



2022年第30期总63期

种质资源保护与创制专题

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2. 植物免疫调节相关蛋白及其应用

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▶ 前沿资讯

1. 蔬菜花卉研究所完成黄瓜抗蔓枯病主效QTL精细定位

简介: 近日,中国农业科学院蔬菜花卉研究所葫芦科蔬菜遗传育种创新团队在黄瓜蔓枯病抗性研究方面取得重要进展。该研究将成株期茎蔓的蔓枯病抗性QTL位点gsb-s6.2定位到34 kb区间内,并预测了2个关键候选基因。相关研究结果以“Fine mapping and candidate gene analysis of gummy stem blight resistance in cucumber stem”为题发表于国际著名植物学期刊Theoretical and Applied Genetics上。蔓枯病(Gummy stem blight, GSB)是黄瓜生产中的主要真菌性病害之一,可导致严重减产与品质下降。然而,黄瓜蔓枯病研究进展缓慢,且在栽培种中缺乏抗源,尚未见对主效QTL或基因进行精细定位的报道。本研究利用近等基因系构建的F₂群体鉴定到97个重组单株,将茎蔓蔓枯病抗性主效位点gsb-s6.2精细定位至34 kb的物理区间内,包含6个基因。结合序列分析与接种前后表达模式分析,将Csa6G046210和Csa6G046240确定为候选基因。Csa6G046210编码肿瘤相关蛋白,在抗感材料间存在多个非同义突变位点,接种后在感病材料中表现出显著高的表达水平;Csa6G046240为MYB转录因子,在启动子区AP2/ERF和MYB motifs上存在多个突变位点。该研究首次实现了黄瓜蔓枯病主效抗性位点的精细定位,并推测2个候选基因可能参与蔓枯病抗性通路,为解析蔓枯病抗性分子机制,及培育蔓枯病抗性新品种奠定了基础。该论文以中国农业科学院蔬菜花卉研究所为第一和通讯作者单位,韩佳楠博士研究生为第一作者,董邵云博士为共同一作,张圣平研究员和顾兴芳研究员为共同通讯作者。该研究受到广东省重点研发、山东省重点研发、现代农业产业技术体系、中国农业科学院创新工程等项目资助。(宣传信息员 董邵云)原文链接: <https://doi.org/10.1007/s00122-022-04172-2>

来源: 中国农业科学院蔬菜花卉研究所

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全文链接:

<https://ivf.caas.cn/xwdt/zhxw/c6b785d8f9774889afebbf4dcc702df2.htm>

2. 华中农业大学在生菜叶卷曲的研究中取得新进展

简介: 近日,我校园艺植物生物学教育部重点实验室匡汉晖教授课题组在“Journal of Experimental Botany”杂志上发表题为“The upregulated LsKN1 gene promotes cytokinin and suppresses gibberellin biosynthesis to generate wavy leaves in lettuce”的研究论文。该论文阐明了LsKN1基因调控生菜叶卷曲性状的遗传和分子机理。生菜是世界上最受欢迎的蔬菜之一。生菜常被用做色拉、火锅配菜等,叶片形态直接关系到其感官品质。通过一个叶卷曲的生菜品种和一个叶平整的生菜品种杂交,构建了叶卷曲表型的遗传分离群体(图1)。遗传定位发现该群体中的一个叶卷曲主效QTL是LsKN1基因。通过互补实验和CRISPR/cas9敲除实验验证了该基因调控叶卷曲。LsKN1基因在不同遗传背景下,可引起不同叶形变化。实验室前期研究表明,该基因的上调表达还导致生菜结球(Yu et al., 2020)和掌状缺刻(Wang et al., 2022)。LsKN1基因通过不同的分子信号途径调控不同的性状,并在不同的遗传背景下出现不同的表型。本研究发现LsKN1影响细胞分裂素(CK)和赤霉素(GA)的合成和降解途径的关键基因,提高了生菜叶片中CK含量并降低了GA含量,导致细胞面积变大、细胞数量增多、次级叶脉变细密,叶脉细胞和叶肉细胞发育紊乱,最终导致卷曲叶片的形成(图2)。卷叶品

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种中LsKN1基因的上调表达是由第一个外显子上一个CACTA转座子的插入导致的。在本研究的遗传转化过程中，偶然获得了3株CACTA转座子发生转座的突变体，这3个突变体的表型由卷叶恢复为平叶，再次证明了LsKN1基因中CACTA转座子的插入是卷曲叶片形成的致变因子（图3）。该研究内容进一步丰富了叶发育理论，并为生菜遗传育种提供理论支持。本研究由我校园艺植物生物学教育部重点实验室莴苣研究团队完成，博士研究生贾越为第一作者，匡汉晖教授和余长春副研究员为共同通讯作者。该研究得到了国家自然科学基金的资助。 原文链接：<https://doi.org/10.1093/jxb/erac311>

来源：园艺林学学院 贾越

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<http://news.hzau.edu.cn/2022/0715/63949.shtml>

