

Exploring Simple Sequence Repeats within Conserved microRNA Precursors Identified from Tea Expressed Sequence Tag (EST) Database

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Abstract : Tea (*Camellia sinensis*) has received substantial attention from the scientific world time to time, not only for its commercial importance, but also for its demand to the health-conscious people across the world for its extensive use as potential sources of antioxidant supplement. These health-benefit traits primarily rely on some regulatory networks of different metabolic pathways. Development of microsatellite markers from the conserved genomic regions is being worthwhile for studying the genetic diversity of closely related species or self-pollinated species. Although several SSR markers have been reported, in tea the trait-specific Simple Sequence Repeats (SSRs) are yet to be identified, which can be used for marker assisted breeding technique. MicroRNAs are endogenous, noncoding, short RNAs directly involved in regulating gene expressions at the post-transcriptional level. It has been found that diversity in miRNA gene interferes the formation of its characteristic hair pin structure and the subsequent function. In the present study, the precursors of small regulatory RNAs (microRNAs) has been fished out from tea Expressed Sequence Tag (EST) database. Furthermore, the simple sequence repeat motifs within the putative miRNA precursor genes are also identified in order to experimentally validate their existence and function. It is already known that genic-SSR markers are very adept and breeder-friendly source for genetic diversity analysis. So, the potential outcome of this in-silico study would provide some novel clues in understanding the miRNA-triggered polymorphic genic expression controlling specific metabolic pathways, accountable for tea quality.

Keywords : micro RNA, simple sequence repeats, tea quality, trait specific marker

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