



2023年第4期总189期

杂交水稻专题

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中国农业科学院农业信息研究所
联系人：于超；罗建军；李亮；顾亮亮
联系电话：0731-84690287

邮箱：agri@ckcest.cn

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▶ 前沿资讯

1. 科研人员发现驯化选择水稻DNA寒害损伤修复机制及其优异模块

简介: 农作物应对全球气候变化引起的异常温度需要具备优异耐受模块, 品种设计需依赖细胞寒害感知防御“信号网络”和“修复机制”的原理。在前期的研究中, 种康院士团队已在水稻寒害感知与防御“信号网络”中已经发现了包括感受器、激酶、叶绿体维生素E-K1代谢途径、转录因子和海藻糖代谢在内的一系列元件及其之间的网络关系。然而, 对于寒害专一的DNA修复系统是如何建立的则知之甚少。科研人员在最新的研究中发现, 具有特异性的人工驯化选择的自然变异耐寒基因模块能够修复寒害引起的DNA损伤。基于数据空间降维理念, 通过数学算法将多维尺度的数据合降维的全基因组关联分析, 即数据整合GWAS (DM-GWAS), 在水稻中系统鉴定到耐寒QTL遗传位点与主效基因COL11, 其突变引起耐寒性的显著降低, 编码区存在GCG密码子重复, 且与DNA修复活性和耐寒性具有正相关性, 受到强的驯化选择。这是首次报道驯化选择的寒害DNA修复优异等位模块新机制。该模块具有重要的应用潜力, 为耐寒分子设计育种中对关键位点进行精细调控开辟了新的途径。

来源: 中国科学院植物研究所

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<http://agri.ckcest.cn/file1/M00/10/1C/Csgk0GPKUbeAAup-AALTbgLEqiI317.pdf>

2. 揭示水稻根响应土壤紧实度的新机制

简介: 近日, 中国农业科学院生物技术研究所作物耐逆性调控与改良创新团队揭示了ABA与生长素协同调控水稻根系响应外界土壤硬度的分子机制, 为培育适应不同土壤硬度作物新品种提供了新的分子途径和有用的基因资源。相关研究成果发表于《Plant Physiology (植物生理学)》上。农业生产中重型农业机械和其他耕作措施等人为因素, 以及土壤干旱等自然因素都会使土壤紧实度产生变化, 当土壤硬度增加时, 会抑制植物根系的生长, 不利于对养分和水分的吸收利用, 从而影响植物的生长和作物的产量。一直以来, 土壤紧实度对作物生长和产量的影响也成为当前关注的热点之一。本研究发现, 紧实土壤抑制水稻根的生长, 与ABA的作用类似。阻断植物体内的ABA合成增强了根穿透紧实土壤的能力。进一步研究发现ABA通过OsZIP46激活生长素合成基因OsYUC8的表达, 促进生长素在根中的积累, 最终导致短而粗的根, 降低了根的钻地性。本研究阐明了ABA通过生长素调控水稻根系响应外界土壤硬度的分子机制, 丰富了植物根系响应土壤紧实度的分子途径, 为未来选育钻地能力强的水稻新品种提供理论基础和有用的基因。

来源: 中国农业科学院生物技术研究所

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▶ 学术文献

1. Combining Ability and Gene Action Controlling Agronomic Traits

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for Cytoplasmic Male Sterile Line, Restorer Lines, and New Hybrids for Developing of New Drought-Tolerant Rice Hybrids (细胞质雄性不育系、恢复系和新杂交种的配合力和控制农艺性状的基因作用)

简介: This study aimed to identify new rice lines and hybrids that are tolerant to water deficit and produce high yields under water stress conditions. A line x tester mating design was used to study the lines and testers' general combining ability (GCA) effects. The specific combining ability (SCA) of the hybrid rice combinations was measured under three different irrigation regimes; 6, 9, and 12 days. The study was carried out at the experimental farm of Sakha Agricultural Research Station, Sakha, Kafr El-Sheikh, Egypt, during the 2018 and 2019 rice growing seasons. Due to the genotypes and their partitions to the parents and the crosses, the mean squares were highly significant for all studied traits under the three irrigation regimes. The additive gene effects play an important role in expressing most of the studied traits. Therefore, the selection procedures based on the accumulation of the additive effect would be successful at improving these traits and the grain yield. The cytoplasmic male sterile (CMS) line G46A (L1) was the best combiner for most yield component traits in the three irrigation regimes. The newly devolved restorer lines T11, T1, T2, T5, T4, and T3, as well as the new hybrids L2 x T10, L2 x T6, L1 x T7, L1 x T5, L1 x T3, L2 x T7, L2 x T9, L2 x T8, L2 x T4, L1 x T4, L2 x T2, L1 x T8, L1 x T9, and L2 x NRL 10, showed good, desirable values of the studied traits such as earliness of flowering, short plant height, number of panicles/plant, panicle length, number of spikelets/panicle, number of filled grains/panicle, panicle weight, 1000-grain weight, hulling percentage, milling percentage, head rice percentage, and grain yield under the irrigation regimes of 6, 9, and 12 days. The hybrids L2 x T10, L2 x T6, L1 x T7, and L1 x T5, showed significant positive SCA effects for grain yield, under all three irrigation regimes.

