

EPIGENETICS

Taking a position on regulatory diversity

Epigenetic differences between individual cells, populations or species are established contributors to differences in gene expression. Whereas previous work has focused mainly on the contribution of proteins that act in *trans* to epigenetic differences, studies using yeast now reveal that differences in nucleosome positioning that contribute to variability and divergence in gene expression can be encoded in the genome.

Choi and Kim looked at promoters of yeast genes that show variability in expression in response to a range of factors. Using data from a previously generated genome-wide map of nucleosome occupancy, they found that these genes have a nucleosome positioned at a site that is crucial for transcriptional regulation and that is nucleosome free in most other

genes. The authors propose that there is variable occupancy at this position, which in turn gives rise to variable expression. Several computational models predicted this position on the basis of sequence, providing evidence that the positioning of this nucleosome is encoded in the genome. Furthermore, the promoters of variably expressed genes are more likely to contain sequences that promote DNA bending and certain periodic dinucleotide patterns — both of which are known to be common in preferred nucleosome binding sites.

In a second study, Field and colleagues used a combination of *in vitro* nucleosome reconstitution and a sequence-based computational model to measure nucleosome occupancy in the promoter regions of a range of yeast species. In general,

growth-related genes that are active under normal conditions had promoters that encoded nucleosome exclusion, whereas the promoters of normally inactive genes encoded higher levels of nucleosome occupancy. Importantly, sets of genes that show divergent expression between two species — such that they are normally active in one species but inactive in the other — consistently show opposite patterns of DNA-encoded promoter nucleosome occupancy. The authors propose that sequence changes that alter nucleosome positioning contribute to evolutionary changes in the responsiveness of genes to growth conditions. The extent to which this applies in other organisms and for other gene classes will be an exciting avenue for future investigation.

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IMAGE SOURCE

ORIGINAL RESEARCH PAPERS Choi, J. K. & Kim, Y. J. Intrinsic variability of gene expression encoded in nucleosome positioning sequences. *Nature Genet.* 1 Mar 2009 (doi:10.1038/ng.319) | Field, Y. *et al.* Gene expression divergence in yeast is coupled to evolution of DNA-encoded nucleosome organization. *Nature Genet.* 1 Mar 2009 (doi:10.1038/ng.324)

FURTHER READING Jiang, C. & Pugh, B. F. Nucleosome positioning and gene regulation: advances through genomics. *Nature Rev. Genet.* 10, 161–172 (2009)