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## 蔬菜育种专题

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## ▶ 前沿资讯

### 1. Every time the small cabbage white butterfly flaps its wings it has us to thank (利用基因组学和公众科学揭示农业害虫菜粉蝶的全球入侵史)

简介: Through close examination of genetic variation and similarities between existing populations, and comparisons of historical data regarding infestations of *Pieris rapae* in Brassicaceae crops, a consortium of researchers document how humans helped the small cabbage white butterfly spread from Europe across the world. Scientists from eight institutions partnered with more than 150 volunteer citizen scientists from 32 countries to detail the pest's range and current genetic diversity.

来源: ScienceDaily

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全文链接:

<http://agri.ckcest.cn/file1/M00/00/02/Csgk0V2B6b0AMoqFAAPCSunzLeM157.pdf>

### 2. Lack of reporting on phosphorus supply chain dangerous for global food security (磷供应链报告的缺失对全球粮食安全构成威胁)

简介: 全球粮食生产系统每年约使用5300万吨磷肥, 这些磷肥是由2.7亿吨磷矿石加工而成的。研究显示, 磷肥从矿厂到农田的损失高达90%。这些损失的很大一部分造成了水体的磷酸盐污染, 甚至产生了“死区”(即海洋中没有生命存在的区域)。2050年粮食需求将增加60%, 这意味着需要更多的磷肥。但这些磷肥来自何处并去往哪里, 目前却知之甚少。

斯德哥尔摩大学和冰岛大学开展的一项新研究表明, 虽然磷是全球粮食安全的关键因素, 但其供应链却是一个黑箱。这可能会导致社会、政治和环境问题, 从而导致磷供应危机。研究结果以“开放获取黑匣子: 报告全球磷供应链的必要性”为题发表在《Ambio》杂志上。

据联合国估计, 到2050年全球人口将增加到90亿, 粮食需求将增长60%。目前世界上有近10亿人营养不良, 但同时浪费的食物却差不多占到了生产量的一半, 这对全球食品供应链和生产系统构成了新的挑战。磷肥的供应是粮食生产的关键因素, 其中大部分来自磷矿石的开采和加工。在磷的整个供应链中, 由于各个阶段都存在损失, 从而使磷从有价值的资源变成了富营养化的主因之一。

研究人员认为, “磷供应链从头到尾的完整报告不仅可以揭示我们为超市货架上的食物所支付的社会、环境、伦理以及经济上的价格, 还可以帮助各国——尤其是大多数依赖进口磷酸盐的国家——制定更好的政策来降低农业部门的脆弱性。

该研究是一项名为“适应新的经济现实”的欧洲大型研究项目的一部分。该研究确定了磷肥供应面临的四个主要挑战。首先, 用于报告磷矿床的术语和方法不统一, 有时也不透明——这使得储量和资源量的估算不准确、不可靠。其次, 磷供应链损失高达90%, 却缺乏记录。损失发生在供应链的各个环节, 这些信息碎片使得很难准确报告损失的数量和位点, 而完善的报告则有助于设计减少损失和提高效率的方法。第三, 磷供应链中存在环境和社会效应。例如, 采矿和加工磷矿石会污染水体, 危害人体健康。此外, 从农用地和污水系统泄漏到水中的磷会导致富营养化和所谓的“死区”。同时磷也存在社

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会和伦理方面的问题。磷矿越来越多地在有争议的地区开采，例如在西撒哈拉地区的“非法开采”。第四，缺乏对磷供应链数据的开放获取。因其与粮食生产直接相关，所以公开磷及其供应链数据就显得十分必要。此外，关于磷的数据报告还将有助于更好地评估一些全球可持续指标的进展情况。

研究认为，可靠和定期的数据收集可以影响企业的社会责任和政治行动，这对解决供应链中发现的许多问题是十分必要的。而提高供应链的透明度则可以促进未来几十年磷及粮食的可持续供应。

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[http://agri.ckcest.cn/file1/M00/0E/C8/Csgk0F2B6LaAbVzNAAPLSRc\\_50k097.pdf](http://agri.ckcest.cn/file1/M00/0E/C8/Csgk0F2B6LaAbVzNAAPLSRc_50k097.pdf)

