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Chapter

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Status and Opportunities of Molecular Breeding Approaches for Genetic Improvement of Tea

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Abstract

Tea is the most popular perennial plantation crop in the Southeast Asian countries because of its attractive aroma, taste, and health benefits. Tea plantations provides an important agro-based, eco-friendly employment generating and export oriented industries in all the tea-growing countries. However, the future of tea industry depends on the availability of high-yielding and high-quality tea clones with greater tolerance to pest, diseases, and environmental stresses. Genetic improvement of tea involves identification, characterization, evaluation, domestication, maintenance, and utilization of germplasm for the development of superior plant material. Conventional breeding program in tea is, however, limited by long gestation period, outbreeding nature, and self-incompatibility. This chapter summarizes the status of emerging molecular genomic information that can expedite the genetic improvement in tea and hence the productivity too. This will also provide a background for possibilities of modern tea breeding together with some current efforts for the development of sequence-based markers such as microsatellites, single-nucleotide polymorphisms (SNPs) and genetic diversity of existing gene pools for the identification of diverse parental s and efficient phenotyping to support operational breeding. Preliminary attempts antitative trait locus (QTL) mapping in tea were also reviewed, and prospectives o provided on power of association genetics to dissect quantitative traits. enges and opportunities to integrate advancement and advent of next-generation sequencing (NGS) technologies to generate genome-wide makers and to integrate genomic information into directional selective breeding are also discussed.

Keywords

Camellia sinensis Genetic diversity Linkage mapping Molecular markers Simple sequence repeat

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