



2019年第16期总56期

小麦遗传育种专题

本期导读

▶ 前沿资讯

1. 用于基因组预测的选择性表型培养种群

▶ 学术文献

1. Triticum和Aegilop基因型中 β -葡聚糖的含量
2. 利用高通量分子标记研究面包小麦主要加工品质基因1的等位效应及其变异
3. 有机低投入常规条件下不同种源小麦品种的品质参数比较

▶ 相关专利

1. 一种西北春小麦全基因组关联分析方法

中国农业科学院农业信息研究所

联系人：唐研

联系电话：0531-66657915

邮箱：agri@ckcest.cn

2019年04月22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. Design of training populations for selective phenotyping in genomic prediction (用于基因组预测的选择性表型培养种群)

简介: 表型分析是当前植物育种的瓶颈,尤其是下一代测序技术在过去20年中降低了10万多倍的基因分型成本。因此,需要在育种计划中优化表型的成本。在设计将基因组选择方案实施到育种周期中时,育种人员需要选择:(1)最大限度地提高基因组预测准确性培养种群的最佳方法;(2)提高精度的同时降低表型成本。在本文中,我们比较了两种场景下选择培养种群的方法:首先,当目标是选择一个训练种群集(TRS)来预测来自相同种群的剩余个体(非靶向),其次,当一个测试集(TS)首先被定义和基因型,然后TRS是围绕着TS(靶向)进行优化。我们的结果表明,包括来自测试集(目标)的信息优化方法显示出最高的准确性,这表明来自TS的先验信息改善了基因组预测。此外,预测能力增强,尤其是当种群规模较小时,这是降低育种项目表型成本的目标。

来源: Nature

发布日期: 2019-02-05

全文链接:

http://agri.ckcest.cn/file1/M00/06/69/Csgk0Fy0HWKAbi1_ADIDT1-NZBw814.pdf

▶ 学术文献

1. β -glucan content in a panel of Triticum and Aegilops genotypes (Triticum和Aegilops基因型中 β -葡聚糖的含量)

简介: 非淀粉多糖是膳食纤维的主要成分,不经小肠消化,对人体健康具有有益作用。在谷物中,大麦、燕麦和黑麦的 β -葡聚糖含量最高(从3%到10%),而小麦、大米和玉米的 β -葡聚糖含量低于1%。本文对栽培和野生的小麦品种中 β -葡聚糖含量进行筛选,以确定小麦育种计划中有用的基因型。在一个由43组栽培和野生的二倍体、四倍体和六倍体小麦品种(Triticum和Aegilops品种)组成的小组中测定了 β -葡聚糖的含量,这些小麦在重复的田间试验中生长了两年。硬粒小麦中 β -葡聚糖的平均含量在2016年和2017年测得的数值分别为0.51%和0.55%,差异在0.39%和0.70%之间;小麦野生种的含量在0.41%到1.33%之间。一些山羊草属物种(Ae. markgrafii, Ae. umbellulata, Ae. biuncialis和Ae. negletta)中 β -葡聚糖含量较高,其值高达7.1%。总的来说,所获得的结果表明,某些Aegilops物种的 β -葡聚糖具有广泛的遗传多样性,可以在种间基因转移计划中考虑到这一点,从而研发 β -葡聚糖含量高于2%的小麦品种,其浓度足以使血液中的胆固醇降低10-15%。

来源: Genetic Resources and Crop Evolution

发布日期: 2019-02-10

全文链接:

<http://agri.ckcest.cn/file1/M00/06/69/Csgk0Fy0KACA00VBAANhkhHfyJo069.pdf>

2. Allelic effects and variations for key bread-making quality genes 1 in bread wheat using high-throughput molecular markers (利用高通

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

量分子标记研究面包小麦主要加工品质基因1的等位效应及其变异)

