

研究论文

水稻白叶枯病数量抗性座位定位及其小种专化性

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摘要 用水稻白叶枯病3个毒力不同的菲律宾小种P2、P6和P9, 对供体Lemont导入到特青背景的178个近等基因导入系群体, 进行白叶枯病数量抗性座位(quantitative resistance loci, QRL)定位及其小种专化性研究。供试亲本Lemont感3个小种, 特青中感P2和P9, 感P6。导入系群体的病斑长度呈连续正态分布。共发现影响病斑长度的10个主效QRL和12对互作QRL, 除第6染色体上的*QBr6c*外, 所有位点上的Lemont等位基因均增加了病斑长度(即降低了抗病性)。在第11染色体RM144~RM123区间检测到1个主效*QBr11*, 推测为*Xa4*基因, 对P2和P9表现为主效QRL, 但完全被P6克服, 在该位点未能检测到任何抗性残余效应。主效和互作QRL对不同小种具有不同的抗性反应, 存在明显的小种专化性, 虽然有些QRL对不同小种的互作方向一致, 但互作效应存在着数量差异。由于在感病亲本中检测到较多的主效和互作QRL, 这些QRL之间的相互作用及其效应的累加, 有利于寄主与病原菌小种之间的稳定化选择, 共同增强寄主抗病性及稳定性效应。

关键词 水稻 白叶枯病 数量抗性座位 小种专化性

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Mapping of Quantitative Resistance Loci to Bacterial Leaf Blight and Their Race Specificity in Rice (*Oryza sativa* L.)

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Abstract The genetic components responsible for quantitative resistance of rice plants to three Philippines races (P2, P6, and P9) of *Xanthomonas oryzae* pv. *oryzae* (Xoo) were dissected using a set of 178 near-isogenic introgression lines (ILs) of Lemont genome introgressed in Teqing background and a complete linkage map with 160 well distributed SSR markers. The japonica cultivar Lemont was susceptible to the three races while the indica cultivar Teqing susceptible to P6 and moderate susceptible to P2 and P9. Transgressive segregations of lesion length for the three races were observed in the IL population, and their distributions were approximately normal. There were significantly positive correlation of resistance among the three races, ranging of correlation coefficients from 0.35 between P2 and P6 to 0.79 between P2 and P9. A total of 10 main-effect QRLs (M-QRL) and 12 pairs of epistatic QRLs (E-QRL) affecting the lesion length of the three races was detected. These QRLs were divided into three groups based on their expressions of resistance to the three races, namely, group 1 QRL which was resistant to one race, group 2 QRL resistant to two races, and group 3 QRL resistant to all the three races. The Lemont alleles at all M-QRLs except *QBr6c* on chromosome 6 were associated with increased lesion length, and decreased resistance. The M-QRL (*QBr11*) detected in the region of RM144-RM123 on chromosome 11, could be allelic to *Xa4* gene, which showed a major additive-effect QRL to moderate virulent races P2 and P9 whereas it was completely defeated by high virulent race P6 and had no any residual effect of resistance. Among 12 E-QRLs, the epistatic effects of the parental type of the three epistatic QRLs (between RM496 and RM120, between RM282 and RM119, and between RM119 and gl-1) were all associated with increased lesion length while the epistatic effects of the recombinant type tended to result in decreased lesion length, and the opposite was true for the other nine epistatic QRLs. Both M-QRL and E-QRL had obvious race specificity, there were differences in magnitude of interaction effects for some QRLs although they shared same directions of interaction. The QRLs detected in this study were compared with those identified in other populations including the recombinant inbred lines derived from the same parents, indicating there are some stable QRLs which expressed across different genetic backgrounds. This study indicated that interaction and cumulative effects of multiple QRLs identified from susceptible parents were favorable to stabilization selection between host and pathogen, which simultaneously provided strong and durable resistance for the host by pyramiding of different stable QRLs.

Key words Rice Bacterial leaf blight Quantitative resistance loci (QRL) Race specificity

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