IN BRIEF

RNA WORLD

MicroRNA target prediction across seven *Drosophila* species and comparison to mammalian targets.

Grün, D. *et al. PLoS Comp. Biol.* **1**, e13 (2005)

Understanding the biological function of microRNAs relies on identifying their targets. These authors used a new computational algorithm (PicTar) and comparative analysis to predict microRNA targets across seven *Drosophila* species. This extensive set of predictions — enriched by a comparison with vertebrates — provides functional information on microRNAs, their evolutionary conservation and the regulatory relationships between them. The predictions are available at http://pictar.bio.nyu.edu

GENOME EVOLUTION

Gene complexity and gene duplicability.

He, X. & Zhang, J. *Curr. Biol.* **15**, 1016–1021 (2005)

The authors examined the complexity of duplicated genes in yeast. On average, these genes were more complex than singletons, in terms of size, functional domains and *cis*-regulatory elements. This is independent of factors that are known to influence the propensity of genes to be duplicated, indicating that complex genes are more likely to be retained after duplication. Duplication therefore seems to increase both genome size and gene complexity, two important contributors to genome complexity.

GENOMICS

Genome-scale identification of nucleosome positioning in *S. cerevisiae*.

Yuan, G.-C. *et al. Science* 16 June 2005 (doi:10.1126/science.1112178)

Nucleosome positioning affects DNA packaging and gene expression. The authors developed a tiled microarray approach to measure nucleosome positions on a genomic scale, based on the susceptibility of the linker DNA to micrococcal nuclease. They report that Pol II promoters and most occupied transcription factor binding motifs are nucleosome-free, indicating that nucleosome positioning determines transcription factor access on a global scale.

RNA INTERFERENCE

RNA-interference-directed chromatin modification coupled to RNA polymerase II transcription.

Schramke, V. *et al. Nature* 19 June 2005 (doi:10.1038/nature03652)

RNA polymerase II is required for RNAi-dependent heterochromatin assembly.

Kato, H. *et al. Science* 9 June 2005 (doi:10.1126/science.1114955)

These papers highlight the role of RNA polymerase II (Pol II) in RNAi-dependent processes. The first group found that Pol II associates with Ago1, a component of the RISC–RITS complex, and its transcribed targets, indicating that RNAi-directed chromatin modification is coupled to transcription. The second paper shows that Pol II is localized to the pericentromere, and couples pericentromeric transcription with siRNA processing and heterochromatin assembly.

URL for WEB

PicTar

http://pictar.bio.nyu.edu