

Genetic Dissection of QTLs in Intraspecific Hybrids Derived from Muskmelon (*Cucumis Melo* L.) and Mangalore Melon (*Cucumis Melo* Var *Acidulus*) for Shelflife and Fruit Quality Traits

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Abstract : Muskmelon is a health-beneficial and refreshing dessert vegetable with a low shelf life. Mangalore melon, a genetic homeologue of muskmelon, has a shelf life of more than six months and is mostly used for culinary purposes. Understanding the genetics of shelf life, yield and yield-related traits and identification of markers linked to such traits is helpful in transfer of extended shelf life from Mangalore melon to the muskmelon through intra-specific hybridization. For QTL mapping, 276 F₂ mapping population derived from the cross Arka Siri × SS-17 was genotyped with 40 polymorphic markers distributed across 12 chromosomes. The same population was also phenotyped for yield, shelf life and fruit quality traits. One major QTL ($R^2 > 10$) and fourteen minor QTLs ($R^2 < 10$) localized on four linkage groups, governing different traits were mapped in F₂ mapping population developed from the intraspecific cross with a LOD > 5.5 . The phenotypic variance explained by each locus varied from 3.63 to 10.97 %. One QTL was linked to shelf-life (qSHL-3-1), five QTLs were linked to TSS (qTSS-1-1, qTSS-3-3, qTSS-3-1, qTSS-3-2 and qTSS-1-2), two QTLs for flesh thickness (qFT-3-1, and qFT-3-2) and seven QTLs for fruit yield per vine (qFYV-3-1, qFYV-1-1, qFYV-3-1, qFYV1-1, qFYV-1-3, qFYV2-1 and qFYV6-1). QTL flanking markers may be used for marker assisted introgression of shelf life into muskmelon. Important QTL will be further fine-mapped for identifying candidate genes by QTLseq and RNAseq analysis. Fine-mapping of Important Quantitative Trait Loci (QTL) holds immense promise in elucidating the genetic basis of complex traits. Leveraging advanced techniques like QTLseq and RNA sequencing (RNA seq) is crucial for this endeavor. QTLseq combines next-generation sequencing with traditional QTL mapping, enabling precise identification of genomic regions associated with traits of interest. Through high-throughput sequencing, QTLseq provides a detailed map of genetic variations linked to phenotypic variations, facilitating targeted investigations. Moreover, RNA seq analysis offers a comprehensive view of gene expression patterns in response to specific traits or conditions. By comparing transcriptomes between contrasting phenotypes, RNA seq aids in pinpointing candidate genes underlying QTL regions. Integrating QTLseq with RNA seq allows for a multi-dimensional approach, coupling genetic variation with gene expression dynamics.

Keywords : QTL, shelf life, TSS, muskmelon and Mangalore melon

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