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摘要: 大豆腐霉菌是黑龙江省大豆根腐病菌群的重要组成部分,为了明确大豆腐霉菌的种类,从黑龙江省黑河市大豆根系土壤分离获得1株腐霉菌PSHH1,应用Rdna-ITS序列分析法对其进行菌种鉴定。Blast和系统进化树结果表明:PSHH1与GenBank上登录号为AB259316.1和AB512973.1等的Pythium sylvaticum亲缘关系最近,rDNA-ITS序列同源性大于99%,因此认定PSHH1为Pythium sylvaticum。为了考察PSHH1的致病性,选取了60份当前大豆主栽品种,应用种子腐烂法和下胚轴接种法进行回接试验。通过计算种子腐烂率和植株茎折率来评价PSHH1的致病性,结果显示,PSHH1仅对13.33%的大豆主栽品种表现出较强的致病力,而对61.67%的大豆主栽品种致病力较弱。

Abstract: Pythium is an important part of soybean root rot fungal population in Heilongjiang province, in order to determine the species of Pythium in Heilongjiang province, PSHH1 has been isolated from the soil of soybean root in Heihe city. And Rdna-ITS sequence analysis was applied to PSHH1. According to the results of the analysis of rDNA-ITS sequences, the sequence homology was more than 99% when it was compared with the sequence of registration number AB259316.1 and AB512973.1 in GeneBank. Therefore, we think PSHH1 was a Pythium sylvaticum. In order to study the pathogenicity of PSHH1, using seed rot method and hypocotyl inoculation method, 60 main soybean cultivars were selected to determine the pathogenicity of PSHH1, and seed rot rate and stem discount rate can be reflected to evaluate the pathogenicity of PSHH1, results showed that PSHH1 had strong pathogenicity to 13.3% main soybean cultivars, at the same time, there were 61.67% main soybean varieties expressed weak pathogenicity to PSHH1.

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