



2019年第18期总58期

# 小麦遗传育种专题

## 本期导读

### ▶ 前沿资讯

1. 在 $\gamma$ -辐射或CRISPR/Cas9引起的六倍体面包小麦基因的缺失或突变中利用GlutEnSeq捕获测序系统蛋白1基因家族

### ▶ 学术文献

1. 在土壤资源丰富的低纬度春小麦中,作物密度、行距和苗床对产量的影响:更新

2. 两个合成W7984×Opata参考群体的密集基因型测序连锁图谱为小麦结构多样性的研究提供了依据

3. 用于农作物育种资源管理和系谱跟踪的黄金种子育种云平台

### ▶ 相关专利

1. 一个小麦白粉病成株期抗性QTL及其分子标记

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](mailto:agri@ckcest.cn)

2019年05月06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. Development of the GlutEnSeq capture system for sequencing gluten 1 gene families in hexaploid bread wheat with deletions or mutations induced by $\gamma$ -irradiation or CRISPR/Cas9 (发展GlutEnSeq捕获测序系统蛋白1基因家族在六倍体面包小麦与缺失或突变引起的 $\gamma$ -irradiation或CRISPR/Cas9)

**简介:** 我们研发了一种溶液中谷蛋白外显体捕获系统GlutEnSeq(谷蛋白基因富集和测序), 覆盖了来自不同小麦类物种和不同品种的数千个原激肽基因的序列变异。我们用光源测序法评估了这种捕获系统在小麦六倍体中的效果。根据中国春(CS)参考基因组序列确定目标区域, 谷蛋白基因序列通常在10000倍左右富集。谷蛋白基因的缺失在CS删除1BS-19/6DS-4线的情况下, 检测到没有谷蛋白基因覆盖在1B和Un染色体(包含未映射的6D染色体的 $\alpha$ -醇溶蛋白基因)。两个 $\gamma$ 射线照射的品种Paragon, 其醇溶蛋白谱显示受到影响, 发现6A染色体中的 $\alpha$ -醇溶蛋白和1B染色体中的 $\gamma$ -醇溶蛋白的纯合缺失。四个Fielder CRISPR/Cas9醇溶蛋白基因编辑的序列显示1B染色体中的 $\gamma$ -醇溶蛋白纯合子缺失, 6A染色体中的 $\alpha$ -醇溶蛋白杂合子缺失。我们还发现一些谷蛋白基因中的谷蛋白基因覆盖率降低。

**来源:** Journal of Cereal Science

**发布日期:** 2019-04-24

**全文链接:**

<http://agri.ckcest.cn/file1/M00/06/6B/Csgk0FzFXDSAwsP8ABFXj8TEeuw501.pdf>

## ▶ 学术文献

### 1. Yield response to plant density, row spacing and raised beds in low latitude spring wheat with ample soil resources: An update (在土壤资源丰富的低纬度春小麦中, 作物密度、行距和苗床对产量的影响: 更新)

**简介:** This paper reviews the results of published and unpublished experiments over 30 years looking at the effect on yield of planting density and row spacing, and of raised bed planting, of modern irrigated short wheat cultivars under the favourable climatic conditions of northwest Mexico. With optimum planting dates (mid Nov. to mid Dec.), regardless of row spacing, wheat yield was remarkably insensitive to planting density within the range normally studied (80400 plants/m<sup>2</sup>). However yield was sensitive to row spacing: the most sensitive cultivars (erect dwarf cultivars) lost yield at spacing 30&thinsp;cm and greater, while the least sensitive (some taller vigorous semidwarf cultivars) tolerated spacing up to at least 50cm without yield loss. Yield sensitivity to wide spacing was unaffected by density but varied between years, being less in favourable cooler years, and was markedly greater with later plantings (Jan.). The response to yield on narrow raised beds (23 rows per bed, 7590&thinsp;cm between bed centres), which have many agronomic advantages, could be

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

explained by the aforementioned yield responses to spacing, in this case the furrow gap or distance between rows on adjacent beds being critical. Yield testing with a furrow gap of 4450 cm appeared to select cultivars more suited to this system, but it wasn't clear whether such cultivars represented the best option under normal 20 cm row spacing in the absence of raised beds. When testing was extended to very low plant densities, yield was remarkably insensitive (maximum yield often achieved with only 16/m<sup>2</sup>), provided the planting date was normal and the planting arrangement did not deviate greatly from a square grid, with the honeycomb design giving an additional small yield advantage. These yield responses reflect the great plasticity in wheat imparted especially by tillering, and appear to be reasonably well explained by the notion that maximum yield requires close to full light interception no later than just before flag leaf emergence, being the onset of dry weight accumulation in growing spikes. Greater leaf greenness and probably higher radiation use efficiency with very low densities (and wide gaps), and associated delays in 50% flowering, may also assist in compensation for gaps. In contrast to much conventional wisdom, it is suggested that a worthwhile breeding objective would be selection for high per spaced-plant yield, with a view to achieving normal (or better) commercial yields at very low plant densities (< 20/m<sup>2</sup>), thereby opening up opportunities for new breeding and agronomic strategies in this era of precision cropping.

