



2019年第36期总76期

小麦遗传育种专题

本期导读

▶ 前沿资讯

1. 合成六倍体小麦对CIMMYT春小麦育种种质资源的遗传贡献

▶ 学术文献

1. 在没有生物控制芽孢杆菌CC09的情况下小麦根中黑曲霉的比较转录组分析
2. 近等基因六倍体小麦的比较转录组特征在2DL FHB抗性QTL下的有效等位基因存在差异
3. 磷改变了与淀粉生物合成与降解有关的小麦籽粒淀粉形态和基因表达

▶ 相关专利

1. 小麦穗粒数主效QTL的紧密连锁的分子标记及其应用

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▶ 前沿资讯

1. Genetic Contribution of Synthetic Hexaploid Wheat to CIMMYT's Spring Bread Wheat Breeding Germplasm (合成六倍体小麦对CIMMYT春小麦育种种质资源的遗传贡献)

简介: 合成六倍体 (SH) 小麦 (AABB D' D') 是通过人工在四倍体硬粒小麦 (*Triticum Turgidum*, AABB) 和二倍体野生山羊草 (*Aegilops Tauschii*, D' D') 之间杂交培育而形成的。30多年来, 国际玉米小麦改良中心 (CIMMYT) 开发并利用SH小麦作为Ae基因转移的桥梁。这是一个成功利用野生亲缘在世界范围内大规模繁殖的独特例子。我们的研究旨在确定SH小麦对CIMMYT全球春小麦育种计划的遗传贡献。我们利用祖先谱系和标记信息估计了 D' 对合成衍生物系的理论和经验贡献。标记估计的平均 D' 贡献率为17.5%, 基因组片段的差异提示了差异选择压力的应用。基于谱系的贡献与基于标记的估计相关, 不提供染色体片段的特异性变异。国际产量试验结果表明, 20%的品系是人工合成的, 平均 D' 贡献率为15.6%。我们的研究结果强调了SH小麦在维持和提高多年来的遗传多样性和遗传增益方面的重要性, 并对制定更具针对性的渗透策略具有重要意义。该研究为CIMMYT全球小麦项目中SH的开发利用提供了回顾性分析。

来源: Nature

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全文链接:

<http://agri.ckceest.cn/file1/M00/OE/80/Csgk0F1siK-Ac76qACTgpnNojLM661.pdf>

▶ 学术文献

1. Comparative Transcriptome Profiling of *Gaeumannomyces graminis* var. *tritici* in Wheat Roots in the Absence and Presence of Biocontrol *Bacillus velezensis* CC09 (在没有生物控制芽孢杆菌CC09的情况下小麦根中黑曲霉的比较转录组分析)

简介: This study aimed to explore potential biocontrol mechanisms involved in the interference of antagonistic bacteria with fungal pathogenicity in planta. To do this, we conducted a comparative transcriptomic analysis of the “take-all” pathogenic fungus *Gaeumannomyces graminis* var. *tritici* (Ggt) by examining Ggt-infected wheat roots in the presence or absence of the biocontrol agent *Bacillus velezensis* CC09 (Bv) compared with Ggt grown on potato dextrose agar (PDA) plates. A total of 4,134 differentially expressed genes (DEGs) were identified in Ggt-infected wheat roots, while 2,011 DEGs were detected in Bv+Ggt-infected roots, relative to the Ggt grown on PDA plates. Moreover, 31 DEGs were identified between wheat roots, respectively infected with Ggt and Bv+Ggt, consisting of 29 downregulated genes coding for potential Ggt pathogenicity factors e.g., para-nitrobenzyl esterase, cutinase 1 and catalase-3, and two upregulated genes coding for tyrosinase and a hypothetical protein in the Bv+Ggt-infected roots when compared with the Ggt-infected roots. In particular, the expression of one gene, encoding the ABA3 involved in the production of Ggt's hormone abscisic acid, was 4.11-fold lower in Ggt-infected roots with Bv than without

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Bv. This is the first experimental study to analyze the activity of Ggt transcriptomes in wheat roots exposed or not to a biocontrol bacterium. Our results therefore suggest the presence of Bv directly and/or indirectly impairs the pathogenicity of Ggt in wheat roots through complex regulatory mechanisms, such as hyphopodia formation, cell wall hydrolase, and expression of a papain inhibitor, among others, all which merit further investigation.

