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杂交水稻专题

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▶ 前沿资讯

1. 揭示新的脂肪酸水解酶协同调控水稻耐盐性与开花时间的分子机制

简介: 在全球气候变化背景下, 日趋加剧的土壤盐碱化制约农作物的生产。土壤中过多的盐分造成植物生长受限, 并消耗大量的能量以适应渗透调节, 最终导致产量损失。因而在遭受到环境胁迫时, 植物演化出多种进化策略以整合外源盐信号和内源发育信号, 从而平衡生长发育和盐胁迫耐受性。其中, 改变开花时间是植物应对环境压力或刺激所采取的积极手段之一。尽管如此, 鉴于不同性状之间的复杂关联, 植物在盐胁迫响应过程中如何协同调控盐胁迫信号并传递到开花途径的作用机制尚不清楚。此外, 尽管已有研究通过各种方法鉴定和克隆了一些水稻耐盐相关基因, 但关于水稻抵抗盐胁迫的机制知之甚少。因此, 深入挖掘水稻耐盐基因资源并解析相关调控机制, 有助于剖析植物和环境的互作, 且在生产应用上亦有重要价值。10月27日, *Molecular Plant* 在线发表了中国科学院分子植物科学卓越创新中心研究员林鸿宣研究组撰写的题为 *An α/β hydrolase family member negatively regulates salt tolerance but promotes flowering through three distinct functions in rice* 的研究论文。该研究分离并克隆了来自非洲稻自然变异位点的一个关键耐盐调控因子, 并揭示了水稻耐盐性和抽穗期协同调控的新机制, 为作物遗传改良及分子设计育种提供了新的基因资源和理论基础。研究组运用正向遗传学方法在非洲稻遗传资源中筛选、鉴定并定位克隆到一个新的控制水稻耐盐性状的关键QTL基因STH1, 其编码一个 α/β 折叠结构域的水解酶, 来源于非洲稻变异形式的STH1由于一个SNP的突变导致其翻译发生提前终止并丧失酶活。转基因遗传实验表明, STH1功能缺失与过量表达株系分别表现出盐胁迫耐受性的增加和降低, 表明该基因是水稻耐盐性状的负调控因子。研究发现, STH1定位于细胞核和细胞质中, 在叶片组织中呈现特异性高表达, 并受盐处理下调其表达, 参与多条盐胁迫响应途径。研究借助广泛靶向代谢组和体外酶活实验, 证实了STH1行使脂肪酸水解酶的功能参与植株体内脂肪酸代谢, 进而影响盐胁迫下质膜组分的完整性和流动性。此外, 研究还发现STH1能够与F box蛋白D3以及耐盐关键调控因子OsHAL3发生两两相互作用, 并在细胞核中形成蛋白复合体, 从而加强D3介导的OsHAL3泛素化降解, 影响其蛋白含量和稳定性。在水稻光周期介导的开花调控网络中, STH1同时扮演锌指蛋白Hd1转录共激活因子的角色, 调节成花素基因Hd3a的表达水平, 影响水稻的抽穗期和产量。导入非洲稻等位形式的STH1基因位点延迟水稻的抽穗时间, 并能够明显提高水稻在正常田间环境和盐胁迫条件下的高产稳产(在高盐胁迫下使水稻产量比对照提高67.14%), 因而在生产上具备潜在的应用价值。该研究阐释了水稻整合耐盐与开花性状的遗传和分子机理, 拓宽了科学家对植物耐盐机制的认识, 并为水稻高产、耐盐育种提供了重要的遗传资源。

来源: 中国科学院

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全文链接:

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<http://agri.ckcest.cn/file1/M00/10/14/Csgk0GNjZhyATohDAAYUZxwVStk987.pdf>

2. 教授团队在香稻施肥调控研究方面取得新进展

简介: 围绕施肥技术如何影响香稻米品质及其生理基础, 研究探讨侧深施肥技术对香稻整精米产量、香气特征物质2-乙酰基-1-吡咯啉(简称2AP)含量和抗氧化生理指标的影响。研究探明了香稻高效益和高品质的施肥方案, 试验中的侧深施肥方案(T3)增加了整精米产量, 提高了稻米外观品质; 提高了2AP积累, 增加了脯氨酸和 Δ^1 -吡咯啉-5-羧酸的积累, 提高了脯氨酸脱氢酶活性; 影响了香稻叶片的抗氧化响应。

来源: 华南农业大学

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全文链接:

