

植物保护—研究报告

青海省大麦黄矮病毒的种类鉴定及基于CP基因的分子进化研究

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摘要:

由大麦黄矮病毒 (Barley Yellow Dwarf Viruses, BYDVs) 引起黄矮病是世界范围的主要的经济危害严重的禾谷类作物病毒病。BYDVs可侵染大麦、小麦、青稞等多种禾谷类作物, 2010年该病害在青海省东部麦区中度流行。为了明确青海麦区大麦黄矮病毒株系种类, 应用酶联免疫吸附法和核酸斑点杂交方法对采集到的112个麦类黄矮病标样进行检测。结果显示, GAV为当地大麦黄矮病毒的流行株系。测定了12个青海GAV分离物的外壳蛋白基因序列; 核苷酸和氨基酸序列间比对分析表明: 青海GAV分离物与中国各地GAV分离物外壳蛋白基因相似性非常高, 变异很小。掌握青海东部麦区大麦黄矮病毒的株系分布及分子变异情况, 对麦类作物的抗病性育种工作提供有价值的参考, 同时对指导该地区小麦黄矮病的防治有着非常重要的意义。

关键词: 外壳蛋白基因

Identification of Barley Yellow Dwarf Viruses (BYDVs) Strains in Qinghai Province and Analysis of Evolution Based on CP Gene

Abstract:

The disease caused by Barley Yellow Dwarf Viruses (BYDVs) is a major, economically important that infect cereal crops including barely, wheat and highland barely worldwide. In 2010, BYDVs are moderately popular in the east of Qinghai Province, in China. In order to identify the serotype of BYDVs, 112 samples were collected from the east regions of Qinghai Province and assayed by ELISA and NASH. The results confirmed that the GAV of BYDV was predominant in these areas. Sequences of coat protein gene of BYDV-GAV isolates obtained from Qinghai Province were aligned at amino acid level and compared with those of other luteoviruses. The results of sequence comparisons showed that the CP gene of GAV shared a high degree of sequence conservation between some isolates from Qinghai and the others from different regions of China. The fact that the main strains and molecular variation of BYDV in the east regions of Qinghai Province were obtained, which would afford a valuable reference to work on breeding resist to BYDVs. It is also essential to direct prevention and cure of BYDVs in these regions.

Keywords: CP gene

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