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中国农业科学院农业信息研究所

联系人：张晓静；祁冉；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. *New Phytologist* | 中国农业大学郭仰东团队揭示番茄抗铝胁迫新机制

**简介:** 近日, *New Phytologist*在线发表了中国农业大学园艺学院郭仰东教授课题组题为“A zinc finger protein S1SZP1 protects S1STOP1 from S1RAE1-mediated degradation to modulate aluminum resistance”的研究论文。该研究发现锌指蛋白S1SZP1通过与抗铝核心转录因子S1STOP1互作参与番茄抗铝胁迫调控。

该研究发现番茄S1SZP1是S1STOP1的互作蛋白。S1SZP1的表达受铝胁迫强烈且快速的诱导。s1szp1、s1stop1单突及s1szp1/s1stop1双突表现为相似的铝不耐受表型,且铝胁迫条件下突变体中S1STOP1下游基因(S1RAE1和S1ASR2)的表达均相较野生型番茄显著下调,暗示着S1SZP1和S1STOP1位于同一条信号通路上。在s1szp1突变体中,S1STOP1蛋白不受铝诱导积累;在S1SZP1-OE株系中,S1STOP1蛋白在正常条件下即可大量积累,表明S1SZP1是影响S1STOP1积累的重要因子。进一步研究发现,E3泛素连接酶S1RAE1能降解S1SZP1或S1STOP1,S1SZP1和S1STOP1互作形成的复合体能够避免二者被S1RAE1降解,使得S1STOP1在铝胁迫条件下得以积累,从而激活其下游抗铝基因的表达,实现番茄抗铝响应。

该研究揭示了S1SZP1在番茄抗铝响应中的角色和功能,构建了S1SZP1-S1STOP1-S1RAE1协同响应铝胁迫的调控模块。通过该模块实现铝胁迫信号的响应和S1STOP1介导的抗铝胁迫调控途径的激活。该研究结果将拓展研究者对STOP1介导的抗铝分子机制的理解。

**来源:** 植物生物技术Pbj

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<http://agri.ckcest.cn/file1/M00/10/08/Csgk0GK9CFqAN741ABLRVhTZ-NM742.pdf>

## ▶ 学术文献

### 1. Genetic variation and QTL analysis of saturated fatty acids in two doubled haploid populations of oilseed rape (*Brassica napus* L.) (甘蓝型油菜两个双单倍体群体饱和脂肪酸的遗传变异及QTL分析)

**简介:** Consumption of foodstuff with low contents of saturated fatty acids is considered beneficial for human health. Reducing saturated fatty acid content in oilseed rape (canola) and other oil and protein crops is a relevant breeding aim. The objective of this work was to study the genetic variation and inheritance of saturated fatty acids in two DH populations of oilseed rape, to map QTL and to identify candidate genes. In addition, the correlation to other seed quality traits was studied. To this end, two half-sib DH populations were tested in up to five field environments in north-western Europe and seeds harvested from open-pollinated seeds were analyzed. Genotyping was performed using Illumina Brassica 15 K SNP chip. In both populations, significant effects for the genotypes and for the environments were detected, and heritability ranged from 68 to 89% for the predominant palmitic acid and stearic acid content. Up to 48 QTL for different fatty acids, oil and acid detergent lignin (ADL) content were mapped in the two populations. Co-locating QTL for palmitic acid, stearic acid, the

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C16/18 fatty acid ratio, the FATB/A ratio, oil and ADL content were identified on different chromosomes. A large number of candidate genes were identified within the vicinity of QTL flanking markers. Identification of several co-locating QTL positions, of associated candidate genes and SNP markers should facilitate oilseed rape breeding for low saturated fatty acid content.

来源: Euphytica

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<http://agri.ckcest.cn/file1/M00/03/36/Csgk0YcTte0AQ1L0AA0EB2IBiBA257.pdf>

## **2. Fine Mapping and Functional Analysis of Major QTL, CRq for Clubroot Resistance in Chinese Cabbage (*Brassica rapa* ssp. *pekinensis*) (大白菜抗根肿病主效QTL CRq的精细定位与功能分析)**

