



2024年第11期总311期

## 小麦遗传育种专题

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## ▶ 前沿资讯

### 1 . Regulation of wheat growth by soil multifunctionality and metagenomic-based microbial functional profiles under mulching treatments (覆盖处理下土壤多功能性和宏基因组微生物功能谱对小麦生长的调控)

简介: Soil microbial functional genes play key roles in biogeochemical processes that are closely related to crop development. However, the regulation of crop growth by the composition and potential interactions of metagenomic-based functional genes is poorly understood. Therefore, in a long-term mulching experiment, the regulation of wheat growth by soil multifunctionality, microbial functional profiles driven by soil properties and microbial activity was studied. Soil properties and microbial activity were significantly separated into distinct mulching treatments, and were significantly declined by plastic film mulching treatment, similar to soil multifunctionality. Only carbon (C) and phosphorus (P) cycling gene compositions were divided significantly into distinct mulching treatments to varying degrees. Similarly, intra- and inter-connected sub-networks associated with C and P cycling genes were more complex and stable than the sub-networks containing nitrogen cycling genes. Despite core functional genes being located in the middle of each network, they were rarely observed in the metagenomic assembly genomes. Subsequently, the dominant soil properties and microbial activity had greater effects on C cycling gene composition and network, which played essential roles in wheat growth regulation. Overall, wheat yield and biomass were affected differently by straw and plastic film mulching treatments, and were mainly regulated by C cycling gene network and soil multifunctionality, respectively. The results of the present study provide novel insights into wheat growth regulation by soil microbial functional profiles, with potential implications for sustainable crop production in mulching conservation agroecosystems.

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<http://agri.nais.net.cn/file1/M00/03/6A/Csgk0WXVq6AJd02ADVQqQeJ00k605.pdf>

### 2 . Genome-wide identification, gene expression and haplotype analysis of the rhomboid-like gene family in wheat (*Triticum aestivum* L.) (小麦菱形基因家族的全基因组鉴定、基因表达及单倍型分析)

简介: The rhomboid-like (RBL) gene encodes serine protease, which plays an important role in the response to cell development and diverse stresses. However, genome-wide identification, expression profiles, and haplotype analysis of the RBL family genes have not been performed in wheat (*Triticum aestivum* L.). This study investigated the phylogeny and diversity of the RBL family genes in the wheat genome through various approaches, including gene structure analysis, evolutionary relationship analysis, promoter cis-acting element analysis, expression pattern analysis, and haplotype analysis. The 41 TaRBL genes

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were identified and divided into five subfamilies in the wheat genome. RBL family genes were expanded through segmented duplication and purification selection. The cis-element analysis revealed their involvement in various stress responses and plant development. The results of RNA-seq and quantitative real-time-PCR showed that TaRBL genes displayed higher expression levels in developing spike/grain and were differentially regulated under polyethylene glycol, NaCl, and abscisic acid treatments, indicating their roles in grain development and abiotic stress response. A kompetitive allele-specific PCR molecular marker was developed to confirm the single nucleotide polymorphism of TaRBL14a gene in 263 wheat accessions. We found that the elite haplotype TaRBL14a-Hap2 showed a significantly higher 1000-grain weight than TaRBL14a-Hap11 in at least three environments, and the TaRBL14a-Hap2 was positively selected in wheat breeding. The findings will provide a good insight into the evolutionary and functional characteristics of the TaRBL genes family in wheat and lay the foundation for future exploration of the regulatory mechanisms of TaRBL genes in plant growth and development, as well as their response to abiotic stresses.

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### **3 . Effect of a QTL on wheat chromosome 5B associated with enhanced root dry mass on transpiration and nitrogen uptake under contrasting drought scenarios in wheat (与根干质量增加相关的5B染色体QTL对不同于旱条件下小麦蒸腾和氮素吸收的影响)**

