



2023年第45期总293期

小麦遗传育种专题

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▶ 前沿资讯

1 . Investigating the response mechanisms of bread wheat mutants to salt stress (面包小麦突变体对盐胁迫的响应机制研究)

简介: Mutation breeding is among the most critical approaches to promoting genetic diversity when genetic diversity is narrowed for a long time using traditional breeding methods. In the current study, 15 wheat mutants created by gamma radiation and three salt-tolerant wheat cultivars were studied under no salinity stress (Karaj) and salinity stress (Yazd) during three consecutive growing seasons from 2017 to 2020 (M05 to M07 generations mutants). Results showed that salinity induced lipid peroxidation and enhanced ion leakage in all genotypes however, M6 and M15 showed the least ion leakage increment. It was also observed that the activity of antioxidant enzymes including SOD, CAT, POX, APX and GR increased with salinity; the maximum increase in antioxidant activity was belonged to M15, M09, M06 and M05. All genotypes had higher protein content in salinity stress conditions; M07 and M12 showed the lowest (1.8%) and the highest (17.3%) protein increase, respectively. Zeleny sedimentation volume increased under salinity stress conditions in all genotypes except M06, C2, C3, and M07. The result indicated that salinity stress increased wet gluten in all genotypes. M10 and M08 showed the highest (47.8%) and the lowest (4%) wet gluten increment, respectively. M06 and M11 mutants showed the lowest (6.1%) and the highest (60.7%) decrement of grain yield due to salinity stress, respectively. Finally, M04, M05, M07, M13, and M14 were known as genotypes with high grain yield in both no salinity and salinity stress conditions. In other word, these genotypes have higher yield stability. The results of the current study revealed that gamma irradiation could effectively be used to induce salinity tolerance in wheat.

来源: Nature

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<http://agri.nais.net.cn/file1/M00/03/60/Csgk0YmXVvSAAGUfABYm3sfnAGg871.pdf>

▶ 学术文献

1 . Grain yield and adaptation of spring wheat to Norwegian growing conditions is driven by allele frequency changes at key adaptive loci discovered by genome-wide association mapping (全基因组关联图谱发现的关键适应位点的等位基因频率驱动的春小麦产量变化)

简介: Adaptation to the Norwegian environment is associated with polymorphisms in the *Vrn-A1* locus. Historical selection for grain yield in Nordic wheat is associated with *TaGS5-3A* and *TaCol-5* loci. Grain yields in Norwegian spring wheat increased by 18 kg ha⁻¹ per year between 1972 and 2019 due to introduction of new varieties. These gains were associated with increments in the number of grains per spike and extended length of the vegetative period. However, little is known about the genetic background of this progress. To fill this

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gap, we conducted genome-wide association study on a panel consisting of both adapted (historical and current varieties and lines in the Nordics) and important not adapted accessions used as parents in the Norwegian wheat breeding program. The study concerned grain yield, plant height, and heading and maturity dates, and detected 12 associated loci, later validated using independent sets of recent breeding lines. Adaptation to the Norwegian cropping conditions was found to be associated with the Vrn-A1 locus, and a previously undescribed locus on chromosome 1B associated with heading date. Two loci associated with grain yield, corresponding to the TaGS5-3A and TaCol-5 loci, indicated historical selection pressure for high grain yield. A locus on chromosome 2A explained the tallness of the oldest accessions. We investigated the origins of the beneficial alleles associated with the wheat breeding progress in the Norwegian material, tracing them back to crosses with Swedish, German, or CIMMYT lines. This study contributes to the understanding of wheat adaptation to the Norwegian growing conditions, sheds light on the genetic basis of historical wheat improvement and aids future breeding efforts by discovering loci associated with important agronomic traits in wheat.

来源: Springer

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<http://agri.nais.net.cn/file1/M00/10/32/Csgk0GVApQ-AWePaAEMiRwZpvYY308.pdf>

2 . Wheat NAC-A18 regulates grain starch and storage proteins synthesis and affects grain weight (NAC-A18调节籽粒淀粉和贮藏蛋白合成, 影响籽粒重)

