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## 杂交水稻专题

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## ▶ 前沿资讯

### 1. 专家团队解析水稻盐胁迫响应调控新机制

**简介:** 盐胁迫是限制植物生长和作物产量的主要非生物胁迫之一，全球盐渍土总面积约8亿公顷，危害粮食安全。水稻是我国重要的粮食作物，对盐胁迫敏感，解析水稻盐胁迫响应的分子机制，对于改良水稻耐盐性具有重要的科学意义。IPA1 (Ideal Plant Architecture 1) 是此前中国科学院遗传与发育生物学研究所李家洋团队鉴定到的一个水稻株型调控的主效基因 (Jiao et al., 2010)，因其在调控水稻分蘖和籽粒大小方面的重要作用，被广泛用于高产水稻育种，但其参与水稻盐胁迫响应的机制并不清楚。近日，该团队通过对IPA1功能缺失突变体ipa1-10和功能获得型ipa1-3D的幼苗进行盐处理，发现IPA1负调控水稻的耐盐性，盐胁迫处理30分钟后IPA1的磷酸化水平升高但蛋白水平降低。为探究IPA1的上游调控因子，研究利用质谱技术系统分析了盐胁迫条件下IPA1的互作蛋白，鉴定到丝裂原活化蛋白激酶 (MAPKs/MPKs) 家族成员OsMPK4。进一步的实验表明，OsMPK4能够与IPA1发生蛋白相互作用，且在盐胁迫条件下，OsMPK4被激活并磷酸化IPA1的Thr180位点，从而促进IPA1的泛素化降解，降低IPA1的蛋白水平并最终提高水稻耐盐性。遗传结果表明，OsMPK4正调控水稻耐盐性并与IPA1在耐盐性调控上位于同一通路中。该项研究阐明了MPK4-IPA1模块调控水稻盐胁迫响应的分子机制，揭示了植物生长和胁迫之间的信号交互，为创制高产耐盐水稻品种提供了新的分子机制与遗传资源。7月5日，相关研究成果以OsMPK4 promotes phosphorylation and degradation of IPA1 in response to salt stress to confer salt tolerance in rice为题，在线发表在Journal of Genetics and Genomics (DOI: 10.1016/j.jgg.2022.06.009) 上。研究工作得到国家自然科学基金、中科院战略先导科技专项、国家水稻产业技术体系等的支持。

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### 2. 科研人员揭示水稻花粉育性的新调控因子

**简介:** 作物花粉不育种质材料是杂种优势利用的基础。花粉有结构复杂的细胞壁（主要由孢粉素组成，可分为花粉外壁与内壁），花粉壁赋予了花粉抗生物和非生物逆境的能力，也参与了花粉与柱头细胞的互作与信息交流，是决定花粉活性和功能的重要因素。目前已发现多个影响孢粉素前体生物合成的基因，但所知道的调控因子非常有限。中科院植物所王台研究组与合作者发现水稻花粉表达的甲基化CpG位点结合蛋白家族成员PEM1是调控花粉外壁形成的重要调控因子。该基因功能缺失导致花粉外壁无定型加厚，乌氏体异常，进而导致花粉降解。进一步研究发现，该基因功能缺失引起转录抑制、信号转导和细胞壁代谢相关基因表达水平的显著增加，以及孢粉素前体角质和蜡质组含量的显著增加，这些结果表明PEM1通过负调控一组基因的表达来调节花粉外壁的发育，可能是花粉发育的主调控因子。序列分析显示PEM1同源序列在单子叶植物中是保守的，暗示PEM1同源基因在其他单子叶植物花粉发育过程中有类似的功能。该研究揭示了一个新的水稻花粉育性的主调控因子，为深入解析花粉外壁发育的调控网络提供了新的切入点，也为植物雄性育性的遗传操作提供了新的基因元件。

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## ➤ 学术文献

### 1. CRISPR/Cas9-Induced Mutagenesis of TMS5 Confers Thermosensitive Genic Male Sterility by Influencing Protein Expression in Rice (*Oryza sativa* L.) (CRISPR/Cas9诱导的TMS5突变通过影响水稻 (*Oryza sativa* L.) 中的蛋白质表达而赋予热敏核雄性不育性)

