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## Preface

Genomic imprinting is the process by which gene activity is regulated according to parent of origin. Usually, this means that either the maternally inherited or the paternally inherited allele of a gene is expressed while the opposite allele is repressed. The phenomenon is largely restricted to mammals and flowering plants and was first recognized at the level of whole genomes. Nuclear transplantation experiments carried out in mice in the late 1970s established the non-equivalence of the maternal and paternal genomes in mammals, and a similar conclusion was drawn from studies of interploidy crosses of flowering plants that extend back to at least the 1930s. Further mouse genetic studies, involving animals carrying balanced translocations (reviewed in Chapter 3), indicated that imprinted genes were likely to be widely scattered and would form a minority within the mammalian genome. The first imprinted genes were identified in the early 1990s; over forty are now known in mammals and the list continues steadily to expand.

*Genomic Imprinting: Methods and Protocols* aims to collect protocols that have been applied to the study of imprinting or imprinted genes. Many of the protocols are based on more widely used embryology or molecular biology techniques that have been adapted for imprinting research. All of the included methods remain gainfully employed in either (or both) the discovery or analysis of imprinted genes. Chapter 1 describes the nuclear transplantation methods, first used in the 1970s, for the generation of mouse embryos with genomes of entirely maternal or entirely paternal origin. The first five chapters are specific to the mouse, though some of the principles could be applied to other species. For instance, the techniques described in Chapters 4 and 5 for generating transgenic mice using large fragments of genomic DNA have resulted in several examples of the faithful reproduction of imprinted gene expression at ectopic loci. The first few imprinted genes have recently been identified in plants and it will be interesting to know whether the imprinting of these genes can be similarly reproduced within plant transgenes.

The majority of protocols describe molecular techniques and most of these allow examination of gene structure or expression in an allele-specific manner, which is an essential aspect of most imprinting studies. Protocols are

included for identifying imprinted genes (Chapters 6–8), for analyzing imprinted gene expression (Chapters 9–12), for the study of DNA methylation and methylation-sensitive DNA-binding proteins (Chapters 13–20), and for examining chromatin structure (Chapters 21–24). The final chapter is a review of genomic imprinting in plants. Although imprinting must have arisen independently in plants and animals, the available evidence suggests that the imprinting mechanisms in these species may share common features, such as the involvement of DNA methylation in distinguishing maternal and paternal alleles. Thus, the molecular methods that are already extensively used to study mammalian imprinted genes will surely find even wider employment as the genomic imprinting field continues to expand.

I thank all of the authors for their outstanding contributions to this volume. On behalf of us all I extend the hope that this effort to make these methods accessible will prove useful to genomic imprinting aficionados everywhere.

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