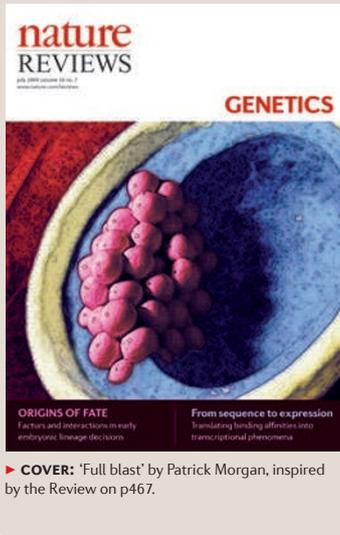




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Controlling the timing, location and level of gene expression is essential for the regulation of biological processes, from cellular responses to external cues to the patterning of a complete organism. Despite huge progress in dissecting transcriptional mechanisms, fundamental questions remain about the different levels at which transcription is regulated. This month, three Reviews consider a selection of these questions.

In the latest addition to our series of articles on Modelling, Segal and Widom (p443) explore how transcriptional information is encoded in DNA regulatory sequences. Protein binding to these regions has long been known to dictate how genes are expressed, but it has been difficult to move from descriptions to predictions of transcriptional output. These authors present a framework that could form the basis of future quantitative models.

To understand transcription *in vivo* we also need to look at its physical context — inside a crowded nucleus in which many genes are being transcribed at once. The observation of discrete foci of transcriptional activity has suggested that nuclear substructures might help to organize and control gene expression. But, as Bickmore and Sutherland discuss in the Review on p457, the importance of these 'transcription factories' remains a hotly debated topic.

At the level of fate decisions in embryogenesis, there is ongoing controversy over what determines the transcriptional programme. On p467, Zernicka-Goetz and colleagues weigh up models of control, which integrate transcription factors, chromatin modifications and positional signals.

This issue also includes the second of our interviews with the 2009 March of Dimes prize winners (p430); this month's interview is with Louis Kunkel.

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on acid-free paper