



2019年第40期总207期

## 蔬菜育种专题

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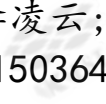
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## ▶ 前沿资讯

### 1. Why the lettuce mitochondrial genome is like a chopped salad (为什么生菜的线粒体基因组像切碎的沙拉)

简介: The genomes of mitochondria are usually depicted as rings or circles. But in plants, 1 ring does not rule them all. A new study of lettuce shows that the mitochondrial genome often forms branching structures with elements that can be swapped around like a chopped salad.

来源: ScienceDaily

发布日期: 2019-09-23

全文链接:

<http://agri.ckcest.cn/file1/M00/0E/CA/Csgk0F2QCq2AM PdAAQ1ahlcCdA957.pdf>

### 2. The next agricultural revolution is here (新的农业革命即将来临)

简介: 不断增长的人口与不断恶化的气候对作物育种提出了重大挑战, 迫切需要利用科学知识和工具开展新一轮农业革命。目前提出的若干解决途径包括增加作物的抗压恢复能力, 将农业扩展到城市生境或干旱易发地区等新环境, 以及促进全球向以植物为主的饮食结构转变。

美国冷泉港实验室 (CSHL) 扎克·利普曼 (Zach Lippman) 教授最近与以色列魏兹曼科学研究所专家尤瓦尔·埃希德 (Yuval Eshed) 合作, 阐述了植物科学和农业的现状和未来。

他们发表在《科学》杂志上的文章列举了过去50年生物学研究中的一些例子, 并强调了推动上一轮农业革命的主要基因突变和遗传修饰, 包括改变植物的开花信号以调整作物的产量, 创造出能够耐肥或适应不同气候的植物, 以及引入高产抗病的杂交种。

这些有益变化最初是偶然发现的, 但现代基因组学已经揭示, 它们大多来源于两个核心激素系统: 控制开花的成花素和影响株高的赤霉素。利普曼和埃希德认为, 现如今的基因编辑技术准确而又高效, 下一次农业革命将无须依赖偶然发现。或许通过改变这两个核心激素系统, 未来就可以克服农业面临的挑战。

在20世纪60年代以前, 为了提高小麦产量而大量施肥, 结果会导致植株徒长和倒伏, 从而造成减产。赤霉素系统的突变, 使小麦和水稻成为了今天的矮秆, 能够抵御那些所谓的灾难性风暴。

利普曼和埃希德还提到了西红柿在欧洲、棉花在中国所经历的变化。在中国, 科研人员利用影响成花素和抗花素的突变把这种在南方通常表现为无限生长的植物改变成了更紧凑、开花更早的灌木状植物, 使其更适合中国北方的气候。西红柿中的一种抗花素突变也是将这种地中海藤蔓作物转化为当今世界农业系统中大规模种植的灌木状作物的催化剂。

核心系统——赤霉素、成花素或两者兼而有之——会受到突变的影响, 从而产生一些有益的性状。这些有益性状偶然被人类发现后, 还需要多年艰苦的育种来调控这种突变的强度, 直至达到育种目标。而CRISPR基因编辑正在加速这一调控过程。利普曼和埃希德认为, 基因编辑的最佳应用可能不仅仅是调控已经存在的革命性突变, 而是识别或引入新的突变。这样不仅会减少进行这种调控的工作量, 还有可能带来一些意外惊喜, 并进一步提高作物生产效率, 或使作物更快地适应新的环境条件。

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通过将基因变异引入这两个核心系统,会有更大的空间创造更多的遗传多样性,这可能会提高生产力,改善边际地区植物的适应性生存,比如干旱条件。

文章认为,过去的农业革命使农作物更加高产,种植的范围更广。鉴于成花素/抗花素和赤霉素/DELLA突变在过去引发了多次农业革命,因而在这两种激素系统中创造新的多样性极有可能会进一步释放农业的潜能。有办法用更多的农作物和更高的频率继续下一轮农业革命,这将是人类的福音。

来源: ScienceDaily

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全文链接:

