



2022年第20期总55期

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中国农业科学院农业信息研究所  
联系人：王丽娟，张玉玮，信丽媛  
联系电话：022-23678616  
邮箱：[agri@ckcest.cn](mailto:agri@ckcest.cn)  
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## ▶ 前沿资讯

### 1. 园艺学院巩振辉教授团队在辣椒抗性研究领域取得系列进展

**简介:** 辣椒 (*Capsicum annuum* L.) 是一种重要的茄科经济作物, 因其富含维生素、辣椒红素、辣椒素等, 在食品及化工产业备受欢迎。现阶段, 干旱和低温胁迫是制约辣椒产业发展的重要环境因素。因此, 探索其抗旱、耐低温分子机制对辣椒产业持续稳定发展具有重要的理论与应用价值。近期, 巩振辉教授团队在《Horticulture Research》、《Journal of Experimental Botany》及《Scientia Horticulturae》期刊发表了关于辣椒抗性的研究论文, 2017级博士研究生马潇为第一作者, 巩振辉教授为通讯作者, 该研究得到了国家自然科学基金项目 (No. 31772309, No. 31860556, No. U1603102) 的资助。本研究探讨了CaCIPK3在调节辣椒干旱胁迫中的功能。在辣椒植株中沉默CaCIPK3会提高植株对干旱的敏感性。在辣椒中瞬时过表达CaCIPK3后, 可通过增强其抗氧化系统的活性和正向调控茉莉酸相关基因的表达, 提高辣椒耐旱性。作为CaCIPK3的互作蛋白, CaCBL2也对耐旱性产生了积极的影响。此外, CaWRKY1和CaWRKY41蛋白通过与CaCIPK3启动子直接结合影响其表达。本研究揭示了CaCIPK3在辣椒干旱调控机制中发挥的重要作用, 为深入解析辣椒的抗旱分子机制奠定了基础。文章链接: <https://www.nature.com/articles/s41438-021-00651-7>

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<https://news.nwafu.edu.cn/xscg/5132849123524f21970e229d89016cc9.htm>

### 2. 西甜瓜种质资源与遗传育种团队在易位二倍体少籽西瓜产生机制研究方面取得新进展

**简介:** 近日, 西甜瓜种质资源与遗传育种团队袁黎教授课题组在《Horticulture Research》期刊在线发表了题为《A 2.09 Mb fragment translocation on chromosome 6 causes abnormalities during meiosis and leads to less seed watermelon》的研究论文。团队教师田树娟为论文第一作者, 已毕业硕士研究生葛洁为共同第一作者, 袁黎教授为通讯作者。西瓜 (*Citrullus lanatus* (Thunb.) Matsum. & Nakai) 因其果实汁多味甜、营养丰富, 在世界范围广泛栽培。西瓜产业在国民经济中占据重要地位, 无籽/少籽西瓜因其具有食用方便、可溶性固形物含量高、口感好等诸多优点备受消费者青睐。其中, 三倍体无籽西瓜由于其适应性、抗逆性强, 耐贮运, 产量高, 具有多倍体和二倍体杂交一代的双重优势, 而深受消费者和种植者欢迎。然而, 三倍体无籽西瓜是由四倍体母本和二倍体父本杂交导致配子染色体失衡产生的无籽(不育), 在生产实践中, 三倍体无籽西瓜的生产技术存在诸多缺点: 如种子生产过程繁琐、冗长; 种子生产成本较高、发芽困难; 种子晚熟等; 而作为非转基因的易位二倍体无籽西瓜恰恰克服了其缺点, 同时避免了使用激素诱导无籽西瓜对药剂处理技术要求严格的问题。因此, 发掘和培育易位二倍体无籽/少籽西瓜资源, 进一步解析其染色体易位机制, 为未来有针对性开展创制精英无籽西瓜新种质具有重要的理论及实践意义。研究人员前期获得了田间自发易位突变体148, 发现该突变体与正常二倍体西瓜“京母”杂交得到的F1代“2018-Z-4”具有明显的少籽表型。进一步实验表明, “148”与其他正常二倍体西瓜亲本“Y83”、“JF”和“M08”的杂交后代也表现出少籽表型。由于雌雄配子不育是少

