



2019年第11期总178期

蔬菜育种专题

本期导读

▶ 前沿资讯

1. 比较不同颜色西红柿中的抗氧化剂水平

▶ 学术文献

1. 甘蓝授粉过程中CML27的分子克隆及表达分析
2. 甘蓝型油菜抗寒性相关数量性状位点图谱
3. 油菜根系对涝渍胁迫反应的蛋白质组学分析
4. 法国菌核病的表型和基因型多样性评估

▶ 科技报告

1. 植物再生的分子机制研究综述

中国农业科学院农业信息研究所

联系人：王爱玲

联系电话：010-51503648

邮箱：agri@ckcest.cn

2019年3月18日

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

▶ 前沿资讯

1. Comparing antioxidants levels in tomatoes of different color (比较不同颜色西红柿中的抗氧化剂水平)

简介: 近年来,天然抗氧化剂因其对健康大有益处而引起了极大关注。墨西哥一所大学的一项研究通过关注8种不同颜色水果的番茄基因型,阐明了不同的抗氧化剂水平。

研究人员对杂交和原生番茄品系中类胡萝卜素、多酚和生育酚含量的变化以及水果抗氧化能力进行测定。此外,来测定了类异戊二烯代谢相关基因和两种色素沉着相关转录因子的表达。

番茄果实是抗氧化剂的主要膳食来源,因其具有抗炎,抗过敏和抗血栓形成的特性,对人体健康有重要贡献。但人们对它们的含量和不同颜色,形状和大小的基因型的调节知之甚少。特定抗氧化剂水平与番茄果实特定颜色的关联性表明这些化合物之间存在“平衡”。

该成果以“不同颜色的番茄基因型中的抗氧化平衡和调节”为题发表在最新一期的“美国园艺学会杂志”上。这项研究的结果有助于在育种计划中使用其基因型来提高现有栽培品种的抗氧化水平。

类胡萝卜素和生育酚是番茄中存在的主要亲脂性抗氧化剂。据报道,多酚是强大的抗氧化剂,具有抗癌作用。主要的番茄多酚是羟基肉桂酸、黄烷酮、黄酮醇和花青素。近年来,已经研究了类胡萝卜素、生育酚和叶绿素的生物合成途径。

研究人员发现,更高水平的特定抗氧化剂与番茄果实的特定着色有关。这些基因型既可以直接用作食物,也可以用于育种计划,以提高功能性化合物的含量,如类胡萝卜素,生育酚,花青素和维生素C等。

来源: AAAS

发布日期: 2019-02-27

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5F/Csgk0Fx8vzmAWgy3AAGHw43QzJM187.pdf>

▶ 学术文献

1. Molecular Cloning And Expression Analysis Of Cml27 In Brassica Oleracea Pollination Process (甘蓝授粉过程中CML27的分子克隆及表达分析)

简介: To keep genetic diversity, flowering plants have developed a self-incompatibility system, which can prevent self-pollination. It has been reported that calcium concentration in pistil papilla cells was increased after self-pollination in transformed self-incompatible Arabidopsis thaliana. In this study, we found that CML27 changed its expression level for both mRNA and protein when compared to transcriptome and proteome. At the same time, CML27 was expressed in the anther and pistil at a high level and reached up to 5-fold up-regulated expression in the pistil at 1 h post-pollination when compared to 0 min. In order to find out potential proteins that may interact with BoCML27, BoCML27 was expressed in and isolated from E. coli. After its co-incubation with Brassica oleracea pistil proteins, the

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

products were separated on SDS-PAGE gels. We found a specific band at the position between 130-180 kDa. Through LC-MS-MS (Q-TOF) analysis, eight proteins were identified from the band. The proteins include 26S proteasome non-ATPase regulatory (26S), Phospholipase D, alpha 2 (PLD α 2) involved in Ca²⁺ binding and Coatomer subunit alpha-2-like (Coatomer) involved in vesicle mediated transport. All of these identified proteins provide new insights for the self-incompatibility response in *B. oleracea*, specific for increasing Ca²⁺ concentration in pistil papilla cells.

来源: ACTA BIOLOGICA CRACOVIENSIA Series Botanica

发布日期:2018-10-01

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5F/Csgk0Fx8u8iAVLJtACldTK921DQ231.pdf>

2. Mapping of quantitative trait loci related to cold resistance in *Brassica napus* L. (甘蓝型油菜抗寒性相关数量性状位点图谱)

简介: Cold stress is one of the major abiotic stresses that seriously limit rapeseed production worldwide. However, few studies on the mechanism of cold resistance in *Brassica napus* have been reported. In this study, an F_{2:3} population including 147 lines was developed to identify the quantitative trait loci (QTLs) related to cold resistance in *B. napus*. As a result, a genetic linkage map based on 333 simple sequence repeat (SSR) markers covering 1317.70 cM was constructed. Up to 11 QTLs for four indicators were identified in the two locations. These QTLs accounted for 1.09% to 42.50% of the phenotypic variations, and six major QTLs accounted for more than 10% of the phenotypic variations. Three QTLs, qSPADYL-6, qSPADYS-6, and qMDAYS-6, were mapped to the same region of linkage group 6 (LG6). Blast analysis indicated that the sequences of the markers related to these three QTLs showed great collinearity with those on the A08 chromosome of *Brassica rapa*, and that the target genes might exist in the region from 1.069 to 15.652 M on A08. Two genes, BnaA08g05330D and BnaA08g15470D, encoding the respective cold-regulated proteins in *B. napus*, were identified. They exhibited high similarity with Bra039858 and Bra010579 (stress-responsive proteins) in the candidate region. RT-qPCR analysis showed a significant difference in gene expression between the two parents. These two genes were hence identified as the genes responsible for cold resistance.

