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Marker-Trait Association Analysis in Horticultural Crops

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Message from the Guest Editor

The world demand for horticultural crop is in continuous increase. To this extent, a deep understanding of the genetic basis regulating phenotypes of interest represents an important prerequisite both to understand the trait physiology and for breeding. The rapid advent of high-throughput genotyping platforms enabled the simultaneous interrogation of hundreds of thousands of single nucleotide polymorphisms (SNP) employing a dedicated array or through whole-genome resequencing (WGS) approaches. The identification of molecular markers in strong linkage with a quantitative trait locus (QTL) provides useful insights to understand the genetic determinism of traits of agronomical relevance. Furthermore, molecular markers can represent a valuable tool for breeders for a genetic-guided seedling or parental selection. Indeed, the use of molecular markers in strong linkage with an agronomical trait allows a fast and relatively inexpensive screening of seedlings with consequent reduction in the time and space needed to develop novel cultivars showing superior phenotypic characteristics.

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Message from the Editor-in-Chief

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