



2019年第11期总51期

# 小麦遗传育种专题

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1. 小麦亩穗数主效QTL的分子标记及其应用

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## ▶ 前沿资讯

### 1. Improved Cd, Zn and Mn tolerance and reduced Cd accumulation in grains with wheat-based cell number regulator TaCNR2 (利用小麦细胞数量调节剂TaCNR2提高小麦对镉、锌、锰的耐受性减少籽粒中镉的积累)

**简介:** 土壤微量元素缺乏和重金属污染影响植物的生长发育, 但通过遗传育种提高微量元素的吸收和减少重金属的积累, 有助于缓解这一问题。小麦细胞数量调节剂2(TaCNR2)与植物抗镉蛋白相似, 可参与调节重金属易位。本研究的目的是了解TaCNR2对重金属耐受性和易位的影响, 研究中, 实时定量PCR表明, 在镉、锌和锰处理下, 小麦幼苗中TaCNR2的表达增加。拟南芥和水稻中TaCNR2的过度表达增强了其对镉、锌和锰的胁迫耐受性, 水稻中TaCNR2的过度表达改善了镉、锌和锰从根到芽的易位。高表达水稻的谷壳镉、锌、锰含量较高, 而糙米的镉含量较野生稻少, 锰含量较高。结果表明, TaCNR2可以运输重金属离子。因此, 本研究为提高作物营养吸收和减少有毒金属积累提供了一种新的基因资源。

**来源:** Nature

**发布日期:** 2019-01-29

**全文链接:**

<http://agri.ckcest.cn/file1/M00/06/60/Csgk0FyGBBuAPMwEAGQdj87qaN8155.pdf>

## ▶ 学术文献

### 1. Yield of chromosomally engineered durum wheat-Thinopyrum ponticum recombinant lines in a range of contrasting rain-fed environments (一系列对比鲜明的雨养环境中硬粒小麦-长穗偃麦草重组系染色体工程产量分析)

**简介:** Introgressions of *Thinopyrum ponticum* 7AgL chromosome segments, spanning 23%, 28% and 40% of the distal end of durum wheat 7AL arm, were previously shown to contain multiple beneficial gene(s)/QTL for yield-related traits, in addition to effective disease resistance (Lr19, Sr25) and quality (Yp) genes. In the present study, durum wheat near isogenic recombinant lines (NIRLs), harbouring each of the three introgressions, were included for the first time in multi-location field trials, to evaluate general and environment-specific effects of the alien chromatin on 26 yield-related traits. Results from nine different trials across contrasting environments of Italy, Morocco and South Australia over four years revealed that the overall impact of 7AgL introgressions into the tetraploid wheat background did not incur, except in one environment, a major yield penalty. The effect of the three 7AgL segments on individual yield-contributing traits resulted in significant increases of biomass m<sup>-2</sup> (+9%), spike number m<sup>-2</sup> (+13%), grain number m<sup>-2</sup> (+11%) and spikelet-1 (+8%), as well as a significant decrease in grain weight (-8%). When the separate NIRLs were analysed, each of the three 7AgL segments were associated with specific yield component variation. The effects of the 40%-long segment proved to be the most stably

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expressed across environments and involved significant increases of spike and grain number m<sup>-2</sup> (13% and 15%, respectively), grain number spike<sup>-1</sup> (10%) and spike fertility index (46%), though accompanied by a significant decrease in thousand grain weight (-23%). In spite of this trade-off between grain number and grain weight, their interplay was such that in four trials, including drier environments, a grain yield advantage was observed. This evidence, and comparison with the two other NIRLs, substantiates the hypothesized existence of major gene(s)/QTL for grain number in the most proximal 2840% 7AgL region, exclusive to the 40%-long 7AgL introgression. The present study represents an important validation of the use of chromosomally engineered genetic stocks for durum wheat improvement, targeting not only disease resistance and quality traits but also relevant yield components.

来源: Field Crops Research

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/60/Csgk0FyGFLGAUeq7ABbgGLFnLpE635.pdf>

## **2. An update of low molecular weight glutenin subunits in durum wheat relevant to breeding for quality (硬粒小麦低分子量谷蛋白亚基的研究进展)**

简介: 低分子量谷蛋白等位基因的鉴定是早期选育优质等位基因组合的重要工具。本研究旨在分析硬粒小麦核心种质谷蛋白的等位基因变异,以提高硬粒小麦育种的遗传变异性,并研究某些亚单位的遗传控制。研究描述了谷蛋白中新的和未分类的等位基因变体,并通过遗传分析确定某些亚单位的遗传控制。研究发现,低分子量谷蛋白亚单位之间以及低分子量谷蛋白和醇溶蛋白之间的联系,对于准确鉴定某些等位基因非常有用。本研究的结果允许更新目前在硬粒小麦中发现的低分子量谷蛋白亚单位(已编目和未编目)。这些信息对于鉴定Glu-3和Glu-B2基因位点的等位基因非常有价值。此外, Glu-B3的一些新等位基因对谷蛋白强度有积极影响,应作为今后研究的目标。

来源: Journal of Cereal Science

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/60/Csgk0FyGIF2AP5NpAA3s2IxzHaw017.pdf>

## **3. Wheat functional genomics in the era of next generation sequencing: An update (小麦功能基因组学在下一代测序时代的一个更新)**

简介: Bread wheat is not only an important cereal crop but also a model for study of an allopolyploid plant with a large, highly repetitive genome. Advances in next-generation sequencing (NGS) technology provide needed throughput to conquer the enormous size of the wheat genome. Multiple high quality reference genome sequences will soon be available. Full-scale wheat functional genomics studies are dawning. In this review we highlight the available tools and methodologies for wheat functional genomics research developed with the assistance of NGS technology and recent progress, particularly the concerted effort in

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generating multiple reference genomes, strategies to attain genome-wide genetic variation, genome-wide association studies, mutant population generation, and NGS-supported gene cloning and functional characterization. These resources and platforms lay a solid foundation for wheat research, leading to a new era of wheat functional genomics that will bridge the gap between genotype and phenotype. Dissection of wheat genomes and gene functions should assist in genomics-assisted selection and facilitate breeding of elite varieties for sustainable agriculture in China and the world.

来源: The Crop Journal

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<http://agri.ckcest.cn/file1/M00/06/60/Csgk0FyGDtCACsPlAAYyYbDKPWA812.pdf>

## ➤ 相关专利

### 1. 小麦亩穗数主效QTL的分子标记及其应用

简介: 本发明公开了一种小麦亩穗数主效QTL的分子标记及其应用。本发明开发了一个与亩穗数主效QTL紧密连锁的Indel标记4BIN2, 可以在苗期有效筛选出不同群体亩穗数的小麦株系, 节约实验成本, 快速筛选出亩穗数多的小麦株系, 提高选择效率, 加速小麦产量育种的进程。

来源: 国家知识产权局专利检索及分析

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<http://agri.ckcest.cn/file1/M00/06/60/Csgk0FyGIpyATSuzAAyn0-51034897.PDF>