

Opening promoters to flexible expression

In a simple world, nucleosomes would behave as roadblocks to transcription, to be lifted whenever access by RNA polymerase was required. A paper that surveys the pattern of nucleosome occupancy at yeast promoters shows that nucleosome patterns might, in fact, help to modulate gene expression, potentially determining how well a gene responds to internal and external signals.

Relying on a recently generated map of nucleosome occupancy across the genome of *Saccharomyces cerevisiae*, Tirosh and Barkai correlated the positioning of nucleosomes in promoter regions with the magnitude of gene expression in response to various conditions, and with the plasticity of expression from each gene. As expected, the more nucleosomes there were in the 150 bp region upstream of the transcription start site (TSS), the lower the level at which a gene was expressed; surprisingly, however, higher occupancy also correlated with higher plasticity, regardless of whether the plastic change involved up- or downregulation of expression.

Even though the overall level of transcription depended on the absolute number of nucleosomes across the promoter, plasticity was determined instead by their precise arrangement. A survey of nucleosomes in the region close (within 150 bp) or distal (from 150–400 bp) to the TSS revealed two classes of promoter: those with less plastic expression were more likely to have low nucleosome occupancy near the TSS and higher occupancy more distally, whereas the more plastic promoters displayed high occupancy close to the start site and more even distribution elsewhere. A strikingly similar connection between promoter structure and transcriptional plasticity was seen in six human cell lines. Promoters of the more plastic gene class in humans and yeast shared other properties — such as high nucleosome turnover, which might facilitate access by transcription factors to promoters.

This level of conservation echoes the conclusions of an earlier paper, by Mavrich, Jiang and colleagues, who generated a high-resolution nucleosome map of *Drosophila*

melanogaster and showed that the positioning of nucleosomes relative to TSSs is conserved with yeast.

Our view of gene expression now has an added dimension, reflecting the fact that fundamental gene properties, such as a propensity for expression variation, can be hard-wired in promoters by adaptive and conserved epigenetic mechanisms.

Tanita Casci

ORIGINAL RESEARCH PAPERS Tirosh, I. & Barkai, N. Two strategies for gene regulation by promoter nucleosomes. *Genome Res.* 30 Apr 2008 (doi:10.1101/gr.076059.108) | Mavrich, T. N. & Jiang, C. *et al.* Nucleosome organization in the *Drosophila* genome. *Nature* 13 Apr 2008 (doi:10.1038/nature06929)

FURTHER READING Henikoff, S. Nucleosome destabilization in the epigenetic regulation of gene expression. *Nature Rev. Genet.* 9, 15–26 (2008)

