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## 杂交水稻专题

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对水稻多重驯化事件的影响

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## ▶ 前沿资讯

### 1. 专家团队在水稻抗旱性研究中取得新进展

**简介：**近日，上海农业生物基因中心科研人员在植物学国际知名期刊Plant Biotechnology Journal上在线发表了题为“Ubiquitin Ligase OsRINGzf1 Regulates Drought Resistance by Controlling the Turnover of OsPIP2;1”的研究论文。研究团队在精细定位的抗旱QTL区间内发现了水稻抗旱新基因OsRINGzf1。过表达OsRINGzf1明显增强了水稻苗期对PEG模拟干旱胁迫及盐胁迫的抗性。与之相反，OsRINGzf1的基因敲除和RNAi植株对于旱较为敏感。在干旱条件下，超表达该基因的水稻产量比对照组高10%以上，从而减少了干旱带来的产量损失。通过分裂泛素膜酵母双杂交系统筛选及酵母双杂交验证发现OsRINGzf1可与OsPIP1;1, OsPIP1;3, OsPIP2;1, OsPIP2;2, OsSIP1;1以及一个预测的TIP等6个水通道蛋白互作。水通道蛋白参与了水分的跨细胞运输，与植物抗旱性相关，但水稻中水通道蛋白的降解调控机制尚不明确。研究人员通过对OsRINGzf1与OsPIP2;1互作的进一步研究揭示了OsRINGzf1通过介导水通道蛋白的泛素化修饰与降解。与野生型相比，OsRINGzf1过表达株系中OsPIP2;1蛋白含量降低，OsRINGzf1过表达株系和OsPIP2;1基因敲除突变体均具有较低的离体叶片失水速率和较高的存活率。研究提示了OsRINGzf1通过介导水通道蛋白的泛素化修饰与降解提高植株保水能力调控水稻抗旱性的新机制，为水稻节水抗旱的分子改良提供了重要的理论基础和基因资源。

**来源：**上海市农业生物基因中心

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**全文链接：**

<http://agri.ckcest.cn/file1/M00/10/04/Csgk0GKPR1GAZ0HdAAKbJwdzo4Y802.pdf>

### 2. 专家团队揭示稻瘟病菌分泌毒力因子抑制植物免疫机制

**简介：**近日，中国农业科学院植物保护研究所粮食作物真菌病害监测与防控团队在《Molecular Plant Pathology (分子植物病理学)》发表题为“Two Magnaporthe appressoria specific (MAS) proteins, MoMas3 and MoMas5, are required for suppressing host innate immunity and promoting biotrophic growth in rice cells”的论文。该论文揭示了稻瘟病菌附着胞特异表达蛋白MoMas3和MoMas5抑制水稻免疫反应，促进稻瘟病菌在植物细胞中活体营养生长的致病新机制。稻瘟病菌侵染水稻过程中分化出附着胞并形成巨大膨压直接穿透寄主表面，同时大量的效应蛋白从附着胞进入侵染菌丝帮助病原菌成功侵染定殖。已有研究表明附着胞特异表达的分泌蛋白与稻瘟病菌侵染和致病过程密切相关，但其与寄主的相互作用机制尚不清楚。该研究解析了稻瘟病菌附着胞特异表达的分泌蛋白MoMas3和MoMas5的功能和作用机制，发现 $\Delta$  MoMas3和 $\Delta$  MoMas5突变体对水稻的致病性减弱；利用水稻叶鞘接种实验进一步发现 $\Delta$  MoMas3和 $\Delta$  MoMas5突变体的侵染菌丝在寄主水稻细胞中的生长扩展受到限制。蛋白亚细胞定位分析发现MoMas3是一个质外体效应因子，而MoMas5则定位在附着胞的细胞质和侵染钉。通过3, 3-二氨基联苯胺 (DAB) 染色二苯基氯化碘盐 (DPI) 处理发现 $\Delta$  MoMas3和 $\Delta$  MoMas5突变体能够恢复由于水稻细胞活性氧 (ROS) 积累导致的侵染菌丝生长扩展缺陷。qRT-PCR检测植物抗病相关基因PR1和PBZ1的表达证明 $\Delta$  MoMas3和 $\Delta$  MoMas5突变体能够诱导植物抗病相关基因的表达，从而增强寄主植物对突变体的抗性。

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该研究发现了稻瘟病菌的两个新毒力因子,通过抑制寄主的先天免疫从而促进病原菌在寄主细胞中的侵染,拓展了稻瘟病菌与水稻互作之间的免疫基础理论。

来源: 中国农业科学院植物保护研究所

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全文链接:

<http://agri.ckcest.cn/file1/M00/03/32/Csgk0Yb1-72A1c-EAAMSYzVD1D8972.pdf>

## ➤ 学术文献

### 1. Genetic Improvement of Rice for Bacterial Blight Resistance: Present Status and Future Prospects (水稻抗白叶枯病遗传改良研究现状与展望)

