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[1] 宁海龙, 吴昊, 李文滨, 等. 大豆四向重组自交系群体全生育期QTL的单标记分析[J]. 大豆科学, 2015, 34(06): 1081-1084, 1089.
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大豆四向重组自交系群体全生育期QTL的单标记分析

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摘要: 以含有160个株系的四向重组自交系为试验材料, 通过188个SSR标记鉴定个体基因型, 利用单标记分析方法, 分析了2年4点试验获得全生育期表型数据, 对该群体的全生育期进行了QTL定位分析。结果表明: 在2013和2014年哈尔滨、克山3个环境下定位了控制大豆全生育期的14个QTL, 分别定位在大豆20个连锁群中的A3、B2、C1、C2、D1b、E、F、G、K、L、N共11个连锁群上, 遗传率为1.34%~9.19%。可延长全生育期的优异等位基因型有BARCSOYSSR_08_0966 (Q3Q3)、Sat_177 (Q2Q2)、Sat_186 (Q3Q3)、Sat_307 (Q3Q3)、Sat_557 (Q1Q1)、Sat_577 (Q2Q2)、Sat_351 (Q1Q1)、Sat_268 (Q1Q1)、Sat_199 (Q1Q1)、Sat_273 (Q3Q3)、Sat_229 (Q1Q1)、Sat_664 (Q1Q1)、Sat_125 (Q4Q4), 能够缩短全生育期的优异等位基因型有BARCSOYSSR_08_0966 (Q2Q2)、Sat_177 (Q1Q1)、Sat_186 (Q1Q1)、Sat_307 (Q2Q2)、Sat_557 (Q2Q2)、Sat_577 (Q4Q4)、Sat_351 (Q2Q2)、Sat_268 (Q3Q3)、Sat_199 (Q3Q3)、Sat_273 (Q2Q2)、Sat_229 (Q3Q3)、Sat_664 (Q3Q3)、Sat_125 (Q3Q3)。Sat_307、Sat_199和Sat_125这3个QTL在2个环境重复检测, 其中Sat_199在两个环境中的遗传率和等位基因的遗传效应差异较小, 受环境条件的影响较小, 可用于分子设计育种。

Abstract: Abstract: In this paper a four-way recombinant inbred lines population with 160 individuals were used to map QTLs underlying the maturity period- 188 SSR primers were used to identify the genotype of the individuals. The maturity period was recorded in the 4 planting environments trails. Single marker analysis method was utilized to analyze the genotypic data and phenotypic data. The result showed that 14 QTLs conditioning maturity period were mapped to located in 11 linkage groups, i.e., A2, B2, C1, C2, D1b, E, F, G, K, L and N, and the heritability varied from 1.34% to 9.19%. The excellent allelic genotype that could delay the maturity include BARCSOYSSR_08_0966 (Q3Q3), Sat_177 (Q2Q2), Sat_186 (Q3Q3), Sat_307 (Q3Q3), Sat_557 (Q1Q1), Sat_577 (Q2Q2), Sat_351 (Q1Q1), Sat_268 (Q1Q1), Sat_199 (Q1Q1), Sat_273 (Q3Q3), Sat_229 (Q1Q1), Sat_664 (Q1Q1), Sat_125 (Q4Q4), and those that could shorten the maturity include BARCSOYSSR_08_0966 (Q2Q2), Sat_177 (Q1Q1), Sat_186 (Q1Q1), Sat_307 (Q2Q2), Sat_557 (Q2Q2), Sat_577 (Q4Q4), Sat_351 (Q2Q2), Sat_268 (Q3Q3), Sat_199 (Q3Q3), Sat_273 (Q2Q2), Sat_229 (Q3Q3), Sat_664 (Q3Q3), Sat_125 (Q3Q3). Among three QTLs i.e., Sat_307, Sat_199 and Sat_125, which were detected in two environments simultaneously, Sat_199 showed little variation in effects of allelic genotypes and heritability across two environments, which showed Sat_199 could be used in molecular design breeding.

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