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**Membrane fluidity is regulated cell nonautonomously by *Caenorhabditis elegans* PAQR-2 and its mammalian homolog AdipoR2, pp. 189–201**

*Rakesh Bodhicharla, Ranjan Devkota, Mario Ruiz, and Marc Pilon*

The properties of cell membranes are determined mostly by the types of fatty acids that they contain. Bodhicharla *et al.* report that a key regulator of membrane fluidity, the PAQR-2/IGLR-2 protein complex, can regulate membrane properties cell non-autonomously in the nematode worm *Caenorhabditis elegans* since expression of PAQR-2 and IGLR-2 in some cells improved membrane properties in the whole worm. They show that AdipoR2, the human homolog of PAQR-2, can also regulate membrane fluidity cell non-autonomously.

**Inferring continuous and discrete population genetic structure across space, pp. 33–52**

*Gideon S. Bradburd, Graham M. Coop, and Peter L. Ralph*

An important step in the analysis of genetic data is to describe and categorize natural variation. Individuals that live close together are, on average, more genetically similar than individuals sampled farther apart, but current statistical methods for inferring population structure cannot accommodate spatial information, leading to the assignment of continuous variation to discrete clusters. Here, Bradburd, Coop, and Ralph report a new method for categorizing natural genetic variation that describes variation as a combination of continuous and discrete patterns. They demonstrate that this method can capture patterns in population genomic data without resorting to splitting populations.

**Relationship between sequence homology, genome architecture, and meiotic behavior of the sex chromosomes in North American voles, pp. 83–97**

*Beth L. Dumont, Christina L. Williams, Bee Ling Ng, Valerie Horncastle, Carol L. Chambers, Lisa A. McGraw, David Adams, Trudy F. C. Mackay, and Matthew Breen*

On the heterogametic sex chromosomes, the homology-driven processes of pairing, recombination, and segregation are restricted to a short region of X/Y homology known as the pseudoautosomal region (PAR). Although failure of X/Y associations in most mammals results in meiotic arrest, several exceptional species have evolved PAR-independent X/Y segregation mechanisms. Dumont *et al*. take advantage of three closely related vole taxa, including one lacking PAR-mediated sex chromosome interactions, to investigate how variable X/Y homology requirements at meiosis shape the evolution of sex chromosome architecture. Their work uncovers dramatic differences in heterochromatic sequence composition among species, hinting at a functional role for low-complexity DNA in non-canonical X/Y segregation.

**Gene regulatory variation in *Drosophila melanogaster* renal tissue, pp. 287–301**

*Amanda Glaser-Schmitt, Aleksandra Zečić, and John Parsch*

This study examines the genetic basis of gene expression variation among strains of *Drosophila melanogaster* from different natural populations. Glaser-Schmitt, Zečić, and Parsch used high-throughput RNA sequencing of inbred strains and their hybrids to determine inheritance patterns of gene expression levels and the underlying basis of expression variation in renal tissue. Their analysis uncovered hundreds of genes with cis-regulatory variation. Functional analysis of a subset of these genes revealed that most cis-regulatory variants were within 2 kb of the affected gene and had tissue-specific effects on gene expression.

**Condensin depletion causes genome decompaction without altering the level of global gene expression in *Saccharomyces cerevisiae*, pp. 331–344**

*Matthew Robert Paul, Tovah Elise Markowitz, Andreas Hochwagen, and Sevinç Ercan*

Gene expression occurs in the context of chromatin organization, but the extent to which higher-order chromatin compaction affects gene expression remains unknown. Here, Paul *et al*. show that gene expression and genome compaction can be uncoupled in *Saccharomyces cerevisiae*. Inactivation of the conserved condensin complex leads to broad genome decompaction in this organism, but unexpectedly, this reorganization has no immediate effect on the transcriptome, indicating that the global gene expression program is resistant to large-scale changes in genome architecture in yeast.

**Micronuclei formation is prevented by Aurora B-mediated exclusion of HP1a from late-segregating chromatin in *Drosophila*, pp. 171–187**

*Brandt Warecki and William Sullivan*

Here, Warecki and Sullivan investigate how late-segregating chromosome fragments pass through nuclear envelope channels to maintain euploidy in the nuclei of *Drosophila* neuroblasts during telophase. The authors find that Aurora B activity prevents the recruitment of HP1a to chromosome fragments, resulting in a regional decrease in the cell's ability to reassemble a nuclear envelope.

**Transgenerational effects of extended dauer diapause on starvation survival and gene expression plasticity in *Caenorhabditis elegans*, pp. 263–274**

*Amy K. Webster, James M. Jordan, Jonathan D. Hibshman, Rojin Chitrakar, and L. Ryan Baugh*

Organisms respond to environmental conditions by altering gene expression; however, it is unclear if organisms retain epigenetic memory of their ancestors' environmental conditions. Webster *et al*. assessed the descendants of two genetically identical populations of *Caenorhabditis elegans*, one of which experienced extended starvation during dauer diapause and one that was never starved. The consequences of extended diapause persisted three generations later, showing effects on starvation survival, lifespan, and gene expression, demonstrating that epigenetic alterations due to ancestral conditions can be inherited for three generations.

**Gene birth contributes to structural disorder encoded by overlapping genes, pp. 303–313**

*Sara Willis and Joanna Masel*

The same nucleotide sequence can encode multiple protein products in different reading frames, and these regions encode higher levels of intrinsic structural disorder than non-overlapping genes. Willis and Masel find that about 32% of this elevation in intrinsic structural disorder can be attributed to the process of *de novo* gene birth but that the frame in which most overlapping genes are born is determined by mutation bias toward greater availability of ORFs rather than by selection for novel genes encoding proteins with higher intrinsic structural disorder. They also report that old genes with high disorder are more likely to be the birthplace of new genes in a different frame.

## This Month's Perspectives

**"Elements" in *Drosophila*: how the search for the genetic basis for speciation led to the birth of comparative genomics, pp. 3–13**

*Stephen W. Schaeffer*

The development of genetic maps multiple species of *Drosophila* to understand the basis for species formation became problematic because visible mutations were not easily compared among species and species-specific linkage groups lacked a standard nomenclature. H. J. Muller published a landmark paper in 1940 that developed a standard nomenclature for *Drosophila* chromosomes that established the concept of gene order conservation and genetic models for how species form. This review examines the history of *Drosophila* genetics that led to the field of comparative genomics and has provided the framework for asking questions about how genomes and species evolve.