小麦遗传育种专题

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前沿资讯

1．Genome-wide linkage mapping of root system architecture-related traits in common wheat (Triticum aestivum L.)（普通小麦根系构型相关性状的全基因组连锁定位）

简介：Identifying loci for root system architecture (RSA) traits and developing available markers are crucial for wheat breeding. In this study, RSA-related traits, including total root length (TRL), total root area (TRA), and number of root tips (NRT), were evaluated in the Doumai/Shi4185 recombinant inbred line (RIL) population under hydroponics. In addition, both the RILs and parents were genotyped using the wheat 90K single-nucleotide polymorphism (SNP) array. In total, two quantitative trait loci (QTLs) each for TRL (QTRL.caas-4A.1 and QTRL.caas-4A.2), TRA (QTRA.caas-4A and QTRA.caas-4D), and NRT (QNRT.caas-5B and QNRT.caas-5D) were identified and each explaining 5.94%9.47%, 6.85%7.10%, and 5.91%10.16% phenotypic variances, respectively. Among these, QTRL.caas-4A.1 and QTRA.caas-4A overlapped with previous reports, while QTRL.caas-4A.2, QTRA.caas-4D, QNRT.caas-5B, and QNRT.caas-5D were novel. The favorable alleles of QTRL.caas-4A.1, QTRA.caas-4A, and QTRA.caas-5B were contributed by Doumai, whereas the favorable alleles of QTRL.caas-4A.2, QTRA.caas-4D, and QTRA.caas-5D originated from Shi 4185. Additionally, two competitive allele-specific PCR (KASP) markers, Kasp_4A_RL (QTRA.caas-4A) and Kasp_5D_RT (QNRT.caas-5D), were developed and validated in 165 wheat accessions. This study provides new loci and available KASP markers, accelerating wheat breeding for higher yields.

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学术文献

1．Optimizing genomic selection of agricultural traits using K-wheat core collection（利用小麦核心种质优化农业性状基因组选择）

简介：The agricultural traits that constitute basic plant breeding information are usually quantitative or complex in nature. This quantitative and complex combination of traits complicates the process of selection in breeding. This study examined the potential of genome-wide association studies (GWAS) and genomewide selection (GS) for breeding ten agricultural traits by using genome-wide SNPs. As a first step, a trait-associated candidate marker was identified by GWAS using a genetically diverse 567 Korean (K)-wheat core collection. The accessions were genotyped using an Axiom® 35K wheat DNA chip, and ten agricultural traits were determined (awn color, awn length, culm color, culm length, ear color, ear length, days to heading, days to maturity, leaf length, and leaf width). It is essential to sustain global wheat production by utilizing accessions in wheat breeding.

Among the traits associated with awn color and ear color that showed a high positive correlation, a SNP located on chr1B was significantly associated with both traits. Next, GS evaluated the prediction accuracy using six predictive models (G-BLUP, LASSO, BayseA, reproducing kernel Hilbert space, support vector machine (SVM), and random forest) and various training populations (TPs). With the exception of the SVM, all statistical models demonstrated a prediction accuracy of 0.4 or better. For the optimization of the TP, the number of TPs was randomly selected (10%, 30%, 50% and 70%) or divided into three subgroups (CC-sub 1, CC-sub 2 and CC-sub 3) based on the subpopulation structure. Based on subgroup-based TPs, better prediction accuracy was found for awn color, culm color, culm length, ear color, ear length, and leaf width. A variety of Korean wheat cultivars were used for validation to evaluate the prediction ability of populations. Seven out of ten cultivars showed phenotype-consistent results based on genomics-evaluated breeding values (GEBVs) calculated by the reproducing kernel Hilbert space (RKHS) predictive model. Our research provides a basis for improving complex traits in wheat breeding programs through genomics assisted breeding. The results of our research can be used as a basis for improving wheat breeding programs by using genomics-assisted breeding.

