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2022年9月2日

前沿资讯

1．园艺学院陈日远课题组在Journal of Integrative Plant Biology发表研究论文

简介：近日，我校园艺学院陈日远团队在国际知名学术期刊Journal of Integrative Plant Biology上发表了题为“The SlTPL3SlWUS Module Regulates Multi-locule Formation in Tomato by Modulating Auxin and Gibberellin Levels in the Shoot Apical Meristem”（全文链接：https://doi.org/10.1111/jipb.13347）的研究论文。畸形果是果菜类蔬菜中常见的一种现象，严重影响果实的外观品质和食用价值。番茄的心室数是影响果实大小性状和畸形果发生率的重要因素，心室数越多，果实越大，畸形果发生率越高。心室的形成与茎尖分生组织的分化与维持密切相关，然而，目前对茎尖分生组织的发育与多心室形成的关系认知仍有很多不足。该研究发现番茄中的TOPLESS转录共抑制子SlTPL3是一个调控茎尖大小的基因，SlTPL3基因的沉默导致茎尖分生组织变大，果实心室数量增加，果实变大。外源IAA以及GA合成抑制剂PAC处理恢复了SlTPL3RNAi植株多心室的表型。SlTPL3定位于细胞核并与转录因子SlWUS互作，SlTPL3和SlWUS蛋白的相互作用增强了SlWUS对下游靶基因SlPIN3、SlGA2ox1的抑制和激活作用。因此，SlTPL3-SlWUS模块通过调控SlPIN3和SlGA2ox1介导IAA分布和GA水平来维持SAM的大小。该结果揭示了SlTPL3-SlWUS作为维持SAM大小的关键调控因子在多心室形成的过程中发挥重要功能，为多心室形成的机制提供了新见解，具有重要意义。　　我校园艺学院宋世威教授为本论文的第一作者，郝彦伟副研究员为通讯作者。我校陈日远教授，法国图卢兹大学Mondher Bouzayen教授、Mohammed Zouine 副教授和胡国建博士对该研究给予了大力支持。我校毕业硕士生黄彬彬和潘赞霖进行了具体的试验研究。该研究得到了国家自然科学基金、广东省自然科学基金以及广州市科技计划项目的资助。

来源：华南农业大学园艺学院

发布日期:2022-08-30

全文链接:

https://www.scau.edu.cn/2022/0830/c11310a322446/page.htm

2．华中农业大学应用真菌团队在香菇镉耐受性分化机制研究中取得进展

简介：8月24日，我校植物科学技术学院边银丙教授领衔的应用真菌团队在国际学术期刊Journal of Hazardous Materials上在线发表了题为“Molecular mechanism underlying cadmium tolerance differentiation in Lentinula edodes as revealed by mRNA and milRNA analyses”的研究论文。该研究使用mRNA和milRNA联合分析的方法解析了香菇镉耐受性分化的分子机制，并验证了α淀粉酶基因LeAmy在增强香菇镉耐受性中的作用，为选育适宜于重金属修复的香菇优良品种奠定了重要的理论基础，这也是milRNA调控大型真菌镉耐受性的首次报道。生物重金属耐受能力和生物修复能力具有重要的研究价值，香菇不同菌株间镉耐受能力存在显著差异。香菇对重金属镉耐受性分化研究对耐基质镉污染的优良品种选育，以及利用香菇菌渣进行环境镉污染修复，都具有重要的科学意义。研究团队通过mRNA和milRNA联合分析揭示了香菇镉耐受性分化的分子机制，细胞壁重塑、转运、重金属螯合、脂质和碳水化合物代谢、转录调控、氧化还原稳态、蛋白水解、信号转导、DNA修复和细胞周期相关的基因及milRNA的差异表达调

控导致了菌株间的镉耐受性分化，进一步建立了香菇镉耐受性分化的分子机制模型。研究团队还通过遗传转化验证了重要候选基因LeAmy的生物学功能。过表达LeAmy基因，镉敏感菌株YS45的镉耐受能力显著提升，且在镉处理条件下产生的蛋白聚集体明显减少，而脂滴数量增加。结果表明LeAmy基因可增强香菇镉耐受能力，碳水化合物及脂质代谢、蛋白水解等生物学过程可影响香菇镉耐受能力。博士生沈楠和硕士生徐晨杰为论文共同第一作者，肖扬副教授为通讯作者。相关研究获得了国家自然科学基金、国家食用菌产业技术体系和湖北省食用菌产业技术体系等项目的资助。通讯作者肖扬副教授一直从事香菇等食用菌的遗传研究，近年来在Journal of Hazardous Materials，Journal of Advanced Research，Computational and Structural Biotechnology Journal，Journal of Fungi，Scientia Horticulturae 等学术期刊发表了一系列研究成果。

