IN BRIEF

DEVELOPMENT

Distinct roles and regulations for *Hoxd* genes in metanephric kidney development.

Di-Poï, N. *et al. PLoS Genet.* **3**, e232 (2007)

A careful analysis using engineered mouse mutations has allowed the authors to dissect the role of genes in the *Hoxd* cluster — one of four mammalian *Hox* clusters — in kidney development. Specific *Hoxd* genes are involved in either the growth or organization of the kidney, and mutations in these genes cause growth defects or diseases that affect the corresponding developmental step. Interestingly, the function of a *Hoxd* gene in kidney morphogenesis is collinear with the position of the gene in the cluster.

GENE REGULATION

Polymorphic Y chromosomes harbor cryptic variation with manifold functional consequences.

Lemos, B. *et al. Science* **319**, 91–93 (2008)

Using isogenic fly strains that only differed by the origin of their Y chromosomes, the authors demonstrate that polymorphic variation on the Y chromosome affects the expression of X-linked and autosomal genes. The common feature of these genes is that they are associated with male functions such as spermatogenesis and temperature sensitivity. Collectively, these results provide a mechanistic explanation for Y-linked adaptive phenotypic variation, and raise the question of how widespread such regulatory variation might be.

GENOMICS

Genome-wide analysis of transcript isoform variation in humans.

Kwan, T. *et al. Nature Genet.* 13 January 2008 (doi:10.1038/ng.2007.57)

Using an exon tiling array covering 17,897 human genes, Kwan *et al.* performed a genome-wide analysis of common genetic variation that affects the expression of different transcript isoforms. They found that splicing variation and alternative 5′- and 3′-UTR usage contributes to differential gene expression in 55% of the genes analysed. Thus, variation that is associated with transcript processing should be considered alongside SNPs and copy-number variants to gain a fuller appreciation of the genetic basis of human variation.

DEVELOPMENT

Predicting expression patterns from regulatory sequence in *Drosophila* segmentation.

Segal, E. *et al. Nature* 2 January 2008 (doi:10.1038/nature06496)

This new mathematical model provides a quantitative explanation of the expression of developmental genes. The model takes the expression levels of specific transcription factors, computes their occupancy on a given DNA sequence and then predicts the expression of nearby genes. Parameters were set using data from *Drosophila melanogaster* segmentation, and the model was validated on data from the related species *Drosophila pseudoobscura*. The model predicted data with reasonable accuracy, although this could be improved by accounting for nucleosome occupancy and non-additive interactions between transcription factors.