IN BRIEF

EVOLUTION

Robustness and plasticity in network evolution

This study describes a new computational approach for studying the evolutionary rewiring of transcriptional regulatory networks by changes in the targets of transcription factors. By applying the approach to the study of 88 transcription factor target binding motifs in 23 species of ascomycete fungi, the authors found that although the biological functions of regulatory networks are conserved, there is considerable plasticity in transcription factor target genes. This suggests a model in which there is selection to maintain the overall function of transcription factors but plasticity with respect to specific targets.

ORIGINAL RESEARCH PAPER Habib, N. *et al.* A functional selection model explains evolutionary robustness despite plasticity in regulatory networks. *Mol. Syst. Biol.* **8**, 619 (2012)

EPIGENETICS

Asymmetric histone distribution in stem cells

Stem cells often divide asymmetrically both to self-renew and to produce daughter cells that enter differentiation. However, it is not known how epigenetic information is transmitted in such divisions. Here the authors tracked 'old' histones (those that were in place before mitosis) and 'new' histones using a system that labelled histone H3 with a different colour before and after heat shock in fruitfly male germ stem cells (GSCs). They found that old H3 (but not the variant histone H3.3) is preferentially distributed to the renewed GSC rather than to the daughter gonialblast cell; this may enable stem-cell-specific epigenetic information to be retained.

ORIGINAL RESEARCH PAPER Tran, V. *et al.* Asymmetric division of *Drosophila* male germline stem cell shows asymmetric histone distribution. *Science* **338**, 679–682 (2012)

COMPLEX DISEASE

Family history versus SNPs for disease predictions

Chuong *et al.* used a theoretical model to compare the ability of family history and SNP-based methods to predict the risk of complex disease. Family-history-based methods were often more effective at predicting risk for more common heritable diseases, such as coronary artery disease, whereas SNP-based approaches had more power to predict less common disorders. The authors also highlight the difficulty in predicting the risk of many diseases using either method alone and advocate that these tests are complementary.

ORIGINAL RESEARCH PAPER Chuong, B. D. *et al.* Comparison of family history and SNPs for predicting risk of complex disease. *PLoS Genet.* **8**, e1002973 (2012)

GENOME EVOLUTION

Orderly gene diversification

Gene diversification is thought to occur largely by duplication followed by functional divergence. Näsvall *et al.* tested whether functional changes might also precede duplication and propose an innovation–amplification–divergence (IAD) model. HisA and TrpF are bacterial enzymes used for the synthesis of histidine and tryptophan, respectively. The authors studied the evolution of multiple lineages of *trpF*-deficient *Salmonella enterica* under amino-acid-limiting conditions. They found that *hisA* evolved dual functionality to act in both the histidine and tryptophan biosynthetic pathways, followed by gene amplification and specialization of the gene copies. Thus, IAD may underlie some evolutionary processes.

ORIGINAL RESEARCH PAPER Näsvall, J. *et al.* Real-time evolution of new genes by innovation, amplification, and divergence. *Science* **338**, 384–387 (2012)