简介: Clubroot disease caused by *Plasmodiophora brassicae* is one of the major threats to Brassica crops. New clubroot resistant varieties of Chinese cabbage (*B. rapa* ssp. *pekinensis*) have been developed through breeding, but the underlying genetic mechanism of clubroot resistance is still unclear. In this study, two Chinese cabbage DH lines, clubroot-resistant Y635-10 and susceptible Y177-47 were crossed to develop F<sub>2</sub> population for fine mapping and cloning resistance gene CRq. After sequence analysis, the expression vector was constructed by gateway technology and transferred into *Arabidopsis thaliana* for functional characterization. Bulk segregant analysis sequencing (BSA-seq) confirmed that CRq is located in the 80 kb genomic region on chromosome A03 between markers GC30-FW/RV and BGA. In silico tools confirmed that the gene length was 3959 bp with 3675 bp coding sequences (CDs), and it has three exons and two introns. In addition, we found 72bp insertion in the third exon of CRq in the susceptible line. We developed and verified functional marker Br-insert1, by which genotyping results showed that 72bp insertion might lead to the destruction of the LRR region of Y177-47, resulting in a loss of resistance relative to clubroot. The results of genetic transformation showed that the roots for wild-type *Arabidopsis thaliana* were significantly enlarged compared with T<sub>2</sub> generation transgenic *Arabidopsis* after treatment by *P. brassicae* spores, and transgenic *Arabidopsis* had certain resistance. Therefore, CRq is a candidate gene of clubroot disease resistance in Chinese cabbage, which could be used as a reference for elucidating disease resistance mechanisms and the marker-assisted breeding of clubroot resistant varieties.

来源: Agronomy

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<http://agri.ckcest.cn/file1/M00/03/36/Csgk0YcTssuAKV-gAB9ngGyNjKM438.pdf>

## **3. Local and systemic responses conferring acclimation of *Brassica napus* roots to low phosphorus conditions (甘蓝型油菜根系适应低磷条件的局部和系统反应)**

简介: Due to the non-uniform distribution of inorganic phosphate (Pi) in the soil, plants

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modify their root architecture to improve acquisition of this nutrient. In this study, a split-root system was employed to assess the nature of local and systemic signals that modulate root architecture of *Brassica napus* grown with non-uniform Pi availability. Lateral root (LR) growth was regulated systemically by non-uniform Pi distribution, by increasing the second-order LR (2<sup>o</sup>LR) density in compartments with high Pi supply but decreasing it in compartments with low Pi availability. Transcriptomic profiling identified groups of genes regulated, both locally and systemically, by Pi starvation. The number of systemically induced genes was greater than the number of genes locally induced, and included genes related to abscisic acid (ABA) and jasmonic acid (JA) signalling pathways, reactive oxygen species (ROS) metabolism, sucrose, and starch metabolism. Physiological studies confirmed the involvement of ABA, JA, sugars, and ROS in the systemic Pi starvation response. Our results reveal the mechanistic basis of local and systemic responses of *B. napus* to Pi starvation and provide new insights into the molecular and physiological basis of root plasticity.

来源: Journal of Experimental Botany

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全文链接:

<http://agri.ckcest.cn/file1/M00/03/36/Csgk0YcTuHuACf91AGt0ym8iKpA891.pdf>

#### **4. Molecular Effects of Biogenic Zinc Nanoparticles on the Growth and Development of *Brassica napus* L. Revealed by Proteomics and Transcriptomics (基于蛋白质组学和转录组学的生物合成纳米锌对甘蓝型油菜生长发育的分子影响)**

简介: Plants are indispensable on earth and their improvement in terms of food security is a need of time. The current study has been designed to investigate how biogenic zinc nanoparticles (Zn NPs) can improve the growth and development of *Brassica napus* L. In this study, Zn NPs were synthesized utilizing *Mentha arvensis* aqueous extracts, and their morphological and optical properties were assessed using UV-Visible spectrophotometry, scanning electron microscopy (SEM), transmission electron microscopy (TEM), and X-ray diffraction (XRD). The synthesized Zn NPs were irregular in shape, indicating aggregation in pattern, with an average particle size of 30 nm, while XRD analysis revealed the crystalline structure of nanoparticles. The growth and development of *B. napus* varieties (Faisal canola and Shiralee) were assessed after foliar treatments with different concentrations of biogenic Zn NPs. In *B. napus* varieties, exposure to 15 mg/L Zn NPs dramatically increased chlorophyll, carotenoid content, and biomass accumulation. Similarly, proteomic analyses, on the other hand, revealed that proteins associated with photosynthesis, transport, glycolysis, and stress response in both *Brassica* varieties were substantially altered. Such exposure to Zn NPs, differential expression of genes associated with photosynthesis, ribosome structural constituents, and oxidative stress response were considerably upregulated in *B. napus* var. (Faisal and Shiralee canola). The results of this study revealed that foliar applications of biogenic Zn NPs influence the transcriptome and protein profiling positively, therefore stimulating plant growth and development.

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