



2019年第1期总41期

小麦遗传育种专题

本期导读

▶ 前沿资讯

1. 小麦品种Toropi耐铝性的遗传及在巴西小麦种质资源中引入该性状的新发现

▶ 学术文献

1. 面包小麦自噬基因家族全基因组序列及表达分析
2. 用新的基因组工具探索野生小麦的过去来改进未来的作物
3. 山羊草 γ -醇溶蛋白基因的克隆、序列分析及其与小麦育种的关系

▶ 相关专利

1. 一种雪霉叶枯病抗性小麦育种新方法

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

2019年01月07日

更多资讯 尽在农业专业知识服务系统：<http://agri.ckcest.cn/>

▶ 前沿资讯

1. Inheritance of aluminum tolerance in the wheat cultivar Toropi and new findings about the introduction of this trait into the Brazilian wheat germplasm (小麦品种Toropi耐铝性的遗传及在巴西小麦种质资源中引入该性状的新发现)

简介: 铝(al)是地壳中含量最丰富的金属,在酸性土壤中,它溶解成植物毒性形式的Al³⁺。对供体基因型铝耐量的遗传分析是开发适应酸性土壤新品种的重要步骤。巴西小麦品种BH1146和Carazinho是世界各地小麦育种项目中耐铝基因的重要供体。这个性状受两个主要基因TaALMT1和TaMATE1B的控制。有趣的是,两个品种都携带这两个基因,但等位基因不同。巴西从当地地方品种发展而来的谱系产生了品种BH1146和Carazinho,以及其他基因型,其中品种Toropi因其在酸性土壤中的优异表现而在此突出。目前尚不清楚在Toropi中,与铝耐受相关的基因和等位基因是否与BH1146和Carazinho携带的基因和等位基因相同。我们分析了一个铝敏感品种Toropi×Anahuac的重组自交系(RIL),结果表明,Toropi的铝耐量受一个基因的控制,对表型有较大影响,而其他影响较小的基因也对这一性状有影响。通过对Toropi×BH1146的RIL分析,发现该主要基因与BH1146携带的基因不同。通过对耐铝巴西小麦品种TAALMT1和TAMATE1B基因的系谱和分子分析,我们可以确定Toropi与Carazinho具有相同的TAMATE1B基因等位基因,但可能来源不同。

来源: Environmental and Experimental Botany

发布日期: 2019-01-01

全文链接:

http://agri.ckcest.cn/file1/M00/06/5B/Csgk0Fwt2PyAa_jnFAB0Av7151RY432.pdf

▶ 学术文献

1. Genome-wide sequence and expressional analysis of autophagy Gene family in bread wheat (*Triticum aestivum* L.) (面包小麦自噬基因家族全基因组序列及表达分析)

简介: Autophagy, a highly conserved intracellular degradation system, is regarded to be responsible for self-defense and protect cells from abiotic stress. Extensive studies have demonstrated that autophagy plays a crucial role in regulating plant growth and development as well as in response to diverse stresses. However, little is known about autophagy-associated genes (ATGs) in wheat, especially those involved in the regulatory network of stress processes. In this study, a total of 108 putative wheat ATGs (TaATG) were obtained based on a genome-wide search approach. Phylogenetic analysis classified them into 13 subfamilies, of which the TaAtg16 subfamily consisted of 29 members, ranking it the largest subfamily. The conserved motif compositions as well as their exon-intron structures were systematically analyzed and strongly supported the classification. The homoeologous genes tended to have similar gene features during wheat polyploidization. Furthermore, a total of 114 putative cis-elements were found, and those related to hormone, stress, and light responsiveness were abundantly presented in the promoter regions. Co-expression network

更多资讯 尽在农业专业知识服务系统:<http://agri.ckcest.cn/>

analysis revealed that orthologous VAMP727 was the hub node of the whole network, and complex interactions were also found. Finally, the expression profiles of TaATGs among different tissues and under abiotic stresses were investigated to identify tissue-specific or stress-responsive candidates, and then 14 were validated by wet-lab analysis. Results showed that the TaAtg8 subfamily played a crucial role in tissue autophagy and stress defense, which could be considered as processes that are candidates for further functional study. This was the first study to comprehensively investigate the ATG family in wheat, which ultimately provided important clues for further functional analysis and also took a step toward uncovering the evolutionary mechanism of ATG genes in wheat and beyond.

