



2019年第41期总208期

蔬菜育种专题

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▶ 前沿资讯

1. 巴斯夫在澳洲上市种子处理杀菌剂（氟吡菌酰胺）防治油菜黑胫病

简介：巴斯夫的新型种子处理杀菌剂ILeV0®已获登记，可供澳大利亚油菜种植者使用，用于防治油菜黑胫病。

黑胫病是澳大利亚油菜中最严重的病害。ILeV0含活性成分氟吡菌酰胺，该成分可转运至油菜根、子叶和第一片真叶。这些部位是黑胫病最先发作的地方，ILeV0集中于上述部位可停止病菌对作物的侵染和进一步损害。

巴斯夫澳新种子技术投资组合经理Arturo de Lucas解释说：“我们为向种植者提供种子处理杀菌剂产品感到高兴，因为管理油菜黑胫病的方法十分有限。连续五年进行的试验结果表明，与目前的行业标准产品相比，ILeV0可更有效地预防黑胫病，并能更好地管理早期叶片感染，减少植物倒伏和内部茎感染。”

巴斯夫澳新地区种子业务负责人Rob Hall说，除了其防病能力之外，ILeV0有其他优势，“它与多种产品兼容，施用量低，甚至可以促进作物出苗和植物早期活力，并且该产品此前未用于防治黑胫病，表现值得期待。”

ILeV0不仅显示出良好的安全性，而且对种子发芽没有影响，还具有很高的兼容性，能够与其他杀菌和杀虫种子处理剂混合使用，从而提供更广泛的保护。

ILeV0补充了巴斯夫针油菜解决方案产品组合，2020年还将在澳大利亚推出InVigor®R4022P，油菜产品组合将继续增长。InVigorR4022P是第一个将新TruFlex®技术与巴斯夫特有PodGuard®性状相结合的产品，可提高杂草防控能力和收获时机，提高作物产量潜力。

来源：世界农化网

发布日期：2019-10-09

全文链接：

<http://agri.ckcest.cn/file1/M00/0E/CB/Csgk0F2ex40AQf7BAAi-mim7qvs028.pdf>

2. Nodulation connected to higher resistance against powdery mildew in legumes (结瘤与豆科植物对白粉病具有较高抗性有关)

简介：科学家早就知道结瘤对植物健康很重要。当根瘤形成于植物（主要是豆科植物）的根部时，根瘤形成与固氮细菌的共生关系，固氮细菌向植物输送营养。这一过程是可持续农业的关键部分，并使豆类成为世界许多地区重要的蛋白质来源。然而，最近来自亚琛大学的研究表明，结瘤可能以其他方式对植物的微生物群产生积极影响。

这项研究于9月份发表在《分子植物与微生物相互作用》上，探讨了结瘤与系统抗性之间的关系，即植物保护自身免受病原体侵害的过程。科学家以豌豆和蒺藜苜蓿（原产于地中海的一种豆科植物）为研究对象，发现结瘤使这些植物在白粉病发作后积累更高水平的水杨酸，这种植物激素有助于防御以宿主为食的生物营养入侵者植物。

此外，这项研究表明，经过结瘤后，这些植物表现出更强的抗白粉病能力，白粉病是一种真菌病，在植物的叶和茎上出现白色白点。科学家们推测这可能与水杨酸水平的上升直接相关。

研究人员表示，这项基础研究有助于我们理解植物防御和植物营养的知识，这将有助于塑造可持续农业。

更多资讯 尽在农业专业知识服务系统：<http://agri.ckcest.cn/>

来源: ScienceDaily

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全文链接:

<http://agri.ckcest.cn/file1/M00/00/02/Csgk0V2e0SuADDSkAAPBFP5thqQ510.pdf>

学术文献

1. Transcriptomic analysis reveals the mechanism of thermosensitive genic male sterility (TGMS) of Brassica napus under the high temperature inducement (转录组分析揭示了高温诱导甘蓝型油菜温敏核不育 (TGMS) 的机理)

简介: Background The thermo-sensitive genic male sterility (TGMS) of Brassica napus facilitates reproductive researches and hybrid seed production. Considering the complexity and little information about the molecular mechanism involved in B. napus TGMS, comparative transcriptomic analyses were performed for the sterile (160S-MS) and fertile (160S-MF) flowers to identify potential crucial genes and pathways associated with TGMS.

Results In total, RNA-seq analysis showed that 2202 genes (561 up-regulated and 1641 down-regulated) were significantly differentially expressed in the fertile flowers of 160S-MF at 25°C when compared the sterile flower of 160S-MS at 15°C. Detailed analysis revealed that expression changes in genes encoding heat shock proteins, antioxidant, skeleton protein, GTPase and calmodulin might be involved in TGMS of B. napus. Moreover, gene expression of some key members in plant hormone signaling pathways, such as auxin, gibberellins, jasmonic acid, abscisic acid, brassinosteroid signalings, were significantly suppressed in the flowers of 160S, suggesting that these genes might be involved in the regulation in B. napus TGMS. Here, we also found that transcription factor MADS, NFY, HSF, MYB/C and WRKY might play a crucial role in male fertility under the high temperature condition.

