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摘要: 利用感大豆胞囊线虫病品种合丰25与抗病品种抗线2号杂交获210个F₂代群体, 利用150对SSR引物, 并采用Windows QTL Cartographer V2.1复合区间法对抗大豆胞囊线虫病的基因进行定位。结果表明: 其中有多态性SSR标记为67个, 占44.67%; 以LOD值大于2.0作为QTL存在的阈值, 检测到2个抗大豆胞囊线虫3号生理小种基因相关的QTL: Qscn-1(Satt163~Satt309), Qscn-2(Sat440~Satt148), 分别定位在MLG G和MLG I上, 且遗传贡献率分别为10.1%和7.6%, 与SSR标记Satt309和Satt148的遗传距离分别为7.2 cM和5.6 cM。

Abstract: Soybean cyst nematode (Heterodera glycines Ichinohe; SCN) is the primary disease responsible for yield loss of soybean [Glycine max (L.) Merr.]. The objectives of this research were to identify quantitative trait loci (QTLs) associated with SCN resistance using the SSR marker technology. In the study, 210 F₂ progeny segregating from a cross between Hefeng 25, a soybean cultivar susceptible to cyst nematode race 3, and Kangxian 2, a soybean cultivar resistance to cyst nematode race 3, were used to screen over 150 SSR markers. A total of 67 SSR markers were distributed in twenty linkage groups. Two QTLs Qscn-1(Satt163~Satt309) and Qscn-2(Sat440~Satt148) relevant to SCN resistance, were detected on MLG G and MLG I when LOD was set as 2.0, and they accounted for 10.1% and 7.6% of the total phenotypic variation, respectively.

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