2024年第12期总312期

小麦遗传育种专题

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2024年03月18日

前沿资讯

1 .Genome-wide identification of the basic leucine zipper transcription factor genes related to starch synthesis in wheat (Triticum aestivum L.)(小麦淀粉合成相关碱性亮氨酸拉链转录因子基因的全基因组鉴定)

简介：In plants, the basic leucine zipper (bZIP) family of transcription factors is known for its large size and diversity. Many studies have shown that bZIP transcription factors play an indispensable role in the growth and development of plants; however, there are few reports about the regulation of starch content in grain. To understand the genetic members of the bZIP family, using newly available wheat genome data, we compared our identification of 181 Triticum aestivum bZIP (TabZIP) genes to those reported in earlier studies. Some duplicate genes and incorrect annotations in previous studies were supplemented and corrected. Through phylogenetic analysis, transcriptome data, quantitative reverse transcription PCR (qRT-PCR), a dual-luciferase reporter (DLR), and subcellular localization analysis were used to identify transcription factors that may be involved in grain starch synthesis. We divided genes into 13 known groups and five unknown groups by phylogenetic analysis. All of the bZIP genes exhibited a minimum of one bZIP motif in their motif distribution and gene structure. Spatial and temporal expression patterns of bZIP family members during various stages of plant growth vary, as suggested by transcriptome data, and several genes were specifically expressed during grain development. As per the expression data obtained via qRT-PCR, over 10 TabZIP genes showed similarity with starch synthesis in wheat. The in-vitro binding activity of TabZIP68 to the promoter of TaWaxy was demonstrated by a DLR assay. Expression level of TabZIP68 was affected by different plant hormones treated with developing grains. Given its potential involvement in starch synthesis, the TabZIP68 gene presents itself as a strong candidate for further investigation.

来源：SpringerLink

发布日期:2024-01-26

全文链接:

http://agri.nais.net.cn/file1/M00/03/6A/CsgkOWXVvJCAerP2ACs5O-aEmVE473.pdf

2 .Genome-wide association mapping for field spot blotch resistance in South Asian spring wheat genotypes(南亚春小麦基因型田间斑点病抗性全基因组关联图谱研究)

简介：Spot blotch caused by Bipolaris sorokiniana ((Sacc.) Shoemaker) (teleomorph: Cochliobolus sativus [Ito and Kuribayashi] Drechsler ex Dastur) is an economically important disease of warm and humid regions. The present study focused on identifying resistant genotypes and single-nucleotide polymorphism (SNP) markers associated with spot blotch resistance in a panel of 174 bread spring wheat lines using field screening and genome-wide association mapping strategies. Field experiments were conducted in Agua Fria, Mexico, during the 2019-2020 and 2020-2021 cropping seasons. A wide range of phenotypic

variation was observed among genotypes tested during both years. Twenty SNP markers showed significant association with spot blotch resistance on 15 chromosomes, namely, 1A, 1B, 2A, 2B, 2D, 3A, 3B, 4B, 4D, 5A, 5B, 6A, 6B, 7A, and 7B. Of these, two consistently significant SNPs on 5A, TA003225-0566 and TA003225-1427, may represent a new resistance quantitative trait loci. Further, in the proximity of Tsn1 on 5B, AX-94435238 was the most stable and consistent in both years. The identified genomic regions could be deployed to develop spot blotch-resistant genotypes, particularly in the spot blotch-vulnerable wheat growing areas.

来源：CSSA

发布日期:2024-01-14

全文链接:

http://agri.nais.net.cn/file1/M00/03/6A/CsgkOWXVwleAQFjbADu8fMOPOFs015.pdf

3．Genome-wide identification and analysis of the GGCT gene family in wheat（小麦GGCT基因家族的全基因组鉴定与分析）

简介：Background γ-glutamylcyclotransferase (GGCT), an enzyme to maintain glutathione homeostasis, plays a vital role in the response to plant growth and development as well as the adaptation to various stresses. Although the GGCT gene family analysis has been conducted in Arabidopsis and rice, the family genes have not yet been well identified and analyzed at the genome-wide level in wheat (Triticum aestivum L.). Results In the present study, 20 TaGGCT genes were identified in the wheat genome and widely distributed on chromosomes 2A, 2B, 2D, 3A, 4A, 5A, 5B, 5D, 6A, 6B, 6D, 7A, 7B, and 7D. Phylogenetic and structural analyses showed that these TaGGCT genes could be classified into three subfamilies: ChaC, GGGACT, and GGCT-PS. They exhibited similar motif compositions and distribution patterns in the same subgroup. Gene duplication analysis suggested that the expansion of TaGGCT family genes was facilitated by segmental duplications and tandem repeats in the wheat evolutionary events. Identification of diverse cis-acting response elements in TaGGCT promoters indicated their potential fundamental roles in response to plant development and abiotic stresses. The analysis of transcriptome data combined with RT-qPCR results revealed that the TaGGCTs genes exhibited ubiquitous expression across plant organs, with highly expressed in roots, stems, and developing grains. Most TaGGCT genes were up-regulated after 6 h under 20% PEG6000 and ABA treatments. Association analysis revealed that two haplotypes of TaGGCT20 gene displayed significantly different Thousand-kernel weight (TKW), Kernel length (KL), and Kernel width (KW) in wheat. The geographical and annual distribution of the two haplotypes of TaGGCT20 gene further revealed that the frequency of the favorable haplotype TaGGCT20-Hap-I was positively selected in the historical breeding process of wheat. Conclusion This study investigated the genome-wide identification, structure, evolution, and expression analysis of TaGGCT genes in wheat. The motifs of TaGGCTs were highly conserved throughout the evolutionary history of wheat. Most TaGGCT genes were highly expressed in roots, stems, and developing grains, and involved in the response to drought stresses. Two haplotypes were developed in the TaGGCT20 gene, where TaGGCT20-Hap-I, as a favorable haplotype, was significantly associated with higher TKW, KL, and KW in wheat, suggesting that the haplotype is used as a

