

IN BRIEF

RECOMBINATION

Genome-wide analysis reveals novel molecular features of mouse recombination hotspots

Smagulova, F. *et al. Nature* **472**, 375–378 (2011)

These authors have developed a molecular approach for directly mapping the initiation sites for meiotic recombination in the mouse genome. The map reveals several interesting features of mammalian recombination hot spots, such as: the existence of a central hot-spot motif; a particular nucleotide skew; a preference to be occupied by a nucleosome; and the presence, in males, of testis-specific trimethylation of lysine 4 on histone H3. The new method can also be applied to other complex genomes.

POPULATION GENOMICSIdentification and functional validation of the novel antimalarial resistance locus *PF10_0355* in *Plasmodium falciparum*Van Tyne, D. *et al. PLoS Genet.* **7**, e1001383 (2011)

In this paper, genome-wide studies were applied to locate variants in the *Plasmodium falciparum* genome that confer resistance to antimalarial drugs. A 17,000-SNP array was used to characterize the genomic diversity in 57 parasite cultures and to identify loci showing signals of selection. This was combined with a genome-wide association study to map loci associated with resistance to 13 antimalarial drugs. Among the loci was a new candidate gene (*PF10_0355*) that, when overexpressed, confers resistance to the drug halofantrine.

GENE REGULATION

Ribosome-mediated specificity in Hox mRNA translation and vertebrate tissue patterning

Kondrashov, N. *et al. Cell* **145**, 383–397 (2011)

Ribosomes are generally considered to have essential but constitutive roles in gene expression; however, this study shows that ribosomal proteins can have regulatory functions. The authors showed that mutations in the gene encoding the mouse ribosomal protein L38 (RPL38) cause a range of developmental patterning defects. Analysis of *Rpl38* mutant embryos revealed no overall change in global protein synthesis, but showed that the translation of a group of Hox mRNAs is regulated by RPL38. Regulation by ribosomal proteins may be widespread, as indicated by distinct expression patterns of different ribosomal proteins in mice embryos.

METAGENOMICS

Enterotypes of the human gut microbiome

Arumugam, M. *et al. Nature* 20 Apr 2011 (doi:10.1038/nature09944)

This study increases the number of individuals and populations from which gut microbiomes have been sequenced. The authors surveyed the gut metagenomes of 22 European individuals and combined the findings with existing data from Japanese and American individuals. They found that the microbiome clusters into distinct phylogenetic groups (enterotypes), which do not reflect country or continent of origin, body mass index, age or gender. However, there were several robust correlations between specific functions encoded in the metagenome and host properties — findings that suggest potential links between gut microbiomes and human health.