来源: Journal of Plant Physiology

发布日期:2018-09-21

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5F/Csgk0Fx8vKqAKtEFACyP7VggLVw436.pdf>

3. Proteomic Analysis of Rapeseed Root Response to Waterlogging Stress (油菜根系对涝渍胁迫反应的蛋白质组学分析)

简介: The overall health of a plant is constantly affected by the changing and hostile environment. Due to climate change and the farming pattern of rice (*Oryza sativa*) and rapeseed (*Brassica napus* L.), stress from waterlogging poses a serious threat to productivity assurance and the yield of rapeseed in China's Yangtze River basin. In order to improve our

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

understanding of the complex mechanisms behind waterlogging stress and identify waterlogging-responsive proteins, we firstly conducted iTRAQ (isobaric tags for relative and absolute quantification)-based quantitative proteomic analysis of rapeseed roots under waterlogging treatments, for both a tolerant cultivar ZS9 and sensitive cultivar GH01. A total of 7736 proteins were identified by iTRAQ, of which several hundred showed different expression levels, including 233, 365, and 326 after waterlogging stress for 4H, 8H, and 12H in ZS9, respectively, and 143, 175, and 374 after waterlogging stress for 4H, 8H, and 12H in GH01, respectively. For proteins repeatedly identified at different time points, gene ontology (GO) cluster analysis suggested that the responsive proteins of the two cultivars were both enriched in the biological process of DNA-dependent transcription and the oxidation-reduction process, and response to various stress and hormone stimulus, while different distribution frequencies in the two cultivars was investigated. Moreover, overlap proteins with similar or opposite tendencies of fold change between ZS9 and GH01 were observed and clustered based on the different expression ratios, suggesting the two genotype cultivars exhibited diversiform molecular mechanisms or regulation pathways in their waterlogging stress response. The following qRT-PCR (quantitative real-time polymerase chain reaction) results verified the candidate proteins at transcription levels, which were prepared for further research. In conclusion, proteins detected in this study might perform different functions in waterlogging responses and would provide information conducive to better understanding adaptive mechanisms under environmental stresses.

来源: Plants

发布日期:2018-09-18

全文链接:

http://agri.ckcest.cn/file1/M00/06/5F/Csgk0Fx8jKACxFEA0_CeparPlo014.pdf

4. Assessing the phenotypic and genotypic diversity of *Sclerotinia sclerotiorum* in France (法国菌核病的表型和基因型多样性评估)

简介: White mould caused by the ascomycete *Sclerotinia sclerotiorum* affects the production of many economically important crops. The incidence of this disease has recently increased in France, especially in melon crops, which were not affected much in the past. One possible explanation for this situation is the emergence of strains with particular characteristics, including increased aggressiveness to melon. To test this hypothesis, 200 isolates of *S. sclerotiorum* were collected from six host crops (bean, brassica oilseed rape, carrot, lettuce, melon, witloof chicory) in different regions. They were genotyped with 16 microsatellites markers. A subsample of 96 isolates were assessed for their aggressiveness on melon leaves. Overall, the isolates from melon did not show higher aggressiveness on melon leaves than those which originated from other host plants. Moreover, the melon isolates did not present distinctive genetic characteristics in comparison with those from other crops and shared several of the 128 identified multilocus haplotypes with isolates collected from carrot, witloof chicory and oilseed rape. Furthermore the Bayesian analysis of the genetic structure indicated that the host plant is not a structuring factor of the three genetic clusters identified, and it suggested instead the occurrence of an isolation-by-distance process. Possible consequences of these results for the management of white mould and alternative hypotheses

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

to explain the recent changes in disease incidence are presented.

来源: European Journal of Plant Pathology

发布日期: 2018-05-08

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5F/Csgk0Fx8gs6AL1NUAA636tZHVrM640.pdf>

科技报告

1. Molecular Mechanisms of Plant Regeneration (植物再生的分子机制研究综述)

简介: Plants reprogram somatic cells following injury and regenerate new tissues and organs. Upon perception of inductive cues, somatic cells often dedifferentiate, proliferate, and acquire new fates to repair damaged tissues or develop new organs from wound sites. Wound stress activates transcriptional cascades to promote cell fate reprogramming and initiate new developmental programs. Wounding also modulates endogenous hormonal responses by triggering their biosynthesis and/or directional transport. Auxin and cytokinin play pivotal roles in determining cell fates in regenerating tissues and organs. Exogenous application of these plant hormones enhances regenerative responses in vitro by facilitating the activation of specific developmental programs. Many reprogramming regulators are epigenetically silenced during normal development but are activated by wound stress and/or hormonal cues.

来源: Annual Review of Plant Biology

发布日期: 2019-02-20

全文链接:

<http://agri.ckcest.cn/file1/M00/06/5F/Csgk0Fx8vliALpiPAE0SwApycGQ769.pdf>