

**GENETIC DIVERSITY AND MOLECULAR
STUDIES ON SOME VEGETABLES**

By

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ABSTRACT

Melon (*Cucumis melo* L.) is a valuable cash crop grown throughout the world. The current research was carried out to identify the genetic diversity among ten melon genotypes conserved in the gene bank, using descriptor morphological traits, and three different molecular markers; Amplified Fragment Length Polymorphism (AFLP), Start Codon Targeted (SCoT), and Simple-Sequence Repeats (SSRs). The fifty studied morphological characters comprised 47 descriptive (qualitative) and three measured (quantitative) characters. The fruit qualitative characters among the studied accessions had great variation and the quantitative traits revealed significant differences among them. The morphology-based dendrogram clustered the accessions into two main clusters fruit surface and corking/netting were the main characters that distinguished the two main clusters. Six AFLP primer combinations were used to characterize the melon accessions. AFLP markers were successfully characterized each of the ten accessions with unique positive/negative markers, with a total of 77 polymorphic amplicons and an average of 12.83 polymorphic amplicons/primer combinations. The percentage of polymorphism ranged from 35.71 to 71.42 % with an average of 54.6%. While, the eight SCoT primers gave 64 polymorphic amplicons with an average of eight amplicons/primer, the percentage of polymorphism ranged from 16.66% to 92.85% with an average of 73.56%. The SSR amplified 21 amplicons, with an average of 2.1 amplicons/primer. Out of ten SSR primer pairs, eight primers revealed 90.47% polymorphism. According to the combined dendrogram based on AFLP, SCoT and SSR the ten melon accessions were distinguished into two main clusters. Where, one accession was distantly away from the others at 0.82 similarity index. While, the second main cluster assigned the other accessions in closed clusters. The obtained results revealed that there is great variability among the melon accessions that could provides good source of diversity that could be used in melon improvement program.

Keywords: *Cucumis melo* L.; morphological characterisation; molecular markers; AFLP; SCoT; SSRs.

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