



2024年第3期总303期

小麦遗传育种专题

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2024年01月15日

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▶ 前沿资讯

1 . Genetic analyses and prediction for lodging- related traits in a diverse Iranian hexaploid wheat collection (伊朗六倍体小麦的宿存相关性状的遗传分析和预测)

简介: Lodging is one of the most important limiting environmental factors for achieving the maximum yield and quality of grains in cereals, including wheat. However, little is known about the genetic foundation underlying lodging resistance (LR) in wheat. In this study, 208 landraces and 90 cultivars were phenotyped in two cropping seasons (20182019 and 20192020) for 19 LR-related traits. A genome-wide association study (GWAS) and genomics prediction were carried out to dissect the genomic regions of LR. The number of significant marker pairs (MPs) was highest for genome B in both landraces (427,017) and cultivars (37,359). The strongest linkage disequilibrium (LD) between marker pairs was found on chromosome 4A (0.318). For stem lodging-related traits, 465, 497, and 478 marker-trait associations (MTAs) and 45 candidate genes were identified in year 1, year 2, and pooled. Gene ontology exhibited genomic region on Chr. 2B, 6B, and 7B control lodging. Most of these genes have key roles in defense response, calcium ion transmembrane transport, carbohydrate metabolic process, nitrogen compound metabolic process, and some genes harbor unknown functions that, all together may respond to lodging as a complex network. The module associated with starch and sucrose biosynthesis was highlighted. Regarding genomic prediction, the GBLUP model performed better than BRR and RRBLUP. This suggests that GBLUP would be a good tool for wheat genome selection. As a result of these findings, it has been possible to identify pivotal QTLs and genes that could be used to improve stem lodging resistance in *Triticum aestivum* L.

来源: Nature

发布日期:2024-01-02

全文链接:

<http://agri.nais.net.cn/file1/M00/10/36/Csgk0GWeWM-ABb9fAFnsjMcHkZs911.pdf>

▶ 学术文献

1 . Genome-wide identification of microsatellites for mapping, genetic diversity and cross-transferability in wheat (*Triticum spp*) (用于小麦 (*Triticum spp*) 测绘、遗传多样性和交叉转移的微卫星全基因组鉴定)

简介: Wheat (*Triticum aestivum* L.) is a crucial global staple crop, and is consistently being improved to enhance yield, disease resistance, and quality traits. However, the development of molecular markers is a challenging task due to its hexaploid genome. Molecular marker system such as simple sequence repeat (SSR) and single nucleotide polymorphism (SNP) are helpful for breeding, but SNP has limitations due to its development cost and its conversion to breeder markers. The study proposed an in-silico

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approach, by utilizing the low-cost transcriptome sequencing of two parental lines, 'TAC 75' and 'WH 1105', to identify polymorphic SSRs for mapping in a recombinant inbred line (RIL) population. This study introduces a new approach to bridge wheat genetics intricacies and next-generation sequencing potential. It presents a comprehensive genome-wide SSR distribution using IWGSC CS RefSeq v2.1 genome assembly and to identify 189 polymorphic loci through in-silico strategy. Of these, 54.76% showed polymorphism between parents, surpassing the traditional low polymorphic success rate. A RIL population screening validated these markers, demonstrating the fitness of identified markers through chi-square tests. The designed SSRs were also validated for genetic diversity analysis in a subset of 37 Indian wheat genotypes and cross-transferability in the wild/relative wheat species. In diversity analysis, a subset of 38 markers revealed 95 alleles (2.5 allele/locus), indicating substantial genetic variation. Population structure analysis unveiled three distinct groups, supported by phylogenetic and PCoA analyses. Further the polymorphic SSRs were also analyzed for SSR-gene association using gene ontology analysis. By utilizing the developing seed transcriptome data within parental lines, the study has enhanced the polymorphic SSR identification precision and facilitated in the RIL population. The undertaken study pioneers the use of transcriptome sequencing and genetic mapping to overcome challenges posed by the intricate wheat genome. This approach offers a cost-effective, less labour-intensive alternative to conventional methods, providing a platform for advancing wheat breeding research.

