



2019年第23期总190期

蔬菜育种专题

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抗性改良为一例

科技报告

1. 美国农业部2028年农业预测

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▶ 前沿资讯

1. Using population genetics, scientists confirm origins of root rot in Michigan ornamentals (通过群体遗传学科学家证实密歇根观赏植物根腐病的起源)

简介: Floriculture is an economically important industry in Michigan. The health of these crops is threatened by *Pythium ultimum* (root rot), a water mold that infects the roots of popular plants. Despite efforts to control of pathogen, root rot occurs annually for many growers. This study confirmed for the first time that the root rot pathogen is likely moved unnoticed within the state via infected plant material as early symptoms of root rot are easily overlooked.

来源: ScienceDaily

发布日期: 2019-06-04

全文链接:

<https://www.sciencedaily.com/releases/2019/06/190604094242.htm>

2. 科学家新发现为达尔文“同种花粉优先”现象提供解释

简介: 北京大学生命科学学院、北大-清华生命科学联合中心教授瞿礼嘉课题组31日在《科学》杂志在线发表题为《富含半胱氨酸小肽信号促进拟南芥的种间遗传隔离》的研究长文。这篇论文揭示了植物内部和种间生殖隔离屏障的分子信号传导机制。该研究有利于未来的育种工作,同时可以通过向作物植物添加期望的农艺性状来增加基因库。

来源: 科学网

发布日期: 2019-06-01

全文链接:

<http://news.sciencenet.cn/htmlnews/2019/6/426995.shtm>

▶ 学术文献

1. 基于家族基因分析的甘蓝MLPK互作PUB蛋白的筛选

简介: MLPK (M位点受体激酶) 是芸薹属自交不亲和正向调控关键元件, 其参与自交不亲和和信号传导的分子机制尚不明确, 同时自交不亲和下游信号元件也有待于进一步分离。为了探索分离MLPK互作蛋白的思路和方法, 构建了不含核定位信号的MLPK短截蛋白 (MLPK-T), 并利用酵母双杂交检测到MLPK与臂重复蛋白1 (ARC1) 作用, 通过全基因组鉴定分别获得了96个甘蓝、101个白菜、70个琴叶拟南芥和62个拟南芥PUB蛋白, 其中含有臂重复序列的PUB蛋白共为127个。通过系统进化分析, 筛选到8个含臂重复序列的甘蓝BoPUB蛋白, 其8个基因全部在柱头内表达, 且成功利用酵母双杂交检测到MLPK与3个含臂重复序列的BoPUB蛋白Bo1008579、Bo1016165和Bo1023511相互作用。

来源: 园艺学报

发布日期: 2019-03-21

全文链接:

<http://agri.ckcest.cn/file1/M00/06/6F/Csgk0Fz4vTSAB8A6ACBPEr2i6XI358.pdf>

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2. Transcriptomic and Proteomic Analysis of Shaan2A Cytoplasmic Male Sterility and Its Maintainer Line in *Brassica napus* (甘蓝型油菜 Shaan 2A细胞质雄性不育系及其保持系的转录和蛋白质组学分析)

