



2023年第50期总298期

小麦遗传育种专题

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▶ 前沿资讯

1 . Genetic architecture of adult-plant resistance to stripe rust in bread wheat (*Triticum aestivum* L.) association panel (面包小麦(*Triticum aestivum* L.) 群体成株抗条锈病遗传结构)

简介: Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici*, is a severe disease in wheat worldwide, including Ethiopia, causing up to 100% wheat yield loss in the worst season. The use of resistant cultivars is considered to be the most effective and durable management technique for controlling the disease. Therefore, the present study targeted the genetic architecture of adult plant resistance to yellow rust in 178 wheat association panels. The panel was phenotyped for yellow rust adult-plant resistance at three locations. Phenological, yield, yield-related, and agro-morphological traits were recorded. The association panel was fingerprinted using the genotyping-by-sequencing (GBS) platform, and a total of 6,788 polymorphic single nucleotide polymorphisms (SNPs) were used for genome-wide association analysis to identify effective yellow rust resistance genes. The marker-trait association analysis was conducted using the Genome Association and Prediction Integrated Tool (GAPIT). The broad-sense heritability for the considered traits ranged from 74.52% to 88.64%, implying the presence of promising yellow rust resistance alleles in the association panel that could be deployed to improve wheat resistance to the disease. The overall linkage disequilibrium (LD) declined within an average physical distance of 31.44 Mbp at $r^2 = 0.2$. Marker-trait association (MTA) analysis identified 148 loci significantly ($p = 0.001$) associated with yellow rust adult-plant resistance. Most of the detected resistance quantitative trait loci (QTLs) were located on the same chromosomes as previously reported QTLs for yellow rust resistance and mapped on chromosomes 1A, 1B, 1D, 2A, 2B, 2D, 3A, 3B, 3D, 4A, 4B, 4D, 5A, 5B, 6A, 6B, 7A, and 7D. However, 12 of the discovered MTAs were not previously documented in the wheat literature, suggesting that they could represent novel loci for stripe rust resistance. Zooming into the QTL regions in IWGSC RefSeq Annotation v1 identified crucial disease resistance-associated genes that are key in plants' defense mechanisms against pathogen infections. The detected QTLs will be helpful for marker-assisted breeding of wheat to increase resistance to stripe rust. Generally, the present study identified putative QTLs for field resistance to yellow rust and some important agronomic traits. Most of the discovered QTLs have been reported previously, indicating the potential to improve wheat resistance to yellow rust by deploying the QTLs discovered by marker-assisted selection.

来源: Frontiers

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<http://agri.nais.net.cn/file1/M00/03/62/Csgk0UEbvciAKKZjALWTBPSqmTQ349.pdf>

2 . Genome-wide association analysis of time to heading and maturity in bread wheat using 55K microarrays (利用55K芯片分析面包小麦抽)

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穗时间和成熟度的全基因组关联)

简介: To investigate the genetic mechanisms underlying the reproductive traits (time to flowering and maturity) in wheat and identify candidate genes associated, a phenotypic analysis was conducted on 239 wheat accessions (lines) from around the world. A genome-wide association study (GWAS) of wheat heading and maturity phases was performed using the MLM (Q+K) model in the TASSLE software, combined with the Wheat 55K SNP array. The results revealed significant phenotypic variation in heading and maturity among the wheat accessions across different years, with coefficients of variation ranging from 0.96% to 1.97%. The phenotypic data from different years exhibited excellent correlation, with a genome-wide linkage disequilibrium (LD) attenuation distance of 3 Mb. Population structure analysis, evolutionary tree analysis, and principal component analysis indicated that the 239 wheat accessions formed a relatively homogeneous natural population, which could be divided into three subgroups. The GWAS results identified a total of 293 SNP marker loci that were significantly associated with wheat heading and maturity stages ($P \leq 0.001$) in different environments. Among them, nine stable SNP marker loci were consistently detected in multiple environments. These marker loci were distributed on wheat chromosomes 1A、1B、2D、3A、5B、6D and 7A. Each individual locus explained 4.03%-16.06% of the phenotypic variation. Furthermore, through careful analysis of the associated loci with large phenotypic effect values and stable inheritance, a total of nine candidate genes related to wheat heading and maturity stages were identified. These findings have implications for molecular marker-assisted selection breeding programs targeting specific wheat traits at the heading and maturity stages. In summary, this study conducted a comprehensive GWAS of wheat heading and maturity phases, revealing significant associations between genetic markers and key developmental stages in wheat. The identification of candidate genes and marker loci provides valuable information for further studies on wheat breeding and genetic improvement targeted at enhancing heading and maturity traits.

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<https://www.frontiersin.org/articles/10.3389/fpls.2023.1296197/full>

3 . Mining *Aegilops tauschii* genetic diversity in the background of bread wheat revealed a novel QTL for seed dormancy (在面包小麦的遗传多样性背景下发现一个新的种子休眠QTL)

简介: Due to the low genetic diversity in the current wheat germplasm, gene mining from wild relatives is essential to develop new wheat cultivars that are more resilient to the changing climate. *Aegilops tauschii*, the D-genome donor of bread wheat, is a great gene source for wheat breeding; however, identifying suitable genes from *Ae. tauschii* is challenging due to the different morphology and the wide intra-specific variation within the species. In this study, we developed a platform for the systematic evaluation of *Ae. tauschii* traits in the background of the hexaploid wheat cultivar 'Norin 61' and thus for the