来源：华中农业大学植物科学技术学院

发布日期:2022-08-26

全文链接:

http://news.hzau.edu.cn/2022/0826/64280.shtml

3．大豆种质资源组学数据库SoyFGBv2.0搭建完成

简介：近日，中国农业科学院作物科学研究所的水稻分子设计技术与应用创新团队和大豆优异基因资源发掘与创新利用团队联手，升级功能基因组育种FGB（Functional Genomics Breeding）数据共享模式，联合搭建大豆代表性种质组学数据库，为将我国大豆种质资源优势转变为基因资源优势和品种优势提供重要信息平台和挖掘工具。相关研究成果发表在《科学通报(Science Bulletin)》。种质资源是作物育种的重要物质基础，是国家战略性资源。大豆起源于中国，我国大豆种质资源在世界上最为丰富。在这个组学时代，海量多组学数据不断产生，如何充分共享组学数据是一直困扰着大豆种质资源工作者的重要问题。该研究团队在《中国科学生命科学（SCIENCE CHINA Life Science）》发表的代表性大豆种质资源重测序和表型数据基础上，采用自主创立的FGB共享模式开展数据平台搭建工作。该模式于2015年发布在《科学通报》，首次应用于3000份水稻测序种质RFGB数据库的构建，并于2020年完成首度升级。针对大豆在基因组和种质资源等方面的特点及用户需求差异，研究团队通过FGB共享模式的再次升级与拓展，建立了SoyFGB v2.0数据平台。SoyFGB v2.0数据平台的特点主要表现在以下3个方面。一是提供离散值的表型数据来帮助用户识别用于育种或遗传研究的“有用”种质资源，实现了2K-SG的33个数量性状与9个质量性状的非下载共享。二是用户可以利用SoyFGB或用户自有的未公开表型数据来实现表型和单倍型变异的相关性在不同基因组分辨率下的在线解析。三是一旦获得基因组作图定位与表型性状相关区域，使用 “搜索”和“浏览”模块，用户可以获取2K-SG 的基因组变异，用于实验验证。根据用户实际体验，与传统Excel表格辅助进行单倍型分析相比，采用SoyFGBv2.0进行特定基因的单倍型分析能够提高效率近60倍。该研究得到国家重点研发计划、国家自然科学基金、中国农业科学院科技创新工程等项目的资助。

来源：中国农业科学院作物科学研究所

发布日期:2022-08-26

全文链接:

https://www.caas.cn/xwzx/kyjz/322396.html

4．黄巍教授团队发现生物钟调控植物细胞自噬节律的新机制

简介：近日，我校生命科学学院、亚热带农业生物资源保护与利用国家重点实验室和岭南现代农业科学与技术广东省实验室黄巍教授团队在Journal of Integrative Plant Biology（影响因子9.1，生物1区）发表了题为“The plant circadian clock regulates autophagy rhythm through LUX ARRHYTHMO”的研究论文。 细胞自噬是真核生物中高度保守的物质稳态机制，通过降解错误折叠的蛋白质和受损的细胞器，实现对营养物质的循环再利用。近年来，越来越多研究表明在动物中自噬途径与生物钟存在着紧密的相互调节的关系。多个生物钟转录因子能够直接调控动物自噬基因的昼夜表达水平，而动物中自噬途径也能够降解生物钟的核心组分从而反馈影响近日节律及其输出途径。然而植物自噬节律与生物钟的调控关系和分子机制仍然不明确。 该研究发现拟南芥细胞自噬在12 h光照/12 h黑暗（LD）条件下和持续光照（LL）条件下都呈现明显的近日节律变化，说明植物自噬过程受生物钟调控。有意思的是，LL条件和LD条件下相比，自噬节律的表达相位大幅提前，但振幅明显降低。进一步研究发现，植物生物钟关键组分LUX基因的突变导致自噬在LL条件下的节律消失，在LD条件下的昼夜振幅显著增强。并且LUX能够直接结合自噬基因ATG2、ATG8a、和ATG11的启动子，并抑制其转录活性。表型分析发现LUX通过维持适度的自噬活性提高了植物对碳饥饿的耐受性。转录组分析发现自噬节律性在不同植物中都广泛存在，说明生物钟调控自噬节律在植物中是一种保守的机制。最近湖南大学于峰课题组发现生物钟基因TOC1在调控植物自噬节律同意发挥着重要作用(Chen et al., 2022)，说明生物钟通过多条途径调控植物自噬节律。华南农业大学博士生杨明康为本文的第一作者，黄巍教授和陈亮副教授为共同通讯作者。中山大学肖仕教授和德国马普学会分子植物生理研究所Bernd Mueller-Roeber教授参与了本研究工作。中科院植物所王雷研究员为本研究提供了实验材料。本研究取得了岭南现代农业实验室项目、广东省重点领域研发计划项目、广东省自然科学基金、广州市科技项目的资助。

