

The capacity to act in *trans* varies among *Drosophila* enhancers, pp. 203–218

Amanda J. Blick, Ilana Mayer-Hirshfeld, Beatriz R. Malibiran, Matthew A. Cooper, Pieter A. Martino, Justine E. Johnson, and Jack R. Bateman

In 1954, Ed Lewis described transvection, an epigenetic phenomenon wherein the expression of a gene is sensitive to the proximity of a homologous chromosome. Transvection can occur via an enhancer on one chromosome activating a promoter on a paired homolog. Although several cases of such enhancer action in *trans* are known, it remains unclear whether this capacity is restricted to a subset of enhancers. Blick *et al.* test a collection of enhancers and find evidence for transvection in all cases, suggesting that this property is common.

Needles: Toward large-scale genomic prediction with marker-by-environment interaction, pp. 543–555

Arne De Coninck, Bernard De Baets, Drosos Kourounis, Fabio Verbosio, Olaf Schenk, Steven Maenhout, and Jan Fostier

Genomic prediction relies on marker information to predict the performance of future hybrid breeds. Since the effect of markers may vary substantially under different environmental conditions, marker-by-environment interaction effects must be taken into account. However, this can lead to a dramatic increase of the computational resources needed for analyzing large-scale data. De Coninck *et al.* describe Needles, a computing solution for large-scale genomic prediction based on distributed computing techniques and a sparse matrix formalism. Needles enables analysis in only a few hours and can identify QTL with a specific effect in certain environments.

Heterochromatin-associated proteins HP1a and Piwi collaborate to maintain the association of achiasmata homologs in *Drosophila* oocytes, pp. 173–189

Christopher C. Giauque and Sharon. E. Bickel

Meiotic chromosome segregation depends on homologous chromosomes staying attached until anaphase I. In *Drosophila* oocytes, homologs that fail to recombine still segregate properly because they remain associated via their pericentric heterochromatin. Giauque and Bickel provide evidence that an interaction between the heterochromatin protein HP1a and the piRNA binding protein Piwi is essential for keeping achiasmata homologs physically associated during meiotic prophase.

When is selection effective? pp. 451–462

Simon Gravel

An animated debate surrounds whether the different demographic histories of human populations have led to differences in the number, distribution, and severity of deleterious variants. Through simulations and analytical calculations, Gravel shows that differences among human populations depend sensitively on selection coefficients, time scales, and the entire history of populations. For this reason, hidden assumptions in commonly used measures of adaptation rate can cause apparent discrepancies between studies.

A pathway analysis of melanin patterning in a hemimetabolous insect, pp. 403–413

Jin Liu, Thomas R. Lemonds, James H. Marden, and Aleksandar Popadić

Liu *et al.* show that melanin genes are employed in a region-specific manner in the hemimetabolous insect, *Oncopeltus fasciatus*. This contrasts with melanin patterning in holometabolous species. These results reveal that black patterning can be accomplished by a “painting” mode, using predominantly melanin promoting factors, and by an “erasing” mode, using mainly melanin suppressing factors. Different combinations of these strategies may account for the vast diversity of melanin patterns observed in insects.

Natural selection and genetic diversity in the butterfly *Heliconius melpomene*, pp. 525–541

Simon H. Martin, Markus Möst, William J. Palmer, Camilo Salazar, W. Owen McMillan, Francis M. Jiggins, and Chris D. Jiggins

Martin *et al.* investigate genetic diversity and the action of selection in the neotropical *Heliconius* butterflies using resequenced genomes from 58 wild-caught individuals of *Heliconius melpomene*, and another 21 resequenced genomes representing 11 related species. The results suggest that positive selection is less pervasive in these butterflies compared to fruit flies, a fact that curiously results in very similar levels of neutral diversity in these very different insects.

Triallelic population genomics for inferring correlated fitness effects of same site nonsynonymous mutations, pp. 513–523

Aaron P. Ragsdale, Alec J. Coffman, PingHsun Hsieh, Travis J. Struck, and Ryan N. Gutenkunst

The proportion of mutations with different effects on fitness is a key parameter in evolutionary genetics, but typical approaches to modeling these distributions cannot account for multiple mutations at the same site. The authors developed a model of correlated fitness effects for mutations at the same protein site. A moderately strong correlation was found when the model was fit to triallelic fruitfly data and it also agreed with direct biochemical measurements, even in different organisms. Thus the correlation of fitness effects may be a universal property of protein evolution.

Multitasking of the piRNA silencing machinery: targeting transposable elements and foreign genes in the bdelloid rotifer *Adineta vaga*, pp. 255–268

Fernando Rodriguez and Irina R. Arkhipova

The genome of the bdelloid rotifer *Adineta vaga* is characterized by massive horizontal gene transfer, low transposon content, and highly diversified RNA-mediated silencing machinery. The authors investigated genome-wide distribution of *A. vaga* piRNAs and found an unexpectedly large fraction matches foreign genes. Small-RNA covered genes show a higher frequency of nearby telomeric repeats and transposons, indicating that gene acquisition occurs largely at the genome periphery, where it can be affected by RNA-based silencing.

This Month in the American Journal of Human Genetics**Analysis of somatic genome rearrangements in human cancers based on whole-exome sequencing, Am. J. Hum. Genet. 98(5)**

Lixing Yang, MiSook Lee, Hengyu Lu, Doo-Yi Oh, Yeon Jeong Kim, Donghyun Park, Gahee Park, Xiaojia Ren, Christopher A. Bristow, Psalm S. Haseley, Soohyun Lee, Angeliki Pantazi, Raju Kucherlapati, Woong-Yang Park, Kenneth L. Scott, Yoon-La Choi, and Peter J. Park

Advances to sequencing technology have ushered in a new era within the realm of clinical oncology. Whole-genome sequencing (WGS) is routinely used to detect a wide range of genomic alterations, including breakpoints that occur in non-coding regions. Although WGS offers greater sensitivity than whole-exome sequencing (WES), WGS data remains more expensive and difficult to analyze. Now, Yang *et al.* now demonstrate that WES presents a viable alternative to WGS for the detection of a range of somatic rearrangements in human cancers. Notably, their analyses reveal a pattern of functional fusion proteins: 5' fusion partners are often housekeeping genes and 3' fusion partners are enriched in tyrosine kinases.