简介: The development of thermosensitive genic male sterile (TGMS) lines is the key to breeding two-line hybrid rice, which has been widely applied in China to increase grain yield. CRISPR/Cas9 has been widely used in genome editing to create novel mutants in rice. In the present study, a super grain quality line, GXU 47, was used to generate a new TGMS line with specific mutations in a major TGMS gene *tms5* generated with CRISPR/Cas9-mediated genome editing in order to improve the rice quality of two-line hybrids. A mutagenesis efficiency level of 75% was achieved, and three homozygous T-DNA-free mutant lines were screened out. The mutants exhibited excellent thermosensitive male fertility transformation characteristics with complete male sterility at  $\geq 24\text{ }^{\circ}\text{C}$  and desirable male fertility at around  $21\text{ }^{\circ}\text{C}$ . Proteomic analysis based on isobaric tags for relative and absolute quantification (iTRAQ) was performed to unveil the subsequent proteomic changes. A total of 192 differentially expressed proteins (DEPs), including 35 upregulated and 157 downregulated, were found. Gene ontology (GO) analysis revealed that the DEPs were involved in a single-organism biosynthetic process, a single-organism metabolic process, oxidoreductase activity, and catalytic activity. Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis showed that the DEPs were involved in ubiquinone and other terpenoid quinone biosynthesis, the biosynthesis of secondary metabolites, metabolic pathways, and phenylpropanoid biosynthesis. Our study shows that high mutation efficiency was achieved in both target sites, and T-DNA-free mutant lines were obtained in the T1 generation. The present study results prove that it is feasible and efficient to generate an excellent mutant line with CRISPR/Cas9, which provides a novel molecular mechanism of male sterility caused by the mutation of *tms5*.

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### 2. Population Dynamics of Wide Compatibility System and Evaluation of Intersubspecific Hybrids by *indica-japonica*

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## Hybridization in Rice (水稻广亲和系统的种群动态及籼粳杂交亚种间杂种的评价)

简介: The exploitation of heterosis through intersubspecific hybridisation between indica and japonica has been a major breeding target in rice, but is marred by the cross incompatibility between the genomes. Wide compatibility (WC) is a triallelic system at the S5 locus on chromosome 6 that ensures the specificity of hybridisation within and between indica and japonica. The S5n allele that favours intercrossing is sparsely distributed in the rice gene pool and therefore warrants identification of diverse WC sources to develop superior intersubspecific hybrids. In this study, we have identified several novel WC sources through the marker-assisted screening of a large set of 950 rice genotypes. Seventeen percent of the genotypes carried S5n, which fell into two subpopulations. The WC genotypes showed wide phenotypic and genotypic variability, including both indica and japonica lines. Based on phenotypic performance, the WC varieties were grouped into three clusters. A subset of 41 WC varieties was used to develop 164 hybrids, of which WC/japonica hybrids showed relative superiority over WC/indica hybrids. The multilocation evaluation of hybrids indicated that hybrids derived from WC varieties, such as IRG137, IRG143, OYR128, and IRGC10658, were higher yielding across all the three different locations. Most of the hybrids showed the stability of performance across locations. The identified diverse set of wide compatible varieties (WCVs) can be used in the development of intersubspecific hybrids and also for parental line development in hybrid rice breeding.

来源: Plants

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<http://agri.ckcest.cn/file1/M00/10/0C/Csgk0GLraiQAWq3aACS8Gof-5vU462.pdf>

## 3. Identification of Male and Female Parents for Hybrid Rice Seed Production Using UAV-Based Multispectral Imagery (基于无人机的多光谱图像识别杂交水稻制种的父本和母本)

简介: Identifying and extracting male and female parent of hybrid rice and then accurately judging the spikelet flowering of male parents is the basis of hybrid rice pollination. Currently, male parent flowering information extraction for hybrid rice is basically obtained by manual recognition. In this study, remote sensing images of parental rice fields were obtained with a multispectral camera carried by a UAV (Unmanned Aerial Vehicle). Six kinds of visible light vegetation indices and four kinds of multispectral vegetation indices, together with two classification methods, pixel-based supervised classification and sample-based object-oriented classification, were applied to identify the male and female parents of hybrid rice, after which the accuracies of the methods were compared. The results showed that the visible vegetation index had a better effect in pixel-based supervised classification. The kappa coefficient of ExGR (Excess Green minus Excess Red index) classification was 0.9256 and the total accuracy was 0.9552. The extraction accuracy was higher than that of the other vegetation indices and object-oriented classification. In pixel-based supervised classification, the maximum likelihood method achieved the highest identification accuracy and shortest

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calculation time. Taking the remote sensing images obtained with a UAV as a data source, maximum likelihood supervised classification based on ExGR index can more effectively and quickly identify the field information of male and female parents of hybrid rice so as to provide a reference for determining optimal pollination timing for hybrid rice in large-scale seed production farms.

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