Evolved differences in cis and trans regulation between the maternal and zygotic mRNA complements in the Drosophila Embryo, pp. 805–821

Emily L. Cartwright and Susan E. Lott

The critical processes of early development require gene products that mothers deposit into eggs, before the zygotic genome is transcriptionally active. Here, Cartwright and Lott determine that patterns of gene regulatory evolution differ for transcripts before and after zygotic genome activation between species of Drosophila. This study indicates that maternal transcript deposition evolves more readily through changes in trans regulation while zygotic transcription changes through a combination of alterations in cis and in trans. The regulatory organization of the maternal and zygotic genomes differ, which likely plays a role in how gene regulation evolves at different developmental timepoints.

Defining the boundaries of polycomb domains in Drosophila, pp. 689–700

Sandip De, Natalie D. Gehred, Miki Fujioka, Fountane W. Chan, James B. Jaynes, and Judith A. Kassis

Polycomb group (PcG) genes are an important group of epigenetic regulators that act to repress transcription. In Drosophila, the PcG group protein complex PR2C is recruited to discrete DNA elements called Polycomb response elements. PR2C tri-methylates histone H3 on flanking nucleosomes, spreading this repressive histone mark for many kilobases to form H3K27me3 or “Polycomb domains”. What stops this spreading process in Drosophila? Here, De et al. show that actively transcribed genes form one type of Polycomb domain end, and that stopping transcription causes Polycomb domains to expand.

Melting dsDNA donor molecules greatly improves precision genome editing in Caenorhabditis elegans, pp. 643–650

Krishna S. Ghanta and Craig C. Mello

Melting and fast cooling double stranded DNA donor molecules prior to injection dramatically increases the frequency of homology-directed repair for edits such as insertions of fluorescent protein markers in Caenorhabditis elegans. Strategies described here enable consistently high editing efficiencies resulting, for example, in up to 100 independent GFP knock-ins from a single injected animal. Such efficiencies make C. elegans by far the easiest metazoan to genome edit, removing barriers to the use and adoption of this facile system as a model for understanding animal biology.

Asymmetric transcription factor partitioning during yeast cell division requires the FACT chromatin remodeler and cell cycle progression, pp. 701–716

Eva Herrero, Sonia Stinus, Eleanor Bellows, Lisa K. Berry, Henry Wood, and Peter H. Thorpe

Most cell divisions are asymmetric with some cellular components distributed preferentially to one of the two nascent daughter cells. These asymmetries are typically important for the developmental fate of the resulting daughter cells. Herrero et al. describe the results of a screen for genes essential for the asymmetric distribution of a transcription factor, Ace2, in budding yeast. They find that a complex required for chromatin organization, FACT, is critical for Ace2 asymmetric distribution. The FACT complex regulates the localization of the RAM kinase network, which in turn control Ace2’s asymmetric distribution during cell division.

Genetic basis of aerobically supported voluntary exercise: results from a selection experiment with house mice, pp. 781–804

David Hillia, Liran Yadgar, George Weinstock, Fernando Parado-Manuel de Villena, Daniel Pomph, Alexandra Fowler, Shizhong Xu, Yingguang Frank Chan, and Theodore Garland

House mice from 4 replicate lines selectively bred for 61 generations for endurance running behavior were compared with 4 non-selected control lines using multiple genome-wide analytical techniques on both haplotype and single nucleotide polymorphism data. Twelve genomic regions were consistently found differentiated across all analytical approaches. These regions are associated with a diverse set of genes that appear related to exercise behavior or motivational systems. Genes related to various organ systems (e.g. heart, brain) known to be physiologically different between test groups were identified. These results highlight candidate genes for detailed studies of exercise behavior and physiology.

Functional divergence of mammalian TFP2a and TFP2b transcription factors for bidirectional sleep control, pp. 735–752

Yang Hu, Alejandra Korovaihak, Marisana Astia, Henning Schroeder, Reanul Islam, Jon Barrenetswa, Andre Fischer, Henrik Oster, and Henrik Brittingmann

Here, Hu et al. show that AP-2 transcription factors have diverged to take on bidirectional control of sleep in mammals. This is the first instance where a sleep gene is shown to have diversified in evolution from a sleep-promoting role in invertebrates to serve bidirectional control of sleep in mammals. Thus, the authors’ work provides an evolutionary principle for how sleep emerged as a simpler state in invertebrates and evolved to more complex states in mammals.

Deep convergence, shared ancestry and evolutionary novelty in the genetic architecture of Heliconius mimicry, pp. 765–780

Jake Morris, Joseph J. Hanly, Simon H. Martin, Steven M. Van Belleghem, Camilo Salazar, Chris D. Jiggins, and Ranchor K. Dasmahapatra

Phenotypic convergence between taxa can be caused by divergent genetic evolution (different genetic pathways), parallel genetic evolution (convergent mutations), or collateral evolution (shared ancestry). Heliconius butterflies have bright mimetic color patterns shared between multiple species, making an excellent model system for looking at convergent genetic evolution. Here, Morris et al. look at patterns of shared ancestry to first identify putative regulatory elements at color genes. They find that all three of novelty, parallel genetic evolution and collateral evolution have driven mimicry between Heliconius species. This adds to recent work that suggests cis-regulatory elements may be a key driver of adaptive convergent evolution.

Sleep architecture in mice is shaped by the transcription factor AP-2β, pp. 753–764

Ayaka Nakai, Tomoyuki Fujiyama, Nanane Nagata, Mitsuki Kashiwagi, Aya Ikkyu, Marina Takagi, Chika Tatsuzawa, Kaeko Tanaka, Miyo Kakizaki, Mika Kanaka, Taizo Kawano, Seiya Mitsuno, Fumihiro Sugiyama, Satoru Takahashi, Takeshi Sakurai, Masashi Yanagisawa, and Yu Hayashi

Humans families carrying mutations in transcription factor AP-2β (TFP2B) self-reported sleep abnormalities. Notably, AP-2β transcription factors play essential roles in invertebrate sleep, implicating a conserved role across the animal phyla. Nakai et al. generated two mutant mouse strains, Tfap2bK144 and Tfap2bK145, each mimicking mutations in the human kindreds, and compared their effects with those of a Tfap2b knockout allele (Tfap2bK144). Tfap2bK145 female mice showed decreased non-rapid eye movement sleep (NREMS). By contrast, Tfap2bK145 male mice exhibited fragmented NREMS, whereas Tfap2bK144 male mice showed reduced NREMS in the dark phase. These findings indicate that TFP2B influences NREMS patterns in mice.

This Month’s Perspectives

The interchromosomal effect: different meanings for different organisms

Danny E. Miller

The interchromosomal effect is a term originally used to describe the change in the distribution of exchange in the presence of an inversion. First described in the 1920s by early Drosophila researchers it has been observed in multiple species. In mammals, the term has been used as a way to describe chromosome nondejuncture in the presence of parental chromosome differences, such as balanced translocations. While it remains unclear if translocations truly affect chromosome segregation in humans the use of the term interchromosomal effect to describe this persists. This article explores the history of the use of the term interchromosomal effect.