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小麦遗传育种专题

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1. 一种小麦高效辐射诱变育种体系构建的方法

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前沿资讯

1. Molecular marker dissection of stem rust resistance in Nebraska bread wheat germplasm (内布拉斯加州面包小麦种质抗锈性分子标记的分离)

简介: 茎锈病 (由禾柄锈菌引起) 是一种主要的小麦疾病。为了解内布拉斯加州冬小麦茎锈病抗性的遗传基础, 对两个苗圃 (DUP22015和TRP2015) 中一组具有330个代表的基因型, 在两次复制中, 对内布拉斯加州茎锈病品种 (QFCSC) 的抗性进行了评估。TRP2015苗圃中还评估了另外13个茎锈病小种的抗性。方差分析显示, 两个群体的基因型在抗茎锈病性方面存在显著差异。对9个茎锈病基因Sr6、Sr31、Sr1RSAmigo、Sr24、Sr36、SrTmp、Sr7b、Sr9b和Sr38进行了预测, 并利用基因特异性标记对其进行了基因分型。遗传分析结果证实了7个茎部抗锈基因的存在。其中一个基因型 (NE15680) 含有5个抗茎锈病基因的目标等位基因, 对不同的品种具有较高的抗茎锈病水平。单标记分析表明, Sr24和Sr38分别与DUP22015和TRP2015苗圃的茎锈病抗性高度相关。连锁不平衡分析发现17个单核苷酸多态性与Sr38特异性标记高度连锁。这些标记Sr38基因的SNPs在其他遗传背景下进行验证后, 可用于标记辅助选择。

来源: Nature

发布日期: 2019-08-12

全文链接:

http://agri.ckcest.cn/file1/M00/OE/7E/Csgk0F1aCCqAb_KbABUXUYevGNc735.pdf

学术文献

1. Genome-Wide Identification and Homoeologous Expression Analysis of PP2C Genes in Wheat (*Triticum aestivum* L.) (小麦PP2C基因的全基因组鉴定及同源表达分析)

简介: Plant protein phosphatase 2Cs (PP2Cs) play crucial roles in phytohormone signaling, developmental processes, and both biotic and abiotic stress responses. However, little research has been conducted on the PP2C gene family in hexaploid wheat (*Triticum aestivum* L.), which is an important cereal crop. In this study, a genome-wide investigation of TaPP2C gene family was performed. A total of 257 homoeologs of 95 TaPP2C genes were identified, of which 80% of genes had all the three homoeologs across A, B, and D subgenomes. Domain analysis indicated that all the TaPP2C homoeologs harbored the type 2C phosphatase domains. Based on the phylogenetic analysis, TaPP2Cs were divided into 13 groups (A-M) and 4 single branches, which corresponded to the results of gene structure and protein motif analyses. Results of chromosomal location and synteny relationship analysis of TaPP2C homoeologs revealed that known chromosome translocation events and pericentromeric inversions were responsible for the formation of TaPP2C gene family. Expression patterns of TaPP2C homoeologs in various tissues and under diverse stress conditions were analyzed using publicly available RNA-seq data. The results suggested that TaPP2C genes regulate wheat developmental processes and stress responses. Homoeologous

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expression patterns of TaPP2C triad homoeologs from A, B, and D subgenomes, revealed expression bias within triads under the normal condition, and variability in expression under different stress treatments. Quantitative real-time PCR (qRT-PCR) analysis of eight TaPP2C genes in group A revealed that they were all up-regulated after abscisic acid treatment. Some genes in group A also responded to other phytohormones such as methyl jasmonate and gibberellin. Yeast two-hybrid assays showed that group A TaPP2Cs also interacted with TaSnRK2.1 and TaSnRK2.2 from subclass II, besides with subclass III TaSnRK2s. TaPP2C135 in group A was transformed into Arabidopsis and germination assay revealed that ectopic expression of TaPP2C135 in Arabidopsis enhanced its tolerance to ABA. Overall, these results enhance our understanding of the function of TaPP2Cs in wheat, and provide novel insights into the roles of group A TaPP2Cs. This information will be useful for in-depth functional analysis of TaPP2Cs in future studies and for wheat breeding.

