



2019年第37期总204期

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中国农业科学院农业信息研究所

联系人: 王爱玲; 李凌云; 顾亮亮

联系电话: 010-51503648

邮箱: [agri@ckcest.cn](mailto:agri@ckcest.cn)

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## ▶ 前沿资讯

### 1. Plant gene discovery could help reduce fertilizer pollution in waterways (植物基因的发现有助于减少肥料污染)

**简介:** 农田过度施肥是一个巨大的环境问题。农田中过量施用的磷经常进入附近的河流和湖泊。由此导致的水生植物生长的繁荣会引起水中的氧气含量骤降,进而导致鱼类死亡和其他有害影响。

来自Boyce Thompson Institute的研究人员发现了一对植物基因的功能,这些基因可以帮助农民提高磷的捕获能力,潜在地减少与施肥相关的环境损害。这项研究于9月2日发表在《Nature Plants》期刊上。

这一发现源于Maria Harrison对植物与丛枝菌根真菌共生关系的关注。AM真菌在植物根部定居,形成一个界面,使植物用脂肪酸交换磷酸盐和氮。这种真菌还可以帮助植物从逆境中恢复,如抵抗干旱。但是用脂肪酸喂养AM真菌是昂贵的,所以植物不会让这种定殖不受控制。

为了发现植物是如何控制真菌定殖量的,文章作者Harrison和她的实验室的博士后Müller研究了植物中编码短蛋白的基因,这些短蛋白被称为短肽(CLE peptides)。

CLE肽参与细胞发育和对胁迫的反应,并且它们存在于从绿藻到开花植物的整个植物王国中。研究人员发现其中两个CLE基因是AM真菌共生的关键调控因子。一种叫做CLE53的基因,一旦根被定殖,就会降低定殖率。另一基因CLE33在植物有足够的磷酸盐时,会降低定殖率。

研究者表示,能够控制真菌在植物根部的定殖水平,即使在较高的磷酸盐条件下也能维持共生关系,这可能对农民有用。例如,你可能想要AM真菌的其他有益效果,如氮吸收和从干旱中恢复,以及磷的进一步吸收等等,可以通过改变植物中这些CLE肽的水平来实现这些效果。

Müller发现CLE肽通过一种叫做SUNN的受体蛋白起作用。他与阿姆斯特丹大学合作,发现这两种CLE肽调节植物合成一种叫做Strigolactone的化合物。植物根向土壤中分泌麦角内酯,该化合物刺激AM真菌生长并定殖于根系。一旦根被定殖或存在大量的磷酸盐,CLE基因就会抑制Strigolactone的合成,从而减少真菌的进一步定殖。

研究人员的下一步将包括找出在定殖和高磷酸盐水平下启动CLE基因的分子。CLE肽非常相似,但它们具有完全不同的功能,Müller还计划将来自本研究的两种CLE肽与具有不同功能的另外的CLE肽进行比较。

**来源:** ScienceDaily

**发布日期:** 2019-09-02

**全文链接:**

<http://agri.ckcest.cn/file1/M00/00/01/Csgk0V14jFmAEVNzAA06iTDfpbw623.pdf>

## ▶ 学术文献

### 1. Transcriptomic response in symptomless roots of clubroot infected kohlrabi (*Brassica oleracea* var. *gongylodes*) mirrors resistant plants (感染根肿病的球茎甘蓝无症状根的转录反应与抗病和易感植

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## 株相似)

**简介:** Background Clubroot disease caused by *Plasmodiophora brassicae* (Phytomyxea, Rhizaria) is one of the economically most important diseases of Brassica crops. The formation of hypertrophied roots accompanied by altered metabolism and hormone homeostasis is typical for infected plants. Not all roots of infected plants show the same phenotypic changes. While some roots remain uninfected, others develop galls of diverse size. The aim of this study was to analyse and compare the intra-plant heterogeneity of *P. brassicae* root galls and symptomless roots of the same host plants (*Brassica oleracea* var. *gongylodes*) collected from a commercial field in Austria using transcriptome analyses.

**Results** Transcriptomes were markedly different between symptomless roots and gall tissue. Symptomless roots showed transcriptomic traits previously described for resistant plants. Genes involved in host cell wall synthesis and reinforcement were up-regulated in symptomless roots indicating elevated tolerance against *P. brassicae*. By contrast, genes involved in cell wall degradation and modification processes like expansion were up-regulated in root galls. Hormone metabolism differed between symptomless roots and galls. Brassinosteroid-synthesis was down-regulated in root galls, whereas jasmonic acid synthesis was down-regulated in symptomless roots. Cytokinin metabolism and signalling were up-regulated in symptomless roots with the exception of one CKX6 homolog, which was strongly down-regulated. Salicylic acid (SA) mediated defence response was up-regulated in symptomless roots, compared with root gall tissue. This is probably caused by a secreted benzoic acid/salicylic acid methyl transferase from the pathogen (PbBSMT), which was one of the highest expressed pathogen genes in gall tissue. The PbBSMT derived Methyl-SA potentially leads to increased pathogen tolerance in uninfected roots.

