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杂交水稻专题

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▶ 前沿资讯

1. 专家团队在水稻镉积累与耐受机理研究方面取得新进展

简介: 水稻镉超标对我国粮食质量和水稻产业发展构成严重威胁。OsNRAMP5 是水稻吸收镉、锰的主效基因,并参与锰从根部向地上部的转运。基因编辑、自然突变和理化诱变获得的 OsNRAMP5功能缺失突变体对镉的吸收均大幅度降低,可使水稻镉含量下降90%以上,因此敲除OsNRAMP5是降低水稻镉超标风险最经济、有效的途径之一。但目前OsNRAMP5敲除突变体的镉耐受性及镉、锰积累特性对不同浓度镉胁迫的响应及其机制尚不清晰。该研究通过镉浓度梯度水培、镉吸收动力学分析和田间小区试验,发现敲除OsNRAMP5可降低水稻镉吸收,但同时会增加镉从根部向地上部的转运;随着生长介质中镉浓度的升高,敲除OsNRAMP5降低镉吸收的效应减弱,而其促进根部镉向地上部转运的效应不变。在低镉胁迫到一定程度高镉胁迫条件下,敲除OsNRAMP5降低镉吸收的效应大于其促进根系镉向地上部转运的效应,从而减少了地上部的镉积累,缓解或解除了镉对生长发育的抑制作用,增强了敲除株系的镉耐受性。但当环境镉浓度继续增高,敲除OsNRAMP5促进根系镉向地上部转运的效应可抵消甚至超过其降低镉吸收的效应,与野生型植株相比,敲除株系地上部的镉含量不变甚至更高,但镉耐受性增强;通过离子组检测、矿质元素缺乏响应基因和金属转运体编码基因的表达分析,发现在高镉胁迫下,野生型植株出现多种矿质元素的缺乏,敲除OsNRAMP5可部分或完全回补矿质元素的缺乏,从而间接提高镉耐受性。此外,该研究还发现水稻拮抗吸收镉、锰的效应主要由OsNRAMP5引起;不同浓度的镉胁迫下,敲除OsNRAMP5均可促使地上部的锰在营养生长期优先分配到幼叶,在生殖生长期优先分配到籽粒。综上所述,随着环境镉浓度的升高,OsNRAMP5转运蛋白对水稻镉吸收的贡献呈降低趋势;从低镉到高镉环境,敲除OsNRAMP5以不同的生理机制增强水稻的镉耐受性,但对地上部镉积累的效应响应环境镉浓度,因此不能通过osnramp5的镉耐受表型判断其茎叶和籽粒的镉积累变化;而OsNRAMP5敲除导致地上部的锰优先分配到幼叶或籽粒,可增强osnramp5对环境的适应性。该研究为OsNRAMP5在镉低积累水稻育种中的应用提供了理论参考。

来源: 湖南省农业科学院

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<http://agri.ckcest.cn/file1/M00/0F/FF/Csgk0GJYzPiAC9bYAALoJpYmZnw638.pdf>

2. 专家研究团队在水稻野生近缘种质资源创新方面取得新进展

简介: 充分利用野生近缘种中丰富的遗传变异是扩宽亚洲栽培稻遗传基础的重要途径。而由于生殖隔离、连锁累赘和背景噪音等的存在,很难将野生近缘种中的遗传多样性直接应用到水稻生产实践中,构建渗入系是解决这一问题的有效途径。目前,虽然利用反复选择回交及全基因组分子标记辅助选择的方法已构建一些种间及籼粳亚种内的水稻单片段染色体渗入系,与供体亲本相比,其中一些渗入系虽然含有供体亲本基因组片段,但没有明显的表型,很难用于基因定位、克隆及育种利用。与此相比,通过以重要农艺性状为标准的表型选择方法来构建渗入系是一种节省时间和人力的策略。稻属AA基因组材料是水稻种质资源的天然基因库,在漫长的独立进化过程中,不同材料独有的特性及生态适应性,形成了极其丰富的遗传多样性,拥有亚洲栽培稻所不具有的或已消失的许多优良遗传基因,但全面系统地构建稻属AA基因组8个种的农艺性状渗入系文库还未见

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报道。近日，云南农业科学院粮食作物研究所陆稻野生稻研究创新团队，在《Frontiers in Plant Science》杂志上发表了题为“A Genetic Resource for Rice Improvement: Introgression Library of Agronomic Traits for All AA Genome Oryza species” (<https://doi.org/10.3389/fpls.2022.856514>)的学术论文。该研究论文以1份长雄野生稻、13份巴蒂野生稻、6份展颖野生稻、8份南方野生稻、19份普通野生稻、20份印度野生稻、103份非洲栽培稻、160份陆稻为供体，3个表现优良的亚洲栽培稻为供体，克服了严重的生殖隔离障碍、花期不育、工作量大等重重难题，在海南三亚进行一年三季的反复表型选择和杂交，经过近十年的努力，培育了26763份遗传材料，其中，具有稳定的散穗、直立穗、密穗、稀穗、芒、匍匐生长、株高、壳色、种皮颜色、光亮、粒长、粒宽、粒重、抗旱性、陆生适应性、抗稻瘟病表型的渗入系材料6372份，育成了全世界供体类型最丰富的种间、亚种间农艺性状渗入系文库。利用这批宝贵的材料，发掘了22个分别控制粒长和粒宽的新的等位变异，基于多供体渗入系文库的优势，发现不同供体的同一座位，可以控制相同的表型，也可以控制完全相反的表型，说明有些位点在不同种中的功能或是保守的，或是不同单倍型的功能存在分化。稻属AA基因组渗入系文库不仅有助于培育具有可持续高产潜能、多样化的品质需求、多抗、环境友好的水稻品种，而且为人类认识水稻重要农艺性状的遗传和分子机制奠定了坚实的基础。

