



2022年第27期总60期

种质资源保护与创制专题

本期导读

▶ 前沿资讯

1. 蔬菜花卉所揭示低温下黄瓜种子萌发的调控机制
2. 菊苣、苦菊、牛蒡和雪莲果参考基因组发布
3. 专家揭示番茄黄曲叶病毒V3蛋白新功能

▶ 学术文献

1. 野生和栽培马铃薯的基因组进化和多样性
2. 美国马铃薯育种计划四十多年来选育的高级无性系的遗传多样性和群体结构
3. 利用根部内生真菌的生物活性改良甘蓝(甘蓝)
4. 特兰西瓦尼亚-罗马尼亚蔬菜遗传多样性保护

▶ 相关专利

1. 一种调控亚麻次生壁合成的LuNAC基因及其应用
2. 一种高效的农杆菌介导甘蔗遗传转化方法
3. 梨类纤维素合成酶基因PbrCSLD5及其应用

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▶ 前沿资讯

1. 蔬菜花卉所揭示低温下黄瓜种子萌发的调控机制

简介: 近日,中国农业科学院蔬菜花卉研究所葫芦科蔬菜遗传育种创新团队在低温胁迫黄瓜种子萌发研究方面取得重要进展。该研究团队克隆了调控低温下黄瓜种子萌发的基因CsGAI,并初步探究了该基因调控低温下种子萌发的网络途径。相关研究结果以“The qLTG1.1 candidate gene CsGAI regulates low temperature seed germination in cucumber”为题发表于国际著名植物学期刊Theoretical and Applied Genetics上。低温降低黄瓜种子发芽率,延缓发芽时间,但迄今为止尚未有黄瓜发芽期耐低温基因被克隆的报道。本研究利用近等基因系将主效位点qLTG1.1精细定位至46.3 kb的物理区间内,包含三个基因;通过序列比对和表达分析确定Csa1G408720为候选基因,该基因为GRAS基因家族的DELLA转录因子GAI,命名为CsGAI;亚细胞定位结果表明该基因位于细胞核;启动子和GUS染色表达分析表明,启动子活性越高,CsGAI基因的转录水平越高;内外源激素GA和ABA含量分析及生物合成代谢途径基因表达等研究表明,CsGAI通过GA和ABA信号途径调控低温下种子萌发。综上,该研究首次克隆了调控低温下黄瓜种子萌发的基因CsGAI,初步解析了该基因通过GA和ABA途径调控低温下黄瓜种子萌发的网络途径。该论文以中国农业科学院蔬菜花卉研究所为第一和通讯作者单位,李彩霞博士研究生为第一作者,董邵云博士为共同一作,顾兴芳研究员和张圣平研究员为共同通讯作者。该研究受到国家自然科学基金、现代农业产业技术体系、中国农业科学院创新工程等项目资助。

原文链接: <https://link.springer.com/article/10.1007/s00122-022-04097-w>

来源: 黄瓜遗传育种课题组 董邵云

发布日期:2022-07-08

全文链接:

<https://ivf.caas.cn/xwdt/kyjz/b11b5abc93284a1c947b3d48bd910411.htm>

2. 菊苣、苦菊、牛蒡和雪莲果参考基因组发布

简介: 近日,中国农业科学院深圳农业基因组研究所农业宏(育种)基因组学创新团队发布了菊苣、苦菊、雪莲果参考基因组,更新了牛蒡基因组,明确了这些物种的分歧时间和近期多倍化事件,对推动菊科植物基因组学基础研究、进一步解析果聚糖代谢分子调控网络具有重要意义,相关成果发表在《分子生态资源(Molecular Ecology Resources)》。果聚糖是菊科植物的重要储能物质,果聚糖不能被人体消化吸收,却能被肠道益生菌利用,常被广泛用作甜味剂、膳食纤维和益生菌等,市场前景广阔。然而,由于缺乏菊科植物的基因组数据资源,对果聚糖代谢基因与调控机制的了解还不深入。研究团队利用PacBio CCS (HiFi) 三代测序、自主开发的scaffolding工具EndHiC等技术构建了菊苣、苦菊、牛蒡、雪莲果染色体水平参考基因组。发现果聚糖代谢酶基因在菊苣、苦菊和牛蒡基因组中为单拷贝,而在雪莲果基因组存在两个拷贝,这与雪莲果特有的全基因组复制(WGD-3)相关。果聚糖聚合度差异主要取决于1-FFT酶的底物选择性,预测1-FFT酶蛋白空间结构并比较种间差异,确定了催化转移反应的关键活性位点,探讨了果聚糖聚合度的影响因素和调控机制。该研究进一步解析雪莲果特有的近期基因组多倍化时间和方式,并揭示影响植物果聚糖聚合度与产量的关键基因及其表达调控机制,为菊科植物的育种提供科学支持。该研究得到中国农业科学院科技创新工