Conclusion High temperature can significantly affect gene expression in the flowers. The findings in the current study improve our understanding of B. napus TGMS at the molecular level and also provide an effective foundation for male fertility researches in other important economic crops.

来源: BMC Genomics

发布日期: 2019-08-13

全文链接:

<http://agri.ckcest.cn/file1/M00/0E/CB/Csgk0F2exTuAVcx3ABYpZX6tKH0102.pdf>

2. Atypical Myrosinase as a Mediator of Glucosinolate Functions in Plants (非典型芥子酶介导植物硫代葡萄糖苷功能的研究)

简介: Glucosinolates (GLSs) are a well-known class of specialized plant metabolites, distributed mostly in the order Brassicales. A vast research field in basic and applied sciences has grown up around GLSs owing to their presence in important agricultural crops and the model plant Arabidopsis thaliana, and their broad range of bioactivities beneficial to human

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health. The major purpose of GLSs in plants has been considered their function as a chemical defense against predators. GLSs are physically separated from a specialized class of beta-thioglucosidases called myrosinases, at the tissue level or at the single-cell level. They are brought together as a consequence of tissue damage, primarily triggered by herbivores, and their interaction results in the release of toxic volatile chemicals including isothiocyanates. In addition, recent studies have suggested that plants may adopt other strategies independent of tissue disruption for initiating GLS breakdown to cope with certain biotic/abiotic stresses. This hypothesis has been further supported by the discovery of an atypical class of GLS-hydrolyzing enzymes possessing features that are distinct from those of the classical myrosinases. Nevertheless, there is only little information on the physiological importance of atypical myrosinases. In this review, we focus on the broad diversity of the beta-glucosidase subclasses containing known atypical myrosinases in *A. thaliana* to discuss the hypothesis that numerous members of these subclasses can hydrolyze GLSs to regulate their diverse functions in plants. Also, the increasingly broadening functional repertoires of known atypical/classical myrosinases are described with reference to recent findings. Assessment of independent insights gained from *A. thaliana* with respect to (1) the phenotype of mutants lacking genes in the GLS metabolic/breakdown pathways, (2) fluctuation in GLS contents/metabolism under specific conditions, and (3) the response of plants to exogenous GLSs or their hydrolytic products, will enable us to reconsider the physiological importance of GLS breakdown in particular situations, which is likely to be regulated by specific beta-glucosidases.

来源: *Frontiers in Plant Science*

发布日期: 2019-08-06

全文链接:

<http://agri.ckcest.cn/file1/M00/0E/CB/Csgk0F2en5WAAWdrAAvxuxH0uBE868.pdf>

3. Knockout of two BnaMAX1 homologs by CRISPR/Cas9-targeted mutagenesis improves plant architecture and increases yield in rapeseed (*Brassica napus* L.) (通过CRISPR/Cas9靶向诱变敲除两个BnaMAX1同源基因可改善油菜(*Brassica napus* L.)的植物结构并提高产量)

简介: Plant height and branch number are essential components of rapeseed plant architecture and are directly correlated with its yield. Presently, improvement of plant architecture is a major challenge in rapeseed breeding. In this study, we first verified that the two rapeseed BnaMAX1 genes had redundant functions resembling those of *Arabidopsis* MAX1, which regulates plant height and axillary bud outgrowth. Therefore, we designed two sgRNAs to edit these BnaMAX1 homologs using the CRISPR/Cas9 system. The T₀ plants were edited very efficiently (56.30%-67.38%) at the BnaMAX1 target sites resulting in homozygous, heterozygous, bi-allelic and chimeric mutations. Transmission tests revealed that the mutations were passed on to the T₁ and T₂ progeny. We also obtained transgene-free lines created by the CRISPR/Cas9 editing, and no mutations were detected in potential off-target sites. Notably, simultaneous knockout of all four BnaMAX1 alleles resulted in semi-dwarf

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and increased branching phenotypes with more siliques, contributing to increased yield per plant relative to wild type. Therefore, these semi-dwarf and increased branching characteristics have the potential to help construct a rapeseed ideotype. Significantly, the editing resources obtained in our study provide desirable germplasm for further breeding of high yield in rapeseed.