简介: Wheat NAC-A18 regulates both starch and storage protein synthesis in the grain, and a haplotype with positive effects on grain weight showed increased frequency during wheat breeding in China. Starch and seed storage protein (SSP) directly affect the processing quality of wheat grain. The synthesis of starch and SSP are also regulated at the transcriptional level. However, only a few starch and SSP regulators have been identified in wheat. In this study, we discovered a NAC transcription factor, designated as NAC-A18, which acts as a regulator of both starch and SSP synthesis. NAC-A18, is predominately expressed in wheat developing grains, encodes a transcription factor localized in the nucleus, with both activation and repression domains. Ectopic expression of wheat NAC-A18 in rice significantly decreased starch accumulation and increased SSP accumulation and grain size and weight. Dual-luciferase reporter assays indicated that NAC-A18 could reduce the expression of TaGBSSI-A1 and TaGBSSI-A2, and enhance the expression of TaLMW-D6 and TaLMW-D1. A yeast one hybrid assay demonstrated that NAC-A18 bound directly to the cis-element "ACGCAA" in the promoters of TaLMW-D6 and TaLMW-D1. Further analysis indicated that two haplotypes were formed at NAC-A18, and that NAC-A18_h1 was a favorable haplotype correlated with higher thousand grain weight. Based on limited population data, NAC-A18_h1 underwent positive selection during Chinese wheat breeding. Our study demonstrates that wheat NAC-A18 regulates starch and SSP accumulation and grain size. A molecular marker was developed for the favorable allele for breeding

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applications.

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全文链接:

<https://link.springer.com/article/10.1007/s00122-023-04365-3>

➤ 科技图书

1 . Contribution and Impact of Mutant Varieties on Food Security (突变品种对粮食安全的贡献和影响)

简介: After the discovery of the mutagenic action of X-rays by Muller and Stadler, experimental mutagenesis in the past 90 years has created a vast amount of genetic variation of both quantitative and qualitative traits. The use of induced mutations over the past five decades has been a key factor in the development of superior plant varieties all around the world. The widespread use of the mutation breeding technique in 228 crop species has resulted in the development and release of more than 3332 mutant cultivars around the globe. The maximum number of mutant varieties are released in cereals, flowers/ornamentals, and grain legumes. Most of them are released in Asia, followed by Europe, North America, Africa, Latin America, Australia, and the Pacific. The varieties released in these crops include direct mutants or mutant derivatives through inter-mutant or cultivar-mutant hybridizations. Some of these mutants' varieties have made a great economic impact in Australia (rice), Bangladesh (rice), China (rice, soybean, and wheat), Europe (Barley), Germany (ornamentals), India (rice, grain legumes, and ornamentals), Italy (durum wheat), Japan (rice, soybean, pear, and ornamentals), Mali (Sorghum), Malaysia (rice and banana), the Netherlands (ornamentals), Pakistan (rice, wheat, and cotton), Thailand (rice), Vietnam (rice and soybean), and the USA (rice, sunflower, and peppermint). Many mutants have made a transnational impact on the yield and quality of several seeds propagated crops since most of the mutant varieties are in cereals, pulses, and oilseeds crops and therefore had a direct impact on global food security and added billions of dollars to the national economy around the world. This chapter reviews the success story of mutation breeding in enhancing food production and the impact of mutation-derived varieties on food security around the globe.

来源: Advanced Crop Improvement

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2 . Colored cereals: Genetics and chemistry of pigments (有色谷物: 色素的遗传学和化学)

简介: This chapter discusses the main pigments derived from colored cereals, their genetic, and variation levels. Many phytochemicals are found in cereals, some of which have a

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substantial impact on their color. The most popular cereals in Europe are wheat, and by far the most popular, maize and barley each account for a third. Barley, oat, rice, rye, triticale, and maize have a comparable spectrum of grain colors to wheat. Blue, purple, or a combination of these colors results from anthocyanins accumulating in the aleurone or pericarp layer. Comparing the spectrum of anthocyanins contained in wheat with other cereals, such as maize and rice, an intermediate diversity of anthocyanins is found in blue-grain wheat and purple wheat. Flavonoids such as yellow C-glycosides of flavones, flavonols, flavanonols, proanthocyanidins, and reddish-colored phlobaphenes are mostly found in the outer layer of grains, whereas carotenoids are found in the endosperm and are responsible for the yellow color. As a result, accumulation of these pigments in grain could be a key target in breeding programs targeted at enhancing bioactive component concentrations in grain and products. Cereal breeders are currently attempting to develop new types of color-grained with improved properties such as quality, yield, and higher pigment contents, which could have a positive impact on nutrition and health. In the fact, in today's modern cultivation, not much of the original varieties of cereal colors and forms are left.

来源: Functionality and Application of Colored Cereals

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