来源: Journal of Plant Physiology

发布日期:2018-07-11

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5B/Csgk0Fwt3q6AScpcAFxuhNctLno913.pdf>

2. New genomic tool searches wheat's wild past to improve crops of the future (用新的基因组工具探索野生小麦的过去来改进未来的作物)

简介: A new genetic directory launched today will enable researchers and breeders to scan the genomes of wild relatives of modern wheat to find disease-fighting properties lost to domestication. The time-travelling trawl is possible following the launch of the Open Wild Wheat, a directory which includes the genetic sequences of 150 wild wheats belonging to a goat grass species called *Aegilops tauschii* ssp. *strangulata*. This wild relative, found in the fertile crescent round the Caspian sea, has contributed the D genome pillar, one of the three genomes found in bread wheat. The directory is the crowd-funded outcome of an international consortium led by wheat researchers at the John Innes Centre, Norwich, UK, and Kansas State University. Contributors from academic institutions and industry spanning 15 countries raised \$150,000 to fund the sequencing.

来源: EurekAlert

发布日期:2018-04-04

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5B/Csgk0Fwt21iAMqjgAABhqY-M7PU385.pdf>

3. Cloning and characterization of novel γ -gliadin genes from *Aegilops markgrafii* in relation to evolution and wheat breeding (山羊草 γ -醇溶蛋白基因的克隆、序列分析及其与小麦育种的关系)

简介: 醇溶蛋白是小麦贮藏蛋白的主要组成部分,对面团的延展性起着重要的作用。本研究采用基于聚合酶链反应(PCR)的方法,从*Aegilops markgrafii*的C基因组中克隆了6个新的全长 γ -醇溶蛋白基因。对推导出的氨基酸序列的分析表明,克隆的基因具有与其他已发现的小麦相关物种 γ -醇溶蛋白肽相似但不完全相同的初级结构。开放读码框架(ORF)的长度从909到963 bp不等,重复性和富含谷氨酰胺的结构域对蛋白质的大小有一定的影响。JX566513序列的重复域中存在一个额外的半胱氨酸残基。在乳糜泻(CD)患者中,我们对标记物进行了搜索,寻找到5个被鉴定为T细胞刺激表位的肽段。肽

更多资讯 尽在农业专业知识服务系统:<http://agri.ckcest.cn/>

gli γ -3在JX566513和JX566514序列中存在, 肽gli γ -5仅在JX566513中存在, 其他醇溶朊不含毒性表位。这些结果为更好地了解Ae. markgrafii在小麦育种中的应用提供了信息。

来源: The Crop Journal

发布日期: 2018-02-08

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5B/Csgk0Fwt3jCAbP8eABhmXa5DaZs570.pdf>

➤ 相关专利

1. 一种雪霉叶枯病抗性小麦育种新方法

简介: 本发明属于小麦育种技术领域, 具体涉及一种雪霉叶枯病抗性小麦育种新方法。该方法选择抗雪霉叶枯病的小麦品种作为母本, 选择性状优良的小麦品种作为父本, 将父本与母本杂交, 收获杂种一代种子F1; 并与回交、自交等步骤联合使用; 在种植杂种一代种子F1、杂种二代种子F2、回交一代种子BC1前, 先将小麦种子浸泡于雪腐格氏霉粗毒素溶液中进行雪霉叶枯病抗性鉴定处理, 即时筛除感病种子, 减少种植样本数, 简化育种步骤, 可提高目的性状的育种效率。

来源: 国家知识产权局专利检索及分析

发布日期: 2018-06-22

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5B/Csgk0Fwt3y6AS64cAAS5swkV9CU975.PDF>