3. 科研人员创制简便高效玉米单倍体诱导系MAGIC

简介:近日,中国农业科学院生物技术研究所作物功能基因组研究中心与国内高校合作,创制出不受材料背景影响、简便高效、单倍体鉴别准确率达99.1%的玉米诱导系MAGIC1和升级版MAGIC2,进一步提升了单倍体育种技术应用效率。相关成果发表在《植物杂志(The Plant Journal)》。单倍体育种技术可极大缩短育种周期,提升育种效率,是现代作物育种的共性关键技术之一。但目前的玉米单倍体育种技术中,鉴别单倍体胚需要剥离全穗所有的胚,并进一步通过光照显色才能区分单倍体和二倍体,效率不高。为提升单倍体胚鉴别效率,该研究将紫胚玉米的花青素积累表型引入单倍体诱导系CAU6,回交转育后形成新的诱导系MAGIC1。MAGIC1与CAU6相比,诱导率没有显著差异,但是单倍体鉴别时间从原来的授粉后21天提前到授粉后9天,准确率从88.3%提高到99.1%。此外,MAGIC1不受材料背景影响,可以用于存在花青素合成抑制基因的玉米种质的单倍体鉴别。研究团队在MAGIC1基础上进一步研发出可利用胚、胚根、叶片等多个组织全生育期鉴别单倍体的升级版MAGIC2,该版本比MAGIC1单倍体识别效率更高,发芽率也更高,进一步提升了玉米单倍体育种技术的简便性和适用性。该研究两个版本的单倍体诱导系实现了单倍体幼胚的直接鉴别,可显著提高单倍体幼胚鉴别与加倍技术应用效率,在单倍体育种中具有较大的应用潜力。相关技术已经获得国家发明专利授权。该研究得到国家重点研发计划等项目的支持。 原文链接:

<https://onlinelibrary.wiley.com/doi/10.1111/tpj.15888>

来源:中国农业科学院生物技术研究所

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<https://www.caas.cn/xwzx/kyjz/321798.html>

➤ 学术文献

1. Comparative bioinformatics analysis and abiotic stress responses of expansin proteins in Cucurbitaceae members: watermelon and melon. (葫芦科成员:西瓜和甜瓜扩展蛋白的比较生物信息学分析和非生物胁迫响应。)

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简介: Watermelon and melon are members of the Cucurbitaceae family including economically significant crops in the world. The expansin protein family, which is one of the members of the cell wall, breaks down the non-covalent bonds between cell wall polysaccharides, causing pressure-dependent cell expansion. Comparative bioinformatics and molecular characterization analysis of the expansin protein family were carried out in the watermelon (*Citrullus lanatus*) and melon (*Cucumis melo*) plants in the study. Gene expression levels of expansin family members were analyzed in leaf and root tissues of watermelon and melon under ABA, drought, heat, cold, and salt stress conditions by quantitative real-time PCR analysis. After comprehensive searches, 40 expansin proteins (22 ClaEXPA, 14 ClaEXPLA, and 4 ClaEXPB) in watermelon and 43 expansin proteins (19 CmEXPA, 15 CmEXPLA, 3 CmEXPB, and 6 CmEXPLB) in melon were identified. The greatest orthologous genes were identified with soybean expansin genes for watermelon and melon. However, the latest divergence time between orthologous genes was determined with poplar expansin genes for watermelon and melon expansin genes. ClaEXPA-04, ClaEXPA-09, ClaEXPB-01, ClaEXPB-03, and ClaEXPLA-13 genes in watermelon and CmEXPA-12, CmEXPA-10, and CmEXPLA-01 genes in melon can be involved in tissue development and abiotic stress response of the plant. The current study combining bioinformatics and experimental analysis can provide a detailed characterization of the expansin superfamily which has roles in growth and reaction to the stress of the plant. The study ensures detailed data for future studies examining gene functions including the roles in plant growth and stress conditions.

来源: Protoplasma

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<http://agri.ckcest.cn/file1/M00/03/3A/Csgk0YdHLOKAZyRnAIMfyrkGpsw738.pdf>

2. A SNP of betaine aldehyde dehydrogenase (BADH) enhances an aroma (2-acetyl-1-pyrroline) in sponge gourd (*Luffa cylindrica*) and ridge gourd (*Luffa acutangula*) (甜菜碱醛脱氢酶 (BADH) 的一个SNP增强了丝瓜 (*Luffa cylindrica*) 和丝瓜 (*Luffa actangula*) 的香气 (2-乙酰-1-吡咯啉)?)

