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杂交水稻专题

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▶ 前沿资讯

1. 科技创新进展：建立正常结实率杂交水稻无融合生殖体系

简介：近日，中国水稻研究所王克剑团队在Molecular Plant杂志上在线发表了题为“Synthetic apomixis with normal hybrid rice seed production”的研究论文。该研究优化了杂交水稻无融合生殖体系，得到了结实率几乎不受影响的无融合生殖杂交水稻植株，实现了对无融合生殖技术体系结实率的大幅提升。杂交稻育种充分发挥了杂种优势的潜能，实现了水稻的高产、稳产，为世界粮食安全提供了重要保障。杂交稻后代种子会发生杂种优势表型分离，因而无法再应用于农业生产，需要每年通过繁琐的程序重制新的杂交种子。杂交制种极易受外界环境影响，生产成本高，种子产量低，价格十分昂贵。因此，如何实现杂交稻自留种，一直被认为是杂交育种的最高目标。自然界中存在一种通过种子进行克隆繁殖的无性生殖方式——无融合生殖。将这种生殖方式引入杂交农作物中，有望可以实现杂交作物自留种。2019年，美国科学家和我所王克剑研究团队分别在常规稻和杂交稻中建立了人工无融合生殖体系，首次获得了水稻的克隆种子，为杂交稻进行自留种提供了可能。但是，这两种人工无融合生殖体系均存在结实率低和克隆种子比例低问题，限制了该技术在农作物中应用。该研究对水稻可诱导孤雌生殖基因BBM1的三个同源基因BBM2、BBM3和BBM4进行系统研究，挖掘相关基因诱导孤雌生殖的潜力。利用拟南芥卵细胞特异性启动子(pDD45)分别驱动BBM2、BBM3和BBM4，获得这三个基因水稻卵细胞异位表达植株EE-BBM2、EE-BBM3和EE-BBM4。接着，借助分子标记技术和流式细胞术对BBMs异位表达植株后代进行分析，发现BBM4卵细胞异位表达植株可以诱导孤雌生殖，单倍体诱导率为3.2%。随后，研究人员测试了BBM4在无融合生殖体系的应用潜力。将异位表达BBM4与有丝分裂代替减数分裂策略MiMe结合，在杂交稻中成功获得了可以发生无融合生殖的Fix2 (Fixation of hybrids 2) 材料。Fix2植株不仅在营养生长阶段表现正常，而且结实率高达80.9–86.1%，与正常杂交稻82.1–86.6%相近。通过细胞倍性检测，在其子代中获得了细胞倍性为二倍体且基因型与亲本保持一致的植株，这些克隆植株的表型也与野生型杂交稻高度相似，同时维持了80.9–82.0%的高结实率。

来源：中国水稻研究所

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2. 科技创新进展：研究揭示水稻卷叶基因SRL10协同调控耐热性

简介：近日，中国水稻研究所水稻生物学国家重点实验室张光恒研究员/钱前院士团队在《植物生物技术杂志》上发表了题为《半卷叶调控基因SRL10通过与过氧化氢酶B互作协同调控水稻叶形及其耐热性》的研究论文。该研究克隆了同时调控水稻株叶形态建成与产量、耐热性的相关的双链RNA结合蛋白编码基因SRL10，并揭示其与过氧化氢酶CATB互作、协同调控水稻耐热性的分子机制，鉴定了SRL10在水稻中具优异耐热性的等位变异。团队利用水稻叶片卷曲和热敏感突变体sr110、染色体片段置换系及自然种质遗传群体，通过正向遗传学方法完成株型发育与耐热协同调控相关的目的基因SRL10的图位克隆，该基因编码双链RNA结合蛋白。研究发现SRL10影响miRNA生物合成，正向调控近轴面泡状细胞发育影响株叶形态和产量，同时参与miRNA介导的耐热性调控进程。SRL10