function marker for the selection in grain yield in wheat breeding.
来源： BMC Genomics
发布日期:2024-01-04
全文链接:
http://agri.nais.net.cn/file1/M00/03/6A/CsgkOWXVqP2AX_GbAFsTdOyRyLY701.pdf

4．Genome-wide analysis and characterization of the TaTLP gene family in wheat and functional characterization of the TaTLP44 in response to Rhizoctonia cerealis(小麦TaTLP基因家族的全基因组分析和鉴定以及TaTLP44对小麦根丝核菌的功能鉴定)

简介： Wheat sharp eyespot is a soil-borne disease caused by Rhizoctonia cerealis, which occurs in many countries worldwide and significantly reduces the yield. Thaumatin-like protein (TLP), also known as PR5, is a member of the pathogen response protein family and plays an essential role in plant resistance to pathogen infection. In this study, 131 TaTLP genes were identified from the wheat genome, of which 38 TaTLPs were newly discovered. The TaTLP gene family contains many tandem duplications and fragment duplications, which is a major pathway for gene amplification. Besides, we also analyzed the physicochemical properties, gene structure and promoter cis-acting regulatory elements of all the TaTLP genes. In addition, the expression patterns of nine TaTLPs in response to R. cerealis were analyzed by RT-qPCR. Six TaTLP proteins expressed in vitro had no significant inhibitory effect on R. cerealis, suggesting that these TaTLP proteins may function in other ways. Finally, we performed gene silencing of TaTLP44 in wheat, which increased the expression of some defense-associated genes and improved resistance to R. cerealis. In summary, we systematically analyzed TaTLP family members and demonstrated that TaTLP44 negatively regulates the resistance to R. cerealis by controlling expression of defense-associated genes. These results provide new insights into the functional mechanism of TaTLP proteins.
来源： ScienceDirect
发布日期:2024-01-02
全文链接:
http://agri.nais.net.cn/file1/M00/10/3D/CsgkOEF_DIiAEb5nAJPW9n8cNsA136.pdf

5．The HC-Pro cistron of Triticum mosaic virus is dispensable for systemic infection in wheat but is required for symptom phenotype and efficient genome amplification(小麦花叶病毒HC-Pro反链在小麦系统感染中是不需要的，但在症状表型和高效基因组扩增中是必需的)

简介： Triticum mosaic virus (TriMV), the type species of the genus Poacevirus in the family Potyviridae, is an economically important wheat curl mite-transmitted wheat-infecting virus in the Great Plains region of the USA. In this study, the functional genomics of helper component-proteinase (HC-Pro) encoded by TriMV was examined using a reverse genetics approach. TriMV with complete deletion of HC-Pro cistron elicited systemic infection in

wheat, indicating that HC-Pro cistron is dispensable for TriMV systemic infection. However, TriMV lacking HC-Pro caused delayed systemic infection with mild symptoms that resulted in little or no stunting of plants with a significant reduction in the accumulation of genomic RNA copies and coat protein (CP). Sequential deletion mutagenesis from the 5′ end of HC-Pro cistron in the TriMV genome revealed that deletions within amino acids 3 to 25, except for amino acids 3 and 4, elicited mild symptoms with reduced accumulation of genomic RNA and CP. Surprisingly, TriMV with deletion of amino acids 3 to 50 or 3 to 125 in HC-Pro elicited severe symptoms with a substantial increase in genomic RNA copies but a drastic reduction in CP accumulation. Additionally, TriMV with heterologous HC-Pro from other potyvirids produced symptom phenotype and genomic RNA accumulation similar to that of TriMV without HC-Pro, suggesting that HC-Pros of other potyvirids were not effective in complementing TriMV in wheat. Our data indicate that HC-Pro is expendable for replication of TriMV but is required for efficient viral genomic RNA amplification and symptom development. The availability of TriMV with various deletions in the HC-Pro cistron will facilitate the examination of the requirement of HC-Pro for wheat curl mite transmission.
来源： PubMed Central
发布日期:2023-11-30
全文链接:
http://agri.nais.net.cn/file1/M00/10/3D/CsgkOEF-_n-ADJBuAJ4m167aS-0198.pdf