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摘要: 以栽培大豆TK780与野生大豆Hidaka4杂交后所得的96个重组自交系 (RILs) 群体为材料, 应用已构建好的连锁图谱, 采用MapQTL5.0MQM作图法 (Multiple-QTL Model) 以及Excel 2007软件对F₁₀代群体的蛋白质含量和油份含量进行QTL定位以及相关分析。结果表明: 蛋白含量与油份含量存在负相关关系。同时在该群体中定位到2个与蛋白质含量有关的QTL, 分布于E、I连锁群上, 分别可解释15.6%和21.1%的表型变异; 定位到3个与油份含量有关的QTL, 分布于E、H、I连锁群上, 分别可解释21.1%、17.2%和28.0%的表型变异。其中在连锁群E、I上定位到的2个QTL同时控制蛋白和油份2个性状。

Abstract: A population consisted of 96 recombinant inbred lines of soybean was developed from an intraspecies cross between Glycine max, TK780 and Glycine soja, Hidaka4. A genetic linkage map of soybean genome had been constructed. MapQTL5.0 multiple-QTL model and Excel 2007 were used to identify quantitative loci (QTLs) associated with protein and oil content in the RIL population, and analyze the relationship between seed protein and oil content. The results indicated that there were a negative phenotypic correlation between protein and oil content, and two QTLs related to seed protein content were identified on E and I linkage groups, explaining 15.6% and 21.1% phenotypic variance, respectively; three QTLs related to seed oil content were identified on E, H and I linkage groups, explaining 21.1%, 17.2% and 28.0% phenotypic variance, respectively. In addition, two QTLs were identified which controlled seed protein and oil content simultaneously on E and I linkage groups.

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