来源：华南农业大学生命科学学院

发布日期:2022-08-18

全文链接:

https://www.scau.edu.cn/2022/0818/c11310a321915/page.htm

学术文献

1．A Review: Agrobacterium-mediated gene transformation to increase plant productivity（农杆菌介导的基因转化提高植物生产力的研究进展）

简介：In genetics and molecular biology, Gene transformation is a gene alteration technique that involves the introduction and expression of a foreign gene into the host organism. There are many gene transformation methods like particle bombardment, electroporation, micro-injection, PEG for different biotechnological experiments. But Plant gene transformation is a widely used procedure for obtaining transgenic plants and plant models to understand gene functions. Agrobacterium tumefaciens is a natural genetic engineer which is rod-shaped, gram-negative soil-born bacteria. Initially, Agrobacterium was utilized to transform only dicot plants but over the year’s modification in plant transformation protocol

it was now utilized in monocot plants as well as in fruits plants too. Agrobacterium tumefaciens inserts its DNA (Transfer DNA-T-DNA) into the host plant. The transmitted DNA is randomly integrated into the host cell's genetic material inside the infected plant cell nucleus. Alternatively, bacterial DNA cantransiently remain in the nucleus without integrating into the genome, but it still replicates alongside the plant genome, using its machinery and expressing its genes to make separate gene products. Besides the traditional method, new research has also been done to transform the plants through agrobacterium. Various methods have been developed to transform monocotyledonous plants such as wheat, maize, rice,and fruity plants. Generally, dicotyledonous plants can be transformed by the traditional method of agrobacterium but various methods have also been developed for dicots for various applications. Here,we have taken an example of a tobacco plant (nicotiana tabacum) transformed with different methods.

来源： The Journal of Phytopharmacology
发布日期: 2022-02-11
全文链接:
http://agri.ckcest.cn/file1/M00/10/0E/CsgkOGMRoE2ABkVeAAZNtVwBuYs617.pdf

2．Optimization of Agrobacterium-mediated transformation and regeneration for CRISPR/Cas9 genome editing of commercial tomato cultivars（农杆菌介导的商业番茄CRISPR/Cas9基因组编辑转化和再生的优化）

简介： Tomato (Solanum lycopersicum) is the second most important horticultural crop worldwide that is widely used as a model plant in genetic manipulation of Solanaceae. CRISPR/Cas9 system has been successfully utilized in several studies for genome edition of model tomato cultivars. However, these genome editing systems should be also optimized for commercial tomato cultivar for direct application of genome editing in field conditions. In this study, we have optimized an Agrobacterium-mediated gene transfer and regeneration system for CRISPR/Cas9 genome editing in two commercial tomato cultivars for the first time. The effect of explant type, genotype, pre-transformation time, Agrobacterium concentration, infection time, and different co-culture periods of bacteria were evaluated to optimize the regeneration and transformation parameters. The highest regeneration capacity of 83% was obtained from cotyledons of Crocker incubated in a medium supplemented with BA (3 mg/L) and IAA (0.1 mg/L). The maximum transformation frequency was obtained by using the following parameters: cotyledon explants of commercial Crocker cultivar that were left for 2 days of pre-transformation incubation, infected with Agrobacterium for 10 min at a concentration of OD600 of 0.6 and co-cultivated with Agrobacterium cells for 48 h. CRISPR/Cas9 system was tested with two gRNAs targeting the phytoene desaturase gene. Fully albino and chimeric plants were successfully produced with optimized transformation and culture conditions in up to 71% of all regenerated plants. In the current study, we optimized the implementation of the CRISPR/Cas9 technique in a commercial tomato cultivar and our method will enable breeders to make necessary changes in traits of interest to improve tomato crops for commercial applications.

来源：Turkish Journal of Agriculture and Forestry
发布日期:2021-12-16
全文链接:
http://agri.ckcest.cn/file1/M00/10/0E/CsgkOGMRnt2Ab-zEADBHAvDPFDo671.pdf

3．Modeling Agrobacterium-Mediated Gene Transformation of Tobacco (Nicotiana tabacum)—A Model Plant for Gene Transformation Studies(烟草（Nicotiana tabacum）的农杆菌介导基因转化模型——基因转化研究的模式植物?
)

