Abstract

Melon (*Cucumis melo*) is one of the most important cucurbit products in Iran. Damping off caused by the soilborne fungus Fusarium oxysporum f.sp. melonis is a serios disease of the plant. the fungus infects the plant in all growth stages. This study aimed to investigate nucleotide diversity and possible recombination occurrence in pathogenic isolates. The melon plants showing yellowing and wilting symptoms were collected from melon forms. Isolation and purification of the strains were performed on PDA medium. After DNA extraction, polymerase chain reaction was performed by CNLl3 and CNS2 primers. 18s-28s rDNA were amplified. PCR product was directly sequenced, and the sequence containing 1076 nucleotide was compared with 33 selected sequences. Phylogenetic analysis was performed by Mega 5 and phylogenetic tree was constructed by the Neighbor Joining method. RDP3 was also used to analyze the recombination between isolates using Boot Scan method. The results of phylogenetic tree classified the isolates into 3 groups the isolates of Golestan province were categorized along the isolates of Isfahan, Yazd, Fars, Markazi, France and America. Percentage of similarity and differences between the isolates was calculated by Meg Align software demonstrating of Golestan province had the greatest similarity with the Kashan isolate. Moreover, the results showed thatno recombination occurred among *Fusarium* isolates isolated from melon in Iran and other parts of the world. The nucleotide sequence of *Fusarium oxysporum* f.sp. *melonis* for the first time in this study was determined.

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Keywords: Fusarium wilt, Melon, Nucleotide diversity, ITS-rDNA

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Mulecular analysis of nucleotide diversity and recombination probability *Fusarium oxysporum* f.sp. *melonis* isolates in Golestan Province

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