



2019年第12期总12期

杂交水稻专题

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2019年9月2日

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▶ 前沿资讯

1. 科学家开发出简单高效鉴定水稻免疫相关的小分泌蛋白质方法

简介: Yoji Kawano研究组和刘仁义研究组设计了一个将转录组学和蛋白组学结合的方法, 利用水稻植株和悬浮细胞两个体系, 筛选能被稻瘟病菌Magnaporthe. oryzae (M. oryzae) 侵染和几丁质处理而诱导的植物细胞因子的前体蛋白质和小分泌蛋白质(SSPs)。通过RNA-seq共鉴定得到2454个基因, 并且利用质谱鉴定到3327个蛋白质被稻瘟病菌和几丁质所激活。最后, 筛选鉴定得到236个小分泌蛋白质, 包括两个已知的植物细胞因子家族, 快速碱化因子(RALFs)和植物磺肽素(PSKs), 以及许多免疫相关的蛋白质家族, 比如蛋白酶抑制剂(PIs)和发病机理相关蛋白家族(PRs)。其中一个命名为免疫应答肽(IRP)的新基因, 它可能编码一个植物细胞因子。细菌肽聚糖和几丁质处理能够诱导IRP的表达并且几丁质可以诱导IRP分泌到水稻细胞外。在过表达IRP的水稻悬浮细胞中, 抗病相关基因PAL1表达被激活。另外, 与野生型相比, 分裂素激活蛋白激酶(MAPKs)的活性在过表达IRP的水稻悬浮细胞中增强, 表明IRP在水稻免疫中起着积极的作用。该研究建立了一个简单且高效的方法, 能够鉴定在水稻免疫过程中发挥重要功能的小分泌蛋白质。更为重要的是, 这个方法将有助于发现在植物生命活动中发挥不同功能的小分泌蛋白质。

来源: 中国科学院

发布日期: 2019-08-29

全文链接:

http://www.cas.cn/syky/201908/t20190828_4711950.shtml

2. 科学家揭示水稻早熟高产新机制

简介: 1998年四川农业大学邓晓建等人发现早粳核不育系“6442S-7”具有完全显性早熟特性, 并初步定位了水稻第3染色体短臂存在的一个显性早熟基因Ef-cd。之后, 通过和中科院遗传与发育生物学研究所储成才研究组合作, 历经多年, 图位克隆了Ef-cd基因。Ef-cd基因因为一个长片段非编码RNA(long noncoding RNA), 通过介导该位点组蛋白甲基化水平, 正向调控另一重要开花基因OsSOC1/OsMADS50的表达, 从而促使水稻早熟。在全国不同纬度(北京、四川成都、浙江嘉兴、福建福州)地区, 对Ef-cd近等基因系及其衍生的早熟杂交稻进行田间比较试验, 结果表明Ef-cd能显著提早水稻抽穗期7-20天, 但对产量没有影响, 甚至在多个地区具有不同程度的增产效果。大规模组学分析表明, 含Ef-cd水稻材料氮代谢、叶绿素代谢及光合作用相关基因表达显著增强; 生理实验也证明, Ef-cd显著提高了水稻硝态氮和铵态氮的吸收能力以及叶片的光合作用效率。这些结果表明Ef-cd基因兼顾早熟和高产两个方面, 具有资源高效利用的显著特征。通过和中科院分子植物科学卓越创新中心/植物生理生态研究所韩斌团队合作, 研究人员对我国目前生产上应用的1439个杂交稻品种基因型和田间抽穗期表型数据分析发现, 所有含Ef-cd基因的杂交稻组合(299份含杂合基因型、16份含纯合基因型)在杭州和三亚两地抽穗期平均提早9-10天。表明Ef-cd在我国杂交水稻生产上做出重大贡献, 是一个具有重大价值的基因。在当前水稻生产新形势下, 该基因的挖掘和利用将有力促进绿色超级稻品种培育的减肥增效需求, 同时, 对解决直播稻和粮经、粮菜、粮油连作稻的早熟丰产以及亚种间杂交稻“超亲晚熟”等问题具有重要价值。

