

研究论文

大豆疫霉根腐病菌的rDNA ITS序列分析

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摘要

采用真菌核糖体基因转录间隔区(ITS)通用引物, PCR扩增了大豆疫霉根腐病菌具有差异的17个菌株的ITS1与ITS2, 经过与DL2000的标准分子量DNA进行比较, 得到了大约800~1000 bp左右的片段, 并对PCR产物进行了序列测定。以

USA 为外类群利用最大简约法构建了大豆疫霉根腐病菌的系统发生树, 并分析了菌株之间的遗传进化关系。结果表明: 不同菌株ITS1和ITS2在碱基构成上有很大差异, 17个菌株大致分为4个谱系中, 且来自于同一地区的菌株大都分布在同一谱系中, 显示出地理上的差异。

关键词 [大豆; 疫霉根腐病菌; rDNA; 系统发育](#)

分类号

Phylogenetic Analysis of the Sequences of rDNA Internal Transcribed Spacer (ITS) of *Phytophthora sojae*

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Abstract

<P>The internal transcribed spacer (ITS) region (ITS1, ITS2 and 5.8S rDNA) of the nuclear ribosomal DNA (nrDNA) was amplified via the PCR method in seventeen different isolates of *Phytophthora sojae* using the common primers of the ITS of fungi. Around 800 bp-1,000 bp fragments were obtained based on the DL2000 marker and the sequences of the PCR products were tested. Taking isolate USA as outgroup, the phylogenetic tree was constructed by means of maximum parsimony analysis, and the genetic evolution among isolates was analyzed. The results showed that there is a great difference between the base constitution of ITS1 and ITS2 among various isolates. The seventeen isolates are classified into three groups, and the isolates from the

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same region belong to the same group, which shows the variation in geography.</P>

Key words [soybean](#); [Phytophthora sojae](#); [rDNA](#); [phylogeny](#)

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