简介: Cytoplasmic male sterility (CMS) lines are widely used for hybrid production in *Brassica napus*. The Shaan2A CMS system is one of the most important in China and has been used for decades; however, the male sterility mechanism underlying Shaan2A CMS remains unknown. Here, we performed transcriptomic and proteomic analysis, combined with additional morphological observation, in the Shaan2A CMS. Sporogenous cells, endothecium, middle layer, and tapetum could not be clearly distinguished in Shaan2A anthers. Furthermore, Shaan2A anther chloroplasts contained fewer starch grains than those in Shaan2B (a near-isogenic line of Shaan2A), and the lamella structure of chloroplasts in Shaan2A anther wall cells was obviously aberrant. Transcriptomic analysis revealed differentially expressed genes (DEGs) mainly related to carbon metabolism, lipid and flavonoid metabolism, and the mitochondrial electron transport/ATP synthesis pathway. Proteomic results showed that differentially expressed proteins were mainly associated with carbohydrate metabolism, energy metabolism, and genetic information processing pathways. Importantly, nine gene ontology categories associated with anther and pollen development were enriched among down-regulated DEGs at the young bud (YB) stage, including microsporogenesis, sporopollenin biosynthetic process, and tapetal layer development. Additionally, 464 down-regulated transcription factor (TF) genes were identified at the YB stage, including some related to early anther differentiation such as SPOROCTELESS (SPL, also named NOZZLE, NZZ), DYSFUNCTIONAL TAPETUM 1 (DYT1), MYB80 (formerly named MYB103), and ABORTED MICROSPORES (AMS). These results suggested that the sterility gene in the Shaan2A mitochondrion might suppress expression of these TF genes in the nucleus, affecting early anther development. Finally, we constructed an interaction network of candidate proteins based on integrative analysis. The present study provides new insights into the molecular mechanism of Shaan2A CMS in *B. napus*.

来源: FRONTIERS IN PLANT SCIENCE

发布日期: 2019-03-04

全文链接:

<http://agri.ckcest.cn/file1/M00/06/6F/Csgk0Fz4vTSAUtPuAJlcPd4FoyA853.pdf>

3. 人工合成甘蓝型油菜抗旱性及DNA甲基化水平分析

简介: 甘蓝型油菜是具有重要经济价值的多倍体物种,是优质食用植物油和饲料蛋白质的重要来源之一。但是其驯化历史较短,遗传背景狭窄,且在整个生命周期中都对于旱胁迫敏感,因此培育高产耐旱品种是甘蓝型油菜的重要育种目标之一。本文用15%PEG-6000模拟干旱胁迫,对人工合成甘蓝型油菜不同世代(S1~S4)及其二倍体亲本进行不同时间的胁迫处理,并结合表型观察,以及叶片中丙二醛(MDA)、可溶性蛋白含量、过氧化物酶(POD)、超氧化物歧化酶(SOD)等生理指标的测定,初步了解上述材料的抗旱性差异。结合表型观察和叶片中相对含水量分析,发现人工合成甘蓝型油菜S1~S4及其亲本的抗旱

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性表现为甘蓝> Bn-S3> Bn-S4> Bn-S1> Bn-S2>白菜型油菜。干旱胁迫后Bn-S3、Bn-S4的POD及SOD活性较高,MDA含量较低,表明Bn-S3和Bn-S4能更加有效地清除活性氧(ROS),对过氧化损伤的防御能力更强。通过HPLC分析发现所有材料的甲基化水平在胁迫12 h时最高,其中亲本白菜型油菜Br的甲基化水平最高, Bn-S1和Bn-S4介于两亲本之间,而Bn-S2和Bn-S3低于两亲本。甲基化敏感多态性分析也显示人工合成甘蓝型油菜在干旱胁迫后,甲基化和去甲基化水平均发生了明显的变化,表明植物的甲基化变化可能有利于提高其抗旱能力。

来源: 作物学报

发布日期:2019-01-17

全文链接:

<http://agri.ckcest.cn/file1/M00/06/6F/Csgk0Fz4vTSAENEuABupj1XoH00787.pdf>

4. Joint QTL mapping and transcriptome sequencing analysis reveal candidate flowering time genes in Brassica napus L (通过联合QTL定位和转录组测序分析揭示甘蓝型油菜 (Brassica napus L) 中的候选开花时间基因)