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identification of QTLs and genes. To validate our platform, we analyzed the seed dormancy trait that confers resistance to preharvest sprouting. We used a multiple synthetic derivative (MSD) population containing a genetic diversity of 43 *Ae. tauschii* accessions representing the full range of the species. Our results showed that only nine accessions in the population provided seed dormancy, and KU-2039 from Afghanistan had the highest level of seed dormancy. Therefore, 166 backcross inbred lines (BILs) were developed by crossing the synthetic wheat derived from KU-2039 with 'Norin 61' as the recurrent parent. The QTL mapping revealed one novel QTL, Qsd.alrc.5D, associated with dormancy explaining 41.7% of the phenotypic variation and other five unstable QTLs, two of which have already been reported. The Qsd.alrc.5D, identified for the first time within the natural variation of wheat, would be a valuable contribution to breeding after appropriate validation. The proposed platform that used the MSD population derived from the diverse *Ae. tauschii* gene pool and recombinant inbred lines proved to be a valuable platform for mining new and important QTLs or alleles, such as the novel seed dormancy QTL identified here. Likewise, such a platform harboring genetic diversity from wheat wild relatives could be a useful source for mining agronomically important traits, especially in the era of climate change and the narrow genetic diversity within the current wheat germplasm.

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➤ 学术文献

1 . Development and characterization of a novel common wheat–Mexico Rye T1DL·1RS translocation line with stripe rust and powdery mildew resistance (小麦–墨西哥黑麦抗条锈病和白粉病易位系T1DL·1RS的选育与鉴定)

简介: Rye (*Secale cereale* L., $2n=2x=14$, RR) is a significant genetic resource for improving common wheat because of its resistance to multiple diseases and abiotic-stress tolerant traits. The 1RS chromosome from the German cultivated rye variety Petkus is critical in wheat breeding. However, its weakened disease resistance highlights the need to identify new resources. In the present study, a novel derived line called D27 was developed from common wheat and Mexico Rye. Cytological observations characterized the karyotype of D27 as $2n=42=21$ II. Genomic in situ hybridization indicated that a pair of whole-arm translocated Mexico Rye chromosomes were inherited typically in the mitotic and meiosis stages of D27. Experiments using fluorescence in situ hybridization (FISH) and gliadin electrophoresis showed that D27 lacked wheat 1DS chromosomes. They were replaced by 1RS chromosomes of Mexico Rye, supported by wheat simple-sequence repeat markers, rye sequence characterized amplified region markers, and wheat 40K SNP array analysis. The wheat 1DS chromosomes could not be detected by molecular markers and wheat SNP array, but the presence of rye 1RS chromosomes was confirmed. Agronomic trait assessments

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indicated that D27 had a higher tiller number and enhanced stripe rust and powdery mildew resistance. In addition, dough properties analysis showed that replacing 1DS led to higher viscosity and lower dough elasticity in D27, which was beneficial for cake making. In conclusion, the novel cytogenetically stable common wheat Mexico Rye T1DL·1RS translocation line D27 offers excellent potential as outstanding germplasm in wheat breeding programs focusing on disease resistance and yield improvement. Additionally, it can be valuable for researching the rye 1RS chromosome's genetic diversity.

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<http://agri.nais.net.cn/file1/M00/10/34/Csgk0EEbu92AWrqeAGSxXhEA9TM270.pdf>

2 . Toward reducing the immunogenic potential of wheat flour: identification and characterization of wheat lines missing omega-5 gliadins encoded by the 1D chromosome (降低小麦粉的免疫原性潜能: 缺失由1D染色体编码的 ω -5麦胶蛋白的小麦品系的鉴定和表征)

简介: Eleven wheat lines that are missing genes for the 1D-encoded omega-5 gliadins will facilitate breeding efforts to reduce the immunogenic potential of wheat flour for patients susceptible to wheat allergy. Efforts to reduce the levels of allergens in wheat flour that cause wheat-dependent exercise-induced anaphylaxis are complicated by the presence of genes encoding omega-5 gliadins on both chromosomes 1B and 1D of hexaploid wheat. In this study, we screened 665 wheat germplasm samples using gene specific DNA markers for omega-5 gliadins encoded by the genes on 1D chromosome that were obtained from the reference wheat Chinese Spring. Eleven wheat lines missing the PCR product corresponding to 1D omega-5 gliadin gene sequences were identified. Two of the lines contained the 1BL·1RS translocation. Relative quantification of gene copy numbers by qPCR revealed that copy numbers of 1D omega-5 gliadins in the other nine lines were comparable to those in 1D null lines of Chinese Spring, while copy numbers of 1B omega-5 gliadins were like those of Chinese Spring. 2-D immunoblot analysis of total flour proteins from the selected lines using a specific monoclonal antibody against the N-terminal sequence of omega-5 gliadin showed no reactivity in regions of the blots containing previously identified 1D omega-5 gliadins. Interestingly, RP-UPLC analysis of the gliadin fractions of the selected lines indicated that the expression of omega-1,2 gliadins was also significantly reduced in seven of the lines, implying that 1D omega-5 gliadin and 1D omega-1,2 gliadin genes are tightly linked on the Gli-D1 loci of chromosome 1D. Wheat lines missing the omega-5 gliadins encoded by the genes on 1D chromosome should be useful in future breeding efforts to reduce the immunogenic potential of wheat flour.

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http://agri.nais.net.cn/file1/M00/03/62/Csgk0UEbxt6AU_9gAC99IT7w7PE587.pdf