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1. 中国杂交水稻种子行业发展趋势分析与未来前景数据统计

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前沿资讯

1．在杂草稻演化及抗旱基因研究中取得重要进展

简介：近期，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研究发现，杂草稻与栽培稻之间存在基因渗入，支持了杂草稻起源于栽培稻的去驯化观点，发掘了杂草稻中的抗旱相关基因PAPH1并验证了其功能，为抗旱基因功能的深入研究与杂草稻的有效利用提供了理论支撑。近日，相关研究成果在《实验植物学杂志(The Journal of Experimental Botany）》在线发表。据韩龙植研究员介绍，杂草稻是稻田里不种自生，伴随栽培稻生长的一种“杂草型稻”，一般表现为落粒、种皮红色、颖壳褐色等特点；同时，杂草稻具有早期生长旺盛、抗病虫、抗逆等优异特性，在新基因发掘和育种研究中具有重要利用价值。该研究表明，杂草稻与水稻地方品种或选育品种存在基因交流，杂草稻的演化与地方品种和选育品种密切相关。生物信息学分析发现，在杂草稻基因组中有158个基因组区段受到了选择，包含37个已注释的抗逆相关基因。基于全基因组关联分析，挖掘出与旱胁迫下叶片干枯程度显著相关的抗旱基因PAPH1，对携带PAPH1基因不同单倍型的水稻自然群体进行抗旱性鉴定表明，拥有单倍型Hap1 和Hap2的种质中，抗旱种质分别占85.45%和77.16% 。进一步研究表明，PAPH1基因敲除突变体的抗旱性明显弱于野生型，而PAPH1基因过表达株系的抗旱性明显强于野生型；与野生型相比，基因敲除突变体叶肉细胞膜内外钙离子和钾离子流速降低，而基因过表达株系叶肉细胞膜内外钙离子和钾离子流速增加，说明PAPH1基因在杂草稻应对旱胁迫过程中发挥着重要作用。该研究为抗旱基因功能的深入研究与杂草稻的有效利用提供了理论支撑。

来源：中国农业科学院作物科学研究所

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http://agri.ckcest.cn/file1/M00/03/2C/CsgkOYalQhWAKUHuAAJOf8I1tm0163.pdf

2．专家组揭示生长素和油菜素甾醇协同调控水稻叶倾角发育

简介：近日，上海市现代种业协同创新中心薛红卫课题组在The Crop Journal在线发表了题为“Rice OsIAA6 interacts with OsARF1 and regulates leaf inclination”的研究论文，揭示了OsIAA6通过 OsIAA6-OsARF1模块抑制生长素信号并参与水稻叶倾角调控。同时OsIAA6作为OsBZR1的下游靶基因参与了BR信号调控的叶倾角形成，为解析生长素和BR协同调控叶倾角发育提供了重要线索。研究者通过筛选水稻T-DNA插入突变体库，获得了一个对生长素不敏感、叶倾角增大的突变体arr1，细胞学分析表明突变体叶倾角增大是由于叶枕部位近轴面细胞伸长增强引起的。遗传分析表明arr1表型是由于T-DNA插入在OsIAA6基因的启动子区域，导致OsIAA6基因表达上调。在利用高通量接合型酵母双杂交系统构建了水稻Aux/IAA 蛋白家族与ARF 蛋白家族的相互作用网络的基础上，发现OsIAA6可与多个OsARF蛋白互作。进一步的遗传实验证明，在arr1/iaa6-D突变体中过表达OsARF1能恢复突变体叶倾角增大的表型。此外，iaa6-D突变体中BR信号也发生了改变，凝胶阻滞实验证实OsBZR1可以直接结合OsIAA6基因启动子区域，表明OsIAA6也参与了BR信号调控的叶倾角形成。 该研究证明了OsIAA6-OsARF1作为功能性模块参与调控水稻叶倾角，为特定组合IAA-ARF的功能阐明提供了线索，也有助于了解生长素和BR协同调控叶倾角形成的机制。

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学术文献

1．Root morphological-physiological traits for japonica_indica hybrid rice with better yield performance under low N conditions（低氮条件下高产粳籼杂交稻根系形态生理特性研究）

