

EDITORS' PREFACE

The current accumulation of complete genome sequences of bacteria is showing that, as genomes increase in size, the number of associated regulatory genes increases exponentially. That is, the more genes a bacterium has, the greater the need to regulate which genes are on or off and so tailor the bacterial properties to the prevailing circumstances, or selected niche. Thus, if we are to make sense of the growing genomic sequence resources, we need to understand not only the genetic content but also the regulatory networks controlling its expression. This symposium volume aims to help readers do just that.

The last time bacterial gene expression was the sole subject of an SGM symposium was '*Regulation of Gene Expression – 25 Years on*' in 1986, which celebrated 25 years of the operon model of Jacob and Monod. The operon model has proved to be a seminal concept in our understanding of gene expression. This symposium aims to show that, in addition to transcription initiation, there are many other levels at which gene expression can be regulated in bacteria. For example, in the low-G + C ratio Gram-positives, regulated anti-termination of transcription is as common a mode of regulation as regulation of the initiation of transcription.

The title of the symposium is meant to reflect the different levels at which gene expression can be controlled in bacteria. Signals and switches activate expression of individual genes and operons. Individual genes and operons can be co-ordinately expressed to form regulons. Activation of expression of one gene can lead to activation of other genes that, in turn, activate still other genes to form cascades of gene expression.

David A. Hodgson
Christopher M. Thomas