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杂交水稻专题

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▶ 前沿资讯

1. 水稻生物钟调控非生物胁迫适应性的新机制

简介: 中国科学院植物研究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。研究通过DAP-seq结合RNA-seq的联合分析, 共筛选出692个OsCCA1的直接靶基因。研究发现, 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。该成果进一步说明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, 并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

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<http://agri.ckcest.cn/file1/M00/03/30/Csgk0YbKRhmACnJhAANuJKRZyMI981.pdf>

2. 揭示通过打破性状连锁突破水稻产量瓶颈的新机制

简介: 近日, 中国科学院遗传与发育生物学研究所李家洋团队揭示了水稻产量核心要素穗重和穗数之间相互制约的分子机制, 旨在通过打破产量性状之间的负相关培育出株型进一步改良的水稻品种。本项研究为打破表型间制约关系提供了一种可行方法, 为突破水稻产量瓶颈提供了新的遗传资源与研究思路, 是该领域的一项重要进展。未来对作物核心基因顺式调控区的系统功能挖掘, 有望为突破现有作物育种瓶颈提供新的分子机制与遗传资源。这一研究成果于2022年4月21日在国际学术期刊《自然-生物技术》发表。不同农艺性状之间常常存在一种此消彼长的权衡效应 (trait trade-off), 例如植物高产与抗病、高产与高品质、产量因素间的负相关性等, 使得这些优异性状难以兼得, 也使得作物育种难以突破瓶颈。这种权衡效应可能由连锁累赘 (linkage drag) 或基因多效性 (gene pleiotropy) 引起。连锁累赘可以通过基因的精细定位和交换重组来解决, 然而, 基因多效性引起的权衡效应仍然没有有效方法进行解除。此外, 目前的基因功能研究主要关注了其产生的优异表型, 而忽略了其同时带来的负效应, 使得育种实践中发现这种负效应难以破除, 造成只有少量基因能够得到很好利用。如何解决基因多效性造成表型间的权衡效应, 对于突破现有育种瓶颈有重要科学意义。为突破IPA1多效性造成的穗部和分蘖的=制约关系, 在此项最新的研究中, 研究团队提出了通过改造IPA1的顺式调控区, 分别调控其在幼穗、茎基部等各组织中的表达水平, 实现不同表型的特异性调控, 从而打破产量因素之间负效应的策略。但由于之前技术方法的制约, 对作物顺式调控区功能的研究极为缺乏, 而对IPA1顺式调控区的功能研究也知之甚少。该团队使用平铺删除 (tiling deletion) 的方法, 通过多靶点CRISPR/Cas9对IPA1的顺式调控区

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进行系统性高覆盖度的片段删除，创制出大量IPA1顺式调控区平铺删除的基因编辑材料，并从中发掘出了一个可以同时提高分蘖数和穗粒数的编辑材料IPA1-Pro10及其对应的54bp关键顺式作用元件。IPA1-Pro10具有穗重和穗数同时增加、株高变高、茎秆和根系粗壮的表型。经田间小区测产鉴定，IPA1-Pro10与对照品种中花11相比能够增产15.9%，大大提高了水稻产量。随后，该研究进一步阐明了IPA1顺式调控区调控穗部表型的分子机制，发现驯化关键转录因子An-1能通过结合54bp关键顺式作用元件中的一个GCGCGTGT基序特异调控IPA1在幼穗的表达水平，进而特异调控穗部表型。此研究通过平铺删除策略，通过编辑筛选水稻关键基因的顺式调控区成功实现了水稻产量关键要素间负相关性的解除，为通过创制全新遗传资源打破水稻产量瓶颈提供了有效策略。

来源：中国科学院遗传与发育生物学研究所

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<http://agri.ckcest.cn/file1/M00/10/02/Csgk0GJzmHaAYU13AAKmdNxX2eY753.pdf>

