



2019年第1期总168期

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1. 1996-2016年转基因作物的环境影响：对农药使用和碳排放的影响

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## ▶ 前沿资讯

### 1. Plants don't like touch: Green thumb myth dispelled (频繁触碰植物会致其生长变慢)

**简介:** 澳大利亚一项新研究发现,植物对触碰极其敏感,频繁碰触会使植物的生长速度显著变慢。这一发现有助于开发优化作物生长及增收的新方法。相关论文发表在《植物杂志》上。

研究发现,即便是对植物的轻微触碰也会触发“基因防御反应”,这种机制反复发生就会导致植物生长变慢。来自人类、动物、昆虫的轻微触碰或者是刮风导致植物之间的互相触碰,都会诱发植物的“基因防御反应”。

实验显示,植物被持续触摸后,“基因防御反应”使其基因组中一定比例的基因发生某种改变,这一过程消耗大量能量,导致植物生长减缓。

研究人员表示,尚不清楚植物为何对触碰反应如此强烈,但这项发现有助于深入理解“基因防御反应”机制,可以寻找新方法降低作物对触碰敏感性以提高产量。下一步的研究,还要弄清降低植物敏感性是否会带来负面后果,比如使植物对某些疾病更易感等。

**来源:** ScienceDaily

**发布日期:** 2018-12-17

**全文链接:**

<http://agri.ckcest.cn/file1/M00/06/5A/Csgk0FwliHGAR9TjAANRjW7159Q718.pdf>

## ▶ 学术文献

### 1. Comparative analysis of cytokinin response factors in Brassica diploids and amphidiploids and insights into the evolution of Brassica species (芸薹属二倍体和双二倍体细胞分裂素反应因子的比较分析及其品种演化的见解)

**简介: Background:** Cytokinin is a classical phytohormone that plays important roles in numerous plant growth and development processes. In plants, cytokinin signals are transduced by a two-component system, which involves many genes, including cytokinin response factors (CRFs). Although CRFs take vital part in the growth of Arabidopsis thaliana and Solanum lycopersicum, little information of the CRFs in the Brassica U-triangle species has been known yet.

**Results:** We identified and compared 141 CRFs in the diploids and amphidiploids of Brassica species, including *B. rapa*, *B. oleracea*, *B. nigra*, *B. napus*, and *B. juncea*. For all the 141 CRFs, the sequence and structure analysis, physiological and biochemical characteristics analysis were performed. Meanwhile, the  $K_a/K_s$  ratios of orthologous and paralogous gene pairs were calculated, which indicated the natural selective pressure upon the overall length or a certain part of the CRFs. The expression profiles of CRFs in different tissues and under various stresses were analyzed in *B. oleracea*, *B. nigra*, and *B. napus*. The similarities and differences in gene sequences and expression profiles among the homologous genes of these

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species were discussed. In addition, AtCRF11 and its ortholog BrCRF11a were identified to be related to primary root growth in Arabidopsis.

**Conclusion:** This study performed a genome-wide comparative analysis of the CRFs in the diploids and amphidiploids of the Brassica U-triangle species. Many similarities and differences in gene sequences and expression profiles existed among the CRF homologous genes of these species. In the bioinformatics analysis, we found the close relativity of the CRF homologous genes in the Brassica A and C genomes and the distinctiveness of those in the B genome, and the CRF homologous genes in B subgenome were considerably influenced by the A subgenome of *B. juncea*. In addition, we identified a new function of the Clade V CRFs related to root growth, which also clarified the functional conservation between Arabidopsis and *B. rapa*. These results not only offer useful information on the functional analysis of CRFs but also provide new insights into the evolution of Brassica species.

来源: BMC Genomics

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全文链接:

[http://agri.ckcest.cn/file1/M00/06/5A/Csgk0Fwlg\\_uAPxJHAEKeLW8SmUM589.pdf](http://agri.ckcest.cn/file1/M00/06/5A/Csgk0Fwlg_uAPxJHAEKeLW8SmUM589.pdf)

## **2. Changes in mineral nutrient concentrations and C - N metabolism in cabbage shoots and roots following macronutrient deficiency (常量营养素亏缺对甘蓝地上部和根部矿质养分含量及C—N代谢的影响)**

**简介:** The responses of metabolic networks to mineral deficiency are poorly understood. Here, we conducted a detailed, broad-scale analysis of macronutrient concentrations and metabolic changes in the shoots and roots of cabbage (*Brassica rapa* L. ssp. *pekinensis*) plants in response to N, P, K, Ca, and Mg deficiency in nutrient solution. To standardize individual macronutrient-deficient treatments, the concentrations of the other nutrients were maintained via substitution with other ions. Individual nutrient deficiencies had various effects on the uptake and accumulation of other mineral nutrients. Phosphorus deficiency had relatively little effect on other mineral nutrient levels compared to the other treatments. Cation deficiency had little effect on N and P concentrations but had a somewhat negative effect on the uptake or concentrations of the other nutrients. Primary metabolic pathways, such as energy production and amino acid metabolism, were greatly affected by mineral nutrient deficiency. Compared to the control treatment, soluble sugar levels increased under N conditions and decreased under Ca and Mg conditions. The levels of several organic acids involved in glycolysis and the TCA cycle decreased in response to N, P, or K treatment. The levels of most amino acids decreased under - N treatment but increased under P, K, Ca, or Mg treatment. Mineral depletion also led to the activation of alternative biochemical pathways resulting in the production of secondary metabolites such as quinate. Notable changes in metabolic pathways under macronutrient deficiency included (1) a quantitative increase in amino acid levels in response to Mg deficiency, likely because the restriction of various pathways led to an increase in protein production and (2) a marked increase in the levels of quinate, a precursor of the shikimate pathway, following cation (K, Ca, and Mg)

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deficiency. These findings provide new insights into metabolic changes in cabbage in response to mineral deficiency and pave the way for studying the effects of the simultaneous deficiency of more than one macronutrient on this crop.

