

论文

从野生二粒小麦导入普通小麦的抗白粉病基因**MIWE18**分子标记定位

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1中国农业大学植物遗传育种系/农业生物技术重点实验室/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/进一步作物杂种优势研究与利用重点实验室, 北京100193; 2北京农学院植物科技学院, 北京102206

摘要:

野生二粒小麦(*Triticum turgidum* var. *dicoccoides*)是小麦抗白粉病遗传改良的重要基因资源。利用野生二粒小麦WE18与普通小麦品种(系)连续多次杂交和自交, 育成对白粉病菌生理小种E09高度抵抗的小麦新品系3D249(京双27//燕大1817/WE18/3/温麦4, F₇)。利用高感白粉病品系薛早和3D249组配杂交组合, 获得杂种F₁代、F₂分离群体和F₃代家系, 进行苗期白粉病抗性鉴定和遗传分析。结果表明, 小麦品系3D249对E09小种的抗性受显性单基因控制, 暂命名该基因为**MIWE18**。利用集群分离分析法(BSA)和分子标记分析, 发现4个简单重复序列(SSR)标记(*Xwmc525*、*Xwmc273*、*Xcfa2040*和*Xcfa2240*)、1个EST-STS标记(*Xmag1759*)和1个EST-STS序列标记(*XE13-2*)与抗白粉病基因**MIWE18**连锁, 在遗传连锁图谱上的顺序为*Xwmc525-Xcfa2040-Xwmc273-XE13-2-Xmag1759-MIWE18-Xcfa2240*。SSR标记的染色体缺失系物理定位结果表明, 抗白粉病基因**MIWE18**位于小麦7A染色体长臂末端的Bin 7AL 16-0.85-1.00。与已知定位于该染色体区域的**Pm**基因遗传连锁图谱比较表明, **MIWE18**与抗白粉病基因**Pm1**、**MIIW72**、**PmU**、**MIm2033**和**MIm80**均位于7AL相同染色体区段。

关键词: 普通小麦品系3D249 野生二粒小麦 抗白粉病基因 **MIWE18** 分子标记

Molecular Mapping of Powdery Mildew Resistance Gene **MIWE18** in Wheat Originated from Wild Emmer (*Triticum turgidum* var. *dicoccoides*)

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Abstract:

Wild emmer (*Triticum turgidum* var. *dicoccoides*) is an important germplasm for wheat improvement especially for resistance to powdery mildew caused by *Blumeria graminis* f. sp. *tritici*. Common wheat line 3D249 (Jingshuang 27//Yanda 1817/WE18/3/Wenmai 4, F₇), a derivative of wild emmer accession WE18 and susceptible elite common wheat lines, was found highly resistant to prevailing powdery mildew isolate E09 at both seedling and adult plant stages in Beijing, China. Genetic analyses of the F₁, F₂ segregating population and their F₃ progenies derived from a cross between susceptible line Xuezao and resistant line 3D249 indicated that the powdery mildew resistance of line 3D249 was controlled by a single dominant gene, temporarily designated **MIWE18**. By bulked segregant analysis (BSA), four SSR markers (*Xwmc525*, *Xwmc273*, *Xcfa2040*, and *Xcfa2240*), one RFLP-derived STS marker (*Xmag1759*) and one EST-STS marker (*XE13-2*) were found to be linked to **MIWE18**, with an order of *Xwmc525-Xcfa2040-Xwmc273-XE13-2-Xmag1759-MIWE18-Xcfa2240* in the genetic linkage map. Using Chinese Spring nullisomic-tetrasomics, ditelosomics, and deletion lines, **MIWE18** was physically mapped on chromosome 7AL terminal bin 7AL 16-0.85-1.00. However, the allelism of wild emmer derived **MIWE18** to known powdery mildew resistance genes **Pm1**, **PmU**, **MIIW72**, **MIm2033**, and **MIm80**, all located on the same chromosome bin, need to be characterized in the future. The common wheat powdery mildew resistance line 3D249 provides useful new germplasm for disease resistance genes pyramiding and marker-assisted

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selection (MAS) in wheat breeding program.

Keywords: Common wheat lin 3D249; Wild emmer (*Triticum turgidum* var. *dicoccoides*) Powdery mildew Resistance genes M_lwe18 Molecular markers

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