



2019年第42期总209期

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(摘要)

## ▶ 科技报告

### 1. 蔬菜和豆类展望

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## ▶ 前沿资讯

### 1. 北京基因组所开发基因组变异-表型关联知识库

**简介:** 近日, 由中国科学院北京基因组研究所开发的国际上首个动植物基因组变异-表型关联知识库(GWAS Atlas)正式上线发表, 该项研究成果以GWAS Atlas: a curated resource of genome-wide variant-trait associations in plants and animals 为题在国际学术期刊《核酸研究》(Nucleic Acids Research) 在线发表。

全基因组关联分析(GWAS), 即指在全基因组范围内找出存在的序列变异, 从中筛选出与疾病、表型性状等相关联的遗传位点, 是挖掘生物复杂性状遗传基础的关键技术。随着高通量测序技术的快速发展, 多个物种产生了越来越多的高质量基因型数据, 并已解析了与许多动植物复杂性状相关联的遗传位点。但这些知识信息都分散在不同文献中, 不利于知识整合、挖掘与再利用。为此国家基因组科学数据中心的科研人员通过关键词检索、人工审编、词条比对注释等技术手段, 结构化整理了现有主要农作物和畜牧动物的基因型-表型关联知识, 开发了世界上首个动植物基因组变异-表型关联知识库GWAS Atlas。

GWAS Atlas知识库整合了9个物种(包括棉花、梅花、玉米、油菜籽、水稻、高粱、大豆7种植物和山羊、猪两种动物)与614个性状关联的75467条基因型-表型(G2P)信息, 并通过语义比对等映射到五个不同的性状本体上(植物性状本体PTO, 家畜性状本体ATOL, 作物本体CO等), 方便用户通过基于本体的层级结构来查找感兴趣的性状及对应的G2P关联信息。此外, 研究人员还分析并定义了与多个性状相关联的多效基因及遗传位点, 支持用户通过不同模块在线浏览、检索与下载。

GWAS Atlas作为首个综合多物种的变异-性状关联知识库, 是全基因组变异信息数据库(GVM)的延伸, 将为未来重要农艺性状的模块化遗传研究和育种应用提供重要资源和平台。该研究得到中科院战略性先导科技专项、中科院国际大科学计划等的资助。

**来源:** 中国科学院

**发布日期:** 2019-10-14

**全文链接:**

<http://agri.ckcest.cn/file1/M00/0E/CD/Csgk0F21gNmAaiRpAAWMWk7jKjQ525.pdf>

### 2. Family of crop viruses revealed at high resolution for the first time(首次以高分辨率揭示作物病毒家族)

**简介:** 黄症病毒科(Luteoviridae)是引起世界范围内主要农作物损失的病原植物病毒。该病毒通过蚜虫传播, 感染多种粮食作物, 包括谷类、豆类、瓜类、甜菜、甘蔗和马铃薯。

到目前为止, 研究人员一直无法生成足够数量的这些病毒以高分辨率研究它们的结构。

现在, 一个研究小组利用植物表达技术的最新进展, 生成足够数量的病原体, 以便用最先进的显微镜技术进行更详细的检查。

该方法涉及用创建病毒样颗粒(VLPs)所必需的基因渗入一种烟草植物。根据插入的遗传信息, VLPs在植物宿主内自组装。这种技术避免了处理传染性病毒的需要。

利用从植物中提取的VLPs, 来自约翰·因内斯中心和利兹大学Astbury生物结构实验室的研究团队可以通过冷冻电子显微镜以高分辨率观察病毒结构。

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这是首次从分子水平上深入了解黄症病毒衣壳的形成过程，并揭示了它是如何通过蚜虫传播的。参与这项研究的团队表示，这种方法可能有助于揭开其他病毒的秘密。

研究人员表示，这一进展为该重要的植物病毒家族提供了开发诊断工具的平台，这些植物病毒在全球范围内造成了巨大的损失。通过植物表达技术和结构生物学的结合，可以了解许多其他类型病毒的结构。

植物病毒感染造成的全球经济损失估计为300亿美元。

黄症病毒科 (Luteoviridae) 攻击植物的脉管系统，导致严重的发育迟缓，造成作物损失。该家族包括大麦黄矮病毒和马铃薯卷叶病毒，在英国每年造成的农作物损失高达4000-6000万英镑。