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籽的主要诱因，传统杂交实验证实，杂交F1代2018-Z-4西瓜的少籽表型是由雌配子半不育所导致。雌配子深埋在孢子体组织中很难接近及鉴定其发育是否正常，已知高等植物中，雌雄配子的发育过程是高度同步、基本一致，因此，可借助检测雄配子发育去判断雌配子的具体发育缺陷时期。进一步染色体展片实验分析表明，“2018-Z-4”小孢子母细胞在减数分裂中期I阶段出现异常的染色体四价体环结构，明确了配子半不育是由染色体易位造成。qRT-PCR分析进一步从侧面证实配子半不育是由染色体易位造成，而不是由减数分裂特异基因的表达降低引起。F2代分离群体遗传分析表明，“148”是易位纯和系材料，且杂交F1代“2018-Z-4”的少籽表型是由一条染色体片段易位造成的。基于基因组重测序、分子标记开发技术、图位克隆等技术，研究人员将易位区段定位于Chr 06染色体上的2.09Mb区间。综上所述，该研究揭示了Chr 06染色体上一段2.09Mb片段发生易位导致少籽西瓜表型的机制，为二倍体水平培育精英无籽西瓜种质提供新方法，同时也为利用人工诱导的染色体易位技术创制无籽西瓜新品种提供了易位片段大小上的参考及前瞻性的研究基础。该研究工作得到了国家级青年人才计划（A279021801）、西北农林科技大学科技大学引进人才启动经费（Z1090221008）、陕西省自然科学基金（2021JM-089）及杨凌种业重点研发项目等项目的支持。原文链接：<https://rdcu.be/cCnaw>

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<https://news.nwafu.edu.cn/xscg/257cd618adc4446191955f77b06e113f.htm>

## ➤ 学术文献

### 1. miRNA Profiling and Its Role in Multi-Omics Regulatory Networks Connected with Somaclonal Variation in Cucumber (*Cucumis sativus* L.) (黄瓜(黄瓜*Cucumis sativus* L.)中与体细胞无性系变异相关的多组分调控网络中的miRNA谱系及其作用)

简介: The role of miRNAs in connection with the phenomenon of somaclonal variation, which occurs during plant in vitro culture, remains uncertain. This study aims to investigate the possible role of miRNAs in multi-omics regulatory pathways in cucumber somaclonal lines. For this purpose, we performed sRNA sequencing (sRNA-seq) from cucumber fruit samples identified 8, 10 and 44 miRNAs that are differentially expressed between somaclones (S1, S2, S3 lines) and the reference B10 line of *Cucumis sativus*. For miRNA identification, we use ShortStack software designed to filter miRNAs from sRNAs according to specific program criteria. The identification of predicted in-silico targets revealed 2,886 mRNAs encoded by 644 genes. The functional annotation of miRNA's target genes and gene ontology classification revealed their association with metabolic processes, response to stress, multicellular organism development, biosynthetic process and catalytic activity. We checked with bioinformatic analyses for possible interactions at the level of target proteins, differentially expressed genes (DEGs) and genes affected by genomic polymorphisms. We assume that miRNAs can indirectly influence molecular networks and play a role in many different regulatory pathways, leading to somaclonal variation. This regulation is supposed to

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occur through the process of the target gene cleavage or translation inhibition, which in turn affects the proteome, as we have shown in the example of molecular networks. This is a new approach combining levels from DNA-seq through mRNA-seq, sRNA-seq and in silico PPI in the area of plants' somaclonal variation.

