



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

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Deadline for manuscript  
submissions:

**closed (30 April 2022)**

### Message from the Guest Editors

Dear Colleagues,

With the merging of methodologies for making reduced-representation/resequencing libraries, RNAseq, next-generation sequencing and bioinformatic approaches have recently emerged for identifying genome-wide SNPs and insertions/deletions (InDELs) for resolving population structure, along with genome-wide association studies (GWAS), QTL/eQTL mapping, and bulk segregant analysis, which can be used to identify genomic regions of interest. In Volume II, we expand the scope of functional genomics involving RNAseq and qRT-PCR validations targeting mapped traits of interest.

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 structures, haplotype networking, and GWAS as emerging tools for plant breeding and ecology research. Original, high-quality contributions that have not yet been published or that are not currently under review by other journals or peer-reviewed conferences are sought.





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## Editor-in-Chief

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## Message from the Editor-in-Chief

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