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1．一种转换纤维素与甘露聚糖活力的纤维素酶突变体及其基

因和应用

2．一种提高纤维素酶活性的方法及纤维素酶突变体5I77-M和应用

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前沿资讯

1．破坏性洋葱病毒进化、传播

简介：根据华盛顿州立大学（WSU）病毒学家的研究，鸢尾黄斑病毒继续通过进化和传播对洋葱作物构成威胁 。鸢尾黄斑病以其原始寄主植物命名，已对世界各地的洋葱作物造成重大损害。感染会削弱带种子的茎，导致它们脱落或倒下，从而有效地破坏下一代种子。该病毒还会降低光合作用，最终使洋葱鳞茎缩小。WSU 教授 Hanu Pappu 和他的研究同事开始使用快速分子测试（一种基因指纹识别）来了解病毒的多样性，以及它的进化和全球传播的可能原因。该研究提供了对这种病毒进化和传播速度的深入了解。部分资金来自美国农业部国家粮食和农业研究所的 特殊作物研究计划。

来源：美国农业部

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全文链接:

https://nifa.usda.gov/announcement/destructive-onion-virus-evolving-spreading

2．微生物潜入番茄防御系统，推进进化战

简介：当我们想到进化时，我们中的许多人都会联想到从猿到人的谱系，这是跨越数百万年的一系列增量变化。但在某些物种中，进化发生得如此之快，我们可以实时观察它。黄单胞菌就是这种情况，这种微生物会导致番茄和辣椒植物中的细菌性叶斑病。像许多世代时间短的微生物一样，它可以以闪电般的速度进化以获得有益的特征，例如逃避宿主防御系统的能力。伊利诺伊大学的一项新研究表明，一种黄单胞菌属物种 X. euvesicatoria (Xe) 已经进化到可以避免被番茄植物的免疫系统检测到。Xe 可以绕过番茄的防御这一事实意味着农民可以更少地依赖固有的抗病性。相反，他们将不得不以其他方式对抗这种疾病，例如喷洒铜基杀虫剂。资金由美国农业部的国家粮食和农业研究所提供。

来源：美国农业部

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全文链接:

https://aces.illinois.edu/news/microbe-sneaks-past-tomato-defense-system-advances-evolutionary-battle

学术文献

1．The jasmonate biosynthesis Gene OsOPR7 can mitigate salinity induced mitochondrial oxidative stress(茉莉酸生物合成基因 osopr7 可以减轻盐度诱导的线粒体氧化应激)

简介：Salinity poses a serious threat to global agriculture and human food security. A better understanding of plant adaptation to salt stress is, therefore, mandatory. In the non-photosynthetic cells of the root, salinity perturbs oxidative balance in mitochondria, leading to cell death. In parallel, plastids accumulate the jasmonate precursor cis

(+)12-Oxo-Phyto-Dienoic Acid (OPDA) that is then translocated to peroxisomes and has been identified as promoting factor for salt-induced cell death as well. In the current study, we probed for a potential interaction between these three organelles that are primarily dealing with oxidative metabolism. We made use of two tools: (i) Rice OPDA Reductase 7 (OsOPR7), an enzyme localised in peroxisomes converting OPDA into the precursors of the stress hormone JA-Ile. (ii) A Trojan Peptoid, Plant PeptoQ, which can specifically target to mitochondria and scavenge excessive superoxide accumulating in response to salt stress. We show that overexpression of OsOPR7 as GFP fusion in tobacco (Nicotiana tabacum L. cv. Bright Yellow 2, BY-2) cells, as well as a pretreatment with Plant PeptoQ can mitigate salt stress with respect to numerous aspects including proliferation, expansion, ionic balance, redox homeostasis, and mortality. This mitigation correlates with a more robust oxidative balance, evident from a higher activity of superoxide dismutase (SOD), lower levels of superoxide and lipid peroxidation damage, and a conspicuous and specific upregulation of mitochondrial SOD transcripts. Although both, Plant PeptoQ and ectopic OsOPR7, were acting in parallel and mostly additive, there are two specific differences: (i) OsOPR7 is strictly localised to the peroxisomes, while Plant PeptoQ found in mitochondria. (ii) Plant PeptoQ activates transcripts of NAC, a factor involved in retrograde signalling from mitochondria to the nucleus, while these transcripts are suppressed significantly in the cells overexpressing OsOPR7. The fact that overexpression of a peroxisomal enzyme shifting the jasmonate pathway from the cell-death signal OPDA towards JA-Ile, a hormone linked with salt adaptation, is accompanied by more robust redox homeostasis in a different organelle, the mitochondrion, indicates that cross-talk between peroxisome and mitochondrion is a crucial factor for efficient adaptation to salt stress.

