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杂交水稻专题

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▶ 前沿资讯

1. 科研人员揭示籼稻血缘渗入对粳稻遗传改良的贡献

简介: 近日,中国农业科学院作物科学研究所水稻优异种质资源发掘与创新利用创新团队系统解析了我国粳稻育成品种的演变规律和改良历史,在基因组层面揭示了籼稻血缘渗入对粳稻遗传改良的贡献,为水稻基因组育种提供了新思路。4月13日,该成果在线发表在《植物通讯(Plant Communications)》杂志上。据韩龙植研究员介绍,在漫长的粳稻品种改良过程中,粳稻品种的基因组上留下了诸多育种印迹,研究粳稻品种基因组的演变规律和改良历史,可为优化粳稻育种路线提供科学依据。该研究对816份我国不同时期代表性粳稻品种进行了重测序,并整合已发表的5500份水稻测序数据,系统分析了不同时期主栽品种的基因组组成。研究发现,自20世纪80年代以来,来自3个不同籼稻亚群的血缘向粳稻品种中的渗入持续增加,使粳稻的重要性状发生了显著变化,如稻瘟病抗性提高、穗粒数增加、单株穗数减少、株型由多穗型向重穗大穗型转变。研究还发现,与株型、产量和抗病虫性相关的等位基因由籼稻渗入到粳稻中,籼稻血缘的渗入贡献了粳稻品种中缺乏的一些优异等位基因,从基因组层面反映了我国粳稻的改良历史。另外,研究还鉴定到一个调控水稻穗粒数的新基因Gnd5,与野生型相比,敲除Gnd5的突变体,水稻穗粒数显著减少。进一步分析发现,Gnd5基因是渗入的靶基因,对育种具有重要的应用价值。此外,通过研究各骨干亲本系谱中穗粒数相关基因单倍型的利用模式,发现多基因的优势单倍型聚合利用存在较强的系谱背景特异性,这将有助于未来在广泛遗传背景下进行数量性状位点聚合和育种路线优化。该研究系统分析了我国粳稻育成品种的演变规律和改良历史,为未来水稻基因组育种提供了新思路。

来源: 中国农业科学院

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<http://agri.ckcest.cn/file1/M00/03/2F/Csgk0YbBFh2AeGKzAAL9heW0Es0335.pdf>

2. 专家团队揭示水稻温敏雄性不育调控的分子机制

简介: 近日,中国科学院遗传与发育生物学研究所李云海团队与海南大学、北京大学研究人员合作发现了水稻温敏不育调控的重要分子机制。该研究发现籼稻TGMS系Tian1S在高温下表现出雄性不育,但在低温下表现出正常的育性,与日长无关。通过遗传分析表明,温敏雄性不育表型由细胞核单个隐性基因OsMS1wenmin1控制。进一步研究发现,高温下OsMS1wenmin1赋予籼粳和粳稻品种温敏不育表型。有意思的是野生型的OsMS1定位于细胞核中,而OsMS1wenmin1定位于细胞质和细胞核中,表明OsMS1保守的L301P的突变影响其亚细胞定位。该研究进一步发现温度调控OsMS1和OsMS1wenmin1的丰度,并且OsMS1wenmin1比OsMS1对温度变化更敏感。在低温条件下,野生型OsMS1和OsMS1wenmin1等位基因分别编码适当水平的OsMS1和OsMS1wenmin1蛋白以保持正常的花粉发育,尽管含有OsMS1wenmin1等位基因的水稻材料中OsMS1wenmin1的水平在细胞核中低于野生型OsMS1。OsMS1和OsMS1wenmin1与转录因子TDR相互作用以激活下游基因的表达,从而产生可育花粉。在高温条件下,OsMS1蛋白的丰度下降,但细胞核中仍有足够的OsMS1蛋白与TDR相互作用以激活下游基因的表达,从而产生可育花粉。相反,高温大大降低了OsMS1wenmin1蛋白水平,因此细胞核中没有足够的OsMS1wenmin1蛋白与TDR相互作用,导致下游基因表达急剧下降并形成不育花粉。该研究揭示了温度调控OsMS1蛋白丰度的

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一种新机制，有意思的是L301P的突变，导致OsMS1wenmin1对温度响应更为敏感，进而导致高温不育的表型。值得注意的是，不同物种中OsMS1高度保守。因此，该研究发现对于进一步阐明温度调控水稻育性转换的分子机制，指导两系杂交稻育种，乃至在其他作物中创制新的温敏不育系具有深远意义。

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学术文献

1. Integrated Crop Management Practices Improve Grain Yield and Resource Use Efficiency of Super Hybrid Rice (作物综合管理措施提高超级杂交水稻的产量和资源利用效率)