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与过氧化氢酶同工酶B (CATB) 交互, 增加蛋白稳定性, 增加SRL10的表达量能显著提高CATB介导的H₂O₂清除能力, 增加耐热性。SRL10的单倍型和等位基因频率分布分析结果表明, 粳稻中大部分品种携带SRL10 Hap1等位变异, 籼稻中同时存在SRL10 Hap2和SRL10 Hap3等位变异, 而大多数aus稻品种携带SRL10 Hap3等位变异。鉴定结果表明: 携带aus稻SRL10 Hap3等位变异的自然品种在高温胁迫下结实率均显著高于携带SRL10 Hap1等位变异的粳稻品种。用遗传背景接近的遗传材料构建分别携带aus稻和粳稻的SRL10等位变异的近等基因系 (NIL-SRL10 Hap3和NIL-SRL10 Hap1)。蛋白稳定性鉴定结果表明: NIL-SRL10 Hap3蛋白热稳定性要显著高于NIL-SRL10 Hap1, 且在人工控制的高温条件下NIL-SRL10 Hap3的结实率和产量均显著高于NIL-SRL10 Hap1。而且, 具有SRL10 Hap3等位变异的品种, SRL10和CATB表达水平较高, 蛋白稳定性强, 使植株具有更强的耐热性。因此, 高温胁迫下SRL10通过与CATB交互调控H₂O₂的积累, 参与ROS代谢, 减轻高温胁迫对植株的伤害, 提高耐热性。携带SRL10 Hap3单倍型在高温环境下为具有提高水稻耐热性有利等位变异。本研究首次将水稻的形态发育和生理抗逆作为一个整体开展研究, 在研究思路和技术上都取得重要突破。研究结果不仅进一步完善了水稻株型与抗逆的协同调控遗传网络, 同时为水稻多性状协同改良和抗逆育种提供新的理论依据和基因资源。

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► 学术文献

1. Development of New Iso-Cytoplasmic Rice-Restorer Lines and New Rice Hybrids with Superior Grain Yield and Grain Quality Characteristics by Utilizing Restorers' Fertility Genes (利用恢复系育性基因培育高产优质等细胞质水稻恢复系和杂交新品种)

简介: This research was carried out at the Experimental Farm of Sakha Agricultural Research Station, Sakha, Kafr El-Sheikh, Egypt, during the 2018-2020 rice-growing seasons to develop and evaluate four iso-cytoplasmic rice-restorer lines: NRL79, NRL80, NRL81, and NRL82, as well as Giza 178, with ten new hybrids in order to estimate genotypic coefficient, phenotypic coefficient, heritability in a broad sense, and advantage over Giza 178 as a check variety (control) of new restorer lines. This study also estimated combining ability, gene action, better-parent heterosis (BP), mid-parents heterosis (MP), and standard heterosis (SH) over Egyptian Hybrid one (IR69A x Giza 178) as a check hybrid (control) for grain yield, agronomic traits, and some grain quality characters in restorer lines and hybrids. The percentage of advantage over commercial-variety Giza 178 (check) was significant, and highly significant among the newly developed restorer fertility lines for all the studied traits. This indicates that the selection is a highly effective factor in improving these traits. New restorer fertility lines showed highly significant positive values over commercial restorer for grain yield; the values ranged from 51% for NRL80 to 100.4% for NRL82, respectively. Meanwhile, in regard to the grain shape of paddy rice, three lines of the promising lines

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showed highly significant negative desirable values compared with Giza 178; the values ranged from -7.7% for the NRL80 to -15.2% for NRL79, respectively. Based on the superiority of the new lines, the new lines can be used as new restorer fertility lines to breed promising new hybrids and new inbred rice lines or varieties. From the results of the testcross experiment, the four promising lines were identified as effective restorer fertility lines for two cytoplasmic male sterile (CMS) lines. Moreover, the six rice hybrids showed values for SH heterosis of grain yield/plant of more than 15% over the check hybrid variety, with high values of 1000-grain weight and desirable grain shape; these hybrids were G46A x NRL81 (125.1%), G46A x NRL80 (66.9%), IR69A x NRL79 (47.2%), G46A x NRL79 (24.6%), IR69A x NRL81 (23.4%), and IR69A x NRL82 (16.2%).

