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[1]李修平,韩英鹏,丁俊杰,等.与耐大豆疫霉根腐病相关的QTL分析[J].大豆科学,2008,27(04):572-575.[doi:10.11861/j.issn.1000-9841.2008.04.0572]

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与耐大豆疫霉根腐病相关的QTL分析

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摘要: 疫霉根腐病是世界范围内的大豆生产上的毁灭性病害。利用470对SSR引物对由耐病品种Conrad×合丰25获得的140个F₂∶5重组自交系(RIL)群体的耐大豆疫霉根腐病基因进行QTL分析,为将耐病基因聚合的分子辅助育种提供理论依据。田间耐病性鉴定于2007年在中国黑龙江省佳木斯和加拿大Woodslee两点进行,并分别采用来自两地的混合菌种进行温室鉴定。经过WinQTL 2.0复合区间法计算,共有4个分子标记(Satt428、Satt600、Satt325和Satt233)与大豆疫霉根腐病显著相关。这些分子标记对病害损失率贡献率从5.47%到27.89%不等。Satt428和Satt600定位在MLG D1b+W上,遗传距离相距10.9 cM; Satt325和Satt233分别定位在MLG F和MLG A2上。通过大环境试验在我国大豆品种合丰25找到与耐大豆疫霉根腐病显著相关的QTL,并定位在MLG A2上。

Abstract: Phytophthora root rot (PRR) caused by Phytophthora sojae M. J. Kaufmann & J. W. Gerdemann is a serious disease of soybean world wide. The objective of this study was to identify the location of quantitative trait loci (QTL) in 'Conrad', a soybean cultivar with broad tolerance to many races of P. sojae, and 'Heifeng 25', a soybean cultivar tolerant to P. sojae in China. The 140 individual of F₂∶5 RIL population derived from Conrad×Heifeng 25 were adopted, and field and green house identification were conducted at Woodslee, Canada and Jiamusi, China in 2007 year, respectively. 470 pair of SSR markers were used and 88 of them showed polymorphism. The genetic map was constructed with Mapmaker/EXP3.0b and QTLs analysis was done by CIM method of WinQTL 2.0. Four markers Satt428, Satt600, Satt325, Satt233, from three linkage group MLG D1b+W, MLG F and MLG A2, were significantly associated with PRR. Each marker explained 5.47% to 27.89% of phenotypic variance. Satt428 and Satt600 were mapped to MLG D1b+W, the genetic distance was 10.9 cM; Satt325 and Satt233 were mapped to MLG F and MLG A2 respectively. Quantitative trait loci on the linkage groups which are associated with PRR was discovered firstly from Heifeng 25, and was mapped to MLG A2. The identified QTLs would be beneficial for marker assistant selection of PRR tolerance varieties against China P. sojae races.

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