



2019年第30期总70期

## 小麦遗传育种专题

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## ▶ 前沿资讯

### 1. Old for new, using ancient genetic variation to supercharge wheat (以旧换新, 利用古老的遗传变异来给小麦增产)

**简介:** 这项由国际小麦产量合作联盟 (IWYP) 资助的研究揭示了辐射利用效率 (RUE, 如何将阳光转化为植物质量) 在提高小麦产量潜力方面的作用: 如何在不牺牲粮食产量的情况下提高植物生物量是一个重大挑战。本研究的重点是: 确定影响春小麦RUE和生物量积累的基因组区域; 如何通过将“外来”小麦战略整合到育种计划中来实现RUE的增长; 鉴定影响产量、生物量和辐射利用效率的常见基因组区域; 在不同生长阶段与RUE相关的基因组区域中与光保护相关的基因的富集; 鉴定可被科学家和育种家利用的未开发的小麦变异。

**来源:** EurekAlert

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<http://agri.ckcest.cn/file1/M00/06/89/Csgk0F01E3mAL6YpAABoi35xrRw823.pdf>

## ▶ 学术文献

### 1. Wheat drought-tolerance to enhance food security in Tunisia, birthplace of the Arab Spring (在阿拉伯之春的发源地突尼斯, 小麦抗旱能力增强了粮食安全)

**简介:** The beginning of the ‘Arab Spring’ in 2011, a regional revolution which started in the Tunisian city of Sidi Bouzid in late 2010, occurred in part as a result of drought-triggered high wheat prices, which in the past led to ‘bread riots’ across several Middle East and North Africa (MENA) nations. Here we present, for the first time, an analysis of possible amelioration of wheat yield loss and greater stability in bread supply resulting from the incorporation of putative drought-tolerant traits into wheat cultivars grown in Tunisia. To this end, we used a simulation crop modeling approach using SSM-Wheat to evaluate yield loss or gain resulting from three types of water-saving traits that have been recently identified in wheat. These consisted in partial stomatal closure at high soil water content, overall decrease in transpiration rate (TR), and partial stomatal closure under elevated vapor pressure deficit (VPD). To capture large gradients in seasonal precipitation across wheat growing areas over a small country such as Tunisia, a grid pattern of 29 × 29 km was established as a basis for the geospatial simulation. Surprisingly, the simulation reflected opposite strategies in terms of water use (water-saving vs aggressive water use). The highest yield gain (30%) resulting from water-saving modification was found to occur in the food-insecure region of Sidi Bouzid. Traits enabling aggressive water use were found to be generally favorable across Tunisia, with one trait leading to up to 80% and 40% increases in yield and its stability in the food-challenged south of the country. However, major yield penalties were found to occur if water-saving traits were to be deployed in the ‘wrong’ region. Those findings could be used as a blueprint to navigate complex trait × environment interactions and to better inform local

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breeding and management programs to improve wheat yield and its stability in Tunisia and the MENA region in general.

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<http://agri.ckcest.cn/file1/M00/06/8A/Csgk0F01GxGAARZeAC5LP500Qpo950.pdf>

## **2. QTL mapping for micronutrients concentration and yield component traits in a hexaploid wheat mapping population (六倍体小麦群体微量营养素浓度和产量组成性状的QTL定位研究)**

简介: Bread wheat is a major staple cereal provides more than 20% of dietary energy and protein supply to global population. However, with increasing population growth, the problem of nutritional deficiencies is increasingly affecting the health of resource people with predominantly cereal-based diet. Therefore, the development of wheat genotypes with micronutrient-dense grains along with high-yield potential is one of the major priorities of wheat biofortification program at CIMMYT. We conducted a QTL mapping study using a recombinant inbred line (RIL) population derived from a cross between a Chinese parental line with highGZnC and a Mexican commercial bread wheat cultivar Roelfs F2007 to identify QTLs that could potentially be integrated in mineral nutrient concentrations and agronomic-related traits breeding. We evaluated 200 RIL lines for mineral nutrient concentrations and agronomic-related traits over two years. A total of 60 QTLs were detected, of which 10 QTLs for GZnC, 9 for GFeC, 5 for GPC and 36 for agronomic-related traits. Moreover, a total of 55 promising candidate genes were identified from the list of associated markers for GFeC and GZnC using the recently annotated wheat genome sequence. We identified the promising genomic regions with high mineral nutrient concentrations and acceptable yield potential, which are good resource for further use in wheat biofortification breeding programs.

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## **3. An eight-year survey of wheat shows distinctive effects of cropping factors on different Fusarium species and associated mycotoxins (8年的小麦调研表明: 不同的种植因子对不同的镰刀菌种及相关真菌毒素有明显的影晌)**

简介: 在8年的时间里, 我们从瑞士的种植者那里获得了686份冬小麦的谷物样本和关于其种植历史的信息。为评估镰刀菌头疫病 (FHB) 的发病风险, 对镰刀菌种发生情况、霉菌毒素含量、镰刀菌 *F. graminearum* (FG) 和 *F. poae* (FP) DNA 的丰度以及 15-乙酰-脱氧雪烯醇 (15ADON)、3-乙酰-脱氧雪烯醇 (3ADON) 和雪烯醇 (NIV) 三种化学类型进行了检测。在所有镰刀菌种中, FG 和 FP 占主导地位, FG DNA 的平均丰度是 FP 的 3 倍。15ADON 化

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学型的平均检出率是3ADON和NIV的两倍。脱氧雪烯醇(DON)、泽拉酮(ZEA)和雪烯醇(NIV)是最常检测到的毒素。11%的DON和7%的ZEA样本都超过了人类食用未加工谷物的欧洲最高限量。此外, NIV最有可能由四种不同的镰刀菌产生。多重对应分析表明, 与早熟作物、少耕、抗FHB性差的品种和含甲氧丙烯酸酯的杀菌剂相比, 作物籽粒样品中的FG和DON含量较高, 其他作物耕作使土壤总氮含量降低了78%至95%。相比之下, 高水平的FP、NIV与耕地和以前的油菜籽样本有关。这些发现以及FP DNA与FG发生率、ZEA和DON之间的负相关关系表明, FP具有不同的生态位或对生长和感染的需求不同。

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## ➤ 相关专利

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

简介: 本发明公开了一种用于检测抗赤霉病QTL Qfhb. hbaas- 5AS的分子标记及使用方法。本发明提供了检测小麦染色体5AS的SNP IWB21456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5AS的SNP IWB21456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- 5AS, 进一步将其关联SNP IWB21456转化为普通PCR标记KASP- Fhb5AS, 两者对240份材料分型一致率为96.7%。该标记可用于检测抗赤霉病QTL Qfhb. hbaas- 5AS的基因型, 并用于抗赤霉病分子育种。

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