

An allosteric network for spliceosome activation revealed by high-throughput suppressor analysis in *Saccharomyces cerevisiae*, pp. 111–124

David A. Brow

This study demonstrates the utility of a custom targeted sequencing panel for identifying spontaneous suppressors of a mutation in the *Saccharomyces cerevisiae* spliceosome. The panel screens 112 genes encoding known or suspected splicing factors for variants in up to 95 suppressor strains simultaneously. Using the cold-sensitive U4-cs1 mutation, which blocks an early step in spliceosome activation, Brow identifies suppressor mutations in five protein-coding genes that were not previously known to harbor suppressors of U4-cs1, providing novel insights into the mechanism of spliceosome activation.

Redundant and cryptic enhancer activities of the *Drosophila* yellow gene, pp. 343–360

Gizem Kalay, Jennifer Lachowicz, Ulises Rosas, Mackenzie R. Dome, and Patricia Wittkopp

Evolutionary changes in enhancers, which control gene expression, often contribute to phenotypic evolution. Here, Kalay *et al.* examine how enhancer activities are encoded within non-coding sequences surrounding the pigmentation gene *yellow* from three *Drosophila* species. *yellow* expression differs among these species in a way that correlates with differences in body pigmentation. The authors find that *yellow*'s *cis*-regulatory sequences are less modular than suggested by prior work and instead have redundant and cryptic enhancer activities. Some of these cryptic enhancers may contribute to divergent *yellow* expression and pigmentation.

Residual heterozygosity and epistatic interactions underlie the complex genetic architecture of yield in diploid potato, pp. 317–332

Alexandre P. Marand, Shelley H. Jansky, Joseph L. Gage, Andy J. Hamernik, Natalia de Leon, and Jiming Jiang

Marand *et al.* use a high-resolution recombination map to dissect the genetic components of yield in diploid potato. Regions of recalcitrant heterozygosity in the inbred parent co-localized with elevated recombination rates, signatures of selection, and tissue-specific gene expression. QTL mapping of yield-related traits uncovered widespread epistatic interactions and elevated dominance that overlaps regions of residual heterozygosity. The authors also investigate the potential contributions of genetic and transcriptomic variation for several candidate genes underlying yield QTLs, paving the way for future investigation.

Centrosome loss triggers a transcriptional program to counter apoptosis-induced oxidative stress, pp. 187–211

John S. Poulton, Daniel J. McKay, and Mark Peifer

Centrosomes are important mediators of mitotic spindle assembly, and loss of centrosomes can lead to mitotic errors and cell death; however, it is also clear that cells can compensate for centrosome loss through multiple mechanisms. To further explore the consequences of acentrosomal mitosis and the mechanisms that respond to it, Poulton, McKay, and Peifer conducted a global transcriptome analysis of acentrosomal *Drosophila* wing cells, finding that centrosome loss leads to oxidative stress and a complex transcriptional response that helps buffer cells against increased levels of reactive oxygen species.

Efficient implementation of penalized regression for genetic risk prediction, pp. 65–74

Florian Privé, Hugues Aschard, and Michael G. B. Blum

Polygenic risk scores (PRS) combine many single-nucleotide polymorphisms into a score reflecting the genetic risk of developing a disease. Privé, Aschard, and Blum present an efficient implementation of penalized logistic regression (PLR) that allows for practical

computation of PRS on modern datasets. They compare PLR with two other methods using both real and simulated data, finding that PLR achieves higher predictive performance, provided that sample size is large enough, while being very fast. They confirm the relevance and feasibility of these results for individual-level data using the UK Biobank.

How linked selection shapes the diversity landscape in *Ficedula* flycatchers, pp. 277–285

Agnes Rettelbach, Alexander Nater, and Hans Ellegren

The effect of selection on linked neutral sites is widely used to detect selected loci. While existing models provide a good description of the patterns expected from background selection or sweeps on a small scale, the picture is less clear at the genomic scale. Rettelbach, Nater, and Ellegren use the density of possible selection targets and recombination rates along chromosomes to calculate the expected reduction of diversity caused by linked selection in the flycatcher genome. They find that, while background selection can explain most of the observed patterns, positive selection is likely to have an influence as well.

Identification of *rfk-1*, a meiotic driver undergoing RNA editing in *Neurospora*, pp. 93–110

Nicholas A. Rhoades, Austin M. Harvey, Dilini A. Samarajeewa, Jesper Svedberg, Aykhan Yusifov, Anna Abusharekh, Pennapa Manitchotpisit, Daren W. Brown, Kevin J. Sharp, David G. Rehard, Joshua Peters, Xavier Ostolaza-Maldonado, Jackson Stephenson, Patrick K. T. Shiu, Hanna Johannesson, and Thomas M. Hammond

A *Neurospora* meiotic drive element known as *Spore killer-2* (*Sk-2*) achieves biased transmission through sexual reproduction by killing siblings that inherit a competing allele. The mechanism is thought to involve at least two critical components: a killer and a resistance protein. Here, Rhoades *et al.* track the killer gene (*rfk-1*) to the right border of the >2 MB *Sk-2* element. In addition, they find that the *rfk-1* transcript undergoes RNA editing during sexual development, raising the possibility that *Sk-2*-based spore killing could be used as a model to study the recently discovered phenomenon of fungal RNA editing.

No cost of complexity in bacteriophages adapting to a complex environment, pp. 267–276

Andrew M. Sackman and Darin R. Rokytta

A longstanding prediction in evolutionary biology is that organisms experience a “cost of complexity” such that an increase in the number of phenotypes under selection results in a decreased rate of adaptation in the population, owing to trade-offs between traits under selection. Sackman and Rokytta present the results of an experiment designed to test this theoretical prediction through the long-term adaptation of bacteriophages in both simple and complex selective environments. We found no evidence for a cost of complexity. Rather, the rate of adaptation was as high, if not higher, in a complex environment as in a simple one.

This Month's Perspectives

Lysenkoism against genetics: the meeting of the Lenin All-Union Academy of Agricultural Sciences of August 1948, its background, causes, and aftermath

Svetlana A. Borinskaya, Andrei I. Ermolaev, and Eduard I. Kolchinsky

This article reviews the ideological, political, economic, social, cultural, personal, moral, and ethical factors that determined the conduct of the Lenin All-Union Academy of Agricultural Sciences session in August 1948, as well as the immediate and delayed consequences of its decisions. In addition, the authors consider current attempts to revise the role of the August Session in order to whitewash Lysenko.