Special Issue

Genomewide SNP Identification and Use for Resolving Population Structure and GWAS of Traits of Interest

Message from the Guest Editors

With the merger of methodologies for making reduced representation libraries, Nextgen sequencing and bioinformatic approaches have emerged recently to identify genomewide SNPs and Insertion/Deletion (InDELs) for resolving population structure and genome-wide association studies (GWAS), QTL mapping, and bulk segregant analysis that can be used to identify genomic regions of interest. These reduced representation methods currently have great impact in studying novel and existing genetic variation for various crop improvement programs as well as non-model plants that have ecological significance. The purpose of this Special Issue is to publish high-quality research papers as well as review articles addressing recent studies involving SNP mining, resolving population structure, haplotype networking, and GWAS as emerging tools for plant breeding and ecology research. Original, high-quality contributions that are not yet published or that are not currently under review by other journals or peer-reviewed conferences are sought.

Guest Editors

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Deadline for manuscript submissions

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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.

Editor-in-Chief

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