Special Issue

Next-Generation Plant Breeding: Integrating Genomics Tools and Marker-Assisted Selection

Message from the Guest Editors

Next-generation plant breeding transforms crop enhancement by incorporating sophisticated genomic technologies alongside marker-assisted selection (MAS). Conventional breeding techniques, although efficacious, are labor-intensive and can lack precision. Conversely, genomics-enabled breeding facilitates the detection and selection of advantageous features at the DNA level, expediting the breeding cycle and enhancing precision. This revolution is fundamentally driven by high-throughput sequencing technology and artificial intelligence capabilities that offer extensive insights into plant genomes. These techniques facilitate the identification of quantitative trait loci (QTLs), single-nucleotide polymorphisms (SNPs), insertions and deletions (InDels), and gene expression patterns linked to agronomically significant features, including yield, drought tolerance, disease resistance, heavy metal resistance and nutritional quality. Upon identification of these markers, MAS can facilitate the monitoring of trait inheritance in breeding populations, enabling more precise and efficient selection.

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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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