2016年第7期总7期

农业生物技术专题

本期导读

前沿资讯

1．中科院“第二粮仓”预研项目达到预期目标

学术文献

1.受体激酶通过整个复杂的RALF信号来抑制拟南芥根系的生长

2．光影响拟南芥中盐诱导的P5CS1转录记忆

3．拟南芥中调节糖转录活性的细菌防御系统

4．利用改造后CRISPR/Cas9系统在水稻中实现靶标基因高效单碱基定点替换

中国农业科学院农业信息研究所
联系人：邹婉侬
联系电话： 010-82109850
邮箱：agri@ckcest.cn
2016年12月19日

前沿资讯

1．中科院“第二粮仓”预研项目达到预期目标

简介：“十三五”规划建议提出，坚持最严格的耕地保护制度，坚守耕地红线，实施“藏粮于地、藏粮于技”战略，提高粮食产能，确保谷物基本自给、口粮绝对安全。“第二粮仓”预研项目紧密结合国家粮食安全重大需求，由中科院科发局组织、中科院合肥物质科学研究院牵头，联合地方政府、科研院所、企业多方力量，以中低产田提质增效为目标，率先在淮北打造周年农业全产业链技术集成和示范样板，为“第二粮仓”计划在全国全面实施提供可复制推广的成功样板和建设方案。

来源：科学网

全文链接：

http://news.sciencenet.cn/htmlnews/2016/12/363200.shtm

学术文献

1．Receptor kinase complex transmits RALF peptide signal to inhibit root growth in Arabidopsis（受体激酶通过整个复杂的RALF信号来抑制拟南芥根系的生长）

简介：A number of hormones work together to control plant cell growth. Rapid Alkalinization Factor 1 (RALF1), a plant-derived small regulatory peptide, inhibits cell elongation through suppression of rhizosphere acidification in plants. Although a receptor-like kinase, FERONIA (FER), has been shown to act as a receptor for RALF1, the signaling mechanism remains unknown. In this study, we identified a receptor-like cytoplasmic kinase (RPM1-induced protein kinase, RIPK), a plasma membrane-associated member of the RLCK-VII subfamily, that is recruited to the receptor complex through interacting with FER in response to RALF1. RALF1 triggers the phosphorylation of both FER and RIPK in a mutually dependent manner. Genetic analysis of the *fer-4* and *ripk* mutants reveals RIPK, as well as FER, to be required for RALF1 response in roots. The RALF1–FER–RIPK interactions may thus represent a mechanism for peptide signaling in plants.

来源：PANS

全文链接：

http://agri.ckcest.cn/ass/NK007-20161219004.pdf

2．Light affects salt stress-induced transcriptional memory of P5CS1 in Arabidopsis（光影响拟南芥中盐诱导的P5CS1转录记忆）

简介：To cope with environmental stresses, plants often adopt a memory response upon primary stress exposure to facilitate a quicker and stronger reaction to recurring stresses. However, it remains unknown whether light is involved in the manifestation of stress memory. Proline accumulation is a striking metabolic adaptation of higher plants during various environmental stresses. Here we show that salinity-induced proline accumulation is memorable and HY5-dependent light signaling is required for such a memory response. Primary salt stress induced the expression of Δ1-pyrroline-5-carboxylate synthetase 1 (*P5CS1*), encoding a proline biosynthetic enzyme and proline accumulation, which were reduced to basal level during the recovery stage. Reoccurring salt stress-induced

stronger *P5CS1* expression and proline accumulation were dependent upon light exposure during the recovery stage. Further studies demonstrated that salt-induced transcriptional memory of *P5CS1* is associated with the retention of increased H3K4me3 level at *P5CS1*during the recovery stage. HY5 binds directly to light-responsive element, C/A-box, in the *P5CS1* promoter. Deletion of the C/A-box or *hy5 hyh* mutations caused rapid reduction of H3K4me3 level at *P5CS1* during the recovery stage, resulting in impairment of the stress memory response. These results unveil a previously unrecognized mechanism whereby light regulates salt-induced transcriptional memory via the function of HY5 in maintaining H3K4me3 level at the memory gene.

来源：PANS

全文链接:

http://agri.ckcest.cn/ass/NK007-20161219005.pdf

3. Regulation of sugar transporter activity for antibacterial defense in Arabidopsis(拟南芥中调节糖转录活性的细菌防御系统)

简介：Microbial pathogens strategically acquire metabolites from their hosts during infection. Here we show that the host can intervene to prevent such metabolite loss to pathogens. Phosphorylation-dependent regulation of sugar transporter 13 (STP13) is required for antibacterial defense in the plant Arabidopsis thaliana. STP13 physically associates with the flagellin receptor flagellin-sensitive 2 (FLS2) and its co-receptor BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 (BAK1). BAK1 phosphorylates STP13 at threonine 485, which enhances its monosaccharide uptake activity to compete with bacteria for extracellular sugars. Limiting the availability of extracellular sugar deprives bacteria of an energy source and restricts virulence factor delivery. Our results reveal that control of sugar uptake, managed by regulation of a host sugar transporter, is a defense strategy deployed against microbial infection. Competition for sugar thus shapes host-pathogen interactions.

来源：Science

全文链接:

http://agri.ckcest.cn/ass/NK007-20161219003.pdf

4. Generation of targeted point mutations in rice by a modified CRISPR/Cas9 system(利用改造后CRISPR/Cas9系统在水稻中实现靶标基因高效单碱基定点替换)

简介：CRISPR/Cas9 (Clustered Regularly Interspaced Short Palindromic Repeats/CRISPR-associated Cas9 endonuclease)-mediated genome editing has revolutionized biological research and crop improvement because of its specificity, simplicity, and versatility (Reviewed in Komor et al., 2016a). Editing a gene by CRISPR/Cas9 only has three requirements: 1) Expression of the nuclear localized Cas9 protein; 2) Production of a guide RNA (gRNA) molecule, whose first 20 nucleotides are complementary to the target gene; 3) the NGG PAM site that is located immediately adjacent to the 3'-end of the target sequence (Fig. 1A). In the presence of a gRNA, Cas9 generates a double-strand break (DSB) at the target sequence. Repairing the DBS by the error-prone, non-homologous end-joining (NHEJ) mechanism often leads to small deletions or insertions at the target site, providing a valuable venue to generate knockout and loss-of-function mutants. The majority of the

reported CRISPR/Cas9-mediated gene editing in plants belongs to this category (Char et al., 2016; Gao et al., 2016; Ma et al., 2015; Miao et al., 2013; Wang et al., 2015; Xie and Yang, 2013). While such mutants are very valuable in defining gene functions, their applications in crop improvement are somewhat limited because many agriculturally important traits are conferred by single nucleotide polymorphisms, or by dominant gain-of-function point mutations. Homology-directed repair (HDR) of a DSB at specific locations can provide a feasible approach to achieve gene replacement. However, it has been very challenging to make use of HDR in plants to introduce point mutations because of the very low frequency of targeted integration.So far only a few special cases of CRISPR/Cas9-mediated HDR have been reported in plants (Sun et al., 2016). NHEJ-mediated repair may also be used to introduce point mutations through gene replacement if the target sequences of CRISPR/Cas9 are located in introns (Li et al., 2016). Nevertheless, it is still a major challenge to generate targeted point mutations in plants.

来源： Molecular Plant

全文链接:

http://agri.ckcest.cn/ass/NK007-20161219002.pdf