Integration of new genes into cellular networks, and their structural maturation, pp. 1407–1417
György Abrusán

De novo formation of genes may be much more prevalent than previously thought; some non-genic sequences can get translated and over time contribute to the proteome. Here the systems properties of new genes in yeast are examined, revealing that new genes seem to acquire regulatory, physical and genetic interactions gradually, most likely due to gene loss and accumulation of neutral mutations.

Resection activity of the Sgs1 helicase alters the affinity of DNA ends for homologous recombination proteins in Saccharomyces cerevisiae, pp. 1241–1251
Kara A. Bernstein, Eleni P. Mimitou, Michael J. Mihalevic, Huan Chen, Ivana Sunjaeric, Lorraine S. Symington, and Rodney Rothstein

How cells process the ends of double-strand breaks (DSBs) is extremely important; when misrepaired, DSBs can lead to chromosomal rearrangements and mutations. One way to target the DNA to the error-free homologous recombination pathway is through resection of the broken ends. This article reports that the Sgs1 helicase, in conjunction with the Sae2 nuclease, is important for efficient resection by enabling removal of other DNA repair proteins from DSB ends. These events are crucial for commitment to error-free DNA repair.

Sex-specific effects of cis-regulatory variants in Drosophila melanogaster, pp. 1419–1422
Joseph D. Coolon, William Webb, and Patricia J. Wittkopp

In addition to often looking quite different, males and females of the same species manifest differences at the molecular level, where sex-specific factors cause differences in gene expression. This raises the possibility that some genetic variants that alter gene expression could have different effects in males and females. Indeed, this article reveals that such sex-specific effects are common among cis-regulatory alleles found in different strains of Drosophila melanogaster.

The evolutionary genetics of the genes underlying phenotypic associations for loblolly pine (Pinus taeda, Pinaceae), pp. 1353–1372

What is the genetic basis of fitness-related traits, and how does it evolve within natural populations? These investigators assessed patterns of nucleotide diversity and divergence in over 7,000 unique expressed sequence tags of loblolly pine (Pinus taeda, Pinaceae), along with the more than 1,000 published genetic associations. As expected for polygenic traits, signals of non-neutral evolution were only apparent when loci were considered at the level of functional sets.

Genetically engineered transvestites reveal novel mating genes in budding yeast, pp. 1277–1290
Lori B. Huberman and Andrew W. Murray

Mating of budding yeast is initiated when two haploid cells of opposite mating types signal to each other using reciprocal pheromones and receptors. Huberman and Murray employed “transvestite” cells carrying the pheromone, pheromone receptor, and pheromone processing factors of the other mating type to discover Abf1 (a-factor barrier), a novel MATα-specific protein that interferes with the pheromone secreted by MATa cells.

APOE modulates the correlation between triglycerides, cholesterol, and CHD through pleiotropy and gene-by-gene interactions, pp. 1397–1405
Taylor J. Maxwell, Christie M. Ballantyne, James M. Cheverud, Cameron S. Guild, Chiadi E. Ndumele, and Eric Boerwinkle

Relationship loci (rQTL) — in which the relationship between two traits varies by genotype — provide a powerful approach to detect gene-by-gene interactions that modulate pleiotropy, and potentially to identify loci that modulate relationships between risk factors and disease. These authors show that APOE, an rQTL that conditionally affects the relationship between cholesterol and triglycerides, affects the risk relationship between these lipids and chronic heart disease. They found other loci that interact with APOE, and show how they contribute to the observed rQTL patterns.

Tolerance of Escherichia coli to fluoroquinolione antibiotics depends on specific components of the SOS response pathway, pp. 1265–1276
Alyssa Theodore, Kim Lewis, and Marin Vulić

Bacteria can survive exposure to antibiotics without becoming genetically resistant. These phenotypically resistant cells, commonly called persisters, can potentially compromise the outcome of antibiotic therapy. Tolerance of Escherichia coli to fluoroquinolione antibiotics (FQs) depends on the SOS DNA damage response pathway, and these investigators found that the DNA repair proteins DinG, UvrD and RuvAB are most needed for survival. They show that the quality of the repair process is a major contributor to survival in the absence of genetic resistance.

Evidence for tissue-specific JAK/STAT target genes in Drosophila optic lobe development, pp. 1291–1306
Hongbin Wang, Xi Chen, Teng He, Yanna Zhou, and Hong Luo

The conserved JAK/STAT pathway plays important roles in development and disease in humans, but the target genes of JAK/STAT signaling remain elusive. These authors identified about 50 target genes in the Drosophila brain. These genes are largely different from the targets identified in other tissues, suggesting that JAK/STAT signaling regulates target genes in a tissue-specific manner.

This Month in the American Journal of Human Genetics

Genetic and epigenetic regulation of human lincRNA gene expression, Am. J. Hum. Gent. 93(6)
Konstantin Popadin, Maria Gutierrez-Arcelus, Emmanouil T. Dermitsakis, and Stylianos E. Antonarakis

When teasing out the function of genes, expression patterns and ways in which expression is regulated can provide functional insight, and this approach could be applied to lincRNAs, which are not well characterized. In this study, Popadin et al. use a genome-wide approach to characterize the cis-eQTLs and DNA methylation patterns that contribute to lincRNA expression variability across three cell types from 195 Europeans. They find that although lincRNAs appear to be less constrained than similar protein-coding genes, they are regulated similarly by many of the same genotype-dependent mechanisms.