简介: *Luffa* is a genus of tropical and subtropical vines belonging to the Cucurbitaceae family. Sponge gourd (*Luffa cylindrica*) and ridge gourd (*Luffa acutangula*) are two important species of the genus *Luffa* and are good sources of human nutrition and herbal medicines. As a vegetable, aromatic luffa is more preferred by consumers than nonaromatic luffa. While the aroma trait is present in the sponge gourd, the trait is not present in the ridge gourd. In this study, we identified *Luffa cylindrica*'s betaine aldehyde dehydrogenase (LcBADH) as a gene associated with aroma in the sponge gourd based on a de novo assembly of public transcriptome data. A single nucleotide polymorphism (SNP: A>G) was identified in exon 5 of LcBADH, causing an amino acid change from tyrosine to cysteine at position 163, which is important for the formation of the substrate binding pocket of the

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BADH enzyme. Based on the identified SNP, a TaqMan marker, named AroLuff, was developed and validated in 370 F2 progenies of the sponge gourd. The marker genotypes were perfectly associated with the aroma phenotypes, and the segregation ratios supported Mendelian's simple recessive inheritance. In addition, we demonstrated the use of the AroLuff marker in the introgression of LcBADH from the aromatic sponge gourd to the ridge gourd to improve aroma through interspecific hybridization. The marker proved to be useful in improving the aroma characteristics of both Luffa species.

来源: Scientific Reports

发布日期: 2022-03-08

全文链接:

<http://agri.ckcest.cn/file1/M00/03/3A/Csgk0YdHK86ALH4BABpwSgzWe2A857.pdf>

3. Integrated analysis of the transcriptome, sRNAome, and degradome reveals the network regulating fruit skin coloration in sponge gourd (*Luffa cylindrica*) (综合转录组、sRNAome和降解组分析, 揭示了丝瓜果实着色的调控网络。)

简介: Sponge gourd fruit skin color is an important quality-related trait because it substantially influences consumer preferences. However, little is known about the miRNAs and genes regulating sponge gourd fruit skin coloration. This study involved an integrated analysis of the transcriptome, sRNAome, and degradome of sponge gourd fruit skins with green skin (GS) and white skin (WS). A total of 4,331 genes were differentially expressed between the GS and WS, with 2,442 down-regulated and 1,889 up-regulated genes in WS. The crucial genes involved in chlorophyll metabolism, chloroplast development, and chloroplast protection were identified (e.g., HEMA, CHLM, CRD1, POR, CAO, CLH, SGR, CAB, BEL1-like, KNAT, ARF, and peroxidase genes). Additionally, 167 differentially expressed miRNAs were identified, with 70 up-regulated and 97 down-regulated miRNAs in WS. Degradome sequencing identified 125 differentially expressed miRNAs and their 521 differentially expressed target genes. The miR156, miR159, miR166, miR167, miR172, and miR393 targeted the genes involved in chlorophyll metabolism, chloroplast development, and chloroplast protection. Moreover, a flavonoid biosynthesis regulatory network was established involving miR159, miR166, miR169, miR319, miR390, miR396, and their targets CHS, 4CL, bHLH, and MYB. The qRT-PCR data for the differentially expressed genes were generally consistent with the transcriptome results. Subcellular localization analysis of selected proteins revealed their locations in different cellular compartments, including nucleus, cytoplasm and endoplasmic reticulum. The study findings revealed the important miRNAs, their target genes, and the regulatory network controlling fruit skin coloration in sponge gourd.

来源: Scientific Reports

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全文链接:

<http://agri.ckcest.cn/file1/M00/10/0C/Csgk0GLwe4eAXc8kAHLVDUotJY4074.pdf>

➤ 相关专利

1. 黄瓜CsLsi2基因及其编码的蛋白和应用(葫芦科YABBY基因家族的全基因组鉴定及在黄瓜中的表达分析。)

简介: 本发明涉及黄瓜CsLsi2基因及其编码的蛋白和应用。所述黄瓜CsLsi2基因核苷酸序列如SEQ ID NO:1所示, 该基因编码的蛋白序列如SEQ ID NO:2所示。本发明通过全基因组关联分析及筛选后克隆得到了与黄瓜果霜性状密切相关的黄瓜CsLsi2基因, 该基因表达水平与黄瓜果霜含量呈正相关, 而在黄瓜基因如SEQ ID NO:1所示序列的第754位的碱基由C变为T后会导致氨基酸翻译的提前终止。黄瓜CsLsi2基因的克隆及表达分析对解决黄瓜果霜基因资源难以筛选的问题起到了很大程度的促进作用。

来源: 佰腾网

发布日期:2021-10-01

全文链接:

<http://agri.ckcest.cn/file1/M00/10/0C/Csgk0GLwfk0ANuk6ABmt0BP3m0000.PDF>

2. 植物免疫调节相关蛋白及其应用

简介: 本发明公开了植物免疫调节相关蛋白MEL及其应用, 涉及植物基因工程领域。本发明发现了一种调控植物免疫相关蛋白MEL, 该蛋白编码一个保守的SWIM结构域, 一个保守的RING结构域以及一个保守的底物识别序列Y ϕ ;NL。植物中调控MEL表达量能够显著提高植物对病原体的广谱抗病性, 提供了一种作物抗病基因工程的方法。

来源: 佰腾网

发布日期:2021-06-15

全文链接:

<http://agri.ckcest.cn/file1/M00/03/3A/Csgk0YdHdQaAc3FOABg108yzagA771.PDF>