



2019年第39期总79期

小麦遗传育种专题

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1. 与小麦穗粒数主效QTL紧密连锁的分子标记及其应用

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▶ 前沿资讯

1. 2019年秋冬季小麦病虫害防控指导意见

简介: 做好小麦播种期及苗期病虫害防治,对压低病虫初始量,预防中后期病虫害的发生,确保全年小麦病虫害有效控制具有重要意义。为加强小麦秋播药剂拌种和秋冬季病虫害防治工作,农业农村部种植业管理司会同全国农业技术推广服务中心组织国家小麦产业体系以及相关植保专家,结合2019年春夏季小麦病虫发生情况,研究制定了我国不同产区秋冬季小麦主要病虫害防控指导意见。

来源: 农业农村部新闻办公室

发布日期: 2019-09-23

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/C9/Csgk0F2JageAP0bDAAJvAyW54Qs449.pdf>

2. Genome-wide identification of and functional insights into the late embryogenesis abundant (LEA) gene family in bread wheat (*Triticum aestivum*) (面包小麦 (*Triticum aestivum*) LEA基因家族的全基因组鉴定及功能研究)

简介: 晚期胚胎产生丰富的蛋白质 (LEA),参与植物对各种非生物胁迫的反应和适应,包括脱水、盐分、高温和低温。本文首次报道了“中国春”小麦LEA基因家族的综合调查,研究共鉴定出179个TaLEA基因,并将其分为8组。所有TaLEA基因均含有LEA保守基序,内含子较少。同属一个类群的TaLEA基因具有相似的基因结构和染色体定位。我们的研究表明,大多数TaLEA基因含有脱落酸(ABA)响应元件(ABREs)、启动子区与应激反应相关的各种顺式作用元件,是在ABA和非生物胁迫处理下诱导产生的。此外,将代表各组的8个基因分别导入大肠杆菌和酵母中,在高温和盐胁迫下TaLEAs产生了保护作用。TaLEAs增强了大肠杆菌和酵母对盐和热的耐受性,表明这些蛋白在应激条件下对宿主细胞具有保护作用。这些结果加深了我们对LEA基因的了解,为今后提高小麦抗逆性的功能研究提供了强有力的候选基因。

来源: Nature

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<http://agri.ckcest.cn/file1/M00/OE/C9/Csgk0F2IjfeABTjAAGCLR12QG-k974.pdf>

▶ 学术文献

1. Genetic Dissection of End-Use Quality Traits in Adapted Soft White Winter Wheat (适应性软质、白粒冬小麦最终用途品质性状的遗传分析)

简介: Soft white wheat is used in domestic and foreign markets for various end products requiring specific quality profiles. Phenotyping for end-use quality traits can be costly, time-consuming and destructive in nature, so it is advantageous to use molecular markers to

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select experimental lines with superior traits. An association mapping panel of 469 soft white winter wheat cultivars and advanced generation breeding lines was developed from regional breeding programs in the U.S. Pacific Northwest. This panel was genotyped on a wheat-specific 90 K iSelect single nucleotide polymorphism (SNP) chip. A total of 15,229 high quality SNPs were selected and combined with best linear unbiased predictions (BLUPs) from historical phenotypic data of the genotypes in the panel. Genome-wide association mapping was conducted using the Fixed and random model Circulating Probability Unification (FarmCPU). A total of 105 significant marker-trait associations were detected across 19 chromosomes. Potentially new loci for total flour yield, lactic acid solvent retention capacity, flour sodium dodecyl sulfate sedimentation and flour swelling volume were also detected. Better understanding of the genetic factors impacting end-use quality enable breeders to more effectively discard poor quality germplasm and increase frequencies of favorable end-use quality alleles in their breeding populations.

来源: Frontiers

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全文链接:

http://agri.ckcest.cn/file1/M00/0E/C9/Csgk0F2Jb_iAQ0mqABzaW4PE59E002.pdf

2. RNAi-Mediated Downregulation of Inositol Pentakisphosphate Kinase (IPK1) in Wheat Grains Decreases Phytic Acid Levels and Increases Fe and Zn Accumulation (RNAi介导的小麦籽粒肌醇五磷酸激酶(IPK1)下调降低了植酸水平,增加了铁和锌的积累)

简介: Enhancement of micronutrient bioavailability is crucial to address the malnutrition in the developing countries. Various approaches employed to address the micronutrient bioavailability are showing promising signs, especially in cereal crops. Phytic acid (PA) is considered as a major antinutrient due to its ability to chelate important micronutrients and thereby restricting their bioavailability. Therefore, manipulating PA biosynthesis pathway has largely been explored to overcome the pleiotropic effect in different crop species. Recently, we reported that functional wheat inositol pentakisphosphate kinase (TaIPK1) is involved in PA biosynthesis, however, the functional roles of the IPK1 gene in wheat remains elusive. In this study, RNAi-mediated gene silencing was performed for IPK1 transcripts in hexaploid wheat. Four non-segregating RNAi lines of wheat were selected for detailed study (S3-D-6-1; S6-K-3-3; S6-K-6-10 and S16-D-9-5). Homozygous transgenic RNAi lines at T4 seeds with a decreased transcript of TaIPK1 showed 2856% reduction of the PA. Silencing of IPK1 also resulted in increased free phosphate in mature grains. Although, no phenotypic changes in the spike was observed but, lowering of grain PA resulted in the reduced number of seeds per spikelet. The lowering of grain PA was also accompanied by a significant increase in iron (Fe) and zinc (Zn) content, thereby enhancing their molar ratios (Zn:PA and Fe:PA). Overall, this work suggests that IPK1 is a promising candidate for employing genome editing tools to address the mineral accumulation in wheat grains.

来源: Frontiers

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全文链接:

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➤ 相关专利

1. 与小麦穗粒数主效QTL紧密连锁的分子标记及其应用

简介：本发明公开了一种与小麦穗粒数主效QTL紧密连锁的分子标记。以小麦基因组DNA为模板，采用PCR引物对进行PCR扩增，扩增产物通过非变性聚丙烯酰胺凝胶电泳分离获得分子标记2A- 654918338；且公开了所述分子标记2A- 654918338在检测小麦品种或品系中是否含有增加小麦穗粒数的QTL位点及小麦分子育种方面的应用。本发明加快了小麦穗粒数的遗传改良进程，大大提高了小麦品种或品系的选择效率和质量，直接实现了目标基因在小麦种质资源以及育种后代中的鉴定，为小麦育种开拓更多新的穗粒数遗传资源。

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