ISSUE HIGHLIGHTS

A neo-sex chromosome that drives postzygotic sex determination in the Hessian fly (*Mayetiola destructor*), pp. 769–777

Thiago R. Benatti, Fernando H. Valicente, Rajat Aggarwal, Chaoyang Zhao, Jason G. Walling, Ming-Shun Chen, Sue E. Cambron, Brandon J. Schemerhorn and Jeffrey J. Stuart

The Hessian fly, a wheat pest, has an unusual sex chromosome. Unlike other sex chromosomes, its segregation determines whether females have all-female or all-male offspring. Females that carry the chromosome produce only daughters; half of these produce females and half produce only males. Males rarely carry the chromosome. The chromosome's effect evolved because sex in this insect is determined by chromosome elimination during embryo development, rather than at conception. The discovery presents an opportunity to investigate sex chromosome evolution and the genes that control chromosome movements during development.

Genetic control of photoperiod sensitivity in maize revealed by joint multiple population analysis, pp. 799–812

Nathan D. Coles, Michael D. McMullen, Peter J. Balint-Kurti, Richard C. Pratt and James B. Holland

Maize from tropical regions responds to long day lengths with delayed flowering. Do genetic pathways controlling photoperiod responses in other plants control the differences seen in maize? These investigators mapped genomic regions controlling photoperiod response in crosses between tropical and temperate maize lines, resolving most of the genetic control to 2% of the genome. Homologs of some major photoperiod genes are not found in these regions, suggesting that the maize photoperiod regulation pathway is only partly shared with other model species.

On the classification of epistatic interactions, pp. 827–837

Hong Gao, Julie M. Granka and Marcus W. Feldman

Application of different quantitative definitions for epistasis can lead to distinct conclusions when constructing genetic interaction networks. But this article suggests that different representations of epistasis (epistatic "subtypes") may be appropriate for different pairs of genes. The authors propose maximum likelihood and model selection methods in a hypothesis-testing framework to choose epistatic subtypes that best represent functional relationships between gene pairs, based on fitness data from single and double mutants in haploid systems. Application of this approach to two datasets from yeast demonstrates that their results are likely to be of biological significance in understanding interaction mechanisms.

A single unpaired and transcriptionally silenced X chromosome locally precludes checkpoint signaling in the *Caenorhabditis elegans* germ line, pp. 613–628

Aimee Jaramillo-Lambert and JoAnne Engebrecht

How are heterogametic sex chromosomes hidden from the surveillance pathways that recognize unpaired chromosomes in meiosis? Analysis of sex determination mutants in the nematode *Caenorhabditis elegans* reveals that even though a single unpaired X chromosome is a substrate of the meiotic recombination machinery, and repair of the resulting breaks is delayed, a single X is not recognized to be unpaired. The authors provide evidence that the chromatin/transcriptional state of a single X enables it to be hidden from the surveillance machinery.

Activation of a poised RNAPII-dependent promoter requires both SAGA and Mediator, pp. 659–672

Sarah K. Lee, Aaron G. L. Fletcher, Lei Zhang, Xu Chen, Julie A. Fischbeck and Laurie A. Stargell

One of the exciting themes emerging in the transcription field is that many genes are regulated at a step after recruitment of the general transcription machinery. TATA-binding protein (TBP) and RNA polymerase II (RNAPII) occupy these poised promoters, even when transcriptional output is not observed, indicating distinct rate-limiting steps from the more traditional recruitment-regulated genes. Using a clever genetic screen, as well as characterization of a genuine postrecruitment-regulated gene, the authors show that the Spt-Ada-Gcn5-acetyltransferase (SAGA) and Mediator coactivator complexes play distinct, and essential, roles in the regulation of gene expression after the formation of the preinitiation complex and the recruitment of RNAPII.

Regulation of *Salmonella enterica* pathogenicity island 1 by DNA adenine methylation, pp. 637–649

Javier López-Garrido and Josep Casadesús

Transcription of certain bacterial genes is controlled by DNA adenine (Dam) methylation. This article shows that Dam methylation regulates expression of the gene cluster in the Salmonella pathogenicity island 1 (SPI-1) by controlling synthesis of an SPI-1 transcription factor, HilD. A surprising observation is that Dam methylation controls *hilD* mRNA stability, not *hilD* transcription. This finding suggests that DNA adenine methylation may play hitherto unknown roles in the bacterial cell.

The Rim101p/PacC pathway and alkaline pH regulate pattern formation in yeast colonies, pp. 707–716

Sarah Piccirillo, Melissa G. White, Jeffrey C. Murphy, Douglas J. Law and Saul M. Honigberg

Pattern formation is ubiquitous in metazoans, but patterns of cell types can form even in unicellular communities. This article reports that colonies of *Saccharomyces cerevisiae* contain sharply divided layers of sporulating and nonsporulating cells. The study reveals two key properties of this type of pattern formation. First, because nutrient environment varies across the colony, different regions express different genes, and sporulation initiates in the overlap between the regions expressing the Ime1p transcription factor and the regions expressing the Ime2p protein kinase. Second, development of sporulation patterns over time requires at least one cell-to-cell signal: alkaline pH, mediated through the Rim101p pathway.

Alternative splicing modulates Ubx protein function in *Drosophila melanogaster*, pp. 745–758

Hilary C. Reed, Tim Hoare, Stefan Thomsen, Thomas A. Weaver, Robert A. H. White, Michael Akam and Claudio R. Alonso

Hox genes shape animal structures by eliciting different developmental programs along the antero-posterior body axis. But how do the products of a single *Hox* gene instruct cells to adopt distinct developmental fates? This article demonstrates that alternative splicing is able to diversify the functions of the Drosophila *Hox* gene *Ultrabithorax,* showing that individual spliced forms of the protein have distinct abilities to activate expression of genes in the embryonic mesoderm, have different ways to pattern larval muscles, and have specific DNA-binding properties. The study thus argues that alternative splicing contributes to *Hox* specificity.