Genetics, Vol. 190, March 2012, Copyright © 2012

**Gene capture by *Helitron* transposons reshuffles the transcriptome of maize, pp. 965–975**

*Allison M. Barbaglia, Katarina M. Klusman, John Higgins, Janine R. Shaw, L. Curtis Hannah, and Shailesh K. Lal*

The *Helitron* family of mobile DNA elements in maize is known for its propensity to capture and multiply gene fragments. Sometimes the captured genes are transcribed into eclectic transcripts that connect different genes. These can evolve into new genes with novel domains and functions. This report provides evidence that alternative splicing and readthrough transcription also generate multiple isoforms of *Helitron*-captured genes. Thus *Helitrons* provide new grist for the mill of natural selection.

**Efficient mapping and cloning of mutations in zebrafish by low-coverage whole-genome sequencing, pp. 1017–1024**

*Margot E. Bowen, Katrin Henke, Kellee R. Siegfried, Matthew L. Warman, and Matthew P. Harris*

Mapping of mutants by standard approaches remains laborious, resulting in a great number of mutants not being reported. Whole-genome sequencing is improving the situation, but it is not clear how useful it will be to find mutations in organisms with large genomes and much genetic variation. These investigators show that this approach, with modifications, can be successfully applied to zebrafish and other organisms with large, complex genomes.

**On the pleiotropic structure of the genotype–phenotype map and the evolvability of complex organisms, pp. 1131–1137**

*William G. Hill and Xu-Sheng Zhang*

How does pleiotropy affect evolvability? Analyses based on statistical significance have concluded that the extent of pleiotropy is limited, and that therefore multi-trait evolution is facilitated. However, these authors show that similar results can be obtained by analyzing simulated data for fully pleiotropic models in which all genes affect all traits to varying extents and have correlated effects. Thus, conclusions on evolutionary constraints are not robust.

**Stringent analysis of gene function and protein-protein interactions using fluorescently tagged genes, pp. 931–940**

*Ralph A. Neumüller, Frederik Wirtz-Peitz, Stella Lee, Young Kwon, Michael Buckner, Roger A. Hoskins, Koen J. T. Venken, Hugo J. Bellen, Stephanie E. Mohr, and Norbert Perrimon*

"Trapping" genes with transposons harboring the green fluorescent protein (GFP) gene is a favorite tactic of gene hunters. The authors of this article teach new tricks to GFP traps in *Drosophila*. One trick silences trapped genes in a tissue-specific manner; another uses GFP traps to isolate endogenous protein complexes. The development of these methods coincides with renewed efforts to trap all genes in *Drosophila*.

**Gene overexpression: Uses, mechanisms, and interpretation, pp. 841–854**

*Gregory Prelich*

The intentional overexpression of genes has a long and productive history. This review summarizes the history, uses, and interpretation of overexpression phenotypes, focusing on the use of overexpression in genetic screens.

**The coalescent with selection on copy number variants, pp. 1077–1086**

*Kosuke M. Teshima and Hideki Innan*

Copy number variation (CNV) in genomes has drawn attention because of its potential effect on phenotype. These investigators develop a coalescent-based simulation tool to generate patterns of single nucleotide polymorphisms (SNPs) in a wide region encompassing the original and duplicated genes. This simulation tool is useful for determining the role of natural selection on CNVs from the pattern of SNPs.

**Going in the right direction: Mating-type switching of Schizosaccharomyces pombe is controlled by judicious expression of two different swi2 transcripts, pp. 977–987**

*Chuanhe Yu, Michael J. Bonaduce, and Amar J. S. Klar*

Yeast mating-type switching is productive: cells usually reconfigure their mating-type locus using as donor the silent copy of the opposite mating-type. How do they know to choose the silent locus with the opposite mating-type gene? This article explains that directionality of mating-type switching in *Schizosaccharomyces pombe* is controlled by judicious expression of two *swi2* transcripts through a cell-type-regulated dual promoter.

## This Month's Perspectives

**Amber mutants of bacteriophage T4D: Their isolation and genetic characterization, pp. 831–840**

*Richard H. Epstein, Antoinette Bolle, and Charles M. Steinberg; Introduction by Franklin W. Stahl*

How often does a groundbreaking piece of research, responsible for founding a whole new approach, itself lay unpublished for 50 years? This issue of GENETICS features such an article, which describes the discovery of "amber" conditional lethal mutants of phage T4. This work launched the systematic study of gene-function relationships in phage and set in place one of the pillars of genetic analysis. An introduction by Frank Stahl, who knew the principals and witnessed the fruits of this work, sets the scene.

## This Month in the American Journal of Human Genetics

**Large-scale gene-centric meta-analysis across 39 studies identifies type 2 diabetes loci, Am. J. Hum. Genet. 90(3)**

*Richa Saxena, Clara C. Elbers, Yiran Guo, Inga Peter, Tom R. Gaunt et al.*

The increasing prevalence of type 2 diabetes (T2D) is a major concern from both a health and economic standpoint. Although previous GWASs have identified candidate variants associated with T2D risk, the findings have been difficult to replicate, especially across different ethnic groups. In this large-scale meta-analysis, Saxena *et al.* identify several previously unknown risk variants, including one for African-Americans (in the HMGA2 locus) and one that predicts risk across ethnicities (in the BCL2 locus). Future studies should help to elucidate the contribution of these risk alleles to the biology of T2D and to improve both diagnostic and therapeutic options for the treatment of T2D.