IN BRIEF

FUNCTIONAL GENOMICS

ChIP-Seq identification of weakly conserved heart enhancers

Blow, M. J. *et al. Nature Genet.* **42**, 806–810 (2010)

How far can sequence conservation predict regulatory elements? These authors surveyed the binding of an enhancer-associated protein across the genome in mouse embryonic heart tissue and identified more than 3,000 potential heart enhancers. Functional assays confirmed the accuracy of these predictions; however, most candidate heart enhancers were found to show less sequence conservation in vertebrates than known enhancers from other tissues. The authors conclude that, depending on the tissue, some sets of enhancers will be hard to predict on the basis of sequence conservation.

QUANTITATIVE TRAITS

Commercially available outbred mice for genome-wide association studies

Yalcin, B. *et al. PLoS Genet.* **6**, e1001085 (2010)

For a population to be useful for genome-wide association (GWA) studies, it must fulfil several requirements: allele frequencies must be high enough to ensure sufficient power; linkage disequilibrium must be low enough to allow fine-scale mapping; and the population must not be structured so as to cause spurious associations. This study assessed these criteria in 66 commercially available outbred mouse colonies and concluded that these populations have good potential for GWA studies. Supporting this conclusion, commercial mouse lines were used to map a molecular change that contributes to variation in an immunological trait.

COMPLEX DISEASE

A *trans*-acting locus regulates an anti-viral expression network and type 1 diabetes risk

Heinig, M. *et al. Nature* 8 Sep 2010 (doi:10.1038/nature09386)

Linking loci identified in genome-wide association (GWA) studies to biological functions is an important challenge in human genetics, and this study shows that a cross-species network-based approach can aid functional annotation. By integrating expression quantitative trait loci data sets from seven rat tissues with transcription factor expression and binding data sets, the authors identified an inflammation-associated gene network and the loci that regulate the network. Examining human gene expression and GWA data in the light of this network led them to a new type 1 diabetes susceptibility locus.

CANCER GENOMICS

Proteomic changes resulting from gene copy number variations in cancer cells

Geiger, T., Cox, J. & Mann, M. *PLoS Genet.* **6**, e1001090 (2010)

A key question in cancer genomics is how the many genetic changes that occur during transformation affect the cellular phenotype. These authors used a global proteomics approach to assess the impact of copy number variation on protein expression for 6,735 proteins in a breast cancer cell line. They show that amplifications of oncogenes, but not adjacent amplified genes, often lead to increased protein expression, suggesting that only some genomic changes have a substantial influence on the phenotype of cancer cells.