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摘要: 大豆疫病严重影响我国及世界各国的农业生产，为探讨多聚半乳糖醛酸酶在大豆疫霉菌致病过程中的作用，采用PCR的方法从大豆疫霉菌中克隆了多聚半乳糖醛酸酶pspg1基因，并利用RT-PCR法对其在大豆中的表达进行了分析。结果表明：大豆疫霉菌pspg1基因开放阅读框长1236 bp，编码一个长412氨基酸的蛋白质。对其进化关系进行分析，发现该基因与其它卵菌的pg基因亲缘关系最近，形成一个独立的分支。RT-PCR分析表明：pspg1基因在接种大豆疫霉菌的大豆下胚轴中大量表达，而在健康大豆下胚轴中未检测到。克隆了大豆疫霉菌pspg1基因，并发现该基因在大豆疫霉菌侵染大豆过程中发挥重要作用。

Abstract: Soybean blight is a worldwide disease, which impacted on agriculture of China and other countries badly, and caused enormous loss on economy. In order to explore the pathogenic role of polygalacturonase from Phytophthora sojae, a polygalacturonase gene pspg1 was cloned from P. sojae by using PCR. And the phylogenetic tree of pspg1 was constructed with PAUP software. Then the expression of pspg1 in soybean was analyzed by RT-PCR. The results showed that the length of open reading frame of pspg1 was 1236 bp, which encoded a protein of 412 amino acid residues. The result of evolutionary analysis indicated that pspg1 was gathered with other pg genes from other oomycetes, which formed an independent branch. More importantly, the evolutionary analysis further defined the status of oomycete in the evolution of the nature. RT-PCR was performed and the results demonstrated that pspg1 expressed in hypocotyl of inoculated soybeans, and the expression was increasing with extending of inoculated time. However, pspg1 was not detected in hypocotyl of healthy soybeans. In this paper, a polygalacturonase gene pspg1 was cloned, and sequence of pspg1 was analyzed. In addition, pspg1 was detected in hypocotyl of inoculated soybeans, which testified that pspg1 played an important role in pathogenic process of P. sojae.

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