

عنوان مقاله:

Investigation of phylogenetic relationship of some isolates of *Magnaporthe oryzae* in different hosts

محل انتشار:

اولین همایش بین المللی و دهمین همایش ملی بیوانفورماتیک ایران (سال: 1400)

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خلاصه مقاله:

Rice is one of the most important agricultural products having more than ۹۰% of its world production in Asia. However, a large amount of that is wasted by pests and diseases. Blast is an influential disease of rice, responsible for a significant yield loss of about ۱۰% to ۳۰% of total rice production every year. The fungal plant pathogen, *Magnaporthe oryzae*, is the causal agent of the devastating rice blast disease. It can infect millet and other grasses, but rice is the most economically significant host. In this study, the phylogenetic relationships of isolates obtained from rice and other wheatgrass are compared based on the ITS regions. The ITS nucleotide sequences were selected from the NCBI gene bank; Then, a strain of *Gaeumannomyces graminis* (GGG۳۱۷ ۱۸S) was used as an out-group array for rooting deciduous trees. The obtained sequences were aligned using BioEdit v. ۰,۹ software and the Clustalw algorithm. Phylogenetic analysis was performed based on the sequence of ITS region using the maximum likelihood algorithm. Also, the validation test of ۱۰۰۰ replications was carried out by MEGA.۶ software. ITS-based phylogenetic analysis of *M. oryzae* isolates, which were isolated from different grasses, were classified into four groups based on their host: group A (Rice), group B (Wheat), group C (Corn, Barley, and so on), and D (Rice). The results indicated that *M. oryzae* was identified for rice isolates in groups A and D, but the Blast agent of Iranian rice was not included in these categories. According to our studies, it can be found that the phylogenetic properties of *M. oryzae* in Iranian rice are similar to group C. Therefore, we conclude the Blast agent in Iran will probably be different from other regions.

کلمات کلیدی:

Iran; ITS region; Phylogenetics; Rice Blast

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