



2023年第6期总191期

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▶ 前沿资讯

1. 研究发现水稻籽粒大小和重量调控的重要途径

简介: 水稻是世界上重要的粮食作物,籽粒大小和粒重是影响水稻产量的重要决定因素。目前已经克隆了一些控制水稻种子大小的重要基因,但水稻种子大小调控的分子机理仍不清楚,进一步阐明水稻籽粒大小的调控机理对于提高水稻产量具有重要的指导意义。近日,中国科学院遗传与发育生物学研究所李云海团队、中国科学院大学柴团耀教授、海南大学徐冉教授合作发现ERAD相关的E2-E3蛋白复合物SMALL GRAIN 3 (SMG3)和DECREASED GRAIN SIZE 1 (DGS1)部分通过油菜素内酯(BR)途径调控水稻籽粒大小和粒重的新途径。水稻SMG3编码拟南芥泛素结合酶UBC32 (UBIQUITIN CONJUGATING ENZYME 32)的同源蛋白,并且与另一籽粒大小调控因子DGS1互作。SMG3或DGS1功能缺失均导致籽粒变小,而过表达则使籽粒变长。进一步分析发现,DGS1是具有活性的E3泛素连接酶,并与SMG3共定位于内质网。此外,DGS1通过泛素化BR受体BRASSINOSTEROID INSENSITIVE 1 (BRI1)并影响其在细胞中的积累量从而参与了BR信号转导通路。遗传分析结果表明,SMG3, DGS1和BRI1三者共同作用调控水稻籽粒大小和粒重。该研究为深入了解ERAD相关途径在水稻籽粒大小调控中的作用,及其与油菜素内酯信号途径的关系提供了分子基础,为高产育种提供了一定的理论依据。

来源: 中国科学网

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2. 水稻天然多抗基因找到了

简介: 水稻是全球最重要的粮食作物之一,但却长期遭受稻瘟病、纹枯病、白叶枯病等主要病害的威胁,穗部病害稻曲病近年来也成为我国水稻主要病害之一。目前,能同时抗多种病害的水稻基因资源十分缺乏。日前,四川农业大学西南作物基因资源发掘与利用国家重点实验室教授王文明团队在《自然-植物》在线发表最新研究论文。论文报道了一个编码蛋白酶体成熟因子的天然等位基因,可改良水稻对多种病害的抗性,同时不影响水稻产量。论文审稿人认为,这项研究对于水稻抗病育种具有很好的指导意义,其实验设计好、数据翔实可靠,将对植保领域产生很大影响。论文共同通讯作者、四川农业大学教授樊晶近年来一直关注稻曲病的发病与抗病机理。他告诉《中国科学报》,稻曲病已成为水稻最严重的穗部病害,被感染的水稻颖花不能结实,从而引起空秕率增加,导致水稻减产。同时,病粒污染健康谷粒后,会降低水稻品质。更严重的是,病粒产生真菌毒素,人畜食用后可能造成腹泻、流产、早产等中毒现象。目前,科学家已经发现了一些多抗基因。例如,bsr-k1可以增强水稻对稻瘟病和白叶枯病的抗性;rod1能提高水稻对稻瘟病、纹枯病和白叶枯病的抗性。研究人员选择了雅恢2115、3个小种特异性抗性的材料和1个感病材料,并把稻瘟菌喷到这些水稻材料的幼苗上,然后检测水稻体内所有基因表达水平的变化。通过比较分析,筛选的基因只在雅恢2115中高表达且被稻瘟菌刺激得更高,而在其他两种材料中均不表达或低表达。研究发现,将雅恢2115中的OsUMP1基因导入感病水稻中,能够提高水稻对多个稻瘟菌菌株的抗性,同时可显著增强对稻曲病、纹枯病、白叶枯病等多种病害的抗性,而其对水稻主要农艺性状和产量没有明显影响。进一步的生理生化与遗传学实验证明,在病原菌入侵时,OsUMP1基因通过增

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加水稻26S蛋白酶体的生物合成与活性, 促进过氧化物酶APX8和过氧化氢酶CatB的降解, 提高侵染位点过氧化氢的积累, 从而增强水稻对多种病原菌的抵御能力。

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► 学术文献

1. Intelligent Identification and Features Attribution of Saline-Alkali-Tolerant Rice Varieties Based on Raman Spectroscopy (基于拉曼光谱的耐盐碱水稻品种智能识别及特征归属)

