ISSUE HIGHLIGHTS

Using reporter gene assays to identify *cis* regulatory differences between humans and chimpanzees, pp. 2069–2076

Adrien Chabot, Ralla A. Shrit, Ran Blekhman and Yoav Gilad

Humans are ~95–99% similar to other apes at the nucleotide level, yet show pronounced phenotypic differences. To reconcile these two observations, King and Wilson proposed that modifications in gene regulation may be responsible for many of the observed phenotypic differences between humans and their close evolutionary relatives. This article describes use of reporter gene assays to identify differences in *cis* regulatory elements between human and chimpanzee for 10 genes that are differentially expressed between the species. For 3 of these genes, changes in *cis* regulatory elements altered the gene expression differences. Moreover, using site-directed mutagenesis, the authors identified three nucleotides that account for a regulatory difference between the species.

Predicting and testing physical locations of genetically mapped loci on tomato pachytene chromosome *1*, pp. 2131–2138

Song-Bin Chang, Lorinda K. Anderson, Jamie D. Sherman, Suzanne M. Royer and Stephen M. Stack

Assignments of the chromosomal locations of mapped markers are often inaccurate because crossing over is not distributed uniformly along chromosomes. This article describes how a physical crossover map based on the distribution of recombination nodules (RNs) can be combined with a genetic linkage map from an interspecific hybrid cross to predict the locations of 17 mapped loci on chromosome *1* of tomatoes. The predicted locations agree well with the locations observed by fluorescence *in situ* hybridization. Once the RN distribution has been determined, the chromosomal location of any mapped locus can be predicted with a high level of confidence.

A genetic mosaic analysis with a repressible cell marker screen to identify genes involved in tracheal cell migration during Drosophila air sac morphogenesis, pp. 2177–2187

Hélène Chanut-Delalande, Alain C. Jung, Li Lin, Magdalena M. Baer, Andreas Bilstein, Clemens Cabernard, Maria Leptin and Markus Affolter

and

A clonal genetic screen for mutants causing defects in larval tracheal morphogenesis in Drosophila, pp. 2279–2291

Magdalena M. Baer, Andreas Bilstein and Maria Leptin

How does a developing organism direct cellular traffic during embryogenesis? These articles describe hunts for mutants that disrupt genes involved in fibroblast growth factor-dependent tracheal cell migration during embryogenesis in *Drosophila melanogaster*. The authors find a range of defects in terminal cells, including failure of lumen formation and reduced or extensive tracheal branching. Other mutations affect cell growth, cell shape, and cell migration.

Prediction of multilocus identity-by-descent, pp. 2307–2315

William G. Hill and Jules Hernández-Sánchez

The probability of identity-by-descent (IBD) is a fundamental quantity that has many applications in analysis of genotypes. Current theory for predicting its magnitude for multiple loci is either approximate or unwieldy. This article develops a fast and accurate chain-rule method for predicting IBD at large numbers of loci. The results can be used in quantitative trait loci mapping by predicting IBD of individuals at the locus from neighboring marker genotypes.

Linkage disequilibrium and recombination rate estimates in the self-incompatibility region of *Arabidopsis lyrata*, pp. 2357–2369

Esther Kamau, Brian Charlesworth and Deborah Charlesworth

Outbreeding of plants is encouraged by self-incompatibility genes. Balancing selection maintains many alleles of these genes (*S* alleles), and this affects diversity of nearby loci. This article models this linked neutral diversity in terms of the number of selectively maintained alleles and the distances from them. This approach is used to estimate the number of different functional *S* alleles, their turnover rate, and recombination rates between the *S*-locus region and other loci. The analysis suggests that there is a small region of very low recombination surrounding the *S*-locus.