来源: Field Crops Research

发布日期: 2019-02-15

全文链接:

<http://agri.ckcest.cn/file1/M00/06/6B/Csgk0FzFZH6AGeVpAAAt0VZS3m1Y130.pdf>

## 2. Dense genotyping-by-sequencing linkage maps of two Synthetic W7984×Opata reference populations provide insights into wheat structural diversity (两个合成W7984×Opata参考群体的密集基因型测序连锁图谱为小麦结构多样性的研究提供了依据)

简介: 小麦 (*Triticum aestivum*) 遗传图谱是遗传学研究的关键工具。利用基因型-测序 (GBS) 衍生标记对W7984杂交组合的重组自交系 (RIL) 和双单倍体 (DH) 群体进行Opata定位, 探讨重组控制的特点。RIL和DH群体、SynOpRIL和SynOpDH分别由906个和92个个体组成。本研究构建了2,842和2,961 cM的高密度遗传连锁骨架图, 分别包含3,634和6,580个标记。利用推算法, 我们在SynOpRIL和SynOpDH地图上分别添加了43,013和86,042个标记。我们观察到端粒区域的优先重组和中心体周围区域的减少重组。重组率在亚基因组间存在差异, 两个种群的D基因组重组率最高, 为0.26-0.27 cM/Mb。QTL映射识别出与交叉数相关的两个加性位点和三个上位性位点。此外, 我们利用SynOpDH发现的POPSEQ数据, 探讨了W7984和Opata的结构变化, 我们发现W7984缺少5AS染色体, 还发现2332个变异大于100kb, 结构变异在远端区域更为丰富, 并重叠了9196个基因, 这两个图谱为性状定位和基因组辅助育种提供了资源。

来源: Nature

发布日期: 2019-02-11

全文链接:

<http://agri.ckcest.cn/file1/M00/06/6B/Csgk0FzFY2WAD8RiAFEL1QrsJHY682.pdf>

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

### 3. Golden seed breeding cloud platform for the management of crop breeding material and genealogical tracking (用于农作物育种资源管理和系谱跟踪的黄金种子育种云平台)

简介: Effectively identifying and analyzing materials are key procedures for breeding novel crop varieties because of the large quantities of materials and their combinations. This paper presents an approach for crop breeding material management, improvement of crop breeding efficiency, and genealogical tracking through the golden seed breeding cloud platform (GSBCP). The system was developed with Java on an Eclipse integrated development environment. To support a large number of users, security, credibility, and expandability, we selected a cloud-based architecture for the system, in which material attribute, pedigree, and trait information were customized by a template. An intelligent retrieval function was provided for the rapid search of breeding materials, and material trait information, historical data, genealogical information, trial data analysis results and material images can be retrieved in the system. For the analysis of the materials' genealogy, the rules of genealogy were regulated. The genealogy of the breeding materials was automatically generated on the basis of these rules, which support many breeding methods, such as selfing, hybridization, double cross, three-way cross, and backcross. The developed system has been successfully applied in many Chinese breeding enterprises and scientific research institutions. The system provided a low-cost and highly efficient solution for crop material information management and genealogical tracking.

来源: Crop Protection

发布日期: 2018-09-01

全文链接:

<http://agri.ckcest.cn/file1/M00/06/6B/Csgk0FzFXh0ABN7kABzcsEbEDU4827.pdf>

## ➤ 相关专利

### 1. 一个小麦白粉病成株期抗性QTL及其分子标记

简介: 本发明属于小麦遗传育种领域, 提供了一个小麦白粉病成株期抗性QTL, 命名为QPm594\_1D (定位结果如图1), 位于普通小麦的1D染色体短臂, 对小麦白粉病表现为成株期抗性, 可以解释至少15%的表型变异; QPm594\_1D与命名为KASPQPm594\_1D高通量分子标记紧密连锁, 该分子标记为单核苷酸多态性位点, SNP位点处为G/A突变; 该分子标记用一组引物检测, 所述引物包括2条正向引物, 1条反向引物; 该QTL位点的正向等位变异来自亲本品种TutoumaiA。该QTL分子标记在辅助育种中、小麦优良性状基因聚合过程中、小麦抗病种质检测中具有较大的应用价值。

来源: 国家知识产权局专利检索与分析

发布日期: 2018-10-28

全文链接:

<http://agri.ckcest.cn/file1/M00/06/6B/Csgk0FzFZT6ACJQxAAi4cWjikRY949.PDF>