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Construction of a Genetic Linkage Map of Citrus with Random Amplified Polymorphic DNA (RAPD) Markers Using a Progeny Population from a Complex Intergeneric Cross

Mehtap ŞAHİN ÇEVİK¹, Gloria A. MOORE²

¹Department of Horticultural Sciences, Faculty of Agriculture, Süleyman Demirel University, 32260 Isparta - TURKEY

²Department of Horticultural Sciences, Plant Molecular and Cellular Biology Program, University of Florida, Gainesville, FL, 32611, USA

 [Keywords](#)
[Authors](#)



bot@tubitak.gov.tr

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Abstract: This study included 30 plants that were randomly selected from a larger progeny population obtained from a complex intergeneric cross of {*C. grandis* (L.) Osb. x [*C. paradisi* Macf. x *Poncirus trifoliata* (L.) Raf.]} x {[*C. paradisi* Macf. x *P. trifoliata* (L.) Raf.] x *C. reticulata* Blanco] x [*C. paradisi* Macf. x *Poncirus trifoliata* (L.) Raf.] x *C. sinensis* (L.) Osb.]. Genomic DNA was extracted from leaf samples of these plants and analysed for polymorphisms by polymerase chain reaction (PCR), using 10-mer random primers. A total of 111 random amplified polymorphic DNA (RAPD) markers were identified using 38 random primers. A genetic linkage map of the progeny population was constructed with these RAPD markers. The map contains 63 markers distributed into 9 linkage groups, which possibly correspond to the 9 haploid chromosomes of Citrus. The total maximum length of the linkage map generated in this study was 314.8 cM, with an average map distance of 5.07 cM between markers.

Key Words: Citrus, DNA markers, RAPD markers, genetic linkage mapping

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