来源: International Journal of Molecular Sciences

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全文链接:

<http://agri.ckcest.cn/file1/M00/03/33/Csgk0Yb0aiqAPx4YAFFeEOK-R08097.pdf>

## **2. Current progress in genetic and genomics-aided breeding for stress resistance in cucumber (*Cucumis sativus* L.) (黄瓜 (*Cucumis sativus* L.) 抗逆遗传和基因组学辅助育种研究进展。)**

简介: Crop plants encounter various biotic and abiotic stresses that hinder life throughout their growth and development. These factors certainly affect the productivity and quality of the final produce. In the post-genomics era, the accumulation of genomic resources has widened the crop breeding for complex traits. Cucumber (*Cucumis sativus* L.) is an important vegetable crop and has been a model plant species to work on genomics in depth as it is the first horticulture crop genome to be sequenced. During the various phases of growth and development, cucumber is exposed to various diseases, insect-pests and abiotic stresses. Resistance breeding in cucumber demands availability of molecular markers associated with trait of interest. The small genome size and existence of full genome sequence of cucumber has facilitated the utilization of genetic and genomics resources to facilitate molecular breeding. The high-density maps and easily accessible high throughput sequencing technologies has allowed quick identification of molecular markers or cloning of candidate genes/QTL for several biotic and abiotic stresses. This review article is attempted to compile the up-to-date available information on genomics enabled tools for haplotype mapping, genetic linkage mapping and functional gene identification for important biotic and abiotic stresses in cucumber.

来源: Scientia Horticulturae

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全文链接:

<http://agri.ckcest.cn/file1/M00/10/05/Csgk0GKdudqAY7XCABko1Szrp3k223.pdf>

## **3. Comparison of Metabolome and Functional Properties of Three Korean Cucumber Cultivars (3个韩国黄瓜品种# 13代谢物及功能特性的比较)**

简介: Cucumber (*Cucumis sativus* L.) is consumed worldwide and various cultivars have been developed to enhance fruit quality. However, few studies have comprehensively evaluated the quality of various cultivars. We carried out a metabolomics approach to study the three different cucumber cultivars (Chuichung, White Dadagi, and Mini) and their parts (peel and flesh) coupled with antioxidant activities. The amino acids, sugars, flavonoids, carotenoids, and chlorophylls were upregulated in Mini flesh; however, in the case of peel,

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they were highly expressed in Chuichung. The highest antioxidant activity was observed in the peel of Chuichung and flesh of Mini. Through correlation analysis between metabolites and antioxidant activity, apigenin and quercetin derivatives, chlorophyll a, chlorophyll b, lutein,  $\alpha$ -carotene, and  $\beta$ -carotene were found to be significantly positively correlated with antioxidant activity. To understand the metabolism of these compounds, we performed a comprehensive pathway analysis using a metabolomics approach and analysis of associated gene expression. In secondary metabolism, the expression levels of carotenoid-related genes (15-cis-phytoene synthase and  $\zeta$ -carotene desaturase) and chlorophyll-related genes (prochlorophyllide reductase and glutamyl-tRNA reductase) were consistent with the metabolome analysis data. Collectively, carotenoid and chlorophyll metabolism were upregulated in Chuichung peel and Mini flesh, which had the highest antioxidant activity in each part. These bioactive compounds can be used as biomarkers of commercial cucumber fruit quality. Accordingly, this study offers integrative insights into the quality of different cucumber cultivars and explores valuable metabolites and genes that are helpful in improving quality with functional properties.

来源: Frontiers in Plant Science

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全文链接:

<http://agri.ckcest.cn/file1/M00/10/05/Csgk0GKduOCAabDjADGEfOPpdNU629.pdf>

#### **4. Genome-wide analysis of OVATE family proteins in cucumber (*Cucumis sativus* L.) (黄瓜OVATE家族蛋白的全基因组分析)**

简介: OVATE family proteins (OFPs) are plant-specific proteins with a conserved OVATE domain that regulate plant growth and development. Although OFPs have been studied in several species, their biological functions remain largely unknown in cucumber (*Cucumis sativus* L.). This study identified 19 CsOFPs distributed on seven chromosomes in cucumber. Most CsOFP genes were expressed in reproductive organs, but with different expression patterns. Ectopic expression of CsOFP12-16c in *Arabidopsis* resulted in shorter and blunt siliques. The overall results indicated that CsOFP12-16c regulates silique development in *Arabidopsis* and may have a similar function in cucumber.

