Special Issue

Plant Genetics and Breeding Research Progress in Genomics to Post-genomics Era

Message from the Guest Editor

Advances in next-generation sequencing technology have revolutionized plant genetics, genomics, and breeding research. High throughput sequencing-based approaches are being used for genome-wide association (GWAS), genomic selection (GS), Mut-map, genetic diversity, and population structure studies. On the other hand, the transcriptome sequencing approach is widely used for identifying gene functions, decoding pathways, and elucidating complex genetic regulation. The aim of this Special Issue is to bring to light the recent progress in the research of plant genetics, genomics, transcriptomics, and bio-informatics.
This Special Issue will focus include articles related to the following topics: Next generation sequencing, assembly, annotation; Genetic mapping, GWAS, multi-parental QTL mapping, and QTLseq; Genomic selection for complex traits; Whole-genome sequencing and resequencing efforts; Haplotype-based breeding; Population genomics, genetic diversity; Plant molecular evolution, genome structure, and genome plasticity; Genomics based precision breeding and novel trait introgression; Transcriptomics, miRNA; Comparative genomics; Epigenomics.

Guest Editor

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The International Journal of Molecular Sciences (*IJMS*, ISSN 1422-0067) is an open access journal, which was established in 2000. The journal aims to provide a forum for scholarly research on a range of topics, including biochemistry, molecular and cell biology, molecular biophysics, molecular medicine, and all aspects of molecular research in chemistry. *IJMS* publishes both original research and review articles, and regularly publishes special issues to highlight advances at the cutting edge of research. We invite you to read recent articles published in *IJMS* and consider publishing your next paper with us.

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