Simple sequence repeat-based association analysis of fruit traits in eggplant

(Solanum melongena)

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ABSTRACT. Association mapping based on linkage disequilibrium (LD) provides a promising tool to identify quantitative trait loci (QTLs) in plant resources. A total of 141 eggplant (Solanum melongena L.) accessions were selected to detect simple sequence repeat (SSR) markers associated with nine fruit traits. Population structure analysis was performed with 105 SSR markers, which revealed that two subgroups were present in this population. LD analysis exhibited an extensive long-range LD of approximately 11 cM. A total of 49 marker associations related to eight phenotypic traits were identified to involve 24 different markers, although no association was found with the trait of fruit glossiness. To our knowledge, this is the 1st approach to use a genome-wide association study in eggplant with SSR markers. These results suggest that the association analysis approach could be a useful alternative to traditional linkage mapping to detect putative QTLs in eggplant.

Key words: SSR; Association mapping; Linkage disequilibrium (LD); Population structure; Eggplant