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## 种质资源保护与创制专题

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## ➤ 前沿资讯

### 1. 蔬菜花卉所发现纳米碳溶液能显著提高青花菜蛋白质含量

**简介：**8月17日，中国农业科学院蔬菜花卉研究所甘蓝类蔬菜遗传育种创新团队在纳米碳溶液对青花菜营养成分和硫甙代谢的影响研究方面取得重要进展，为青花菜深加工助力乡村振兴和采用科技手段精准调控其营养提供了技术支撑和科学依据。该研究结果以“Effects of nanocarbon solution treatment on the nutrients and glucosinolate metabolism in broccoli”为题发表于应用化学Top期刊Food Chemistry: X (IF=6.443/Q1)上。青花菜是一种富含蛋白质、维生素C和矿物质（钙、锌、镁、铁、硒等）等营养成分的国际流行蔬菜，被誉为“蔬菜皇冠”。Nature portfolio报道了全球8032种果蔬、粮食与肉禽的营养评价，包括东西方不同烹饪方式下各种食品的营养分值，其中青花菜（broccoli）总体处于Top系列（<https://doi.org/10.1038/s43016-021-00381-y>）。本研究考察了不同纳米碳（生物炭）溶液对青花菜生育期花球中主要营养成分包括蛋白质、维生素C、总糖以及硫甙组分含量的变化影响，研究发现，纳米碳溶液能显著提高花球中蛋白质的积累，18.75 L·ha<sup>-1</sup>的纳米碳溶液能够提高有益硫甙4-甲基亚磺酰基丁基硫甙(glucoraphanin)22.9%的生成量，同时也显著减低了4种吲哚族硫甙(glucobrassicin、4-methoxyglucobrassicin、4-hydroxyglucobrassicin和neoglucobrassicin)的含量，纳米碳能够直接上调青花菜中调脂肪族硫甙代谢关键调控基因MAM1、IPMI2、CYP79F1、FM0gs-ox2、AOP2和TGG1，为实现青花菜内源营养成分的精准调控提供了新途径和科学依据，也将极大提升我国青花菜生产中的科技管理水平，服务大健康产业。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，李占省副研究员为第一和通讯作者，北京市农林科学院农产品加工与食品营养研究所刘光敏博士为共同一作(2/2)。该研究得到了国家自然科学基金、国家大宗蔬菜产业技术体系、中央级公益性科研院所基本科研业务费专项及中国农科院创新工程等项目的资助。原文链接：<https://doi.org/10.1016/j.foodchx.2022.100429>

**来源：**李占省

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**全文链接：**

<https://ivf.caas.cn/xwdt/zhxw/38bdc8cd26d94aeab92fe74fa24710d2.htm>

### 2. 李博教授课题组揭示增强子转录调控植物免疫的新机制

**简介：**7月21日，李博教授课题组在《BMC Biology》上发表了题为“Dynamic enhancer transcription associates with reprogramming of immune genes during pattern triggered immunity in *Arabidopsis*”的研究论文。该研究构建了基于拟南芥基因间区染色质开放和转录水平的潜在活性增强子库，鉴定了响应不同微生物相关分子模式(MAMPs)的免疫相关增强子，并联合分析了免疫基因激活与增强子动力学的调控网络，首次揭示了增强子顺式调控基因表达的是植物免疫的重要组成部分。增强子是真核生物中的一类顺式调控元件(CRE)，通过激活相关基因的转录在基因表达调控中发挥重要作用。哺乳动物增强子转录产物——eRNA的生物合成和功能研究较多，被认为是活性增强子的重要指标，但是植物增强子转录本的特征和功能尚未得到系统定义。微生物相关分子模式(MAMPs)触发的免疫反应PTI是植物先天免疫的重要环节，精准的转录重编程

