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## 杂交水稻专题

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## ▶ 前沿资讯

### 1. 中国4‰盐度下耐盐常规稻再破纪录，亩产超691公斤

**简介:** 青岛的耐盐碱水稻产量有了新突破!10月11日,随着青岛海水稻研究发展中心(以下简称“中心”)组织的耐盐碱水稻专家测评会圆满完成,中国海水稻实现4‰盐度下耐盐常规稻产量新高度。当日上午,中心邀请山东省水稻产业技术体系首席专家周学标研究员、国家品种审定委员会水稻专业组委员张保友研究员、山东省农业科学院作物所李升东副研究员担任测产专家。对耐盐常规稻材料22ZS-39和22ZS-44进行了小面积试验田测产验收。种植试验田土壤含盐量0.34‰, pH值7.9, 测产水稻材料以及对照品种全生育期进行4‰的咸水灌溉。此次测产材料22ZS-39产量608.9kg/亩; 22ZS-44产量691.8kg/亩, 均超过了对照品种盐稻21号516.9kg/亩的产量。这两个耐盐碱常规稻产量打破往年纪录, 实现了4‰盐度下耐盐常规稻产量新高度。据青岛海水稻研究发展中心技术研发事业部部长万吉丽介绍,测产的两个水稻材料非常有代表性。“22ZS-44亩产量已经达到了691.8kg, 是一个非常不错的成绩, 很有发展潜力。2017年中心测产的一个杂交籼稻品种, 在千分之六的咸水灌溉下, 产量达到620.95kg/亩。但因为它是杂交稻品种, 杂交稻普遍比常规稻产量高很多, 所以今天测产的两两种水稻材料在全生育期盐度4‰的咸水灌溉的条件下, 产量应该是很不错了, 在全国来说也是比较高的。” 青岛海水稻研究发展中心团队自2012年在袁隆平院士的带领下开始做耐盐碱水稻育种研究。育种过程中通过杂交育种、诱变育种及生物育种相结合的育种手段, 缩短育种周期。2019年耐盐常规稻的产量为295.9 kg/亩, 2021年耐盐常规稻的产量为590.6 kg/亩, 2022年4‰盐度下耐盐常规稻的最高产量为691.8kg/亩。团队在育种方面不断突破, 并且每年持续不断输出新的稳定的耐盐碱水稻新品种。与此同时, 十年间, 中国海水稻已从科研试验阶段, 发展到产业化规模化推广, 实现了“从无到有、从小到大”的飞跃。截至2021年底, 中国海水稻种植面积达到60万亩, 分布在黑龙江、山东、江苏、新疆、内蒙古、浙江等十多个省份, 品种覆盖全国四大类典型盐碱地。2022年, 中国推广海水稻种植的面积突破100万亩。

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### 2. 重度盐碱地种上水稻 万亩荒滩变良田

**简介:** 百谷盈满为丰, 颗粒归仓为收。近日, 中国科学院吉林大安农田生态系统国家野外科学观测研究站在大安市红岗子乡中科院“黑土粮仓”科技会战盐碱地水田万亩核心示范区, 召开盐碱地“良田+良种+良法”高效治理模式专家现场测产交流会。在场的院士、专家们看到“不长粮”的盐碱地通过酸性磷石膏改良的重度盐碱地水稻产量达到517.39公斤/亩, 无不感到惊喜。10月7日上午, 测产交流会在吉林省大安市红岗子乡按时举行。经过推选, 中国科学院院士、华南农业大学刘耀光教授担任本次测产组的组长。测产要通过收割、丈量、称重、除水、去杂等严格程序。首先进行的收割机进行收割, 记者注意到通过土壤改良的稻田地里稻子长势喜人, 在同一块地没有经过土壤改良的稻叶已经枯萎。通过土壤剖面可以清晰的看到, 改良的盐碱地泥土发生了巨大变化, 稻子根系已经扎得很牢固。而没有经过改良的稻田地土壤依然白花花一片。通过测产组测产,

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利用酸性磷石膏改良的重度盐碱地（改良前土壤pH 10.58，EC 0.42mS/cm）水稻产量达到517.39公斤/亩，而未实施土壤改良的水田产量仅为35.16公斤/亩，增产高达13.7倍。按此推算，每改造1000亩盐碱地即可增产粮食100万斤以上。

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## ➤ 学术文献

### **1. Analysis of parental genetic diversity and its impact on grain yield and quality of japonica hybrid rice in northern China (北方杂交粳稻亲本遗传多样性及其对产量和品质的影响)**

