



2019年第34期总201期

蔬菜育种专题

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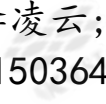
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▶ 前沿资讯

1. Accelerating Growth: IAEA Launches Plant Mutation Breeding Network for Asia and the Pacific (国际原子能机构启动亚洲及太平洋植物突变育种网络)

简介: 突变育种作为育种的重要方法广泛使用。随着人口的快速增长,特别是在亚洲和太平洋地区,农民和科学家们更多地利用辐照来开发新的作物品种并满足农民的需求:更高、更稳定的产量,能够抵御病害和气候变化的优质植物。

据粮农组织/国际原子能机构粮食负责人称,在亚太地区,有记录的作物品种中,突变育种占了近2000种。到目前为止,发布的使用诱变技术的826种水稻品种中,有699种来自亚太地区,其中290种仅来自中国。中国第二大应用最广泛的小麦品种,种植面积超过360万公顷,是通过诱变育种培育出来的。

植物突变育种网络(MBN)旨在提高整个地区作物突变育种的效率。由国际原子能机构和联合国粮食及农业组织(FAO)牵头的一项倡议正在把该区域的专家聚集在一起,相互支持,并在彼此的研究、育种及其成果的基础上进一步发展。这包括从加速发现植物中更好的性状,到推进快速育种技术以获得更好的性状,以及促进农民获得改良种子。MBN的最终目标是通过区域合作和知识与技术交流,确保粮食和营养安全,改善民生。

遗传与科技交流

交换种质资源。除了加强各国在植物突变育种和相关生物技术方面的能力外,预计参与的各国政府还将交换种质资源——种子或任何种植后能够生长的东西。这是关键,因为它可以让孟加拉国等国的农民种植越南科学家开发的耐旱水稻。这样的双边转让将大大有助于研究和发展以及能力建设,并节省有关国家的努力。

同样,通过MBN,科学家将能够实施航天育种,这涉及在不同地点连续种植,以使生长过程更快。事实上,MBN旨在促进不同国家的多环境田间试验,以确定作物在哪里生长得更好。

交换新技术。交换新技术也在该网络的列表中。为了改善植物的性状,科学家们用伽马射线或x射线照射植物的种子或其他部分。然后,他们种植种子或培育受辐射的材料,以产生专家所说的突变群体。

在突变群体中的数千种植物中,植物育种者需要确定适合其特定气候、土壤和流行植物病害的正确组合。为了加速这一选择过程,科学家们开发了新的分子技术。这个工具不仅可以用来选择新的性状,还可以在不同的地区或大陆传播具有所需性状的作物。

建立全球种子库。MBN另一个目标是支持在挪威斯瓦尔巴德的全球种子库中保护改良突变植物品种的样本。该储藏库在冰覆盖的岩石中挖掘,充当天然冰柜,来自世界各地的种子被保存。该种子库的建立是为了保护各种植物种子,这些种子是重复样本或“备用”拷贝,以防止在大规模区域或全球危机期间其他基因库中种子的丢失。种子库距离北极约1300公里。

合作与交流。在该网络的框架下,有望通过研讨会、科学访问和研究基金在区域内分享这种快速育种技术。该网络鼓励建立平台,使交换技术和感兴趣的已知基因成为可能。

该网络的参与者正在开发一个网站,提供关于国家作物和性状优先次序、现有品种、国家能力和现有基础设施、突变育种的文献以及关于培训和会议机会的最新信息。

MBN目前由来自孟加拉国,中国,印度,印度尼西亚,老挝人民民主共和国,马来

西亚, 蒙古, 缅甸, 巴基斯坦, 菲律宾, 斯里兰卡, 泰国和越南的专家组成。它的第一次会议于上个月在中国北京召开, 非洲和拉丁美洲的科学家也受邀参加了会议。MBN合作伙伴愿意扩大网络, 以满足食品和营养安全, 并改善其他地区的生计, 这取决于该网络成功与否。

来源: IAEA

发布日期: 2019-08-16

全文链接:

