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Repeated selection of alternatively adapted haplotypes creates sweeping genomic remodeling in stickleback, pp. 921–939

Susan Bassham, Julian M. Catchen, Emily Lescak, Frank A. von Hippel, and William Cresko

After the catastrophic 1964 Alaskan earthquake, marine stickleback colonized newly created ponds on seismically uplifted islands. Bassham and Catchen *et al*. show that, in replicate populations, as much as a quarter of the genome changed in the first dozens of generations during freshwater adaptation, and identical haplotypes were repeatedly selected from standing genetic variation. Marine fish harbor significant frequencies of these genotypes, providing potential for rapid exploitation of new freshwater habitats. These findings give insight into the adaptive capacity of species that exist across variable environments, particularly during accelerating climate and land-use change.

Spermiogenesis and male fertility require the function of suppressor of hairy-wing in somatic cyst cells of *Drosophila*, pp. 757–772

Tingting Duan and Pamela K. Geyer

Drosophila Suppressor of Hairy-wing [Su(Hw)] is a multivalent transcription factor. Although best known for its *gypsy* retrotransposon insulator function, its functions at non-*gypsy* genomic binding sites are poorly understood. Duan and Geyer study the newly-discovered requirement for Su(Hw) in spermatogenesis, showing that Su(Hw) is required in testis cyst cells for sustained male fertility. Additionally, their studies build evidence that the prominent function of Su(Hw) at non-*gypsy* binding sites is as a transcriptional repressor, with its loss causing cell-specific changes in gene expression.

An association mapping framework to account for potential sex difference in genetic architectures, pp. 685–698

Eun Yong Kang, Cue Hyunkyu Lee, Nicholas A. Furlotte, Jong Wha J. Joo, Emrah Kostem, Noah Zaitlen, Eleazar Eskin, and Buhm Han

Recent genome-wide association studies suggest that the human genetic architecture of complex traits may vary between males and females; however, traditional approaches for association mapping cannot fully account for these between-sex differences. Here, Kang *et al*. propose a novel association mapping framework that comprehensively accounts for the genetic architecture differences between males and females. Using simulations and real data, they show that their method provides higher statistical power than traditional approaches for detecting associated loci.

The evolution of polymorphic hybrid incompatibilities in house mice, pp. 845–859

Erica L. Larson, Dan Vanderpool, Brice A. J. Sarver, Colin Callahan, Sara Keeble, Lorraine P. Provencio, Michael D. Kessler, Vanessa Stewart, Erin Nordquist, Matthew D. Dean, and Jeffrey M. Good

Reproductive barriers are often assumed to arise from fixed genetic differences between species, despite frequent individual variation in the strength of reproductive isolation between populations. Larson *et al*. report polymorphism at several hybrid male sterility loci in house mice, and their results demonstrate that selection against deleterious hybrid interactions can drive the introgression of hybrid incompatibilities and highlights the need for more extensive sampling of natural variation in speciation studies.

Dynamic copy number evolution of X- and Y-linked ampliconic genes in human populations, pp. 907–920

Elise A. Lucotte, Laurits Skov, Jacob Malte Jensen, Moisès Coll Macià, Kasper Munch, and Mikkel H. Schierup

Ampliconic genes are multicopy genes often located on sex chromosomes and enriched for testis-expressed genes. Here, Lucotte *et al*. developed new bioinformatic approaches to investigate the ampliconic gene copy number and their coding sequence turnover using the Simons Genome Diversity Project, which provided genomic sequences of 276 individuals from 128 human populations. They report extensive copy number variation for testis-expressed ampliconic genes, providing the first world-wide picture of the diversity of ampliconic genes in humans.

Comparison of genotypic and phenotypic correlations: Cheverud's conjecture in humans, pp. 941–948

Sebastian M. Sodini, Kathryn E. Kemper, Naomi R. Wray, and Maciej Trzaskowski

Cheverud's conjecture asserts that the use of phenotypic correlations as proxies for genetic correlations in situations where genetic data is not available is appropriate. Although empirical evidence for this has been found across plant and animal species, it has not been systematically tested in humans; to address this, Sodini *et al*. used cutting-edge methodology paired with the largest genetic sample to date. Their results support consistency between genetic and phenotypic correlations in humans. This finding may be of interest in anthropological studies and extends out to studies of modern humans, where genetic data of rare or more obscure traits are not available.

Serrate-notch signaling regulates the size of the progenitor cell pool in *Drosophila* imaginal rings, pp. 829–843

Sheng-An Yang and Wu-Min Deng

Drosophila imaginal rings are larval precursors for adult guts and salivary glands. Yang and Deng show that the proliferation of these cells is regulated by the canonical Notch pathway and that both cis- and trans-interactions between Notch and its ligand are involved. Their findings indicate that Notch signaling is the primary growth-promoting signal, demonstrating that imaginal rings are excellent models for studies on how the size of the progenitor pool is controlled in development.

This Month's Perspectives

One hundred years of linkage disequilibrium, pp. 629–636

John A. Sved and William G. Hill

The year 2018 marks 100 years since the concept of linkage disequilibrium (LD) was introduced, and 50 years since the importance of chance segregation in generating LD was recognized. Genome-Wide Association Studies (GWAS) now use the huge array of genetic markers that result from this LD to map genetic diseases, to understand the basis for quantitative characters such as human height, and as an aid in animal and plant breeding.