**Conclusions** Infected and uninfected roots of clubroot infected plants showed transcriptomic differences similar to those previously described between clubroot resistant and susceptible hosts. The here described intra-plant heterogeneity suggests, that for a better understanding of clubroot disease targeted, spatial analyses of clubroot infected plants will be vital in understanding this economically important disease.

**来源:** BMC Plant Biology

**发布日期:**2019-07-01

**全文链接:**

<http://agri.ckcest.cn/file1/M00/0E/C8/Csgk0F14i2SAKIKgACEvy6DKyRs679.pdf>

## 2. Draft genome sequence of cauliflower (*Brassica oleracea* L. var. *botrytis*) provides new insights into the C genome in Brassica species (花椰菜(*Brassica oleracea* L. var. *botrytis*)基因组序列草图为芸苔属植物C基因组的研究提供了新的视角)

**简介:** Cauliflower is an important variety of *Brassica oleracea* and is planted worldwide. Here, the high-quality genome sequence of cauliflower was reported. The assembled cauliflower genome was 584.60 Mb in size, with a contig N50 of 2.11 Mb, and contained 47,772 genes; 56.65% of the genome was composed of repetitive sequences. Among these sequences, long terminal repeats (LTRs) were the most abundant (32.71% of the genome),

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followed by transposable elements (TEs) (12.62%). Comparative genomic analysis confirmed that after an ancient paleohexaploidy ( $\gamma$ ) event, cauliflower underwent two whole-genome duplication (WGD) events shared with Arabidopsis and an additional whole-genome triplication (WGT) event shared with other Brassica species. The present cultivated cauliflower diverged from the ancestral *B. oleracea* species  $\sim$ 3.0 million years ago (Mya). The speciation of cauliflower ( $\sim$ 2.0 Mya) was later than that of *B. oleracea* L. var. capitata (approximately 2.6 Mya) and other Brassica species (over 2.0 Mya). Chromosome no. 03 of cauliflower shared the most syntenic blocks with the A, B, and C genomes of Brassica species and its eight other chromosomes, implying that chromosome no. 03 might be the most ancient one in the cauliflower genome, which was consistent with the chromosome being inherited from the common ancestor of Brassica species. In addition, 2,718 specific genes, 228 expanded genes, 2 contracted genes, and 1,065 positively selected genes in cauliflower were identified and functionally annotated. These findings provide new insights into the genomic diversity of Brassica species and serve as a valuable reference for molecular breeding of cauliflower.

来源: Horticulture Research

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全文链接:

<http://agri.ckcest.cn/file1/M00/OE/C8/Csgk0F14mQWAbDBByAB3YCF7x8kk342.pdf>

### **3. Genome-wide identification of stress-associated proteins (SAP) with A20/AN1 zinc finger domains associated with abiotic stresses responses in Brassica napus (甘蓝型油菜非生物胁迫反应相关的A20/AN1锌指域的应激相关蛋白 (SAP) 的全基因组鉴定)**

简介: Stress-associated proteins (SAP) that contain the A20/AN1 zinc-finger domain play important roles in plants abiotic stress responses. However, little is known about the SAP gene family in *Brassica napus* (genome AnAnCnCn), was formed by recent allopolyploidy between ancestors of *Brassica rapa* (genome ArAr) and *Brassica oleracea* (genome CoCo). To explore the distribution and expression patterns of these genes, a genome-wide identification and a systematic analysis of genes in the SAP family in *B. napus* were performed. A total of 57 genes encoding SAP were identified, and subsequently classified into 5 groups. In contrast to results seen in other plant species, further analyses of gene structures and conserved protein motifs revealed that a large percentage of the BnaSAP (16/57) genes were A20-type or AN1-type SAP genes, most of which were not found to have homologous genes in *B. rapa* or *B. oleracea*. The cis-elements of the BnaSAP promoters, and BnaSAP gene expression levels in different tissues, and under different stress treatments, were also investigated based on RNA-seq data. All the typical A20-AN1-type and AN1-AN1(-C2H2)-type BnaSAP genes were constitutively expressed among all tissues, except 4 members in Group II. In contrast, almost all A20 type and AN1 type members showed very low detection levels in all the tested rapeseed tissues from which the transcriptome data was derived. Additionally, most of the typical A20-AN1-type and AN1-AN1-type BnaSAP genes were found to be induced by multiple stresses and