简介：The relationship between parental genetic differences and the quality and yield of japonica hybrid rice strongly influences japonica hybrid rice breeding. In this study, 137 parental lines of japonica hybrid rice were genotyped using 8K rice SNP-Chips to characterize their genetic diversity, population structure, and indica -genotype proportion. The genetic diversity of total parental lines averaged 0.264, with values of 0.287 for restorer lines and 0.148 for the sterile lines. The introduction of indica lineage increased the genetic diversity of restorer lines relative to that of sterile lines. By model-based population structure analysis, the 137 lines were divided into 14 groups. According to the grouping results, eight restorer lines and five sterile lines were selected from different groups for cross breeding, yielding 40 japonica hybrid rice combinations (F1). Investigation of the yield and quality of these combinations showed that high -yield combinations could be obtained by increasing parental genetic distance to 0.8-0.9, a result accomplished largely by the introduction of indica genomic components of restorer lines. To further improve grain quality, the genetic distance between parents should be reduced to 0.4-0.5, suggesting an indica -genotype proportion of 30%-40% for restorer lines. This study may provide a reference for breeding of japonica hybrid rice.(c) 2022 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. This is an open access article under the CC BY-NC -ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

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### **2. Transcriptome profiling of two super hybrid rice provides insights into the genetic basis of heterosis (两个超级杂交水稻的转录组分析提供了杂种优势遗传基础的见解)**

简介：Background: Heterosis is a phenomenon that hybrids show superior performance over

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their parents. The successful utilization of heterosis has greatly improved rice productivity, but the molecular basis of heterosis remains largely unclear. Results: Here, the transcriptomes of young panicles and leaves of the two widely grown two-line super hybrid rice varieties (Jing-Liang-You-Hua-Zhan (JLYHZ) and Long-Liang-You-Hua-Zhan (LLYHZ)) and their parents were analyzed by RNA-seq. Transcriptome profiling of the hybrids revealed 1,778 similar to 9,404 differentially expressed genes (DEGs) in two tissues, which were identified by comparing with their parents. GO, and KEGG enrichment analysis showed that the pathways significantly enriched in both tissues of two hybrids were all related to yield and resistance, like circadian rhythm (GO:0,007,623), response to water deprivation (GO:0,009,414), and photosynthetic genes (osa00196). Allele-specific expression genes (ASEGs) were also identified in hybrids. The ASEGs were most significantly enriched in ionotropic glutamate receptor signaling pathway, which was hypothesized to be potential amino acid sensors in plants. Moreover, the ASEGs were also differentially expressed between parents. The number of variations in ASEGs is higher than expected, especially for large effect variations. The DEGs and ASEGs are the potential reasons for the formation of heterosis in the two elite super hybrid rice. Conclusions: Our results provide a comprehensive understanding of the heterosis of two-line super hybrid rice and facilitate the exploitation of heterosis in hybrid rice breeding with high yield heterosis.

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### **3. The Next Generation of Rice: Inter-Subspecific Indica-Japonica Hybrid Rice (下一代水稻: 亚种间籼粳杂交水稻)**

简介: Rice (*Oryza sativa*) is an important food crop and has two subspecies, indica and japonica. Since the last century, four generations of rice varieties have been applied to rice production. Semi-dwarf rice, intra-subspecific hybrid rice, and inter-subspecific introgression rice were developed successively by genetic modification based on the first generation of tall rice. Each generation of rice has greater yield potential than the previous generation. Due to the stronger heterosis of indica-japonica hybrids, utilization of the inter-subspecific heterosis has long been of interest. However, indica-japonica hybrid sterility hinders the utilization of heterosis. In the past decades, indica-japonica hybrid sterility has been well understood. It is found that indica-japonica hybrid sterility is mainly controlled by six loci, S5, Sa, Sb, Sc, Sd, and Se. The indica-japonica hybrid sterility can be overcome by developing indica-compatible japonica lines (ICJLs) or wide-compatible indica lines (WCILs) using genes at the loci. With the understanding of the genetic and molecular basis of indica-japonica hybrid sterility and the development of molecular breeding technology, the development of indica-japonica hybrid rice has become possible. Recently, great progress has been made in breeding indica-japonica hybrid rice. Therefore, the indica-japonica hybrid rice will be the next generation of rice. It is expected that the indica-japonica hybrid rice will be widely applied in rice production in the near future.

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