来源: Frontiers

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全文链接:

http://agri.ckcest.cn/file1/M00/0E/7E/Csgk0F1aCwqAUwbhAH_xRKRZXos559.pdf

2. Identification and Characterization of Wheat Yellow Striate Virus, a Novel Leafhopper-Transmitted Nucleorhabdovirus Infecting Wheat (一种新型叶蝉传播的小麦黄纹病毒的识别与表征)

简介: A new wheat viral disease was found in China. Bullet-shaped viral particles within the nucleus of the infected wheat leaf cells, which possessed 180210 nm length and 3540 nm width, were observed under transmission electron microscopy. A putative wheat-infecting rhabdovirus vectored by the leafhopper *Psammotettix alienus* was identified and tentatively named wheat yellow striate virus (WYSV). The full-length nucleotide sequence of WYSV was determined using transcriptome sequencing and RACE analysis of both wheat samples and leafhoppers *P. alienus*. The negative-sense RNA genome of WYSV contains 14,486 nucleotides (nt) and seven open reading frames (ORFs) encode deduced proteins in the order N-P-P3-M-P6-G-L on the antisense strand. In addition, WYSV genome has a 76-nt 3' leader RNA and a 258-nt 5' trailer, and the ORFs are separated by conserved intergenic sequences. The entire genome sequence shares 58.1 and 57.7% nucleotide sequence identity with two strains of rice yellow stunt virus (RYSV-A and RYSV-B) genomes, respectively. The highest amino acid sequence identity was 63.8% between the L proteins of the WYSV and RYSV-B, but the lowest was 29.5% between the P6 proteins of these viruses. Phylogenetic analysis firmly established WYSV as a new member of the genus Nucleorhabdovirus. Collectively, this study provided evidence that WYSV is likely the first nucleorhabdovirus described infecting wheat via leafhopper *P. alienus* transmission.

来源: Frontiers

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全文链接:

<http://agri.ckcest.cn/file1/M00/0E/7E/Csgk0F1aDISAFSMXACmK7q0dcYE794.pdf>

3. Genetic Diversity and Population Structure of F3:6 Nebraska Winter Wheat Genotypes Using Genotyping-By-Sequencing (采用基因型测序法研究F3:6内布拉斯加州冬小麦基因型的遗传多样性和群体结构)

简介: The availability of information on the genetic diversity and population structure in wheat (*Triticum aestivum* L.) breeding lines will help wheat breeders to better use their genetic resources and manage genetic variation in their breeding program. The recent advances in sequencing technology provide the opportunity to identify tens or hundreds of thousands of single nucleotide polymorphism (SNPs) in large genome species (e.g., wheat). These SNPs can be utilized for understanding genetic diversity and performing genome wide association studies (GWAS) for complex traits. In this study, the genetic diversity and population structure were investigated in a set of 230 genotypes (F3:6) derived from various crosses as a prerequisite for GWAS and genomic selection. Genotyping-by-sequencing provided 25,566 high-quality SNPs. The polymorphism information content (PIC) across chromosomes ranged from 0.09 to 0.37 with an average of 0.23. The distribution of SNPs markers on the 21 chromosomes ranged from 319 on chromosome 3D to 2,370 on chromosome 3B. The analysis of population structure revealed three subpopulations (G1, G2, and G3). Analysis of molecular variance identified 8% variance among and 92% within subpopulations. Of the three subpopulations, G2 had the highest level of genetic diversity based on three genetic diversity indices: Shannon's information index (I) = 0.494, diversity index (h) = 0.328 and unbiased diversity index (uh) = 0.331, while G3 had lowest level of genetic diversity (I = 0.348, h = 0.226 and uh = 0.236). This high genetic diversity identified among the subpopulations can be used to develop new wheat cultivars.

来源: Frontiers

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➤ 相关专利

1. 一种小麦高效辐射诱变育种体系构建的方法

简介: 本发明公开了一种小麦高效辐射诱变育种体系构建的方法, 通过本发明, 300Gy⁶⁰Co的 γ 射线辐照处理干种子作为亲本密播且迟播, 促进花期相遇; 以未经辐照处理小麦亲本为母本和辐照处理后的亲本种子为父本进行杂交, 较杂交后F1代种子低剂量辐射处理操作简单, 较常规不辐射杂交变异的可能性大, 较辐照当代为母本未辐射亲本为父本杂交产生变异度更大; F2和F3低世代采用常规密度小区种植有利于保留更多的变异类型, 同时也可用于材料耐密性筛选。

来源:

<http://pss-system.cnipa.gov.cn/sipopublicsearch/patentsearch/showViewList-jumpToView.shtml>

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