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## 小麦遗传育种专题

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## ➤ 前沿资讯

### 1 . Breeding effects on durum wheat traits detected using GWAS and haplotype block analysis (利用GWAS和单倍型块分析检测硬粒小麦性状的育种效应)

**简介:** Introduction: The recent boosting of genomic data in durum wheat (*Triticum turgidum* subsp. durum) offers the opportunity to better understand the effects of breeding on the genetic structures that regulate the expression of traits of agronomic interest. Furthermore, the identification of DNA markers useful for marker-assisted selection could also improve the reliability of technical protocols used for variety protection and registration. Methods: Within this motivation context, 123 durum wheat accessions, classified into three groups: landraces (LR), ancient (OC) and modern cultivars (MC), were evaluated in two locations, for 34 agronomic traits, including UPOV descriptors, to assess the impact of changes that occurred during modern breeding. Results: The association mapping analysis, performed with 4,241 SNP markers and six multi-locus-GWAS models, revealed 28 reliable Quantitative Trait Nucleotides (QTNs) related to plant morphology and kernel-related traits. Some important genes controlling flowering time and plant height were in linkage disequilibrium (LD) decay with QTNs identified in this study. A strong association for yellow berry was found on chromosome 6A (Q.Yb-6A) in a region containing the nadh-ubiquinone oxidoreductase subunit, a gene involved in starch metabolism. The Q.Kcp-2A harbored the PPO locus, with the associated marker (Ku\_c13700\_1196) in LD decay with Ppo-A1 and Ppo-A2. Interestingly, the Q.FGSGIs-2B.1, identified by RAC875\_c34512\_685 for flag leaf glaucosity, mapped less than 1 Mb from the Epistatic inhibitors of glaucousness (Iw1), thus representing a good candidate for supporting the morphological DUS traits also with molecular markers. LD haplotype block approach revealed a higher diversity, richness and length of haploblocks in MC than OC and LR (580 in LR, 585 in OC and 612 in MC), suggesting a possible effect exerted by breeding programs on genomic regions associated with the agronomic traits. Discussion: Our findings pave new ways to support the phenotypic characterization necessary for variety registration by using a panel of cost-effectiveness SNP markers associated also to the UPOV descriptors. Moreover, the panel of associated SNPs might represent a reservoir of favourable alleles to use in durum wheat breeding and genetics.

**来源:** Frontiers

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[http://agri.nais.net.cn/file1/M00/10/31/Csgk0GUJTNSA0Tv\\_ACqgyOXDplo020.pdf](http://agri.nais.net.cn/file1/M00/10/31/Csgk0GUJTNSA0Tv_ACqgyOXDplo020.pdf)

### 2 . Multi-target genome editing reduces polyphenol oxidase activity in wheat (*Triticum aestivum* L.) grains (多靶点基因组编辑降低小麦 (*Triticum aestivum* L.) 籽粒多酚氧化酶活性)

**简介:** Introduction: Polyphenol oxidases (PPO) are dual activity metalloenzymes that

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catalyse the production of quinones. In plants, PPO activity may contribute to biotic stress resistance and secondary metabolism but is undesirable for food producers because it causes the discolouration and changes in flavour profiles of products during post-harvest processing. In wheat (*Triticum aestivum* L.), PPO released from the aleurone layer of the grain during milling results in the discolouration of flour, dough, and end-use products, reducing their value. Loss-of-function mutations in the PPO1 and PPO2 paralogous genes on homoeologous group 2 chromosomes confer reduced PPO activity in the wheat grain. However, limited natural variation and the proximity of these genes complicates the selection of extremely low-PPO wheat varieties by recombination. The goal of the current study was to edit all copies of PPO1 and PPO2 to drive extreme reductions in PPO grain activity in elite wheat varieties. Results: A CRISPR/Cas9 construct with one single guide RNA (sgRNA) targeting a conserved copper binding domain was used to edit all seven PPO1 and PPO2 genes in the spring wheat cultivar 'Fielder'. Five of the seven edited T1 lines exhibited significant reductions in PPO activity, and T2 lines had PPO activity up to 86.7% lower than wild-type. The same construct was transformed into the elite winter wheat cultivars 'Guardian' and 'Steamboat', which have five PPO1 and PPO2 genes. In these varieties PPO activity was reduced by >90% in both T1 and T2 lines. In all three varieties, dough samples from edited lines exhibited reduced browning. Discussion: This study demonstrates that multi-target editing at late stages of variety development could complement selection for beneficial alleles in crop breeding programs by inducing novel variation in loci inaccessible to recombination.

