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SEQUENCING OF LRR DOMAIN OF FOM-2 GENE IN TWO MELON (CUCUMIS MELO L.) GENOTYPES

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Soil-borne fungus *Fusarium oxysporum* f.sp.*melonis* causes important losses in melon and reduces the quality of the fruit. Since the race 1 of this disease is economically very important in Iran and *Fom-2* gene induces resistance toward race 0 and 1, in this study cloning and sequencing of LRR domain from *Fom-2* gene in two melon accessions was carried out. In this study, the genomic DNA was extracted from Isabelle and Garmak. In order to perform polymerase chain reaction primers based on the sequence of Fom-2 retrieved from the NCBI database using the software Primer-3 were designed. The single-band of PCR products of the expected size (1300 bp) was observed via electrophoresis. Amplified DNA was ligated in pGEM-T Easy vector and cloned in E-coli strain DH5α. Recombinant colonies were selected after growth in selective culture medium of LB/Amp/X-Gal. To verify the cloning, recombinant plasmids of colonies were extracted and digested with restriction enzyme of *Eco*RI and the expected band pattern and the presence of the target DNA in the vector was confirmed. After the sequencing, sequence alignment revealed that the cloned LRR domain is different between the resistant and susceptible accessions. 28 nucleotide substitutions were found between resistant and susceptible alleles. The reported differences can help developing molecular markers for marker assisted selection.

Keywords: gene cloning, marker assisted selection, resistance gene, wilt disease