简介: We developed and validated high-throughput Kompetitive Allele-Specific PCR (KASP) assays for key genes underpinning bread-making quality, including the wbm gene on chromosome 7AL and over-expressed glutenin Bx7^{OE} (Glu-B1a1) gene. Additionally, we used pre-existing KASP assay for Sec1 (1B.1R translocation) gene on chromosome 1B. The newly developed KASP assays were compared with gel-based markers for reliability and phenotypically validated in a diversity panel for Mixograph, Rapid Visco Analyzer (RVA) and Mixolab traits. Genotypes carrying the 1B.1R translocation had significantly lower Mixolab parameters than those without the translocation. Similarly, superior effects of the wbm+ and Bx7^{OE} alleles on Mixograph and RVA properties and their extremely low frequencies in global wheat collections supported the idea of using these genes for bread-making quality improvement. The allele frequencies of wbm+ and Bx7^{OE} were extremely low in historical Chinese and CIMMYT wheat germplasm, but were relatively higher in synthetic hexaploid wheats and their breeding derivatives. In both the Vavilov and Watkins global landrace collections, the frequency of wbm+ was 6.4 and 3.5%, and frequency of Bx7^{OE} was 3.2% and 7.0%, respectively. The high-throughput marker resources and large-scale global germplasm screening provided further opportunities to exploit these genes in wheat breeding to enhance bread-making quality.

来源: Journal of Cereal Science

发布日期:2018-12-07

全文链接:

<http://agri.ckcest.cn/file1/M00/06/69/Csgk0Fy0IIuABQc AAnUREC57EE012.pdf>

3. Comparison of quality parameters of wheat varieties with different breeding origin under organic and low-input conventional conditions (有机低投入常规条件下不同种源小麦品种的品质参数比较)

简介: The processing quality of 37 wheat varieties grown in Hungary and Austria (2011/2013) were assessed under organic and conventional low input management. The varieties studied were developed using three breeding strategies (conventional, organic and their combination: BFOA). The aim was to evaluate the effect of the field management and to assess the performance of varieties developed using different breeding methods, based on their quality traits under different managements. Furthermore, properties were identified that could characterize wheat quality and be used effectively for selection under both types of growing conditions. Strong year and genotype effects were found for all the quality traits (protein, starch, gluten, GI, Zeleny, Farinograph water absorption, development time, stability and quality number, falling number, flour yield, hardness index) of the studied varieties, while the effect of the management was significant for the physical properties (test weight, thousand-kernel weight, hardness) and gluten quality characters (gluten spread, GI, dough stability) of the grain. The standard deviation of the gluten quality traits characterized the differences between the breeding strategies. It proved possible to pre select organic varieties for quality traits with high broad-sense heritability under conventional growing conditions,

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

but direct selection in organic fields is suggested for gluten quality characters.

来源: Journal of Cereal Science

发布日期: 2016-05-22

全文链接:

<http://agri.ckcest.cn/file1/M00/06/69/Csgk0Fy0IeKAEwqbABJBbFZGanY230.pdf>

➤ 相关专利

1. 一种西北春小麦全基因组关联分析方法

简介: 本发明公开了一种西北春小麦全基因组关联分析方法, 包括: 选择小麦种子种植; 成熟期测株高、穗长、小穗数、穗粒数、基部不孕小穗数; 成熟后收获种子, 测种子粒宽、粒长、重量, 计算千粒重; 用CTAB法提取DNA, 制备DArT芯片; 采用STRUCTURE计算小麦品种群体结构, 利用贝叶斯模型划分群体结构, 采用TASSEL进行群体连锁不平衡分析, 获得与产量和种子特性相关的DArT分子标记; 包括12个株高关联标记; 2个穗长相关标记; 8个小穗数相关标记; 3个穗粒数关联标记; 4个不实小穗数关联标记; 3个粒长关联标记; 1个千粒重关联标记; 4个粒宽关联标记。本发明的DArT分子标记可应用于农业育种中。

来源: 国家知识产权局专利检索与分析

发布日期: 2018-12-05

全文链接:

<http://agri.ckcest.cn/file1/M00/06/69/Csgk0Fy0K00AbEaQABg5W67uAfI560.PDF>