



2018年第35期总35期

## 小麦遗传育种专题

### 本期导读

#### ▶ 前沿资讯

1. 快速育种技术为新的绿色革命播下了种子

#### ▶ 学术文献

1. 测定小麦苗期盐耐性和微量营养素含量的数量性状基因图谱
2. 美国冬小麦抗白粉病的全基因组关联分析
3. 英国小麦秆锈病再次出现的可能性研究

#### ▶ 相关专利

1. 小麦分子标记及其在鉴定小麦白粉病抗性中的应用

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)

2018年11月26日

## ▶ 前沿资讯

### 1. Speed breeding technique sows seeds of new green revolution (快速育种技术为新的绿色革命播下了种子)

**简介:** 先进的技术将加速全球对作物改良的诉求,这一发展与战后的绿色革命如出一辙。昆士兰大学(University of Queensland)的约翰英尼斯中心(John Innes Centre)和悉尼大学(University of Sydney)的研究团队开发了一种快速培育平台,该平台利用温室或人工环境和光照的增强,创造出密集的全天环境,以加速寻找性能更好的作物。利用这项技术,研究小组在短短8周内就完成了从种子到种子的小麦育种过程,这些结果发表在《自然植物》杂志上。这意味着现在每年可以种植6季小麦——比目前育种家和研究人员使用的育种技术增加了三倍。

**来源:** EurekAlert!

**发布日期:** 2018-11-06

**全文链接:**

<http://agri.ckcest.cn/file1/M00/02/9C/Csgk0Fvub6WABPg7AADgateR3ts079.pdf>

## ▶ 学术文献

### 1. Mapping QTLs conferring salt tolerance and micronutrient concentrations at seedling stage in wheat (测定小麦苗期盐耐性和微量营养素含量的数量性状基因图谱)

**简介:** Soil salinization and degradation is one of the consequences of climate change. Identification of major salt tolerance genes and marker assisted selection (MAS) can accelerate wheat breeding for this trait. We genotyped 154 wheat F<sub>2</sub> lines derived from a cross between salt tolerant and susceptible cultivars using the Axiom Wheat Breeder's Genotyping Array. A high-density linkage map of 988 single nucleotide polymorphisms (SNPs) was constructed and utilized for quantitative trait loci (QTL) mapping for salt tolerance traits and mineral concentrations under salinity. Of 49 mapped QTLs, six were for Na<sup>+</sup> exclusion (NAX) and two QTLs (qSNAX.2 A.1, qSNAX.2 A.2) on chromosome 2 A coincided with a reported major NAX QTL (Nax1 or HKT1;4). Two other major NAX QTLs were mapped on 7 A, which contributed 11.23 and 18.79% of the salt tolerance respectively. In addition to Ca<sup>+2</sup> and Mg<sup>+2</sup> QTLs, twenty-seven QTLs for tissue Phosphorus, Zinc, Iron, Manganese, Copper, Sulphur and Boron concentrations under salinity were also mapped. The 1293 segregating SNPs were annotated/located within genes for various ion channels, signalling pathways, transcription factors (TFs), metabolic pathways and 258 of them showed differential expression in silico under salinity. These findings will create new opportunities for salt tolerance breeding programs.

**来源:** Nature

**发布日期:** 2017-11-15

**全文链接:**

<http://agri.ckcest.cn/file1/M00/02/9D/Csgk0FvzZJ6A0mquACmAgThj0iM862.pdf>

## 2. Genome-wide Association Analysis of Powdery Mildew Resistance in U.S. Winter Wheat (美国冬小麦抗白粉病的全基因组关联分析)

**简介:** Wheat powdery mildew (PM), caused by *Blumeria graminis* f. sp. *tritici*, is a major fungal disease of wheat worldwide. It can cause considerable yield losses when epidemics occur. Use of genetic resistance is the most effective approach to control the disease. To determine the genomic regions responsible for PM resistance in a set of U.S. winter wheat and identify DNA markers in these regions, we conducted a genome-wide association study on a set of 185 U.S. winter wheat accessions using single nucleotide polymorphism (SNP) markers from 90 K wheat SNP arrays. We identified significant SNP markers linked to nine quantitative trait loci (QTLs) and simple sequence repeats (SSR) markers linked to three QTLs for PM resistance. Most of the QTLs in the US winter wheat population have been reported previously, but some such as these on chromosomes 1A, 6A and 1B have not been reported previously, and are likely new QTLs for PM resistance in U.S. winter wheat. The germplasm with immunity to PM are good sources of resistance for PM resistance breeding and the markers closely linked to the QTLs can be used in marker-assisted selection to improve wheat PM resistance after further validation.

**来源:** Nature

**发布日期:**2017-09-18

**全文链接:**

<http://agri.ckcest.cn/file1/M00/02/9D/Csgk0FvzY6GAP73zAB562W0s4YQ181.pdf>

## 3. Potential for re-emergence of wheat stem rust in the United Kingdom (英国小麦秆锈病再次出现的可能性研究)

**简介:** 小麦秆锈病是一种由秆锈菌引起的小麦和大麦的毁灭性病害。然而，近年来却发生了独立的暴发疫情。在此，我们研究了现代欧洲品种缺乏耐药性、交替寄生以及气候条件的变化是否有助于其复苏。我们报道了近60年来英国首次发生小麦秆锈病，只有20%的英国小麦品种对这个菌株有抗性。过去25年的气候变化也表明病菌感染的条件越来越有利。此外，我们还记录了英国几十年来第一次发生在的*P. graminis*感染。我们的数据表明，小麦秆锈病确实发生在英国，如果气候条件有利，可能会严重损害小麦和大麦的生产。

**来源:** Nature

**发布日期:**2018-02-08

**全文链接:**

<http://agri.ckcest.cn/file1/M00/02/9D/Csgk0FvzYhGAJI8cAC06GuanNIc498.pdf>

### ➤ 相关专利

#### 1. 小麦分子标记及其在鉴定小麦白粉病抗性中的应用

**简介:** 本发明公开了小麦分子标记及其在鉴定小麦白粉病抗性中的应用。本发明公开的小麦分子标记为下述M1 )或M2 )：M1 )小麦基因组DNA中对应于序列表中序列4的第18位的核苷酸；M2 )含有M1 )的DNA片段；本发明还制备了用于检测该小麦分子标记的P

引物组、K-IWB41105引物组和Str-IWB41105引物组。本发明所提供的小麦分子标记及引物组可用于小麦白粉病成株抗性分子育种和白粉病成株抗性性状的鉴定。本发明的专用引物将在小麦抗病育种中发挥重要作用。

**来源：**国家知识产权局专利检索及分析

**发布日期：**2018-03-01

**全文链接：**

<http://agri.ckcest.cn/file1/M00/02/9D/Csgk0FvzZV6ACSfoAB71451uBEM387.PDF>