来源: Plant Biotechnology Journal

发布日期:2019-08-01

全文链接:

http://agri.ckcest.cn/file1/M00/00/02/Csgk0V2exnKAZX1TAER_x2vs8jY471.pdf

4. Genome-wide exploration and characterization of miR172/euAP2 genes in Brassica napus L. for likely role in flower organ development (甘蓝型油菜miR172/euAP2基因的全基因组研究及其在花器官发育中的作用)

简介: **Background** APETALA2-like genes encode plant-specific transcription factors, some of which possess one microRNA172 (miR172) binding site. The miR172 and its target euAP2 genes are involved in the process of phase transformation and flower organ development in many plants. However, the roles of miR172 and its target AP2 genes remain largely unknown in Brassica napus (*B. napus*).

Results In this study, 19 euAP2 and four miR172 genes were identified in the *B. napus* genome. A sequence analysis suggested that 17 euAP2 genes were targeted by Bna-miR172 in the 3' coding region. EuAP2s were classified into five major groups in *B. napus*. This classification was consistent with the exon-intron structure and motif organization. An analysis of the nonsynonymous and synonymous substitution rates revealed that the euAP2 genes had gone through purifying selection. Whole genome duplication (WGD) or segmental duplication events played a major role in the expansion of the euAP2 gene family. A cis-regulatory element (CRE) analysis suggested that the euAP2s were involved in the response to light, hormones, stress, and developmental processes including circadian control, endosperm and meristem expression. Expression analysis of the miR172-targeted euAP2s in nine different tissues showed diverse spatiotemporal expression patterns. Most euAP2 genes were highly expressed in the floral organs, suggesting their specific functions in flower development. BnaAP2-1, BnaAP2-5 and BnaTOE1-2 had higher expression levels in late-flowering material than early-flowering material based on RNA-seq and qRT-PCR, indicating that they may act as floral suppressors.

Conclusions Overall, analyses of the evolution, structure, tissue specificity and expression of the euAP2 genes were performed in *B. napus*. Based on the RNA-seq and experimental data, euAP2 may be involved in flower development. Three euAP2 genes (BnaAP2-1, BnaAP2-5 and BnaTOE1-2) might be regarded as floral suppressors. The results of this study provide insights for further functional characterization of the miR172/euAP2 module in *B. napus*.

来源: BMC Plant Biology

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全文链接:

<http://agri.ckcest.cn/file1/M00/0E/CB/Csgk0F2ew76AWWeHACR0sdWi80s551.pdf>

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5. Targeted expression of a cysteine protease (AdCP) in tapetum induces male sterility in Indian mustard, Brassica juncea (半胱氨酸蛋白酶 (ADCP) 在绒毡层中的靶向表达诱导印度芥菜 (Brassica juncea) 雄性不育)

简介: The development of male sterile plants is a prerequisite to developing hybrid varieties to harness the benefits of hybrid vigor in crops and enhancing crop productivity for sustainable agriculture. In plants, cysteine proteases have been known for their multifaceted roles during programmed cell death, and in ubiquitin- and proteasome-mediated proteolysis. Here, we showed that *Arachis diogeni* cysteine protease (AdCP) expressed under the TA-29 promoter induced complete male sterility in Indian mustard, *Brassica juncea*. The herbicide resistance gene bar was used for the selection of transgenic plants. Mustard transgenic plants exhibited male sterile phenotype and failed to produce functional pollen grains. Irregularly shaped aborted pollen grains with groove-like structures were observed in male sterile plants during scanning electron microscopy analysis. The T₁ progeny plants obtained from the seed of primary transgenic male sterile plants crossed with the wild-type plants exhibited segregation of the progeny into male sterile and fertile plants with normal seed development. Further, male sterile plants exhibited higher transcript levels of AdCP in anther tissues, which is consistent with its expression under the tapetum-specific promoter. Our results clearly suggest that the targeted expression of AdCP provides a potential tool for developing male sterile lines in crop plants by the malfunction of tapetal cells leading to male sterility as shown earlier in tobacco transgenic plants (Shukla et al. 2014, *Funct Integr Genomics* 14:307-317).

来源: *Functional & Integrative Genomics*

发布日期: 2019-04-09

全文链接:

<http://agri.ckcest.cn/file1/M00/00/02/Csgk0V2exH-AWzazAFLZDvUVZ6s201.pdf>

➤ 标准

1. 食品安全国家标准 食品中农药最大残留限量 (GB 2763—2019)

简介: 根据国家卫生健康委员会、农业农村部和国家市场监督管理总局公告2019年第5号,《食品安全国家标准 食品中农药最大残留限量》(GB 2763—2019,代替GB 2763—2016和GB 2763.1—2018)等3项食品安全国家标准自发布之日起6个月正式实施。

来源: 中国农产品质量安全网

发布日期: 2019-09-18

全文链接:

http://agri.ckcest.cn/file1/M00/00/02/Csgk0V2enr0APFPhAFvi_iSZFJI522.pdf