2022年 第1期 总36期

种质资源保护与创制专题

本期导读

前沿资讯

1. 科研人员研发出4套基于CRISPR/Cas系统的病原体核酸检测工具

2. 基因编辑“流水线” 助力作物病害防控

3. 江苏省自主创新资金项目“精准基因编辑技术研发及非转基因抗除草剂优质水稻新材料创制”启动会顺利召开

4. PLoS Pathogens— 朱勃/陈功友联合团队研究揭示植物病原细菌sRNA致病新机制

学术文献

1.AtPHB6和AtSOT12之间的两个相互作用蛋白通过ROS信号调节植物抗盐性

2. 盐生植物基因ScVTC2通过AsA介导的光合增强作用赋予植物对氧化胁迫的抗性

3.bZIP72通过激活ADH1促进浸没水稻种子萌发和胚芽鞘伸长

4.TaFLZ2D通过优越的离子胁迫耐受能力和ROS解毒能力增强耐盐胁迫能力

5. 水稻（Oryza sativa L.）1号染色体长臂上两个排斥力连锁的粒重数量性状位点的分离

相关专利

1. 一种提高纤维素酶催化效率的方法及突变体5I77-M2

2. 耐低温纤维素酶突变体

中国农业科学院农业信息研究所
联系人：王丽娟，张玉玮，信丽媛
联系电话：022-23678616
邮箱：agri@ckcest.cn
2022年1月7日

前沿资讯

1．科研人员研发出4套基于CRISPR/Cas系统的病原体核酸检测工具

简介：近日，中国农业科学院作物科学研究所作物分子育种技术和应用创新团队鉴定了RfxCas13d靶向RNA引发“反式切割”活性的基本特征，研制出基于RfxCas13d、LwaCas13a、LbCas12a与AsCas12a的多套核酸检测工具，并研发出田间实时可视化灵敏定性定量检测方法，为动植物病原体检测提供了高效、低成本的开发途径，具有广阔的技术开发场景与应用价值。相关研究结果在线发表在《中国科学:生命科学（Science China-Life Sciences）》上。据谢传晓研究员介绍，植物真菌性病害、细菌性病害及病毒性病害严重危害作物生产与品质安全，如禾谷镰孢菌和拟轮枝镰孢菌是玉米穗粒腐、茎腐病、小麦赤霉病的罪魁祸首；水稻黑条矮缩病毒则通过灰飞虱在水稻、小麦和玉米宿主之间迁移传播，严重威胁水稻、小麦和玉米生产。建立快速、准确、灵敏及便携的病原体诊断技术，可为病害的早期预警与绿色防控提供重要依据。针对以上植物病害病原体，团队成员研制了多套基于CRISPR-Cas12a和CRISPR-Cas13系统“反式切割”活性的病原体核酸诊断技术。通过优化样本处理方法，可实现田间实际样本粗提物稀释液的灵敏检测，且可利用小型手持式荧光仪或试纸条进行田间现场定性读取结果。此外，以禾谷镰孢与拟轮枝镰孢菌复合侵染为样本，建立了基于Cas12/Cas13联合应用的复合检测，实现了一个检测能诊断判读多种病原，进一步拓展了检测工具的应用场景与潜力。此外，该系列检测方法还可应用于食品安全质量检验、动植物检疫、转基因检测、动植物群体的基因分型与基因表达检测等，具有重要的应用价值。该研究得到国家自然科学基金和中国农科院科技创新工程等项目资助。

来源：中国农业科学院作物科学研究所

发布日期:2022-01-06

全文链接:

https://www.caas.cn/xwzx/kyjz/318666.html

2．基因编辑“流水线” 助力作物病害防控

简介：华中农业大学谢卡斌课题组开发出一套名为“FLASH”的基因编辑“流水线”，不仅优化了整个基因编辑流程，还可用来快速鉴别基因编辑材料的“身份”，帮助找出农作物中与抗病、抗逆、产量等重要农艺性状相关的基因。近日，华中农业大学作物遗传改良国家重点实验室暨湖北洪山实验室谢卡斌教授课题组，在《分子植物》发表的研究论文，报道了一种大规模、高通量编辑植物基因的方法，并利用该方法编辑了水稻中全部受体激酶基因，为快速鉴定抗病、抗逆相关的基因提供了新资源。

