

Special Issue

Epigenetics and Genome Evolution in Plants

Message from the Guest Editor

Accumulating evidence many of those were from plant systems suggests the contribution of epigenetic mechanisms to genome evolution. For example, DNA methylation is vital for the silencing of transposable elements, enabling the colonization of a substantial proportion of repetitive sequences in plant genomes. During evolution, these genomic elements are capable of moving and self-replicating in germlines in waves (i.e., epigenetic assimilation), potentially resulting in genetic diversity and genome plasticity. Furthermore, these epigenetically controlled dynamics may also steer the ecological and evolutionary advantage of hybridization and polyploid events by perhaps modulating the transcriptional expression of nearby genes. This special issue aims to collect a wide body of research studies dealing with epigenomics, population epigenetics, and functional genomics in model and non-model plant species that have significant relevance in genome evolution, adaptation, ecological speciation, and diversification.

Guest Editor

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Message from the Editor-in-Chief

Plants is an open access journal which provides an advanced forum for research findings in areas related to plant function, its physiology, biology, taxonomy, stresses, and its interactions with other organisms. It publishes original research articles, reviews, reports, conference proceedings (peer reviewed full articles) and communications. In original research papers, it is important that full experimental details are provided. We also encourage timely reviews and commentaries on topics of interest to the plant research community.

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