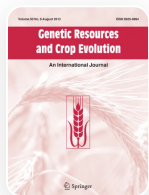


Genotypic characterization on the basis of chilling requirement in apple (*Malus × domestica* Borkh.) using simple sequence repeat (SSR) markers

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Abstract

Molecular characterization was performed using simple sequence repeat (SSR) markers among apple (*Malus × domestica* Borkh.) cultivars categorized based on the chilling requirement in this study. In total, 191 alleles, with an average of 3.47 per locus, were revealed utilizing 55 informative polymorphic SSR primers among the 84 total SSRs initially screened. The mean per cent polymorphism was obtained to be 96.21 in the characterized cultivars, with an average number of monomorphic (0.13) and polymorphic (3.35) bands. The mean polymorphic information content, effective multiplex ratio, Shannon index, expected heterozygosity value, observed heterozygosity, observed allele number, effective allele number, marker index, and resolving power were 0.65, 3.26, 0.93, 0.61, 0.84, 2.93, 2.45, 2.19, and 4.23, respectively. The similarity coefficient range was 0.26–0.96. The population structure showed an admixture of two genetic pools in the

examined cultivars. Cluster analysis divided the subjected apple cultivars into two major clusters: the first cluster of high-chilling cultivars, while the second cluster of mid-chilling and low-chilling cultivars. The present study inferred clear and distinct characterization of low, mid, and high chilling cultivars using SSR markers that confirms the standard classification in accordance with the available literature. Hence, the results so obtained will serve as a base for further research towards developing trait-specific markers and to unfold the genetic base behind varied chilling requirements in apples.



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Data Availability

No datasets were generated or analysed during the current study.

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M.T.: conducted PCR-based research, data recording, R.S.: Conceptualization, methodology, overall supervision, funding acquisition, manuscript editing and finalization; P.V.: Procurement of germplasm; P.S.: Supervision, PCR-based analysis, manuscript editing and finalization; M.S.: PCR-based research, data recording; P.: PCR-based research, data analysis; A.T.: Writing rough draft of the manuscript; data recording; PCR-based analysis; A.S.: PCR-based research. All authors reviewed the manuscript.

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Ethics declarations

Conflict of interest

The authors declare no competing interests.

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