

ISSUE HIGHLIGHTS

Natural selection and the distribution of identity-by-descent in the human genome, pp. 295–308

Anders Albrechtsen, Ida Moltke and Rasmus Nielsen

These authors scan human populations for regions with excess identity-by-descent (IBD) sharing in order to identify regions in the human genome that have been under strong, very recent selection. The HLA region is by far the one with the most extreme signal, suggesting that much of the strong recent selection acting on the human genome has been immune related.

Gene duplication, gene conversion and the evolution of the Y chromosome, pp. 277–286

Tim Connallon and Andrew G. Clark

and

Y not a dead end: Epistatic interactions between Y-linked regulatory polymorphisms and genetic background affect global gene expression in *Drosophila melanogaster*, pp. 109–118

Pan-Pan Jiang, Daniel L. Hartl and Bernardo Lemos

The Y chromosome has been seen as an evolutionary dead end because of its non-recombining nature, but these two articles belie that view. JIANG *et al.* show that Y-by-background interaction effects modulate expression of many genes throughout the genome, some of which are important for male fitness, like those involved in pheromone detection and immune response. CONNALLON and CLARK show that gene conversion between duplicates is a powerful force for maintaining functional genes on the Y.

Accidental amplification and inactivation of a methyltransferase gene eliminates cytosine methylation in *Mycosphaerella graminicola*, pp. 67–77

Braham Dhillon, Jessica R. Cavaletto, Karl V. Wood and Stephen B. Goodwin

Repeat-induced point mutation (RIP) is a well-known genome-defense mechanism in fungi that targets repetitive sequences, especially transposable elements. This article shows that RIP can influence the evolutionary trajectory of duplicate genes and cause rapid, species-wide modification of gene function. It describes analysis of a recently amplified gene encoding cytosine methyltransferase in a wheat pathogen. All copies of this gene, including the original, were targeted and mutated by RIP, causing complete loss of cytosine methylation, most likely within the past 10,500 years.

The next generation of molecular markers from massively parallel sequencing of pooled DNA samples, pp. 207–218

Andreas Futschik and Christian Schlötterer

The authors compare individual sequencing with pooling designs for “next generation” DNA sequencing data. The focus is on population genetic inference, as well as SNP detection and allele frequency estimation. The article explores the conditions under which pooling provides better estimates at lower cost compared to individual sequencing. An accompanying commentary considers the limits of such pooling strategies.

QIP, a component of the vegetative RNA silencing pathway, is essential for meiosis and suppresses meiotic silencing in *Neurospora crassa*, pp. 127–133

Dong Whan Lee, Ryan Millimaki and Rodolfo Aramayo

and

QIP, a protein that converts duplex siRNA into single strands, is required for meiotic silencing by unpaired DNA, pp. 119–126

Hua Xiao, William G. Alexander, Thomas M. Hammond, Erin C. Boone, Tony D. Perdue, Patricia J. Pukila and Patrick K. T. Shiu

A segment of DNA not present on the homologous chromosome can trigger the silencing of both unpaired and paired homologous DNA segments. Such meiotic silencing was originally described in *Neurospora crassa*, but has since been observed in nematodes and mammals. These two articles reveal that QIP, an exonuclease that degrades the passenger strand of siRNA, is required for meiotic silencing and is essential for early sexual development. These observations establish QIP as a connection between the vegetative and the meiotic RNAi pathways of *Neurospora*.

Regulation of odor receptor genes in trichoid sensilla of the *Drosophila* antenna, pp. 79–95

Carson J. Miller and John R. Carlson

Each olfactory *receptor neuron* expresses only a few—and often only one—of a family of 60 *Odor receptor* genes. This article, describing a genetic dissection of the upstream regulatory regions of four odor receptor genes, illuminates the logic of the remarkable restriction of expression of this large gene family.

Miniature inverted-repeat transposable elements of *Stowaway* are active in potato, pp. 59–66

Masaki Momose, Yutaka Abe and Yoshihiro Ozeki

Miniature inverted-repeat transposable elements (MITEs) are prevalent in eukaryotic genomes. While MITEs are potential endogenous mutagens that could contribute to gene evolution, almost all of them are inactive. Active MITEs have been found only in rice. These investigators find that MITEs of dicotyledons are mobile. These active MITEs promise to be a useful tool for learning how these transposable elements have shaped genomes.

A pathogenic relationship between a regulator of the actin cytoskeleton and serum response factor, pp. 147–157

Angela M. Verdoni, Keaton J. Schuster, Brian S. Cole, Akihiro Ikeda, Winston W. Kao and Sakae Ikeda

Cell hyperproliferation, inflammation, and angiogenesis are central to the pathogenesis of numerous diseases. Mice deficient for actin depolymerizing factor (ADF) display these abnormalities in the cornea and provide a model to examine the basis of these maladies. The authors of this article show that aberrant expression of the serum response transcription factor (SRF) is responsible for development of a diseased cornea. This result reveals a new genetic relationship between a regulator of the actin cytoskeleton and SRF, and shows that abnormal SRF regulation can lead to development of several common pathologies.