

植物保护

马铃薯及番茄晚疫病菌的核糖体DNA-ITS区段序列分析*

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收稿日期 2004-11-22 修回日期

摘要 取3个不侵染马铃薯的番茄晚疫病菌菌株和3个不侵染番茄的马铃薯晚疫病菌菌株,以及2个可交叉侵染马铃薯和番茄的菌株,提取DNA全基因组后,用引物ITS1和ITS4进行扩增,得到约850 bp左右的扩增产物并进行测序,比较同源性,结果显示这些菌株的全基因组DNA序列与Genebank上登录的3个序列AF228084,AF228083,AY269995.1的同源性均为100%。3个番茄菌株之间的同源性大小为98.22%,3个马铃薯菌株之间的为99.52%,较番茄菌株的同源性高。不可交叉的两类菌株间的同源性为98.28%,可交叉侵染的番茄菌株和马铃薯菌株之间的同源性为99.17%,比不可交叉侵染的菌株间的同源性高,说明相似的序列使得生物学特性也很相似,反之,同源性有差异的,在生物特性上也表现出一定差异。

关键词 [晚疫病菌](#); [交叉侵染](#); [ITS区段序列](#)

分类号 [S 435.32](#)

Analysis on Sequence of Ribosomal DNA-ITS of *Phytophthora infestans* from Potato and Tomato

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Abstract

3 isolates of *P. infestans* from tomato that couldn't infect potato, 3 isolates from potato that couldn't infect tomato and 2 isolates of *P. infestans* that could infect both tomato and potato was amplified using polymerase chain reaction (PCR) and the universal primers internal transcribed spacer ITS 1 and ITS4. PCR products were an approximately 850 base pair and checked the sequences. The sequences of ribosomal DNA-ITS of 8 isolates were compared with 3 sequence logging in GeneBank and their homologies were 100%. The homologous character of 3 isolates from tomato were 98.22% and 3 isolates from potato were 99.52%. The homologies of 2 isolates that couldn't cross infect potato and tomato were 98.28%. The homologies of 2 isolates that could infect tomato and potato were 99.17%, it was higher than isolates that couldn't cross infect. The resembling sequences led to the resemble biological characters. On the contrary, the different sequences led to different biological characters.

Key words [Phytophthora infestans](#) [crossed infection](#) [ITS region sequence](#)

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