来源：华中农业大学

发布日期:2021-12-09

全文链接:

http://news.hzau.edu.cn/2021/1209/62198.shtml

3．江苏省自主创新资金项目“精准基因编辑技术研发及非转基因抗除草剂优质水稻新材料创制”启动会顺利召开

简介：近日，由卓越创新中心主持的江苏省农业科技自主创新资金项目“精准基因编辑

技术研发及非转基因抗除草剂优质水稻新材料创制[CX(21)1002]”实施方案论证暨项目启动会顺利召开。江苏省科技厅农村处处长杨天和、科教处处长姜雪忠、种业处处长何旭平、江苏省财政厅农业农村处副处长储惠平、江苏省植保植检站站长田子华、江苏省农药总站站长邓建平等专家应邀对项目实施方案进行指导。科研处、卓越创新中心等相关负责人，项目参加单位骨干等20余人参加了会议。会议由院科研处处长余向阳主持。项目负责人杨郁文研究员从研究背景、研究内容、实施方案、任务分工及经费分配管理等方面进行了详细汇报。项目参加单位南京农业大学、江苏润扬种业股份有限公司项目骨干对项目背景及实施方案作补充说明。与会专家围绕项目实施方案及项目管理进行了细致的讨论，肯定了项目选题意义、方案的可行性和创新性。同时，专家从技术创新、子课题间的衔接、实际应用等方面提出了建设性意见和建议。还与项目负责人交流讨论了“精准基因编辑技术研发”、“抗除草剂种质创新利用”、以及“除草剂科学 使用”等问题。 通过项目论证咨询，进一步优化了研究方案，为项目的实施与推进奠定了坚实基础。

来源：江苏省农业科学院

发布日期:2021-11-12

全文链接:

http://newkeyan.jaas.ac.cn/show-1534-990-1.html

4. PLoS Pathogens— 朱勃/陈功友联合团队研究揭示植物病原细菌sRNA致病新机制

简介：国际著名学术期刊PLoS Pathogens于2021年7月24日在线发表了上海交通大学农业与生物学院朱勃、陈功友联合团队研究成果“A key antisense sRNA modulates the oxidative stress response and virulence in Xanthomonas oryzae pv. oryzicola”，揭示了稻黄单胞菌稻生致病变种Xanthomonas oryzae pv. oryzicola (Xoc)中sRNA适应氧化应激环境下对水稻致病性的研究机制。原核生物和真核生物中除了三种经典的RNA，如 tRNA, rRNA,和 mRNA 外，还存在着一类新型的具有重要调控功能的非编码RNA（ncRNA），在细菌中被统称为 small RNA（sRNA），大小在 50-500nt 之间，主要作用方式是通过碱基互补配对与靶标基因 mRNA结合，进而影响 mRNA 的稳定性和翻译从而在转录水平上调控基因表达。研究团队发现sRNA Xonc3711通过碱基互补配对靶标DNA结合蛋白Xoc_3982影响其转录水平，ChIP-Seq表明Xoc_3982能够与三型效应因子XopC2结合从而影响其致病性。sRNA Xonc3711通过增加生物膜的形成来增加氧化应激耐受性和和在水稻上的毒性(图)。目前对于稻黄单胞菌稻生致病变种Xoc中sRNA的生物学功能仍处于研究初始阶段，因此开展sRNA 的研究，并发现具有重要功能的 sRNA，对进一步揭示细菌致病机理等和防控所致的植物病害提供了新的思路。上海交通大学农业与生物学院博士研究生吴言和王赛为论文的共同第一作者，上海交通大学长聘教轨副教授朱勃和长聘教授陈功友为论文的共同通讯作者。朱勃博士2017年以长聘教轨副教授任职交大农业与生物学院。该研究得到了科技部重点研发（项目编号2017YFD0201108和2018YFD0201202）等项目的资助。

来源：上海交通大学农业与生物学院

发布日期:2021-07-26

全文链接:

http://www.agri.sjtu.edu.cn/Data/View/5925

学术文献

1. Two interaction proteins between AtPHB6 and AtSOT12 regulate plant salt resistance through ROS signaling(AtPHB6和AtSOT12之间的两个相互作用蛋白通过ROS信号调节植物抗盐性)

简介：In the past, the PHB gene function was mainly focused on anti-cell proliferation and antitumor effects. But the molecular mechanism of the PHB gene regarding saline and oxidative stresses is unclear. To study the role of AtPHB6 in salt and oxidative stress, AtPHB6 was cloned from A. thaliana. Bioinformatics analysis showed that AtPHB6 was closely related to AtPHB1 and AtPHB2, which are both type II PHB. RTqPCR results indicated that the AtPHB6 in the leaves and roots of A. thaliana was obviously induced under different stress treatments. AtPHB6-overexpressing plants were larger and more lush than wild-type and mutant plants when placed under stress treatments during seed germination. The root length and fresh weight of AtPHB6 transgenic plants showed the best resistance compared to wild-type plants under different treatments, in contrast, the AtPHB6 mutants had the worst resistance during the seedling stage.AtSOT12 was an interacting protein of AtPHB6, which screened by yeast two-hybrid system. The interaction between the two proteins were further confirmed using in vitro pull-down experiments and in vivo BiFC experiments. Subcellular localization showed both AtPHB6 and AtSOT12 protein expressed in the nucleus and cytoplasm. The H2O2 content in both the transgenic AtPHB6 and AtSOT12 plants were lower than that in the wild type under stresses. Thus, AtPHB6 increased plant resistance to salt stress and interacted with the AtSOT12 protein.

