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论文

不同生态环境条件下小麦籽粒灌浆速率及千粒重QTL分析

王瑞霞1;张秀英1;伍玲2;王瑞3;海林1;闫长生1;游光霞1;肖世和1,*

1 中国农业科学院作物科学研究所 / 国家农作物基因资源与基因改良重大科学工程, 北京100081; 2 四川省农业科学院作物研究所,四川成都610066; 3 安徽省农业科学院作物研究所, 安徽合肥230036 摘要:

以142个和尚麦/豫8679的F7:8重组自交系及其亲本为试验材料,分析了籽粒平均灌浆速率、最高灌浆速率及千粒重在北京(2006, 2007)、安徽合肥(2007)和四川成都(2007)4个生态环境下的性状表现,并利用已构建的含有170个SSR标记和2个EST标记的遗传图谱,对这3个性状进行了QTL定位分析。共检测到54个QTLs,涉及小麦1A、1B、2A、2D、3A、3B、3D、4A、4D、5A、5B、6D 和7D染色体。其中,17个与平均灌浆速率相关,可解释表型变异的7.17%~20.83%; 16个与最高灌浆速率相关,可解释表型变异的6.31%~15.95%; 21个与千粒重相关,可解释表型变异的4.36%~16.80%。另外,在1A、1B、2A、3B、4D、6D和7D染色体上发现10个涉及"一因多效"或紧密连锁位点的基因组区段,有助于了解籽粒灌浆和籽粒产量相关性状的遗传基础。

关键词: 小麦 数量性状位点 重组自交系 灌浆速率 千粒重

QTL Mapping for Grain Filling Rate and Thousand-Grain Weight in Dif-ferent Ecological Environments in Wheat

1 Institute of Crop Sciences, Chinese Academy of Agricultural Sciences / National Key Facility for Crop Gene Resources and Genetic Improvement, Beijing 100081; 2 Crop Research Institute, Sichuan Academy of Agricultural Sciences, Chengdu 610066, Sichuan; 3 Crop Research Institute, Anhui Academy of Agricultural Sciences, Hefei 230036, Anhui, China

1 Institute of Crop Sciences, Chinese Academy of Agricultural Sciences / National Key Facility for Crop Gene Resources and Genetic Improvement, Beijing 100081; 2 Crop Research Institute, Sichuan Academy of Agricultural Sciences, Chengdu 610066, Sichuan; 3 Crop Research Institute, Anhui Academy of Agricultural Sciences, Hefei 230036, Anhui, China

Abstract:

The duration and rate of grain filling determine the individual grain size, thousand-grain weight (TGW), and final grain yield. Several reports have focused on the physiological basis of grain filling in wheat (Triticum aestivum L.), but rare on the genetic mechanism and QTL mapping due to its complexity. To identify QTLs related to grain filling, the $F_{7.8}$ generation of 142 recombinant inbred lines (RILs) derived from the cross between Yu 8679 (large spike) and Heshangmai (small spike) were planted in four ecological environments in Beijing (2006 and 2007), Hefei (2007), and Chengdu (2007). Three agronomic traits including mean grain filling rate (GFR $_{\rm mean}$), maximum grain filling rate (GFR $_{\rm max}$), and TGW were evaluated. A genetic map comprising 170 SSR and 2 EST markers (Tx23-24 and Tx37-38) was constructed based on the 142 RILs. According to the genetic map and phe-notypic data, quantitative trait loci were identified for these agronomic traits using the composite interval mapping (CIM) method. A total of 54 QTLs located on chromosomes 1A, 1B, 2A, 2D, 3A, 3B, 3D, 4A, 4D, 5A, 5B, 6D, and 7D for the three traits were identified over four environments. Among them, 17 for GFR_{mean}, 16 for GFR_{max}, and 21 for TGW, accounted for variations of GFR_{mean} , GFR_{max} , and TGW by 7.17–20.83%, 6.31– 15.95%, and 4.36-16.80%, respectively. Ten genomic sections involving chromosomes 1A, 1B, 2A, 3B, 4D, 6D, and 7D with "pleiotropic effects" were detected. These QTLs with pleiotropic effects are useful for understanding the relationship between grain filling and other related grain yield traits at gene level.

Keywords: Wheat Quantitative trait locus (QTL) Recombinant inbred lines (RILs) Grain filling rate Thousand-grain weight

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