

水稻幼苗根际联合固氮能力的QTL定位

季天委¹; 方萍¹; 邢永忠²; 贾小明³

1. 浙江大学环境与资源学院 浙江杭州310029; 2. 华中农业大学作物遗传改良国家重点实验室 湖北武汉430070; 3. 浙江大学生命科学院 浙江杭州310029

Mapping quantitative trait loci for associative nitrogen fixation ability in rhizosphere of rice seedling

JI Tian-wei¹; FANG Ping¹; XING Yong-zhong²; JIA Xiao-ming³*

1 College of Envir. and Resour. Sci.; Zhejiang Univ.; Hangzhou 310029; China; 0070; China; 3 College of Life Sci.; Zhejiang Univ.; Hangzhou 310029; China

[摘要](#)[参考文献](#)[相关文章](#)Download: [PDF \(418KB\)](#) | [HTML 0KB](#) | Export: [BibTeX](#) or [EndNote \(RIS\)](#) | [Supporting Info](#)

摘要 以珍汕97×明恢63杂交组合的重组自交系(RIL)群体的241个株系和高效固氮菌株W12以及固氮菌株FY为材料,在严格限菌条件下,利用改进的SpermosphereModel技术,测定RIL群体及其亲本与两个固氮菌株的联合固氮能力表型值。采用MAPMAKER/QTL软件对获得的表型性状进行QTL定位分析,在第2染色体上,检测到控制与W12联合固氮能力(W12.NFA)和与FY联合固氮能力(FY.NFA)的QTL各1个;前者位于标记区间RM208~RM207,后者位于标记区间R712~RM324。分别对这两个QTLs的等位标记RM208与R712作单因子方差分析,得W12.NFA在RM208不同标记基因型间差异的F值为8.28,达0.0044显著性水平;FY.NFA在等位R712不同标记基因型间差异的F值为13.81,达0.0003显著性水平。显然,本研究检出的控制固氮菌株W12和FY与水稻根际联合固氮能力的QTL是相互独立的。

关键词: 固氮菌 重组自交系(RILs)群体 联合固氮能力 QTL 水稻 固氮菌 重组自交系(RILs)群体 联合固氮能力 QTL 水稻

Abstract: In order to reduce production cost and address environmental pollution due to heavy use of chemical nitrogen fertilizer for high rice yield, there is a strong interest in developing high efficiency of rice rhizosphere associative nitrogen fixing system. For this purpose, it is important to breed rice varieties with strong associative nitrogen fixing ability to get high nitrogen fixing efficiency bacteria strains. A strain with high nitrogen fixing efficiency has been isolated in our previous study. In order to breed such rice varieties, we studied the genetic basis of rice associative nitrogen fixing ability. A recombinant inbred lines (RILs) population consisting of 241 recombination lines, derived from an elite combination, Zhenshan97×Minghui 63 and two strains of high efficient nitrogen-fixing bacteria named as W12 and FY were used in this study. The strain W12 with higher nitrogenase activity was isolated from cotton rhizosphere in Egypt and the strain FY was provided by Chinese Academy of Agricultural Sciences. An improved spermosphere mode method was use to detect the nitrogenase activity of each RILs line associated with each nitrogen-fixing bacteria strain. Based on the molecular marker linkage map of RILs population, the QTLs mapping of associated nitrogen fixation ability in rice rhizosphere was done by the method of QTL interval mapping using the program MAPMAKER/QTL. A QTL for each strain was detected at tow independent intervals on the chromosome 2, separately. The qWNFA-2 for W12 is flanked by interval RM208~RM207 with LOD score 2.81 accounting for about 5.4% of the total phenotypic variance and the qFYNFA-2 for FY is flanked by interval R712~RM324 with LOD score 2.98 accounting for about 5.8 % of the total phenotypic variance. According to this result, it was supposed that rice rhizosphere associative nitrogen fixing ability associated with two strains was controlled by different genes.

Keywords:

引用本文:

季天委¹; 方萍¹; 邢永忠²; 贾小明³. 水稻幼苗根际联合固氮能力的QTL定位[J] 植物营养与肥料学报, 2005, V11(3): 394-

JI Tian-wei¹; FANG Ping¹; XING Yong-zhong²; JIA Xiao-ming³. Mapping quantitative trait loci for associative nitrogen fixation ability in rhizosphere of rice seedling [J] Acta Metallurgica Sinica, 2005, V11(3): 394-

Service

- ▶ [把本文推荐给朋友](#)
- ▶ [加入我的书架](#)
- ▶ [加入引用管理器](#)
- ▶ [Email Alert](#)
- ▶ [RSS](#)

[作者相关文章](#)