

## Abstract

Pumpkin scientific name *Lagenaria vulgaris* is the most common and most widely melons world. Soil fungus *Fusarium* wilt disease caused by *Fusarium oxysporum* f.sp. pumpkin cucurbit pumpkin is the most common disease of unknown cause that much damage to imported products-makes and economic importance is special. The aim of this study was to evaluate changes in the nucleotide sequence of the fungus *Fusarium* strains Mazandaran using primers designed and comparison with other sequences in the gene bank was strains this fungus. Therefore, in the summer of 1393 from pumpkin farms province (Behshahr) visited and suspicious plants with symptoms of *Fusarium* wilt-Breda and transferred to the laboratory. In order to isolate the cause pieces of the root zone (the border between healthy and diseased tissue) formation and surface disinfection with sodium hypochlorite after 1% were cultured on PDA. Isolates were purified to single spore method. isolate on morphological and physiological characteristics were determined using valid identification key and DNA was extracted by CTAB method was based Murray and Thompson after PCR amplification of DNA fragments to obtain the sequence of ITS region mushrooms, primer pairs *Fusarium* were used. PCR products were sequenced directly obtained sequences were compared with 29 sequences of Gen Bank. The results of sequencing Isolates coat protein gene region of Mazandaran strain FOC other software in the world, MegAlign, CLUSTALX, Editseq, Blast was revealed that the strain of Mazandaran highest percentage of similarity with isolates Spain with an average of 97/1 percent had the nucleotide level. RDP3 was used for the analysis of recombination between strain software reviews recombination between the E. ITS region, recombination between strains from other countries, the results showed that the isolates belonged to Saudi Arabia (LN892999) a recombinant fragment of the isolates Spain (FN598931) was observed as well as strain of India (AM261767) recombination it was found that the recombinant fragment of strain Spain (FN598931) was. MEGA5 was used for phylogenetic tree software, resulting in strain Taxonomic position Iranian FOC and compare it with other Isolates world and the emergence of this strain in Iran could shed light on the evolutionary origins.

Keywords: *Fusarium*, Wilt, Squash, Recombinatio,ITS-rDNA



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**Thesis Submitted in Partial Fulfillment of the Requirement  
for the degree of Master of Science (M. Sc) in the field of  
Plant Pathology**

**Assessment the molecular analysis and recombination  
probability of *Fusarium oxysporum* f.sp. *cucurbitae*, the  
agent cucurbit wilt disease, in Mazandaran province**

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December 2016