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http://agri.ckcest.cn/file1/M00/03/1F/CsgkOYZItQqAOthoADc4QcRcsmU195.pdf

2. Biotinylated subunit of 3-methylcrotonyl-CoA carboxylase encoding gene (AtMCCA) participating in Arabidopsis resistance to carbonate Stress by transcriptome analysis(转录组分析3- 甲基 crotonyl-coa 羧化酶编码基因(atmcca)的生物素化亚基参与拟南芥抗碳酸盐胁迫)

简介： Soil salinization is a major factor impacting modern agricultural production, and alkaline soils contain large amounts of NaHCO3. Therefore, understanding plant tolerance to high levels of NaHCO3 is essential. In this study, a transcriptome analysis of shoot and root tissues of wild-type Arabidopsis thaliana was conducted at 0, 4, 12, 24 and 48 h after exposure to a 3 mM NaHCO3 stress. We focused on differentially expressed genes (DEGs) in roots identified in the early stages (4 h and 12 h) of the NaHCO3 stress response that were enriched in GO term, carboxylic acid metabolic process, and utilize HCO3?. Six genes were identified that exhibited similar expression patterns in both the RNA-seq and qRT-PCR data.

We also characterized the phenotypic response of AtMCCA-overexpressing plants to carbonate stress, and found that the ability of AtMCCA-overexpressing plants to tolerate carbonate stress was enhanced by the addition of biotin to the growth medium.

来源：Plant Science

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全文链接:

http://agri.ckcest.cn/file1/M00/03/1F/CsgkOYZIt4OAZoRfAGNRZr7MJ9k646.pdf

3. Applications of CRISPR/Cas9 in a rice protein expression system via an intron-targeted insertion approach(Crispr/cas9在大米蛋白表达系统中的应用)

简介：The sugar starvation-inducible rice αAmy3 promoter and signal peptide are widely used to produce valuable recombinant proteins in rice suspension culture cells. Conventionally, the recombinant gene expression cassette is inserted into the genome at random locations by Agrobacterium- or particle bombardment-mediated transformation. CRISPR/Cas9 gene editing enables gene insertion at a precise target site in the genome. In this study the CRISPR/Cas9 approach was modified for intron-targeted insertion by adding an artificial 3′ splicing site upstream of the recombinant gene. Knock-in transgenic rice cell lines containing the recombinant GFP gene inserted in intron 1 of αAmy3 were generated. The endogenous αAmy3 promoter regulated recombinant gene expression and the αAmy3 signal peptide directed secretion of the recombinant GFP protein into the culture medium. In addition, the recombinant GFP protein was localized in amyloplasts, identical to the subcellular localization of endogenous αAmy3 reported previously. This modified CRISPR/Cas9 knock-in approach is simple and highly efficient, and the recombinant gene insertion frequency attained 12.5%. The approach can be applied in the production of pharmaceutical proteins in rice suspension cell cultures. The high efficiency of the GFP reporter gene knock-in method and the maintenance of target gene behavior also make the strategy applicable to endogenous gene functional studies in rice.

来源：Plant Science

影响因子：4.729/Q2

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全文链接:

http://agri.ckcest.cn/file1/M00/0F/F1/CsgkOGHyBkOAR6JmADC_P-y3VHI992.pdf

4. Calcium-dependent Protein Kinase 5 (CPK5) positively modulates drought tolerance through phosphorylating ABA-Responsive Element Binding Factors in oilseed rape (Brassica napus L.)(钙依赖蛋白激酶5(cpk5)通过磷酸化 aba 反应元件结合因子调节油菜的抗旱性)

