



2019年第31期总198期

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## ▶ 前沿资讯

### 1. Worm Pheromones Protect Major Crops (蛔貳信息素可保护主要作物免受病虫害)

**简介:** 保护农作物免受病虫害而不使用有毒农药,是农业长期以来的目标。美国博伊斯汤普森研究所(BTI)的研究人员发现,一种来源奇特(来源于土壤蛔虫)的化合物可以达到这个目的。这些化合物有助于保护主要作物免受各种病原体的侵害,从而提高农业的可持续性。研究成果发表在《植物病理学杂志》上。

研究团队研究了一种叫做ascr 18的蛔虫代谢产物对植物健康的影响。ascr 18是蛔貳信息素的一种,是由土壤中的蛔虫所产生的。

研究人员用低剂量的ascr 18处理大豆、水稻、小麦和玉米植株,然后用病毒、细菌、真菌或卵菌纲病菌感染这些植株,几天后经测定发现,与未经处理的植株相比,经ascr 18处理的植株对病原体的抵抗力显著增强。

研究人员认为,植物的根经常暴露于土壤中的蛔虫,因此植物进化到能够感知害虫的程度,并在预期受到攻击时发挥免疫系统的功能是不无道理的。由于蛔貳只是增强植物的免疫系统,而不是杀死害虫和病原体,所以它不是杀虫剂。因此,这可能比目前许多害虫和病原体的控制手段更安全。

蛔貳是一种对植物、动物、人类和环境安全的天然化合物,研究人员相信它可以为植物提供更环保的保护,以防止害虫和病原体侵害。

在之前的研究中,研究人员已经证明了ascr 18和其他的蛔貳增加了番茄、土豆、大麦和拟南芥对害虫和病原体的抵抗力。研究团队通过将研究范围扩大到主要作物,并将重点放在最重要的病原体上,确定了蛔貳具有提高作物产量的潜力。

研究证明,ascr 18可保护水稻免受白叶枯病(通常导致亚洲国家水稻产量损失10%-50%)的侵害,保护小麦免受小麦壳针孢叶枯病(小麦最严重的叶类病害之一)的侵害,保护玉米免受南方叶枯病的侵害,保护大豆免受大豆疫霉菌(一种能在数天内杀死受感染植物的卵菌)以及丁香假单胞菌和大豆花叶病毒的侵害。

研究发现,极低浓度的蛔貳足以使植物抵抗病原体。有趣的是,最佳浓度似乎取决于植物种类,而不是病原体。

研究人员认为,不同植物种类具有不同最佳剂量的原因可能与植物细胞对ascr 18的受体有关。不同的植物种类可能表达不同数量的ascr 18受体,并且受体可能对蛔貳具有不同的亲和力。这些差异将影响触发植物免疫系统所需的ascr 18的数量。

该小组目前正在研究蛔貳如何激活植物免疫系统的分子机制。BTI和美国康奈尔大学的一家初创公司正在将这一成果商品化。

该研究团队的成员来自于美国康奈尔大学、肯塔基大学、加利福尼亚大学、戴维斯大学和德国Justus-Liebig大学。

该研究得到了美国农业部国家食品和农业研究所、农业食品与研究计划,美国科罗拉多州农业试验站、肯塔基州大豆促进委员会和德国教育与研究部部长基金的资助。

**来源:** BTI

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## 学术文献

### 1. 羽衣甘蓝的BoRACK1基因抗病性分析

**简介:** [目的]RACK1可与多种信号分子相互作用并影响不同的信号转导途径,可能参与了植物在生物和非生物逆境胁迫中的多种应答。[方法]为研究羽衣甘蓝RACK1对抗病性中的功能,通过农杆菌介导的遗传转化方法获得转化植株,并对3个独立转基因株系进行抗逆性分析。[结果]接种后转基因植株表现明显的抗病表型,抗病防御相关基因和表达量显著高于野生型。[结论]RACK1基因在羽衣甘蓝抗病过程中具有正调控作用,通过上调逆性相关基因的表达量增强抗逆性。

**来源:** 西南农业学报

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### 2. 甘蓝型油菜桔黄花色基因的QTL-seq遗传分析及InDel分子标记开发

**简介:** 本研究以甘蓝型油菜黄色花株系16G097和桔黄色花株系J为亲本,回交获得BC1F1世代花色分离群体。对该分离群体的花色差异单株,通过混池分离分析法(BSA)与全基因组重测序(QTL-seq)技术,对桔黄色花性状调控基因进行初步的遗传分析。结果表明,一个主要的候选区域位于甘蓝型油菜的C09染色体区域(C09:4.64~8.28 Mb)。根据该区域的插入/缺失(InDel)变异位点,开发InDel分子标记,经过筛选获得与桔黄色花性状连锁的共显性分子标记2个(BnaC0919, BnaC0934),这个结果也验证了桔黄色调控基因的候选区域。这些研究结果有利于进一步分离桔黄色调控基因的候选区段,并为甘蓝型油菜遗传学研究和分子育种提供有价值的资源。

**来源:** 分子植物育种

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[http://agri.ckcest.cn/file1/M00/06/8C/Csgk0F0\\_7GmAT-8-ABIxzkzTqcc678.pdf](http://agri.ckcest.cn/file1/M00/06/8C/Csgk0F0_7GmAT-8-ABIxzkzTqcc678.pdf)

### 3. Genome-wide identification of silique-related traits based on high-density genetic linkage map in Brassica napus (基于高密度遗传连锁图谱的甘蓝型油菜角果相关性状的全基因组鉴定)

**简介:** The yield of rapeseed is directly and indirectly influenced by silique-related traits, the genetic dissection, and improvement of the silique-related traits are thus the most important research project in rapeseed. Seven silique-related traits, including seed number per silique (SPS), silique length (SL), silique width (SW), silique thickness (ST), silique volume (SV), silique density (SD), and thousand seed weight (TSW) were further analyzed through quantitative trait locus (QTL) mapping based on a high-density genetic linkage map in KN population. A total of 273 identified QTLs were integrated into 230 consensus QTLs, in which 84.78% of consensus QTLs were considered to be environment-specific QTLs and 15.22% of consensus QTLs were considered to be environmentally stable expression QTLs.

