

研究论文

玉米抗甘蔗花叶病毒资源的遗传多样性研究

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摘要 利用人工接毒方法对46份我国主要玉米自交系进行了两年抗甘蔗花叶病毒鉴定, 筛选出高抗系8份(K22、CN962、P138、齐318、中自01、金黄96B、齐319、Pa405), 抗病系7份(早21、中自03、早23、农大178、获白、K12、黄早四)。用SSR标记研究了46份自交系的遗传多样性。49对引物共检测出168个等位基因变异, 每对引物检测等位基因2~10个, 平均为3.43个。UPGMA聚类分析表明, 供试自交系可分为7群, 划群结果与系谱和育种家经验基本相符。15份抗病毒自交系分散于4群(A、B、E、G), 依据杂种优势原理, 可用于改良同一群内感病系的抗性; 其中群E和亚群GII被鉴定为抗病种质, 可用于组建抗病群体。本文的研究结果为抗甘蔗花叶病毒玉米种质改良提供了重要信息。

关键词 [玉米](#) [SSR标记](#) [杂种优势群](#) [甘蔗花叶病毒](#) [抗性鉴定](#)

分类号 [S513](#)

Genetic Diversity of Elite Maize Germplasm for Resistant to SCMV

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Abstract Forty-six elite maize (*Zea mays* L.) inbred lines were evaluated for reaction to sugarcane mosaic virus under field conditions with artificial inoculation in 1999 and 2000. The results showed that 8 lines (K22, CN962, P138, Qi318, Zhongzi 01, Jinhuang96B, Qi319, and Pa405) were highly resistant to SCMV, and 7 (Han21, Zhongzi03, Han23, Nongda178, Huobai, K12, and Huangzao4) were resistant. The germplasm basis for resistance to SCMV in 46 inbreds was investigated by SSR markers. The average number of alleles per SSR locus was 3.43 with a range from 2 to 10. The UPGMA cluster analysis showed that the 46 inbreds could be classified into 7 distinct groups with several subgroups, which were generally consistent to their known pedigree information and breeder's experiences. Fifteen resistant inbreds were found in 4 groups (A, B, E, G), which could be used in germplasm improvement for SCMV resistance based on heterotic pattern, respectively. Group E and subgroup GII were identified as two important sources of resistance, which can be employed to synthesize the composite s for SCMV resistance. The study provided useful information for germplasm improvement for resistance to SCMV.

Key words [Zea mays L.](#) [SSR marker](#) [Heterotic group](#) [Sugarcane mosaic virus](#) [Resistance evaluation](#)

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