## 学术文献

### 1. 十字花科蔬菜硫代葡萄糖苷合成相关转录因子调控研究进展

简介: 硫代葡萄糖苷是十字花科植物中重要的次生代谢产物，其衍生产物和降解产物在植物防卫反应、特殊风味形成和人体防癌抗癌等方面具有特殊作用。硫苷的合成代谢，可以概括为：氨基酸侧链的延伸、核心结构的合成及R侧链的修饰，涉及BCATs、MAMs、CYP79s、CYP83s和AOPs等多个基因家族。综述了硫苷合成过程中几种重要的转录因子，其中MYB转录因子家族12亚族的MYB28、MYB29、MYB76、MYB34、MYB51和MYB122对十字花科植物硫苷合成起主要的调控作用，MYB28和MYB34分别为调控脂肪族硫苷和吲哚族硫苷的主效基因。bHLH类转录因子MYC2、MYC3和MYC4通过作用于MYB类转录因子对硫苷合成起调控作用，WRKY类转录因子WRKY18和WRKY40协同CYP81F2负调控吲哚族硫苷的合成。此外，还介绍了上述几种转录因子在外源生物或非生物刺激后的响应，及参与调控硫苷合成的作用机理。通过对调控硫苷合成的转录因子的研究，可进一步丰富硫苷合成的调控网路，为高硫苷含量的十字花科蔬菜作物的分子育种、优质栽培、病虫害生物防治提供新思路和新方法。

来源: 园艺学报

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<http://agri.ckcest.cn/file1/M00/00/02/Csgk0V2B5L2Aer0PAA16qG1uaLI477.pdf>

### 2. Analysing the genetic architecture of clubroot resistance variation in Brassica napus by associative transcriptomics (利用联合转录组学分析甘蓝型油菜根肿病抗性变异的遗传结构)

简介: Clubroot is a destructive soil-borne pathogen of Brassicaceae that causes significant recurrent reductions in yield of cruciferous crops. Although there is some resistance in oilseed rape (a crop type of the species Brassica napus), the genetic basis of that resistance is poorly understood. In this study, we used an associative transcriptomics approach to elucidate the genetic basis of resistance to clubroot pathotype ECD 17/31/31 across a genetic diversity panel of 245 accessions of B. napus. A single nucleotide polymorphism (SNP) association

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analysis was performed with 256,397 SNPs distributed across the genome of *B. napus* and combined with transcript abundance data of 53,889 coding DNA sequence (CDS) gene models. The SNP association analysis identified two major loci (on chromosomes A2 and A3) controlling resistance and seven minor loci. Within these were a total of 86 SNP markers. Altogether, 392 genes were found in these regions. Another 21 genes were implicated as potentially involved in resistance using gene expression marker (GEM) analysis. After GO enrichment analysis and InterPro functional analysis of the identified genes, 82 candidate genes were identified as having roles in clubroot resistance. These results provide useful information for marker-assisted breeding which could lead to acceleration of pyramiding of multiple clubroot resistance genes in new varieties.

来源: Molecular Breeding

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全文链接:

<http://agri.ckcest.cn/file1/M00/00/02/Csgk0V2B6AaARMCaACiSLNxSE0I839.pdf>

### **3. Comparative effect of elicitors on the physiology and secondary metabolites in broccoli plants (诱导子对西兰花植物生理和次生代谢产物的比较效应)**

简介: Elicitation is an economic and sustainable technique for increasing the content of secondary metabolites, mainly bioactive compounds, in plants grown for better human nutrition. The aim of this study was to compare the physiological responses (water relations and mineral nutrition) and the enrichment in glucosinolates (GLSs) and phenolic compounds of broccoli plants (*Brassica oleracea* L. var. *italica*) receiving different elicitation treatments. The treatments involved the priming of seeds with KCl and the exposure of plants to elicitors, including K<sub>2</sub>SO<sub>4</sub> and NaCl solutions and foliar sprays of methyl jasmonate (MeJA), salicylic acid (SA), and methionine (Met). The physiological response of the plants in terms of root hydraulic conductance was improved by priming with KCl and elicitation with MeJA or Met. Foliar application of Met significantly increased the plant biomass and enhanced mineral nutrition. In general, all treatments increased the accumulation of indole GLSs, but K<sub>2</sub>SO<sub>4</sub> and MeJA gave the best response and MeJA also favored the formation of a newly described compound, cinnamic-GLS, in the plants. Also, the use of Met and SA as elicitors and the supply of K<sub>2</sub>SO<sub>4</sub> increased the abundance of phenolic compounds; K<sub>2</sub>SO<sub>4</sub> also enhanced growth but did not alter the water relations or the accumulation of mineral nutrients. Therefore, although the response to elicitation was positive, with an increased content of bioactive compounds, regulation of the water relations and of the mineral status of the broccoli plants was critical to maintain the yield.

