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杂交水稻专题

本期导读

前沿资讯

学术文献

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前沿资讯

1. 发现新的水稻黑条矮缩病抗性基因

简介：水稻病毒病有水稻“癌症”之称，严重威胁水稻的生产安全。近年来，由水稻黑条矮缩病毒（RBSDV）和南方水稻黑条矮缩病毒（SRBSDV）引起的病毒病对我国的水稻生产危害严重，后者被农业农村部列为水稻上仅有的两个一类农作物病虫害之一。江苏农业科学院周彤团队近20年以来一直致力于水稻病毒病的研究，在水稻病毒病的抗性鉴定与评价方法、抗性资源筛选、以及抗病基因的发掘与利用等方面开展了深入系统的研究，取得了重大突破和一系列阶段性成果。在该研究中，通过对水稻资源的自然接种和人工接种鉴定，筛选出高抗水稻黑条矮缩病的水稻品种乌壳。利用乌壳构建的分离群体，定位了抗黑条矮缩病的QTL，其中第6染色体上的QTL qRBSDV6效应最强，位于1.8 Mb的区间内。通过对该区段内基因的序列对比分析，筛选出蛋白质功能区域在亲本间存在差异的候选基因进行转基因验证。发现OsGLK1过表达后转基因植株的抗性显著增强。同时，使用RNAi干扰抑制OsGLK1的表达后，转基因植株对黑条矮缩病的抗性显著降低。结果表明OsGLK1是主效QTL qRBSDV6的功能基因，其编码蛋白含有Myb结构域，属于Golden 2-like1转录因子家族。这是该团队继首次公布水稻RBSDV抗性基因OsAP47后鉴定出的水稻上第二个RBSDV抗性基因，这一结果对水稻品种的抗性改良具有重要意义。

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2. 杂交水稻全程机械化制种关键技术研究取得新进展

简介：种子是农业的“芯片”，水稻种子是保障粮食安全的关键，我国水稻常年种植面积约4.5亿亩，其中杂交水稻占50%，年用种量超过2.2亿公斤。杂交水稻制种产量的高低和种子质量的好坏，直接关系到杂交水稻的生产发展与粮食安全。针对福建省省杂交水稻制种用工多以及种子收晒难导致制种规模难以扩大的问题，福建省农业科学院水稻研究所水稻遗传育种科技创新团队历经9年联合科技攻关，取得了创新性成果。开展密集烤房干燥水稻种子技术研究，首创密集烤房干燥水稻种子技术，实现种子及时烘干，提高种子质量；发明的静态批式谷物烘干机在保持卧式烘干机的优点下，实现种子破损率低和自动进出仓；开展杂交水稻制种授粉后立即割除父本技术研究，明确授粉后割除父本时间、父本高度、稻秆放置等技术指标，实现阴雨天气种子迅速抢收，促进制种增产增收；优化福建省杂交水稻制种母本机插技术，研发制种专用插秧机并成为主流机型，开展了育秧、母本机插、单行父本机插等技术研究，集成一套适于福建丘陵山区的杂交水稻机械化制种技术，在耕整、育插秧、喷施农药及赤霉素、父本割除、收获、烘干等环节实现机械化。该成果获得授权专利7件，其中发明专利1件；制定了福建省地方标准《密集烤房干燥水稻种子技术规程》，入选福建省农业主推技术2项，发表论文12 篇。2019-2021年在我国杂交水稻制种区域累计推广188.8万亩次，新增稻种1483.9万千克，新增产值3.2亿元，节约成本1.0亿元，增收节支4.2亿元。其中利用密集烤房干燥种子量占全省制种总产量的77.2%。