<http://agri.ckcest.cn/file1/M00/OE/CA/Csgk0F2QCgKANzQuAARY1zkfJ1s871.pdf>

## ➤ 学术文献

### 1. 甘蓝型油菜NBS-LRR基因家族的鉴定及密码子偏好性分析

**简介:** NBS-LRR(nucleotide binding site and leucine rich repeat)是庞大且复杂的基因家族,对植物的抗病性具有非常重要的作用。为深入了解甘蓝型油菜NBS-LRR基因家族,合理开发利用基因资源,对甘蓝型油菜(*Brassica napus* L.)及相关物种的NBS-LRR基因进行了生物信息学分析,包括基因家族鉴定、系统进化分析、保守基序、基因结构、染色体定位以及密码子偏好性分析等。以拟南芥为参考,在甘蓝型油菜中鉴定到463个NBS-LRR基因家族成员,根据结构域将其分成TIR-NBS-LRR和CC-NBS-LRR两类,再分别细分为4和8个亚组。19条染色体均有NBS-LRR基因,其中ChrC09上分布最多,达到53个;NBS-LRR基因以基因簇形式存在居多,可推测抗病基因NBSLRR发生了大规模片段复制。分析5个物种(甘蓝、白菜、甘蓝型油菜、水稻和拟南芥)的NBS-LRR家族基因密码子偏好性,结果发现,甘蓝型油菜抗病基因有效密码子数范围与甘蓝(*B. oleracea* L.)更加相近。然后进一步对甘蓝型油菜和白菜(*B. rapa* L.)与甘蓝的共线直系同源关系进行偏好性分析,并获得相同发现,推测甘蓝型油菜可能和甘蓝在抗病基因密码子的使用偏好上更为相似。

来源: 中国油料作物学报

发布日期: 2019-09-23

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/CA/Csgk0F2QCMGAP6CxAFGMBqjEShg819.pdf>

### 2. Construction of a high-density genetic linkage map and identification of quantitative trait loci associated with clubroot resistance in radish (*Raphanus sativus* L.) (萝卜(*Raphanus sativus* L.)高密度遗传连锁图谱的构建及抗根肿病性状QTL鉴定)

**简介:** Clubroot is a devastating disease caused by *Plasmodiophora brassicae*, leading to substantial yield loss of cruciferous plants, especially radish (*Raphanus sativus*) in China. Thus, there is a need to elucidate the mechanisms underlying the pathogenicity of *P. brassicae* and to breed clubroot-resistant radish cultivars. In the present study, we constructed a high-density linkage map of *R. sativus* by restriction-site-associated DNA sequencing

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(RAD-Seq) using an F2 population derived from a cross between the clubroot-resistant and clubroot-susceptible inbred lines “BJJ” and “XNQ,” respectively. The genetic map spans 794.3 cM and has 1148 SNPs distributed across nine linkage groups corresponding to the nine chromosomes of *R. sativus*. The average distance between the adjacent markers is 0.7 cM. A set of five QTLs (viz., RsCr1, RsCr2, RsCr3, RsCr4, and RsCr5) associated with resistance to clubroot was detected on chromosomes 8 and 9. The limit of detection values of quantitative trait loci (QTLs) ranged from 5.23 to 7.65, accounting for 7.26-31.38% of the observed phenotypic variance. Synteny analysis showed that RsCr1 is homologous to the clubroot resistance gene *Crr1* in *Brassica rapa*. This high-density genetic map of *R. sativus* provides valuable information for clubroot resistance gene selection and resistant variety breeding, while the QTL mapping results provide a reference dataset for effective gene exploration and marker-assisted breeding programs.

来源: Molecular Breeding

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全文链接:

<http://agri.ckcest.cn/file1/M00/OE/CA/Csgk0F2QBtOAZMAwABcaoRpkmgI006.pdf>

### 3. Development of a marker for detection of *Xanthomonas campestris* pv. *campestris* races 1 and 2 in *Brassica oleracea* (甘蓝中十字花科黑腐病菌1号和2号生理小种检测标记物的建立)

简介: *Xanthomonas campestris* pv. *campestris* (Xcc) is a plant pathogen of cruciferous crops that causes black rot disease throughout the world. At present, based on the host-pathogen interactions among differential cultivars of *Brassica* crops, 11 pathogenic Xcc races have been identified, but the race identification method based on host-pathogen interactions is time-consuming. However, early and rapid detection of the pathogen could reduce economic loss by allowing appropriate control measures against black rot disease to be taken more quickly. In this study, a PCR-based molecular marker has been developed for identifying the Xcc race 1 and Xcc race 2 bacterial strains together. The specificity of the marker was tested by PCR using 8 available Xcc races, *X. campestris* strains, and other bacteria. Upon amplification, a polymorphic band was observed in the PCR amplicon with a size of 1523 bp and 929 bp in Xcc races 1 and 2, respectively. A deletion of 594 bp conferred the specificity in Xcc race 2 compared to race 1. The identified PCR-based molecular marker clearly discriminated the Xcc race 1 and race 2 from other races when tested in artificially infected cabbage leaves. Thus, PCR-based development of an Xcc race 1- and 2-specific marker could be a valuable tool for the accurate detection of Xcc race 1 and 2 together for implementing control measures more quickly.

