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杂交水稻专题

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▶ 前沿资讯

1. 科研人员发现水稻生物钟调控非生物胁迫适应性的新机制

简介: 中科院植物所王雷研究组发现生物钟核心组分OsCCA1 (*Oryza sativa* CIRCADIAN CLOCK ASSOCIATED 1) 正向调控水稻对高盐、干旱以及渗透胁迫的适应性, 其功能缺失的突变体导致对多种逆境胁迫更加敏感。此外, 高盐环境直接导致oscca1突变体的产量严重降低。通过DAP-seq结合RNA-seq的联合分析, 共筛选出692个OsCCA1的直接靶基因。深入解析发现OsCCA1在高盐环境中参与ABA信号通路, 调控着多个A类OsPP2Cs成员以及下游bZIP类转录因子如OsbZIP46的表达, 进而激活它们在多种逆境中高水平的转录。因此, oscca1突变体中诸多胁迫应答相关基因的表达不能有效地被激活, 导致水稻对胁迫环境更加敏感。另外, oscca1材料对外源施加的脱落酸更敏感, 低浓度条件下株高受到显著的抑制作用, 高浓度直接导致幼苗存活率明显降低。该结果进一步说明OsCCA1直接参与脱落酸信号通路, 当其突变以后会导致脱落酸信号传导受阻, 使得水稻对脱落酸更加敏感。该研究系统解析了生物钟核心组分OsCCA1协调脱落酸信号网络增强水稻对多种非生物逆境胁迫适应的分子机制。该研究进一步揭示了植物生物钟系统调控非生物胁迫适应性的分子网络, 为生物钟调控水稻耐逆性提供了新的理论依据, 为研发具有多重抗逆性的水稻品种提供了设计育种的靶点和优质遗传资源。

来源: 中国科学院植物研究所

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<http://agri.ckcest.cn/file1/M00/03/31/Csgk0YbTdYGAHE5RAALQ2DHMye0899.pdf>

2. 专家团队揭示水稻PRC2复合体维持茎尖分生组织活性的表观遗传机制

简介: 近日, 作物遗传改良国家重点实验室和湖北洪山实验室周道绣和赵毓教授课题组在The Plant Cell 杂志上在线发表题为“A coiled-coil protein associates Polycomb Repressive Complex2 (PRC2) with KNOX/BELL transcription factors to maintain H3K27me3 and gene repression in shoot apex”的研究论文, 揭示了PRC2相关蛋白PACP通过调控组蛋白H3K27me3修饰参与水稻茎尖分生组织(SAM)活性维持的表观遗传机制。组蛋白H3第27位赖氨酸三甲基化(H3K27me3)是一类维持基因和基因组沉默的关键组蛋白修饰, 在动植物生长发育和环境适应性应答中发挥着重要的调控作用。H3K27me3修饰由多梳蛋白复合物2 (PRC2) 催化建立和维持, 组蛋白去甲基化酶负责去除(Li et al., The Plant Cell, 2013)。植物茎顶端分生组织发育是地上部分所有器官的来源, 是决定农作物地上部分的生物量、产量和品质的重要因素。本课题组前期研究发现, PRC2及其参与催化的H3K27me3修饰在水稻顶端分生组织活性的维持和侧生器官建成过程中发挥着重要功能(Liu et al., The Plant Cell. 2015; Cheng et al., Nucleic Acids Research, 2018), 但其具体调控机制尚不清楚。本项目从水稻PRC2特异的靶向招募机制入手, 以鉴定和研究水稻PRC2非核心组分为切入点, 对PRC2及H3K27me3参与SAM发育的调控机制进行了解析。本研究利用免疫沉淀偶联质谱(IP-MS)和酵母双杂交等方法鉴定到一类新的PRC2相关因子, 命名为PACP (PRC2 Associated Coiled-coil Protein), 该蛋白C端含有特殊的Coiled-coil结构域。研究发现PACP蛋白除了能够形成同源二聚体外, 还可以与PRC2核心组分以及SAM发育的重要调控因子KNOX/BELL相互作用。PACP

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蛋白在植物进化中极其保守，最早在轮藻中出现，这表明该蛋白可能在植物的形态建成中发挥重要的功能。PACP与PRC2核心组分功能缺失的水稻植株都表现为植株矮化、分蘖增多和早花等表型。细胞学进一步分析发现这些突变体的顶端分生组织都变小；突变体转录组数据分析发现大量侧生器官发育相关的基因在SAM中异位高表达。同时，PACP功能缺失导致了水稻基因组中H3K27me3修饰以及PRC2结合水平都显著降低，这些结果表明PACP维持SAM活性依赖于PRC2及H3K27me3对SAM中促进侧生器官发育基因的抑制。染色质免疫沉淀数据分析表明PACP与PRC2在水稻全基因组的分布模式相似，它们直接调控的下游基因大部分都可以被KNOX蛋白OSH1结合。该研究解析了PACP参与PRC2的募集机制以及在招募位点通过H3K27me3修饰维持顶端分生组织活性的机制，建立了染色质修饰、SAM活性以及基因表达调控之间的直接联系，为PRC2介导的水稻顶端分生组织发育调控机制的阐明奠定了基础。

