



2019年第10期总50期

小麦遗传育种专题

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前沿资讯

1. Research on the biophoton emission of wheat kernels based on permutation entropy (基于排列熵的小麦籽粒光子辐射研究)

简介: 为研究小麦籽粒光子辐射信号的非线性动态特征,引入排列熵来区分正常籽粒和受感染籽粒。本文研究了排列熵在不同程度超弱发光小麦信号中的应用以及嵌入维数和时滞对排列熵的影响。小麦超微弱发光信号分析的实验结果表明,排列熵是检测正常小麦与感染小麦差异的有效手段。

来源: Optik

发布日期:2019-02-01

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5F/Csgk0Fx-HmGAQvZLABXw1nQUU1g018.pdf>

学术文献

1. A catalog of gliadin alleles: Polymorphism of 20th-century common wheat germplasm (醇溶蛋白等位基因序列:20世纪常见小麦种质的多态性)

简介: A new, improved version of the catalog of 182 alleles at the six Gli loci of common wheat (*T. aestivum* L.) shown in electrophoregrams of 128 standard genotypes was used for analysis of 1060 cultivars and lines bred in the 20th century. The most frequent alleles in the studied germplasm occurred with frequencies of 18%40%, with 30 unique alleles, one in each cultivar. Extremely high genetic diversity was found (average H for the six main Gli loci was 0.870 ± 0.046), nearly identical in winter (H = 0.831) and spring (H = 0.856) wheats but differing among 28 groups of cultivars released in 22 countries. Each country or region was characterized by its own specific set of the most frequent Gli alleles, and the 28 cultivar groups formed five main relationship clusters if polymorphism at the six Gli loci was considered. However, different levels of similarity between groups of cultivars were found if polymorphism of the A, B, or D genomes of common wheat was tested separately. In general, the 20th century germplasm of common wheat was differentiated and structured by country or region and cultivar type (spring or winter). Each elemental genome (in particular, A and D) contributed to the structure of the polymorphism studied. We propose that the structure of the wheat germplasm was a result of natural selection under the eco-climatic conditions of cultivation specific to each country or region. As many as 27.4% of cultivars studied violated the requirement of the DUS rules for uniformity, being represented by mixtures of two or more closely related genotypes. However, the composition of a cultivar as a set of related but different genotypes may contribute to its adaptivity, and thereby to the known high plasticity of common wheat.

来源: The Crop Journal

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<http://agri.ckcest.cn/file1/M00/06/60/Csgk0Fx-KGyABhy1ABBg0WzaspA736.pdf>

2. The landscape of molecular mechanisms for salt tolerance in wheat (小麦耐盐性分子机制的研究进展)

简介: 小麦是重要的粮食作物之一, 其产量受到高盐度和其他非生物胁迫的严重制约。许多研究试图阐明与小麦耐盐性相关的主要生理过程, 并确定控制这些过程的基因。本文综述了高亲和力钾转运蛋白(HKT)基因在提高小麦耐盐性中的重要作用。通过对一条小麦基因渗入系的综合研究, 探讨了活性氧(ROS)维持小麦内部稳定与耐盐性之间的关系, 并描述了一组参与这一过程基因的作用。基于最近的组学进展, 将继续讨论并揭示小麦耐盐机制的新研究策略。

来源: The Crop Journal

发布日期: 2018-02-01

全文链接:

<http://agri.ckcest.cn/file1/M00/06/60/Csgk0Fx-Jl6AHJv1AAiquh0zu18003.pdf>

3. Genetic gains in wheat in Turkey: Winter wheat for dryland conditions (土耳其小麦的遗传增益: 旱地条件下的冬小麦)

简介: Wheat breeders in Turkey have been developing new varieties since the 1920 s, but few studies have evaluated the rates of genetic improvement. This study determined wheat genetic gains by evaluating 22 winter/facultative varieties released for rainfed conditions between 1931 and 2006. The study was conducted at three locations in Turkey during 2008-2012, with a total of 21 test sites. The experimental design was a randomized complete block with four replicates in 2008 and 2009 and three replicates in 2010-2012. Regression analysis was conducted to determine genetic progress over time. Mean yield across all 21 locations was 3.34 t ha⁻¹ but varied from 1.11 ha⁻¹ to 6.02 t ha⁻¹ and was highly affected by moisture stress. Annual genetic gain was 0.50% compared to Ak-702, or 0.30% compared to the first modern landmark varieties. The genetic gains in drought-affected sites were 0.75% compared to Ak-702 and 0.66% compared to the landmark varieties. Modern varieties had both improved yield potential and tolerance to moisture stress. Rht genes and rye translocations were largely absent in the varieties studied. The number of spikes per unit area decreased by 10% over the study period, but grains spike⁻¹ and 1000-kernel weight increased by 10%. There were no significant increases in harvest index, grain size, or spike fertility, and no significant decrease in quality over time. Future use of Rht genes and rye translocations in breeding programs may increase yield under rainfed conditions.

来源: The Crop Journal

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<http://agri.ckcest.cn/file1/M00/06/60/Csgk0Fx-IJ6AId0gAAZR6Lv0j5U833.pdf>

➤ 相关专利

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1. 一种用于检测中麦895抗条锈病QTL的分子标记及使用方法

简介: 本发明公开了一种用于检测中麦895抗条锈病QTL的分子标记及使用方法。本专利利用小麦660K SNP芯片分析扬麦16/中麦895双单倍体群体(Doubled Haploid, DH)基因型, 构建高密度连锁图谱, 结合田间条锈病抗性鉴定, 在2A染色体长臂(2AL)上定位到一个主效抗条锈病位点Q Yr .caas - 2AL , 解释表型变异高达44 .0%~56 .4%, 抗性等位基因来自中麦895。在此基础上, 本发明开发了与QYr .caas-2AL紧密连锁的CAPS(cleaved amplified polymorphic sequences)标记Yr-2AL-CAPS, 为抗条锈病小麦育种提供了良好工具。

来源: 国家知识产权局专利检索及分析

发布日期:2018-09-05

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<http://agri.ckcest.cn/file1/M00/06/60/Csgk0Fx-KayAC6p6AA5GtZ6Hhkg967.PDF>