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植物遗传学

小麦品种梭条花叶病抗性基因遗传分析及分子标记筛选

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摘要 选用3个抗梭条花叶病的小麦品种 “仪宁小麦”、“徐87-633”和“西风”为抗病亲本、以感病品种“镇9523”为感病亲本配制了三个杂交组合，对四个亲本及其杂种后代（F1及F2代）单株的田间抗病鉴定表明，三个抗病亲本的抗性均由核基因控制，为显性遗传方式。“仪宁小麦”和“西风”的抗性受两对表现互补效应的显性基因控制；“徐87-633”的抗性受一对显性基因控制。选取涉及小麦21条染色体上的266对SSR引物在“仪宁小麦”和“镇9523”间进行筛选，其中108对引物在两亲本间表现多态。根据“仪宁小麦”×“镇9523” F2代单株的田间抗病鉴定结果，采用BSA的方法，将已初筛的108对引物在抗、感池间进行扩增，发现引物Xgwm261在抗、感池间表现多态，表明该引物与“仪宁小麦”的抗病基因连锁，并将该抗病位点初步定位于2DS上。用该标记对F2代224个单株进行PCR扩增，根据扩增结果，采用Mapmaker 3.0软件计算遗传距离，结果显示，该标记与抗病位点间的遗传距离为22.9 cM。

关键词 小麦,梭条花叶病,遗传,SSR

分类号

Inheritance Analysis and Molecular Marker Selection of Genes for Wheat Spindle Streak Mosaic Resistance

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Abstract

Three wheat spindle streak mosaic viruses (WSSMV) resistant cultivars (‘Yining Xiaomai’, ‘Xu87-633’, and ‘Xifeng’) and one susceptible cultivar (‘Zhen9523’) were used as parents of 3 crosses in this experiment. WSSMV resistance of the parents, F1, and F2 was evaluated under field condition. Based on the segregation ratios of resistant and susceptible plants in F1 and F2 populations, it was deduced that the resistance to WSSMV was dominant and the inheritable factors controlling WSSMV resistance were encoded by the nuclear genome. WSSMV resistances in ‘Yining Xiaomai’ and ‘Xifeng’ were controlled by two pairs of alleles, which showed complementary effects. However the resistance in‘Xu-87633’ was controlled by a single dominant gene. 266 pairs of SSR primers located on 21 wheat chromosomes were used for polymorphic analysis of the two resistant and the susceptible parents ‘Yining Xiaomai’ and ‘Zhen9523’, and 108 of them amplified polymorphic DNA products. By Bulk Segregant Analysis of resistant and susceptible pools, one pair of primer located on chromosome arm 2DS, Xgwm261, were found being linked to WSSMV resistance. The 224 F2 individuals were then amplified with marker Xgwm261. The statistic genetic distance between Xgwm261 and the resistance locus was calculated to be 22.9 cM using the software Mapmaker 3.0.

Key words wheat wheat spindle streak mosaic virus inheritance SSR

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