<http://agri.ckcest.cn/file1/M00/03/42/Csgk0Ye6PbKAeEzHAAGB1Pd6nJM152.pdf>

► 学术文献

1. Polyploidization Increases the Lipid Content and Improves the Nutritional Quality of Rice (多倍体化提高稻米的脂肪含量并改善营养品质)

简介: Plant polyploidization is frequently associated with changes in nutrient contents. However, the possible contribution of metabolites to this change has not been investigated by characterizing the metabolite contents of diploid and tetraploid forms of rice (*Oryza sativa* L.). We compared the metabolites of a group of diploid-tetraploid japonica brown rice and a group of diploid-tetraploid indica brown rice based on liquid chromatography-tandem mass spectrometry. In total, 401 metabolites were identified; of these, between the two diploid-tetraploid groups, 180 showed opposite expression trends, but 221 showed the same trends (147 higher abundance vs. 74 lower abundance). Hierarchical cluster analysis of differential metabolites between diploid and tetraploid species showed a clear grouping pattern, in which the expression abundance of lipids, amino acids and derivatives, and phenolic acids increased in tetraploids. Further analysis revealed that the lipids in tetraploid rice increased significantly, especially unsaturated fatty acids and phospholipids. This study provides further basis for understanding the changes in rice nutritional quality following polyploidization and may serve as a new theoretical reference for breeding eutrophic or functional rice varieties via polyploidization.

来源: PLANTS-BASEL

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全文链接:

http://agri.ckcest.cn/file1/M00/03/42/Csgk0Ye6G9CAMUhfAEhxPSBJd_w925.pdf

2. Development and regeneration of wheat-rice hybrid zygotes produced by in vitro fertilization system (小麦-水稻杂交合子的体外

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受精发育与再生)

简介: Hybridization plays a decisive role in the evolution and diversification of angiosperms. However, the mechanisms of wide hybridization remain open because pre- and post-fertilization barriers limit the production and development of inter-subfamily/intergeneric zygotes, respectively. We examined hybridization between wheat and rice using an in vitro fertilization (IVF) system to bypass these barriers. Several gamete combinations of allopolyploid wheat-rice hybrid zygotes were successfully produced, and the developmental profiles of hybrid zygotes were analyzed. Hybrid zygotes derived from one rice egg cell and one wheat sperm cell ceased at the multicellular embryo-like structure stage. This developmental barrier was overcome by adding one wheat egg cell to the wheat-rice hybrid zygote. In the reciprocal combination, one wheat egg and one rice sperm cell, the resulting hybrid zygotes failed to divide. However, doubling the dosage of rice sperm cell allowed the hybrid zygotes to develop into plantlets. Rice chromosomes appeared to be progressively eliminated during the early developmental stage of these hybrid embryos, and c. 20% of regenerated plants showed abnormal morphology. These results suggest that hybrid breakdown can be overcome through optimization of gamete combinations, and the present hybrid will provide a new horizon for utilization of inter-subfamily genetic resources.

来源: NEW PHYTOLOGIST

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全文链接:

<http://agri.ckcest.cn/file1/M00/10/14/Csgk0GNjgSuAZdgXACpVi-sEHg4031.pdf>

3. Overexpression of OsLCT2, a Low-Affinity Cation Transporter Gene, Reduces Cadmium Accumulation in Shoots and Grains of Rice (低亲和力阳离子转运蛋白基因OsLCT2的过度表达降低了水稻茎和籽粒中镉的积累)

简介: Cadmium (Cd)-contaminated rice is a serious issue affecting food safety. Understanding the molecular regulatory mechanisms of Cd accumulation in rice grains is crucial to minimizing Cd concentrations in grains. We identified a member of the low-affinity cation transporter family, OsLCT2 in rice. It was a membrane protein. OsLCT2 was expressed in all tissues of the elongation and maturation zones in roots, with the strongest expression in pericycle and stele cells adjacent to the xylem. When grown in Cd-contaminated paddy soils, rice plants overexpressing OsLCT2 significantly reduced Cd concentrations in the straw and grains. Hydroponic experiment demonstrated its overexpression decreased the rate of Cd translocation from roots to shoots, and reduced Cd concentrations in xylem sap and in shoots of rice. Moreover, its overexpression increased Zn concentrations in roots by up-regulating the expression of OsZIP9, a gene responsible for Zn uptake. Overexpression of OsLCT2 reduces Cd accumulation in rice shoots and grains by limiting the amounts of Cd loaded into the xylem and restricting Cd translocation from roots to shoots of rice. Thus, OsLCT2 is a promising genetic resource to be engineered to reduce Cd accumulation in rice grains.

来源: RICE

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