# 杂交水稻专题

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## 前沿资讯

## 1．科研人员开发出水稻高效引导编辑系统

**简介**：近日，中国水稻研究所水稻基因组编辑及无融合生殖研究创新团队和中国科学院遗传与发育生物学研究所科研团队合作，成功在水稻中开发了高效引导编辑系统。这一系统的开发为推动引导编辑在农业育种、作物改良等方面的快速应用奠定了技术基础。相关研究成果在线发表在《中国科学：生命科学（Science China Life Sciences）》引导编辑系统(Prime Editor, PE)可以在基因组的靶位点处实现任意碱基替换和小片段精准删除、插入，为植物基因组精准编辑提供了有效工具。但是，引导编辑系统目前在植物中的应用存在精准编辑效率低、靶点依赖性强等问题，严重限制了其在农作物育种上的应用。研发团队以植物引导编辑PPE3系统为基础，尝试在引导RNA的 3'末端添加结构性RNA基序以增强引导编辑系统的稳定性，建立了PPE3-evopreQ1和PPE3-mpknot两种新型引导编辑系统。研究人员分别利用上述2种新型引导编辑系统对水稻内源OsCDC48、OsALS、OsDEP1、OsEPSPS以及OsROC5基因进行单个以及多个碱基的精准替换。结果表明，无论是在原生质体、抗性愈伤以及转基因植株中，优化的PPE3-evopreQ1和PPE3-mpknot系统的基因精准编辑效率均得到显著提升，其中PPE3-evopreQ1系统显著优于PPE3-mpknot系统，利用PPE3-evopreQ1系统得到的转基因植株中，精准编辑平均效率达到10%以上，最高达到47.5%。鉴于逆转录酶M-MLV的最适工作温度为42℃，高于水稻愈伤及植株培养温度，研究人员进一步尝试在抗性愈伤培养阶段给予适当的42℃高温处理以期增加引导编辑系统效率，结果表明，适当的高温处理确实可以大幅提高引导编辑系统的精准编辑效率。重要的是，优化的PPE3-evopreQ1系统和适当的高温处理相结合，达到了最佳编辑效率组合，所测试的8个靶位点均得到了精准编辑的植株，精准编辑效率平均达到20%以上，最高达到了60.5%。该高效引导编辑系统的开发基本解决了之前精准编辑效率低、靶点依赖性强的问题，为突破农作物现有种质资源限制、根据生产需求人工定向进化优异性状提供了重要工具，将极大加速农作物育种进程。

**来源**：中国农业科学院

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http://agri.ckcest.cn/file1/M00/03/37/CsgkOYcc-3mAWUfoAAQtlP26KUQ590.pdf

## 2．揭示过氧化氢酶介导稻瘟病抗性的新机制

**简介**：近日，中国农业科学院植物保护研究所作物病原生物功能基因组研究创新团队在《植物生理》（ Plant Physiology ）上在线发表了题为"Rice catalase OsCATC is degraded by the E3 ligase APIP6 to negatively regulate immunity"的研究论文，报道了稻瘟菌效应蛋白AvrPiz-t和水稻E3泛素连接酶APIP6共同靶向过氧化氢酶OsCATC，通过调控活性氧的积累调节稻瘟病抗性的分子机制。泛素介导的蛋白质降解是真核生物体内最重要的翻译后修饰调控机制之一，在植物的生长、发育和逆境胁迫应答过程中发挥着重要作用。其中E3泛素连接酶决定了对靶蛋白的特异性选择，因此E3泛素连接酶和靶蛋白的鉴定是泛素化研究的重点和热点。该团队前期研究发现稻瘟菌效应蛋白AvrPiz-t与水稻E3泛素连接酶APIP6相互作用，并互相促进降解。水稻中异源表达AvrPiz-t和沉默 APIP6 都会显著抑制flg22激发的活性氧产生。然而,AvrPiz-t和APIP6如何调控活性氧的积累还不清楚。该研究发现APIP6与过氧化氢酶OsCATC直接相互作用，

并降解OsCATC从而抑制其清除过氧化氢（活性氧的主要成分）的效率，水稻 oscatc 突变体积累大量的过氧化氢，诱导细胞死亡的发生并增强对稻瘟菌的抗病性。进一步发现AvrPiz-t也能与OsCATC相互作用，并促进其清除过氧化氢的效率。该研究证明，当稻瘟菌侵染水稻时，稻瘟菌分泌效应蛋白AvrPiz-t促进OsCATC清除过氧化氢，为稻瘟病侵染创造更有利的条件；为了抵御稻瘟菌的侵染，E3泛素连接酶APIP6同时靶向稻瘟菌AvrPiz-t和水稻OsCATC进行降解，以增加活性氧的产生，从而激活水稻防御反应。该研究率先鉴定了降解过氧化氢酶的E3泛素连接酶，揭示了稻瘟菌与水稻互作过程中通过调控过氧化氢酶清除活性氧效率介导抗病性的分子机制，为水稻抗病分子育种提供了理论依据和基因资源。

来源：中国农业科学院植物保护研究所

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## 学术文献

### 1. Evaluation of Chilo suppressalis resistance and analysis of CRY1C expression in transgenic rice(转基因水稻二化螟抗性评价及CRY1C表达分析)