简介：The multilayer perceptron (MLP) topology of an artificial neural network (ANN) was applied to create two predictor models in Agrobacterium-mediated gene transformation of tobacco. Agrobacterium-mediated transformation parameters, including Agrobacterium strain, Agrobacterium cell density, acetosyringone concentration, and inoculation duration, were assigned as inputs for ANNMLP, and their effects on the percentage of putative and PCR-verified transgenic plants were investigated. The best ANN models for predicting the percentage of putative and PCR-verified transgenic plants were selected based on basic network quality statistics. Ex-post error calculations of the relative approximation error (RAE), the mean absolute error (MAE), the root mean square error (RMS), and the mean absolute percentage error (MAPE) demonstrated the prediction quality of the developed models when compared to stepwise multiple regression. Moreover, significant correlations between the ANN-predicted and the actual values of the percentage of putative transgenes (R2 = 0.956) and the percentage of PCR-verified transgenic plants (R2 = 0.671) indicate the superiority of the established ANN models over the classical stepwise multiple regression in predicting the percentage of putative (R2 = 0.313) and PCR-verified (R2= 0.213) transgenic plants. The best combination of the multiple inputs analyzed in this investigation, to achieve maximum actual and predicted transgenic plants, was at OD600 = 0.8 for the LB4404 strain of Agrobacterium × 300 μmol/L acetosyringone × 20 min immersion time. According to the sensitivity analysis of ANN models, the Agrobacterium strain was the most important influential parameter in Agrobacterium-mediated transformation of tobacco. The prediction efficiency of the developed model was confirmed by the data series of Agrobacterium-mediated transformation of an important medicinal plant with low transformation efficiency. The results of this study are pivotal to model and predict the transformation of other important Agrobacterium-recalcitrant plant genotypes and to increase the transformation efficiency by identifying critical parameters. This approach can substantially reduce the time and cost required to optimize multi-factorial Agrobacterium-mediated transformation strategies.
来源：Frontiers in Plant Science
发布日期:2021-07-23
全文链接:
http://agri.ckcest.cn/file1/M00/03/3C/CsgkOYdoUHKAc3j7ACKIS1OPXCs152.pdf

4．Development of an efcient in?planta Agrobacterium?mediated transformation method for Iranian purslane (Portulaca oleracea L.)using sonication and vacuum infltration(利用超声波和真空注入技术，为伊朗马齿苋（Portulaca oleracea L.）开发一种高效的植物内农杆菌介导的转化方法)

简介：Purslane (Portulaca oleracea L.), a valuable medicinal herb, is used as a source of pharmaceutical components such as favonoids, alkaloids, fatty acids, terpenoids, and sterols. Regeneration of transgenic purslane plantlets from transformed cells is a time-consuming procedure and needs hard work. In this study, in-planta transformation of purslane, using sonicationand vacuum infltration, is reported. The purslane seeds were infected through Agrobacterium tumefaciens strain LBA4404 having the uidA gene on pBI121 vector. Efective selection of transformants was performed by supplementing MS media with 250 mg l?1 kanamycin. Several factors afecting the in-planta procedure including pre-culture duration, acetosyringone dose, sonication, and vacuum infltration duration were investigated. The results demonstrated that the highest number of GUS-positive purslane plantlets was obtained when the pre-cultured seeds were sonicated and vacuum-infltered for 2 min in agro-bacterial cell suspension, and then co-cultivated in MS media having 100 μM acetosyringone. The integration and expression of uidA gene in transgenic purslane was successfully corroborated by southern blot and GUS histochemical analyses.

来源：Acta Physiologiae Plantarum

发布日期:2021-01-12

全文链接:

http://agri.ckcest.cn/file1/M00/03/3C/CsgkOYdoTsOAH9nbABB2bqMLz1w547.pdf

相关专利

1．番茄miR482基因在控制植物分枝上的应用方法

简介：本发明公开了番茄miR482基因在控制植物分枝中的应用方法，该方法是利用miR482前体序列以及pLP-35S载体来构建番茄miR482基因的超表达载体，然后通过农杆菌介导法转化番茄植株，番茄miR482基因调控植株分枝发育；所述miR482前体序列的核苷酸序列如SEQ ID NO.1所示。该方法能够控制miR482的表达，使植物分枝明显增多。

来源：佰腾网

发布日期:2021-07-16

全文链接:

http://agri.ckcest.cn/file1/M00/03/3D/CsgkOYdsSUeAL3g-AAv87_f_eYc116.pdf

2．一种农杆菌介导的番茄遗传转化方法

简介：本发明涉及植物基因工程技术领域，提供了一种农杆菌介导的番茄遗传转化方法。所述方法具体包括：无菌番茄叶片外植体的获得；农杆菌侵染叶片外植体；外植体的抗性筛选；外植体的继代培养；外植体的生根培养；转基因植株的移土培养；本发明方法简化了遗传转化的程序，整体过程较为简单，有效地缩短了转化周期；使得转基因后代

遗传趋于稳定，操作简单，外源基因得到了表达水平明显提升，使得转化效率大大提高。
来源：佰腾网
发布日期:2020-10-30
全文链接:
http://agri.ckcest.cn/file1/M00/10/0F/CsgkOGMVmT2AUzJOAApe-qEyAgw239.pdf

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