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我国玉米上一个水稻黑条矮缩病毒重排体的ORF序列(英文)

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Optimization of RT-PCR detection system for rice black-streaked dwarf virus and detection of its natural hosts

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摘要 玉米粗缩病20世纪50年代和90年代中后期在我国部分地区严重发生,2008年至今,该病在黄淮海地区又呈暴发趋势[1]。引起我国北方玉米粗缩病的主要是水稻黑条矮缩病毒(*Rice black-streaked dwarf virus*,RBSDV)[2]。田间寄主植物和传毒昆虫灰飞虱(*Laodelphax striatellus* Fallen)的发生数量、带毒率与玉米粗缩病的发生密切相关[1]。因此,建立快速灵敏的RBSDV检测体系,明确RBSDV的田间寄主,对有效控制玉米粗缩病具有重要意义。

关键词:

Abstract: To establish and optimize the RT-PCR detection system of rice black-streaked dwarf virus (RBSDV), and identify the natural host of RBSDV in the field, four pairs of primers were designed according to the nucleotide sequences of RBSDV S10. RT-PCR detection system for RBSDV was optimized after comparing primer pair, concentration of Mg^{2+} and *Taq* polymerase, and times of RNA dilution. The fourth pair of primers (F4 and R4) was proved to be the most sensitive one. The optimal RT-PCR system was 10× PCR buffer 2.5 μL, 25 mmol/L $MgCl_2$ 1.5 μL, dNTP (each 2.5 mmol/L) 2.0 μL, primers F4 and R4 (10 μmol/L) each 1.0 μL, 5 U/μL *Taq* DNA polymerse 0.2 μL, template RNA 5.0 μL and sterilized water 11.8 μL to make a total volume of 25 μL. With the method established, RBSDV could be detected from RNA extracted from single *Laodelphax striatellus* or 30 ng infected maize leaves. Besides plants of family *Gramineae, Sonchus brachyotus* and *Eclipta prostrate* from family *Asteraceae*, and *Amaranthus retroflexus* from *Amaranthaceae* were also natural hosts of RBSDV.

Key words: *Rice black-streaked dwarf virus* (RBSDV) detection RT-PCR natural host

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