来源: 中国科学院

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发布日期:2019-08-28

全文链接:

http://www.cas.cn/syky/201908/t20190827_4711756.shtml

3. 水稻穗发芽机制研究中取得新进展

简介:中国科学院遗传与发育生物学研究所植物基因组学国家重点实验室储成才研究组一直致力于水稻穗发芽分子机制研究。通过大规模突变体筛选,获得了一系列水稻穗发芽突变体,并已报道了植物激素脱落酸(ABA)合成途径基因的突变体(phs1至phs7)都表现出穗发芽表型(Fang et al., 2008; Fang and Chu, 2008)。而PHS8的突变导致胚乳中小分子糖的积累,从而抑制胚中的ABA信号传递,导致了穗发芽表型(Du et al., 2018)。对一个新的穗发芽突变体phs9的研究表明,PHS9编码一个高等植物特有的CC类型谷氧还蛋白,并且主要在发育后期的胚中表达。PHS9通过与一个ABA受体互作蛋白OsGAP相互作用,整合了活性氧(ROS)信号和ABA信号,从而调控水稻穗发芽。更为有意思的是,在江浙主栽品种淮稻5号和武运粳27号敲除PHS9基因能够显著抑制新鲜收获的种子的萌发,表明可以通过基因编辑PHS9来有效缓解水稻穗发芽。

来源: 中国科学院

发布日期:2019-08-26

全文链接:

http://www.cas.cn/syky/201908/t20190823_4711161.shtml

学术文献

1. High Nitrogen Levels Alleviate Yield Loss of Super Hybrid Rice Caused by High Temperatures During the Flowering Stage (高氮水平减轻超级杂交稻开花期高温造成的产量损失)

简介: The effect of high temperatures on rice production has attracted considerable research attention. It is not clear, however, whether nitrogen (N) management can be used to alleviate the damaging effects of high temperatures on flowering in rice. In this study, we compared the yields of five elite super hybrid rice varieties and examined their heat tolerance under four N treatments in two seasons with contrasting temperatures at flowering: 2015 (normal temperature) and 2016 (high temperature). The average daily temperature during the flowering stage in 2016 was 31.1°C which was 4.5°C higher than that in 2015. There was a significant positive correlation between grain yield and N level ($R^2 = 0.42$, $P < 0.01$). However, mean grain yield of the five rice varieties in 2015 was 10.5% higher than that in 2016. High N levels reduced yield losses in plants exposed to high temperature in 2016. The mean seed-set percentage in 2016 was 13.0% lower than that in 2015 at higher N levels, but spikelets per panicle increased by 7.6% at higher N levels compared with lower N levels. Higher N levels reduced the number of degenerated spikelets under high temperatures. Spikelets per panicle and N treatment level were positively correlated at high temperatures ($R^2 = 0.32$, $P < 0.05$). These results confirmed that increasing N application could alleviate yield losses caused by high temperatures in super hybrid rice during the flowering stage.

更多资讯 尽在农业专业知识服务系统:<http://agri.ckcest.cn/>

来源: Frontiers in Plant Science

发布日期: 2019-03-26

全文链接:

<http://agri.ckcest.cn/file1/M00/0E/80/Csgk0F1ny8-AES3oAB048ugDx2g950.pdf>

2. Extensive allele-level remodeling of histone methylation modification in reciprocal F-1 hybrids of rice subspecies (水稻亚种互交F-1杂种组蛋白甲基化修饰的广泛等位基因水平重塑)

简介: Epigenetic mechanisms play a major role in heterosis, partly as a result of the remodeling of epigenetic modifications in F1 hybrids. Based on chromatin immunoprecipitation-sequencing (ChIP-Seq) analyses, we show that at the allele level extensive histone methylation remodeling occurred for a subset of genomic loci in reciprocal F1 hybrids of *Oryza sativa* (rice) cultivars Nipponbare and 93-11, representing the two subspecies japonica and indica. Globally, the allele modification-altered loci in leaf or root of the reciprocal F1 hybrids involved ca. 12% to > 43% or more of the genomic regions carrying either of two typical histone methylation markers, H3K4me3 (>21 000 genomic regions) and H3K27me3 (>11 000 genomic regions). Nevertheless, at the total modification level, the majority (from ca. 43% to >90%) of the modification-altered alleles lay within the range of parental additivity in the hybrids because of concerted alteration in opposite directions, consistent with an overall attenuation of allelic differences in the modifications. Importantly, of the genomic regions that did show non-additivity in total modification level by either marker in the two tissues of hybrids, >80% manifested transgressivity, which involved genes enriched in specific functional categories. Extensive allele-level alteration of H3K4me3 alone was positively correlated with genome-wide changes in allele-level gene expression, whereas at the total level, both H3K4me3 and H3K27me3 remodeling, although affecting just a small number of genes, contributes to the overall non-additive gene expression to variable extents, depending on tissue/marker combinations. Our results emphasize the importance of allele-level analysis in hybrids to assess the remodeling of epigenetic modifications and their relation to changes in gene expression.

来源: PLANT JOURNAL

发布日期: 2019-02-13

全文链接:

<http://agri.ckcest.cn/file1/M00/0E/80/Csgk0F1nmLyA00f0AB7IW9NIwcs975.pdf>