



Gene-Based SNP Discovery and Diversity of Forests Trees

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Message from the Guest Editors

Dear Colleagues,

Single Nucleotide Polymorphisms (SNPs) are the most abundant and widely distributed markers in plant genomes. The rapid advancement of next-generation sequencing technologies and their associated cost reduction, along with the development of the required bioinformatics resources, has democratized the large-scale discovery of SNPs in forest tree species. Different goals can guide SNP discovery and genotyping. High-throughput SNP genotyping has become a powerful tool to address a range of research areas related to structural and functional genomics, populations genomics, association genomics, conservation genomics, or genomic selection. The acquisition of a large number of SNPs in both candidate genes and random loci across the genome, and the development of high throughput genotyping are pivotal to understand the molecular basis of adaptation of natural forest tree populations and to support tree breeding.

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Guest Editors





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