<http://agri.ckcest.cn/file1/M00/0E/7F/Csgk0F1eM-uASmSuAAUMbg4jrDw741.pdf>

学术文献

1. PEG模拟干旱胁迫下花椰菜种质资源萌发特性及抗旱性评价

简介: 为鉴定和筛选花椰菜耐旱种质资源, 以12个花椰菜种质资源为试验材料, 测定不同浓度PEG[0 (CK)、100、150和200 g·L⁻¹]模拟干旱胁迫对花椰菜的相对发芽率 (RGP)、相对发芽势 (RGR)、相对发芽指数 (RGI)、相对活力指数 (RVI)、相对苗高 (RSH) 和相对根长 (RRL) 等6个指标的影响, 并采用隶属函数法进行抗旱性的综合评价。结果表明, 100 g·L⁻¹PEG胁迫对花椰菜种子萌发的影响不大, 150~200 g·L⁻¹PEG胁迫则显著抑制花椰菜种子萌发。100~150 g·L⁻¹PEG胁迫对RRL具有一定的促进作用, 而150~200 g·L⁻¹PEG胁迫则会明显抑制RSH, 表明150~200 g·L⁻¹PEG可作为花椰菜萌发期抗旱性筛选的适宜浓度。基于RGP、RGR、RGI、RVI、RSH和RRL 6个指标, 通过隶属函数法综合评价发现, 12个花椰菜材料的抗旱性依次表现为P3>P6>A1>P8>P7>P2>P1>P4>P5>A2>A3>P9。本研究结果为花椰菜抗旱品种选育提供了一定的理论依据。

来源: 核农学报

发布日期: 2019-07-22

全文链接:

<http://agri.ckcest.cn/file1/M00/0E/7F/Csgk0F1eMamAL3UqABsYiUezn9g582.pdf>

2. Fine mapping and candidate gene analysis of the yellow petal gene ckpc in Chinese kale (*Brassica oleracea* L. var. *alboglabra* Bailey) by whole-genome resequencing (利用全基因组测序技术对芥蓝 (*Brassica oleracea* L. var. *alboglabra* Bailey) 黄色花瓣基因ckpc进行精细定位及候选基因分析)

简介: Chinese kale is a characteristic vegetable crop originating from China and being suggested to be a possible ancestor of various cultivated *B. oleracea* vegetables. It has both white and yellow petals and is therefore a desirable plant for use in research on petal color formation. In our study, the Chinese kale landrace YCK-1 (yellow petals) was crossed with the Chinese kale inbred line Lb07M (white petals) to construct mapping populations for genetic analysis and fine mapping of the petal color gene. The results indicated that yellow petal color is controlled by a single recessive gene named ckpc, which was preliminarily located in a 2.06-Mb candidate region of chromosome C03 using whole-genome

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resequencing combined with bulked segregant analysis (BSA). Fine mapping with traditional molecular marker technology was used to narrow down the ckpc gene in a 69.0-kb interval flanked by the markers M916 and SNP4 at genetic distances of 0.07 cM and 0.04 cM, respectively. Gene annotation revealed 5 genes in that region, and Bo3g158650 was annotated as a carotenoid cleavage dioxygenase 4 (CCD4) gene, which is known to function in flower and flesh color formation. Sequence analysis revealed that the Bo3g158650 gene in the white-petaled parent, Lb07M, had an identical sequence to that in the 'TO1000' reference genome, while a 7.61-kb CACTA-like transposable element 1 (TE1) insertion was found in this gene in the yellow-petaled parent, YCK-1. These results increase the understanding of the mechanism underlying petal color formation in Brassica.

来源: Molecular Breeding

发布日期: 2019-06-26

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/7F/Csgk0F1eMPSAaRA1ABplvSLMX0E134.pdf>

3. Dynamic variation of glucosinolates and isothiocyanates in broccoli sprouts during hydrolysis (水解过程中西兰花芽苗中硫代葡萄糖苷和异硫氰酸酯的动态变化)

简介: In this study, the glucosinolates (GLs) content and isothiocyanates (ITCs) formation in broccoli sprouts and their dynamic variation during hydrolysis were investigated. The results showed that 7 kinds of GLs were detected and glucoraphanin (GRA) was the dominating component. After hydrolysis, three kinds of ITCs and 2 kinds of nitriles were detected in broccoli sprouts, however, the corresponding nitriles of 4-isothiocyanato-1-butene and 1-isothiocyanato-butane were not detectable. This inferred that the inter-transformation among ITCs existed during sprouts hydrolysis. According to the identification, 4-isothiocyanato-1-butene had another source in addition to gluconapin (GNA), 1-isothiocyanato-butane stemmed from glucoerucin (GER). Moreover, the affinity of MYR in broccoli sprouts was stronger to GER than to GRA and other GLs.

