

Programmed cell death in *Neurospora crassa* is controlled by the allorecognition determinant *rcd-1*, pp. 1387–1400

Asen Daskalov, Pierre Gladieux, Jens Heller, and N. Louise Glass

Programmed cell death preventing heterokaryon formation in fungi has been proposed to represent a defense mechanism against conspecific genome exploitation and mycoviruses. Here, Daskalov *et al.* identified a novel genetic determinant of allorecognition *rcd-1, regulator of cell death-1*, controlling cell death in germlings of *Neurospora crassa*. The authors show that *rcd-1* carries evolutionary marks of balancing selection and trans-species polymorphism, previously associated with allorecognition genes. They found that *rcd-1* is a member of a large and widespread gene family in fungi. The finding suggests that the gene is of general importance in the fungal kingdom and extends the repertoire of fungal PCD determinants.

Stress-Induced neuron remodeling reveals differential interplay between neurexin and environmental factors in *Caenorhabditis elegans*, pp. 1415–1430

Michael P. Hart

Hart characterizes a novel interaction between genetics and environmental stress on experience-dependent neuron remodeling and plasticity in *Caenorhabditis elegans*, defining an interplay between different forms of adolescent stress and the autism-associated gene neurexin. The results show that the morphology of a GABAergic neuron is altered by three environmental stressors, specifically during sexual maturation. Outgrowth of axon-like neurites following adolescent stress is due to altered morphologic plasticity in adulthood. This axonal remodeling is induced by each of the three stressors; however, only nutritional stress impacts downstream behavior with outgrowth being dependent on neurexin/*nrx-1*.

Position effects influence transvection in *Drosophila melanogaster*, pp. 1289–1299

Thomas D. King, Justine E. Johnson, and Jack R. Bateman

Transvection is a form of gene regulation the depends on interactions between regulatory elements on separate chromosomes. In one form of transvection that is prevalent in *Drosophila*, an enhancer can act in *trans* to activate a promoter on a closely paired homologous chromosome. While prior analyses have suggested that the *Drosophila* genome is generally permissive to enhancer action in *trans*, King, Johnson, and Bateman find that the degree to which transvection is supported varies significantly at different genomic locations. The data are consistent with a model wherein position effects on transvection are largely mediated by the local chromatin state, whereas variation in the degree to which homologous chromosomes are paired does not appear to have a significant impact.

Scalable nonparametric prescreening method for searching higher-order genetic interactions underlying quantitative traits, pp. 1209–1224

Juho A. J. Kontio and Mikko J. Sillanpää

The Gaussian process (GP) regression is theoretically capable of capturing higher-order gene-by-gene interactions important to trait variation non-exhaustively with high accuracy. Unfortunately, GP approach is scalable only for 100-200 genes and thus, not applicable for high-throughput sequencing datasets. Kontio and Sillanpää present a multi-stage procedure based on a generalized Haseman-Elston method that preserves virtually all the major benefits of GP regression and extends its scalability to datasets with tens of thousands of genes (running time is in seconds).

How boundaries form: linked nonautonomous feedback loops regulate pattern formation in yeast colonies, pp. 1373–1386

Sarah Piccirillo, Abbigail H. McCune, Samuel R. Dedert, Cassandra G. Kempf, Brian Jimenez, Shane R. Solst, LeAnn M. Tiede-Lewis, and Saul M. Honigberg

How do boundaries between cells of different types form? Such boundaries are critical for metazoan development, but even in microorganisms, boundaries between cells of different types form in communities such as colonies and biofilms. This organization presumably enhances the fitness of the community. For example, colonies of the budding yeast (*Saccharomyces cerevisiae*) form a sharp boundary between a layer of meiotic cells at the top of the colony and a layer of feeder cells at the bottom of the colony, and these feeder cells may supply nutrients to meiotic layer. In the current report, Piccirillo *et al.* present evidence that the boundary between these layers is established through the combined action of two nonautonomous positive-feedback loops. Each loop is active on only one side or the other of the boundary. The symmetry of this regulation suggests it may be a general mechanism for boundary formation.

The genomic basis for short-term evolution of environmental adaptation in maize, pp. 1479–1494

Randall J. Wisser, Zhou Fang, James B. Holland, Juliana E. C. Teixeira, John Dougherty, Teclemariam Weldekidan, Natalia de Leon, Sherry Flint-Garcia, Nick Lauter, Seth C. Murray, Wenwei Xu, and Arnel Hallauer

The geographical distribution of many crop species spans far beyond their centers of origin and the native range of their wild ancestors. Maize is exemplary of this adaptability, which has contributed to its agricultural significance on multiple continents. Wisser *et al.* report a new study design used to explore how a tropical landrace of maize harbors genetic variation enabling adaptiveness to a temperate environment, showing that a complex genomic basis for short-term evolution results in the maintenance of genetic diversity during phenotypic selection.