来源: GENES

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http://agri.ckcest.cn/file1/M00/03/4A/Csgk0Ygg_deAJnTVABsu5fKVhgE038.pdf

2. Whole-Genome Sequencing of 117 Chromosome Segment Substitution Lines for Genetic Analyses of Complex Traits in Rice (用于水稻复杂性状遗传分析的117个染色体片段代换系的全基因组测序)

简介: Rice is one of the most important food crops in Asia. Genetic analyses of complex traits and molecular breeding studies in rice greatly rely on the construction of various genetic populations. Chromosome segment substitution lines (CSSLs) serve as a powerful genetic population for quantitative trait locus (QTL) mapping in rice. Moreover, CSSLs containing target genomic regions can be used as improved varieties in rice breeding. In this study, we developed a set of CSSLs consisting of 117 lines derived from the recipient 'Huanghuazhan' (HHZ) and the donor 'Basmati Surkb 89-15' (BAS). The 117 lines were extensively genotyped by whole-genome resequencing, and a high-density genotype map was constructed for the CSSL population. The 117 CSSLs covered 99.78% of the BAS genome.

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Each line contained a single segment, and the average segment length was 6.02 Mb. Using the CSSL population, we investigated three agronomic traits in Shanghai and Hangzhou, China, and a total of 25 QTLs were detected in both environments. Among those QTLs, we found that RFT1 was the causal gene for heading date variance between HHZ and BAS. RFT1 from BAS was found to contain a loss-of-function allele based on yeast two-hybrid assay, and its causal variation was a P to S change in the 94th amino acid of the RFT1 protein. The combination of high-throughput genotyping and marker-assisted selection (MAS) is a highly efficient way to construct CSSLs in rice, and extensively genotyped CSSLs will be a powerful tool for the genetic mapping of agronomic traits and molecular breeding for target QTLs/genes.

来源: RICE

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<http://agri.ckcest.cn/file1/M00/10/1B/Csgk0GPKRbmAAke-ABoqx0yoqBY118.pdf>

3. Rice Brittle Culm19 Encoding Cellulose Synthase Subunit CESA4 Causes Dominant Brittle Phenotype But has No Distinct Influence on Growth and Grain Yield (编码纤维素合成酶亚基CESA4的水稻脆性秆19引起显性脆性表型, 但对生长和产量没有显著影响)

简介: Background Mechanical strength is a crucial agronomic trait in rice (*Oryza sativa*), and brittle mutants are thought suitable materials to investigate the mechanism of cell wall formation. So far, almost all brittle mutants are recessive, and most of them are defected in multiple morphologies and/or grain yield, limiting their application in hybrid breeding and in rice straw recycling. Results We identified a semi-dominant brittle mutant Brittle culm19 (Bc19) isolated from the japonica variety Nipponbare through chemical mutagenesis. The mutant showed the same apparent morphologies and grain yield to the wild type plant except for its weak mechanical strength. Its development of secondary cell wall in sclerenchyma cells was affected, along with reduced contents of cellulose, hemicellulose, lignin and sugars in culms and leaves. Positional cloning suggested that the Bc19 gene was allelic to OsCESA4, encoding one of the cellulose synthase A (CESA) catalytic subunits. In this mutant, a C-to-T substitution occurred in the coding sequence of BC19, causing the P507S missense mutation in its encoded product, which was located in the second cytoplasmic region of the OsCESA4 protein. Furthermore, introducing mutant gene Bc19 into the wild-type plant resulted in brittle plants, confirming that the P507S point mutation in OsCESA4 protein was responsible for the semi-dominant brittle phenotype of Bc19 mutant. Reverse correlation was revealed between cellulose contents and expression levels of mutant gene Bc19 among the homozygous mutant, the hybrid F-1 plant, and the Bc19 overexpression transgenic plants, implying that gene Bc19 might affect cellulose synthesis in a dosage-dependent manner. Conclusions Bc19, a semi-dominant brittle mutant allele of gene OsCESA4, was identified using map-based cloning approach. The mutated protein of Bc19 possessing the P507S missense mutation behaved in a dosage-dependent semi-dominant manner. Unique brittle effect on phenotype and semi-dominant genetic quality of gene Bc19 indicated its potential

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application in grain-straw dual-purpose hybrid rice breeding.

来源: RICE

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