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程、深圳市重点实验室基金等项目的资助。

原文链接: <https://onlinelibrary.wiley.com/doi/abs/10.1111/1755-0998.13675>

来源: 中国农业科学院深圳农业基因组研究所

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全文链接:

<https://www.caas.cn/xwzx/kyjz/321745.html>

3. 专家揭示番茄黄曲叶病毒V3蛋白新功能

简介: 近日, 中国农业科学院植物保护研究所作物病原生物功能基因组研究创新团队, 揭示了番茄黄曲叶病毒编码的新蛋白V3, 可以沿着细胞质内的微丝到达胞间连丝, 并促进病毒在细胞间的移动。相关研究成果发表在《中国科学-生命科学 (Science China-Life Sciences)》。双生病毒是一类世界范围内广泛发生的单链环状DNA病毒, 已在全球粮食和经济作物上造成严重危害。番茄黄化曲叶病毒是双生病毒科中的代表种, 是番茄危害最严重的病毒。该团队的前期研究发现, 双生病毒基因组编码大量具备特殊细胞器定位的小蛋白, 其中番茄黄化曲叶病毒编码的新基因V3为定位于高尔基体, 为RNA沉默抑制子。深入研究表明, V3具备胞间连丝定位, 通过使用微丝标记及相关抑制剂发现, V3在细胞质内沿着微丝高速运动, 并可以促进病毒在细胞间的移动, 具备运动蛋白的一系列特征, V3是促进双生病毒进行细胞间运动的新蛋白。该研究拓展了对双生病毒运动机制的认知。该研究得到国家自然科学基金等项目的资助。

原文链接: <https://link.springer.com/article/10.1007/s11427-021-2063-4>

来源: 中国农业科学院植物保护研究所

发布日期:2022-06-29

全文链接:

<https://www.caas.cn/xwzx/kyjz/321510.html>

学术文献

1. Genome evolution and diversity of wild and cultivated potatoes (野生和栽培马铃薯的基因组进化和多样性)

简介: Potato (*Solanum tuberosum* L.) is the world's most important non-cereal food crop, and the vast majority of commercially grown cultivars are highly heterozygous tetraploids. Advances in diploid hybrid breeding based on true seeds have the potential to revolutionize future potato breeding and production^{1,2,3,4}. So far, relatively few studies have examined the genome evolution and diversity of wild and cultivated landrace potatoes, which limits the application of their diversity in potato breeding. Here we assemble 44 high-quality diploid potato genomes from 24 wild and 20 cultivated accessions that are representative of *Solanum* section *Petota*, the tuber-bearing clade, as well as 2 genomes from the neighbouring section, *Etuberosum*. Extensive discordance of phylogenomic relationships suggests the complexity of potato evolution. We find that the potato genome substantially expanded its repertoire of disease-resistance genes when compared with closely related seed-propagated solanaceous crops, indicative of the effect of tuber-based propagation strategies on the evolution of the

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potato genome. We discover a transcription factor that determines tuber identity and interacts with the mobile tuberization inductive signal SP6A. We also identify 561,433 high-confidence structural variants and construct a map of large inversions, which provides insights for improving inbred lines and precluding potential linkage drag, as exemplified by a 5.8-Mb inversion that is associated with carotenoid content in tubers. This study will accelerate hybrid potato breeding and enrich our understanding of the evolution and biology of potato as a global staple food crop.