简介: Super hybrid rice genotypes have transformed the rate of genetic yield gain primarily due to intersubspecific heterosis, although the physiological basis underpinning this yield transformation has not been well quantified. We assessed the radiation use efficiency (RUE) and nitrogen use efficiency (NUE) of novel hybrid rice genotypes under four management practices representative of rice cropping systems in China. Y-liangyou 900 (YLY900), a new super hybrid rice widely adopted in China, was examined in field experiments conducted in Jingzhou and Suizhou, Hubei Province, China, from 2017 to 2020. Four management practices were conducted: nil fertilizer (CK), conventional farmer practice (FP), optimized cultivation with reduced nitrogen (OPT-N), and optimized cultivation with increased nitrogen (OPT+N). Yield differences across the treatment regimens were significant ($p < 0.05$). Grain yield of OPT+N in Jingzhou and Suizhou were 11 and 12 t ha⁻¹, which was 14 and 27% greater than yields obtained under OPT-N and FP, respectively. Relative to OPT-N and FP, OPT+N had greater panicle numbers (9 and 18%), spikelets per panicle (7 and 12%), spikelets per unit area (17 and 32%), and total dry weight (9 and 19%). The average RUE of OPT+N was 2.7 g MJ⁻¹, which was 5 and 9% greater than that of OPT-N and FP, respectively, due to higher intercepted photosynthetically active radiation (IPAR). The agronomic efficiency of applied N (AE(N)) of OPT+N was 17 kg grain kg⁻¹ N, which was 9 and 68% higher than that of OPT-N and FP. These results show that close correlations exist between yield and both the panicles number ($R^2 = 0.91$) and spikelets per panicle ($R^2 = 0.83$) in OPT+N. We conclude that grain yields of OPT+N were associated with greater IPAR, RUE, and total dry matter. We suggest that integrated cropping systems management practices are conducive to higher grain yield and resource use efficiency through expansion of sink potential in super hybrid rice production.

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2. Construction of a weight-based seed sorting system for the third-generation hybrid rice (基于重量的第三代杂交水稻种子分选系统的构建)

简介: Background The third-generation hybrid rice technology can be constructed by transforming a recessive nuclear male sterile (NMS) mutant with a transgenic cassette containing three functional modules: the wild type male fertility gene to restore the fertility of the mutant, the pollen killer gene that specifically kills the pollen grains carrying the transgene, and the red fluorescence protein (RFP) gene to mark the transgenic seed (maintainer). The transgenic plant produces 1:1 NMS seeds and maintainer seeds that can be distinguished by the RFP signal. However, the RFP signals in the partially filled or pathogen-infected maintainer seeds are often too weak to be detected by RFP-based seed sorting machine, resulting in intermingling of the maintainer seeds with NMS seeds. Results Here we constructed a weight-based seed sorting system for the third-generation hybrid rice technology by silencing the genes encoding ADP-glucose pyrophosphorylase (AGP) essential for endosperm starch biosynthesis via endosperm-specific expression of artificial microRNAs (amiRNAs). In this system, the NMS seeds have normal endosperm and are heavy, but the maintainer seeds have shrunken endosperms and are light-weighted. The maintainer seeds can be easily and accurately sorted out from the NMS seeds by weight-sorting machines, so pure and fully filled NMS seeds are available. Conclusions The weight-based seed sorting system shows obvious advantages over the RFP-based seed sorting system in accuracy, efficiency, and cost for propagation of pure male sterile seeds. These characteristics will significantly increase the value and transgenic safety of the third-generation hybrid rice technology.

来源: RICE

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3. Parental variation in CHG methylation is associated with allelic-specific expression in elite hybrid rice (亲本CHG甲基化变异与优质杂交水稻等位基因特异性表达相关)

简介: Heterosis refers to the superior performance of hybrid lines over inbred parental lines. Besides genetic variation, epigenetic differences between parental lines are suggested to contribute to heterosis. However, the precise nature and extent of differences between the parental epigenomes and the reprogramming in hybrids that govern heterotic gene expression remain unclear. In this work, we analyzed DNA methylomes and transcriptomes of the widely cultivated and genetically studied elite hybrid rice (*Oryza sativa*) SY63, the reciprocal hybrid, and the parental varieties ZS97 and MH63, for which high-quality reference genomic sequences are available. We showed that the parental varieties displayed substantial variation in genic methylation at CG and CHG (H=A, C, or T) sequences. Compared with their parents,

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the hybrids displayed dynamic methylation variation during development. However, many parental differentially methylated regions (DMRs) at CG and CHG sites were maintained in the hybrid. Only a small fraction of the DMRs displayed non-additive DNA methylation variation, which, however, showed no overall correlation relationship with gene expression variation. In contrast, most of the allelic-specific expression (ASE) genes in the hybrid were associated with DNA methylation, and the ASE negatively associated with allelic-specific methylation (ASM) at CHG. These results revealed a specific DNA methylation reprogramming pattern in the hybrid rice and pointed to a role for parental CHG methylation divergence in ASE, which is associated with phenotype variation and hybrid vigor in several plant species.

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