来源: AAAS

发布日期: 2019-10-11

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/CD/Csgk0F21gqGAJEdNAAYfNWqt1gs286.pdf>

## ➤ 学术文献

### 1. Biased gene retention during diploidization in Brassica linked to three-dimensional genome organization (芸薹属植物二倍化过程中与三维基因组结构相关的偏向基因保留)

简介: The non-random three-dimensional (3D) organization of the genome in the nucleus is critical to gene regulation and genome function. Using high-throughput chromatin conformation capture, we generated chromatin interaction maps for *Brassica rapa* and *Brassica oleracea* at a high resolution and characterized the conservation and divergence of chromatin organization in these two species. Large-scale chromatin structures, including A/B compartments and topologically associating domains, are notably conserved between *B. rapa* and *B. oleracea*, yet their KNOT structures are highly divergent. We found that genes retained in less fractionated subgenomes exhibited stronger interaction strengths, and diploidization-resistant duplicates retained in pairs or triplets are more likely to be colocalized in both *B. rapa* and *B. oleracea*. These observations suggest that spatial constraint in duplicated genes is correlated to their biased retention in the diploidization process. In addition, we found strong similarities in the epigenetic modification and Gene Ontology terms of colocalized paralogues, which were largely conserved across *B. rapa* and *B. oleracea*, indicating functional constraints on their 3D positioning in the nucleus. This study presents an investigation of the spatial organization of genomes in Brassica and provides insights on the role of 3D organization in the genome evolution of this genus.

来源: Nature Plants

发布日期: 2019-08-05

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/CD/Csgk0F21eV6AAyi2AD2A2S1kI6o165.pdf>

### 2. Five Newly Collected Turnip Mosaic Virus (TuMV) Isolates from

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## **Jeju Island, Korea are Closely Related to Previously Reported Korean TuMV Isolates but Show Distinctive Symptom Development**(来自韩国济州岛的五种新收集的芜菁花叶病毒 (TuMV) 分离株与之前报道的韩国TuMV分离株密切相关, 但显示出独特的症状发展)

**简介:** For several years, temperatures in the Korean peninsula have gradually increased due to climate change, resulting in a changing environment for growth of crops and vegetables. An associated consequence is that emerging species of insect vector have caused increased viral transmission. In Jeju Island, Korea, occurrences of viral disease have increased. Here, we report characterization of five newly collected turnip mosaic virus (TuMV) isolates named KBJ1, KBJ2, KBJ3, KBJ4 and KBJ5 from a survey on Jeju Island in 2017. Full-length cDNAs of each isolate were cloned into the pJY vector downstream of cauliflower mosaic virus 35S and bacteriophage T7 RNA polymerase promoters. Their fulllength sequences share 98.9-99.9% nucleotide sequence identity and were most closely related to previously reported Korean TuMV isolates. All isolates belonged to the BR group and infected both Chinese cabbage and radish. Four isolates induced very mild symptoms in *Nicotiana benthamiana* but KBJ5 induced a hypersensitive response. Symptom differences may result from three amino acid differences uniquely present in KBJ5; Gly(382)Asp, Ile(891)Val, and Lys(2522)Glu in P1, P3, and NIb, respectively.

**来源:** The Plant Pathology Journal

**发布日期:** 2019-08-01

**全文链接:**

<http://agri.ckcest.cn/file1/M00/OE/CD/Csgk0F21eC6ATJ0YAB-Ng9FcqcY338.pdf>

## **3. Natural variation in a calreticulin gene causes reduced resistance to Ca<sup>2+</sup> deficiency-induced tipburn in Chinese cabbage (*Brassica rapa* ssp. *pekinensis*)**(钙网蛋白基因的自然变异导致大白菜 (*Brassica rapa* ssp. *pekinensis*) 对Ca<sup>2+</sup> 缺乏诱导的干烧心病抗性降低)

