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摘要: 通过生物学纯化与血清学鉴定（ELISA）得到5个大豆花叶病毒(SMV)分离物，利用RT-PCR法扩增其CP、HC-Pro、P1和P3基因片段并进行测序。结果表明：5个分离物P1基因全长均为927个核苷酸，编码产生309个氨基酸。同源性分析表明，5个分离物核苷酸序列同源性为88.0%~99.9%，由此推导的氨基酸序列同源性为86.1%~100.0%。此外，5个分离物4个SMV基因CP、HC-Pro、P1和P3长度均为4 137个核苷酸，编码1 378个氨基酸。分析结果显示，5个分离物之间的核苷酸及氨基酸的同源性分别为92.6%~99.3%和95.1%~99.2%。根据系统进化树的分析，结合5个分离物在10个大豆鉴别寄主上的致病性反应，发现SMV的4个基因CP、HC-Pro、P1和P3与SMV的致病力及病样的来源地之间具有一定的关系。同时，这4个SMV基因能够将传统的SMV株系分离物与重组性分离物进行区分。

Abstract: Five SMV isolates were obtained by using biological purification and serology (DAS-ELISA). The CP, HC-Pro, P1 and P3 gene regions were amplified by reverse transcription polymerase chain reaction (RT-PCR) Sequences analysis showed that P1 gene of the each SMV isolates had 927 nucleotides in length, encoding 309 amino acids. Comparison of the sequences of P1 genes between different isolates showed they shared 88.0%-99.9% nucleotide acids identities and 86.1%-100.0% amino acids identities with each other. The four genes from the 5 SMV isolates were composed of 4 137 nucleotides, encoding 1 378amino acids, and shared 92.6%-99.3% nucleotide sequence identities and 95.1%-99.2% amino acid sequence identities. The results also revealed that the sequences variation in the CP, HC-Pro, P1 and P3 genes of virus were correlated with the level of virulence and the source of the virus isolates based on the symptom reaction of SMV on differential hosts and the phylogenetic analyses .Meanwhile, the normal soybean mosaic virus isolates and recombinant isolates could be differentiated through the sequences variation of CP, HC-Pro, P1 and P3genes.

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