



2019年第40期总80期

小麦遗传育种专题

本期导读

▶ 前沿资讯

1. 稻米同源基因TaAPO-A1与欧洲优良六倍体冬小麦 (*Triticum aestivum* L.) 穗粒数的关系

▶ 学术文献

1. 在ZIP4 (Ph1基因) 突变体小麦-野生杂交种减数分裂过程中增加了同源交叉的频率

2. 面包小麦Sr6茎秆抗锈病新基因SNP标记的全基因组关联研究

3. 利用小麦55K SNP序列对主QTL进行映射以获取分蘖数的时间表达式

▶ 相关专利

1. 与小麦抗条锈病基因Yr1152紧密连锁的分子标记及其应用

中国农业科学院农业信息研究所

联系人：唐研；孟静；顾亮亮

联系电话：0531-66657915

邮箱：agri@ckcest.cn

2019年10月07日

更多资讯 尽在农业专业知识服务系统：<http://agri.ckcest.cn/>

▶ 前沿资讯

1. TaAPO-A1, an ortholog of rice ABERRANT PANICLE ORGANIZATION 1, is associated with total spikelet number per spike in elite European hexaploid winter wheat (*Triticum aestivum* L.) varieties (稻米同源基因TaAPO-A1与欧洲优良六倍体冬小麦(*Triticum aestivum* L.)穗粒数的关系)

简介: 对欧洲518个优质冬小麦品种进行了小穗总数(TSN)、穗长(SL)和开花时间(FT)等性状的遗传基础分析。基于39,908个SNP标记的全基因组关联研究(GWAS)显示,2D、7A、7B染色体上TSN的数量性状位点(QTL)、5A染色体上SL的数量性状位点(QTL)和2D染色体上FT的数量性状位点(QTL)均具有高度显著性,其中2D-QTL是Ppd-D1基因的功能标记。TSN的7A-QTL的物理区域揭示了小麦与AP01-a基因的同源性(TaAPO-A1),而AP01-a基因正是调控着圆锥花序上的小穗数。TaAPO-A1同源基因的种间分析表明,TaAPO-A1是一种高度保守的基因,对花的发育具有重要意义,广泛存在于陆生植物中。对小麦TaAPO-A1基因型的种内研究表明,在保守的F-box区域存在多态性,并定义了两种单倍型。在多态位点发育的KASP标记表明TaAPO-A1与TSN高度显著相关,占总基因型变异的23.2%。此外,TaAPO-A1等位基因在SL和籽粒产量上表现出显著的差异。结果表明,利用小麦序列资源对重要性状的候选基因进行遗传分析具有重要意义。

来源: Nature

发布日期: 2019-09-25

全文链接:

http://agri.ckcest.cn/file1/M00/OE/C9/Csgk0F2MfPGALa2oADJ_n8rINIE660.pdf

▶ 学术文献

1. Magnesium Increases Homoeologous Crossover Frequency During Meiosis in ZIP4 (Ph1 Gene) Mutant Wheat-Wild Relative Hybrids (在ZIP4 (Ph1基因)突变体小麦-野生杂交种减数分裂过程中镁增加了同源交叉的频率)

简介: Wild relatives provide an important source of useful traits in wheat breeding. Wheat and wild relative hybrids have been widely used in breeding programs to introduce such traits into wheat. However, successful introgression is limited by the low frequency of homoeologous crossover (CO) between wheat and wild relative chromosomes. Hybrids between wheat carrying a 70 Mb deletion on chromosome 5B (ph1b) and wild relatives, have been exploited to increase the level of homoeologous CO, allowing chromosome exchange between their chromosomes. In ph1b-rye hybrids, CO number increases from a mean of 1 CO to 7 COs per cell. CO number can be further increased up to a mean of 12 COs per cell in these ph1b hybrids by treating the plants with Hoagland solution. More recently, it was shown that the major meiotic crossover gene ZIP4 on chromosome 5B (TaZIP4-B2) within the 70 Mb deletion, was responsible for the restriction of homoeologous COs in wheat-wild relative hybrids, confirming the ph1b phenotype as a complete Tazip4-B2 deletion mutant

更多资讯 尽在农业专业知识服务系统:<http://agri.ckcest.cn/>

(Tazip4-B2 ph1b). In this study, we have identified the particular Hoagland solution constituent responsible for the increased chiasma frequency in Tazip4-B2 ph1b mutant-rye hybrids and extended the analysis to Tazip4-B2 TILLING and CRISPR mutant-Ae variabilis hybrids. Chiasma frequency at meiotic metaphase I, in the absence of each Hoagland solution macronutrient (NH₄ H₂PO₄, KNO₃, Ca (NO₃)₂·4H₂O or Mg SO₄·7H₂O) was analyzed. A significant decrease in homoeologous CO frequency was observed when the Mg²⁺ ion was absent. A significant increase of homoeologous CO frequency was observed in all analyzed hybrids, when plants were irrigated with a 1 mM Mg²⁺ solution. These observations suggest a role for magnesium supplementation in improving the success of genetic material introgression from wild relatives into wheat.