简介: Background Optimum flowering time is a key agronomic trait in Brassica napus. To investigate the genetic architecture and genetic regulation of flowering time in this important crop, we conducted quantitative trait loci (QTL) analysis of flowering time in a recombinant inbred line (RIL) population, including lines with extreme differences in flowering time, in six environments, along with RNA-Seq analysis. Results We detected 27 QTLs distributed on eight chromosomes among six environments, including one major QTL on chromosome C02 that explained 1125% of the phenotypic variation and was stably detected in all six environments. RNA-Seq analysis revealed 105 flowering time-related differentially expressed genes (DEGs) that play roles in the circadian clock/photoperiod, autonomous pathway, and hormone and vernalization pathways. We focused on DEGs related to the regulation of flowering time, especially DEGs in QTL regions. Conclusions We identified 45 flowering time-related genes in these QTL regions, eight of which are DEGs, including key flowering time genes PSEUDO RESPONSE REGULATOR 7 (PRR7) and FY (located in a major QTL region on C02). These findings provide insights into the genetic architecture of flowering time in B. napus.

来源: BMC Genomics

发布日期:2019-01-09

全文链接:

<http://agri.ckcest.cn/file1/M00/06/6F/Csgk0Fz4vTKAJLZ0AC82QMsA9HA574.pdf>

5. Mapping of a novel clubroot resistance QTL using ddRAD-seq in Chinese cabbage (Brassica rapa L.) (利用 ddRAD-seq 在大白菜 (Brassica rapa L.) 中定位新型的根肿病抗性QTL)

简介: Background Plasmodiophora brassicae is a soil-borne plant pathogen that causes clubroot disease, which results in crop yield loss in cultivated Brassica species. Here, we

investigated whether a quantitative trait locus (QTL) in *B. rapa* might confer resistance to a Korean *P. brassicae* pathotype isolate, Seosan. We crossed resistant and susceptible parental lines and analyzed the segregation pattern in a F2 population of 348 lines. We identified and mapped a novel clubroot resistance QTL using the same mapping population that included susceptible Chinese cabbage and resistant turnip lines. Forty-five resistant and 45 susceptible F2 lines along with their parental lines were used for double digest restriction site-associated DNA sequencing (ddRAD-seq). High resolution melting (HRM)-based validation of SNP positions was conducted to confirm the novel locus. Results A 3:1 ratio was observed for resistant: susceptible genotypes, which is in accordance with Mendelian segregation. ddRAD-seq identified a new locus, CRs, on chromosome A08 that was different from the clubroot resistance (CR) locus, Crr1. HRM analysis validated SNP positions and constricted CRs region. Four out of seventeen single nucleotide polymorphisms (SNPs) positions were within a 0.8-Mb region that included three NBS-LRR candidate genes but not Crr1. Conclusion The newly identified CRs locus is a novel clubroot resistance locus, as the cultivar Akimeki bears the previously known Crr1 locus but remains susceptible to the Seosan isolate. These results could be exploited to develop molecular markers to detect Seosan-resistant genotypes and develop resistant Chinese cabbage cultivars.

来源: BMC Plant Biology

发布日期:2019-01-08

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<http://agri.ckcest.cn/file1/M00/06/6F/Csgk0Fz4vTKAT4NXACWYXKZJeeo096.pdf>

6. Germinative and Post-Germinative Behaviours of Brassica napus Seeds Are Impacted by the Severity of S Limitation Applied to the Parent Plants (母株的S限制程度影响甘蓝型油菜种子的萌发和后发芽行为)

简介: In oilseed rape (*Brassica napus* L.), sulphur (S) limitation leads to a reduction of seed yield and nutritional quality, but also to a reduction of seed viability and vigour. S metabolism is known to be involved in the control of germination *sensu stricto* and seedling establishment. Nevertheless, how the germination and the first steps of plant growth are impacted in seeds produced by plants subjected to various sulphate limitations remains largely unknown. Therefore, this study aimed at determining the impact of various S-limited conditions applied to the mother plants on the germination indexes and the rate of viable seedlings in a spring oilseed rape cultivar (cv. Yudal). Using a 34S-sulphate pulse method, the sulphate uptake capacity during the seedling development was also investigated. The rate of viable seedlings was significantly reduced for seeds produced under the strongest S-limited conditions. This is related to a reduction of germination vigour and to perturbations of post-germinative events. Compared to green seedlings obtained from seeds produced by well-S-supplied plants, the viable seedlings coming from seeds harvested on plants subjected to severe S-limitation treatment showed nonetheless a higher dry biomass and were able to enhance the sulphate uptake by roots and the S translocation to shoots.

