

High-density genetic map construction and identification of quantitative trait loci controlling leaf abscission in citrus (Abstract)

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ABSTRACT

We constructed a high-density genetic map of citrus using simple sequence repeat and single-nucleotide polymorphism markers evenly distributed across the genome. The sex-averaged linkage map contains 4163 markers with an average distance of 1.12 cM between loci. The female clementine mandarin linkage map contains 1478 markers with a length of 1093.90 cM. A dense genetic map of male parent *Poncirus trifoliata* was also constructed, with a length of 1227.03 cM and 2976 markers. Collinearity between physical and genetic distances of all markers in nine linkage groups indicated the high quality of the genetic map. The linear order of common markers was highly conserved between clementine mandarin and *P. trifoliata*. *Poncirus* has deciduous leaves, representing a distinct phenotype from evergreen true citrus trees. Based on this high-density integrated citrus genetic map and two years of deciduous phenotype analysis, two potential quantitative trait loci (QTLs) were identified in linkage groups 1 and 8, and 137 candidate genes were identified from these regions based on integrative analysis of resequencing and transcriptome analysis. The high-density citrus genetic map will greatly facilitate QTL mapping and genome studies, and successful localization of the deciduous trait is valuable for understanding the underlying mechanism and improving citrus breeding.

Keywords: QTL mapping, leaf abscission, citrus.

