

Editorial

A special issue on ‘epigenetics’

The term epigenetics was coined by Waddington CH in 1940s as a portmanteau of the words *genetics* and *epigenesis* to describe the differentiation of cells from their initial totipotent state in embryonic development. With the explosion of knowledge in this field in the recent 10 years, epigenetics is now typically defined as the study of heritable changes in gene expression that are not due to changes in the nucleotide sequence of DNA. The field of epigenetics is revolutionizing our understanding of biology and medicine. Recent studies have been focusing on the mechanisms of epigenetic regulation, including DNA methylation, histone modification, chromatin remodeling, etc., and on their contributions to development and diseases. In this special issue, nine review articles written by prominent experts in this field are put together, trying to give our readers a broad picture of epigenetics and a summary of most recent research progress in this field. Here is a preview of what you will find in this issue.

Epigenetic changes are clonally inheritable from mother cell to daughter cells in order to maintain the cell identity; however, the molecular mechanisms remain largely unknown. Qing Li and Zhiguo Zhang have summarized the recent studies of the maintenance of heterochromatin and epigenetic inheritance during DNA replication and discussed the roles of DNA replication factors and histone chaperones in heterochromatin silencing.

The epigenetic regulations at the chromatin level include DNA methylation, histone modification, ATP-dependent chromatin remodeling, and the recently discovered non-coding RNAs. Several articles in this issue are focusing on these issues. Xiaobing Shi and his colleagues have briefly reviewed all the enzymes known to regulate histone lysine methylation, and have further summarized the current knowledge of lysine methylation of non-histone proteins and its role in regulating proteins involved in diverse cellular processes. Yuanyuan Li and Haitao Li have described the latest progresses of plant homeodomain (PHD) finger, one of the reader modules of the histone lysine methylation, especially from the perspective of structural biology, and highlighted the versatile binding features and biological significance of PHD fingers. Wenqiang Yu and his colleagues have depicted the genome-wide expression of non-coding RNA (ncRNA) according to genome location

and discussed how ncRNAs guide and recruit chromatin modification complex to specific loci of genome to modulate gene expression by affecting chromatin state.

Epigenetic mechanisms are crucial for normal development and aberrant epigenetic programming has been linked to the occurrence of diseases. A series of reviews in this issue discussed this topic. Bo Wen and his colleagues have highlighted recent advances on chromatin signatures in pluripotent stem cells and differentiated cells, focusing on large chromatin domains which affect higher-order chromatin and nuclear architecture. Jiang Wu has summarized the functions of BAF subunits, a group of prototypical ATP-dependent chromatin remodeling complexes, during mammalian development and in the progression of various cancers, and has discussed the mechanisms underlying the functional diversity and specificities of BAF complexes. Jing Huang and his colleagues have described the potential biological functions of protein lysine methyltransferases/demethylases in cancers, and have also discussed the potentials and caveats of targeting histone methylation with the inhibitors to treat cancers. Xiangjiao Yang and his colleagues have provided an overview of histone acetylation, listed the major groups of histone acetyltransferases and deacetylases, and covered in relatively more detail the recent studies that suggest the links of these enzymes to gastrointestinal carcinogenesis. Sean M. Wu and his colleagues have discussed the epigenetic regulation of embryonic cardiac development and their implications and contribution to congenital heart diseases.

In summary, this special issue covers a broad, although not complete, aspect of epigenetic regulation mechanism and biological function. We sincerely hope that our readers will get the introductory knowledge of epigenetic as well as the up-to-date information in this rapidly progressing field from this collection of reviews.

Finally, we would like to thank all the authors of this issue for their fine contributions to this journal. We are also grateful to Dr Xiaobing Shi, Dr Xiangjiao Yang, and Dr Jing Huang for their recommendations. We really appreciate all the reviewers, Prof. Taiping Chen, Prof. Mridul Mukherji, Prof. Ching-Pin Chang, Prof. Rho H. Seong, Prof. Bin Zhou, Prof. Joseph Wu, Prof. Guohong Li, Prof. Renjie Jiao, Prof. Takayoshi Suzuki, Prof. Jia Fang, Prof.

Patrick M. Woster, Prof. Joya Chandra, Prof. In-Hyun Park, Prof. Xiaohua Shen, Prof. DeLong Liu, Prof. Lingling Chen, Prof. Andrew Xiao, Dr Kevin C Wang, and Dr Yu Zhang, for their critical comments which help us to present these excellent review articles to our readers. We hope that the readers will enjoy this special issue and many more

articles on the fascinating topic of epigenetics in future issues of *Acta Biochimica et Biophysica Sinica*.

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