

2018年第22期总136期

蔬菜育种专题

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> 前沿资讯

1. Close relative of the cultivated tomato is resistant to many insects(荷兰发现抗多种虫害的番茄近缘野生种)

简介:野生番茄比栽培番茄具有较强的抗虫性,但问题是大部分野生番茄都是栽培番茄的远缘种,到目前为止尚未成功杂交出所需的性状。荷兰瓦格宁根大学及研究中心(WUR)的科研人员最近发现了一种能够抵抗多种害虫的近缘野生番茄,有望通过杂交使栽培种获得抗虫性。这种野生番茄(Solanum galapagense)可抵抗包括粉虱、桃蚜和甜菜夜蛾在内的多种害虫,其抗性被编码在单一染色体内,因而与栽培番茄的杂交变得更加容易。预计该研究会给田间和热带地区的番茄种植带来更多好处。

来源: Wageningen University & Research

发布日期:2018-04-12

全文链接:

https://www.wur.nl/en/Expertise-Services/Research-Institutes/plant-research/show-wpr/Close-relative-of-the-cultivated-tomato-is-resistant-to-many-insects.htm

≻ 学术文献

1. Genome Wide Identification and Expression Profiling of SWEET Genes Family Reveals Its Role During Plasmodiophora brassicae-Induced Formation of Clubroot in Brassica rapa(基因组广 泛鉴定和SWEET基因家族表达谱揭示了其在甘蓝型油菜诱导的芸薹 属根瘤菌形成过程中的作用)

简介: Plasmodiophora brassicae is a soil borne pathogen and the causal agent of clubroot, a devastating disease of Brassica crops. The pathogen lives inside roots, and hijacks nutrients from the host plants. It is suggested that clubroot galls created an additional nutrient sink in infected roots. However, the molecular mechanism underlying P. brassicae infection and sugar transport is unclear. Here, we analyzed sugar contents in leaves and roots before and after P. brassicae infection using a pair of Chinese cabbage near-isogenic lines (NILs), carrying either a clubroot resistant (CR) or susceptible (CS) allele at the CRb locus. P. brassicae infection caused significant increase of glucose and fructose contents in the root of CS-NIL compared to CR-NIL, suggesting that sugar translocation and P. brassicae growth are closely related. Among 32 B. rapa SWEET homologs, several BrSWEETs belonging to Clade I and III were significantly up-regulated, especially in CS-NIL upon P. brassicae infection. Moreover, Arabidopsis sweet11 mutant exhibited slower gall formation compared to the wild-type plants. Our studies suggest that P. brassicae infection probably triggers active sugar translocation between the sugar producing tissues and the clubbed tissues, and the SWEET family genes are involved in this process.

来源: Frontiers in Plant Science 发布日期:2018-02-28 http://agri.ckcest.cn/ass/f4aefd40-7dce-48f3-8cf4-40a92de6a036.pdf

2. Proteomic analysis of the interaction between Plasmodiophora brassicae and Chinese cabbage (Brassica rapa L. ssp. Pekinensis) at the initial infection stage(芸薹根肿菌与大白菜在初步感染阶段相互 作用的蛋白质组学分析)

简介: The interaction between plants and pathogens that induces a defense response has been shown in previous studies. In our research, we used Plasmodiophora brassicae Woronin (Plasmodiophoraceae), the causal agent of clubroot disease, to infect the roots of Brassica rapa seedlings. Electron microscopic observation showed that the roots could be infected by Plasmodiophora brassicae on the fifth day after inoculation. We identified 438 and 414 differentially expressed proteins (DEPs) in the inoculated and control groups, respectively. Mass spectrometry was performed to identify 18 of the DEPs in which the relative protein abundance varied by > 2-fold. In general, Gene Ontology (GO) analysis revealed that the DEPs reflected a wide range of molecular functions, including "response to stimuli" (39%) and "plant defense reaction" (8%) in the Biological Process domain. Among these, two proteins (DEPs 3038 and 3129) were found to be related to salicylic acid (SA)-mediated systemic acquired resistance (SAR), two proteins (DEPs 3414 and 2358) were found to be related to jasmonic acid (JA)/ ethylene (ET)-mediated induced systemic resistance (ISR), and DEP 4043 participated in both SAR and ISR. In addition, one pathogenesis-related protein (PR-1) was found in the extracellular cell component group, and KEGG analysis indicated that a DEP participates in plant-pathogen interaction signaling pathways. KEGG analysis also confirmed that these two pathways show some degree of cross-talk, rather than acting independently.

来源: Scientia Horticulturae 发布日期:2018-02-16 全文链接: http://agri.ckcest.cn/ass/9b40e98d-a247-4b49-86f6-c540d66f86c2.pdf

3. Temporal-spatial patterns of ABCDE model genes expressed in new flowers that emerge from the centres of existing flowers in Chinese cabbage(在大白菜花心出现的新花中的ABCDE模型基因表达 时空模式)

简介: We examined the formation of flower buds and floral organs at five growth stages and compared between normal flowers and those that emerged from the centre of another flower (i.e. flowers-in-flower). Gene expression was analysed via qRT-PCR. When compared with normal flowers, expression of nine genes at corresponding time periods showed clearly different trends in the flowers-in-flower samples, depending upon whether those abnormal structures were of the first types (1-1 and 1-2) or the second types (2-1 and 2-2). For example, at each time point, expression of AP2, STK and SHP was notably higher in 2-1 flowers than in either 1-1 or 1-2 flowers. By contrast, AG expression was up-regulated more between

Stages 4 and 5 for normal flowers than for the other types. Furthermore, when compared with normal floral organs, AP1 transcripts were barely detected in the stamens and pistils of mutant samples, and expression was lower in the flowers-in-flower sepals and petals. Except for 2-2 flowers at Stage 5, STK and SHP expression was higher in the mutant organs than in the normal organs. These results suggest that formation of the flowers-in-flower morphology is closely related to down-regulation of AP1 and AG and up-regulation of AP2, STK, and SHP.

来源: The Journal of Horticultural Science and Biotechnology 发布日期:2017-08-28 全文链接: http://agri.ckcest.cn/ass/b447d419-4d49-43c5-bd73-f31147cd5f80.pdf

4. Transcript levels of orf288 are associated with the hau cytoplasmic male sterility system and altered nuclear gene expression in Brassica juncea (orf288转录水平与hau细胞质雄性不育系统和改造后的芥菜 核基因表达有关)

简介: Cytoplasmic male sterility (CMS) is primarily caused by chimeric genes located in the mitochondrial genomes. In Brassica juncea, orf288 has been identified as a CMS-associated gene in the hau CMS line; however, neither the specific abortive stage nor the molecular function of the gene have been determined. We therefore characterized the hau CMS line, and found that defective mitochondria affect the development of archesporial cells during the L2 stage, leading to male sterility. The expression level of the orf288 transcript was higher in the male-sterility line than in the fertility-restorer line, although no significant differences were apparent at the protein level. The toxicity region of ORF288 was found to be located near the N-terminus and repressed growth of Escherichia coli. However, transgenic expression of different portions of ORF288 indicated that the region that causes male sterility resides between amino acids 73 and 288, the expression of which in E. coli did not result in growth inhibition. Transcriptome analysis revealed a wide range of genes involved in anther development and mitochondrial function that were differentially expressed in the hau CMS line. This study provides new insights into the hau CMS mechanism by which orf288 affects the fertility of Brassica juncea.

来源: Journal of Experimental Botany 发布日期:2018-01-02 全文链接: http://agri.ckcest.cn/ass/d93556d3-3d37-44f4-ac91-29989b056708.pdf