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杂交水稻专题

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▶ 前沿资讯

1. 研究在表观遗传修饰调控稻瘟菌致病机制方面获得新进展

简介: 近日, 华中农业大学农业微生物学国家重点实验室、植物科学技术学院陈小林课题组研究成果以“MTA1-mediated RNA m6A modification regulates autophagy and is required for infection of the rice blast fungus”为题在*New Phytologist*发表。研究以稻瘟菌-水稻为模式系统, 揭示了N6-甲基腺苷修饰(N6-methyladenosine RNA, m6A)调控植物病原真菌侵染结构功能的新机制。RNA m6A修饰是真核生物中mRNA最普遍的修饰, 近年来在人类, 动物, 植物和酵母等物种中均被发现广泛参与不同的生物学过程, 在不同的生物体内均发挥着关键调控作用。在这些物种中, METTL3/IME4是m6A甲基化转移酶复合体中一个最重要的组成蛋白, 主要负责催化RNA分子在N6-甲基腺嘌呤上发生m6A修饰。然而, 由于在丝状真菌中一直未发现与METTL3/IME4同源的蛋白, 因此m6A修饰在植物病原真菌中是否存在并发挥功能, 一直未得到系统的研究。本研究中, 研究者鉴定到一个与人类METTL4(通常被认为编码DNA m6A修饰的关键酶)同源的蛋白MTA1, 随后证明该蛋白参与稻瘟菌RNA m6A修饰(但可能并不参与DNA m6A修饰)。MTA1基因敲除后导致稻瘟菌总m6A修饰显著降低, 同时病菌致病力严重降低。进一步分析发现, 致病力降低是由于敲除体附着胞功能受到影响, 同时侵染菌丝扩展能力也受到抑制。敲除体附着胞形成过程中, 糖原和脂质体利用能力显著受限, 细胞自噬过程受阻, 同时附着胞膨压显著降低。由于MTA1在附着胞中发挥关键作用, 随后收集野生型和MTA1敲除体的附着胞材料, 进行MeRIP-seq和RNAseq联合分析。与野生型菌株比较发现, MeRIP-seq分析在 Δ mta1菌株的附着胞中鉴定出595个mRNA的659个位点m6A甲基化水平降低。其中, 糖类代谢和脂类代谢, 以及细胞自噬相关的信号通路被富集。结合RNAseq数据, 发现其中的114个m6A修饰水平与mRNA丰度呈负相关, 暗示m6A修饰可能参与mRNA的降解。进一步分析表明, 一些调控细胞自噬过程的ATG基因的转录本受到m6A修饰, 包括ATG8。通过网站预测到ATG8的转录本3'非翻译区位点A982可能为m6A修饰位点, 随后将该位点进行了点突变。MeRIP-qPCR分析表明, A982位点突变导致ATG8 m6A修饰水平严重降低; 同时qRT-PCR分析表明A982位点突变导致ATG8 mRNA水平升高, 表明m6A负调控ATG8的mRNA丰度。A982位点突变后, 同时导致ATG8蛋白水平升高, 附着胞细胞自噬过程紊乱, 从而影响着胞功能, 导致致病力减弱。综合以上研究发现, 在稻瘟菌附着胞形成过程中, m6A修饰可能参与细胞自噬蛋白mRNA丰度的调控, 从而协调附着胞细胞自噬, 调控功能性附着胞的形成, 帮助稻瘟菌致病。本研究首次系统揭示了RNA m6A修饰调控植物病原真菌过程的分子机制, 为深入理解植物病原真菌的致病机理提供了新的视角, 可能为开发真菌病害防控策略提供新的思路, 为研发新的杀菌剂提供新的候选靶标。

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2. 科技创新进展: 发现调控水稻氮素利用率、产量和稻米品质的关键因子

简介: 近日, 中国水稻研究所胡培松院士研究团队在*Journal of Genetics and Genomics*在线发表了题为“Alanine aminotransferase (OsAlaAT1) modulates nitrogen

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utilization, grain yield and quality in rice” 的研究论文。该研究发现编码水稻丙氨酸转氨酶(OsAlaAT1)的基因LNUE1在调控水稻氮素利用率(NUE)、产量和稻米品质中起着关键的作用,为水稻产量与品质遗传改良提供了新的理论基础与基因资源。氮是影响水稻生长发育最重要的大量元素之一,其广泛利用显著地提高了水稻产量,但过度的氮肥施用不仅导致农业成本上升和稻米品质降低,还造成水体富营养化、土壤酸化等环境问题。因此提高水稻氮肥利用率,在少施氮肥的情况下提高水稻产量与品质,对现代水稻品种选育及生产尤为重要。研究人员筛选到了一个低氮素利用率的水稻突变体lnue1,在大田间里种植时,lnue1的株高降低,分蘖数、穗粒数减少,胚乳呈现严重垩白,粒重、单株产量显著降低。相较于野生型,lnue1的氮肥利用率(NUE)显著降低,而茎秆等组织中氮含量增加。图位克隆发现LNUE1编码丙氨酸转氨酶(OsAlaAT1)。进一步研究发现,突变中lnue1中丙氨酸转氨酶活性极显著下降,氮吸收相关基因上调,而氮的长距离运输相关基因下调表达,这可能导致了突变体从土壤中吸收的氮素无法运输至种子而大量积累在茎秆中。突变体幼苗和发育胚乳中积累大量的丙酮酸,丙酮酸向淀粉转化的相关基因表达下调,导致其胚乳淀粉合成不足出现严重垩白。此外,在野生型和lnue1背景下过表达LNUE1均能够提高氮素利用率与单株产量。本研究证明LNUE1(OsAlaAT1)是调节水稻氮素利用率影响产量和稻米品质的关键因子,对提高水稻的氮肥利用率以及实现产量和品质协同改良具有重要意义。