简介：The insect resistance of Bacillus thuringiensis (Bt) transgenic rice (Oryza sativa L.) is mainly determined by the transcription of the CRY1C gene and the translation process of the Cry1C protein. With this in mind, we analyzed CRY1C expression and Cry1C protein content in a transgenic Bt insect-resistant restorer line and its F1 hybrids, evaluated the resistance to Chilo suppressalis of various lines of rice, and determined the 50% lethal concentration (LC50) of Cry1C for C. suppressalis. In four transgenic rice lines, the relative expression of CRY1C was highest at the heading stage in most tissues. Among different tissues from the same developmental stage, CRY1C expression was highest in leaves, followed by stems and panicles. The relative expression of CRY1C was higher in the parent restorer line than in the F1 hybrids. The LC50 of the Cry1C protein for C. suppressalis was 4.016 mu g g(-1), and the Cry1C protein expression level of transgenic insect-resistant rice exceeded this threshold at the heading stages and in stems. We next analyzed the lethality of each strain toward C. suppressalis. After 48 h, the mortality rate of second-instar C. suppressalis larvae feeding on transgenic stem tissue was higher at the heading stage than at the tiller stage and varied from 66.7 to 91.7%. By documenting the temporal and spatial expression of CRY1C and evaluating C. suppressalis resistance to Bt transgenic rice, the risk of pests and diseases during the rice production process can be greatly reduced.

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## 2. Early Domestication History of Asian Rice Revealed by Mutations and Genome-Wide Analysis of Gene Genealogies(突变和基因谱系全基因组分析揭示亚洲水稻的早期驯化史)

简介：Background: Asian rice (Oryza sativa L.) has been a model plant but its cultivation history is inadequately understood, and its origin still under debate. Several enigmas remain, including how this annual crop shifted its growth habit from its perennial ancestor, O. rufipogon, why genetic divergence between indica and japonica appears older than the history of human domestication, and why some domestication genes do not show signals of introgression between subgroups. Addressing these issues may benefit both basic research and rice breeding.Results: Gene genealogy-based mutation (GGM) analysis shows that history of Asian rice is divided into two phases (Phase I and II) of about equal lengths. Mutations occurred earlier than the partition of indica and japonica to Os genome mark Phase-I period. We diagnosed 91 such mutations among 101 genes sampled across 12 chromosomes of Asian rice and its wild relatives. Positive selection, detected more at 5' regions than at coding regions of some of the genes, involved 22 loci (e.g., An-1, SH4, Rc, Hd3a, GL3.2, OsMYB3, OsDFR, and OsMYB15), which affected traits from easy harvesting, grain color, flowering time, productivity, to likely taste and tolerance. Phase-I mutations of OsMYB3, OsHd3a and OsDFR were experimentally tested and all caused enhanced functions of the genes in vivo. Phase-II period features separate cultivations, lineage-specific selection, and expanded domestication to more genes. Further genomic analysis, along with phenotypic comparisons, indicates that O. sativa is hybrid progeny of O. rufipogon and O. nivara, inherited slightly more genes of O. rufipogon. Congruently, modern alleles of the sampled genes are approximately 6% ancient, 38% uni-specific, 40% bi-specific (mixed), and 15% new after accumulating significant mutations. Results of sequencing surveys across modern cultivars/landraces indicate locus-specific usages of various alleles while confirming the associated mutations.Conclusions: Asian rice was initially domesticated as one crop and later separate selection mediated by human resulted in its major subgroups. This history and the hybrid origin well explain previous puzzles. Positive selection, particularly in 5' regions, was the major force underlying trait domestication. Locus-specific domestication can be characterized and the result may facilitate breeders in developing better rice varieties in future.

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## 3. Reduced nitrogen application rate with dense planting improves rice grain yield and nitrogen use efficiency: A case study in east China(密植降低施氮量提高水稻产量和氮素利用效率：以华东地区为例)

简介：Dense planting could be a feasible method for reducing nitrogen (N) application rates without compromising rice grain yield in northeast and central China. It is still unclear

whether reduced N application with dense planting (RNDP) can achieve higher rice yield and N use efficiency (NUE) in Jiangsu, east China. Three japonica inbred rice (JI) and three indica hybrid rice (IH) cultivars were grown in a field experiment. Their grain yield, NUE, and related traits were compared under two cultivation treatments: conventional high-yielding practice (CHYP) and RNDP. JI showed similar yields under the two treatments, while IH showed lower yield under RNDP than under CHYP, and the partial factor productivity of N and N use efficiency for grain yield increased ($P < 0.05$) in both JI and IH under RNDP. Compared with CHYP, RNDP reduced spikelets per panicle but increased panicles per m(2) and filled-kernel percentage of JI and IH, and JI's kernel weight was increased ($P < 0.05$) under RNDP. Shoot biomass weight and nonstructural carbohydrate (NSC) content in the stem at heading and maturity of JI and IH were reduced under RNDP, while harvest index and NSC remobilization reserve were increased ($P < 0.05$) under RNDP, especially for JI. Our results suggest that RNDP could achieve a higher rice grain yield and NUE, particularly for JI, a dominant rice cultivar type in Jiangsu. For JI, the increased panicles per m(2), sink-filling efficiency, harvest index, and NSC remobilization after heading under RNDP contributed to a grain yield similar to that under CHYP. (C) 2021 Crop Science Society of China and Institute of Crop Science, CAAS. Production and hosting by Elsevier B.V. on behalf of KeAi Communications Co., Ltd.

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