



2023年第7期总192期

杂交水稻专题

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▶ 前沿资讯

1. 广东丝苗米品种的核心粒形基因组合方面取得新进展

简介: 广东丝苗米是一系列具有显著地方特色优质籼稻的总称,有“南稻珍宝,广东丝苗”之誉。粒形细长是广东丝苗米品种的主要特征之一,这是在育种过程中通过高强度的人工选择实现的。然而目前,广东丝苗米中被人工选择的粒形等位基因组合是未知的。本研究通过比较粒形变异丰富的国际籼稻和粒形细长的广东丝苗米品种的群体分化指数,发现有4个粒形基因(GS3, GS5, GW5和GL7)被人工选择,这四个谷粒形状基因可以分别解释谷粒长度、宽度和长宽比的共68.3%、72.1%和86.1%的表型变异。研究通过进一步分析这四个基因的等位基因和频率分布表明:GS3allele3和GW5allele2在丝苗米中占96.2%,GL7allele2和GS5allele2分别占76.9%和74.5%;在广东丝苗米的主要3种粒形基因组合中都携带GS3allele3+GW5allele2,而组合(GS3allele3+GW5allele2+GL7allele1+GS5allele2)和组合(GS3allele3+GW5allele2+GL7allele2+GS5allele2)由于GL7等位基因的不同,在粒长和长宽比上都有显著差异;粒形基因组合(GS3allele3+GW5allele2+GL7allele2+GS5allele2)出现的比例最高(51.9%)。研究再通过对广8A的保持系广8B的系谱分析表明,亲本和广8B都携带GS3allele3+GW5allele2+GS5allele2,而GL7等位基因不同,导致了谷粒大小的显著差异。可见,GS3和GW5是控制广东丝苗米品种细长粒形的核心基因;而GL7则决定了广东丝苗米品种的谷粒大小。综上,本研究首次剖析了广东丝苗米品种的粒形遗传基础,其结果将有助于广东丝苗米的分子育种。

来源: 广东省农业科学院

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<http://agri.ckcest.cn/file1/M00/03/4B/Csgk0Yg7VjSAYfFHAUFUoRUGaJc671.pdf>

2. “工厂化”水稻育秧跑出生产“加速度”

简介: 农时催人,当下正是水稻育秧的关键期。在湖北省襄阳市襄州区的育秧工厂内,集约化育秧为水稻提质增产跑出“加速度”。在“工厂化”水稻育秧生产线上,秧盘经过铺底土、浇水、播种、盖土等工序制成后,被运送至增温大棚进行暗化催芽处理。齐芽后,送入育秧苗床进行培养扶壮。当秧苗长到机械插秧作业的要求标准时,移入大田进行机插作业,全流程基本实现自动化。据了解,与传统的人工育秧相比,水稻“工厂化”育秧大幅削减用工规模与强度,出苗率提高8%-10%,移栽时间可提前2-3天,移栽后秧苗返青快,预计每亩稻田增产70公斤以上。

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▶ 学术文献

1. Development of Multiple-Heading-Date mtl Haploid Inducer Lines

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in Rice (水稻多抽穗期mtl单倍体诱导系的选育)

简介: In vivo doubled haploid (DH) production based on crossing heterozygous germplasm with mtl haploid inducer lines promises to transform modern rice (*Oryza sativa*) breeding. However, this technology is limited, as haploid inducers and pollen acceptors have asynchronous heading dates. To address this obstacle, we developed a panel of multiple-heading-date mtl haploid inducer lines that produce pollen for more than 35 days. We edited the MTL gene in a hybrid rice with the CRISPR-Cas9 system. We then selected transgene-free homozygous mutants in the T-1 generation and reproduced to T-4 generation by single-seed descent method. We obtained 547 mtl haploid inducers with diverse heading dates (from 73 to 110 days) and selected 16 lines comprising a core population with continuous flowering. The seed-setting rate and haploid induction rate (HIR) of the core panel were 4.0-12.7% and 2.8-12.0%, respectively. Thus, our strategy of using multiple-heading-date mtl haploid inducers could accelerate the use of in vivo DH technology in rice breeding.

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2. Population Structure of a Worldwide Collection of Tropical Japonica Rice Indicates Limited Geographic Differentiation and Shows Promising Genetic Variability Associated with New Plant Type (全球热带粳稻的种群结构表明地理分化有限, 并显示出与新植物类型相关的潜在遗传变异性)

简介: Abating the approaching yield plateau in rice requires taking advantage of potential technologies that requires knowledge on genetic diversity. Hybrid breeding, particularly in indica rice, requires the recruitment of large genetic variability from outside because the available genetic diversity of the cultivated pool has already been utilized to a great extent. In this study, we examined an assembly of 200 tropical japonica lines collected worldwide for population genetic structure and variability in yield-associated traits. Tested along with 30 indica and six wild rice lines belonging to India, the tropical japonica lines indicated great phenotypic variability, particularly related to new plant type (NPT) phenology, and formed six clusters. Furthermore, a marker-based characterization using a universal diversity marker panel classified the genotype assembly into four clusters, of which three encompassed tropical japonica lines, while the last cluster included mostly indica lines. The population structure of the panel also revealed a similar pattern, with tropical japonica lines forming three subpopulations. Remarkable variation in the allelic distribution was observed between the subpopulations. Superimposing the geographical sources of the genotypes over the population structure did not reveal any pattern. The genotypes sourced closer to the center of origin of rice showed relatively little diversity compared with the ones obtained from other parts of the world, suggesting migration from a common region of origin. The tropical japonica lines can be a great source of parental diversification for hybrid development after

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confirming the presence of widely compatible genes.

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3. Genetic behavior of earliness and yield traits of some rice (*Oryza sativa* L.) genotypes (一些水稻 (*Oryza sativa* L.) 基因型早熟性和产量性状的遗传行为)

简介: Rice (*Oryza sativa* L.) is a critical staple food crop that provides more than half of the world's population with its primary nutritional source. Breeders and growers of rice would profit from robust genotypes with improved morphological and yield-related characteristics. The aim of this work is to determine the nature and magnitude of gene action on yield quantity and quality, to define the best combinations of earliness and yield characters, develop hybrids that perform better on yield quantity and quality. Three replications were used in the experiment's randomized complete block design (RCBD). During the 2016 season, seven different parents, namely Sakha 101, Sakha 104, Sakha 105, Giza 177, Black rice 1, Black rice 2, and Black rice 3, were crossed using A 7 x 7 half-diallel set analysis without reciprocals to generate 21 F1 crosses. The results indicated that genotype-dependent mean squares were very significant for main characteristics. Significant combining ability SCA variance estimates were more considerable than general combining ability (GCA) variance for all characters except days to 50% flowering. It demonstrated that both additive and non-additive genetic variance played a role in expressing the attributes investigated. The Parents, Black rice, Sakha 105, and Sakha 101, were recognized as the best general combiner for most growth and yield attributes. Sakha105 x Black Rice 1, Sakha105 x Black Rice 2, Sakha101 x Sakha104, Sakha105 x Giza 177, and Sakha101 x Giza 177 all demonstrated non-additive gene activity for the majority of maturity and yield traits. Heterosis breeding would be most efficient for qualities where high performance was determined by dominance and dominance gene effects. The increased yield of crosses results from parents with a diverse genetic background and genetic diversity.(c) 2022 The Authors. Published by Elsevier B.V. on behalf of King Saud University. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

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