来源: Scientia Horticulturae

发布日期: 2019-05-20

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/7F/Csgk0F1eBxiAVdhLAC1JGUnKZ1w987.pdf>

4. First Report of Stem and Root Rot of Chinese Kale Caused by Fusarium incarnatum-equiseti Species Complex in China (由镰刀菌 (Fusarium incarnatum-equiseti) 复合种引起的芥蓝茎、根腐病研究初报)

简介: Chinese kale (*Brassica oleracea* var. *alboglabra*) is an important green leaf crop in China. In October 2018, plants of cultivar 'Sujie' in the experimental field of the Vegetable Research Institute at the Guangdong Academy of Agricultural Sciences (VRI-GAAS) in Guangzhou, China, exhibited stem rot symptoms. Disease incidence was up to 30%.

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Symptom development was first observed on 2-month-old plants. Symptoms appeared as wilting and yellowing of leaves, followed by rotting of stem and root tissues. Infected plants had reduced growth, and severely infected plants died.

来源: Plant Disease

发布日期: 2019-05-16

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/7F/Csgk0F1eA8WABDLLAAGdywMVZOI656.pdf>

5. Genome-wide haplotype analysis improves trait predictions in Brassica napus hybrids (全基因组单倍型分析提高甘蓝型油菜杂种性状预测)

简介: Combining ability is crucial for parent selection in crop hybrid breeding. Many studies have attempted to provide reliable and quick methods to identify genome regions in parental lines correlating with improved hybrid performance. The local haplotype patterns surrounding densely spaced DNA markers include a large amount of genetic information, and analysis of the relationships between haplotypes and hybrid performance can provide insight into the underlying genome regions which might contribute to enhancing combining ability. Here, we generated 24,403 single-copy, genome-wide SNP loci and calculated the general combining ability (GCA) of 950 hybrids from a diverse panel of 475 pollinators of spring-type canola inbred lines crossed with two testers for days to flowering (DTF) and seed glucosinolate content (GSL). We performed a genome-wide analysis of the haplotypes and detected eight and seven haplotype regions that were significantly associated with the GCA values for DTF and seed GSL, respectively. Additionally, two haplotype blocks containing orthologs of flowering time genes FLOWERING LOCUS T (FT) and FLOWERING LOCUS C (FLC) on chromosome A02 showed additive epistatic interactions influencing flowering time. Moreover, two homoeologous haplotype regions on chromosomes A02 and C02 corresponded to major quantitative trait loci (QTL) for GSL which showed additive effects related to reduction of seed GSL in F1 hybrids. Our study showed that haplotype analysis has the potential to substantially improve the efficiency of hybrid breeding programs.

来源: Plant Science

发布日期: 2019-03-13

全文链接:

<http://agri.ckcest.cn/file1/M00/OE/7F/Csgk0F1eBIWAB4Z1ADDIbCVrz4Y784.pdf>

6. Simultaneous Transcriptome Analysis of Host and Pathogen Highlights the Interaction Between Brassica oleracea and Sclerotinia sclerotiorum (寄主和病原体的同时转录组分析突出了甘蓝和菌核病之间的相互作用)

简介: White mold disease caused by *Sclerotinia sclerotiorum* is a devastating disease of Brassica crops. Here, we simultaneously assessed the transcriptome changes from lesions produced by *S. sclerotiorum* on disease-resistant (R) and -susceptible (S) *B. oleracea* pools bulked from a resistance-segregating F2 population. Virulence genes of *S. sclerotiorum*,

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including polygalacturonans, chitin synthase, secretory proteins, and oxalic acid biosynthesis, were significantly repressed in lesions of *R. B. oleracea* at 12h postinoculation (hpi) but exhibited similar expression patterns in *R* and *S. B. oleracea* at 24 hpi. Resistant *B. oleracea* induced expression of receptors potentially to perceive *Sclerotinia* signals during 0 to 12hpi and deployed complex strategies to suppress the pathogen establishment, including the quick accumulation of reactive oxygen species via activating Ca^{2+} signaling and suppressing pathogen oxalic acid generation in *S. sclerotiorum*. In addition, cell wall degradation was inhibited in the resistant *B. oleracea* potentially to prevent the expansion of *Sclerotinia* hyphae. The transcriptome changes in *S. sclerotiorum* and host revealed that resistant *B. oleracea* produces strong responses against *S. sclerotiorum* during early infection.

来源: Phytopathology

发布日期:2019-03-12

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<http://agri.ckcest.cn/file1/M00/OE/7F/Csgk0F1eBgKABG6DABxbBdqDo3Q630.pdf>