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不同世代间大豆蛋白质和脂肪含量相关QTL的稳定性分析

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摘要: 以高油大豆东农46为母本,高蛋白大豆L-100为父本,建立F₂、F_{2:3}、F_{2:4}、F_{2:5}代群体。应用SSR标记技术,对不同世代在不同地点条件下遗传群体的蛋白质、脂肪含量进行QTL分析。结果表明:不同世代群体的蛋白质含量、脂肪含量均接近于正态分布,其中群体脂肪含量偏向于东农46,蛋白质含量偏向于L-100。在F_{2:4}代检测到2个与蛋白质含量相关的QTL,分别位于D2和K连锁群,能够解释的表型变异率为1.92%~2.03%,其中位于Satt226附近的QTL在F₂、F_{2:3}和F_{2:5}代能够稳定地被检测到。在F_{2:4}代检测到2个与脂肪含量相关的QTL,分别位于F和B2连锁群,能够解释的表型变异率为2.56%~6.98%,其中位于Satt577附近的QTL在F_{2:3}、F_{2:5}代能够稳定地被检测到。因此,本研究获得1个与蛋白质含量相关的稳定QTL和1个与脂肪含量相关的稳定QTL。

Abstract: In this study, F₂, F_{2:3}, F_{2:4} and F_{2:5} generation families were formed from a cross between high oil content cultivar Dongnong 46 and the high protein content line L-100. QTL analysis of protein, oil contents for genetic populations were carried via using SSR markers under different generations in different locations. Distribution of the protein and oil content in different generations nearly fitted normal distribution. The expression of the oil content trait in the populations trended to that of the parent Dongnong 46, and the expression of the protein content trait trended to that of the parent L-100. In F_{2:4} generation, 2 QTLs of protein content were detected, located in MLG D2, K, and explained the phenotypic variation from 1.92% to 2.03%; especially the QTL in the vicinity of Satt226 in F₂, F_{2:3} and F_{2:5} generations under different environmental conditions could be stably detected. In F_{2:4} generation, 2 QTLs of oil content were detected, located in MLG F, B2, and explained the phenotypic variation from 2.56% to 6.98%; especially the QTL in the vicinity of Satt577 in F_{2:3} and F_{2:5} generations under different environmental conditions could be stably detected. This study obtained a stable QTL associated with protein content and oil content, separately.

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