来源：Plant Physiology and Biochemistry

影响因子：4.270/Q1

发布日期:2021-12-01

全文链接:

http://agri.ckcest.cn/file1/M00/03/1E/CsgkOWHpBOGAZtXpALKdrtY-deU001.pdf

2. The halophyte gene ScVTC2 confers resistance to oxidative stress via AsA-mediated photosynthetic enhancement(盐生植物基因ScVTC2通过AsA介导的光合增强作用赋予植物对氧化胁迫的抗性)

简介：Various abiotic stresses commonly cause excessive production of reactive oxygen species (ROS) and result in oxidative stress, which challenges the physiological homeostasis of plants. Maintaining a delicate balance between ROS generation and removal is critical for plants to cope with stressful environments. Suaeda corniculata is a typical euhalophyte with strong tolerance to salt stress, but its mechanism of ROS detoxification to prevent oxidative stress is unknown. Here, a combined analysis of RNA-Seq and photosynthetic assays was performed on S. corniculata under oxidative stress to uncover the underlying mechanism that modulates oxidative tolerance. Our results showed that all genes involved in the pathway of ROS scavenging, especially the AsA-GSH pathway, were highly enriched under oxidative stress. Notably, VTC2 (GGPase), which functions in the L-galactose pathway of AsA

synthesis, was significantly upregulated. Arabidopsis transgenic plants with heterologous expression of ScVTC2 showed elevated AsA and increased tolerance to oxidative stress. Furthermore, ScVTC2 also established better photosynthetic capacity in these plants upon oxidative treatment. Thus, ScVTC2 not only functioned as an effective ROS scavenger but also as a protector of the photosynthetic apparatus in S. corniculata and allowed plants to respond to and tolerate oxidative stress.

来源：Plant Physiology and Biochemistry

影响因子：4.270/Q1

发布日期:2021-11-03

全文链接:

http://agri.ckcest.cn/file1/M00/0F/F0/CsgkOGHpBPmAFsMOAH-gNVsA0iM339.pdf

3. bZIP72 promotes submerged rice seed germination and coleoptile elongation by activating ADH1(bZIP72通过激活ADH1促进浸没水稻种子萌发和胚芽鞘伸长?)

简介：Seed germination and coleoptile elongation in response to flooding stress is an important trait for the direct seeding of rice. However, the genes regulating this process and the underlying mechanisms are little understood.In this study, bZIP72 was identified as a positive regulator of seed germination under submergence. Transcriptionof bZIP72 was submergence induced. Over-expression of bZIP72 enhanced submerged seed germination and coleoptile elongation, while bzip72 mutants exhibited the opposite tendency. Using biochemical interaction assays, we showed that bZIP72 directly binds to the promoter of alcohol dehydrogenase 1 (ADH1), enhances its activity, and subsequently produces more NAD+, NADH and ATP involved in the alcoholic fermentation and glycolysis pathway, ultimately providing necessary energy reserves thus conferring tolerance to submergence. In summary, this research provides novel insights into bZIP72 participation in submerged rice seed germination and coleoptile elongation.

来源：Plant Physiology and Biochemistry

影响因子：4.270/Q1

发布日期:2021-11-02

全文链接:

http://agri.ckcest.cn/file1/M00/0F/F0/CsgkOGHpAy-AL_u-ADexo8Cvr90775.pdf

4. TaFLZ2D enhances salinity stress tolerance via superior ability for ionic stress tolerance and ROS detoxification(TaFLZ2D通过优越的离子胁迫耐受能力和ROS解毒能力增强耐盐胁迫能力)

