

## **Abstract**

Rice stem rot disease is one of the most common fungal pathogen of this product in Iran and many rice-producing countries that is damaging to produce of this product. Causes the disease is *Magnaporthe salvinii* (anamorph: *Sclerotium oryzae*) the heterotallic fungus. To examine morphology, genetic and pathogenic diversity of this species, sampling were taken at random from the province. Samples were cultured on WA medium, followed by purification was performed using the tip of hyphae. And a total of 45 isolates were isolated and used for further studies. Isolates on PDA medium have gray-white blackish colonies and spherical and semi spherical black sclerotes. Studying morphological diversity of isolates and data analysis with SAS software showed that the growth rate measurements were in 13 groups and were in 23 groups with the diameter of sclerotia measure and were in one groups the length and width of the conidi. The maximum diameter of the isolates was Sa.2 from Sari and the minimum diameter was F.1 from Fereidoonkenar. The largest sclerotia and the smallest sclerotiawere A.13 and A.1 isolates from Amol. To investigate the pathogenicity test, wsa used of cultivar ahlami tarum rice. Symptoms were recorded 10 days after infection. Analysis of the data showed that the isolates were divided into three groups. Isolates Be.32, Ra.1 and A.22 respectively belonging to the Behshahr, Ramsar and Amol cities showed more disease severity. Study of genetic diversity were individually with four UP markers, which the isolates were classified into nine genetic groups. The results show that there was relatively high genetic diversity among the isolates from this Province. Although between the severity pathogenesis and genetic diversity was no observed a direct relationship.

**Keywords:** DNA Fingerprinting, Genetic diversity, Rice stem rot, UP-PCR



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**The Thesis Submitted for the Degree of M. Sc  
(in the Field of Plant Pathology)**

**Studying genetic and pathogenic  
diversity of *Magnaporthe salvinii*, the  
causal agent of rice stem rot isolated  
from rice in Mazandaran Province**

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November 2012