A genetic analysis of the Drosophila *mcm5* gene defines a domain specifically required for meiotic recombination, pp. 2151–2163

Cathleen M. Lake, Kathy Teeter, Scott L. Page, Rachel Nielsen and R. Scott Hawley

Minichromosome maintenance (Mcm) proteins play roles in many essential cellular processes. The genetic analysis of the *mcm5* gene presented in this article demonstrates that Mcm5 has two distinct and separable functions in Drosophila: it is essential for mitotic DNA replication and it has a specialized function in meiotic recombination. These results strengthen the view that Mcm proteins have functions outside of DNA replication.

The Bro1-domain protein, EGO-2, promotes Notch signaling in *Caenorhabditis elegans*, pp. 2265–2277

Ying Liu and Eleanor M. Maine

A puzzling aspect of Notch signaling is the observation that endocytosis in the signaling cell promotes transduction of the signal in the receiving cell. The authors show that EGO-2, which contains a Bro1 domain characteristic of certain endosomal proteins, promotes Notch signaling in *Caenorhabditis elegans*. EGO-2 activity in the soma is critical for Notch signaling in the germline, consistent with a role for it in production of ligand by the signaling cell. The authors propose that EGO-2 functions in endosome-localized processes in the signaling cells that promote Notch signaling.

Genetic screens for *Caenorhabditis elegans* mutants defective in left/right asymmetric neuronal fate specification, pp. 2109–2130

Sumeet Sarin, M. Maggie O'Meara, Eileen B. Flowers, Celia Antonio, Richard J. Poole, Dominic Didiano, Robert J. Johnston, Jr., Sarah Chang, Surinder Narula and Oliver Hobert

This article describes comprehensive genetic screens that identify a large number of genes involved in an interesting cell-fate decision in the nematode *Caenorhabditis elegans*.

Cytotype regulation by telomeric *P* elements in *Drosophila melanogaster*: Interactions with *P* elements from M' strains, pp. 1957–1966

Michael J. Simmons, Jarad B. Niemi, Don-Felix Ryzek, Cecile Lamour, Joseph W. Goodman, Wojciech Kraszkiewicz and Ryan Wolff

and

Cytotype regulation by telomeric *P* elements in *Drosophila melanogaster*: Evidence for involvement of an RNA interference gene, pp. 1945–1955

Michael J. Simmons, Don-Felix Ryzek, Cecile Lamour, Joseph W. Goodman, Nicole E. Kummer and Peter J. Merriman

These two articles provide strong evidence that cytotype regulation of transposable *P* elements in Drosophila involves RNA interference (RNAi). *P* elements inserted at the left telomere of the *X* chromosome evoke the P cytotype, a maternally inherited condition that regulates the *P*-element family in the Drosophila germline. The authors show that this regulation is disrupted in flies heterozygous for mutations in *aubergine*, which encodes a protein involved in RNAi. It is likely that this RNAi mechanism is tied to the system that regulates the accumulation of retrotransposons at the ends of Drosophila chromosomes.

SYP-3 restricts synaptonemal complex assembly to bridge paired chromosome axes during meiosis in *Caenorhabditis elegans*, pp. 2015–2025

Sarit Smolikov, Andreas Eizinger, Kristina Schild-Prufert, Allison Hurlburt, Kent McDonald, JoAnne Engebrecht, Anne M. Villeneuve and Mónica P. Colaiácovo

and

Synapsis-defective mutants reveal a correlation between chromosome conformation and the mode of double-strand break repair during *Caenorhabditis elegans* meiosis, pp. 2027–2033

Sarit Smolikov, Andreas Eizinger, Allison Hurlburt, Eric Rogers, Anne M. Villeneuve and Mónica P. Colaiácovo

How do cells ensure that only aligned pairs of homologous chromosomes form synaptonemal complexes (SCs)? This article describes SYP-3, a coiled-coil protein that helps ensure that assembly of the SC occurs only in the appropriate context. Analysis of *syp-3* mutants provides insight into the relationship between chromosome conformation and the repair of meiotic double-strand breaks.