



2024年第5期总305期

## 小麦遗传育种专题

### 本期导读

#### ▶ 前沿资讯

1. 小麦根系结构与锌变异的关系
2. 小麦(*Triticum aestivum* L.)籽粒形成过程中蛋白质含量的转录组和代谢组
3. 小麦Pm55等位基因与一种抑制剂表现出显著的相互作用,由此产生不同的白粉病抗性

#### ▶ 学术文献

1. 内源穗细胞分裂素与春小麦籽粒数性状的关系

#### ▶ 科技图书

1. 小麦四倍体与六倍体育种创新的基因流动

山东省农业科学院农业信息与经济研究所

中国农业科学院农业信息研究所

联系人: 唐研; 孟静; 顾亮亮

联系电话: 0531-66657915

邮箱: [agri@ckcest.cn](mailto:agri@ckcest.cn)

2024年01月29日

更多资讯 尽在农业专业知识服务系统:<http://agri.nais.net.cn/>

## ▶ 前沿资讯

### 1 . Root system architecture associated zinc variability in wheat (*Triticum aestivum* L.) (小麦根系结构与锌变异的关系)

简介: Root system architecture (RSA) plays a fundamental role in nutrient uptake, including zinc (Zn). Wheat grains are inheritably low in Zn. As Zn is an essential nutrient for plants, improving its uptake will not only improve their growth and yield but also the nutritional quality of staple grains. A rhizobox study followed by a pot study was conducted to evaluate Zn variability with respect to RSA and its impact on grain Zn concentration. The grain Zn content of one hundred wheat varieties was determined and grown in rhizoboxes with differential Zn (no Zn and 0.05 mg L<sup>-1</sup> ZnSO<sub>4</sub>). Seedlings were harvested 12 days after sowing, and root images were taken and analyzed by SmartRoot software. Using principal component analysis, twelve varieties were screened out based on vigorous and weaker RSA with high and low grain Zn content. The screened varieties were grown in pots with (11 mg ZnSO<sub>4</sub> kg<sup>-1</sup> soil) and without Zn application to the soil. Zinc translocation, localization, and agronomic parameters were recorded after harvesting at maturity. In the rhizobox experiment, 4% and 8% varieties showed higher grain Zn content with vigorous and weaker RSA, respectively, while 45% and 43% varieties had lower grain Zn content with vigorous and weaker RSA. However, the pot experiment revealed that varieties with vigorous root system led to higher grain yield, though the grain Zn concentration were variable, while all varieties with weaker root system had lower yield as well as grain Zn concentration. Zincol-16 revealed the highest Zn concentration (28.07 mg kg<sup>-1</sup>) and grain weight (47.9 g). Comparatively higher level of Zn was localized in the aleurone layer than in the embryonic region and endosperm. It is concluded that genetic variability exists among wheat varieties for RSA and grain Zn content, with a significant correlation. Therefore, RSA attributes are promising targets for the Zn biofortification breeding program. However, Zn localization in endosperm needs to be further investigated to achieve the goal of reducing Zn malnutrition.

来源: <https://www.nature.com/articles/s41598-024-52338-3>

发布日期: 2024-01-20

全文链接:

<http://agri.nais.net.cn/file1/M00/10/36/Csgk0EFaFzaANb1JAC4Mx-8yC7s609.pdf>

### 2 . Comparison of the transcriptome and metabolome of wheat (*Triticum aestivum* L.) proteins content during grain formation provides insight (小麦(*Triticum aestivum* L.)籽粒形成过程中蛋白质含量的转录组和代谢组)

简介: Introduction: Wheat is a food crop with a large global cultivation area, and the content and quality of wheat glutenin accumulation are important indicators of the quality of wheat flour. Methods: To elucidate the gene expression regulation and metabolic characteristics related to the gluten content during wheat grain formation, transcriptomic and metabolomic analyses were performed for the high gluten content of the Xinchun 26

更多资讯 尽在农业专业知识服务系统: <http://agri.nais.net.cn/>

cultivar and the low proteins content of the Xinchun 34 cultivar at three periods (7 d, 14 d and 21 d) after flowering. Results: Transcriptomic analysis revealed that 5573 unique differentially expressed genes (DEGs) were divided into two categories according to their expression patterns during the three periods. The metabolites detected were mainly divided into 12 classes. Lipid and lipid-like molecule levels and phenylpropanoid and polyketide levels were the highest, and the difference analysis revealed a total of 10 differentially regulated metabolites (DRMs) over the three periods. Joint analysis revealed that the DEGs and DRMs were significantly enriched in starch and sucrose metabolism; the citrate cycle; carbon fixation in photosynthetic organisms; and alanine, aspartate and glutamate metabolism pathways. The genes and contents of the sucrose and gluten synthesis pathways were analysed, and the correlation between gluten content and its related genes was calculated. Based on weighted correlation network analysis (WGCNA), by constructing a coexpression network, a total of 5 specific modules and 8 candidate genes that were strongly correlated with the three developmental stages of wheat grain were identified. Discussion: This study provides new insights into the role of glutenin content in wheat grain formation and reveals potential regulatory pathways and candidate genes involved in this developmental process.