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► 学术文献

1. Is the Two-Line Hybrid Rice a Hindrance to the Efficient Use of Nitrogen Fertilizer in China (两系杂交水稻是中国氮肥高效利用的障碍吗)

简介: Two-line hybrid rice (2LH) is accompanied by more nitrogen (N) input. To explore the difference in response of two-line and three-line hybrid rice (3LH) to N application, a three-year split-plot experiment was conducted. Three 2LHs and three 3LHs were set as main plots, and four N rates including 0 kg ha⁻¹ (N0), 90 kg ha⁻¹ (N90), 150 kg ha⁻¹ (N150), and 210 kg ha⁻¹ (N210) were set as subplots. 3LH had more panicles and yielded 7.95%, 6.31%, and 5.48% higher than 2LH in N0, N90, and N150, respectively. 2LH had a greater panicle weight in N210 and yielded 1.45% higher than 3LH. Leaf area index (LAI) had the greatest effect on the yields of both 2LH and 3LH, while the contribution of light extinction coefficient (K) was 46.35% and 12.80% those of LAI, respectively. The LAI, K, and radiation interception rate (RIR) of 2LH were smaller than those of 3LH in N0 and N90. The K of 2LH increased significantly as the N rate increased from 150 kg ha⁻¹ to 210 kg ha⁻¹, while that of 3LH showed no significant change, making the maximum RIR of 2LH greater than that of 3LH. 2LH, which intercepted more radiation through greater leaf extension to achieve higher yields, was able to use nitrogen fertilizer efficiently under a high N rate in China.

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2. New Hybrid Spikelet Sterility Gene Found in Interspecific Cross between *Oryza sativa* and *O. meridionalis* (水稻种间杂交中发现新的杂交小穗不育基因)

简介: Various kinds of reproductive barriers have been reported in intraspecific and interspecific crosses between the AA genome *Oryza* species, to which Asian rice (*O. sativa*) and African rice (*O. glaberrima*) belong. A hybrid seed sterility phenomenon was found in the progeny of the cross between *O. sativa* and *O. meridionalis*, which is found in Northern Australia and Indonesia and has diverged from the other AA genome species. This phenomenon could be explained by an egg-killer model. Linkage analysis using DNA markers showed that the causal gene was located on the distal end of chromosome 1. Because no known egg-killer gene was located in that chromosomal region, this gene was named HYBRID SPIKELET STERILITY 57 (abbreviated form, S57). In heterozygotes, the eggs carrying the *sativa* allele are killed, causing semi-sterility. This killer system works incompletely: some eggs carrying the *sativa* allele survive and can be fertilized. The distribution of alleles in wild populations of *O. meridionalis* was discussed from the perspective of genetic differentiation of populations.

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3. Molecular Breeding of a Novel PTGMS Line of WDR for Broad-Spectrum Resistance to Blast Using *Pi9*, *Pi5*, and *Pi54* Genes (利用*Pi9*、*Pi5*和*Pi54*基因选育广谱抗稻瘟病的WDR PTGMS新品系)

简介: Background The two-line method based on the photoperiod and thermo-sensitive genic male sterile (PTGMS) lines is more cost-effective, simple, and efficient than the three-line system based on cytoplasmic male-sterility. Blast and drought are the most prevalent biotic and abiotic stress factors hampering rice production. Molecular techniques demonstrate higher efficacy in the pyramiding of disease resistance genes, providing green performance under the background of water-saving and drought-resistance rice. Results This study employed molecular marker-assisted selection, conventional hybridization, and high-intensity stress screening to integrate three broad-spectrum blast resistance genes *Pi9*, *Pi5*, and *Pi54* into Huhan 1S. Subsequently, a novel water-saving and drought-resistance rice (WDR) PTGMS line Huhan 74S was developed. The drought resistance of the new PTGMS line Huhan 74S was comparable to that of Huhan 1S. Pathogenicity assays involving the inoculation of 14 blast prevalent isolates in the glasshouse showed that the blast resistance

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frequency of Huhan 74S was 85.7%. Further evaluation under natural blast epidemic field conditions showed that Huhan 74S and its hybrids were resistant to leaf and neck blast. The critical temperature point of fertility-sterility alteration of Huhan 74S was 23 degrees C daily mean temperature. The complete male sterility under natural growth conditions in 2017 at Shanghai lasted for 67 days. Also, both the agronomic and grain quality traits met the requirement for two-line hybrid rice production. Conclusion These results indicate that the newly bred PTGMS line Huhan 74S can be used to breed high-yielding, good-quality, disease-resistant two-line hybrid water-saving and drought-resistance rice (WDR), hence promoting sustainable rice production in China.

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