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## 蔬菜育种专题

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## ➤ 前沿资讯

### 1. Quantitative and functional posttranslational modification proteomics reveals that TREPH1 plays a role in plant touch-delayed bolting (植物接触形态建成的分子调控机制)

**简介:** 诸如风、触碰等环境的机械外力会引起植物基因表达调控和发育的改变, 这叫做“接触形态建成”, 说明了植物能够感知外界刺激的能力。在拟南芥中, 接触形态建成最主要的响应就是延迟抽薹, 也就是花茎的形成被延迟。触碰响应下游在植物中的机械传导还有很多需要深入研究的地方。来自中国香港科技大学、南京农业大学和美国莱斯大学等机构的研究团队基于拟南芥稳定同位素标记的高通量磷酸化蛋白质组定量鉴定来绘制拟南芥中40秒的触碰处理所导致的蛋白磷酸化改变。在鉴定到的24个触碰响应磷酸化蛋白, 大部分来自于激酶、磷酸酶、细胞骨架蛋白、膜蛋白及离子转运蛋白。另外, 先前未被报道的触碰相关磷酸化蛋白TREPH1在受触碰刺激的植株中快速积累, 免疫印迹试验验证了这一点。TREPH1作为可溶性蛋白, 对于由触碰引起的抽薹延迟和基因表达改变是必须的。此外, 不能被磷酸化的TREPH1 S625A异构体不能拯救trep1-1突变体触碰诱导的开花延迟表型, 说明了S625对于TREPH1发挥功能是必要的, 同时也说明了受触碰调控的TREPH1磷酸化的功能相关性。总之, 该研究鉴定了一个调控拟南芥接触形态建成的磷酸化蛋白, 同时也表明了TREPH1及其触碰诱导的磷酸化在拟南芥接触形态建成的重要响应, 即延迟抽薹中发挥着非常重要的作用。

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<http://agri.ckcest.cn/ass/2290711e-75a4-4038-870b-2ff873570db9.pdf>

## ➤ 学术文献

### 1. An Integration of Genome-Wide Association Study and Gene Co-expression Network Analysis Identifies Candidate Genes of Stem Lodging-Related Traits in Brassica napus (结合全基因组关联研究和基因共表达网络分析识别甘蓝型油菜茎秆倒伏相关性状的候选基因)

**简介:** Lodging is a persistent problem which severely reduce yield and impair seed quality in rapeseed (*Brassica napus* L.). Enhancing stem strength (SS) has proven to be an effective approach to decrease lodging risk. In the present study, four interrelated stem lodging-related traits, including stem breaking resistance (SBR), stem diameter (SD), SS, and lodging coefficient (LC), were investigated among 472 rapeseed accessions. A genome-wide association study (GWAS) using Brassica 60K SNP array for stem lodging-related traits identified 67 significantly associated quantitative trait loci (QTLs) and 71 candidate genes. In parallel, a gene co-expression network based on transcriptome sequencing was constructed. The module associated with cellulose biosynthesis was highlighted. By integrating GWAS and gene co-expression network analysis, some promising candidate genes, such as

ESKIMO1 (ESK1, BnaC08g26920D), CELLULOSE SYNTHASE 6 (CESA6, BnaA09g06990D), and FRAGILE FIBER 8 (FRA8, BnaC04g39510D), were prioritized for further research. These findings revealed the genetic basis underlying stem lodging and provided worthwhile QTLs and genes information for genetic improvement of stem lodging resistance in *B. napus*.

来源: *Frontiers in Plant Science*

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<http://agri.ckcest.cn/ass/5ec6a4d4-clf1-4a34-94c0-c59e0c81db21.pdf>

## **2. Virulence and pathotype classification of *Plasmodiophora brassicae* populations collected from clubroot resistant canola (*Brassica napus*) in Canada (加拿大抗根瘤病油菜中芸苔属根瘤菌种群毒性及致病型分类)**

