



2024年第2期总302期

小麦遗传育种专题

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1. 基于SNP的地中海小麦选育

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▶ 前沿资讯

1 . Dual RNA-sequencing of Fusarium head blight resistance in winter wheat (冬小麦中镰刀菌头疫病抗性的双RNA测序)

简介: Fusarium head blight (FHB) is a devastating fungal disease responsible for significant yield losses in wheat and other cereal crops across the globe. FHB infection of wheat spikes results in grain contamination with mycotoxins, reducing both grain quality and yield. Breeding strategies have resulted in the production of FHB-resistant cultivars, however, the underlying molecular mechanisms of resistance in the majority of these cultivars are still poorly understood. To improve our understanding of FHB-resistance, we performed a transcriptomic analysis of FHB-resistant AC Emerson, FHB-moderately resistant AC Morley, and FHB-susceptible CDC Falcon in response to *Fusarium graminearum*. Wheat spikelets located directly below the point of inoculation were collected at 7-days post inoculation (dpi), where dual RNA-sequencing was performed to explore differential expression patterns between wheat cultivars in addition to the challenging pathogen. Differential expression analysis revealed distinct defense responses within FHB-resistant cultivars including the enrichment of physical defense through the lignin biosynthesis pathway, and DON detoxification through the activity of UDP-glycosyltransferases. Nucleotide sequence variants were also identified broadly between these cultivars with several variants being identified within differentially expressed putative defense genes. Further, *F. graminearum* demonstrated differential expression of mycotoxin biosynthesis pathways during infection, leading to the identification of putative pathogenicity factors.

来源: Frontiers

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http://agri.nais.net.cn/file1/M00/10/36/Csgk0GWWW6CAJyToAJLFz_BTy8860.pdf

2 . Critical assessment of wheat biofortification for iron and zinc: a comprehensive review of conceptualization, trends, approaches, bioavailability, health impact, and policy framework (小麦铁锌生物强化的关键评估: 概念、趋势、方法、生物可得性、健康影响和政策框架的综合审查)

简介: Addressing global hidden hunger, particularly in women of childbearing age and children under five, presents a significant challenge, with a focus on iron (Fe) and zinc (Zn) deficiency. Wheat, a staple crop in the developing world, is crucial for addressing this issue through biofortification efforts. While extensive research has explored various approaches to enhance Fe and Zn content in wheat, there remains a scarcity of comprehensive data on their bioavailability and impact on human and animal health. This systematic review examines the latest trends in wheat biofortification approaches, assesses bioavailability, evaluates the effects of biofortified wheat on health outcomes in humans and animals, and analyzes global policy frameworks. Additionally, a meta-analysis of per capita daily Fe and

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Zn intake from average wheat consumption was conducted. Notably, breeding-based approaches have led to the release of 40 biofortified wheat varieties for commercial cultivation in India, Pakistan, Bangladesh, Mexico, Bolivia, and Nepal, but this progress has overlooked Africa, a particularly vulnerable continent. Despite these advancements, there is a critical need for large-scale systematic investigations into the nutritional impact of biofortified wheat, indicating a crucial area for future research. This article can serve as a valuable resource for multidisciplinary researchers engaged in wheat biofortification, aiding in the refinement of ongoing and future strategies to achieve the Sustainable Development Goal of eradicating hunger and malnutrition by 2030.

来源: Frontiers

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<http://agri.nais.net.cn/file1/M00/03/63/Csgk0WVVVG2Ab3ILAE831jV4s783.pdf>

3 . Transcriptomic insights into the molecular mechanism for response of wild emmer wheat to stripe rust fungus (转录组揭示野生小麦对条锈病菌反应的分子机制)

简介: A higher number of DEGs were identified in the moderately (Pst-resistant genotype), while the highly (Pst-resistant genotype) exhibited a greater enrichment of pathways. Nonetheless, there were consistent patterns in the enrichment of pathways between the two genotypes at the same time of inoculation. At 24 hpi, a majority of pathways such as the biosynthesis of secondary metabolites, phenylpropanoid biosynthesis, phenylalanine metabolism, and alpha-Linolenic acid metabolism exhibited significant enrichment in both genotypes. At 72 hpi, the biosynthesis of secondary metabolites and circadian rhythm-plant pathways were notably and consistently enriched in both genotypes. The majority of (WRKY, MADs, and AP2-ERF families) were found to be involved in the initial stage of response to Pst invasion (24 hpi), while the MYB, NAC, TCP, and b-ZIP families played a role in defense during the later stage of Pst infection (72 hpi).

