



2019年第29期总69期

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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](mailto:agri@ckcest.cn)

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## ▶ 前沿资讯

### 1. 10天3破全国冬小麦单产纪录, 山东为何这么牛

**简介:** 纵观全国冬小麦高产“冠军”队伍, 不乏山东品种的身影。由山东省农科院培育的济麦22, 2009年取得单产789.9公斤的成绩, 一举打破了尘封10年之久的全国冬小麦单产最高纪录。在2009年至2017年的秋播中, 济麦22连续9年种植面积全国最大, 至今累计推广2.7亿亩。山东, 小麦育种科研队伍强大, 为业界所首肯。其中, 尤其以山东农业大学、山东省农科院、烟台市农科院成果最多。

**来源:** 中华人民共和国农业农村部

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<http://agri.ckcest.cn/file1/M00/06/88/Csgk0F0r2fuAD06MAAJY7T0zTF4437.pdf>

## ▶ 学术文献

### 1. Simultaneous selection for grain yield and protein content in genomics- assisted wheat breeding (基因组辅助小麦育种中籽粒产量和蛋白质含量的同时选择)

**简介:** Genomic selection has been implemented in many national and international breeding programmes in recent years. Numerous studies have shown the potential of this new breeding tool; few have, however, taken the simultaneous selection for multiple traits into account that is though common practice in breeding programmes. The simultaneous improvement in grain yield and protein content is thereby a major challenge in wheat breeding due to a severe negative trade-off. Accordingly, the potential and limits of multi-trait selection for this particular trait complex utilizing the vast phenotypic and genomic data collected in an applied wheat breeding programme were investigated in this study. Two breeding strategies based on various genomic-selection indices were compared, which (1) aimed to select high-protein genotypes with acceptable yield potential and (2) develop high-yielding varieties, while maintaining protein content. The prediction accuracy of preliminary yield trials could be strongly improved when combining phenotypic and genomic information in a genomics-assisted selection approach, which surpassed both genomics-based and classical phenotypic selection methods both for single trait predictions and in genomic index selection across years. The employed genomic selection indices mitigated furthermore the negative trade-off between grain yield and protein content leading to a substantial selection response for protein yield, i.e. total seed nitrogen content, which suggested that it is feasible to develop varieties that combine a superior yield potential with comparably high protein content, thus utilizing available nitrogen resources more efficiently.

**来源:** Springer

**发布日期:** 2019-06-01

**全文链接:**

<https://link.springer.com/article/10.1007%2Fs00122-019-03312-5>

## 2. Genetic mapping and expressivity of a wheat multi-pistil gene in mutant 12TP (小麦多雌蕊基因12TP突变体的遗传定位与表达)

**简介:** 2012年, 我们从一个F2育种群体中鉴定出了一个小麦(*Triticum aestivum* L.) 多雌蕊突变体, 命名为12TP(一朵小花中有三个雌蕊)。遗传分析表明, 一个显性基因位点控制着雌蕊的多性状。使用来源于原突变体12TP的纯合正常和多雌蕊系(近等基因系; NILs), 通过简单序列重复(SSR)标记法定位于染色体臂2DL上的12TP位点。4个SSR标记分别在 15.85 cM、10.47 cM、2.89 cM 和 10.37 cM 处与 12TP 连接, 顺序为 Xcfd233&rarr;Xcfd62-12TP&rarr;Xwmc41&rarr;Xcfd168。在7个纯合子12TP系中, “一花三雌蕊”性状的平均遗传表达率超过98%; 然而, 杂合F1植株的平均遗传表达率约为49%。因此, 12TP是一个半显性基因座, 与以前报道的所有多雌蕊突变体不同。突变体12TP是研究小麦花发育和高产小麦育种的一种新种质资源。

**来源:** ScienceDirect

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**全文链接:**

<http://agri.ckcest.cn/file1/M00/00/01/Csgk0V0r2zuAR9NCAxmt0rQAI551.pdf>

## 3. Dissecting the genetics underlying the relationship between protein content and grain yield in a large hybrid wheat population (从遗传学角度分析了杂交小麦群体蛋白质含量与籽粒产量之间的关系)

**简介:** Grain yield and quality-related traits such as protein content and sedimentation volume are key traits in wheat breeding. In this study, we used a large population of 1604 hybrids and their 135 parental components to investigate the genetics and metabolomics underlying the negative relationship of grain yield and quality, and evaluated approaches for their joint improvement. We identified a total of nine trait-associated metabolites and show that prediction using genomic data alone resulted in the highest prediction ability for all traits. We dissected the genetic architecture of grain yield and quality-determining traits and show results of the first mapping of the derived trait grain protein deviation. Further, we provide a genetic analysis of the antagonistic relation of grain yield and protein content and dissect the mode of gene action (pleiotropy vs linkage) of identified QTL. Lastly, we demonstrate that the composition of the training set for genomic prediction is crucial when considering different quality classes in wheat breeding.

**来源:** Springer

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<http://agri.ckcest.cn/file1/M00/00/01/Csgk0V0r3sCALSL0ABRsI8vkyzI995.pdf>

### ➤ 相关专利

#### 1. 一种用于检测抗赤霉病QTL Qfhb . hbaas-5AL的分子标记及使用 方法

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**简介：**本发明公开了一种用于检测抗赤霉病QTL Qfhb.hbaas-5AL的分子标记及使用方法。本发明提供了检测小麦染色体5AL的SNP IWB42293位点的基因型的物质在鉴定或辅助鉴定小麦赤霉病抗性中的应用；还提供了检测小麦染色体5AL的SNP IWB42293位点的基因型的物质在制备鉴定或辅助鉴定小麦赤霉病抗性产品中的应用。本发明通过全基因组关联分析(GWAS)发现了位于小麦5A染色体短臂上抗赤霉病位点Qfhb.hbaas-5AL，进一步将其关联SNP IWB42293转化为普通PCR标记M-5AL-Fhb，该标记可用于检测抗赤霉病QTL Qfhb.hbaas-5AL的基因型，并用于抗赤霉病分子育种。

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