来源: nature

发布日期:2022-06-08

全文链接:

http://agri.ckcest.cn/file1/M00/10/0A/Csgk0GLY_ryAJ1wqANnf8019XX4009.pdf

2. Genetic diversity and population structure of advanced clones selected over forty years by a potato breeding program in the USA (美国马铃薯育种计划四十多年来选育的高级无性系的遗传多样性和群体结构)

简介: Knowledge regarding genetic diversity and population structure of breeding materials is essential for crop improvement. The Texas A&M University Potato Breeding Program has a collection of advanced clones selected and maintained in-vitro over a 40-year period. Little is known about its genetic makeup and usefulness for the current breeding program. In this study, 214 potato clones were genotyped with the Infinium Illumina 22 K V3 Potato Array. After filtering, a total of 10,106 single nucleotide polymorphic (SNP) markers were used for analysis. Heterozygosity varied by SNP, with an overall average of 0.59. Three groups of tetraploid clones primarily based on potato market classes, were detected using STRUCTURE software and confirmed by discriminant analysis of principal components. The highest coefficient of differentiation observed between the groups was 0.14. Signatures of selection were uncovered in genes controlling potato flesh and skin color, length of plant cycle and tuberization, and carbohydrate metabolism. A core set of 43 clones was obtained using Core Hunter 3 to develop a sub-collection that retains similar genetic diversity as the whole population, minimize redundancies, and facilitates long-term conservation of genetic resources. The comprehensive molecular characterization of our breeding clone bank collection contributes to understanding the genetic diversity of existing potato resources. This analysis could be applied to other breeding programs and assist in the selection of parents, fingerprinting, protection, and management of the breeding collections.

来源: Scientific Reports

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全文链接:

<http://agri.ckcest.cn/file1/M00/10/0A/Csgk0GLZAJ6AHVqsADyJV3k9LBc483.pdf>

3. Brassica oleracea var. acephala (kale) improvement by biological activity of root endophytic fungi (利用根部内生真菌的生物活性改良甘蓝(甘蓝))

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简介: Brassica oleracea var. acephala (kale) is a cruciferous vegetable widely cultivated for its leaves and flower buds in Atlantic Europe and the Mediterranean area, being a food of great interest as a "superfood" today. Little has been studied about the diversity of endophytic fungi in the Brassica genus, and there are no studies regarding kale. In this study, we made a survey of the diversity of endophytic fungi present in the roots of six different Galician kale local populations. In addition, we investigated whether the presence of endophytes in the roots was beneficial to the plants in terms of growth, cold tolerance, or resistance to bacteria and insects. The fungal isolates obtained belonged to 33 different taxa. Among those, a Fusarium sp. and Pleosporales sp. A between Setophoma and Edenia (called as Setophoma/Edenia) were present in many plants of all five local populations, being possible components of a core kale microbiome. For the first time, several interactions between endophytic fungus and Brassica plants are described and is proved how different interactions are beneficial for the plant. Fusarium sp. and Pleosporales sp. B close to Pyrenophora (called as Pyrenophora) promoted plant growth and increased cold tolerance. On the other hand, isolates of Trichoderma sp., Pleosporales sp. C close to Phialocephala (called as Phialocephala), Fusarium sp., Curvularia sp., Setophoma/Edenia and Acrocalymma sp. were able to activate plant systemic resistance against the bacterial pathogen Xanthomonas campestris. We also observed that Fusarium sp., Curvularia sp. and Setophoma/Edenia conferred resistance against Mamestra brassicae larvae.

