

## IN BRIEF

**EVOLUTION**

Chimpanzee and human Y chromosomes are remarkably divergent in structure and gene content

Hughes, J. F. *et al. Nature* **463**, 536–539 (2010)

The authors report the finished sequence of the male-specific region of the Y chromosome (MSY) in chimpanzees. Comparing the MSY sequence of chimpanzees and humans reveals that far from being an evolutionarily stagnant region of the genome, as previously assumed, the two MSYs have in fact been diverging rapidly over the past 6 million years. Proposed contributing forces include species-specific mating behaviour, the role of MSY in sperm production and frequent ectopic recombination.

**POPULATION GENETICS**

The genetic signature of conditional expression

Van Dyken, J. D. & Wade, M. J. *Genetics* **184**, 557–570 (2010)

How does natural selection affect genes that are conditionally expressed and therefore not constantly visible to evolutionary forces? Using analytical methods and computer simulations, the authors show that the strength of selection on sequence variation is weakened to a similar degree in the presence of spatial or temporal conditional expression. The smaller the number of individuals expressing a gene, the higher the chance that a gene will accumulate deleterious mutations and lose phenotypic plasticity. The frequency of expression of genes should therefore be incorporated into studies of sequence variation.

**SPLICING**

Regulation of alternative splicing by histone modifications

Luco, R. F. *et al. Science* 4 Feb 2010 (doi:10.1126/science.1184208)

This paper shows for the first time a direct role for histone modification in modulating the outcome of alternative splicing. In human cells, the authors found that certain modifications — particularly trimethylation of lysine 36 at histone H3 (H3K36me3) — are enriched at alternative exons. The inclusion of these alternative exons is repressed by the polypyrimidine tract-binding protein PTB, and Luco *et al.* showed that the chromatin-binding protein MRC15 'reads' H3K36me3 and recruits PTB. Similar systems involving other histone marks might exist and help to control splicing in development and differentiation.

**GENETIC VARIATION**

Genotype and gene expression associations with immune function in *Drosophila*

Sackton, T. B., Lazzaro, B. P. & Clark, A. G. *PLoS Genet.* **6**, e1000797 (2010)

This study shows that polymorphisms in infection-induced genes have different effect sizes depending on their position in the immune pathway. The authors analysed the expression of immunity-related genes and bacterial load in *Drosophila melanogaster* infected with various strains of bacteria. Polymorphisms in pathogen-recognition genes — upstream components of immune signalling — were most significantly associated with bacterial load. The authors suggest that amplification of the effects of minor upstream variations through the immune signalling cascade can lead to substantial effects on organismal phenotype.