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研究报告与简报

大麦黄矮病毒GPV株系基因组末端序列的克隆和分析 张文蔚,成卓敏

(中国农业科学院植物保护研究所,植物病虫害生物学国家重点实验室, 北京 100193) 摘要:

利用5′RACE、3′RACE和RT-PCR完成了大麦黄矮病毒GPV株系5′和3′末端序列的克隆和分析。分析结果显示,GPV株系5′末端长302 nt,包含起始密码子ATG和长100 nt的5′UTR。与马铃薯卷叶病毒属其他病毒比较,5′UTR的长度差异大且不保守。3′末端长328 nt,包含终止密码子TGA和长93 nt的3′UTR。比RPV 3′UTR短74 nt,同源性为40%,但末端较为保守,与RPV 3′UTR末端序列同源性达84.34%。关键词: 大麦黄矮病毒GPV株系;5′RACE;3′RACE;5′UTR;3′UTR

Cloning and Analysis of the Terminal Sequence of Barley Yellow Dwarf Virus GPV

ZHANG Wen-wei, CHENG Zhuo-min

(State Key Laboratory for Biology of Plant Diseases and Insect Pests, Institute of Plant Protection, Chinese Academy of Agricultural Sciences, Beijing 100193, China)

Abstract:

The authentic 5' and 3' terminal sequences of genome of barley yellow dwarf virus

(BYDV) GPV were obtained by 5' and 3' RACE and RT-PCR techniques. The analysis showed that 5' terminal sequence in the genome of GPV was 302 nt long, which included the start codon ATG and 5' un-translated region (UTR) of 100 nt. Compared with other virus of Polerovirus, the length of 5' UTR was variable and un-conservative. While 3' terminal sequence in the genome of GPV was 328 nt long, including the terminator codon TGA and 3' UTR of 93 nt. 3'UTR was 74 nt shorter than that of RPV. The homology of 3'UTR between GPV and RPV was 40%, but the terminal of 3'UTR was conservative. The homology was 84.34% between GPV and RPV.

Keywords: barley yellow dwarf virus GPV 5'RACE; 3'RACE; 5'UTR; 3'UTR 收稿日期 2008-09-24 修回日期 2008-11-28 网络版发布日期

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通讯作者:成卓敏,研究员,主要从事小麦病毒研究。E-mail: zmcheng@ippcaas.cn

作者简介: 张文蔚,助理研究员,硕士,主要从事分子植物病理学研究。E-mail: zwwei@sohu.com。

作者Email:

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大麦黄矮病毒GPV株系; 5′ ▶ RACE; 3'RACE; 5'UTR; 3' UTR

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