简介：Newly bred japonica/indica hybrid rice (JIHR) cultivars might produce more grain yield and have better nitrogen-use efficiency (NUE) under low N conditions. This study determined whether an improved root system in JIHR cultivars could benefit shoot growth, physiological processes, and thereby grain yield and NUE. Four rice cultivars, including two JIHR cultivars and two local high-yielding japonica hybrid rice (JHR) cultivars were field-grown under two N application levels: 120 kg ha(-1) (low application of N, LN) and 180 kg ha(-1) (normal application of N, NN). Grain yield and the amount of N taken up from the soil were higher in JIHR cultivars than in JHR cultivars by 12.1% and 18.1% under NN and 12.5% and 14.0% under LN, respectively. Compared with JHR cultivars, JIHR cultivars had higher N partial factor productivity (PFPN) under both N treatments and higher internal N-use efficiency (IEN) and N harvest index only under LN treatment. Under LN treatment, JIHR cultivars had several improved root morphological and physiological traits, for instance, greater root dry weight (DW), root length density and root volume, longer root length, larger specific root length, deeper root distribution, larger root total and active absorption area, higher root oxidation activity (ROA), and concentration of zeatin (Z) plus zeatin riboside (ZR) in root-bleeding sap, than JHR cultivars. Generally, the results suggest that improved root morphological and physiological traits might benefit shoot growth, physiological processes, and thereby grain yield and NUE for JIHR cultivars under low N conditions.
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2．Generation of a New Glutinous Photothermosensitive Genic-Male-Sterile (PTGMS) Line by CRISPR_Cas9-Directed Mutagenesis of Wx in Rice (Oryza sativa L.)（CRISPR_Cas9对水稻（Oryza sativa L.）Wx的定向诱变产生一个新的糯光温敏核不育系（PTGMS））

简介：The Photothermosensitive Genic-Male-Sterile (PTGMS) line, Y58S, an indica rice variety, combines high-quality and high-light-efficiency use, disease and stress resistance, and excellent plant type and mating force. Y58S is widely used to assemble two-line hybrid

rice varieties, especially super hybrids. The Wx gene is the main effector gene for controlling amylose synthesis, which determines the amylose content (AC) of rice grains. By editing this gene, a glutinous line with a low AC can be obtained. In this study, the CRISPR/Cas9 system was used to mediate the editing of the Wx gene, which caused ultra-low AC mutations that produced a PTGMS glutinous rice strain with excellent waxiness. The results showed that 18 positively transformed plants were obtained from the T-0 generation, with a mutation rate of 64.29%, of which six were homozygous mutant plants, indicating that the gene-editing target had a higher targeting efficiency and a higher homozygosity mutation rate. Compared to the wild type, the AC of the mutants was significantly lower. Through molecular marker detection and screening of T-1 and T-2 generations, five homozygous T-DNA-free mutant strains were identified that were consistent with Y58S in fertility and other agronomic traits except for AC. Among these, the AC of the W-1-B-5 homozygous mutant, the glutinous PTGMS line wx-Y58S, was as low as 0.6%. Our research revealed that the Wx gene of excellent PTGMS rice can be edited to generate a new waxy PTGMS line using the CRISPR/Cas9 system. This study provided a simple and effective strategy for breeding high-yield, high-quality, and glutinous two-line hybrid rice, and provided excellent sterile lines for their large-scale application. Once put into use, waxy hybrid rice will greatly improve the yield of glutinous rice and increase social benefits.

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统计数据

1．中国杂交水稻种子行业发展趋势分析与未来前景数据统计

简介：杂交水稻种子供应过剩的态势将进一步加剧，我国的水稻种子市场一方面杂交稻改种常规趋势明显，另一方面隆平高科等优势种子企业逐渐占据垄断地位，对优质资源的控制力越来越强。2020年，全国杂交水稻落实制种面积115万亩，减幅为17%，其中早稻落实制种面积19.3万亩，中稻落实制种面积75万亩，晚稻落实制种20.7万亩，江西、湖南两省部分制种基地受连日雨水和持续低温天气影响，早制品种出现倒伏、结实率低与穗上芽等现象;福建基地病虫害发生情况好于往年。据初步统计，2021年中国杂交水稻制种面积达158万亩。从总供给看，2020年杂交水稻制种产量达2.8亿公斤左右。据初步统计，2021年杂交水稻制种面积、制种单产较2020年实现双增，新产种子2.9亿公斤。我国杂交水稻供需情况基本稳定，供需差基本保持在0.5亿公斤以内。2020年，我国杂交水稻需种量约为2.2亿公斤。2021年杂交水稻季末有效库存约0.84亿公斤，2022年杂交水稻商品种子有效供给量将超过3.5亿公斤，预计2022年杂交水稻大田用种与出口需求合计2.35亿公斤，种子供给量超出需求量约1.15亿公斤，种子供应过剩的态势将进一步加剧。2021年上半年我国杂交水稻种子市场行业CR4为31%。其中，垦丰种业、隆平高科、苏垦农发、荃银高科的业务收入达到6.93亿元、6.19亿元、3.68亿元、2.86亿元，市占率分别为10.93%、9.76%、4.51%和5.80%。

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