



2022年第38期总361期

蔬菜育种专题

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➤ 前沿资讯

1. Researchers identify three genes involved in melon ripening - New research would allow the development of melon varieties with a longer shelf life, thus helping reduce food waste (西班牙研究人员确定控制甜瓜成熟的重要基因)

简介: 西班牙农业基因组学研究中心(CRAG)、西班牙农业食品研究与技术研究所(IRTA)和法国高等师范学院生物研究所(IBENS)进行了一项合作研究,发现了3个与甜瓜果实成熟有关的基因—— CmCTR1、CmROS1和CmNAC-NOR,并利用CRISPR/Cas9技术对其进行基因突变,确定了它们的重要作用。研究发现,通过抑制CmCTR1、CmROS1基因表达,可以加速果实成熟。在研究CmNAC-NOR功能过程中,研究人员获得了两个CRISPR/Cas9介导的突变体(nor-3和nor-1)。突变体nor-3可以成功将果实成熟延迟约8天而不影响果实质量,突变体nor-1则可以完全抑制果实成熟。这一发现揭示了甜瓜的成熟机制,有助于开发早熟甜瓜新品种,还可以延长甜瓜保质期,减少食物浪费。研究结果分别于6月10日和4月8日发表于《植物科学前沿》和《实验植物学杂志》。

来源: seedquest

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全文链接:

<http://agri.ckcest.cn/file1/M00/10/10/Csgk0GMii-iATogTAI OXnx bsk407.pdf>

➤ 学术文献

1. Assessment of Sclerotinia Stem and Leaf Rot Resistance and its Association with Physical Strength Attributes in Brassicaceae with Special Emphasis on Brassica Juncea (十字花科植物核盘菌茎叶腐病抗性评价及其与体力属性的关系研究)

简介: The Brassicaceae family includes many economically important species that are grown worldwide and used mainly for vegetable oils. Sclerotinia stem and leaf rot, caused by *Sclerotinia sclerotiorum*, is a devastating disease that affects many Brassicaceae species and threatens their long-term productivity and profitability. There are currently no genetic sources known to have a high level of resistance to this pathogen. In this study, 338 accessions from 13 cultivated and wild Brassicaceae species, including 266 accessions from *Brassica juncea*, were evaluated for *Sclerotinia* rot resistance and stem physical strength attributes. Large variation of resistance was found in Brassicaceae, with maximum differences of 23.08- and 8.25-folds in stem and leaf resistance, respectively. *B. juncea* IC 589660, *D. tenuisiliqua* and *S. alba* SA 1 showed high level of resistance to stem rot while *B. carinata* HC 0214, *B. juncea* IC 589660, *B. juncea* IC 491160, *B. juncea* IC 73231, and *B. juncea* IC 491463 exhibited high level of resistance to leaf rot. These accessions showed significantly lower disease scores than the resistant control. Among all the evaluated accession, *B. juncea* IC 589660 is the only genotype exhibited high resistance to both stem and leaf rot and could prove useful for *S. sclerotiorum* resistance breeding programs. The lack of association between leaf lesion

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size and stem lesion length revealed separate genetic regulation for stem vs leaf resistance. While, significant negative correlation detected between stem lesion length, and stem physical strength attributing traits indicated that stem physical strength-mediated resistance (SPSMR) factors were responsible for Sclerotinia stem rot resistance in Brassicaceae. Hard and woody stem is a prominent resistance factor that could be targeted in durable resistance breeding programs against stem rot. These findings pave the door for further research into the molecular basis of SPSMR's response to Sclerotinia stem rot in Brassica oilseeds and other hosts. Sclerotinia stem and leaf rot resistant accessions identified in this study will be of considerable benefit not only in increasing our understanding of resistance mechanisms across different Brassicaceae species, but also in generating resistant cultivars against Sclerotinia sclerotiorum.

