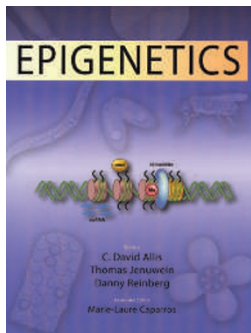


Epigenetics for big and small



Epigenetics

Edited by C. David Allis, Thomas Jenuwein & Danny Reinberg
Associate editor: Maire-Laure Caparros

Cold Spring Harbor Press 2007
£85/\$150

Reviewed by Asifa Akhtar

The availability of the human genome sequence has opened new avenues to broaden our understanding of human biology. Certainly, this information is key to facilitating examination of the molecular similarities and differences between individuals in the normal and diseased state. However, it is also becoming increasingly evident that knowledge of the DNA sequence of chromosomes does not completely reflect the genetic complexity of an organism. In recent years, we have seen exciting developments in the field of epigenetics, which promise to answer some of the open questions in the post-genomic era, such as why two neighbouring cells with identical genotypes can have different phenotypes.

Epigenetics is the first textbook in this field that is dedicated towards current understanding of epigenetic phenomena. Thanks to the remarkable efforts of its editors David Allis, Thomas Jenuwein, Danny Reinberg and the associate editor Marie-Laure Caparros, the book, which aims to educate the reader about the various biological processes that form the basis of epigenetic research, comes at an opportune time.

Conrad Waddington was the first to coin the term epigenetics in the early 1950s, which referred to the phenotypic changes that occur in the cells of an organism during development without a corresponding change in genotype. More recently, epigenetics has been defined as the study of mitotically and/or meiotically heritable changes in DNA. Cellular DNA is not “naked”, but is compacted into chromatin by histones. Interestingly, wrapping of histones around DNA not only compacts DNA, but also imparts regulatory potential. Chromatinized DNA can be made accessible in a variety of ways, such as ATP-dependent chromatin-remodelling complexes, histone variants and DNA methylation. Yet another way to remodel chromatin is via the amino-terminal tails of histones, which can be post-translationally modified such that the chromatin fibre can become more or less accessible to nuclear factors. Over the past decade, there has been an explosion in the identification of the number and variety of post-translational modifications that occur on histone tails, including acetylation, methylation, phosphorylation, ubiquitination, sumoylation, ribosylation and isomerization. Interestingly, just like histones, most of the histone modifications are also evolutionarily conserved across

species, suggesting a fundamental role in a number of cellular events. The rich plethora of these modifications, the identification of proteins that bind to some of these modifications and the diversity of the functional output associated with various modifications have paved the way for a more molecular definition of epigenetics. Epigenetics is defined by Allis, Jenuwein and Reinberg in the book as “the sum of the alterations to the chromatin template that collectively establish and propagate different patterns of gene expression (transcription) and silencing from the same genome”. Although it is clear that DNA methylation is epigenetic in the classical meaning of the term, it remains to be seen how many of the histone modifications will follow this rule.

From a historical perspective, epigenetics has been viewed as a collection of a number of interesting phenomena, such as position effect variegation in *Drosophila*, X inactivation and imprinting in mammals, or paramutation in maize. These processes, although unique in their own right, have intriguing similarities at the molecular level, especially when it comes to certain histone modifications. These disparate observations have brought together scientists from various fields, such as RNA interference, heterochromatin formation, prion proteins and researchers working on different model organisms. From this perspective, the book captures the essence of the field very well. It begins with historical accounts describing the evolution of the field in chapters 1 and 2. This provides the reader with an immediate perspective on the progress made over the past 50 years. The editors provide an overview of how they envision present and future progress of epigenetics in chapter 3. An important strength of the book is the recognition and acknowledgement that an understanding of key epigenetic principles has come from studying model organisms. Compilation of information generated across species has made the field move forward by leaps and bounds. As a reflection of this appreciation, chapters 4–9 focus on studies in model organisms, including fungi, ciliates, flies and plants. This is followed by an in-depth analysis of some of the classical epigenetic phenomena, such as position-effect variegation, dosage compensation in flies, worms and mammals, DNA methylation and imprinting in mammals in chapters 10–19. Chapters 20–22 discuss stem-cell pluripotency, lymphopoiesis and nuclear transplantation and reprogramming processes, which are intimately linked with epigenetic regulation. Finally, the last two chapters address the close relationship between genomes and epigenomes with diseases such as cancer.

In addition to the cutting-edge epigenetic research that is highlighted in this book by eminent scientists in the field, the summaries at the beginning of each chapter, and the multiple tables and colourful illustrations used throughout the book will prove useful in guiding the reader through a discussion of complex biological processes. Undoubtedly, some of these illustrations will be widely used by students and teacher of epigenetics. It is evident that the importance of epigenetics has become widely recognized and this book will be an excellent read for beginners as well as experts in this field.

COMPETING FINANCIAL INTERESTS

The author declares no competing financial interests.

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