简介: Clubroot, caused by *Plasmodiophora brassicae* Wor., is an important soilborne disease of canola (*Brassica napus* L.) in Canada that is managed mainly by planting clubroot-resistant (CR) cultivars. Populations of *P. brassicae* representing 106 fields in Alberta were obtained from galled roots of CR canola plants collected in 2014-2016 and characterized for virulence on seven CR canola cultivars. Sixty-one of these populations could overcome resistance in at least one CR cultivar and were evaluated further by inoculation on 13 *Brassica* hosts termed the Canadian Clubroot Differential (CCD) Set. The CCD Set included the differentials of Williams (1966) and Som é et al. (1996), selected hosts of the European Clubroot Differential Set, and the *B. napus* cultivars 'Brutor', 'Mendel', 'Westar' and '45H29'. Each unique virulence pattern on the CCD Set represented a distinct pathotype and was identified with a letter. Five reference isolates, obtained prior to the introduction of CR canola, also were assessed. A total of 17 pathotypes were detected using the CCD Set, compared with five pathotypes using the system of Williams and two with the system of Som é et al., suggesting that the CCD Set has a greater differentiating capacity. Pathotype A, a variant of pathotype 3 (as per Williams) which is able to overcome the resistance in CR *B. napus*, was predominant. The original pathotype 3, which is avirulent on CR canola, was classified as CCD pathotype H. An integrated strategy, combining other tools in addition to resistance, will be needed for the sustainable management of clubroot.

来源: *Canadian Journal of Plant Pathology*

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## **3. Using antagonistic soil bacteria and their cell - free filtrates to control the black rot pathogen *Xanthomonas campestris* pv. *Campestris* (利用拮抗土壤细菌及其无细胞滤液控制黑腐病病原体)**

简介: *Xanthomonas campestris* pv. *campestris* (Xcc) is a phytopathogenic bacteria, and it is the causative agent of black rot in crucifers. Recent studies have shown that *Bacillus* species

have strong biological control on *Xanthomonas*. One of the mechanisms of this control is secondary metabolites production. A collection of 257 bacteria isolated from a suppressive soil was evaluated for in vitro antagonistic activity against *X. campestris*, and 92 isolates (44.6%) were able to inhibit its growth. Among the 92 isolates evaluated in the double-layer technique, 51 (55.43%) inhibited Xcc growth on the inhibition tests with cell-free filtrates (CFF) in liquid medium. Thirteen of these isolates presented 50% or more growth inhibition, and five isolates presented 100% growth inhibition of Xcc. The CFF of the isolate TCDT-08, which belongs to the *Paenibacillus* genus, was used for in vivo tests with kale crops. The artificial inoculation of kale with Xcc-629IBSBF pretreated with CFF from the isolate TCDT-08 demonstrated that the bacterium loses the ability of colonizing kale and of causing black rot. A *Paenibacillus* sp. isolate has strong inhibitory activity against *X. campestris* pv. *campestris*, and further studies can result in the use of this isolate to protect kale from Xcc infection.

来源: Journal of Phytopathology

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<http://agri.ckcest.cn/ass/5cc805de-baea-4788-9047-36823b4c6f60.pdf>

#### **4. Genome-Wide Association Study Reveals Both Overlapping and Independent Genetic Loci to Control Seed Weight and Silique Length in *Brassica napus* (全基因组关联研究揭示控制油菜粒重及角果长度的重叠和独立基因位点)**

简介: Seed weight (SW) is one of three determinants of seed yield, which positively correlates with silique length (SL) in *Brassica napus* (rapeseed). However, the genetic mechanism underlying the relationship between seed weight (SW) and silique length (SL) is largely unknown at present. A natural population comprising 157 inbred lines in rapeseed was genotyped by whole-genome re-sequencing and investigated for SW and SL over four years. The genome-wide association study identified 20 SNPs in significant association with SW on A01, A04, A09, C02, and C06 chromosomes and the phenotypic variation explained by a single locus ranged from 11.85% to 34.58% with an average of 25.43%. Meanwhile, 742 SNPs significantly associated with SL on A02, A03, A04, A07, A08, A09, C01, C03, C04, C06, C07, and C08 chromosomes were also detected and the phenotypic variation explained by a single locus ranged from 4.01 to 48.02% with an average of 33.33%, out of which, more than half of the loci had not been reported in the previous studies. There were 320 overlapping or linked SNPs for both SW and SL on A04, A09, and C06 chromosomes. It indicated that both overlapping and independent genetic loci controlled both SW and SL in *B. napus*. On the haplotype block on A09 chromosome, the allele variants of a known gene *BnaA.ARF18.a* controlling both SW and SL were identified in the natural population by developing derived cleaved amplified polymorphic sequence (dCAPS) markers. These findings are valuable for understanding the genetic mechanism of SW and SL and also for rapeseed molecular breeding programs.

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<http://agri.ckcest.cn/ass/641b79c8-12fe-439b-9a53-944c54ee7a0c.pdf>