

两种环境下甘蓝型油菜含油量差异的QTL分析

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QTL Analysis of Oil Content Difference in Two Environments in *Brassica napus* L.

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摘要

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摘要 利用本实验室构建的遗传连锁图谱和复合区间作图法检测重组自交系GH06×P174(SWU-1)和GH06×中油821(SWU-2)群体在2个环境中含油量差值的QTL。以SWU-1群体在2个环境中检测到2个含油量差值QTL, 分别位于2个不同的连锁群, 单个QTL可解释表型变异的10.31%~12.45%; 以SWU-2群体在2个环境中检测到3个含油量差值QTL, 分别位于2个不同的连锁群, 单个QTL可解释表型变异的6.60%~10.58%。分析结果表明, 含油量受环境影响较大, 差值的变异幅度达到0~18.66个百分点, 变异系数达到58.24%, 说明在油菜的油脂合成中, 存在对环境敏感和钝感的基因。含油量差值QTL与2个环境中分别检测到的含油量QTL没有明显的连锁关系, 初步分析说明对环境敏感或钝感的基因与油脂合成基因不是同一个系统。

关键词: 甘蓝型油菜 含油量 环境 差值QTL

Abstract: According to the genetic linkage map established by our laboratory and composite interval mapping (CIM), the QTLs oil content difference between two environments were detected using the recombinant inbred lines (RIL) SWU-1 and SWU-2 in *Brassica napus* L. two QTLs of the oil content difference were located in the two linkage groups, each of the QTLs explained 10.31% - 12.45% of phenotypic variation in SWU-1; three QTLs of the oil content difference were located in the two linkage groups, each of them explained 6.60% - 10.58% of phenotypic variation in SWU-2. The results showed that the oil content difference of the different genotypes was quite different, ranging from 0 to 18.66% and the coefficient of variation was up to 58.24%, which means there are different environment insensitive genes for oil content in the different genotypes. There were no visible linkage relationship between the QTLs of oil content difference and the QTLs of oil content in two environments, which indicated that sensitive and insensitive genes do not have the same genetic expression system as the oil synthesis genes.

Keywords: *Brassica napus* L. Oil content Environment Difference QTL

Received 2010-08-10; published 2010-12-20

Fund:

本研究由国家高技术研究发展计划(863计划)项目(2008AA10Z147), 国家科技支撑计划项目(2009BADA8B01), 国家自然科学基金项目(31071450)和贵州省农科院创新基金项目[黔农科合(创新基金)2010007号]资助。

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引用本文:

李超, 李波, 曲存民, 阎星颖, 付福友, 刘利钊, 谌利, 李加纳. 两种环境下甘蓝型油菜含油量差异的QTL分析[J] 作物学报, 2011, V37(02): 249-254

LI Chao, LI Bei, QU Cun-Min, YAN Xing-Ying, FU Fu-You, LIU Li-Zhao, CHEN Li, LI Jia-Na. QTL Analysis of Oil Content Difference in Two Environments in *Brassica napus* L. [J] Acta Agron Sin, 2011, V37(02): 249-254

链接本文:

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