



2017年第24期总86期

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## ▶ 前沿资讯

### 1. Scientists find way to surgically strike out weeds that impede crop growth (科学家们找到了一种治疗植物生长的杂草的方法)

简介: By using a combination of fumigants, scientists believe they can surgically strike out some weeds that otherwise get in the way of vegetable growth. Researchers say this will help growers as they try to manage pests in areas where they cause the most trouble.

来源: Science Daily

发布日期: 2017-06-05

全文链接:

<https://www.sciencedaily.com/releases/2017/06/170605092404.htm>

## ▶ 学术文献

### 1. The complete genome sequence, occurrence and host range of Tomato mottle mosaic virus Chinese isolate (番茄斑驳花叶病毒中国分离株全基因组序列、发生及寄主范围)

简介: Background: Tomato mottle mosaic virus (ToMMV) is a recently identified species in the genus Tobamovirus and was first reported from a greenhouse tomato sample collected in Mexico in 2013. In August 2013, ToMMV was detected on peppers (*Capsicum* spp.) in China. However, little is known about the molecular and biological characteristics of ToMMV. Methods: Reverse transcription-polymerase chain reaction (RT-PCR) and rapid identification of cDNA ends (RACE) were carried out to obtain the complete genomic sequences of ToMMV. Sap transmission was used to test the host range and pathogenicity of ToMMV. Results: The full-length genomes of two ToMMV isolates infecting peppers in Yunnan Province and Tibet Autonomous Region of China were determined and analyzed. The complete genomic sequences of both ToMMV isolates consisted of 6399 nucleotides and contained four open reading frames (ORFs) encoding 126, 183, 30 and 18 kDa proteins from the 5' to 3' end, respectively. Overall similarities of the ToMMV genome sequence to those of the other tobamoviruses available in GenBank ranged from 49.6% to 84.3%. Phylogenetic analyses of the sequences of full-genome nucleotide and the amino acids of its four proteins confirmed that ToMMV was most closely related to Tomato mosaic virus (ToMV). According to the genetic structure, host of origin and phylogenetic relationships, the available 32 tobamoviruses could be divided into at least eight subgroups based on the host plant family they infect: Solanaceae-, Brassicaceae-, Cactaceae-, Apocynaceae-, Cucurbitaceae-, Malvaceae-, Leguminosae-, and Passifloraceae-infecting subgroups. The detection of ToMMV on some solanaceous, cucurbitaceous, brassicaceous and leguminous plants in Yunnan Province and other few parts of China revealed ToMMV only occurred on peppers so far. However, the host range test results showed ToMMV could infect most of the tested solanaceous and cruciferous plants, and had a high affinity for the solanaceous plants. Conclusions: The complete nucleotide sequences of two Chinese ToMMV isolates from

naturally infected peppers were verified. The tobamoviruses were divided into at least eight subgroups, with ToMMV belonging to the subgroup that infected plants in the Solanaceae. In China, ToMMV only occurred on peppers in the fields till now. ToMMV could infect the plants in family Solanaceae and Cucurbitaceae by sap transmission.

来源: Virology Journal

发布日期: 2017-01-31

全文链接:

<http://agri.ckcest.cn/ass/NK002-20170612001.pdf>

## **2. Broccoli and radish sprouts are safe and rich in bioactive phytochemicals (西兰花和萝卜芽是安全和富含生物活性的植物化学物质)**

简介: Cruciferous sprouts (e.g. broccoli and red radish) are rich source of health-promoting phytochemicals that are more concentrated than in the adult plant edible organs; however, these tiny microgreens need cold storage conditions to preserve their quality to reach the consumers in microbiologically safe conditions, maintaining their composition and acceptability. In this work, the microbiological status and phytochemical composition of broccoli and radish sprouts were evaluated at harvest (Day 0), and after seven and fourteen days of storage at 5 and 10°C. Pathogenic microorganisms were absent during shelflife; nevertheless, the slight growth of *Enterobacteriaceae* organisms, aerobic mesophilic and psychotropic bacteria, molds and yeasts was assessed. The storage temperature influenced the quality and content of bioactives in the sprouts, and for practical applications, storage at 5°C is the most suitable option. Moreover, these fresh crucifers remain acceptable for consumers after 14 d storage period, being an interesting option for consuming fresh and naturally-functional foods.

来源: Postharvest Biology and Technology

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<http://agri.ckcest.cn/ass/NK002-20170612002.pdf>

## **3. Molecular Characterization of a Leaf Senescence-Related Transcription Factor BrWRKY75 of Chinese Flowering Cabbage (一种叶子的衰老相关转录因子brwrky75菜心的分子特征)**

简介: WRKY is a plant-specific transcription factor (TF) involved in the regulation of many biological processes; however, its role in leaf senescence of leafy vegetables remains unknown. In the present work, a WRKY TF, termed BrWRKY75 was isolated from Chinese flowering cabbage [*Brassica rapa* L. ssp. *chinensis* (L.) Mokino var. *utilis* Tsen et Lee]. Analysis of deduced amino acid sequence and the phylogenetic tree showed that BrWRKY75 has high homology with WRKY75 from *Brassica oleracea* and *Arabidopsis thaliana*, and belongs to the II c sub-group. Sub-cellular localization and transcriptional activity analysis revealed that BrWRKY75 is a nuclear protein with transcriptional repression activity, and was up-regulated during leaf senescence. Electrophoretic mobility shift assay confirmed that

BrWRKY75 directly bound to the W-box (TTGAC) *cis*-element. Collectively, these results provide a basis for further investigation of the transcriptional regulation of Chinese flowering cabbage leaf senescence.

来源: Horticultural Plant Journal

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<http://agri.ckcest.cn/ass/NK002-20170612004.pdf>

#### **4. Genetic Analysis and Mapping of the Purple Gene in Purple Heading Chinese Cabbage (大白菜紫心性状遗传规律分析及其基因初步定位)**

简介: To analyze genetic linkage and map purple gene (*BrPur*) controlling purple inner leaves trait of Chinese cabbage, a F<sub>2</sub> population was constructed by selfing a F<sub>1</sub> plant from homozygous purple heading line '14S839' and homozygous orange heading line '14S162'. The phenotype investigation of head color showed that the segregation ratio of purple to non-purple individuals was consistent with the expected ratio of 3:1, which indicated that purple inner leaves trait is controlled by a single dominant gene. A total of 297 SSRs in whole genome of Chinese cabbage were tested by modified Bulk Segregant Analysis (BSA) method. Two linked markers flanking *BrPur*, A710 and A714, were obtained and *BrPur* was mapped on linkage group A07 based on the sequence of these two markers. Subsequently, two new markers flanking *BrPur*, CL-12 and B214-87, were developed based on two known anthocyanins-related genes, Br4CL3 and Bra004214. Genetic mapping of all markers in the F<sub>2</sub> mapping population showed CL-12 and B214-87 linked to *BrPur* with the genetic distance of 3.1 cM and 3.5 cM, respectively.

来源: Horticultural Plant Journal

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<http://agri.ckcest.cn/ass/NK002-20170612003.pdf>