来源: Frontiers

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全文链接:

http://agri.ckcest.cn/file1/M00/OE/80/Csgk0F1ss7GASOk_ABUfHNWOKNE819.pdf

2. Comparative Transcriptome Profiles of Near-Isogenic Hexaploid Wheat Lines Differing for Effective Alleles at the 2DL FHB Resistance QTL (近等基因六倍体小麦的比较转录组特征在2DL FHB抗性QTL下的有效等位基因存在差异)

简介: Fusarium head blight (FHB), caused by the fungus *Fusarium graminearum*, represents one of the major wheat diseases worldwide, determining severe yield losses and reduction of grain quality due to the accumulation of mycotoxins. The molecular response associated with the wheat 2DL FHB resistance QTL was mined through a comprehensive transcriptomic analysis of the early response to *F. graminearum* infection, at 3 days post-inoculation, in spikelets and rachis. The analyses were conducted on two near isogenic lines (NILs) differing for the presence of the 2DL QTL (2-2618, resistant 2DL+ and 2-2890, susceptible null). The general response to fungal infection in terms of mRNAs accumulation trend was similar in both NILs, even though involving an higher number of DEGs in the susceptible NIL, and included down-regulation of the primary and energy metabolism, up-regulation of enzymes implicated in lignin and phenylpropanoid biosynthesis, activation of hormones biosynthesis and signal transduction pathways and genes involved in redox homeostasis and transcriptional regulation. The search for candidate genes with expression profiles associated with the 2DL QTL for FHB resistance led to the discovery of processes differentially modulated in the R and S NILs related to cell wall metabolism, sugar and JA signaling, signal reception and transduction, regulation of the redox status and transcription factors. Wheat FHB response-related miRNAs differentially regulated were also identified as putatively implicated in the superoxide dismutase activities and affecting genes regulating responses to biotic/abiotic stresses and auxin signaling. Altered gene expression was also observed for fungal non-codingRNAs. The putative targets of two of these were represented by the wheat gene WIR1A, involved in resistance response, and a gene encoding a jacalin-related lectin protein, which participate in biotic and abiotic stress response, supporting the presence of a cross-talk between the plant and the fungus.

来源: Frontiers

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<http://agri.ckcest.cn/file1/M00/OE/80/Csgk0F1suZKARpkTALWFYJVC8zI880.pdf>

3. Phosphorus Alters Starch Morphology and Gene Expression Related to Starch Biosynthesis and Degradation in Wheat Grain (磷改变了与淀粉生物合成与降解有关的小麦籽粒淀粉形态和基因表达)

简介: Phosphorus is an essential plant macronutrient which profoundly affects the yield and quality of wheat starch. In this study, scanning electron microscopy showed that P fertilizer amount (0, 46, and 92 kg P ha⁻¹) had no significant effect on the shape of starch granules in wheat (cv. Xindong 20) grain. However, confocal laser scanning microscopy with 3-(4-carboxybenzoyl) quinoline-2-carboxaldehyde and methanolic merbromin stains indicated that P amount influenced the microstructure of the starch granules. Starch granules from the 46 kg P ha⁻¹ treatment released significantly more reducing sugars than those from the 0 and 92 kg P ha⁻¹ treatments during digestion with alpha-amylase and amyloglucosidase digestion. Phosphorus application (especially the 46 kg P ha⁻¹ treatments) significantly increased the relative expression of genes related to starch synthesis (especially during early to mid-grain filling) and starch degradation (especially during mid- and late grain filling). Phosphorus application also increased the transcript abundance of amylase genes at the periphery of the endosperm. We propose that P application, especially the 46 kg P ha⁻¹ treatment, enhanced channels in wheat starch granules. These channels facilitated the transport of substances required for starch biosynthesis, thus increasing starch accumulation in wheat endosperm. These results provide insight into the potential mechanisms through which P influences the microstructure and biosynthesis of wheat starch.

来源: Frontiers

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<http://agri.ckcest.cn/file1/M00/0E/80/Csgk0F1stuuANzDtACg1oraPV0k363.pdf>

➤ 相关专利

1. 小麦穗粒数主效QTL的紧密连锁的分子标记及其应用

简介: 本发明公开了一种小麦穗粒数主效QTL的紧密连锁的分子标记及其应用。本发明还提供了一种用于鉴定或辅助鉴定小麦穗粒数性状的引物组，为能够扩增得到如下DNA片段的引物组：所述DNA片段是以小麦基因组DNA为模板，采用如SEQ ID NO:1和SEQ ID NO:2所示引物对进行PCR扩增所得的DNA片段，以及采用如SEQ ID NO:3-5所示引物对进行PCR扩增所得的DNA片段。以小麦基因组DNA为模板，采用上述引物组进行PCR扩增所得产物即为与小麦穗粒数性状相关的分子标记本发明可用于小麦穗粒数的分子标记，为小麦产量性状分子育种提供优异基因资源和选择工具。

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http://agri.ckcest.cn/file1/M00/0E/80/Csgk0F1su_uAQvAUABR7ciiL6Dg587.PDF