



2018年第49期总109期

农业生物技术专题

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▶ 前沿资讯

1. 中科院稻米新品种努力破解“优质稻不高产”难题

简介: 日前,由安徽省种子管理总站、安徽省农技推广总站以及安徽农业大学相关专家组成的专家组,对中科院合肥物质科学研究院技术生物所培育的稻米新品种“科辐粳9号”现场测产,在稻虾共养的生态模式下实收亩产569.4公斤,努力破解“优质稻不高产”的农业传统难题。“科辐粳9号”被称为“科技稻”,是近期中科院科研人员利用分子设计育种技术培育出的新品种。其多项品质指标均达到国内顶尖优质稻水平,适应种植范围广,在安徽淮河以南及江苏、浙江、上海等地区均可种植。今年以来,科研人员在安徽省庐江县、宿松县、长丰县等地实施了600亩“科辐粳9号”稻虾共养示范种植,整体效果突出。产量高、米质优良,未使用化学农药但无病虫害发生。同时实行订单回收生产,回收价格比市场普通水稻高约40%,每亩实现虾、稻收益超过5000元,达到常规种植效益的3倍以上。

来源: 科学网

发布日期:2018-11-23

全文链接:

<http://news.sciencenet.cn/htmlnews/2018/11/420295.shtm>

2. California pesticide regulators recommend new chlorpyrifos restrictions (美国加州农药监管机构提议设立新毒死蜱限用法案)

简介: The California Department of Pesticide Regulation (DPR) announced last Thursday that it has recommended new interim restrictions on the use of the pesticide chlorpyrifos, which is used on more than 800,000 acres and more than 60 crops in the state including tree nuts, grapes, citrus, vegetables, cotton, and alfalfa. The new measures will provide increased protections from potential exposure to the pesticide while DPR completes a formal regulatory process to list chlorpyrifos as a “toxic air contaminant” and develops permanent restrictions on its use. The department is recommending that county agricultural commissioners (CAC’s) begin implementing the interim measures on Jan. 1. “DPR has been working with growers for years to find alternatives to this pesticide while also taking action to curtail its use through the regulatory process,” said DPR Director Brian Leahy. “These interim measures represent a significant step in our ongoing effort to protect human health and the environment.”

来源: AgroNews

发布日期:2018-11-19

全文链接:

<http://news.agropages.com/News/NewsDetail—28426.htm>

▶ 学术文献

1. Adaption of roots to nitrogen deficiency revealed by 3-D quantification and proteomic analysis (通过3-D量化和蛋白质组学分析揭示根对氮缺乏的适应性)

简介: Rapeseed (*Brassica napus* L.) is an important oil crop worldwide. However, severe inhibition of rapeseed production often occurs in the field due to nitrogen (N) deficiency. The root system is the main organ to acquire N for plant growth, but little is known about the mechanisms underlying rapeseed root adaptations to N deficiency. Here, dynamic changes in root architectural traits of N-deficient rapeseed plants were evaluated by 3-D in situ quantification. Root proteome responses to N deficiency were analyzed by the tandem mass tag (TMT)-based proteomics method, and related proteins were further characterized. Under N deficiency, rapeseed roots become longer, with denser cells in the meristematic zone and larger cells in the elongation zone of root tips, and also become softer with reduced solidity. A total of 171 and 755 differentially expressed proteins (DEPs) were identified in short- and long-term N-deficient roots, respectively. The abundance of proteins involved in cell wall organization or biogenesis was highly enhanced, but most identified peroxidases were reduced in the N-deficient roots. Notably, peroxidase activities were also decreased, which might promote root elongation while lowering the solidity of N-deficient roots. These results were consistent with the cell wall components measured in the N-deficient roots. Further functional analysis using transgenic *Arabidopsis thaliana* plants demonstrated that the two root-related DEPs contribute to the enhanced root growth under N-deficiency conditions. These results provide insights into global changes of rapeseed root responses to N deficiency and may facilitate the development of rapeseed cultivars with high N use efficiency through root-based genetic improvements.

来源: Plant Physiology 期刊

发布日期: 2018-11-02

全文链接:

<http://agri.ckcest.cn/file1/M00/02/9D/Csgk0Fv7VzSAbYqJACf4GY22cAc198.pdf>

2. Resistance protein Pit interacts with the GEF OsSPK1 to activate OsRac1 and trigger rice immunity (抗性蛋白Pit与GEF OsSPK1相互作用以激活OsRac1并触发水稻免疫)

简介: Resistance (R) genes encode intracellular nucleotide-binding/leucine-rich repeat-containing (NLR) family proteins that serve as critical plant immune receptors to induce effector-triggered immunity (ETI). NLR proteins possess a tripartite domain architecture consisting of an N-terminal variable region, a central nucleotide-binding domain, and a C-terminal leucine-rich repeat. N-terminal coiled-coil (CC) or Toll-interleukin 1 receptor (TIR) domains of R proteins appear to serve as platforms to trigger immune responses, because overexpression of the CC or TIR domain of some R proteins is sufficient to induce an immune response. Because direct downstream signaling molecules of R proteins remain obscure, the molecular mechanisms by which R proteins regulate downstream signaling are largely unknown. We reported previously that a rice R protein named Pit triggers ETI through a small GTPase, OsRac1, although how Pit activates OsRac1 is unclear. Here, we identified OsSPK1, a DOCK family guanine nucleotide exchange factor, as an interactor of Pit and activator for OsRac1. OsSPK1 contributes to signaling by two disease-resistance genes, Pit and Pia, against the rice blast fungus *Magnaporthe oryzae* and

facilitates OsRac1 activation in vitro and in vivo. The CC domain of Pit is required for its binding to OsSPK1, OsRac1 activation, and the induction of cell death. Overall, we conclude that OsSPK1 is a direct and key signaling target of Pit-mediated immunity. Our results shed light on how R proteins trigger ETI through direct downstream molecules.

来源: PNAS期刊

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全文链接:

<http://agri.ckcest.cn/file1/M00/02/9D/Csgk0Fv7U46AFMNIACADZcJITe8391.pdf>

相关专利

1. 植物基因组改造中常用的在核苷酸序列上修饰植物基因组的方法和工具

简介: 提供了以定向的方式修饰包含嵌合基因的转基因植物的植物基因组的方法和工具, 其中所述嵌合基因具有植物分子生物学中常用的DNA元件。提供了重新设计的大范围核酸酶, 用于切割此类常用于植物分子生物学中的元件。

来源: 国家知识产权局

发布日期:2018-11-20

全文链接:

<http://agri.ckcest.cn/file1/M00/02/9D/Csgk0Fv7Y0eADwwOADXvGN60ZgI191.pdf>