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Leaf transcriptome sequencing for SSR development and linkage map construction in bottle gourd

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Despite the worldwide consumption and medicinal importance of bottle gourd (*Lagenaria siceraria*) is not thoroughly investigated in molecular biology barring a few reports on genetic diversity analyses. Using high-throughput Illumina RNA sequencing, we analyzed a *L. siceraria* (variety *Pusa Santushti*) leaf transcriptome and 17.4 million clean reads were assembled into 19594 unigenes averaging 1195 bp. Among them, 18000 (91.8%) unigenes were annotated with a BLAST search against the NCBI Non-Redundant (NR) database and 2592 (13.3%) were detected that contained one or more simple sequence repeats (SSRs). From these SSR-containing sequences, 808 candidate SSR markers were developed and experimentally tested, validating (%) novel polymorphic SSR markers. Then, a consensus SSR-based linkage map was constructed with SSR markers distributed in 11 linkage groups. Both transcriptome information and the genetic map of *L. siceraria* presented here offer a valuable foundation for molecular biology investigations such as functional gene isolation, QTL mapping and marker-assisted selection breeding in this important vegetable species as well as related cucurbit crops.

Biography

Manjusha Verma is a Senior Scientist with an excellent experience in the emerging genomic technologies as well as their integration with the established methods for the understanding of genetic variation in horticultural crops especially cucurbitaceous crops. She has evaluated genetic variability based on morphological traits, biochemical and molecular markers in several horticultural crops and millets. She has developed thousands of microsatellite markers in bottle gourd, sponge gourd, watermelon and small millets with potential and demonstrated relevance to the analyses of genetic diversity, cultivar identification and marker assisted selection.

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