



2018年第45期总105期

农业生物技术专题

本期导读

▶ 前沿资讯

1. 阿根廷修改微生物技术监管法规 促进新型农业投入品发展
2. IHARA生物农药获得登记 开创巴西采后生物防治先河
3. CRISPR新工具开辟更多可编辑基因组位点

▶ 学术文献

1. 通过中介复合物23调控印迹细胞的终末成熟
2. 氮相关代谢和生长的转录调节

中国农业科学院农业信息研究所

联系人：邹婉侬

联系电话：010-82109850

邮箱：agri@ckcest.cn

2018年11月5日

▶ 前沿资讯

1. 阿根廷修改微生物技术监管法规 促进新型农业投入品发展

简介: 阿根廷政府农业部秘书处近期修改了微生物技术监管法案，增加了针对转基因微生物的监管条款。该法规公布在了政府官方公报上。修改法规的目的在于促进新型农业投入品的发展，加强对微生物技术的监管。该法规确保在田间、温室、生物安全箱内开展的转基因微生物试验处于可控条件下，优化试验程序。食品和生物经济秘书处已开始执行。此前1992年的法案仅针对作为兽用疫苗使用的微生物进行了监管。而目前法案的监管对象覆盖了所有用于农业的DNA重组微生物。因此该法案涉及大量科技前沿和新的应用，以及二十多年来积累的该技术领域的管理经验。此外，还需要为农资产品简化不必要的程序，并且去除官僚化。“这次修改法案将会通过提高生产力和生产的可持续性，工业发展将会带动农业附加的提升，进而促进新生物制品的研发。新法规更加清晰，更具有针对性，所要求的信息能够用以开展高效科学的评估。这次修改法案还扩大并优化了此前的监管程序，” 阿根廷政府表示。“我们生物技术法律体系中的旧法规以此获得了更新，通过良好监管新生物技术的试验和安全使用，有利于生产力的提高，” 农业部秘书处总结道。

来源: 食品资讯中心网

发布日期:2018-10-23

全文链接:

<http://news.foodmate.net/2018/10/489642.html>

2. Brazil gains its first biopesticide from IHARA for post-harvest application (IHARA生物农药获得登记 开创巴西采后生物防治先河)

简介: IHARA, a company specializing in crop protection technologies, has just gained the country's first register for use of a post-harvest biopesticide. Launched in 2017 for pre-harvest uses, Eco-shot biofungicide will now help to protect the quality and value of farmers' production even after the products have left the field. About 45 percent of fruit and vegetable production is lost worldwide, according to estimates by the United Nations Food and Agriculture Organization. Of this total, 40 percent of the losses occur after harvest. "Every link in the chain loses with waste and loss of quality, but this is mainly reflected in the price paid to the grower", says the manager of IHARA's Biological Products, Mauricio Hideki Ouchi. "By protecting the quality of production before and after harvest, Eco-shot is also protecting the farmer's profit," he explains. The fact that Brazil has a biological product to avoid the proliferation of fungi after harvest has strategic implications for the domestic market and for exports. The use of fungicides after harvest raises the shelf life of the food before it deteriorates, which is extremely important so that the product can face the long journeys to the importing countries. However, importing countries follow strict standards of maximum residue limits of chemical pesticides in food. As it is a biofungicide, Eco-shot does not face these restrictions, which opens up new possibilities for Brazil to meet external markets. This potential is enormous, especially in the fruit segment. Though it is the third major global fruit producer, Brazil is the 23rd country in the export ranking of these products, sending abroad only 2.5% of the volume produced, according to the data from

Brazilian Association of Producers Exporting Fruit and Vegetables (Abrafrutas). "Phytosanitary barriers are one of the main impediments for Brazil to improve its position on this list, therefore it is so important to have a registered biofungicide for the post-harvest," says Hideki.

