Assessment of genetic variability and genotyping of some Citrus accessions using molecular markers

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ABSTRACT

Genotyping of 14 Citrus accessions was carried out using RAPD and SCAR markers.The genetic variability among the 14 Citrus accessions was estimated using forty decamer RAPD primers. The total number of amplicons detected was 531, including 349 polymorphic amplicons. This represents a level of polymorphism of 65.7% and an average number of 8.7 polymorphic bands per primer. RAPD markers detected genetic similarity ranging from 10.8% to 87.7% between TC and each of WM, AWM and BSO and between MSG and RRG, respectively. The similarity matrices were employed in the cluster analysis to generate a dendrogram using the UPGMA method. The dendrogram separated Troyer citrange from the other Citrus genotypes. Moreover, accessions belonging to the same species always clustered together. Thirty-four out of the forty RAPD primers identified 13 out of the 14 Citrus accessions by unique positive and or negative markers.Each of the three primers OPC04, OPK16 and OPO13 revealed unique markers characterizing five different accessions. While, the other primers identified 1 to 4 accessions. Seven out of the eight RAPD primers and one out of three SCAR primers detected markers known to be linked to Citrus tristeza virus resistance in four and one Citrus accessions, respectively. On the other hand, three RAPD primers and one SCAR primer were used to detect markers linked to low fruit acidity with the 14 Citrus accessions.

Key words: *Citrus, RAPD, SCAR, genotyping, Citrus tristeza virus (ctv), acitric fruits.*

INTRODUCTION

Citrus is one of the major fruit crops all over the world. The coventional methods in *Citrus* cultivars identification relied on morphological features and isozymes (Protopapadadis, 1988). Using morphological traits, it is difficult to distinguish between many *Citrus* cultivars because some cultivars are distinguishable only by fruit traits and *Citrus* trees usually do not bear fruits until 3-4 years after planting. Moreover, isozyme markers can be mediated by secondary processes so that the normal patterns of expression are suppressed. Phenotypic diversity, polyembryony, hybridization and mutations have prevented cosensus on systematic classification of *Citrus* (Coletta *et al*., 1998) and hampered *Citrus* improvement programs.

The development of molecular markers based on DNA sequences has provided an