

不同水分胁迫下小麦胚芽鞘和胚根长度的QTL分析

袁倩倩, 李卓坤, 田纪春*, 韩淑晓*

山东农业大学 / 作物生物学国家重点实验室小麦品质育种室, 山东泰安 271018

QTL Mapping for Coleoptile Length and Radicle Length in Wheat under Different Simulated Moisture Stresses

YUAN Qian-Qian, LI Zhuo-Kun, TIAN Ji-Chun*, HAN Shu-Xiao*

Group of Quality Wheat Breeding of Key Laboratory of Crop Biology / Shandong Agricultural University, Tai'an 271018, China

摘要

参考文献

相关文章

Download: PDF (397KB) HTML 1KB Export: BibTeX or EndNote (RIS) Supporting Info

摘要 小麦胚芽鞘和胚根在不同渗透溶液下的长度变化是鉴别小麦幼苗抗逆性的重要指标。以小麦花培3号×豫麦57的DH株系衍生的含168个组合的永久F₂ (immortalized F₂, IF₂)群体为材料,在蒸馏水(正常条件)以及10%、20%和30%聚乙二醇(PEG-6000)模拟水分胁迫处理下,进行胚芽鞘长和胚根长度的数量性状基因(QTL)定位分析。利用完备区间作图法,共检测到影响胚芽鞘和胚根长度的23个QTL,单个QTL对表型的贡献率为4.93%~35.37%。位于4B染色体区间Xcfd39.2 - Xcfd22.2上影响胚芽鞘长度的位点QCI4B,具有最大的遗传效应,贡献率为35.37%;在3D染色体Xcfd223 - Xbarc323区段,正常条件和20% PEG-6000处理下同时检测到影响胚芽鞘长度的QTL, QCI3D-a,其贡献率分别为7.83%和11.74%。另外,在10% PEG-6000处理下,3D染色体上的相近区域还定位出了影响胚芽鞘长度的QCI3D-b位点;在染色体1A和染色体5A1上各检测出与胚根长度有关的2个和3个不同的QTL;在6D染色体Xswes679.1 - Xcfa2129和Xwmc412.1 - Xcfd49区间分别检测到2个影响胚芽鞘长度和胚根长度的QTL。这些主效QTL可用于胚芽鞘和根系的分子标记辅助选择。

关键词: 小麦 “永久F₂”群体 胚芽鞘长度 胚根长度 QTL

Abstract: Coleoptile length and Radicle length are the important indexes to evaluate resistance of wheat (*Triticum aestivum* L.) seedlings to stresses. For mapping quantitative trait loci (QTLs) for lengths of coleoptile and Radicle in wheat, a set of immortalized F₂ (IF₂) population (168 lines) from Huapei 3 × Yumai 57 double haploid (DH) lines was treated with distilled water (normal condition) and 10%, 20%, and 30% of polyethylene glycol (PEG-6000). The coleoptile length (CL) and radicle length (RL) of the parents and the 168 IF₂ lines were measured after 7 d of treatment. QTLs for CL and RL were detected using 323 SSR markers, which were distributed in the whole genome of wheat. Based on inclusive composite interval mapping (ICIM) method, we identified 11 additive QTLs for CL and 12 additive QTLs for RL under normal and the three stress conditions. Each locus explained 4.93% - 35.37% of phenotypic variance. In the interval between Xcfd39.2 and Xcfd22.2 on chromosome 4B, QTL QCI4B had the phenotypic contribution of 35.37%. Another QTL QCI3D-a located between Xcfd223 and Xbarc323 on chromosome 3D was detected in both normal and 20% PEG-6000 treatments, and explained phenotypic variances of 7.83% and 11.74%, respectively. QTL QCI3D-b was located on the same chromosome and close to QCI3D-a. In the linkage groups 1A and 5A1, three and two QTLs associated with RL were detected respectively. On chromosome 6D, two QTLs for CL and RL were found in the interval between Xswes679.1 and Xcfa2129 and the interval between Xwmc412.1 and Xcfd49, respectively. The major QTLs identified can be applicable in marker-assisted selection in wheat breeding for coleoptile and root.

Keywords: Wheat Immortalized F₂ population Coleoptile length Radicle length Quantitative trait locus

Received 2010-05-18; published 2010-12-15

Fund:

本研究由国家重点基础研究计划(973计划)项目(2009CB118301),国家自然科学基金项目(30971764)和农业部行业科研基金(nyhyzx07-002)资助。

Corresponding Authors: 田纪春, E-mail: jctian@sdau.edu.cn, Tel: 0538-8242040 Email: cartooncecily@163.com

引用本文:

袁倩倩, 李卓坤, 田纪春, 韩淑晓. 不同水分胁迫下小麦胚芽鞘和胚根长度的QTL分析[J] 作物学报, 2011, V37(02): 294-301

YUAN Qian-Qian, LI Zhuo-Kun, TIAN Ji-Chun, HAN Chu-Xiao. QTL Mapping for Coleoptile Length and Radicle Length in Wheat under Different

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

- ▶ 袁倩倩
- ▶ 李卓坤
- ▶ 田纪春
- ▶ 韩淑晓

链接本文:

<http://211.155.251.148:8080/zwx/CN/10.3724/SP.J.1006.2011.00294> 或 <http://211.155.251.148:8080/zwx/CN/Y2011/V37/I02/294>