来源: Horticulture, Environment, and Biotechnology

发布日期: 2019-07-18

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/CA/Csgk0F2QCC2AfNjQAA7oZDZ8ROs192.pdf>

### 4. Characterization and expression analysis of *BcAMT1;4*, an

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## **ammonium transporter gene in flowering Chinese cabbage (菜薹中氨转运基因BcAMT1;4的特征与表达分析)**

**简介:** Ammonium ( $\text{NH}_4^+$ ) is generated during many endogenous metabolic processes in the leaves of plants, and there is increasing evidence that ammonium transporters (AMTs) play important roles in  $\text{NH}_4^+$  transmembrane transport and distribution. However, the expression of different AMT genes is tissue-type specific and their functions differ. Information about AMT genes and their expression under different environmental conditions in flowering Chinese cabbage (*Brassica campestris* L.) is currently limited. Here, we isolated and characterized an AMT gene, BcAMT1;4, in flowering Chinese cabbage. BcAMT1;4 was localized to the plasma membrane and complemented  $\text{NH}_4^+$  transport in  $\text{NH}_4^+$  uptake-deficient yeast. The highest expression levels of BcAMT1;4 were detected in the flowers and leaves of flowering Chinese cabbage. The expression of BcAMT1;4 was induced by nitrogen deficiency and significantly inhibited by the reapplication of  $\text{NH}_4^+$  ( $\text{NH}_4\text{Cl}$  or  $\text{NH}_4\text{NO}_3$ ). In contrast, when plants pre-cultured in nitrate were transferred to an  $\text{NH}_4^+$  nutrient solution, BcAMT1;4 expression was significantly enhanced. BcAMT1;4 exhibited a diurnal expression pattern, with higher expression levels during the light period than during the dark period, and a peak expression at the later stage of the light period. Knowledge of AMT genes in flowering Chinese cabbage will lay a foundation for enhancing our understanding of the functional roles of different AMT members in the regulation of its growth by  $\text{NH}_4^+$ , as BcAMT1;4 seems to play an important role in leaf  $\text{NH}_4^+$  transport.

**来源:** Horticulture, Environment, and Biotechnology

**发布日期:** 2019-07-08

**全文链接:**

<http://agri.ckcest.cn/file1/M00/OE/CA/Csgk0F2QB4SAZJxABUKBMvpRCK950.pdf>

## **5. Abscisic acid and ethylene biosynthesis-related genes are associated with anthocyanin accumulation in purple ornamental cabbage (*Brassica oleracea* var. *acephala*) (脱落酸和乙烯生物合成相关基因与紫色观赏甘蓝 (*Brassica oleracea* var. *acephala*) 中的花青素积累有关)**

**简介:** Purple ornamental cabbage (*Brassica oleracea* var. *acephala*) is a popular decorative plant, cultivated for its colorful leaf rosettes that persist in cool weather. It is characterized by green outer leaves and purple inner leaves, whose purple pigmentation is due to the accumulation of anthocyanin pigments. Phytohormones play important roles in anthocyanin biosynthesis in other species. Here, we identified 14 and 19 candidate genes putatively involved in abscisic acid (ABA) and ethylene (ET) biosynthesis, respectively, in *B. oleracea*. We determined the expression patterns of these candidate genes by reverse-transcription quantitative PCR (RT-qPCR). Among candidate ABA biosynthesis-related genes, the expressions of BoNCED2.1, BoNCED2.2, BoNCED6, BoNCED9.1, and BoAAO3.2 were significantly higher in purple compared to green leaves. Likewise, most of the ET biosynthetic genes (BoACS6, BoACS9.1, BoACS11, BoACO1.1, BoACO1.2, BoACO3.1, BoACO4, and BoACO5) had significantly higher expression in purple compared to green

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leaves. Among these genes, BoNCED2.1, BoNCED2.2, BoACS11, and BoACO4 showed particularly strong associations with total anthocyanin content of the purple inner leaves. Our results suggest that ABA and ET might promote the intense purple pigmentation of the inner leaves of purple ornamental cabbage.

来源: Genome

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全文链接:

<http://agri.ckcest.cn/file1/M00/OE/CA/Csgk0F2QBiqAbDkZADbiPIqjH7k113.pdf>

## ➤ 专业会议

### 1. III Asian Horticultural Congress - AHC2020 (第三届亚洲园艺大会-AHC2020)

简介: On behalf of the Congress's Organizing Committee, it is a great pleasure and honor for me to invite you to the Third Asian Horticultural Congress 2020 (AHC 2020) which will be held at Bangkok International Trade and Exhibition Centre (BITEC), Bangkok, Thailand, during 7-9 May 2020 under the theme "Asian Horticulture for a Sustainable World". The Congress will be hosted by the Horticultural Science Society of Thailand, the International Society for Horticultural Science, the Department of Agriculture, Department of Agricultural Extension, the Ministry of Agriculture and Cooperatives, Kasetsart University and VNU Exhibitions Asia Pacific Co., Ltd. with the support from National Research Council of Thailand, Thailand Research Fund, Agricultural Research Development Agency (Public Organization) and Thailand Convention and Exhibition Bureau (TCEB).

来源: ISHS

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