来源：华中农业大学

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► 学术文献

1. Concurrent Disruption of Genetic Interference and Increase of Genetic Recombination Frequency in Hybrid Rice Using CRISPR_Cas9 (CRISPR_Cas9对杂交水稻遗传干扰的同时破坏和遗传重组频率的提高)

简介: Manipulation of the distribution and frequency of meiotic recombination events to increase genetic diversity and disrupting genetic interference are long-standing goals in crop breeding. However, attenuation of genetic interference is usually accompanied by a reduction in recombination frequency and subsequent loss of plant fertility. In the present study, we generated null mutants of the ZEP1 gene, which encodes the central component of the meiotic synaptonemal complex (SC), in a hybrid rice using CRISPR/Cas9. The null mutants exhibited absolute male sterility but maintained nearly unaffected female fertility. By pollinating the zep1 null mutants with pollen from indica rice variety 93-11, we successfully conducted genetic analysis and found that genetic recombination frequency was greatly increased and genetic interference was completely eliminated in the absence of ZEP1. The findings provided direct evidence to support the controversial hypothesis that SC is involved in mediating interference. Additionally, the remained female fertility of the null mutants makes it possible to break linkage drag. Our study provides a potential approach to increase genetic diversity and fully eliminate genetic interference in rice breeding.

来源: FRONTIERS IN PLANT SCIENCE

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<http://agri.ckcest.cn/file1/M00/03/31/Csgk0YbTcIaABKPAAFzfM6LYm7Q075.pdf>

2. Transcriptomic Analysis of Short-Term Salt-Stress Response in Mega Hybrid Rice Seedlings (超级杂交水稻幼苗短期盐胁迫反应的转录组学分析)

简介: Salinity is a major abiotic stressor that leads to productivity losses in rice (*Oryza sativa* L.). In this study, transcriptome profiling and heterosis-related genes were analyzed by ribonucleic acid sequencing (RNA-Seq) in seedlings of a mega rice hybrid, Liang-You-Pei-Jiu (LYP9), and its two parents 9311 and Pei-ai64s (PA64s), under control and two different salinity levels, where we found 8292, 8037, and 631 salt-induced differentially expressed genes (DEGs), respectively. Heterosis-related DEGs were obtained higher after 14 days of salt treatment than after 7 days. There were 631 and 4237 salt-induced DEGs related to heterosis under 7-day and 14-day salt stresses, respectively. Gene functional classification showed the expression of genes involved in photosynthesis activity after 7-day stress treatment, and in metabolic and catabolic activity after 14 days. In addition, we correlated the concurrence of an expression of DEGs for the bHLH transcription factor and a shoot length/salinity-related quantitative trait locus qSL7 that we fine-mapped previously, providing a confirmed case of heterosis-related genes. This experiment reveals the transcriptomic divergence of the rice F1 hybrid and its parental lines under control and salt stress state, and enlightens about the significant molecular mechanisms developed over time in response to salt stress.

来源: AGRONOMY-BASEL

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http://agri.ckcest.cn/file1/M00/10/03/Csgk0GJ8v0WAJa_QACY-m-3tXKA280.pdf

3. Compositional equivalence assessment of insect resistant genetically modified rice using multiple statistical analyses (基于多重统计分析的抗虫转基因水稻成分等效性评估)

简介: The safety of transgenic Bt rice containing bacteria-derived mCry1Ac gene from *Bacillus thuringiensis* (Bt) was assessed by conducting field trials at two locations for two consecutive years in South Korea, using the near-isogenic line comparator rice cultivar ('Ilmi', non-Bt rice) and four commercial cultivars as references. Compositional analyses included measurement of proximates, minerals, amino acids, fatty acids, vitamins, and antinutrients. Significant differences between Bt rice and non-Bt rice were detected; however, all differences were within the reference range. The statistical analyses, including analysis of % variability, analysis of similarities (ANOISM), similarity percentage (SIMPER) analysis, and permutational multivariate analysis of variance (PERMANOVA) were performed to study factors contributing to compositional variability. The multivariate analyses revealed that environmental factors more influenced rice components' variability than by genetic factors. This approach was shown to be a powerful method to provide meaningful evaluations between Bt rice and its comparators. In this study, Bt rice was proved to be compositionally equivalent to conventional rice varieties through multiple statistical methods.

来源: GM CROPS & FOOD-BIOTECHNOLOGY IN AGRICULTURE AND THE FOOD

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