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phytohormones. Among the identified BnaSAP genes, four members of Group III (BnaA07g15770D, BnaC06g14100D, BnaC04g27800D, and BnaC08g24010D) were induced following various low-temperature stresses in leaves, and were induced by NaCl and PEG stress in roots. BnaA06g02460D and BnaC06g04440D from Group IV were induced by heat stress, while BnaA06g31640D and BnaC07g25010D from Group V were induced by heat stress and salicylic acid (SA) treatment. This study provides a comprehensive analysis of SAP genes in rapeseed, and may aid in future efforts to identify the functions of A20/AN1-type proteins and the responses of rapeseed under a variety of abiotic stresses.

来源: Environmental and Experimental Botany

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<http://agri.ckcest.cn/file1/M00/OE/C7/Csgk0F14Zg2AIK6CALMxhJHLRIA531.pdf>

#### **4. Mutation in EMB1923 gene promoter is associated with chlorophyll deficiency in Chinese cabbage (*Brassica campestris* ssp. *pekinensis*) (大白菜(*Brassica campestris* ssp. *pekinensis*) EMB1923基因启动子突变与叶绿素缺乏相关)**

简介: Leaf color mutants are widespread in higher plants and can be used as markers in crop breeding or as important material in understanding the regulatory mechanisms of chlorophyll biosynthesis and chloroplast development. A stably inherited plant etiolated mutation (pem) was obtained from its wild-type 'FT' (a doubled haploid line of the Chinese cabbage variety 'Fukuda 50') by combining 60Co- $\gamma$  radiation and isolated microspore culture in Chinese cabbage. Compared to the wild-type 'FT', the chlorophyll content in the pem mutant was decreased, the photosynthetic capacity was reduced and the chloroplast development was retarded. These physiological changes may lead to a reduction in growth and yield in the pem mutant line. Genetic analysis showed that the mutant phenotype was controlled by the single recessive nuclear pem gene. The pem gene was mapped to a 25.88 kb region on the A03 chromosome. Cloning and sequencing results showed that there was only one DNA sequence variation in this region, which was a 30 bp deletion on the promoter of Bra024218. Its homologous gene encodes EMBRYO DEFECTIVE 1923 (EMB1923) in *Arabidopsis thaliana*. We therefore predicted that Bra024218 was the mutated gene associated with etiolated leaves in Chinese cabbage. The pem mutant is a useful line for researching chloroplast development and the mechanism of leaf color mutation in Chinese cabbage.

来源: Physiologia Plantarum

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[http://agri.ckcest.cn/file1/M00/OE/C7/Csgk0F14Z2aAKadYA0y\\_3WrMjWM151.pdf](http://agri.ckcest.cn/file1/M00/OE/C7/Csgk0F14Z2aAKadYA0y_3WrMjWM151.pdf)

#### **5. BjuWRR1, a CC-NB-LRR gene identified in *Brassica juncea*, confers resistance to white rust caused by *Albugo candida* (芥菜中发现的CC-NB-LRR基因BjuWRR1对白念珠菌引起的白锈病具有抗性)**

简介: **Key message** BjuWRR1, a CNL-type R gene, was identified from an east European

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gene pool line of *Brassica juncea* and validated for conferring resistance to white rust by genetic transformation.

**Abstract** White rust caused by the oomycete pathogen *Albugo candida* is a significant disease of crucifer crops including *Brassica juncea* (mustard), a major oilseed crop of the Indian subcontinent. Earlier, a resistance-conferring locus named AcB1-A5.1 was mapped in an east European gene pool line of *B. juncea*—Donskaja-IV. This line was tested along with some other lines of *B. juncea* (AABB), *B. rapa* (AA) and *B. nigra* (BB) for resistance to six isolates of *A. candida* collected from different mustard growing regions of India. Donskaja-IV was found to be completely resistant to all the tested isolates. Sequencing of a BAC spanning the locus AcB1-A5.1 showed the presence of a single CC-NB-LRR protein encoding R gene. The genomic sequence of the putative R gene with its native promoter and terminator was used for the genetic transformation of a susceptible Indian gene pool line Varuna and was found to confer complete resistance to all the isolates. This is the first white rust resistance-conferring gene described from *Brassica* species and has been named BjuWRR1. Allelic variants of the gene in *B. juncea* germplasm and orthologues in the Brassicaceae genomes were studied to understand the evolutionary dynamics of the BjuWRR1 gene.

来源: Theoretical and Applied Genetics

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<http://agri.ckcest.cn/file1/M00/0E/C7/Csgk0F14iAqAdwAoADBga94JCGo579.pdf>