对于植物启动快速有效的防御反应至关重要，而增强子是否参与植物免疫并发挥重要调控功能还不清楚。通过去除核糖体RNA和高深度的转录组测序，并结合全基因组染色质可及性、DNA甲基化和组蛋白修饰等分析，鉴定到了与拟南芥部分增强子区域相对应的转录本，且其与动物增强子RNA具有相似的特征。这些从拟南芥增强子单向或双向转录的eRNA，大多数不具有polyA结构。转录的增强子可视为活性增强子，具有较低程度的DNA甲基化、高水平的染色质可及性以及RNA Pol II和组蛋白乙酰化标记的显著富集等特性。从而揭示了“转录枢纽”的形成是植物活性增强子的关键特征，而增强子转录本的产生是增强子活性的良好标志。基于不同MAMPs诱导后eRNA的差异表达，解析了PTI诱导的拟南芥免疫相关增强子活性动态变化，这些增强子的转录受f1g22、chitin和nlp20，以及植物损伤相关分子模式pep2等的诱导，被定义为模式诱导的核心增强子（CIPE）。研究证明了增强子和靶基因之间的表达模式有很强的关联，在植物免疫中起着重要的调节作用。该研究还确定了特定的免疫相关转录因子（包括WRKYs和SARD1）是免疫诱导增强子转录的潜在元件，绘制了一个由“转录因子—增强子—靶标基因”组成的免疫基因调控网络。总体而言，该研究创新性地探究了植物增强子的转录活性特征及其对植物免疫基因表达的关键作用，相关结果可以作为研究植物免疫增强子和基因表调控的良好资源。我院在读博士研究生章颖为该论文的第一作者，李博教授为论文的通讯作者，姜道宏教授和付艳萍教授等参与此项研究。该研究得到了国家自然科学基金、中央高校基本科研业务费专项基金和华中农业大学自主创新基金等项目的资助。

来源：华中农业大学植物科学技术学院

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全文链接:

<http://cpst.hzau.edu.cn/info/1037/12497.htm>

## ➤ 学术文献

### 1. Effects of squirting cucumber (*Ecballium elaterium*) fruit juice on *Agrobacterium tumefaciens*-mediated transformation of plants (喷瓜(喷瓜)果汁对农杆菌介导的植物转化的影响)

**简介：**Different concentrations of squirting cucumber (*Ecballium elaterium* (L.) A. Rich.) fruit juice were added to *Agrobacterium tumefaciens* growth, leaf disc inoculation, and cocultivation media, to investigate its effect on the transformation frequency of tobacco and potato. *A. tumefaciens* strain GV2260 harboring p35S GUS-INT and pAOPR1-GUS-INT plasmids were used separately in the transformation experiments. Neomycin phosphotransferase (NPT-II) gene was used as a plant selectable marker at a concentration of 100 mg L<sup>-1</sup>. The addition of 5-10 mg L<sup>-1</sup> squirting cucumber fruit juice to bacterial nutrient medium increased *A. tumefaciens* growth significantly by 6 h. Moreover, the use of high concentrations (2.5-20 mL L<sup>-1</sup>) of fruit juice resulted in excessive bacterial growth on cocultivation and selection media around the explants, which was difficult to eliminate by subculture or higher levels of antibiotics. On the other hand, lower concentrations (0.2-1.6 mL L<sup>-1</sup>) of squirting cucumber fruit juice significantly increased the transformation frequency in both tobacco and potato. Kanamycin-resistant tobacco shoots, rooted in a medium containing 100 mg L<sup>-1</sup> kanamycin, were transferred to pots containing organic soil

and perlite in growth cabinets for acclimatization. Transgenic plants grew normally and set seeds. The presence of T-DNA in these transformants was confirmed by PCR and GUS analysis.

来源: Turkish journal of biology

发布日期:2015-05-01

全文链接:

[http://agri.ckcest.cn/file1/M00/10/0E/Csgk0GMId3uAX\\_rTAHiegTL6gkg145.pdf](http://agri.ckcest.cn/file1/M00/10/0E/Csgk0GMId3uAX_rTAHiegTL6gkg145.pdf)

## **2. High-efficiency Agrobacterium tumefaciens- mediated transformation of cucumber ( *Cucumis sativus L.*) using stem nodes as explants. (以茎节为外植体高效转化黄瓜的研究(根癌农杆菌))**

简介: An efficient Agrobacterium- mediated transformation system was developed for cucumber ( *Cucumis sativus L.* 'Jinyan') using stem nodes as explants. Stem nodes were isolated from cucumber seedlings 10 d after germination, wounded four-to-five-times with a knife, infected for 30 min with Agrobacterium tumefaciens strain EHA105 harbouring the binary vector pCAMBIA 1303, then co-cultured for 5 d. Adding a washing step after co-culturing, and using 25 mg l<sup>-1</sup> meropenem to suppress bacterial growth in the regeneration medium, eliminated any overgrowth of Agrobacterium and significantly improved the efficiency of transformation when 15 mg l<sup>-1</sup> hygromycin was applied as a selection agent. Finally, a transformation efficiency of 7.1% was achieved with a high frequency (50%) of single-copy T-DNA integration 2 months after co-culture. On average, two-to-three independent transformation events occurred from each original explant.