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2 . Development of diagnostic SNP markers for identification of rye 1RS translocations in wheat（黑麦1RS易位诊断SNP标记的建立）

简介：Wheat (Triticum aestivum L.) wild relatives are rich genetic resources for genetic improvement of wheat. The short arm of rye (Secale cereale L.) chromosome 1 (1RS) contains many beneficial genes for resistance to drought, insects, and diseases, therefore the 1RS wheat translocations have been widely used in wheat breeding programs worldwide. To facilitate marker-assisted identification of 1RS in wheat breeding, we designed a set of Kompetitive allele-specific polymerase chain reaction (KASP) markers to detect the translocations of 1RS with long arm from wheat chromosome 1A (1RS.1AL) and 1RS with long arm from wheat chromosome 1B (1RS.1BL) based on the sequence flanking single nucleotide polymorphisms (SNPs) generated by genotyping-by-sequencing (GBS) between wheat and rye panels. We identified a set of three SNP markers for diagnosis and differentiation of the two 1RS translocations in wheat. Among the three KASP markers, 1AS-05056 is 1RS specific, and clearly separated the genotypes with 1RS (1RS.1AL and 1RS.1BL) from those without the two 1RS translocations; whereas 1AS-29875 clearly identified the 1RS.1AL translocation and 1BS-16654 separated 1RS.1BL from 1RS.1AL. The three new KASP markers together accurately identified the presence of 1RS translocation on either 1A or 1B chromosome in a panel of 95 representative U.S. winter wheat accessions, which were further validated in two additional U.S. hard winter wheat panels. Therefore, they can be used for routine screening of 1RS.1BL and 1RS.1AL translocation lines in wheat breeding programs.

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➤ 科技图书

1．Physiological, Biochemical, and Molecular Responses to Salt Stress and Seed Priming Approach to Enhance Salt Tolerance in Bread Wheat（盐胁迫对面包小麦生理生化和分子反应的影响及种子诱导提高耐盐性的研究）

简介：Soil and water salinization induced by climate change and anthropogenic activities is a major threat to the wheat production, globally. Wheat is a major source of calories for two-thirds of the global population. Salt stress adversely affects seed germination, plant growth and development, and physiological processes through reduction in chlorophyll content, hormonal imbalance, alteration in metabolic activities, and modification in household gene expression, which ultimately decreases the yield of wheat. Therefore, detailed understanding of the effects of salt stress in wheat crop is essential to devise the remedial measures for reducing its adverse effect of the crop. In the past, various approaches including management of saline soils, selection of salt-tolerant germplasm, and development of salt-tolerant cultivars through conventional and molecular breeding approaches have been applied to a limited extent. However, various crop management practices, such as seed priming, nutrient management, and exogenous applications of organic (phytohormones, osmolytes) and inorganic chemicals, were found to be more effective in managing the adverse effects of salinity in wheat crop as the biological approaches are very costly, time consuming, and labor intensive. Therefore, in this chapter, we reviewed from available literature the salt stress induced effects on physiological, biochemical, and molecular responses of wheat and the advantage of seed priming with chemical in plant growth and grain yield improvement of wheat under salt stress.

来源：Salinity and Drought Tolerance in Plants
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2．Importance of Integrating Physiological Breeding to Augment Crop Breeding（整合生理育种对加强作物育种的重要性）

简介：Global food consumption is expected to surpass the crops genetic gain by 2050, and climate change threatens the breeding programmes by hampering yield advantages. The current yield gain achieved is mostly through conventional breeding, and there is an urgent need for exploring new breeding approaches for augmenting the food demand. Recently, the physiological breeding and specifically trait-based breeding approaches are more

explored in different crop breeding programmes and shown significant cumulative effect on yield advantage under both control and stress conditions. This helped in having complete information of genetic resource and the capability to improve favourable alleles by phenomic screening of offspring. This chapter mainly discusses the importance and role of physiological breeding, success stories of physiological breeding and the methods and need for integrating physiological breeding with all conventional crop improvement programmes to achieve significant yield advantages.

来源：Translating Physiological Tools to Augment Crop Breeding

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