Tentative Outline

Special Issue for "Current Genomics"

(The critical role of epigenetic regulation in developmental programming of higher organisms)

Guest Editor: Dr. Luis María Vaschetto

Aims & Scope:

Recent advancements in epigenetics represent key milestones to us in order to understand how genetic mechanisms underlie the basis of complex biological processes. Different research areas including, among others, non-coding RNA, DNA methylation, histone code, genome architecture, etc., are providing an exponentially growing amount of insights into the relationships between the epigenetic mechanisms and evolutionary conserved signaling pathways in both animal and plant systems, thereby providing a more realistic vision of the developmental programs in these species. This thematic issue proposes bring together latest findings into epigenetics research and thus outline how such mechanisms control development in higher organisms.

Proposed topics (titles and abstracts)

1- First potential topic: 3D genome architecture

Abstract: Recently, molecular techniques such as chromosome Conformation Capture (3C) assay have enabled to manipulate the chromatin conformation and thus understand the mode in which 3D genome landscape is linked with gene expression. The objective of this topic is to unrevealing how 3D chromosome architecture is associated with gene expression patterns and how it affects development in higher organisms.

2- Second potential topic: non coding RNAs

Abstract: ncRNAs can play important roles in the configuration of the 3D-nuclear landscape. For instance, in mammals, the X-chromosome inactivation (XIST) lncRNA is known to play a central role in regulating master development programing by silencing one X chromosome and thus regulate dosage effects. The objective of this topic is to understand how ncRNAs may act to control developmental pathways.

3- Third potential topic: small ncRNAs, chromatin remodeling complexes and histone/DNA modifications in signaling pathways

Abstract: short ncRNAs are versatile molecules that control transcription of target genes by recruiting chromatin remodeling enzyme complexes which epigenetically alter the chemical state of histones and DNA sequences in specific chromosome regions. The objective of this topic is to understand how small ncRNAs and chromatin remodeling complexes trigger histone/DNA modifications and thus modulate downstream signaling pathways.

4- Fourth potential topic: repetitive/duplicated sequences in genome organization and function

Abstract: Sequence duplication is an important evolutionary mechanism of eukaryote genomes, and it is nowadays recognized to generate adaptive diversity capable of modulating transcriptional activity. The objective of this topic is to highlight the role of duplicated and repetitive sequences on transcriptional activity and the importance of both in genome evolution and developmental programing.

Keywords: epigenetic reprograming, non-coding RNAs; gene expression; chromatin remodeling complexes; DNA methylation; histone code; chromosome architecture, repetitive sequences, transposable elements.

Subtopics:

Specific topics of particular interest include, but are not limited to:

- 3D genome architecture in epigenetic programing
- Non-coding RNAs in epigenetic programing
- Small non-coding RNAs, histone/DNA modifications and signaling developmental pathways
- Chromatin remodeling complexes, histone/DNA modifications and signaling developmental pathways
- Repetitive/duplicated sequences in genome organization, evolution, function and development

Schedule:

- Manuscript submission deadline: 30 April 2019
- Peer Review Due: 15 July 2019
- Revision Due: 15 October 2019
- Announcement of acceptance by the Guest Editors: 30 November 2019
- Final manuscripts due: 1 April 2020

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