简介: The production and productivity of rice has been challenged due to biotic and abiotic factors. Bacterial blight (BB) disease, caused by *Xanthomonas oryzae* pv. *oryzae*, is one of the important biotic stress factors, which reduces rice production by 20%-50%. The deployment of host plant resistance is the most preferred strategy for management of BB disease, and breeding disease resistant varieties remains a very economical and effective option. However, it is difficult to develop rice varieties with durable broad-spectrum resistance against BB using conventional approaches alone. Modern biotechnological tools, particularly the deployment of molecular markers, have facilitated the cloning, characterization and introgression of BB resistance genes into elite varieties. At least 46 BB resistance genes have been identified and mapped from diverse sources till date. Among these, 11 genes have been cloned and characterized. Marker-assisted breeding remains the most efficient approach to improve BB resistance by introducing two or more resistance genes into target varieties. Among the identified genes, xa5, xa13 and Xa21 are being widely used in marker-assisted breeding and more than 70 rice varieties or hybrid rice parental lines have been improved for their BB resistance alone or in combination with genes/QTLs conferring tolerance to other stress. We review the developments related to identification and utilization of various resistance genes to develop BB resistant rice varieties through marker-assisted breeding.

来源: RICE SCIENCE

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<http://agri.ckcest.cn/file1/M00/03/32/Csgk0Yb13pGAcmjAAQqsiYpeBg656.pdf>

### 2. Identification of QTL Combinations that Cause Spikelet Sterility in Rice Derived from Interspecific Crosses (种间杂交水稻小穗不育性QTL组合的鉴定)

简介: Background: The exploitation of useful genes through interspecific and intersubspecific crosses has been an important strategy for the genetic improvement of rice. Postzygotic reproductive isolation routinely occurs to hinder the growth of pollen or embryo sacs during

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the reproductive development of the wide crosses. Result: In this study, we investigated the genetic relationship between the hybrid breakdown of the population and transferred resistance genes derived from wide crosses using a near-isogenic population composed of 225 lines. Five loci (qSS12, qSS8, qSS11, ePS6-1, and ePS6-2) associated with spikelet fertility (SF) were identified by QTL and epistatic analysis, and two out of five epistasis interactions were found between the three QTLs (qSS12, qSS8 and qSS11) and background marker loci (ePS6-1 and ePS6-2) on chromosome 6. The results of the QTL combinations suggested a genetic model that explains most of the interactions between spikelet fertility and the detected loci with positive or negative effects. Moreover, the major-effect QTLs, qSS12 and qSS8, which exhibited additive gene effects, were narrowed down to 82- and 200-kb regions on chromosomes 12 and 8, respectively. Of the 13 ORFs present in the target regions, Os12g0589400 and Os12g0589898 for qSS12 and OS8g0298700 for qSS8 induced significantly different expression levels of the candidate genes in rice at the young panicle stage. Conclusion: The results will be useful for obtaining a further understanding of the mechanism causing the hybrid breakdown of a wide cross and will provide new information for developing rice cultivars with wide compatibility.

来源: Rice

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全文链接:

<http://agri.ckcest.cn/file1/M00/10/04/Csgk0GKPLR2AfxUWADtL8zFJg8s550.pdf>

### **3. Genetic and Geographic Patterns of Duplicate DPL Genes Causing Genetic Incompatibility Within Rice: Implications for Multiple Domestication Events in Rice (导致水稻遗传不亲和的DPL重复基因的遗传和地理模式: 对水稻多重驯化事件的影响)**

简介: Strong genetic incompatibilities exist between two primary rice subspecies, indica and japonica. However, the wild ancestors of rice, *O. nivara* Sharma et Shastry and *O. rufipogon* Griff., are genetically compatible. How this genetic incompatibility became established has not been clearly elucidated. To provide insights into the process, we analyzed a pair of hybrid sterility genes in rice, DOPPELGANGER 1 (DPL1) and DOPPELGANGER 2 (DPL2). Either of the two loci can have one defective allele (DPL1- and DPL2-). Hybrid pollen carrying both DPL1- and DPL2- alleles is sterile. To explore the origination of DPL1- and DPL2-, we sequenced the DPL1 and DPL2 genes of 811 individual plants, including *Oryza sativa* (132), *O. nivara* (296) and *O. rufipogon* (383). We then obtained 20 DPL1 and 34 DPL2 sequences of *O. sativa* from online databases. Using these sequences, we analyzed the genetic and geographic distribution patterns of DPL genes in modern rice and its wild ancestors. Compared with the ancestral populations, DPL1- and DPL2- showed reduced diversity but increased frequency in modern rice. We speculated that the diversity reduction was due to a historic genetic bottleneck, and the frequency had likely increased because the defective alleles were preferred following this artificial selection. Such results indicated that standing variances in ancestral lines can lead to severe incompatibilities among descendants. Haplotype analysis indicated that the DPL1- haplotype of rice emerged from an *O. nivara*

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population in India, whereas the DPL2- haplotype emerged from *O. rufipogon* in South China. Hence, the evolutionary history of DPLs conforms to the presumed multiple domestication events of modern rice.

来源: RICE SCIENCE

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