**简介:** Tipburn is an irreversible physiological disorder of Chinese cabbage that decreases crop value. Because of a strong environmental component, tipburn-resistant cultivars are the only solution, although tipburn resistance genes are unknown in Chinese cabbage. We studied three populations of Chinese cabbage over four growing seasons under field conditions: (a) 194 diverse inbred lines, (b) a doubled haploid (DH100) population, and (c) an F2 population. The 194 lines were genotyped using single nucleotide polymorphism markers, and genome-wide-association mapping showed that 24 gQTLs were significantly associated with tipburn disease index. Analysis of the DH100 and F2 populations identified a shared tipburn-associated locus, gqbTRA06, that was found to cover the region defined by one of the 24 gQTLs. Of 35 genes predicted in the 0.14-Mb quantitative trait locus region, Bra018575 (calreticulin family protein, BrCRT2) showed higher expression levels during disease development. We cloned the two BrCRT2 alleles from tipburn-resistant (BrCRT2<sup>R</sup>) and tipburn-susceptible (BrCRT2<sup>S</sup>) lines and identified a 51-bp deletion in BrCRT2<sup>S</sup>.

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Overexpression of BrCRT2<sup>R</sup> increased Ca<sup>2+</sup> storage in the Arabidopsis crt2 mutant and also reduced cell death in leaf tips and margins under Ca<sup>2+</sup>-depleted conditions. Our results suggest that BrCRT2 is a possible candidate gene for controlling tipburn in Chinese cabbage.

来源: PLANT CELL AND ENVIRONMENT

发布日期:2019-07-13

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/CD/Csgk0F21d0WABrmSADsMDccVz50176.pdf>

#### **4. High ambient temperature leads to reduced FT expression and delayed flowering in Brassica rapa via a mechanism associated with H2A.Z dynamics (高环境温度通过与H2 A. Z动力学相关的机制导致油菜FT表达降低和开花延迟)**

简介: Flowering time is a relevant agronomic trait because is crucial for the optimal formation of seeds and fruits. The genetic pathways controlling this developmental phase transition have been studied extensively in Arabidopsis thaliana. These pathways converge in a small number of genes including FT, the so-called florigen, which integrates environmental cues like ambient temperature. Nevertheless, detailed and functional studies about flowering time in Brassica crops are scarce. Here we study the role of the FT Brassica rapa homologues and the effect of high ambient temperature on flowering time in this crop. Phenotypic characterization and gene-expression analyses suggest that BraA.FT.a (BraA02g016700.3C) is decisive for initiating floral transition; consequently, braa.ft.a loss-of-function and hypomorphic mutations result in late flowering phenotypes. We also show that high ambient temperature delays B. rapa floral transition by reducing BraA.FT.a expression. Strikingly, these expression changes are associated with increased histone H2A.Z levels and less accessible chromatin configuration of the BraA.FT.a locus at high ambient temperature. Interestingly, increased H2A.Z levels at high ambient temperature were also observed for other B. rapa temperature-responsive genes. Previous reports delimited that Arabidopsis flowers earlier at high ambient temperature due to reduced H2A.Z incorporation in the FT locus. Our data reveal a conserved chromatin-mediated mechanism in B. rapa and Arabidopsis in which the incorporation of H2A.Z at FT chromatin in response to warm ambient temperature results in different flowering time responses. This work will help to develop improved Brassica crop varieties with flowering time requirements to cope with global warming.

来源: The Plant Journal

发布日期:2019-07-01

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/CD/Csgk0F21cPKAULNbABZofCIRsf0771.pdf>

## **会议论文**

### **1. 8th International conference on management of the diamondback**

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## **moth and other crucifer insect pests (Abstracts) (第八届小菜蛾及其他十字花科害虫防治国际会议论文集 (摘要))**

简介: 8th International conference on management of the diamondback moth and other crucifer insect pests, Shanhua, Tainan, Taiwan, 4-8 March 2019. Meeting information, schedule and abstracts.

来源: World Vegetable Center

发布日期: 2019-03-08

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/CD/Csgk0F21fuiAHBbwABEpX2LIEQo582.pdf>

### **➤ 科技报告**

#### **1. Vegetables and Pulses Outlook (蔬菜和豆类展望)**

简介: This report covers basic supply, demand, price, and trade analysis for fresh-market vegetables, processing vegetables, potatoes, and pulses.

来源: USDA

发布日期: 2019-09-27

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/CD/Csgk0F21gCWAE55tAArFzgSH0eM359.pdf>