来源: Plants

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发布日期:2019-01-05

全文链接:

<http://agri.ckcest.cn/file1/M00/06/6F/Csgk0Fz4vTGAHd16ABqQWqFfREA143.pdf>

7. Synchronous improvement of subgenomes in allopolyploid: a case of Sclerotinia resistance improvement in Brassica napus (异源多倍体中亚基因组的同步改良: 以甘蓝型油菜菌核病抗性改良为一例)

简介: The rare chance of homoeologous exchange results in a low efficiency to transfer elite locus between subgenomes of allopolyploid in vivo. Here, we propose a breeding strategy to synchronously improve the subgenomes of allopolyploid, as a case of Sclerotinia sclerotiorum resistance improvement in Brassica napus. The resistance of both parental species was firstly improved by identifying resistance source in B. oleracea and transferring the resistance loci from resistant B. oleracea into B. rapa. The resistance loci from B. rapa and B. oleracea were then pyramided by resynthesizing B. napus. Four groups of resynthesized B. napus, comprising of 37 lines with or without resistance loci from B. rapa and/or B. oleracea, were evaluated for Sclerotinia resistance across 3 years. Significant differences were found among the four groups for both leaf and stem resistance. The group of resynthesized B. napus carrying resistance loci from B. rapa and B. oleracea exhibited the highest level of resistance, out of which one prominent line showed 2.7-fold higher stem resistance than “Zhongshuang 9,” a partial resistant Chinese rapeseed variety. Our data highlights that the strategy of synchronous improvement of subgenomes can efficiently improve allopolyploids.

来源: Molecular Breeding

发布日期:2019-01-04

全文链接:

<http://agri.ckcest.cn/file1/M00/06/6F/Csgk0Fz4vTKAOGfVAD3kKpgZnG8015.pdf>

➤ 科技报告

1. USDA Agricultural Projections to 2028 (美国农业部2028年农业预测)

简介: This report provides projections for the agricultural sector to 2028. Projections cover agricultural commodities, agricultural trade, and aggregate indicators of the sector, such as farm income. The projections are based on specific assumptions about macroeconomic conditions, policy, weather, and international developments, with no domestic or external shocks to global agricultural markets. The Agricultural Act of 2014 is assumed to remain in effect through the projection period. The projections are one representative scenario for the agricultural sector for the next decade and reflect a composite of model results and judgment-based analyses. The projections in this report were prepared July 2018 through February 2019. While agricultural prices are tending to trend upwards, ongoing U.S. trade disputes with China have dampened expectations for soybeans. These trade disputes are

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assumed to last the duration of the projection period. Planted acreage drops slightly overall, primarily due to an expected drop in soybean plantings, while corn and wheat plantings are expected to offset the bulk of the loss in soybean acreage. Energy costs are expected to remain relatively low with crude oil import prices remaining below \$93 per barrel over the coming 10 years. Low feed costs and continued strong global demand provide economic incentives for expansion in the livestock sector. Long-run developments for global agriculture reflect steady world economic growth and continued global demand for biofuel feedstocks, factors which combine to support longer run increases in disappearance, trade, and prices of agricultural products. Although a relatively strong U.S. dollar is expected to dampen growth in U.S. agricultural exports, the United States remains competitive in global agricultural markets, in part due to efficiency and quality margins. Net farm income is expected to increase a little over 8 billion dollars in 2019 to just over 77.5 billion dollars and remain relatively steady, fluctuating between 75 and 80 billion dollars for the remainder of the decade.

来源: 美国农业部

发布日期: 2019-03-01

全文链接:

<http://agri.ckcest.cn/file1/M00/06/6F/Csgk0Fz4vTSAGG1QABUewrF4174313.pdf>