简介：Salinity stress severely affects plant growth and crop productivity. FCS-like zinc finger family genes (FLZ) play important roles in plant growth and stress responses. But most information of this family obtained was involved in sucrose signaling, limited function has been known in response to salinity stress. In this study, a novel FLZ gene TaFLZ2D has been

isolated and characterized in response to salinity stress in wheat. TaFLZ2D was induced by both salinity stress and exogenous abscisic acid (ABA). Its transcript level was substantially higher in the salt resistant wheat cultivar SR3 than in its closely related but salt sensitive cultivar JN177. Transient expression in Nicotiana benthamiana leaf epidermal cells demonstrated TaFLZ2D was localized both in the cytoplasm membrane and nucleus. Constitutive expression of TaFLZ2D in Arabidopsis thaliana improved salinity stress tolerance and ABA sensitivity. Phenotype analysis under KCl and mannitol treatment demonstrated TaFLZ2D increased salinity stress tolerance mainly due to the superior ability to cope with ionic stress. TaFLZ2D over-expressing lines increased abscisic acid synthesis, peroxidase activity and reduced rate of water loss. Transcriptomic analysis demonstrated over-expression of TaFLZ2D regulated ABA-dependent and independent signaling pathway related genes expression and activated antioxidant related genes expression under normal condition and Ca2+ signaling related genes expression under NaCl treatmemt. Taken together, TaFLZ2D is a positive regulator of salinity stress tolerance, which contributes to salinity stress mainly through superior ability for ionic stress tolerance and ROS detoxification.、

来源：Plant Physiology and Biochemistry

影响因子：4.270/Q1

发布日期:2021-11-01

全文链接:

http://agri.ckcest.cn/file1/M00/03/1E/CsgkOWHpBeSASFYCAKZmocoxb80941.pdf

5．Dissection of two quantitative trait loci for grain weight linked in repulsion on the long arm of chromosome 1 of rice (Oryza sativa L.)(水稻（Oryza sativa L.）1号染色体长臂上两个排斥力连锁的粒重数量性状位点的分离?
)

简介：Grain weight is a key determinant of grain yield in rice. Three sets of rice populations with overlapping segregating regions in isogenic backgrounds were established in the generations of BC2F5, BC2F6 and BC2F7, derived from Zhenshan 97 and Milyang 46, and used for dissection of quantitative trait loci (QTL) for grain weight. Two QTL linked in repulsion phase on the long arm of chromosome 1 were separated. One was located between simple sequence repeat (SSR) markers RM11437 and RM11615, having a smaller additive effect with the enhancing allele from the maintainer line Zhenshan 97 and a partially dominant effect for increasing grain weight. The other was located between SSR markers RM11615 and RM11800, having a larger additive effect with the enhancing allele from the restorer line Milyang 46 and a partially dominant effect for increasing grain weight. When the two QTL segregated simultaneously, a residual additive effect with the enhancing allele from Milyang 46 and an over-dominance effect for increasing grain weight were detected. This suggests that dominant QTL linked in repulsion phase might play an important role in heterosis in rice. Our study also indicates that the use of populations with overlapping segregating regions in isogenic backgrounds is helpful for the dissection of minor linked QTL.

来源： The Crop Journal
影响因子： 4.407/Q3
发布日期:2013-10-01
全文链接:
http://agri.ckcest.cn/file1/M00/0F/F0/CsgkOGHpA-iAFOP5AAiOCPHX-3g094.pdf

相关专利

1．一种提高纤维素酶催化效率的方法及突变体5I77-M2

简介：本发明涉及基因工程领域，具体涉及一种提高纤维素酶催化效率的方法及突变体5I77-M2。所述方法包括将氨基酸序列如SEQ ID NO：1所示的野生型纤维素酶的第300位的氨基酸Thr突变为氨基酸Pro和将第307位点的氨基酸Asp突变为氨基酸Pro、以及第193位的氨基酸Asn突变为Ala的步骤。酶促反应的最适pH值、最适温度并未发生变化；以羧甲基纤维素钠为底物时，本发明的突变体5I77-M2的比活力比突变体5I77-M提高了50%。
来源： 佰腾网
发布日期:2021-11-23
全文链接:
http://agri.ckcest.cn/file1/M00/0F/F0/CsgkOGHpB92AUFMEAAZfyeBTv-k605.PDF

2．耐低温纤维素酶突变体

简介：本发明涉及基因工程与蛋白质改造技术领域，具体涉及一种耐低温纤维素酶突变体及其应用。本发明提供的突变体在选自下组中的至少一个位置上包含氨基酸的取代：120，130，179。所述突变体在40℃低温条件下的相对酶活均得到显著提高，从而有利于纤维素酶在纺织领域中的广泛应用。
来源： 佰腾网
发布日期:2021-05-14
全文链接:
http://agri.ckcest.cn/file1/M00/0F/F0/CsgkOGHpBwCAVbF8AAfBV70RPvk538.PDF