

Survey of Simple Sequence Repeat (SSR) markers in guava (*Psidium guajava* L.) genome; towards establishment of molecular genetic map of guava

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Guava (*Psidium guajava* L., $2n=22$) which is considered to be “poor man’s fruit” or “apple of tropics”, is most economically important perennial fruit crop of the family Myrtaceae. In spite of the sophistication and availability of present technology the genomics of this crop hasn’t been much explored till date. The present study involves genotyping of two parental lines viz *Psidium guajava* var Kamsari and *Psidium guajava* var Purple Local, differing in fruit quality traits viz seed strength (Hardness/Softness), Fruit weight and TSS, and their mapping population comprising of 96 progenies using SSR markers. Initial survey, with a set of 62 SSR markers, revealed 63% polymorphism i.e. 39 polymorphic markers between the parental lines that have been further used for high through-put genotyping of the mapping population involving the amplification of microsatellites by following M13-Tailed PCR principle and thereby identifying the alleles through Genetic Analyzer by performing Gene Scan Analysis. Thus the generated genotyping data helps in constructing a Linkage Map in *Psidium guajava* which plays a vital role in QTL analysis, Map-based cloning and identification of trait(s)-linked marker(s).

Biography

Padmakar B. is pursuing his Doctoral degree from Jawaharlal Nehru Technological University, Hyderabad. Currently working on various aspects of molecular markers, their applications and identification in Horticultural crops at Molecular Biology Lab in Division of Biotechnology, IIHR at Bangalore. He has published 3 papers in reputed journals.

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