简介：Drought is an environmental stress that causes severe crop loss. Drought stress can

induce abscisic acid (ABA) accumulation and cytoplasmic calcium oscillation. Calcium-dependent protein kinases (CPKs) constitute a group of Ser/Thr protein kinases decoding calcium signals. However, the function and molecular mechanisms of most CPKs in oilseed rape (Brassica napus) remain unknown. Here, we report the functional characterization of BnaCPK5 in drought stress tolerance. BnaCPK5 belongs to Group I of the CPK family and was localized at the plasma membrane and nuclei. Overexpression of BnaCPK5 enhanced drought stress tolerance compared with the control. A screening of interacting proteins identified that BnaCPK5 interacted strongly with two ABA-Responsive Element Binding Factors (ABF/AREBs), BnaABF3 and BnaABF4. BnaCPK5 was shown to phosphorylate both BnaABF3 and BnaABF4 in a kinase assay. Further, it was found that the phosphorylation of BnaABF3 and BnaABF4 by BnaCPK5 increased their transcriptional activities against the famous drought stress marker gene, Responsive to Dehydration (RD) 29B and protein stability. Taken together, these data demonstrate that BnaCPK5 acts as a positive regulator of drought tolerance by, at least in part, phosphorylating two core ABA-signaling components to modulate Late-Embryogenesis Abundant (LEA)-like RD29B expression.

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5．GmWRKY46, a WRKY transcription factor, negatively regulates phosphorus tolerance primarily through modifying root morphology in soybean（Gmwrky46是一种转录因子，主要通过改变大豆根系形态来负向调节耐磷性）

简介：Phosphorus (P) deficiency affects soybean growth and development, resulting in significant reduction of yields. However, the regulatory mechanism of P deficiency tolerance in soybean is still largely unclear. WRKY transcription factors are a family of regulators involved in a variety of abiotic stresses in plants while rarely reported in P deficiency. Here, we demonstrated that a soybean GmWRKY46 gene, belonging to group III of WRKY TF family, was involved in the regulation of P deficiency tolerance in soybean. The expression of GmWRKY46 in low P sensitive soybean varieties was significantly higher than that in tolerant soybean varieties. It was primarily expressed in roots and strongly induced by P deprivation. GmWRKY46 was localized in the nucleus. Compared with the control expressing the empty vector, overexpression of GmWRKY46 in soybean hairy roots exhibited more sensitive phenotypes to low P stress, while the RNA interfered GmWRKY46 significantly enhanced P deficiency tolerance by increasing the proliferation, elongation and P absorption efficiency of hairy roots. Expression patterns of a number of P-responsive genes (GmPht1;1, GmPht1;4, GmPTF1, GmACP1, GmPAP21 and GmExpansin-A7) were altered in both overexpression and gene silenced plants. The results provided a novel insight into how soybean responds to low P stress and new gene that may be used to improve soybean

low P tolerance through gene editing approach.
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相关专利

1. 一种转换纤维素与甘露聚糖活力的纤维素酶突变体及其基因和应用

简介： 本发明涉及农业生物技术领域，具体涉及一种转换纤维素与甘露聚糖活力的纤维素酶突变体及其基因和应用。本发明通过对氨基酸序列如SEQ ID No：1所示的野生型纤维素酶的N105位点实施定点突变获得N100V突变体，该以两种底物测定时，酶促反应的最适pH值不变，最适温度提高5℃；以角豆胶为底物时，突变体的甘露聚糖比活力比野生型提高了约630%。
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https://www.baiten.cn/patent/detail/57658b842a4e81892f958facc37e1b78842e1e8b1cb3101b?sc=&fq=&type=&sort=&sortField=&q=%E4%B8%80%E7%A7%8D%E8%BD%AC%E6%8D%A2%E7%BA%A4%E7%BB%B4%E7%B4%A0%E4%B8%8E%E7%94%98%E9%9C%B2%E8%81%9A%E7%B3%96%E6%B4%BB%E5%8A%9B%E7%9A%84%E7%BA%A4%E7%BB%B4%E7%B4%A0%E9%85%B6%E7%AA%81%E5%8F%98%E4%BD%93%E5%8F%8A%E5%85%B6%E5%9F%BA%E5%9B%A0%E5%92%8C%E5%BA%94%E7%94%A8&rows=10#1/CN202010809506.2/sqdetail/abst

2. 一种提高纤维素酶活性的方法及纤维素酶突变体5I77-M和应用

简介： 本发明涉及农业生物技术领域，具体涉及一种提高纤维素酶活性的方法及纤维素酶突变体5I77-M和应用。本发明通过对氨基酸序列如SEQ ID NO：1所示的野生型纤维素酶的T300/D307位点实施定点突变获得T300P/D307P突变体。结果表明，与野生型纤维素酶相比，突变体的最适pH值、最适温度并未发生变化，而以羧甲基纤维素钠为底物时，突变体的比活力比野生型提高了约60%。
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