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摘要: 大豆与根瘤菌共生固氮是大豆生长发育所需氮素的主要来源。由于根瘤菌与大豆两者基因型的不同,接种根瘤菌后大豆固氮能力也不同。以合丰25×固新野生大豆杂交组合的重组自交系(RIL)群体F₁₁的104个株系为材料,在严格控菌条件下,用固氮菌株2178进行结瘤匹配鉴定,测定RIL群体及其亲本固氮酶活性、结瘤数目、侧根数目、根瘤鲜重、茎干重5个指标,对所得数据进行正态分布检验,结合SSR分子数据利用复合区间作图法对其QTL定位分析。结果表明:RIL群体各性状均表现超亲分离,均值介于双亲之间,其偏度和峰度均较小,符合正态分布。这表明所考察性状均为数量性状遗传。应用复合区间作图法进行固氮性状的QTL定位,在A1、L、O、D1b、D2、C2、I连锁群,检测控制固氮的QTL有8个,解释表型变异的7.65%~15.05%,这些QTL及分子标记位点可用于大豆固氮性状的分子标记选择。

Abstract: Nitrogen demand of soybean can be supplied via biological nitrogen fixation. Because genotype of soybean and soybean rhizobium is different, the symbiotic ability is significantly different among soybeans after inoculation. In this study, the F₁₁ populations derived from G. max HeFeng 25×G. soja Guxin were inoculated with B. japonicum strain 2178, and five indexes of RILs population and parents, including activity of nitrogen fixation, No. of nodulation, No. of lateral root, weight of nodulation and weight of stem, were identified at seedling stage. QTL mapping was performed by characteristics of nitrogen fixation trait combined with the composite interval mapping. All the nitrogen fixation traits at seedling stage showed a normal distribution in RIL population, which were suitable to QTL mapping analysis. Eight QTLs on chromosomes A1, L, D1b, D2, C2, I and O associated with nodulation traits at seedling stage were detected, which explained the range of the observed phenotypic variance from 7.65% to 15.05%. These markers can be used in molecular marker selection of soybean nitrogen fixation traits.

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