来源: Scientific Reports

发布日期: 2020-11-19

全文链接:

http://agri.ckcest.cn/file1/M00/03/38/Csgk0YcvsveAPvBdABi40dyuj_g519.pdf

4. Conservation of vegetable genetic diversity in Transylvania-Romania (特兰西瓦尼亚-罗马尼亚蔬菜遗传多样性保护)

简介: The conservation of plant and animal genetic heritage is not a purpose in itself, but it represents the sine qua non condition for practicing a sustainable agriculture and to ensure nutrition and food security on long-term. Our research focused on identifying the areas with the richest genetic diversity of vegetables in Transylvania, Romania, as well as the main vulnerabilities related to seed production for the local vegetables. Our trips included 210 locations where 338 small seed producers were surveyed. The questionnaire method with fixed questions and undisguised multiple-choices was used. A number of 316 out of 565 cultivars taken into study have been proven to be authentic and valuable landraces, meaning 55.9%. In Transylvania, the richest genetic diversity of vegetables is found in the counties of Maramures, Bistrita-Nasaud and Hunedoara—where the cooperativization was lower before the year 1989. The most important risk in losing vegetable landraces is the old age of small growers (68.4%). However, it is encouraging that many NGOs interested in identifying, conserving and promoting local varieties have emerged in the last decade. Therefore, so-called "seed houses" have been set up to facilitate the exchange of seeds, and on the other hand, the expansion of organic farming requires local varieties that are better adapted to harsh

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environmental conditions.

来源: Scientific Reports

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全文链接:

<http://agri.ckcest.cn/file1/M00/03/38/Csgk0YcvS-JqAHBCxABFmpZsCKiw549.pdf>

➤ 相关专利

1. 一种调控亚麻次生壁合成的LuNAC基因及其应用

简介: 本发明提供了一种调控亚麻次生壁合成的LuNAC基因及其应用。本发明采用病毒诱导的基因沉默技术,通过农杆菌介导法获得LuNAC基因沉默亚麻株系SE。LuNAC转录因子通过调控下游LuMyb42、LuMyb46、LuMyb69、LuMyb103、LuNST1、LuNST3、LuNAC12及LuNAC73纤维细胞次生壁合成的二级开关转录因子,及纤维素、半纤维素及木质素合成关键酶基因LuCesA4、LuCesA8B、LuCslA1、LuCslG3.2、LuCCoAOMT、LuCOMT的表达,进而实现对细胞壁组分纤维素、半纤维素及木质素合成的调控。本发明为改良亚麻纤维品质的分子育种提供了重要基因资源。

来源: 佰腾网

发布日期: 2022-04-15

全文链接:

<http://agri.ckcest.cn/file1/M00/03/38/Csgk0YcvuLKAN5ISAAg42YQZUx4075.PDF>

2. 一种高效的农杆菌介导甘蔗遗传转化方法

简介: 本发明是一种高效的农杆菌介导甘蔗遗传转化方法,其以甘蔗的茎顶端的幼嫩的轮生叶片作为外植体,诱导其产生高质量的胚性愈伤组织,以优质的胚性愈伤组织作为农杆菌侵染的受体材料。侵染过程中通过纤维素酶R-10、离析酶R-10和果胶酶Y-23消化部分植物的细胞壁,并将侵染的条件设置在28℃黑暗培养7-10天,提高转化的效率。经过20-40天的0.01-0.1%的除草剂抗性培养后,再进行分化培养,获得抗性转化植株后移栽。本发明是一项可以高效获得转基因甘蔗植株的转化方法,实验成本低,方法简单。

来源: 佰腾网

发布日期: 2022-02-18

全文链接:

http://agri.ckcest.cn/file1/M00/03/38/Csgk0YcvtS-AXWoAAAS_9Nh6yZk028.PDF

3. 梨类纤维素合成酶基因PbrCSLD5及其应用

简介: 本发明公开一种梨类纤维素合成酶基因PbrCSLD5及其应用,该基因具有如SEQ ID No. 1所示的核苷酸序列。通过农杆菌介导遗传转化方法在拟南芥中过表达PbrCSLD5基因,获得转基因植株,经生物学功能验证,表明本发明克隆的PbrCSLD5基因具有调控梨花粉管细胞壁纤维素合成的作用。

来源: 佰腾网

发布日期: 2021-10-22

全文链接:

<http://agri.ckcest.cn/file1/M00/10/0A/Csgk0GLZA4iABibFAAt3WoRusls610.PDF>

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