

IN BRIEF

COMPLEX TRAITS

Localization of type 1 diabetes susceptibility to the MHC class I genes *HLA-B* and *HLA-A*.

Nejentsev, S., Howson, J. M. M. *et al. Nature* 15 November 2007 (doi:10.1038/nature06406)

The major histocompatibility complex (MHC) locus is associated with many complex traits. This group mapped two new major susceptibility genes for type 1 diabetes to the MHC class I genes *HLA-A* and *HLA-B*, adding to established associations for two MHC class II genes. A total of 1,729 polymorphisms were typed in two independent studies involving thousands of cases and controls. The results have implications for understanding disease aetiology and preventing its development.

FUNCTIONAL GENOMICS

Analysis of sequence conservation at nucleotide resolution.

Asthana, S. *et al. PLoS Comput. Biol.* 14 November 2007 (doi:10.1371/journal.pcbi.0030254.eor)

A method for detecting single conserved nucleotides has been applied to 1% of the human genome. Most conserved non-coding nucleotides were shown to lie outside the stretches of conserved sequence that other methods would predict; furthermore, these positions are experiencing ongoing selection. Known functional regions were found to be enriched for both individual conserved nucleotides and short conserved sequences of less than 15 bp, suggesting that there are many small fragments of conserved non-coding sequence in the human genome.

MODEL ORGANISMS

Significant gene content variation characterizes the genomes of inbred mouse strains.

Cutler, G. *et al. Genome Res.* 7 November 2007 (doi:10.1101/gr.6754607)

Although they are less frequent than SNPs, because copy number variants (CNVs) affect whole stretches of sequence they may have a bigger phenotypic impact. Using array comparative genomic hybridization (CGH) on 42 Mouse Phenome Consortium priority strains, the authors identified more than 2,000 putative CNVs. Strains might therefore differ by hundreds of genes, with some complete or partial deletions and other multicopy genes. By comparing CNV number with the time of strain emergence, the authors demonstrate that structural genomic variation can develop surprisingly quickly within a species.

GENOMICS

Transposase-derived transcription factors regulate light signaling in *Arabidopsis*.

Lin, R. *et al. Science* **318**, 1302–1305 (2007)

These authors show that FHY3 and FAR1, both related to Mutator-like transposases, modulate signalling through the photoreceptor phytochrome A. By directly binding to the promoters of *FHY1* and *FHL*, the transposases activate transcription to ensure correct responses to far-red light. Phylogenetic and functional analyses imply that one or more MULE transposase genes gave rise to *FHY3*- and *FAR1*-related genes during angiosperm evolution, which allowed them to adapt to changing light conditions. The results also confirm that transposable elements can be a source of new transcription factors during evolution.