EDITORIAL

The Critical Role of Epigenetic Regulation in Developmental Programming of Higher Organisms

In the last years, research efforts have been focused on the understanding of the evolutionary mechanisms linked to the control of the transcriptional activity and developmental processes. The study of developmental mechanisms has advanced significance over the last decade, and developmental programs that have undergone evolutionary specialization among species have recently been characterized. Epigenetics, which includes analysis of DNA methylation, histone code (*i.e.*, histone methylation/demethylation, acetylation/deacetylation, phosphorylation, ubiquitination, *etc.*), noncoding RNA (ncRNA) pathways and 3D genome organization, has made important progress towards understanding of the complexity of developmental processes. Epigenetic factors involved in the regulation of development are increasingly being identified in organisms ranging from yeast to humans, and it has been shown that epigenetic phenomena such as genomic imprinting, paramutation and transgenerational epigenetic inheritance are often closely linked to these processes. The main objective of this thematic issue is to present current research into the epigenetic mechanisms involved in developmental programming, their evolution and their roles in disease states.

In the first article of this issue, Vaschetto and Ortiz [1] provide an opinion on the role of the duplication of sequence in the mechanisms of gene regulation and its importance in genome evolution and developmental programming. By the analysis of information based on master developmental genes (*i.e.*, HOX genes), repetitive ribosomal DNA (rDNA) arrays, sequences encoding noncoding RNAs (ncRNAs,) and distinct classes of Transposable Elements (*i.e.,* MITEs, SINEs, R2, *etc.*), the authors explain how sequence duplication may function as an evolutionary strategy to regulate the transcriptional expression at genome-level. In the next article, Csaba [2] provides a review on the mechanisms associated with the hormonal imprinting, an epigenetic phenomenon that involves the first encounter between a hormone and the target receptor, which occurs in the perinatal period. Remarkably, Dr. Csaba postulated the theory of hormonal imprinting [3], and his laboratory has made important research efforts to understand the faulty hormonal imprinting in the Developmental Origin of Health and Disease (DOHaD).

In the third article, Şanlı and Kabaran [4] examine the consequences of the maternal obesity and maternal overnutrition on fetal programming. In this article, the authors analyze how maternal obesity is associated with epigenetic modifications that influence fetal growth and underlie metabolic diseases during adulthood. Next, Lecoutre *et al.* review the mechanisms for which maternal obesity may induce adipose tissue remodeling of offspring and explore the role of the epigenetic inheritance in developmental programming of obesity [5].

In the next article, Alsayegh *et al.* [6] examine the potential of pluripotent stem cells (PSCs) as *de novo* source of Hematopoietic Stem Cells (HSCs), and the mechanism of regulation of HOX and GATA factors in hematopoiesis. In this review, the authors also evaluate the relationships existing between the HOX and GATA master regulators and microRNA (miRNA) pathways. Lastly, Kadayifci *et al*. [7] discuss the importance of the epigenetic mechanisms for the nutritional programming of Type 2 Diabetes Mellitus and their roles in the developmental origin of this worldwide chronic disease.

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