来源: Frontiers

发布日期: 2018-04-20

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/CA/Csgk0F2QNkSAADibABiQvVJjgDc891.pdf>

2. Genome-Wide Association Study for Identification and Validation of Novel SNP Markers for Sr6 Stem Rust Resistance Gene in Bread Wheat (面包小麦Sr6茎秆抗锈病新基因SNP标记的全基因组关联研究)

简介: Stem rust (caused by *Puccinia graminis* f. sp. *tritici* Erikss. & E. Henn.), is a major disease in wheat (*Triticum aestivum* L.). However, in recent years it occurs rarely in Nebraska due to weather and the effective selection and gene pyramiding of resistance genes. To understand the genetic basis of stem rust resistance in Nebraska winter wheat, we applied genome-wide association study (GWAS) on a set of 270 winter wheat genotypes (A-set). Genotyping was carried out using genotyping-by-sequencing and ~35,000 high-quality SNPs were identified. The tested genotypes were evaluated for their resistance to the common stem rust race in Nebraska (QFCSC) in two replications. Marker-trait association identified 32 SNP markers, which were significantly (Bonferroni corrected $P < 0.05$) associated with the resistance on chromosome 2D. The chromosomal location of the significant SNPs (chromosome 2D) matched the location of Sr6 gene which was expected in these genotypes based on pedigree information. A highly significant linkage disequilibrium (LD, r^2) was found between the significant SNPs and the specific SSR marker for the Sr6 gene (Xcfd43). This suggests the significant SNP markers are tagging Sr6 gene. Out of the 32 significant SNPs, eight SNPs were in six genes that are annotated as being linked to disease resistance in the IWGSC RefSeq v1.0. The 32 significant SNP markers were located in nine haplotype blocks. All the 32 significant SNPs were validated in a set of 60 different genotypes (V-set) using single marker analysis. SNP markers identified in this study can be used in marker-assisted selection, genomic selection, and to develop KASP (Kompetitive Allele Specific PCR) marker for the Sr6 gene.

来源: Frontiers

发布日期: 2018-03-27

全文链接:

http://agri.ckcest.cn/file1/M00/OE/CA/Csgk0F2QNJaAdvR8AB6nT_8AZUs840.pdf

更多资讯 尽在农业专业知识服务系统:<http://agri.ckcest.cn/>

3. Utilization of a Wheat55K SNP Array for Mapping of Major QTL for Temporal Expression of the Tiller Number (利用小麦55K SNP序列对主QTL进行映射以获取分蘖数的时间表达式)

简介: Maximum tiller number and productive tiller number are important traits for wheat grain yield, but research involving the temporal expression of tiller number at different quantitative trait loci (QTL) levels is limited. In the present study, a population set of 371 recombinant inbred lines derived from a cross between Chuan-Nong18 and T1208 was used to construct a high-density genetic map using a Wheat55K SNP Array and to perform dynamic QTL analysis of the tiller number at four growth stages. A high-density genetic map containing 11,583 SNP markers and 59 SSR markers that spanned 4,513.95 cM and was distributed across 21 wheat chromosomes was constructed. A total of 28 single environmental QTL were identified in the recombinant inbred lines population, and among these, seven QTL were stable and used for multi-environmental and dynamic analysis. These QTL were mapped to chromosomes 2D, 4A, 4D, 5A, 5D, and 7D, respectively. Each QTL explained 1.6321.22% of the observed phenotypic variation, with an additive effect from -20.51 to 11.59. Dynamic analysis showed that cqTN-2D.2 can be detected at four growth stages of tillering, explaining 4.9217.16% of the observed phenotypic variations and spanning 13.71 Mb (AX-109283238-AX-110544009: 82189047-95895626) according to the physical location of the flanking markers. The effects of the stable QTL were validated in the recombinant inbred lines population, and the beneficial alleles could be utilized in future marker-assisted selection. Several candidate genes for MTN and PTN were predicted. The results provide a better understanding of the QTL selectively expressing the control of tiller number and will facilitate future map-based cloning. 9.17% SNP markers showed best hits to the Chinese Spring contigs. It was indicated that Wheat55K Array was efficient and valid to construct a high-density wheat genetic map.

来源: Frontiers

发布日期: 2018-03-15

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/CA/Csgk0F2QM50AVtd-ABt6zowYIIE582.pdf>

➤ 相关专利

1. 与小麦抗条锈病基因Yr1152紧密连锁的分子标记及其应用

简介: 本发明涉及分子生物学技术领域, 具体涉及与小麦抗条锈病基因Yr1152紧密连锁的分子标记及其应用。本发明提供小麦抗条锈病新基因Yr1152的精细定位以及与Yr1152基因紧密连锁的2个STS分子标记ID250和ID260。本发明提供的STS分子标记及其特异性引物对可用于高效、快速、准确鉴定抗条锈病小麦品种以及小麦品种是否含有抗条锈病基因Yr1152, 且不受小麦品种的限制, 在小麦抗条锈病基因Yr1152的克隆和检测、抗条锈病小麦鉴定和抗条锈病小麦育种中具有重要意义。

来源: 国家知识产权局

发布日期: 2019-06-21

全文链接:

更多资讯 尽在农业专业知识服务系统: <http://agri.ckcest.cn/>

<http://agri.ckcest.cn/file1/M00/0E/CA/Csgk0F2QN3eAEHriAAwzE5eQEig422.PDF>

业知识服务系统
[/agri.ckcest.cn](http://agri.ckcest.cn)

 农业专业知识服务系统
<http://agri.ckcest.cn>

 农业专
<http://agri.ckcest.cn>

业知识服务系统
[/agri.ckcest.cn](http://agri.ckcest.cn)

 农业专业知识服务系统
<http://agri.ckcest.cn>

 农业专
<http://agri.ckcest.cn>

业知识服务系统
[/agri.ckcest.cn](http://agri.ckcest.cn)

 农业专业知识服务系统
<http://agri.ckcest.cn>

 农业专
<http://agri.ckcest.cn>

更多资讯 尽在农业专业知识服务系统:<http://agri.ckcest.cn/>