



2019年第33期总73期

小麦遗传育种专题

本期导读

▶ 前沿资讯

1. 小麦根、茎代谢产物的基因型变异表明持续、优先的碳分配是激发磷效率的潜在机制

▶ 学术文献

1. 硬粒小麦高度遗传农艺性状的全基因组关联研究
2. 基因生物强化丰富了稻米和小麦籽粒的铁含量：从基因到产品
3. 提高小麦黑斑病抗性的实用育种策略

▶ 相关专利

1. 一种基于多基因聚合创制持久抗白粉病小麦育种元件的方法

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2019年08月19日

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▶ 前沿资讯

1. Genotypic Variation in the Root and Shoot Metabolite Profiles of Wheat (*Triticum aestivum* L.) Indicate Sustained, Preferential Carbon Allocation as a Potential Mechanism in Phosphorus Efficiency (小麦根、茎代谢产物的基因型变异表明持续、优先的碳分配是激发磷效率的潜在机制)

简介: 植物代谢产物对营养缺乏反应水平的变化可以反映植物如何利用稀缺资源。本项目研究了不同磷利用效率(PUE)下小麦根、芽代谢产物基因型的变化。在低磷和播种后的28天(DAS), 小麦育种系RAC875 (P有效率)比小麦品种多产生42%的芽生物量, 而Wyalkatchem (P低效)。在低磷胁迫下, 叶片和根系的代谢产物谱发生了明显的变化, 且存在显著的基因型变异。在低磷条件下, 两种小麦基因型的根中棉子糖和1-蔗糖三糖均有明显的增加, RAC875的积累量高于Wyalkatchem; 植株叶片中棉子糖和1-蔗糖三糖含量无显著增加。低磷对两种基因型的蔗糖、麦芽糖、葡萄糖和果糖水平均无显著影响, 而RAC875中磷酸化糖(葡萄糖-6-P和果糖-6-P)保持不变, 而在Wyalkatchem中, 葡萄糖-6-P在根中显著降低, 果糖-6-P在叶和根中含量显著降低。在低磷胁迫下, 两种小麦基因型的根中甘油-3-P含量均降低了2倍。在根中, RAC875的富马酸盐、苹果酸盐、马来酸盐和依他酸盐含量明显低于Wyalkatchem, 而在RAC875中, 低磷增强了有机酸的渗出, 而在Wyalkatchem中则没有。RAC875显示更高的天冬氨酸积累, 谷氨酰胺和 β -丙氨酸叶子比Wyalkatchem在低P供应。更高棉子糖的积累; 1-蔗糖三糖在根部的积累; 天冬氨酸、谷氨酰胺和 β -丙氨酸在叶子中的积累似乎与RAC875增强有关。葡萄糖-6-P和果糖-6-P对糖酵解具有重要作用, 维持这些代谢产物可以使RAC875在缺磷条件下维持碳水化合物代谢和地上植株生物量。本项研究表明在PUE和关键代谢途径下, 不同的小麦品种之间可以观察到代谢物谱的差异, 并在有效的基因型中维持代谢途径的差异, 以确保在低磷条件下的碳供应。

来源: Frontiers

发布日期: 2019-08-06

全文链接:

<http://agri.ckcest.cn/file1/M00/0E/7D/Csgk0F1M1tGafDnoACov2ygyqhk317.pdf>

▶ 学术文献

1. A Genome-Wide Association Study of Highly Heritable Agronomic Traits in Durum Wheat (硬粒小麦高度遗传农艺性状的全基因组关联研究)

简介: Uncovering the genetic basis of key agronomic traits, and particularly of drought tolerance, addresses an important priority for durum wheat improvement. Here, a genome-wide association study (GWAS) in 493 durum wheat accessions representing a worldwide collection was employed to address the genetic basis of 17 agronomically important traits and a drought wilting score. Using a linear mixed model with 4 inferred subpopulations and a kinship matrix, we identified 90 marker-trait-associations (MTAs)

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defined by 78 markers. These markers could be merged into 44 genomic loci by linkage disequilibrium ($r^2 > 0.2$). Based on sequence alignment of the markers to the reference genome of bread wheat, we identified 14 putative candidate genes involved in enzymes, hormone-response, and transcription factors. The GWAS in durum wheat and a previous quantitative trait locus (QTL) analysis in bread wheat identified a consensus QTL locus.4B.1 conferring drought tolerance, which was further scanned for the presence of potential candidate genes. A haplotype analysis of this region revealed that two minor haplotypes were associated with both drought tolerance and reduced plant stature, thought to be the effect of linkage with the semi-dwarfing gene Rht-B1. Haplotype variants in the key chromosome 4B region were informative regarding evolutionary divergence among durum, emmer and bread wheat. Over all, the data are relevant in the context of durum wheat improvement and the isolation of genes underlying variation in some important quantitative traits.

