



2023年第52期总300期

## 小麦遗传育种专题

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1. 小麦测序：泛基因组和加速育种的机会

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## ➤ 前沿资讯

### 1 .Epigenetic modifications regulate cultivar-specific root development and metabolic adaptation to nitrogen availability in wheat (表观遗传修饰调节小麦品种特异性根系发育和对氮素有效性的代谢适应)

简介: The breeding of crops with improved nitrogen use efficiency (NUE) is crucial for sustainable agriculture, but the involvement of epigenetic modifications remains unexplored. Here, we analyze the chromatin landscapes of two wheat cultivars (KN9204 and J411) that differ in NUE under varied nitrogen conditions. The expression of nitrogen metabolism genes is closely linked to variation in histone modification instead of differences in DNA sequence. Epigenetic modifications exhibit clear cultivar-specificity, which likely contributes to distinct agronomic traits. Additionally, low nitrogen (LN) induces H3K27ac and H3K27me3 to significantly enhance root growth in KN9204, while remarkably inducing NRT2 in J411. Evidence from histone deacetylase inhibitor treatment and transgenic plants with loss function of H3K27me3 methyltransferase shows that changes in epigenetic modifications could alter the strategy preference for root development or nitrogen uptake in response to LN. Here, we show the importance of epigenetic regulation in mediating cultivar-specific adaptation to LN in wheat.

来源: Nature

发布日期:2023-12-12

全文链接:

<http://agri.nais.net.cn/file1/M00/03/62/Csgk0WWD3qiALDAKAEONv5IUDuI459.pdf>

## ➤ 学术文献

### 1 . Wheat cultivar replacement drives soil microbiome and microbial cooccurrence patterns (小麦品种更替驱动土壤微生物组和微生物共生模式)

简介: While wheat domestication is reported to influence the soil microbial community, few studies have evaluated the influence of cultivar replacement in modern breeding on both bacterial and fungal communities. Especially, few studies reported the bacterial-fungal interkingdom association by analysis of taxa co-occurrence or co-exclusion between different wheat growth stages. In this study, we selected major wheat cultivars from different decades to investigate their genetic relatedness, plant traits, soil bacterial and fungal communities in the rhizosphere and proximal root zone, and the relationships between them. Our results indicated that host selection had the greatest impact on bacterial and fungal communities compared to growth stage and sampling location ( $P < 0.001$ ). At flowering, the soil microbial community in the genotype group consisting of the 1950s ( $W_{50s}$ ) and 1960s ( $W_{60s}$ ) cultivars could be clearly distinguished from those in later genotype groups. Plant traits explained the largest source of variation in microbial  $\beta$ -diversity (12.820.6%) ( $P = 0.01$ ), with plant height, aboveground dry matter, leaf area per

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plant and specific root length being associated with the divergence in microbial composition or quantity among cultivars. The cultivar from the 1970 s (W<sub>70s</sub>) enriched a greater number of microbial taxa with the highest relative abundance, suggesting that old cultivar could be considered as a source of cultivar-microbe interaction. The cultivar from the 2000 s (W<sub>00s</sub>) enriched taxa from the bacterial genus Nocardioideae and increased the fungal phylum Glomeromycota in the rhizosphere. At three growth stages, W<sub>00s</sub> root-zone exhibited the highest bacteria/fungi ratio (B/F) and contained more phosphorus cycle-related bacterial phoD-genes than W<sub>50s</sub> and W<sub>60s</sub>. The co-occurrence network revealed more operational taxonomic units (OTUs) from the bacterial order Rhizobiales in the largest module of W<sub>00s</sub>. The increased B/F ratio and the aforementioned taxa are reported to be involved in soil nitrogen and phosphorus availability, suggesting that contemporary cultivar may recruit beneficial bacteria and fungi while weaken the association with other fungi. These findings contribute to the development of microbiome-based breeding strategies for sustainable wheat farming.

来源: ScienceDirect

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<http://agri.nais.net.cn/file1/M00/03/62/Csgk0WWD5JSABRVTAHULu81K7Tg033.pdf>

## 2 . Genomics for Yield and Yield Components in Durum Wheat (硬粒小麦产量及其构成因素的基因组学研究)

简介: In recent years, many efforts have been conducted to dissect the genetic basis of yield and yield components in durum wheat thanks to linkage mapping and genome-wide association studies. In this review, starting from the analysis of the genetic bases that regulate the expression of yield for developing new durum wheat varieties, we have highlighted how, currently, the reductionist approach, i.e., dissecting the yield into its individual components, does not seem capable of ensuring significant yield increases due to diminishing resources, land loss, and ongoing climate change. However, despite the identification of genes and/or chromosomal regions, controlling the grain yield in durum wheat is still a challenge, mainly due to the polyploidy level of this species. In the review, we underline that the next-generation sequencing (NGS) technologies coupled with improved wheat genome assembly and high-throughput genotyping platforms, as well as genome editing technology, will revolutionize plant breeding by providing a great opportunity to capture genetic variation that can be used in breeding programs. To date, genomic selection provides a valuable tool for modeling optimal allelic combinations across the whole genome that maximize the phenotypic potential of an individual under a given environment.

来源: MDPI

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<http://agri.nais.net.cn/file1/M00/03/62/Csgk0WWD6byAcKCIACbm-4K2uvE154.pdf>

## 3 . Historic trends and sources of year-over-year stability in Montana

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## winter wheat yields (蒙大纳州冬小麦产量逐年稳定的历史趋势和缘由)

简介: Producers desire cultivars that consistently perform with high yields and end-use qualities. Unlike easily recognized average yield improvements, yield stability over time is less examined, especially when considering the role of breeding relative to other factors like management and changing climatic conditions. Our study system was a 70-year historical dataset from which we estimated the year-over-year stability of winter wheat (*Triticum aestivum* L.) cultivars released by Montana's Agricultural Experimental Station. We examined yield stability within six locations representing diverse growing conditions across Montana and found no evidence that breeding has improved stability, that stability may be decreasing over time at one location, and that the year-over-year stability of a cultivar is sensitive to location. We examined the role of climatic conditions, including temperature, and rainfall to understand if increased climatic variability was masking improved patterns of stability. However, the lack of impact of breeding remained. These findings suggest that Montana's winter wheat may benefit from selective breeding for increased stability within locations.

来源: Crop Science

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<http://agri.nais.net.cn/file1/M00/10/35/Csgk0GWD5e2AP02AABASpe9IbP4355.pdf>

## ➤ 科技图书

### 1 . Wheat Sequencing: The Pan-Genome and Opportunities for Accelerating Breeding (小麦测序: 泛基因组和加速育种的机会)

简介: Wheat is a crucial crop globally, with widespread cultivation and significant economic importance. To ensure food security amidst the increasing human population and new production challenges, such as climate change, it is imperative to develop novel wheat varieties that exhibit better quality, higher yield, and enhanced resistance to biotic and abiotic stress. To achieve this, leveraging comprehensive genomic resources from global breeding programs can aid in identifying within-species allelic diversity and selecting optimal allele combinations for superior cultivars. While previous single-reference genome assemblies have facilitated gene discovery and whole-genome level genotype-phenotype relationship modeling, recent research on variations within the pan-genome of all individuals in a plant species underscores their significance for crop breeding. We summarize the different approaches and techniques used for sequencing the large and intricate wheat genome, while highlighting the challenge of generating high-quality reference assemblies. We discuss the computational methods for building the pan-genome and research efforts that are aimed at utilizing the wheat pan-genome in wheat breeding programs.

来源: The Wheat Genome

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