
Preface

DNA is the key to the inheritance of the genetic information in living organisms, and the mechanism of duplication of double-stranded DNA is arguably the molecular process with the widest appreciation in the general public. However, almost since their discovery, it was known that the nucleobases could be further modified by the addition of methyl groups. DNA methylation patterns are often heritable, leading to their classification as epigenetic mark. We now know that DNA methylation has very important functions in almost all species, ranging from bacteria to higher and low eukaryotes and plants. Moreover, changes in DNA methylation are associated with the development of human diseases, and the field of epigenetics is currently exploding with connections to nutrition, behavior, and transgenerational inheritance of traits. The comprehension of the relevance of DNA methylation in various fields of biology and medicine has also brought a lot of attention to the enzymes responsible for the transfer of methyl group to DNA, the so-called DNA methyltransferases (MTases), which are the key subject of this book.

We both have studied DNA methyltransferases for many years, attracted by their complicated mechanisms, beautiful structures and medical relevance; actually, these enzymes faithfully accompanied us through almost our entire career. Therefore, we felt very honored and excited by the offer from *Springer* to edit a book on these fascinating enzymes and happily took up this challenge. This book on DNA methyltransferases provides a compilation of chapters that recapitulate and update many of the developments made in the field, including past achievements and future challenges. Many of the chapters were written by renowned experts, who themselves made central contributions to the developing field.

The introduction of the book (Chap. 1) by Jurkowska and Jeltsch recaptures the development of the field over the past more than 60 years, highlighting and conceptualizing many critical key discoveries. In Chap. 2, Motorin et al. place DNA methylation and DNA MTases into the larger subject of nucleic acid modification focusing on the alkylation of pyrimidines in RNA and DNA. Chapter 3 written by Casadesus describes bacterial DNA methyltransferases and the important roles of DNA methylation in bacteria. The next four chapters cover DNA methylation and DNA MTases in mammals. Tajima et al. focus in Chap. 4 on the structural aspects of the mammalian DNA MTases, and Jurkowska and Jeltsch describe their enzymatic properties and regulation in cells (Chap. 5). In Chap. 6, Dan and Chen review the important contributions of genetic studies to our current understanding

of DNA methylation and DNA MTases. Chapter 7 by Lakshminarasimhan and Liang recapitulates the role of DNA methylation in cancer. Next, structures and mechanisms of plant DNA methyltransferases are described in Chap. 8 written by Du, and in Chap. 9, Wedd and Maleszka present the role of DNA methylation in honeybees as an example for DNA methylation in lower eukaryotes. The ongoing progress of science in the field is illustrated by the recent discovery of adenine-N6 methylation in several higher eukaryotes and the discussion whether this mark, still controversial in some cases, functions as an epigenetic signal, as described in Chap. 10 by O’Brown and Greer. The next chapters focus on the pathways of DNA demethylation (Chap. 11 written by Dean) and the structure and mechanism TET enzymes, which are involved in this reaction (Chap. 12 contributed by Yin and Xu). In Chap. 13, Shimbo and Wade summarize the biological processes involved in DNA methylation readout, and Hong and Cheng review base flipping as a basic mechanism involved in setting, reading, and erasing DNA methylation in Chap. 14. The last part of the book is devoted to the technological developments. In Chap. 15, Tost reviews current methods to study DNA methylation. Based on this, Lopez et al. provide an overview over the development and potential application of DNMT inhibitors in cancer and other diseases (Chap. 16), and Stolzenburg et al. describe emerging approaches to edit DNA methylation patterns in a targeted manner (Chap. 17). Finally, in Chap. 18, Laurino et al. summarize achievements in the design of DNA methyltransferases, and in Chap. 19, Tomkuvienė et al. describe applications of DNMTs as molecular biology tools to label DNA.

We anticipate many more years of exciting research focusing on DNA methylation and DNA MTases, with many new and groundbreaking discoveries to come. The aim of this book is to serve as a rich and reliable source of information for specialist scientists, but also for students and researchers entering the field, providing them with a solid fundament for future work. At the same time, it should help researchers to get into this fascinating subject, allowing them to catch up with the current level of knowledge and learn about recent trends.

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