来源: Frontiers

发布日期: 2024-01-18

全文链接:

<http://agri.nais.net.cn/file1/M00/10/36/Csgk0EFaFXGAPhAbAKTi0z1TinU110.pdf>

### **3 . Wheat Pm55 alleles exhibit distinct interactions with an inhibitor to cause different powdery mildew resistance (小麦Pm55等位基因与一种抑制剂表现出显著的相互作用，由此产生不同的白粉病抗性)**

简介: Powdery mildew poses a significant threat to wheat crops worldwide, emphasizing the need for durable disease control strategies. The wheat-Dasypyrum villosum T5AL • 5V#4 S and T5DL • 5V#4S translocation lines carrying powdery mildew resistant gene Pm55 shows developmental-stage and tissue-specific resistance, whereas T5DL • 5V#5S line carrying Pm5V confers resistance at all stages. Here, we clone Pm55 and Pm5V, and reveal that they are allelic and renamed as Pm55a and Pm55b, respectively. The two Pm55 alleles encode coiled-coil, nucleotide-binding site-leucine-rich repeat (CNL) proteins, conferring broad-spectrum resistance to powdery mildew. However, they interact differently with a linked inhibitor gene, SuPm55 to cause different resistance to wheat powdery mildew. Notably, Pm55 and SuPm55 encode unrelated CNL proteins, and the inactivation of SuPm55 significantly reduces plant fitness. Combining SuPm55/Pm55a and Pm55b in wheat does not result in allele suppression or yield penalty. Our results provide not only insights into the suppression of resistance in wheat, but also a strategy for breeding durable resistance.

来源: Nature

发布日期: 2024-01-13

全文链接:

<http://agri.nais.net.cn/file1/M00/03/64/Csgk0WWwyJmANdUbACK8eJgwTWc990.pdf>

更多资讯 尽在农业专业知识服务系统: <http://agri.nais.net.cn/>

## 学术文献

### 1 . Associations between endogenous spike cytokinins and grain-number traits in spring wheat genotypes (内源穗细胞分裂素与春小麦籽粒数性状的关系)

简介: Genetic variation in grain number has been positively associated with levels of cytokinins in inflorescences in cereals, although studies quantifying endogenous levels in the field are currently lacking. The present study, using a spring wheat association mapping panel (HiBAP II) of 150 lines, quantified associations between spike hormone levels and grain number and associated traits. The HiBAP II panel was grown in the field in NW Mexico under irrigated conditions for one year and a subset of ten genotypes in the glasshouse under well-watered conditions for three years. The spike levels of four cytokinins (trans-zeatin riboside, trans-zeatin, isopentenyladenosine, and isopentenyladenine) were measured by using ultra-high-performance liquid chromatography coupled with electrospray ionization tandem mass spectrometry. In the glasshouse experiments, spike hormone levels were measured at booting and anthesis, and in the field experiment at anthesis. In the glasshouse experiments, cytokinin levels were also measured in the basal, central, and apical spikelets separately in addition to at the whole spike level. The spike cytokinin levels did not differ significantly between the basal, central and apical sections of the spike. or show a spike position  $\times$  genotype interaction. In the glasshouse experiments, significant genetic variation was detected for the expression of the four cytokinins in spikes at booting. At booting, spike trans-zeatin concentration ranged amongst genotypes from 4.5 to 16.0 ng g<sup>-1</sup> FW and was positively correlated with grain number per main shoot ( $r = 0.77$ ,  $P < 0.05$ ). In the field at anthesis, the spike levels of each of trans-zeatin, trans-zeatin riboside and isopentenyl adenosine were positively correlated with grains per m<sup>2</sup> ( $r = 0.170.19$ ,  $P < 0.05$ ). Our results indicated that selection for high spike cytokinin levels in wheat germplasm offers scope to raise grain number and yield potential in wheat.

来源: Science Direct

发布日期: 2024-01-01

全文链接:

<http://agri.nais.net.cn/file1/M00/03/64/Csgk0WWxtFWAceKiADi6zat7fhI517.pdf>

## 科技图书

### 1 . Gene Flow Between Tetraploid and Hexaploid Wheat for Breeding Innovation (小麦四倍体与六倍体育种创新的基因流动)

简介: Durum and bread wheat are two related species with different ploidy levels but a high similarity between the common A and B genomes. This feature, which allows a continuous gene flow between the two species, can be exploited in breeding programs to improve key traits in both crops. Therefore, durum wheat, despite covering only 5% of cultivated wheat worldwide, also represents an asset for the genetic improvement of bread wheat.

更多资讯 尽在农业专业知识服务系统: <http://agri.nais.net.cn/>

Tetraploid wheat, with a very large availability of wild and domesticated accessions, durum landraces, and cultivars, offers a large gene reservoir to increase the genetic diversity of A and B genomes in bread wheat. Moreover, thanks to the possibility of crossing durum wheat with *Aegilops tauschii*, synthetic hexaploid lines are generated which show a much larger genetic diversity also in the D genome compared to common wheat. The genome sequences of wild emmer, durum, and bread wheat provide power tools for gene cloning and comparative genomics that will also facilitate the shuttling of genes between tetraploid and hexaploid wheats.

来源: The Wheat Genome

发布日期: 2023-11-14

全文链接:

<http://agri.nais.net.cn/file1/M00/10/36/Csgk0EFbBhuAPC3GAMbnL-N4bbI885.pdf>