来源: Journal of Plant Growth Regulation

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<http://agri.ckcest.cn/file1/M00/03/3E/Csgk0Yd5PDCAIUkfACAjjVhsobc887.pdf>

2. Establishment and Validation of Reference Genes of Brassica napus L. for Digital PCR Detection of Genetically Modified Canola (甘蓝型油菜转基因油菜数字PCR检测参考基因的建立与验证)

简介: As an effective tool for genetically modified organism (GMO) quantification in complex matrices, digital PCR (dPCR) has been widely used for the quantification of genetically modified(GM) canola events; however, little is known about the quantification of GM canola events using endogenous reference gene (ERG) characteristics by dPCR. To calculate and quantify the content of GM canola using endogenous reference gene (ERG) characteristics, the suitability of several ERGs of canola, such as cruciferin A (CruA), acetyl-CoA carboxylase (BnAcc), phosphoenolpyruvate carboxylase (PEP), cruciferin storage (BnC1), oleoyl hydrolase (Fat(A)), and high-mobility-group protein I/Y (HMG-I/Y), was investigated by droplet dPCR. BnAcc and BnC1 were more specific and stable in copy number in the genome of Brassica napus L. than the other genes. By performing intra-laboratory validation of the suitability of ERG characteristics for the quantification of GM canola events, the ddPCR methods for BnAcc and BnC1 were comprehensively demonstrated in dPCR assays. The methods could provide technical support for GM labeling regulations.

来源: Foods

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<http://agri.ckcest.cn/file1/M00/10/10/Csgk0GMiiPKAKkBAABcaK8zoQDc795.pdf>

3. Identification of Two Bacillus Strains with Antimicrobial Activity and Preliminary Evaluation of Their Biocontrol Efficiency (两种具有抗菌活性的芽孢杆菌菌株的鉴定及其生防效果初步评价)

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简介: Cabbage Fusarium Wilt (CFW) is a serious disease caused by *Fusarium oxysporum* f. sp. *conglutinans* in many parts of the world. The use of chemical fungicides has placed a heavy burden on the environment and is prone to drug resistance in plant pathogens. As a method with great potential, biological control has attracted the attention of many academics both at home and abroad. In this study, we have found that strains B5 and B6 had a strong inhibitory effect on various pathogens and significantly inhibited mycelium growth. They were both identified as *Bacillus velezensis* by morphological features, biochemical determinations, 16S rRNA gene and *gyrA* gene sequence analysis. When different concentrations of bacterial suspension were applied to cabbage seeds, hypocotyl and taproot length increased to varying degrees. The *in vivo* results showed that B5 and B6 decreased the incidence of cabbage seedling wilt disease, with B6 performing significantly better. Furthermore, *B. velezensis* B6 had the ability to colonize cabbage plants and rhizosphere soil. Thus, strain B6 has great potential for biocontrol development and this research could lead to the development of a promising biological agent for CFW.

来源: Horticulturae

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<http://agri.ckcest.cn/file1/M00/03/3E/Csgk0Yd50qeAaR7mAC9XqVM38RA658.pdf>

4. Interspecific Hybridization of Transgenic *Brassica napus* and *Brassica rapa*-An Overview (转基因油菜和油菜的种间杂交)

简介: In nature, interspecific hybridization occurs frequently and can contribute to the production of new species or the introgression of beneficial adaptive features between species. It has great potential in agricultural systems to boost the process of targeted crop improvement. In the advent of genetically modified (GM) crops, it has a disadvantage that it involves the transgene escaping to unintended plants, which could result in non-specific weedy crops. Several crop species in the *Brassica* genus have close kinship: canola (*Brassica napus*) is an ancestral hybrid of *B. rapa* and *B. oleracea* and mustard species such as *B. juncea*, *B. carinata*, and *B. nigra* share common genomes. Hence, intraspecific hybridization among the *Brassica* species is most common, especially between *B. napus* and *B. rapa*. In general, interspecific hybrids cause numerous genetic and phenotypic changes in the parental lines. Consequently, their fitness and reproductive ability are also highly varied. In this review, we discuss the interspecific hybridization and reciprocal hybridization studies of *B. napus* and *B. rapa* and their potential in the controlled environment. Further, we address the fate of transgenes (herbicide resistance) and their ability to transfer to their progenies or generations. This could help us to understand the environmental influence of interspecific hybrids and how to effectively manage their transgene escape in the future.

来源: Genes

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