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2. Transcriptome and Metabolome Profiling Reveal the Resistance Mechanisms of Rice against Brown Planthopper (转录组和代谢组分析揭示水稻对褐飞虱的抗性机制)

简介: Brown planthopper (*Nilaparvata lugens* Stal, BPH) is one of the most destructive insects affecting rice production. To better understand the physiological mechanisms of how rice responds to BPH feeding, we analyzed BPH-induced transcriptomic and metabolic changes in leaf sheaths of both BPH-susceptible and -resistant rice varieties. Our results demonstrated that the resistant rice reduced the settling, feeding and growth of BPH. Metabolic analyses indicated that BPH infestation caused more drastic overall metabolic changes in the susceptible variety than the resistant rice. Differently accumulated metabolites (DAMs) belonging to flavonoids were downregulated in the susceptible rice but upregulated in resistant variety. Transcriptomic analyses revealed more differentially expressed genes (DEGs) in susceptible rice than resistant rice, and DEGs related to stimulus were significantly upregulated in resistant rice but downregulated in susceptible rice. Combined analyses of transcriptome and metabolome showed that many DEGs and DAMs were enriched in phenylpropane biosynthesis, flavonoid biosynthesis, and plant hormone signal transduction. We conducted correlation analyses of DEGs and DAMs in these pathways and found a high correlation between DEGs and DAMs. Then, we found that the contents of endogenous indole 3-acetic acid (IAA) in resistant rice was lower than that of susceptible rice after BPH feeding, while the salicylic acid (SA) content was the opposite. For functional analysis, an exogenous application of IAA decreased rice resistance to BPH, but the exogenous application of SA increased resistance. In addition, biochemical assessment and quantitative PCR analysis showed that the lignin content of resistant accession was constitutively higher than in susceptible accession. By adding epigallocatechin, the substrate of anthocyanidin reductase (ANR), to the artificial diet decreased the performance of BPH. We first combined a transcriptome-metabolome-wide association study (TMWAS) on rice resistance to BPH in this study. We demonstrated that rice promoted resistance to BPH by

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inducing epigallocatechin and decreasing IAA. These findings provided useful transcriptomic and metabolic information for understanding the rice-BPH interactions.

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3. Identification and Analysis of Genes Involved in Double Fertilization in Rice (水稻双受精相关基因的鉴定与分析)

简介: Double fertilization is a key determinant of grain yield, and the failure of fertilization during hybridization is one important reason for reproductive isolation. Therefore, fertilization has a very important role in the production of high-yield and well-quality hybrid of rice. Here, we used RNA sequencing technology to study the change of the transcriptome during double fertilization with the help of the mutant fertilization barrier (feb) that failed to finish fertilization process and led to seed abortion. The results showed that 1669 genes were related to the guided growth of pollen tubes, 332 genes were involved in the recognition and fusion of the male-female gametes, and 430 genes were associated with zygote formation and early free endosperm nuclear division. Among them, the genes related to carbohydrate metabolism; signal transduction pathways were enriched in the guided growth of pollen tubes, the genes involved in the photosynthesis; fatty acid synthesis pathways were activated by the recognition and fusion of the male-female gametes; and the cell cycle-related genes might play an essential role in zygote formation and early endosperm nuclear division. Furthermore, among the 1669 pollen tube-related genes, it was found that 7 arabinogalactan proteins (AGPs), 1 cysteine-rich peptide (CRP), and 15 receptor-like kinases (RLKs) were specifically expressed in anther, while 2 AGPs, 7 CRPs, and 5 RLKs in pistil, showing obvious unequal distribution which implied they might play different roles in anther and pistil during fertilization. These studies laid a solid foundation for revealing double fertilization mechanism of rice and for the follow-up investigation.

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