



2023年第40期总288期

小麦遗传育种专题

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2023年10月02日

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➤ 前沿资讯

1 . Candidate effectors for leaf rust resistance gene Lr28 identified through transcriptome and in-silico analysis (通过转录组和计算机分析鉴定抗叶锈病基因Lr28的候选效应子)

简介: Puccinia spp. causing rust diseases in wheat and other cereals secrete several specialized effector proteins into host cells. Characterization of these proteins and their interaction with host's R proteins could greatly help to limit crop losses due to diseases. Prediction of effector proteins by combining the transcriptome analysis and multiple in-silico approaches is gaining importance in revealing the pathogenic mechanism. The present study involved identification of 13 Puccinia triticina (Pt) coding sequences (CDSs), through transcriptome analysis, that were differentially expressed during wheat-leaf rust interaction; and prediction of their effector like features using different in-silico tools. NCBI-BLAST and pathogen-host interaction BLAST (PHI-BLAST) tools were used to annotate and classify these sequences based on their most closely matched counterpart in both the databases. Homology between CDSs and the annotated sequences in the NCBI database ranged from 79 to 94% and with putative effectors of other plant pathogens in PHI-BLAST from 24.46 to 54.35%. Nine of the 13 CDSs had effector-like features according to EffectorP 3.0 (>0.546 probability of these sequences to be effector). The qRT-PCR expression analysis revealed that the relative expression of all CDSs in compatible interaction (HD2329) was maximum at 11 days post inoculation (dpi) and that in incompatible interactions (HD2329 + Lr28) was maximum at 3 dpi in seven and 9 dpi in five CDSs. These results suggest that six CDSs (>0.8 effector probability as per EffectorP 3.0) could be considered as putative Pt effectors. The molecular docking and MD simulation analysis of these six CDSs suggested that candidate Lr28 protein binds more strongly to candidate effector c14094_g1_i1 to form more stable complex than the remaining five. Further functional characterization of these six candidate effectors should prove useful for a better understanding of wheat-leaf rust interaction. In turn, this should facilitate effector-based leaf rust resistance breeding in wheat.

来源: Frontiers

发布日期: 2023-09-17

全文链接:

<http://agri.nais.net.cn/file1/M00/10/31/Csgk0GUQ7u2AYbUrAD08YwVYa7c048.pdf>

➤ 学术文献

1 . Character variation of root space microbial community composition in the response of drought-tolerant spring wheat to drought stress (耐旱春小麦根系空间微生物群落组成对于旱胁迫响应的特征变化)

简介: Drought is the most prevalent environmental stress in crop production, posing a significant danger to food security. Microorganisms in the crop root zone affect crop growth

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and development, enhance effective nutrient use, and resist adversity hazards. To analyze the changes and functional differences of root space microbial (endosphere-rhizosphere-bulk soil) communities in spring wheat under drought stress. In this study, the root, rhizosphere, and bulk soil of the drought-tolerant group (DTG, three varieties) and drought-sensitive group (DSG, three varieties) were collected. The control (CK, 2528%), moderate drought (MD, 1518%), and severe drought (SD, 912%) were analyzed by high-throughput sequencing and bioinformatics. The results showed significant differences in the diversity of Bacteria and Fungi in the root space of spring wheat under drought stress ($P < 0.05$), with the drought-tolerant group exhibiting higher microbial diversity. The microbial community change in spring wheat root space was mainly determined by the niche differentiation of endosphere, rhizosphere, and bulk soil and declined from endosphere to bulk soil due to drought. The antagonism between microbial and root-space species increased, and the community's complexity and stability deteriorated. Enriching drought-resistant preference groups like Actinobaciota, Variovorax, Streptomyces, and Conocybe altered the structure and function of the microbial community in the root space of spring wheat. Spring wheat's root space Bacteria and Fungi have different strategies to respond to drought.

