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杂交水稻专题

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▶ 前沿资讯

1. 研究揭示水稻种子内生核心微生物组垂直传播机制

简介: 近日,中国农业科学院农业资源与农业区划研究所农业微生物资源创新团队建立了水稻内生微生物资源库,并通过多尺度微生物组学分析,阐明了种子内生核心微生物组功能及其垂直传播机制。相关成果发表在《微生物组 (Microbiome)》上。植物相关微生物组被称为植物的“第二基因组”,而内生微生物组是植物相关微生物组的核心,与植物进化、抗病抗逆、营养转化具有最密切的联系。该研究利用两代水稻、六个品种、四个种植区、五个取样部位,进行了高通量微生物组深度解析,构建了以水稻内生微生物为基础的资源库。进一步阐明了水稻微生物群落组装的偏好性及在水稻不同部位的动态变化,发现了14个水稻内生核心分类单元(ASV),并成功分离到可垂直传播的3个泛菌种类和1个糖黄单胞种类。功能基因组学分析表明,这两类细菌基因组简单、无致病特征、产特殊次生代谢物质和酶类等,且具有溶磷、促生等益生特点。该研究提出并通过组学分析验证了水稻种子内生微生物的垂直传播机制,在微生物-植物共进化学理论方面具有重要的创新意义。此外,水稻内生微生物资源库的建立为开发利用这一特殊生境微生物提供了资源基础,一些重要微生物类群在营养转化与吸收、抗病抗逆、耐胁迫等方面表现出的巨大潜力,将为微生物肥料、微生物农药、微生物种衣剂、微生物防腐剂的研发开辟新的思路。

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2. 杂交水稻技术再有重大突破

简介: 一项由香港浸会大学(浸大)理学院生物系讲座教授张建华领导的研究,通过开创雌性不育技术,为杂交水稻的制种过程带来突破。相比生产杂交水稻种子常用的雄性不育技术「三系法」,该崭新的技术不会产生「恢复系」自花授粉所孕育的水稻种子,从而提升杂交水稻种植的效率。新技术可实现以机器全面自动化收割杂交种子,令制种成本大幅降低。研究结果已于近期刊登在尖端国际科学期刊《Cell Research》。经过近十年不断研究,浸大理学院生物系讲座教授张建华带领的研究团队,在水稻田种植过程中,从一个优质的水稻品种发现「自发性温敏雌性不育1」(TFS1)基因突变。在正常或高温下(即高于25℃),该基因突变会令水稻呈现雌性不育,而在低温(即23℃)下则恢复部份育性。这个基因突变没有令水稻的生长出现异常。团队观察到出现TFS1基因突变的水稻,可产生雄性育性正常的健康花粉。育性正常的水稻接受了带有TFS1基因突变的水稻花粉后,可结出正常的种子。研究进一步显示,在正常或高温下,当花粉在带有TFS1基因突变的水稻的柱头上萌发后,它们长出的花粉管未能进入胚囊,故未能产生胚胎并结出种子。但在低温下,育性及产生胚胎的能力可部分获得恢复。团队运用基因克隆(gene cloning)及分子技术进行一系列基因分析,发现雌性不育基因突变,是由一个出现在基因区域Argonaute7(AGO7)的点突变所产生。AGO7属于一种Argonaute(AGO)蛋白复合物,负责制造小分子干扰核糖核酸tasiR-ARFs。tasiR-ARFs的下游调控能控制花粉管进入胚囊,但在正常或高温下,此调控机制在带有TFS1基因突变的水稻中失效,因而无法完成双受精过程。为评价TFS1作为杂交水稻制种基因工具的

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潜质,团队在香港及湖南省进行种植实验。团队通过基因渗入及基因编辑的方法,把TFS1突变基因导入三个水稻品种,培植出温敏雌性不育种质的水稻,用作提供花粉的「恢复系」。另外三种雄性不育的水稻品种则用作「雄性不育系」。团队把「恢复系」按传统杂交制种的做法种植于「雄性不育系」旁,或把它们随机混合在农田上种植。在香港,两个种植方案均可以在超过三成的「雄性不育系」水稻花穗收成杂交种子,湖南省则有超过四成。这个种子收成比例,与沿用现有「恢复系」的杂交制种收成比例相若,但无须于收割杂交种子前移除「恢复系」。

来源: 香港浸会大学

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➤ 学术文献

1. Genes and Their Molecular Functions Determining Seed Structure, Components, and Quality of Rice (决定水稻种子结构、成分和品质的基因及其分子功能)