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4 . Genome-wide association study of common resistance to rust species in tetraploid wheat (四倍体小麦抗锈病的全基因组关联研究)

简介: Rusts of the genus *Puccinia* are wheat pathogens. Stem (black; Sr), leaf (brown; Lr), and stripe (yellow; Yr) rust, caused by *Puccinia graminis* f. sp. *tritici* (Pgt), *Puccinia triticina* (Pt), and *Puccinia striiformis* f. sp. *tritici* (Pst), can occur singularly or in mixed infections and pose a threat to wheat production globally in terms of the wide dispersal of their urediniospores. The development of durable resistant cultivars is the most sustainable method for controlling them. Many resistance genes have been identified, characterized, genetically mapped, and cloned; several quantitative trait loci (QTLs) for resistance have

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also been described. However, few studies have considered resistance to all three rust pathogens in a given germplasm. A genome-wide association study (GWAS) was carried out to identify loci associated with resistance to the three rusts in a collection of 230 inbred lines of tetraploid wheat (128 of which were *Triticum turgidum* ssp. *durum*) genotyped with SNPs. The wheat panel was phenotyped in the field and subjected to growth chamber experiments across different countries (USA, Mexico, Morocco, Italy, and Spain); then, a mixed linear model (MLM) GWAS was performed. In total, 9, 34, and 5 QTLs were identified in the A and B genomes for resistance to Pgt, Pt, and Pst, respectively, at both the seedling and adult plant stages. Only one QTL on chromosome 4A was found to be effective against all three rusts at the seedling stage. Six QTLs conferring resistance to two rust species at the adult plant stage were mapped: three on chromosome 1B and one each on 5B, 7A, and 7B. Fifteen QTLs conferring seedling resistance to two rusts were mapped: five on chromosome 2B, three on 7B, two each on 5B and 6A, and one each on 1B, 2A, and 7A. Most of the QTLs identified were specific for a single rust species or race of a species. Candidate genes were identified within the confidence intervals of a QTL conferring resistance against at least two rust species by using the annotations of the durum (cv. 'Svevo') and wild emmer wheat ('Zavitan') reference genomes. The 22 identified loci conferring resistance to two or three rust species may be useful for breeding new and potentially durable resistant wheat cultivars.

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➤ 相关专利

1 . SNP based panel for mediterranean wheat plant selection and breeding (基于SNP的地中海小麦选育)

简介: However, the complexity of the wheat genome presents some challenges for applying new technologies in molecular marker identification generating large numbers of molecular markers (SNPs) for use in genetic analyses such as genomics-assisted breeding in a range of plant species. Genomic selection models have already proven to be advantageous but they are still quite laborious requiring the access to high throughput genotyping platforms and well trained and experienced personnel on bioinformatics and biostatistics to conduct prediction based on mathematical models. According to recent data, despite the increasing wheat plantings in 2021 in the United States of America and Canada, adverse climatic conditions decreased yield prospects for the main winter wheat crop and consequently wheat production is expected to be below average. Although in European Union the expansion of winter wheat planting is expected to lead to higher production yields, wheat production in the Southern Mediterranean countries is mostly dependent on weather conditions and water availability, being especially fragile under very high spring temperatures and long periods of land drought. Grain yield (GY) improvement is one of the

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most challenging objectives in wheat breeding due to the complex genetic architecture and low heritability. Wheat production in the Southern European region is facing problems of long periods of groundwater decreasing, limiting irrigation frequency and causing the abandonment of wheat crop production by farmers. Although conventional breeding attempts to increase grain yield potential, advances are relatively slow as GY is a complex trait, strongly associated with spike number per unit area, kernel number per spike and thousand-kernel weight (TKW). In Mediterranean-climate regions, temperate cereals like wheat are usually exposed to a severe water deficit during the grain filling period. This water deficit leads to reductions in canopy photosynthesis and lower levels of assimilate transfer to the grain, leading to low kernel weights and GY.

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