来源: Frontiers

发布日期: 2023-09-15

全文链接:

<http://agri.nais.net.cn/file1/M00/03/5F/Csgk0Y1nqUWA0JieAKqK1-ti-u8571.pdf>

2 . From genes to policy: mission-oriented governance of plant-breeding research and technologies (从基因到政策: 以使命为导向的植物育种研究和技术治理)

简介: Mission-oriented governance of research focuses on inspirational, yet attainable goals and targets the sustainable development goals through innovation pathways. We disentangle its implications for plant breeding research and thus impacting the sustainability transformation of agricultural systems, as it requires improved crop varieties and management practices. Speedy success in plant breeding is vital to lower the use of chemical fertilizers and pesticides, increase crop resilience to climate stresses and reduce postharvest losses. A key question is how this success may come about? So far plant breeding research has ignored wider social systems feedbacks, but governance also failed to deliver a set of systemic breeding goals providing directionality and organization to research policy of the same. To address these challenges, we propose a heuristic illustrating the core elements needed for governing plant breeding research: Genetics, Environment, Management and Social system (GxExMxS) are the core elements for defining directions for future breeding. We illustrate this based on historic cases in context of current developments in plant phenotyping technologies and derive implications for governing research infrastructures and breeding programs. As part of mission-oriented governance we deem long-term investments into human resources and experimental set-ups for agricultural systems necessary to ensure a symbiotic relationship for private and public

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breeding actors and recommend fostering collaboration between social and natural sciences for working towards transdisciplinary collaboration.

来源: Frontiers

发布日期:2023-09-04

全文链接:

http://agri.nais.net.cn/file1/M00/10/31/Csgk0GUQ832AG0TzABWe_Lhes4s037.pdf

3 . Novel Genetic Loci from Triticum timopheevii Associated with Gluten Content Revealed by GWAS in Wheat Breeding Lines (GWAS在小麦育种系中发现与面筋含量相关的新遗传位点)

简介: The content and quality of gluten in wheat grain is a distinctive characteristic that determines the final properties of wheat flour. In this study, a genome-wide association study (GWAS) was performed on a wheat panel consisting of bread wheat varieties and the introgression lines (ILs) obtained via hybridization with tetraploid wheat relatives. A total of 17 stable quantitative trait nucleotides (QTNs) located on chromosomes 1D, 2A, 2B, 3D, 5A, 6A, 7B, and 7D that explained up to 21% of the phenotypic variation were identified. Among them, the QTLs on chromosomes 2A and 7B were found to contain three and six linked SNP markers, respectively. Comparative analysis of wheat genotypes according to the composition of haplotypes for the three closely linked SNPs of chromosome 2A indicated that haplotype TT/AA/GG was characteristic of ten ILs containing introgressions from *T. timopheevii*. The gluten content in the plants with TT/AA/GG haplotype was significantly higher than in the varieties with haplotype GG/GG/AA. Having compared the newly obtained data with the previously reported quantitative trait loci (QTLs) we inferred that the locus on chromosome 2A inherited from *T. timopheevii* is potentially novel. The introgression lines containing the new locus can be used as sources of genetic factors to improve the quality traits of bread wheat.

来源: MDPI

发布日期:2023-08-27

全文链接:

<http://agri.nais.net.cn/file1/M00/03/5F/Csgk0Y1n2FOAEL0tABg-DvKGuJg755.pdf>

4 . Screening of the Effect of Mutation Breeding On Biotic Stress Tolerance and Quality Traits of Durum Wheat (突变育种对硬粒小麦生物抗逆性及品质性状影响的筛选)

简介: Breeding is a promising tool to increase genetic diversity in crop plants for the selection and transfer of favorable genes. Mutation breeding techniques were considered as an evolutionary breeding tool for creating a new elite genotypes resistant to multiple biotic and abiotic stresses. In this context, a total of 70 M4 and 37 M5 mutants selected from three levels of gamma irradiation (100, 150, and 250 Gy) were evaluated for disease resistance and quality traits. Under field conditions, M5 selected mutants at 150 Gy showed higher diseases resistance (Septoria tritici blotch, tan spot, yellow rust, and leaf rust) as well as better grain quality parameters(thousand kernel weight, grain protein content, test

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weight, gluten content, and wet gluten content). Positive correlations were established for most of the considered parameters on M5 along with a negative association with *Septoria tritici* blotch, yellow rust, thousand kernel weight, and test weight. Principal component analysis (PCA) showed that 100 Gy and 150 Gy were good gamma irradiation dose levels in improving and giving effective desirable traits, especially 150 Gy which ensures the best disease resistance and grain quality. These findings are promising tools for exploring the implication of mutation on genetic mechanisms and the transfer of complex traits on elite genotypes.

来源: Springer

发布日期: 2022-10-18

全文链接:

<http://agri.nais.net.cn/file1/M00/10/31/Csgk0GURH3yAfvtmABYJhniunW4148.pdf>