来源: Journal of Plant Physiology

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全文链接:

<http://agri.ckcest.cn/file1/M00/0E/C8/Csgk0F2B530Aboh1AAoHvVJa0F4857.pdf>

### **4. Allele specific DNA marker for fusarium resistance gene FocBo1**

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## in *Brassica oleracea* (甘蓝镰刀菌抗性基因FocBo1的等位基因特异性DNA标记)

简介: The fusarium yellows resistance (YR) gene FocBo1 was previously identified and the DNA markers were developed to assist the breeding of YR cultivars in *Brassica oleracea*. However, the further analysis revealed discrepancies between the phenotypes and the genotypes predicted by those DNA markers in cabbage commercial cultivars. Since this discrepancy seemed to be due to unknown susceptible alleles of focbo1, we sequenced the gene in 19 accessions to determine the sequence variations between alleles and found that there were two resistant FocBo1 alleles and six susceptible alleles in the investigated population. The newly designed PCR markers detected three mutations in the susceptible alleles that generate premature termination codons. These were shown to accurately distinguish resistant and susceptible alleles in more than 200 accessions of *B. oleracea* inbred lines and cultivars. The study revealed that the locus is represented by 37.2% resistant and 62.8% susceptible alleles within seventy-eight commercial cultivars. Structural analysis of the gene revealed that a part of the allelic variation comes from intragenic recombination between alleles. Our results enable a more precise prediction of the phenotype by marker assisted selection, promoting the production of YR cultivars in *B. oleracea*.

来源: Breeding Science

发布日期: 2019-05-08

全文链接:

<http://agri.ckcest.cn/file1/M00/00/02/Csgk0V2B5nWAb66rABAHLhEhjQ8301.pdf>

## 5. Development of *Plasmodiophora brassicae* in the root cortex of cabbage over time (甘蓝根皮层中芸薹根肿菌的发展)

简介: Pathogen development in the root cortex of three cabbage (*Brassica oleracea* var. capitata) cultivars that differed in clubroot reaction (susceptible 'Bronco', partially resistant 'B-2819', resistant 'Tekila') was assessed over time in plants inoculated with  $1 \times 10^6$ ,  $1 \times 10^7$  and  $2 \times 10^8$  spores  $\text{mL}^{-1}$  of *Plasmodiophora brassicae* in a controlled environment study. Cortical colonization and symptom development in 'Bronco' and 'B-2819' were affected by inoculum concentration. When inoculated at  $1 \times 10^6$  and  $1 \times 10^7$  spores  $\text{mL}^{-1}$ , clubroot levels were generally higher on 'Bronco' relative to 'B-2819'. However, there were no differences at  $2 \times 10^8$  spores because incidence and severity in both 'Bronco' and 'B-2819' were near the maximum. Similarly, the area colonized by *P. brassicae* (%) on root cross-sections was much higher in 'Bronco' than 'B-2819' at  $1 \times 10^6$  spores, but differences in cortical colonization, if any, were small at higher inoculum concentrations. The concentration of *P. brassicae* DNA in inoculated roots (assessed using qPCR) was higher in 'Bronco' relative to 'B-2819' at  $1 \times 10^6$  spores, and there were no differences between the two cultivars at the highest inoculum concentration, which matched with the pattern of symptom development. In contrast, symptom development in 'B-2819' lagged behind increases in DNA level at  $1 \times 10^7$  spores. No cortical infection was observed in 'Tekila' at the two lower inoculum concentrations, and only a few spindle clubs developed at the highest concentration. These results demonstrated that this source of partial resistance was strongly affected by inoculum concentration, while

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strong resistance was much less affected.

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