来源: Journal of Integrative Agriculture

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全文链接:

[http://agri.ckcest.cn/file1/M00/03/33/Csgk0Yb0aQaAIwDvACMs-F\\_sPVo171.pdf](http://agri.ckcest.cn/file1/M00/03/33/Csgk0Yb0aQaAIwDvACMs-F_sPVo171.pdf)

### 相关专利

#### **1. 一种木霉菌疏水蛋白Thfb6及其菌株、植物ISR激发子及激发方法**

简介: 本发明“一种木霉菌疏水蛋白Thfb6及其菌株、植物ISR激发子及激发方法”属于分子生物学领域。所述木霉菌疏水蛋白Thfb6的氨基酸序列如SEQ ID NO. 1。基于所述木霉菌疏水蛋白Thfb6, 本发明还提供一种植物ISR激发子及其激发方法以及一种TMV抗性

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诱导剂及其诱导方法。本发明的木霉菌疏水蛋白Thfb6能够引起植物叶片发生活性氧爆发、诱导细胞胞外碱化、胼胝质和酚类物质积累等早期防御反应，提高叶片中PAL、POD、PPO等抗逆性酶活性提高，诱导病程相关蛋白基因PR-1b、系统抗性标记基因NPR1以及防御反应关键酶基因PAL的表达，并诱导烟草提高对烟草花叶病的抗病性，同时还能诱导黄瓜对枯萎病抗性。

**来源：**佰腾网

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**全文链接：**

<http://agri.ckcest.cn/file1/M00/10/05/Csgk0GKdu3KACxARABXgVxjjza8513.PDF>

## 2. 黄瓜6-磷酸葡萄糖酸内酯酶CsPmR1在抗瓜类疫病中的应用

**简介：**本发明首次公开了6-磷酸葡萄糖酸内酯酶CsPmR1在抗瓜类疫病中的应用。特别是CsPmR1对侵染瓜类的瓜类疫霉(*Phytophthora melonis*)具有抗病功能。过量表达CsPmR1基因能够使黄瓜、南瓜子叶对疫病的抗性较对照明显增强，而在黄瓜子叶中瞬时沉默CsPmR1基因则使黄瓜子叶对疫病的抗性较对照明显减弱。CsPmR1基因对黄瓜、南瓜等瓜类抗疫病起着非常重要的作用，具有广泛的应用前景。

**来源：**佰腾网

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**全文链接：**

<http://agri.ckcest.cn/file1/M00/03/33/Csgk0Yb0bRGAI02yAA7Wgh7w9tE662.PDF>

## 3. 黄瓜CsGL2-LIKE基因及其参与调控雄花部分败育中的应用

**简介：**本发明提供了黄瓜CsGL2-LIKE基因及其参与调控雄花部分败育中的应用。本发明提供的黄瓜CsGL2-LIKE基因的核苷酸序列如SEQ ID NO. 2所示，其编码蛋白的氨基酸序列如SEQ ID NO. 1所示。本发明构建了CsGL2-LIKE基因的干扰载体，并利用农杆菌介导的转化技术将其转入黄瓜中，证明CsGL2-LIKE基因的下调造成黄瓜雄蕊的形态以及花粉活力发生变化，导致转基因植物的雄花部分败育，花粉活力下降，花粉管伸长能力受阻，而雌花没有受到影响，说明CsGL2-LIKE的功能与黄瓜雄花部分败育相关，暗示该基因可在黄瓜育种及品质改良中具有重要改良潜能作用。

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