来源: JOURNAL OF PLANT NUTRITION AND SOIL SCIENCE

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<http://agri.ckcest.cn/file1/M00/06/5A/Csgk0FwIheOAA2MAACzXg007Hb0781.pdf>

### **3. Tissue culture and genetic transformation of cabbage (*Brassica oleracea* var. *capitata*): an overview (甘蓝组织培养及遗传转化研究进展)**

简介: *Main conclusion* The main goal of this publication is an overview of the biotechnological achievements concerning in vitro cultures and transformation of *Brassica oleracea* var. *capitata*.

Faced with the requirements of the global food market, intensified work on the genetic transformation of economically important plants is carried out in laboratories around the world. The development of efficient procedures for their regeneration and transformation could be a good solution for obtaining, in a shorter time than by traditional methods, plants with desirable traits. Furthermore, conventional breeding methods are insufficient for crop genetic improvement not only because of being time-consuming but also because they are severely limited by sexual incompatibility barriers. This problem has been overcome by genetic engineering, which seems to be a very good technique for cabbage improvement. Despite the huge progress that has been made in the field of plant regeneration and transformation methods, up to now, no routine transformation procedure has been developed in the case of cabbage. This problem stems from the fact that the efficiency of cabbage transformation is closely related to the genotype and some varieties are recalcitrant to transformation. It is obvious that it is not possible to establish one universal regeneration and transformation protocol for all varieties of cabbage. Therefore, it seems fully justified to develop the above-mentioned procedures for individual economically important cultivars. Despite the obstacles of cabbage transformation in laboratories of many countries, especially those where this vegetable is extremely popular (e.g., China, India, Korea, Malaysia, Pakistan), such attempts are made. This article reviews the achievements in the field of tissue culture and cabbage transformation from the last two decades.

来源: Planta

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全文链接:

[http://agri.ckcest.cn/file1/M00/06/5A/Csgk0FwIgcGAbd-0ABPr\\_Z7Cn6I129.pdf](http://agri.ckcest.cn/file1/M00/06/5A/Csgk0FwIgcGAbd-0ABPr_Z7Cn6I129.pdf)

### **4. Effect of ambient temperature fluctuation on the timing of the transition to the generative stage in cauliflower (环境温度变化对花椰菜生育期转换时间的影响)**

简介: Cauliflower (*Brassica oleracea* ssp. *botrytis*) is an important vegetable that is grown

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worldwide from the tropics to temperate zones. The harvested product is the curd, which consists of arrested inflorescence meristems. The switch from vegetative development to curd formation in cauliflower, referred to as the generative switch, is strongly temperature responsive in the majority of varieties. We aimed at measuring the delay in timing of the generative switch by high ambient temperature, and how temperature affects the expression of genes with a potential role in timing of this switch. A seven day increase of six degrees in day and night temperature during vegetative development, results in a substantial delay of the generative switch and increased variation in timing of this switch in sensitive cultivars only. The expression level of the Cauliflower FRUITFULL-like gene BoFULc increased significantly at the generative switch and therefore can be used as marker for this developmental phase change. The expression profiles of the majority of the other investigated cauliflower flowering time genes resembled the expression behaviour of their homologous genes in the model plant Arabidopsis thaliana during the vegetative stage and flowering induction. An exception was the expression of two FLC paralogues BoFLC-1 and BoFLC-3, which showed opposite expression profiles of which the pattern of BoFLC-1 resembles the pattern expected based on Arabidopsis FLC. This interesting observation suggests different roles for these two FLC paralogs in regulation of the timing of the generative switch in cauliflower. Unexpectedly, high temperatures did not delay timing of expression of the majority of investigated genes in meristems and leaves of sensitive cultivars that were delayed in the switch to the generative stage. However, expression of a few potential flowering-time genes was affected by the high temperature treatment in a sensitive cultivar, making them potential candidates to be causal for the observed delay in generative switch.

来源: Environmental and Experimental Botany

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<http://agri.ckcest.cn/file1/M00/06/5A/Csgk0FwlgxCAMwt2ABe63IaYDvc679.pdf>

## ➤ 科技报告

### **1. Environmental impacts of genetically modified (GM) crop use 1996-2016: Impacts on pesticide use and carbon emissions (1996-2016年转基因作物的环境影响: 对农药使用和碳排放的影响)**

简介: This paper updates previous assessments of the environmental impacts associated with using crop biotechnology in global agriculture. It focuses on the environmental impacts associated with changes in pesticide use and greenhouse gas emissions arising from the use of GM crops since their first widespread commercial use over 20 years ago. The adoption of GM insect resistant and herbicide tolerant technology has reduced pesticide spraying by 671.4 million kg (8.2%) and, as a result, decreased the environmental impact associated with herbicide and insecticide use on these crops (as measured by the indicator, the Environmental Impact Quotient (EIQ)) by 18.4%. The technology has also facilitated important cuts in fuel use and tillage changes, resulting in a significant reduction in the release of greenhouse gas emissions from the GM cropping area. In 2016, this was equivalent to removing 16.7 million

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cars from the roads.

来源: GM Crops & Food-Biotechnology in Agriculture and the Food Chain

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<http://agri.ckcest.cn/file1/M00/06/5A/Csgk0FwliAGAVRICAAsjFTxj0SaI124.pdf>