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3. 节水抗旱稻新品种“沪旱1516”成功转化

简介：11月9日上午，上海农业科学院基因中心选育的节水抗旱稻“沪旱1516”单一品种在第三个区域达成独占实施许可交易。“籼型常规节水抗旱稻‘沪旱1516’湖南省、湖北省15年独占实施许可”项目通过上海农村产权交易所竞价系统完成报价，并在上海国际商品拍卖有限公司拍卖平台落锤，经过3位意向竞买人实时在线13轮竞价，最终实现交易溢价30%，受让方为江西俊谷生物科技有限公司。此项成果转化也是首次组织操作的单一品种分区域实施许可的新方式。此前，“‘沪旱1516’ 江西省、福建省15年独占实施许可”项目以及“‘沪旱1516’ 安徽省、江苏省15年独占实施许可”项目均通过上海农村产权交易所分别转化给江西俊谷生物科技有限公司和安徽荃银高科种业股份有限公司。“沪旱1516”是首个即将通过国审的籼型常规节水抗旱稻品种，取得了植物新品种权（CNA20191006109），其在长江中下游作一季稻种植，全生育期114.5天，比对照早熟0.5天，结实率86.9%，千粒重22.6克。抗性:中感稻瘟病；抗旱性3级；中感白叶枯病；中抗褐飞虱；抽穗期耐热性强。米质达部标三级。2019－2020年参加长江中下游节水抗旱稻组区域试验，两年区域试验平均亩产553.8千克，比对照增产2.2%。目前，基因中心的节水抗旱稻系列品种已转化给上海天谷、江苏丰大、安徽荃银高科、湖北中垦锦绣华农、四川荃银天府、江西俊谷等种业企业。中心将继续与合作企业共同携手，在节水抗旱稻的科技研发、应用推广、配套栽培技术、市场服务等各个领域紧密合作，共同推进节水抗旱稻事业的发展，助力我国乡村振兴、粮食安全、食品安全和生态安全。

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学术文献

1. Genetic relationships and identification of core germplasm among rice photoperiod- and thermo-sensitive genic male sterile lines（水稻光温敏核不育系的遗传关系及核心种质鉴定）

简介：BackgroundHarnessing heterosis is one of the major approaches to increase rice yield and has made a great contribution to food security. The identification and selection of outstanding parental genotypes especially among male sterile lines is a key step for exploiting heterosis. Two-line hybrid system is based on the discovery and application of photoperiod- and thermo-sensitive genic sensitive male sterile (PTGMS) materials. The development of wide-range of male sterile lines from a common gene pool leads to a narrower genetic diversity, which is vulnerable to biotic and abiotic stress. Hence, it is valuable to ascertain the genetic background of PTGMS lines and to understand their relationships in order to select and design a future breeding strategy.ResultsA collection of

118 male sterile rice lines and 13 conventional breeding lines from the major rice growing regions of China was evaluated and screened against the photosensitive (pms3) and temperature sensitive male sterility (tms5) genes. The total gene pool was divided into four major populations as P1 possessing the pms3, P2 possessing tms5, P3 possessing both pms3 and tms5 genes, and P4 containing conventional breeding lines without any male sterility allele. The high genetic purity was revealed by homozygous alleles in all populations. The population admixture, principle components and the phylogenetic analysis revealed the close relations of P2 and P3 with P4. The population differentiation analysis showed that P1 has the highest differentiation coefficient. The lines from P1 were observed as the ancestors of other three populations in a phylogenetic tree, while the lines in P2 and P3 showed a close genetic relation with conventional lines. A core collection of top 10% lines with maximum within and among populations genetic diversity was constructed for future research and breeding efforts.ConclusionThe low genetic diversity and close genetic relationship among PTGMS lines in P2, P3 and P4 populations suggest a selection sweep and they might result from a backcrossing with common ancestors including the pure lines of P1. The core collection from PTGMS panel updated with new diverse germplasm will serve best for further two-line hybrid breeding.

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2. Genomic selection: A breakthrough technology in rice breeding(基因组选择：水稻育种的突破性技术)

简介：Rice (Oryza sativa) provides a staple food source for more than half the world population. However, the current pace of rice breeding in yield growth is insufficient to meet the food demand of the ever-increasing global population. Genomic selection (GS) holds a great potential to accelerate breeding progress and is cost-effective via early selection before phenotypes are measured. Previous simulation and experimental studies have demonstrated the usefulness of GS in rice breeding. However, several affecting factors and limitations require careful consideration when performing GS. In this review, we summarize the major genetics and statistical factors affecting predictive performance as well as current progress in the application of GS to rice breeding. We also highlight effective strategies to increase the predictive ability of various models, including GS models incorporating functional markers, genotype by environment interactions, multiple traits, selection index, and multiple omic data. Finally, we envision that integrating GS with other advanced breeding technologies such as unmanned aerial vehicles and open-source breeding platforms will further improve the efficiency and reduce the cost of breeding. (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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