来源: Frontiers

发布日期: 2019-07-17

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/7D/Csgk0F1M2p-ANUgzADZbs5Ghofg539.pdf>

2. Genetic Biofortification to Enrich Rice and Wheat Grain Iron: From Genes to Product (基因生物强化丰富了稻米和小麦籽粒的铁含量: 从基因到产品)

简介: The micronutrient iron (Fe) is not only essential for plant survival and proliferation but also crucial for healthy human growth and development. Rice and wheat are the two leading staples globally; unfortunately, popular rice and wheat cultivars only have a minuscule amount of Fe content and mainly present in the outer bran layers. Unavailability of considerable Fe-rich rice and wheat germplasm limits the potential of conventional breeding to develop this micronutrient trait in both staples. Agronomic biofortification, defined as soil and foliar fertilizer application, has potential but remains quite challenging to improve grain Fe to the significant level. In contrast, recent accomplishments in genetic biofortification can help to develop Fe-enriched cereal grains to sustainably address the problem of “hidden hunger” when the roadmap from proof of concept to product and adoption can be achieved. Here, we highlight the different genetic biofortification strategies for rice and wheat and path to develop a product.

来源: Frontiers

发布日期: 2019-07-16

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/7D/Csgk0F1M2RGAVAmDAAXTn5wBAAsc290.pdf>

3. Practical breeding strategies to improve resistance to Septoria tritici blotch of wheat (提高小麦黑斑病抗性的实用育种策略)

简介: Septoria tritici blotch (STB), caused by fungal agent Zymoseptoria tritici (previously known as Mycosphaerella graminicola) is a devastating foliar wheat diseases globally. Importance and potential threat of STB have been discussed historically and geographically.

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This paper reviews information on the *Z. tritici*—wheat pathosystem and proposes approaches to identify resistance genes and to advance in breeding for STB resistance. Screening of resistant lines/cultivars, QTL mapping analysis within genetic populations derived from crosses, detection of new resistance gene(s) and finally application of Stb gene carrier line/cultivar in crosses are the major stages of a practical wheat-breeding program against STB of wheat. Phenotyping and genotyping outputs on the top of each other should confirm each other, so it needs to expose a resistance gene carrier line/cultivar in the epidemic condition at seedling/adult plant stage to confirm resistance performance of detected gene(s) in the real condition. On the other word, detecting an associated QTL to resistance should not be considered as the end of investigation. Climate change resulted geographical disease pattern conversion where some diseases became more important in some area where they had not been serious in the past and vice versa. Hence, a reconsideration of wheat disease importance zone is necessary to predict regions where STB is and will be a limitation for wheat yield improvement.

来源: Springer

发布日期: 2018-07-01

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/7D/Csgk0F1M39-AIZ2NACv1hFd-kNg631.pdf>

➤ 相关专利

1. 一种基于多基因聚合创制持久抗白粉病小麦育种元件的方法

简介: 本发明公开了一种基于多基因聚合创制持久抗白粉病小麦育种元件的方法,包括:根据育种目标,对亲本材料进行聚合育种,获得持久抗白粉病小麦;所述的育种目标至少包括聚合“pm21+pm8+pm4+pm38”和抗白粉病。亲本材料为镇麦9号、宁麦23、扬麦11和平原50。本发明通过选择携带不同抗白粉病基因的亲本,利用基因重组和累加效应从而创造出聚合pm21、pm8、pm4和pm38四个基因后代,得到持久抗白粉病、分蘖力强、矮秆抗倒、广适高产稳产的小麦,同时具有大穗大粒、熟相好,综合农艺性状突出等优点,本发明培育出的抗白粉病小麦具有对白粉病稳定、持久抗性,高产稳产性好,综合农艺性状突出,解决了单一抗性基因抗性丧失的问题。

来源: 国家知识产权局

发布日期: 2019-06-25

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/7D/Csgk0F1M4V-AIjQ7AAckPmZry8Q030.PDF>