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Two major QTLs, including cqSW.C6-5 for SW and cqSPS.C6-3 for SPS were identified on C06. According to QTLs integrated from different silique traits, 48 unique QTLs were identified with pleiotropy that involved in 2-5 silique-related traits. In addition, 185 epistatic locus pairs were identified with the PV ranging from 0.96 to 15.98%. QTL comparison were made between the KN population and other mapping populations, a total of 164 QTLs for silique-related traits (48 for SPS, 31 for SL, 7 for SD, and 78 for TSW) from nine previously reported researches were aligned to the Brassica napus reference genome, in which 23 QTLs were considered as new QTLs (8 for SD, 4 for SL, 7 for SPS, 4 for TSW). More importantly, cqSPS.C6-3 for SPS might be a novel major QTL. Furthermore, 82 candidate genes in B. napus corresponding to 48 candidate genes in Arabidopsis thaliana were identified, which were involved in transcription factors, enzymes, protein structure units, phytohormone response factors, and transporters, etc. These findings not only provided more comprehensive insights into the genetic basis for silique-related traits but also new cues for improving silique and increasing seed yield in B. napus.

来源: Molecular Breeding

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#### **4. A unique strategy to improve the floral traits and seed yield of Brassica oleracea cytoplasmic male sterile lines through honey bee-mediated selection (一种通过蜜蜂介导的选择来改善甘蓝细胞质雄性不育系的花性状和种子产量的独特策略)**

简介: Improvement in flower structure and seed yield is one of the main objectives when developing cytoplasmic male sterile lines (CMS) in vegetable Brassicas for their successful use in the development of F1 hybrids. However, it is found that the introgression of alien cytoplasm alters the reproductive structure of Brassica oleracea genotypes and the altered floral structure in these lines can be improved only marginally even after several generations of manual selection. We have tested an alternative selection strategy using honey bee (*Apis cerena indica*) as the selection agent in five selection cycles in three CMS lines of cauliflower (Ogu1A, Ogu2A and Ogu3A). Selected plants with the highest seed yield, determined through honey bee selection, were bulked to raise the plants for next generation. The reproductive structures of the CMS plants improved significantly after five cycles of honey bee-mediated selection. Seed yield/plant, nectar quantity, size of nectary and flower size improved significantly in all three CMS lines at the end of the selection cycles. Quantity of nectar increased from 0.45  $\mu$ l and from 0.37 to 1.49  $\mu$ l per flower in CMS lines Ogu1A and Ogu3A, respectively, after five cycles of selection; similarly, quantity of seeds per plant improved from 13.48 to 20.71 g and from 12.77 to 17.57 g in the same CMS lines, respectively. The extent of improvement in nectar quantity and seed yield was comparatively lower in CMS line Ogu2A. The occurrence of different floral deformities was also reduced in all three CMS lines after five cycles of honey bee-mediated selection. CMS lines Ogu1A and Ogu3A responded better to honey bee-mediated selection than did CMS line Ogu2A. This

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novel strategy of honey bee-mediated selection can be used to develop CMS lines with higher seed yield in different crops where cytoplasmic male sterility is commercially used in hybrid seed production.

来源: Euphytica

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## **5. First Report of the Sugar Beet Cyst Nematode, *Heterodera schachtii*, on Brassica sp. in Japan (甜菜孢囊线虫 (*Heterodera Schachtii*) 在日本芸苔属植物上的首次报道)**

简介: The sugar beet cyst nematode, *Heterodera schachtii* Schmidt, is the most economically important pest of sugar beet (*Beta vulgaris* L.) and causes serious yield losses in all major sugar beet production areas of the world. This nematode also causes serious economic losses on Brassicaceae crops.

来源: Plant Disease

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## **6. Changes in phenylpropanoid pathway gene expression in roots and leaves of susceptible and resistant Brassica napus lines in response to *Plasmodiophora brassicae* inoculation (芸苔根肿菌侵染后甘蓝型油菜感病品系和抗病品系根和叶中苯丙烷途径基因表达的变化)**

简介: Clubroot, caused by the obligate parasite *Plasmodiophora brassicae*, is currently one of the most severe diseases of the Brassicaceae. As a soil-borne pathogen, *P. brassicae* infects the roots of host plants, inducing the formation of galls and negatively affecting plant growth and productivity. Roots and leaves of two clubroot susceptible and one resistant *Brassica napus* lines, inoculated with *P. brassicae* spores, were monitored for disease progression at four time points after inoculation. Quantitative gene expression analysis of phenylpropanoid pathway genes in these tissues showed increased expression of several genes involved in lignin biosynthesis in response to infection. In leaves, a higher expression of genes involved in flavonoid biosynthesis was also observed. In both roots and leaves of the resistant line, phenylpropanoid pathway genes were upregulated at more time points and at higher levels than in susceptible lines. The differential expression of phenylpropanoid pathway genes between resistant and susceptible lines, suggests that this pathway is instrumental in resistance to clubroot disease progression in the resistant line.

来源: Physiological and Molecular Plant Pathology

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