简介: With the improvement of people's living standards and rice trade worldwide, the demand for high-quality rice is increasing. Therefore, breeding high quality rice is critical to meet the market demand. However, progress in improving rice grain quality lags far behind that of rice yield. This might be because of the complexity of rice grain quality research, and the lack of consensus definition and evaluation standards for high quality rice. In general, the main components of rice grain quality are milling quality (MQ), appearance quality (AQ), eating and cooking quality (ECQ), and nutritional quality (NQ). Importantly, all these quality traits are determined directly or indirectly by the structure and composition of the rice seeds. Structurally, rice seeds mainly comprise the spikelet hull, seed coat, aleurone layer, embryo, and endosperm. Among them, the size of spikelet hull is the key determinant of rice grain size, which usually affects rice AQ, MQ, and ECQ. The endosperm, mainly composed of starch and protein, is the major edible part of the rice seed. Therefore, the content, constitution, and physicochemical properties of starch and protein are crucial for multiple rice grain quality traits. Moreover, the other substances, such as lipids, minerals, vitamins, and phytochemicals, included in different parts of the rice seed, also contribute significantly to rice grain quality, especially the NQ. Rice seed growth and development are precisely controlled by many genes; therefore, cloning and dissecting these quality-related genes will enhance our knowledge of rice grain quality and will assist with the breeding of high quality rice. This review focuses on summarizing the recent progress on cloning key genes and their functions in regulating rice seed structure and composition, and their corresponding contributions to rice grain quality. This information will facilitate and advance future high quality rice breeding programs.

来源: RICE

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2. DNA Methylation Alterations and Their Association with High Temperature Tolerance in Rice Anthesis (水稻花药DNA甲基化变化及其与耐高温性的关系)

简介: DNA methylation is an important epigenetic mechanism involved in gene regulation under environmental stresses in plants. However, little information is available regarding its responses to high temperature (HT) and association with HT tolerance in rice. In this study, fourteen rice genotypes were classified into the susceptible, moderate, and tolerant groups by the high temperature susceptibility index (HTSI) after HT treatment. The changes of DNA methylation in rice anthesis under normal and HT30 conditions were investigated using methylation-sensitive amplified polymorphism³¹ (MSAP). The MSAP results showed that the DNA methylation level significantly increased in the susceptible rice group and decreased in the tolerant rice group under HT treatment, while no significant difference was observed in the moderate rice group. More hypomethylation events were detected in the tolerant rice group, while more hypermethylation was detected in the susceptible rice group. Forty-four differentially methylated epiloci (DME) were generated under both control and HT conditions, which can clearly distinguish the susceptible, moderate, and tolerant genotypes via PCoA analysis. Approximately 43.18% of DMEs were determined to be tolerance-associated epiloci (TAEs). 63.15% TAEs were sequenced and annotated into 12 genes. Quantitative RT-PCR analysis showed that 12 TAE genes were mainly upregulated in 14 rice genotypes, and their expression levels were related to the HT tolerance of rice. Here, DEGs, generated from a number of genotypes, indicate higher probabilities for association with stress tolerance. Overall, these results suggest that DNA methylation regulation might play a key role in adaptation to HT stress in rice.

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3. Domain Unknown Function DUF1668-Containing Genes in Multiple Lineages Are Responsible for F-1 Pollen Sterility in Rice (含有多个谱系基因的域未知功能DUF1668与水稻F-1花粉不育)

简介: Postzygotic reproductive isolation maintains species integrity and uniformity and contributes to speciation by restricting the free gene flow between divergent species. In this study we identify causal genes of two Mendelian factors S22A and S22B on rice chromosome 2 inducing F-1 pollen sterility in hybrids between *Oryza sativa japonica*-type cultivar Taichung 65 (T65) and a wild relative of rice species *Oryza glumaepatula*. The causal gene of S22B in T65 encodes a protein containing DUF1668 and gametophytically expressed in the anthers, designated S22B_j. The *O. glumaepatula* allele S22B_g, allelic to S22B_j, possesses three non-synonymous substitutions and a 2-bp deletion, leading to a

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frameshifted translation at the S22B C-terminal region. Transcription level of S22B-j and/or S22B_g did not solely determine the fertility of pollen grains by genotypes at S22B. Western blotting of S22B found that one major band with approximately 46 kDa appeared only at the mature stage and was reduced on semi-sterile heterozygotes at S22B, implying that the 46 kDa band may associated in hybrid sterility. In addition, causal genes of S22A in T65 were found to be S22A_j1 and S22A_j3 encoding DUF1668-containing protein. The allele of a wild rice species *Oryza meridionalis* Ng at S22B, designated S22B_m, is a loss-of-function allele probably due to large deletion of the gene lacking DUF1668 domain and evolved from the different lineage of *O. glumaepatula*. Phylogenetic analysis of DUF1668 suggested that many gene duplications occurred before the divergence of current crops in Poaceae, and loss-of-function mutations of DUF1668-containing genes represent the candidate causal genetic events contributing to hybrid incompatibilities. The duplicated DUF1668-domain gene may provide genetic potential to induce hybrid incompatibility by consequent mutations after divergence.

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