3. 专家揭示敲除OsNRAMP5对镉胁迫的响应机制

简介：近日，湖南杂交水稻研究中心赵炳然研究员团队在国际知名期刊Science of the Total Environment（环境科学一区，TOP期刊）发表了题为“Knockout of OsNRAMP5 enhances rice tolerance to cadmium toxicity in response to varying external cadmium concentrations via distinct mechanisms”的研究论文，阐明了敲除OsNRAMP5对不同浓度镉胁迫的响应机制。该研究通过镉浓度梯度水培、镉吸收动力学分析和田间小区试验，发现敲除OsNRAMP5可降低水稻镉吸收，但同时会增加镉从根部向地上部的运输；随着生长介质中镉浓度的升高，敲除OsNRAMP5降低镉吸收的效应减弱，而其促进根部镉向地上部运输的效应不变。在一定程度镉胁迫条件下，敲除OsNRAMP5降低镉吸收的效应大于其促进根系镉向地上部运输的效应，从而减少了地上部的镉积累，缓解或解除了镉对生长发育的抑制作用，增强了敲除株系的镉耐受性。但当环境镉浓度继续增高，敲除OsNRAMP5促进根系镉向地上部运输的效应可抵消甚至超过其降低镉吸收的效应，与野生型植株相比，敲除株系地上部的镉含量不变甚至更高，但镉耐受性增强；通过离子组检测、矿质元素缺乏响应基因和金属转运体编码基因的表达分析，发现在高镉胁迫下，野生型植株出现多种矿质元素的缺乏，敲除OsNRAMP5可部分或完全回补矿质元素的缺乏，从而间接提高镉耐受性。此外，该研究还发现水稻拮抗吸收镉、锰的效应主要由OsNRAMP5引起；不同浓度的镉胁迫下，敲除OsNRAMP5均可促使地上部的锰在营养生长期优先分配到幼叶，在生殖生长期优先分配到籽粒。综上所述，随着环境镉浓度的升高，OsNRAMP5转运蛋白对水稻镉吸收的贡献呈降低趋势；从低镉到高镉环境，敲除OsNRAMP5对地上部镉积累的效应受环境镉浓度影响，以不同的生理机制增强水稻的镉耐受性，因此不能通过OsNRAMP5的镉耐受表型判断其茎叶和籽粒的镉积累变化；而OsNRAMP5敲除导致地上部的锰优先分配到幼叶或籽粒，可增强OsNRAMP5对环境的适应性。该研究为OsNRAMP5在镉低积累水稻育种中的应用提供了理论参考。

来源：湖南省农业科学院

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学术文献

1. Molecular Genetic Diversity and Combining Ability for Some Physiological and Agronomic Traits in Rice under Well-Watered and Water-Deficit Conditions (水分充足和水分亏缺条件下水稻某些生理和农艺性状的分子遗传多样性和配合力)

简介: Water deficit is a pivotal abiotic stress that detrimentally constrains rice growth and production. Thereupon, the development of high-yielding and drought-tolerant rice genotypes is imperative in order to sustain rice production and ensure global food security. The present study aimed to evaluate diverse exotic and local parental rice genotypes and their corresponding cross combinations under water-deficit versus well-watered conditions, determining general and specific combining ability effects, heterosis, and the gene action controlling important traits through half-diallel analysis. In addition, the research aimed to assess parental genetic distance (GD) employing simple sequence repeat (SSR) markers, and to determine its association with hybrid performance, heterosis, and specific combining ability (SCA) effects. Six diverse rice genotypes (exotic and local) and their 15 F-1 hybrids were assessed for two years under water-deficit and well-watered conditions. The results revealed that water-deficit stress substantially declined days to heading, plant height, chlorophyll content, relative water content, grain yield, and yield attributes. Contrarily, leaf rolling and the sterility percentage were considerably increased compared to well-watered conditions. Genotypes differed significantly for all the studied characteristics under water-deficit and well-watered conditions. Both additive and non-additive gene actions were involved in governing the inheritance of all the studied traits; however, additive gene action was predominant for most traits. The parental genotypes P-1 and P-2 were identified as excellent combiners for earliness and the breeding of short stature genotypes. Moreover, P-3, P-4, and P-6 were identified as excellent combiners to increase grain yield and its attributes under water-deficit conditions. The hybrid combinations; P-1 x P-4, P-2 x P-5, P-3 x P-4, and P-4 x P-6 were found to be good specific combiners for grain yield and its contributed traits under water-deficit conditions. The parental genetic distance (GD) ranged from 0.38 to 0.89, with an average of 0.70. It showed lower association with hybrid performance, heterosis, and combining ability effects for all the studied traits. Nevertheless, SCA revealed a significant association with hybrid performance and heterosis, which suggests that SCA is a good predictor for hybrid performance and heterosis under water-deficit conditions. Strong positive relationships were identified between grain yield and each of relative water content, chlorophyll content, number of panicles/plant, number of filled grains/panicle, and 1000-grain weight. This suggests that these traits could be exploited as important indirect selection criteria for improving rice grain yield under water-deficit conditions.

来源: PLANTS-BASEL

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<http://agri.ckcest.cn/file1/M00/03/30/Csgk0YbKSG6AG-1bADWqu7X9FdQ345.pdf>

2. Genome-wide Association Study and Genomic Prediction for Yield and Grain Quality Traits of Hybrid Rice (杂交水稻产量和品质性状的全基因组关联研究及基因组预测)

简介: Genomic selection is an efficient tool for breeding selection, especially for quantitative traits controlled by multiples genes with low heritability. To validate the application of genomic selection in hybrid rice breeding, the yield and grain quality traits of 404 hybrid rice breeding lines were investigated, and the same accessions were genotyped by using a 56 K SNP chip. There were wide variances among the tested accessions for all the measured traits, and most of the traits were correlated. A total of 67 significant loci were identified for the yield-related traits, and 123 significant loci were identified for the grain quality traits by GWAS. Two of these loci associated with increasing grain yield but decreasing grain quality. The GEBVs of all the yield and grain quality traits were calculated by using 15 different prediction algorithms. The plant height, panicle length, thousand grain weight, grain length and width ratio, amylose content, and alkali value have higher predictability than other traits. However, the predictive accuracy of different GS models is different for different traits. This study provided useful information for genomic selection of specific trait using proper markers and prediction models.

来源: MOLECULAR BREEDING

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