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摘要: 2012年对河北大豆产区13个县(区)市28个采样点采集的273份大豆花叶病毒(SMV)病样进行了生物纯化,最终共获得67个分离物,经ELISA和RT-PCR检测确认其中56个为SMV分离物。利用全国统一的SMV鉴别体系将这些分离物归为9个株系。与以往的研究结果相比,河北地区SMV株系组成和分布发生一定的变化,其中SC7和SC11仍为流行株系,SC8所占比例有所下降;未检测到SC12、SC13和SC15;发现SC1、SC3和SC18共3个新株系。今后应对SC3株系的发展动态予以密切关注。

Abstract: A total of 273 virus samples of SMV were collected from 28 locations distributed in 13 counties of Hebei province in 2012. The isolates were biologically purified from collected samples and detected by ELISA and RT-PCR. Then, SMV isolates were classified by the unified national identification system. Finally, 67 virus isolates were obtained and 56 virus isolates were identified to be SMV isolates by ELISA and RT-PCR. Based on the differential host responses to these isolates, these SMV isolates were classified into 9 strains. Compared with previous studies, composition and distribution of SMV strains in Hebei had showed some changes, however SC7 and SC11 were still popular strain; the percentage of SC8 strain decreased; SC12, SC13 and SC15 were undetected; three new strains SC1, SC3 and SC18 were first discovered in Hebei, and the development of SC3 strains should be given more attention.

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