

2023年第32期总280期

## 小麦遗传育种专题

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#### > 前沿资讯

# **1**. Sequencing trait-associated mutations to clone wheat rust-resistance gene YrNAM(小麦抗锈病基因YrNAM克隆的性状相关 突变序列分析)

简介: Stripe (yellow) rust, caused by Puccinia striiformis f. sp. tritici (Pst), can significantly affect wheat production. Cloning resistance genes is critical for efficient and effective breeding of stripe rust resistant wheat cultivars. One resistance gene (Yr10CG) underlying the Pst resistance locus Yr10 has been cloned. However, following haplotype and linkage analyses indicate the presence of additional Pst resistance gene(s) underlying/near Yr10 locus. Here, we report the cloning of the Pst resistance gene YrNAM in this region using the method of sequencing trait-associated mutations (STAM). YrNAM encodes a non-canonical resistance protein with a NAM domain and a ZnF-BED domain. We show that both domains are required for resistance. Transgenic wheat harboring YrNAM gene driven by its endogenous promoter confers resistance to stripe rust races CYR32 and CYR33. YrNAM is an ancient gene and present in wild wheat species Aegilops longissima and Ae. sharonensis; however, it is absent in most wheat cultivars, which indicates its breeding value.

来源: Nature 发布日期:2023-07-19 全文链接: <u>http://agri.ckcest.cn/file1/M00/10/2F/Csgk0GTGGDyAMX3mACX5zKcBLvI730.pdf</u>

## > 学术文献

# **1**. The use of PI 277012-derived Fusarium head blight resistance QTL in winter wheat breeding (PI 277012衍生抗枯萎病QTL在冬小麦育种中的应用)

简介: Fusarium head blight (FHB) caused by Fusarium graminearum results in substantial grain yield and quality losses in common wheat (Triticum aestivum L.). Genetic resistance is partial but crucial for effective, integrated management of the disease. Host resistance is conditioned by numerous small effect quantitative trait loci (QTL) that are strongly affected by the environment and genetic background. Qfhb.rwg-5A.1 and Qfhb.rwg-5A.2 (PI 277012 is the source for both genes) are two recently discovered FHB resistance QTL that also occur in spring wheat GP80 (PI 277012 derivative). To transfer the PI 277012 resistance from GP80 to hard winter wheat (HWW), GP80 was first crossed with Novus-4. The F1 hybrid was crossed with SY Monument, following which marker-selected progeny were crossed with, and backcrossed to, ND Noreen. To potential carriers of FHB resistance QTL among the 22 F1 of the ND Noreen cross, simple sequence repeat (SSR) markers, Illumina 90 K single nucleotide polymorphism (SNP) haplotypes and greenhouse FHB Type II resistance tests were done. Likely homozygotes for Qfhb.rwg.5A.1 and Qfhb.rwg.5A.2, were selected and backcrossed to ND Noreen. In the B1F1, 131 plants were evaluated for SNP haplotypes, SSR

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markers and FHB resistance. Nine B1F2:3 lines were derived, and their resistance confirmed in a third greenhouse FHB trial. The results suggested that eight lines had higher resistance and were comparable to GP80 with the Qfhb.rwg-5A.2 markers occurring in all eight and the Qfhb.rwg-5A.1 markers occurring in four lines. The eight selections constitute a valuable HWW resistance breeding resource.

来源: Elsevier 发布日期:2023-04-01 全文链接: http://agri.ckcest.cn/file1/M00/03/5D/Csgk0YkcyymAdBVvABoQdkQZ7oY546.pdf

# 2. Preliminary Dissection of Grain Yield and Related Traits at Differential Nitrogen Levels in Diverse Pre-Breeding Wheat Germplasm Through Association Mapping(利用关联图谱初步剖析不同氮素水平下小麦种质产量及相关性状)

简介: Development of nutrient efficient cultivars depends on effective identification and utilization of genetic variation. We characterized a set of 276 pre-breeding lines (PBLs) for several traits at different levels of nitrogen application. These PBLs originate from synthetic wheats and landraces. We witnessed significant variation in various traits among PBLs to different nitrogen doses. There was ~ 4-18% variation range in different agronomic traits in response to nitrogen application, with the highest variation for the biological yield (BY) and the harvest index. Among various agronomic traits measured, plant height, tiller number, and BY showed a positive correlation with nitrogen applications. GWAS analysis detected 182 marker-trait associations (MTAs) (at p-value<0.001), out of which 8 MTAs on chromosomes 5D, 4A, 6A, 1B, and 5B explained more than 10% phenotypic variance. Out of all, 40 MTAs observed for differential nitrogen application response were contributed by the synthetic derivatives. Moreover, 20 PBLs exhibited significantly higher grain yield than checks and can be selected as potential donors for improved plant nitrogen use efficiency (pNUE).

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# ▶ 科技图书

# **1**. Wheat quality testing in a breeding program (育种项目中的小麦品 质检测)

简介: The major objective of wheat breeding programs is the development of new cultivars with increased grain yield potential, disease resistance, tolerance to abiotic stresses, and quality. However, most of the tests typically used to determine wheat quality are difficult, expensive, and require a relatively large amount of grain which limits quality analysis to the

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later stages of the breeding process. Such constraints often result in promising wheat cultivars that do not satisfy the requirements of the millers, food processors, and consumers and therefore may not be released. To avoid this problem, the proper integration of quality testing in the breeding process is fundamental. In this chapter, we will focus on explaining the operation of a conventional wheat breeding program and the analyses that can be done to address the quality requirements demanded each process and product.

来源: ICC Handbook of 21st Century Cereal Science and Technology

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http://agri.ckcest.cn/file1/M00/03/5D/Csgk0Ykcxx2AVH3JAAsZzuY8M-A688.pdf

#### 2. Strategies to Develop Heat and Drought-Tolerant Wheat Varieties Following Physiological Breeding(小麦生理育种下耐热耐旱品种的培 育策略)

简介: Worldwide, abiotic stresses including heat and drought are the major obstructions that threaten the agricultural production. Development of climate-resilient cultivars is the easy and economical way to combat drought and heat stress with limited resources. Plants do follow adaptation strategies to mitigate the impact of stress and lead to alteration in some of the morphological traits such as leaf rolling, leaf angle, cuticular wax content, stomatal conductance, deep root system, altered signalling and metabolic pathways. Targeting such traits along with the economical yield will help to identify suitable genotypes which perform better under stress environment. The basic step is to explore the available physiological trait variation among the cultivars, germplasm set and wild relatives to main stream alleles of importance to breeding material from the donor parent. Conventional and advanced breeding strategies can be implemented to develop climate-resilient cultivars with the suitable breeding and screening methods. As a key factor hybridization and selection along with the implication of advanced breeding methods like MABB, MARS, GS and transgenic approach make it easy and accurate to develop varieties in less time. Linkage, QTL and genome-wide association mapping helps to identify the genomic region of interest to target during marker-aided breeding approaches. A cocktail of breeding methods from conventional to transgenic may help in the development of high-yielding climate-resilient varieties which can help to serve farmers to escape from glitch of crop loss due to dry spell during cropping season. The recent advancement and methodologies regarding drought and heat tolerance breeding in wheat are discussed in this chapter along with the difficulties posed.

来源: Translating Physiological Tools to Augment Crop Breeding 发布日期:2023-04-20 全文链接: http://agri.ckcest.cn/file1/M00/10/2F/Csgk0GTGFHmAQ0dIAAxAQHD21kw018.pdf