来源: The Journal of Horticultural Science & Biotechnology

发布日期:2009-02-01

全文链接:

<http://agri.ckcest.cn/file1/M00/03/3C/Csgk0YdfKO-ABPkHABnxJTURBC8235.pdf>

## **3. Cloning of tryptophan monooxygenase gene in *Pseudomonas syringae* and transformation into cucumber. (假单胞杆菌色氨酸单加氧酶基因的克隆及转化黄瓜的研究)**

简介: Tryptophan monooxygenase iaaM gene was cloned from *P. syringae* pv. *syringae* 3023 by PCR. The results of nucleotide sequence determination showed that the complete nucleotide sequence was 1674 bp in length, and the GENBANK accession number was AY530536. The 2A12 promoter gene was cloned from tomato cultivar Dongnong 706 by using the same method. We constructed the expression vector pCAM-2AiaaT with the iaaM gene, and driven by fruit specific promoter 2A12. The iaaM gene was transferred into cucumber cultivar 649 mediated by Agrobacterium tumefaciens, and transgenic cucumber plants were confirmed by PCR and Southern blot.

来源: Acta Horticulturae

发布日期:2007-07-01

全文链接:

<http://agri.ckcest.cn/file1/M00/03/3C/Csgk0YdfJ-iAWVj5AAygyYaagwU669.pdf>

## **4. In vitro organogenesis and genetic transformation in popular Cucumis sativus L. through Agrobacterium tumefaciens(黄瓜的离体器官发生和根癌农杆菌遗传转化)**

**简介:** The effect of growth regulators and culture conditions on the morphogenetic response of cotyledonary leaf discs was studied in popular cucumber variety (Cucumis sativus cv. Sheetal). Organogenesis was induced directly without any intervening callusphase on Murashige and Skoog medium supplemented with different concentrations of benzyladenine and indole propionic acid. Best results (93 percent)were obtained in the presence of the 4mg/L benzyladenine and 1mg/L IPA. The elongated shoots were rooted in basal medium with 1mg/L indole butyric acid, hardened and transferred to the field conditions. Genetic transformation system has been established for Cucumis sativus cv. Sheetal, plants by infecting cotyledonary explants with Agrobacterium tumefaciensstrain LBA4404 carrying binary plasmid pBI121, which contains scorable marker, #beta#-glucuronidase and selectable marker nptII under the CaMV 35S promoter. Infection was most effective when explants were infected with Agrobacterium for 15 min and co-cultivated for 2 days in the co-cultivation medium. Shoots were regenerated directly from cotyledonary leaf explants in the presence of kanamycin (50#mu#g/ml) and analysed. Southern blot analysis confirmed that transformation had occurred. This method willallow genetic improvement of this crop by the introduction of agronomically important genes.

**来源:** Indian Journal of Experimental Biology

**发布日期:** 2002-03-04

**全文链接:**

<http://agri.ckcest.cn/file1/M00/10/0E/Csgk0GM1eI2ANhgIADwATbytdfk180.pdf>

### **相关专利**

#### **1. 与果形指数紧密相关分子标记的特异性引物及应用-**

**简介:** 本发明涉及分子生物学领域, 具体涉及与果形指数紧密相关分子标记的特异性引物及应用。本发明确定了一个与果形显著相关的SNP, 并确定了其为控制辣椒果形指数的候选基因, 通过设计扩增及测序引物, 对包含此SNP的区段进行PCR扩增, 对PCR扩增产物进行Sanger测序, 根据测序结果鉴定此SNP位点的基因型。

**来源:** 佰腾网

**发布日期:** 2022-05-31

**全文链接:**

[http://agri.ckcest.cn/file1/M00/10/0E/Csgk0GM1gseARbeuAA0y\\_220ESQ163.PDF](http://agri.ckcest.cn/file1/M00/10/0E/Csgk0GM1gseARbeuAA0y_220ESQ163.PDF)

#### **2. 一种农杆菌介导的菜心遗传转化方法**

**简介:** 本发明涉及植物基因工程应用领域, 具体涉及一种农杆菌介导的菜心遗传转化方法。本发明将菜心种子经表面消毒后置于播种培养基上进行培养, 然后苗龄为3d的无菌苗的带柄子叶作为外植体, 进行预培养、侵染、共培养、恢复培养和继代培养; 将继代

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培养后的不定芽转移至生根培养基中进行生根培养，得到组培苗，组培苗今后一步开瓶炼苗，后正常管理，得到转基因植物。本发明以菜心为材料，构建了菜心遗传转化体系，获得转基因植株，操作简单高效，污染率低，综合性能高，为芸薹属植物基因功能研究和分子育种奠定基础。

**来源：**佰腾网

**发布日期:**2020-11-06

**全文链接:**

<http://agri.ckcest.cn/file1/M00/03/3C/Csgk0YdfMuaABQy8ABGjZdeqhe0170.PDF>