来源: Frontiers

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<http://agri.nais.net.cn/file1/M00/03/5F/Csgk0Y1gEBaAeN2UAekp5HiwIKA738.pdf>

## ➤ 学术文献

### 1 . Genetic improvement in grain yield and quality of Australian durum wheat over six decades of breeding (60年来澳大利亚硬粒小麦产量和品质的遗传改良)

简介: Durum wheat breeding commenced in Australia in the 1930s by the New South Wales Department of Primary Industries (NSW DPI), Australia. Dural was developed in 1956 from a cross between North African landraces. Since then, another 20 varieties have been released in the following six decades by NSW DPI and the University of Adelaide. These were evaluated for agronomic and detailed quality traits including pasta-making quality over three seasons. This study aimed to quantify progress achieved in Australian durum breeding for yield, quality, and some agronomic traits since the release of Dural.

来源: Wiley

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<http://agri.nais.net.cn/file1/M00/03/5F/Csgk0Y1iVLiAe2ioAF0hrUk1RIY731.pdf>

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## 2 . Reducing the generation time in winter wheat cultivars using speed breeding (利用速成育种缩短冬小麦品种培育的世代时间)

简介: Reducing generation time is critical to achieving the goals of genetic gain in important crops like wheat (*Triticum aestivum*). Speed breeding (SB) has been shown to considerably reduce generation times in crop plants. Unlike spring wheat cultivars, winter wheat varieties require typically 69 weeks of cold treatment, called vernalization, for flowering which extends the generation time for the development of improved winter wheat cultivars. Here, we optimized the SB method using a set of 48 diverse soft red winter wheat (SRWW) cultivars by testing vernalization duration, light and temperature requirements, and the viability of seeds harvested after different durations post-anthesis under extended daylight conditions. We have found that using a 22-h setting (22 h day/2 h night, 25°C/22 °C) in high-density 50-cell trays results in rapid generation advancement. We used genotypic data for a panel of soft red winter wheat varieties from the regional programs to determine the impact of photoperiod and vernalization alleles on the efficiency of the SB approach. Using a set of 48 SRWW cultivars and germplasm from Maryland and four other public breeding programs, we establish that this protocol can allow for the advancement of four generations per year in controlled conditions for winter wheat varieties, experimental lines, or emerging cultivars. Our work shows the potential to reduce generation time by ~30 days per generation faster than what had been reported in the SB strategies for winter wheat, thus allowing for a quicker turnaround time from original cross to genetically stable experimental genotypes that can be tested in field settings.

来源: American Society of Agronomy

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<http://agri.nais.net.cn/file1/M00/03/5F/Csgk0Y1iUTaAEF9tABR26C1huyU586.pdf>

## 3 . Combining datasets to routinely predict fusarium head blight resistance in a wheat breeding program (结合数据集常规预测小麦育种项目中赤霉病的抗性)

简介: Fusarium head blight (FHB; *Fusarium graminearum* Schwabe) is a devastating fungal disease of wheat (*Triticum aestivum* L.) that can significantly reduce yield and grain quality. Datasets from different stages of field evaluation can be combined into a training population to predict FHB resistance. Our objective was to determine if FHB resistance among F5 lines can be predicted accurately with historical lines, parental lines, and a subset of F5 lines. Lines at the F5 and preliminary yield trial (PYT) stages in the University of Minnesota wheat breeding program were evaluated in two locations from 2016 to 2020 and were genotyped with 3679 single nucleotide polymorphism markers. Historical datasets with 368 to 3015 lines had predictive abilities of -0.01 to 0.20, whereas F5 subsets had predictive abilities of 0.040.32. Adding subsets of F5 lines to the historical datasets led to incremental improvements in predictive abilities in most cases, especially when the subset was selected via the pedigree or k-means approach. The most effective training populations were those that contained a subset of 200 F5 lines chosen via the k-means method, the F5

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parents, and the PYT lines tested in the same year, with predictive abilities that were usually higher than that of the F5 subset. We have started to use such combinations of datasets to routinely predict FHB resistance of F5 lines in our breeding program.

来源: American Society of Agronomy

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