来源：云南省农业科学院

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➤ 学术文献

1. Assessment of Genetic Parameters and Gene Action Associated with Heterosis for Enhancing Yield Characters in Novel Hybrid Rice Parental Lines (杂交水稻新亲本产量性状杂种优势相关遗传参数和基因作用的评估)

简介: The technology of hybrid rice utilizing heterosis is an essential requirement for achieving food security. The current study was aimed at assessing the genetic parameters and the gene actions of 15 yield-component traits associated with heterosis, in 9 new parental lines of hybrid rice and their generated hybrids. Five cytoplasmic male sterile (CMS) lines were crossed with four restorer (R) lines using twenty generated line × tester designation hybrid combinations. The results revealed that all the traits were controlled by additive and non-additive gene actions. However, the additive variance was the main component of the total genotypic variance. Assessment of the general combining ability (GCA) detected the best combiners among the genotypes. The hybrid combinations that expressed the highest-positive specific combining ability (SCA) for grain-yield were detected. The correlation between the GCA and SCA was evaluated. The hybrid crosses with high-positive heterosis, due to having a better parent for grain yield, were detected. The principal component analysis (PCA) recorded the first four principal axis displayed Eigenvalues >1 and existing variation cumulative of 83.92% in the genotypes for yield component characteristics. Three-dimensional plots corresponding to the studied traits illustrated that the

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genotypes Guang8A × Giza181, Quan-9311A × Giza179, II-32A × Giza181, and II-32A × Giza179 are classified as possessing superior grain yield.

来源: PLANTS-BASEL

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2. Flowering Synchronization in Hybrid Rice Parental Lines at Different Sowing Dates (杂交水稻亲本在不同播期的开花同步)

简介: : Hybrid seed set on the female line depends primarily on its flowering synchronization with the restorer line (R), therefore, the sowing of male and female lines must be planned properly to achieve this. Field experiments on different sowing dates (May 1st, May 15th, and May 30th) of R lines (Giza 178R, Giza 179R, and Giza 181R) and cytoplasmic male sterile (CMS) lines (IR69625A, IR70368A, IR58025A, K17A, and G46A) were carried out at the farm of Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt during 2019 and 2020 to study the effect of sowing dates on flowering synchronization in hybrid rice. The results indicated that the synchronization of flowering between CMS lines and R lines has highly significant effects on the days to 50% heading, number of leaves, effective accumulated temperature (EAT), plant height, panicle exertion percentage, panicle length, number of fertile panicles, panicle weight, seed set percentage, harvest index and seed yield of hybrid rice. The highest seed yield (1.72 and 1.41 t ha⁻¹, respectively in 2019 and 2020) was recorded from the sowing date May 1st and the hybrid combination of Giza 178R × IR58025A (2.06 and 2.12 t ha⁻¹ in 2019 and 2020, respectively). The grain yield had a significant and highly significant positive correlation with the plant height (cm), panicle exertion percentage, panicle length, number of panicles plant⁻¹, panicle weight, seed set percentage, and harvest index. In Egypt, May 1st is the best time for the synchronization of hybrid rice lines and a combination of Giza 178R × IR58025A may be recommended for better performance.

来源: SUSTAINABILITY

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3. DNA methylation modification in heterosis initiation through analyzing rice hybrid contemporary seeds (通过分析杂交水稻当代种子, DNA甲基化修饰在杂种优势启动中的作用)

简介: Heterosis is an important biological phenomenon and widely applied in agriculture. Although many studies have been performed by using vegetative organs of F-1 hybrid plants, how heterosis (or hybrid vigor) is initiated and formed, particularly the underlying molecular mechanism, remain elusive. Hybrid contemporary seeds of rice indica varieties 9311 and PA64 were innovatively used and analysis of DNA methylome of embryo and endosperm at early developing stages revealed the globally decreased DNA methylation. Genes, especially

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those relate to hormones function and transcriptional regulation present non-additive methylation. Previously identified heterosis-related superior genes are non-additively methylated in early developing hybrid contemporary seeds, suggesting that key genes/loci responsible for heterosis are epigenetically modified even in early developing hybrid seeds and hypomethylation of hybrid seeds after cross-pollination finally result in the long-term transcriptional change of F-1 hybrid vegetative tissues after germination, demonstrating that altered DNA methylation in hybrid seeds is essential for initiation regulation and maintenance of heterosis exhibiting in F-1 hybrid plants. Notably, a large number of genes show non-additive methylation in the endosperm of reciprocal hybrids, suggesting that endosperm might also contribute to heterosis. (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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