简介: Planting rice in saline-alkali land can effectively improve saline-alkali soil and increase grain yield, but traditional identification methods for saline-alkali-tolerant rice varieties require tedious and time-consuming field investigations based on growth indicators by rice breeders. In this study, the Python machine deep learning method was used to analyze the Raman molecular spectroscopy of rice and assist in feature attribution, in order to study a fast and efficient identification method of saline-alkali-tolerant rice varieties. A total of 156 Raman spectra of four rice varieties (two saline-alkali-tolerant rice varieties and two saline-alkali-sensitive rice varieties) were analyzed, and the wave crests were extracted by an improved signal filtering difference method and the feature information of the wave crest was automatically extracted by `scipy.signal.find peaks`. Select K Best (SKB), Recursive Feature Elimination (RFE) and Select F Model (SFM) were used to select useful molecular features. Based on these feature selection methods, a Logistic Regression Model (LRM) and Random Forests Model (RFM) were established for discriminant analysis. The experimental results showed that the RFM identification model based on the RFE method reached a higher recognition rate of 89.36%. According to the identification results of RFM and the identification of feature attribution materials, amyllum was the most significant substance in the identification of saline-alkali-tolerant rice varieties. Therefore, an intelligent method for the identification of saline-alkali-tolerant rice varieties based on Raman molecular spectroscopy is proposed.

来源: Web of Science

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2. Balancing selection and wild gene pool contribute to resistance in global rice germplasm against planthopper (平衡选择和野生基因库有助于全球水稻种质对稻飞虱的抗性)

简介: Interactions and co-evolution between plants and herbivorous insects are critically

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important in agriculture. Brown planthopper (BPH) is the most severe insect of rice, and the biotypes adapt to feed on different rice genotypes. Here, we present genomics analyses on 1,520 global rice germplasms for resistance to three BPH biotypes. Genome-wide association studies identified 3,502 single nucleotide polymorphisms (SNPs) and 59 loci associated with BPH resistance in rice. We cloned a previously unidentified gene Bph37 that confers resistance to BPH. The associated loci showed high nucleotide diversity. Genome-wide scans for trans-species polymorphisms revealed ancient balancing selection at the loci. The secondarily evolved insect biotypes II and III exhibited significantly higher virulence and overcame more rice varieties than the primary biotype I. In response, more SNPs and loci evolved in rice for resistance to biotypes II and III. Notably, three exceptional large regions with high SNP density and resistance-associated loci on chromosomes 4 and 6 appear distinct between the resistant and susceptible rice varieties. Surprisingly, these regions in resistant rice might have been retained from wild species *Oryza nivara*. Our findings expand the understanding of long-term interactions between rice and BPH and provide resistance genes and germplasm resources for breeding durable BPH-resistant rice varieties.

来源: JOURNAL OF INTEGRATIVE PLANT BIOLOGY

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<http://agri.ckcest.cn/file1/M00/10/1C/Csgk0GPbfIqADEMUACPZaBShBrw582.pdf>

3. Genotypic Variation in Nutrient Uptake Requirements of Rice Using the QUEFTS Model (利用QUEFTS模型研究水稻养分吸收需求的基因型变异)

简介: Nutrient requirements for single-season rice using the quantitative evaluation of the fertility of tropical soils (QUEFTS) model in China have been estimated in a previous study, which involved all the rice varieties; however, it is unclear whether a similar result can be obtained for different rice varieties. In this study, data were collected from field experiments conducted from 2016 to 2019 in Zhejiang Province, China. The dataset was separated into two parts: japonica/indica hybrid rice and japonica rice. To produce 1000 kg of grain, 13.5 kg N, 3.6 kg P, and 20.4 kg K were required in the above-ground plant dry matter for japonica/indica hybrid rice, and the corresponding internal efficiencies (IEs) were 74.0 kg grain per kg N, 279.1 kg grain per kg P, and 49.1 kg grain per kg K. For japonica rice, 17.6 kg N, 4.1 kg P, and 23.0 kg K were required to produce 1000 kg of grain, and the corresponding IEs were 56.8 kg grain per kg N, 244.6 kg grain per kg P, and 43.5 kg grain per kg K. Field validation experiments indicated that the QUEFTS model could be used to estimate nutrient uptake of different rice varieties. We suggest that variety should be taken into consideration when estimating nutrient uptake for rice using the QUEFTS model, which would improve this model.

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