

Cell cycle-regulated transcription of CENP-A by the MBF complex ensures optimal level of CENP-A for centromere formation, pp. 861–875

David Aristizabal-Corrales, Jinpu Yang, and Fei Li

In most eukaryotes, the histone H3 variant CENP-A serves as the epigenetic mark for centromeres. CENP-A transcription is subject to cell-cycle regulation, but the molecular mechanism underlying the regulation remains elusive. Through a genetic screen, Aristizabal-Corrales, Yang, and Li identify the MBF complex as a key regulator of temporal control of CENP-A transcription in fission yeast, providing insight into the mechanism for regulating cell cycle-dependent CENP-A transcription. They also show that timing of CENP-A transcription is dispensable for its centromeric localization but is important for proper maintenance of CENP-A level across generations.

Tissue-specific *trans* regulation of the mouse epigenome, pp. 831–845

Christopher L. Baker, Michael Walker, Seda Arat, Guruprasad Ananda, Pavlina Petkova, Natalie R. Powers, Hui Tian, Catrina Spruce, Bo Ji, Dylan Rausch, Kwangbom Choi, Petko M. Petkov, Gregory W. Carter, and Kenneth Paigen

While much is known about the enzymes that deposit and remove epigenetic modifications, less is known about the *trans*-acting system that determines when and where these modifications occur. By looking at four diverse cell types, Baker *et al.* find that epigenetic marks at regulatory elements can be greatly influenced by regions of the genome distal to the element itself. Using male germ cells, they identify several loci that function to decrease the levels of one epigenetic mark associated with active chromatin. Together, these observations suggest cell-type specific genetic control of the epigenome.

The role of miRNAs in *Drosophila melanogaster* male courtship behavior, pp. 925–942

Hina Iftikhar, Nicholas L. Johnson, Matthew L. Marlatt, and Ginger E. Carney

The role of non-coding RNAs in the development and maintenance of sex-specific characteristics in *Drosophila* is not well understood. Iftikhar *et al.* present results of a genetic screen demonstrating that ~39% of tested miRNAs affect male courtship behavior. *miR-957* mutant males displayed high levels of male-male courtship. They demonstrate that reduced ability to process inhibitory pheromones from courtship subjects, particularly the gustatory pheromone 7-T, likely accounts for male-male courtship. This study provides new insights into possible roles of miRNAs in regulation of complex physiological and behavioral processes in adult *D. melanogaster*.

Pervasive linked selection and intermediate-frequency alleles are implicated in an evolve-and-resequencing experiment of *Drosophila simulans*, pp. 943–961

John K. Kelly and Kimberly A. Hughes

Evolve-and-Resequencing (E&R) experiments, where researchers allow populations to evolve within one or more controlled environments and then whole-genome sequence the resultant populations, are increasingly important in evolutionary genetics methodology. Here, Kelly and Hughes develop a set of analytical and simulation tools for E&R experiments and apply them to a new study of rapid evolution in *Drosophila simulans*. They find that 138 polymorphisms across the genome experience strong parallel selection in the laboratory. The allele frequency spectrum at these sites suggests that loci responding to selection may be balanced polymorphisms in nature.

Modelling sex-specific crossover patterning in *Arabidopsis*, pp. 847–859

Andrew Lloyd and Eric Jenczewski

Males and females of many organisms show distinct patterns of inheritance. Here, Lloyd and Jenczewski model crossover patterning in

Arabidopsis to gain insights into what causes the large differences in recombination rates and patterns in the male and female germlines. Their findings suggest that recombination is mechanistically identical in both sexes and that differences in crossover patterning observed between males and females are due to differences in the length of the chromosome axes.

Establishment and maintenance of chromatin architecture are promoted independently of transcription by the histone chaperone FACT and H3-K56 acetylation in *Saccharomyces cerevisiae*, pp. 877–892

Laura L. McCullough, Trang H. Pham, Timothy J. Parnell, Zaily Connell, Mahesh B. Chandrasekharan, David J. Stillman, and Tim Formosa

Using a combination of *in vitro* biochemistry, genetics, and genomics, McCullough and Pham *et al.* explore how the histone:DNA contact at the entry/exit site of nucleosomes affects the functions of the histone chaperone FACT in the yeast *Saccharomyces cerevisiae*. They find that FACT and histone H3-K56 acetylation collaborate to establish the appropriate chromatin architecture. This role appears to be important for maintaining the features of chromatin independent of ongoing transcription as well as in response to the effects of transcription on chromatin integrity.

Deleterious mutation burden and its association with complex traits in sorghum (*Sorghum bicolor*), pp. 1075–1087

Ravi Valluru, Elodie E. Gazave, Samuel B. Fernandes, John N. Ferguson, Roberto Lozano, Pradeep Hirannaiah, Tao Zuo, Patrick J. Brown, Andrew D. B. Leakey, Michael A. Gore, Edward S. Buckler, and Nonoy Bandillo

Sorghum (*Sorghum bicolor* (L.) Moench) is a major staple food cereal for millions of people worldwide. Valluru *et al.* identify putative deleterious mutations among ~5.5M segregating variants of 229 diverse sorghum lines and show that about 33% of nonsynonymous substitutions are putatively deleterious. Mutation burden varies appreciably among racial groups, which negatively correlated with phenotypes. The contribution of deleterious variants to phenotypic diversity appears to be dependent on the genetic architecture of traits. Overall, the results suggest that including putatively deleterious variants in genomic models do not significantly improve breeding accuracy because of extensive linkage.

The genetics of mating song evolution underlying rapid speciation: linking quantitative variation to candidate genes for behavioral isolation, pp. 1089–1104

Mingzi Xu and Kerry L. Shaw

A common component of divergence in mating behavior is the distinctive mating songs of insects, and identifying genes underlying natural variation in acoustic behavior is important for understanding targets of selection during speciation. Here, Xu and Shaw examine the largest quantitative trait locus underlying an interspecific difference in the male mating song of two closely related species of Hawaiian crickets, characterize its genetic and phenotypic effects, and refine its map location. They identify an ion channel gene as a promising candidate underlying behavioral isolation between the two cricket species.

This Month's Perspectives

Martynas Yčas: The "Archivist" of the RNA Tie Club

Bernard S. Strauss

The records of correspondence of Yčas with the physicist George Gamow and with Francis Crick throw some light on the genesis of our understanding about the role of messenger RNA. The story of the "RNA Tie Club" illustrates the difficulty in assigning credit for important discoveries and underscores the importance of a free exchange of information even (or especially) among competitors.