

论文

野生二粒小麦导入普通小麦的抗白粉病基因 *MIWE29* 分子标记定位

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中国农业大学植物遗传育种系/农业生物技术国家重点实验室/农业部作物基因组学与遗传改良重点开放实验室/北京市作物遗传改良重点实验室/教育部作物杂种优势研究与利用重点实验室, 北京100193

摘要:

小麦白粉病是严重影响小麦生产的重要病害之一, 培育和应用抗病品种是有效控制和减少病害的最经济有效的方法。野生二粒小麦是硬粒小麦和普通小麦的四倍体野生祖先种, 是小麦抗病性遗传改良的重要基因资源。本研究利用来自以色列的野生二粒小麦WE29与普通小麦杂交, 再用普通小麦连续回交和自交, 育成高抗白粉病 (*Blumeria graminis* f. sp. *tritici*) 小麦新品系3D258(系谱为燕大1817/WE29//5*87-1, BC₄F₆)。将3D258和高感小麦白粉病的普通小麦品种薛早配制杂交组合, 对其F₁、F₂代分离群体和F₃代家系进行白粉病抗性鉴定和遗传分析。结果表明3D258携带抗白粉病显性单基因, 暂命名为 *MIWE29*。利用集群分离分析法(BSA)和分子标记分析, 发现6个SSR标记(*Xgwm335*、*Xgwm213*、*Xgwm639*、*Xwmc415*、*Xwmc289*和*Xwmc75*)和5个EST-STS标记(*BE494426*、*BE442763*、*CD452476*、*BE445282*和*BE407068*)与抗白粉病基因 *MIWE29* 连锁。利用中国春缺体-四体系、双端体系和缺失系将抗白粉病基因 *MIWE29* 标记物理定位于5BL染色体的0.59–0.79区域。这一普通小麦抗白粉病种质资源的创制及其连锁分子标记的建立为小麦抗病基因分子标记辅助选择、基因积聚和分子育种提供了新的物质基础。

关键词: 白粉病 野生二粒小麦 抗白粉病基因 分子标记

Molecular Mapping of Powdery Mildew Resistance Gene *MIWE29* in Wheat Originated from Wild Emmer (*Triticum turgidum* var. *dicoccoides*)

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Abstract:

Powdery mildew, caused by *Blumeria graminis* f. sp. *tritici*, is one of the most important wheat diseases in many regions in the world. Breeding for the resistance is the most economical and effective method for controlling this disease. Wild emmer (*Triticum turgidum* var. *dicoccoides*) is the immediate progenitor of cultivated tetraploid and hexaploid wheats and has been proven to be an important resource of disease resistance improvement. In this study, a common wheat line 3D258 with powdery mildew resistance was developed by crossing wild emmer accession WE29 with common wheat landrace Yanda1817 and backcrossing with common wheat line 87-1 (Yanda 1817/WE29//5*87-1, F₆). Genetic analysis of the F₂ population and their F₃ families, developed from 3D258 and a susceptible common wheat cultivar Xueza0, indicated that the powdery mildew resistance in 3D258 was controlled by a single dominant gene, designated temporarily as *MIWE29*. Molecular markers and the bulked segregant analysis were used to characterize the powdery mildew resistance gene *MIWE29*. Six SSR markers (*Xgwm335*, *Xgwm213*, *Xgwm639*, *Xwmc415*, *Xwmc289*, and *Xwmc75*) and five EST-STS markers (*BE494426*, *BE442763*, *CD452476*, *BE445282*, and *BE407068*) were found to be linked to *MIWE29*. Using Chinese Spring nullisomic-tetrasomics, ditelosomics and deletion lines, *MIWE29* was physically mapped on chromosome 5BL bin 0.59–0.79. The common wheat line 3D258 and its resistance gene linked molecular markers could be used in disease resistance genes pyramiding and marker-assisted selection in wheat breeding program.

Keywords: *Blumeriagraminis* f.sp. *tritici* *Triticum turgidum* var. *dicoccoides* Powdery mildew resistance gene Molecular markers

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