来源: Science Direct

发布日期: 2023-11-28

全文链接:

<http://agri.nais.net.cn/file1/M00/03/63/Csgk0WWeWyiASGrPAGvA6jCK69E817.pdf>

2 . Development of novel wheat-rye 6RS small fragment translocation lines with powdery mildew resistance and physical mapping of the resistance gene PmW6RS (新型小麦-黑麦6RS小片段易位系的开发和PmW6RS抗性基因的物理映射)

简介: Rye (*Secale cereale* L., RR) contains valuable genes for wheat improvement. However, most of the rye resistance genes have not been successfully used in wheat cultivars. Identification of new rye resistance genes and transfer of these genes to wheat by developing small fragment translocation lines will make these genes more usable for wheat breeding. In this study, a broad-spectrum powdery mildew resistance gene PmW6RS was localized on rye chromosome arm 6RS using a new set of wheat-rye disomic and telosomic addition lines. To further study and use PmW6RS, 164 wheat-rye 6RS translocation lines were developed by ⁶⁰Co-γ-ray irradiation. Seedling and adult stage powdery mildew resistance analysis showed that 106 of the translocation lines were resistant. A physical map of 6RS was constructed using the 6RS translocation and deletion lines, and PmW6RS was localized in the 6RS-0.580.66-bin, flanked by markers X6RS-3 and X6RS-10 corresponding to the physical interval of 50.2368.61 Mb in Weining rye genome. A total of 23 resistance-related genes were annotated. Nine markers co-segregate with the

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6RS-0.580.66-bin, which can be used to rapidly trace the 6RS fragment carrying PmW6RS. Small fragment translocation lines with powdery mildew resistance were backcrossed with wheat cultivars, and 39 agronomically acceptable homozygous 6RS small fragment translocation lines were obtained. In conclusion, this study not only provides novel gene source and germplasm for wheat resistance breeding, but also laid a solid foundation for cloning of PmW6RS.

来源: SpringerLink

发布日期: 2023-08-07

全文链接:

<http://agri.nais.net.cn/file1/M00/10/36/Csgk0GWeXG6AG9jBACgzIFwODtI304.pdf>

3 . Screening and evaluation of drought resistance traits of winter wheat in the North China Plain (华北平原冬小麦抗旱特性的筛选与评价)

简介: From 2019 to 2021, 16 representative winter wheat cultivars were cultivated in the field, and 24 traits, including morphological, photosynthetic, physiological, canopy, and yield component traits, were measured to evaluate the drought tolerance of the cultivars. Principal component analysis (PCA) was used to transform 24 conventional traits into 7 independent, comprehensive indices, and 10 drought tolerance indicators were screened out by regression analysis. The 10 drought tolerance indicators were plant height (PH), spike number (SN), spikelet per spike (SP), canopy temperature (CT), leaf water content (LWC), photosynthetic rate (A), intercellular CO₂ concentration (C_i), peroxidase activity (POD), malondialdehyde content (MDA), and abscisic acid (ABA). In addition, through membership function and cluster analysis, 16 wheat varieties were divided into 3 categories: drought-resistant, drought weak sensitive, and drought-sensitive.

来源: Frontiers

发布日期: 2023-06-16

全文链接:

<http://agri.nais.net.cn/file1/M00/10/36/Csgk0GWeXmaATszyAJB622hENKE299.pdf>

4 . Genetic gains in grain yield in wheat (*Triticum aestivum* L.) cultivars developed from 1965 to 2020 for irrigated production conditions of northwestern plains zone of India (1965-2020年印度西北平原地区灌溉生产条件下小麦(*Triticum aestivum* L.)产量的遗传收益)

简介: Field trials with 13 landmark wheat cultivars released between 1965 and 2020 were conducted at 15 different locations during 2019-2020 and 2020-2021, providing data from 30 environments. The study of the historical set of spring wheat varieties from the North-Western Plains Zone (NWPZ) of India developed in the last 55 years demonstrated an improvement of grain yield from 3208 to 6275 kg ha⁻¹ or a genetic gain of 1.21% year⁻¹ over long-term check cultivar C306. In real terms, the yield has increased at a rate of 44.14 kg ha⁻¹ year⁻¹. To compare the present genetic gain study, a trend analysis based on historical

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grain yield data in standard AVT in the zone from 1980 to 2020 was also attempted, which revealed that the percent yield increase was 0.78 per annum. To achieve a higher rate of genetic gain, it requires greater breeding efficiency in the national breeding program through more systematic use of genetic diversity to introduce novel alleles as well as application of new breeding approaches like speed breeding and genomic selection.

来源: SpringerLink

发布日期:2022-08-16

全文链接:

<http://agri.nais.net.cn/file1/M00/03/63/Csgk0WwEXWmAPRQVABiP4ckyrmA867.pdf>