简介: Background A sufficient nitrogen supply is crucial for high-quality wheat yields. However, the use of nitrogen fertilization can also negatively influence ecosystems due to leaching or volatile atmospheric emissions. Drought events, increasingly prevalent in many crop production areas, significantly impact nitrogen uptake. Breeding more efficient wheat varieties is necessary to achieve acceptable yields with limited nitrogen and water. Crop root systems play a crucial role as the primary organ for absorbing water and nutrients. To investigate the impact of an enhanced root system on nitrogen and water use efficiency in wheat under various irrigation conditions, this study conducted two experiments using precision phenotyping platforms for controlled drought stress treatment. Experiment 1 involved four contrasting winter wheat genotypes. It included the Chinese variety Ning0604, carrying a quantitative trait locus (QTL) on chromosome 5B associated with a higher root dry biomass, and three elite German varieties, Elixer, Genius, and Leandrus. Experiment 2 compared near-isogenic lines (NIL) of the three elite varieties, each containing introgressions of the QTL on chromosome 5B linked to root dry mass. In both experiments, nitrogen partitioning was tracked via isotope discrimination after fertilization with 5 Atom % <sup>15</sup>N-labeled KNO<sub>3</sub>. Results In experiment 1 the quantification by <sup>15</sup>N isotope discrimination revealed significantly ( $p < 0.05$ ) higher nitrogen derived from fertilizer in the root organ for Ning0604 than those of the three German varieties. In experiment 2, two out of three NILs showed a significantly ( $p < 0.05$ ) higher uptake of N derived from fertilizer than their

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respective recipient line under well-watered conditions. Furthermore, significantly lower transpiration rates ( $p < 0.1$ ) were observed in one NIL compared to its respective recipient. Conclusions The combination of the DroughtSpotter facility coupled with  $^{15}\text{N}$  tracer-based tracking of N uptake and remobilization extends the insight into the impact of genetically altered root biomass on wheat NUE and WUE under different water availability scenarios. The study shows the potential for how a modified genetic constitution of the locus on wheat chromosome 5B can reduce transpiration and enhance N uptake. The dependence of the observations on the recipient and water availability suggests a need for further research to investigate the interaction with genetic background traits.

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## ➤ 学术文献

### 1 . Wheat landraces as sources of high grain quality and nutritional properties (小麦地方品种是高品质和营养特性的来源)

简介: Background. Improving the grain quality of modern spring bread wheat cultivars is a highly relevant task of breeding. To solve this problem, old and local wheat varieties (landraces) are of considerable interest. A rich collection of them is available among the plant genetic resources preserved at VIR. With this in view, the aim of this research was to identify sources of high protein, gluten, macro- and micronutrient content out of the landraces from the VIR collection for improvement of wheat grain quality through breeding. Materials and methods. Field and laboratory research were conducted in the experimental field of Omsk State Agrarian University under the conditions of the southern forest-steppe of Western Siberia in 20202021. Sowing was carried out on fallow on conventional sowing dates. Mineral composition in the grain of the studied landraces was analyzed at the Kurchatov Genomic Center, Novosibirsk, using atomic absorption spectrometry techniques. Results. The research results showed that landraces from different regions of Russia, Kazakhstan, Tajikistan, and Kyrgyzstan were characterized by high levels of protein (18.418.8%) and gluten (35.936.0%) in grain. Landraces from Kazakhstan had low Zn content (on average 38.3 mg/kg), while those from Kyrgyzstan, on the contrary, had high content of Zn (41.9 mg/kg) and Fe (55.1 mg/kg), and landraces from Tajikistan had high K content (3820 mg/kg). A positive relationship between the concentrations of Mg, Mn, Fe, and Zn was found in the grain of wheat landraces. Conclusion. Wheat landraces are of interest as genetic resources for the development of high-protein cultivars with improved nutritional value of grain for the milling and breadmaking industries.

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## 2 . Dissection of a rapidly evolving wheat resistance gene cluster by long-read genome sequencing accelerated the cloning of Pm69 (通过长读长测序技术对快速进化的小麦抗性基因簇解剖加速Pm69的克隆)

简介: Gene cloning in repeat-rich polyploid genomes remains challenging. Here, we describe a strategy for overcoming major bottlenecks in cloning of the powdery mildew resistance gene (R-gene) Pm69 derived from tetraploid wild emmer wheat. A conventional positional cloning approach was not effective owing to suppressed recombination. Chromosome sorting was compromised by insufficient purity. A Pm69 physical map, constructed by assembling Oxford Nanopore Technology (ONT) long-read genome sequences, revealed a rapidly evolving nucleotide-binding leucine-rich repeat (NLR) R-gene cluster with structural variations. A single candidate NLR was identified by anchoring RNA sequencing reads from susceptible mutants to ONT contigs and was validated by virus-induced gene silencing. Pm69 is likely a newly evolved NLR and was discovered in only one location across the wild emmer wheat distribution range in Israel. Pm69 was successfully introgressed into cultivated wheat, and a diagnostic molecular marker was used to accelerate its deployment and pyramiding with other R-genes.

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