来源: AgroNews

发布日期: 2018-10-29

全文链接:

<http://news.agropages.com/News/NewsDetail---28195.htm>

3. CRISPR新工具开辟更多可编辑基因组位点

简介: 据最新一期《科学进展》报道, 美国麻省理工学院 (MIT) 研究人员发现了一种可靶向几乎一半基因组位点的Cas9酶, 从而极大地扩展了基因编辑工具的适用范围。尽管基因编辑工具近年来取得了相当大的成功, 但CRISPR-Cas9在基因组上可访问的位点数量仍然有限。这是因为CRISPR需要在基因组靶向位点侧翼的一段特定序列——原型间隔区相邻基序 (PAM) 来识别该位点。最广泛使用的Cas9酶——化脓性链球菌Cas9, 需要两个G核苷酸作为其PAM序列, 这极大地限制了其可靶向的位点数量 (约占基因组上9.9%的位点)。MIT分子机器研究小组负责人约瑟夫·雅各布森教授表示, CRISPR就像一个非常准确和高效的邮政系统, 只要邮政编码以零结尾, 就可以精确到达想要去的任何地方。但正因为其非常准确和具体, 也限制了可以去到的地点数量。为了开发更通用的CRISPR系统, 研究人员利用算法对细菌序列进行生物信息学检索, 以确定是否存在类似的、对PAM限制性要求较低的酶。为此, 他们开发了一种数据分析软件工具, 并在实验室中构建了CRISPR的合成版本, 以评估新发现酶的性能。研究最终发现, 最成功的酶是来自犬链球菌的ScCas9, 其与目前广泛使用的Cas9酶非常相似, 但能够靶向常用酶不能靶向的DNA序列。新酶只需要一个而不是两个G核苷酸作为其PAM序列, 从而在基因组上开辟了更多的靶向位点, 允许CRISPR靶向许多先前已经超出系统范围的特异性疾病突变。例如, 一个典型的基因长度约为1000个碱基, 如果只是简单地敲除整个基因, 其可为研究人员提供许多不同的靶向位点。但镰状细胞性贫血等疾病是由单一碱基突变引起的, 这使其更难以靶向。雅各布森认为, 碱基编辑不仅仅是找到基因中1000个碱基的任意位置并将其敲除的问题, 而是一个以非常精确的方式进入并纠正想要改变的基因的问题。新的CRISPR工具在这些应用中具有非常大的潜力, 未来或能追踪基因组上的每个位点。

来源: 科学网

发布日期: 2018-10-26

全文链接:

<http://news.sciencenet.cn/htmlnews/2018/10/419132.shtm>

➤ 学术文献

1. Regulation of the terminal maturation of iNKT cells by mediator complex subunit 23 (通过中介复合物23调控印迹细胞的终末成熟)

简介: Invariant natural killer T cells (iNKT cells) are a specific subset of T cells that

recognize glycolipid antigens and upon activation rapidly exert effector functions. This unique function is established during iNKT cell development; the detailed mechanisms of this process, however, remain to be elucidated. Here the authors show that deletion of the mediator subunit Med23 in CD4+CD8+ double positive (DP) thymocytes completely blocks iNKT cell development at stage 2. This dysregulation is accompanied by a bias in the expression of genes related to the regulation of transcription and metabolism, and functional impairment of the cells including the loss of NK cell characteristics, reduced ability to secrete cytokines and attenuated recruitment capacity upon activation. Moreover, Med23-deficient iNKT cells exhibit impaired anti-tumor activity. Our study identifies Med23 as an essential transcriptional regulator that controls iNKT cell differentiation and terminal maturation.

来源: Nature Communications 期刊

发布日期: 2018-09-24

全文链接:

<http://agri.ckcest.cn/file1/M00/00/10/Csgk0FvX1xCAPdPWACR7qMyZf9w231.pdf>

2. Transcriptional regulation of nitrogen-associated metabolism and growth (氮相关代谢和生长的转录调节)

简介: Nitrogen is an essential macronutrient for plant growth and basic metabolic processes. The application of nitrogen-containing fertilizer increases yield, which has been a substantial factor in the green revolution¹. Ecologically, however, excessive application of fertilizer has disastrous effects such as eutrophication². A better understanding of how plants regulate nitrogen metabolism is critical to increase plant yield and reduce fertilizer overuse. Here we present a transcriptional regulatory network and twenty-one transcription factors that regulate the architecture of root and shoot systems in response to changes in nitrogen availability. Genetic perturbation of a subset of these transcription factors revealed coordinate transcriptional regulation of enzymes involved in nitrogen metabolism. Transcriptional regulators in the network are transcriptionally modified by feedback via genetic perturbation of nitrogen metabolism. The network, genes and gene-regulatory modules identified here will prove critical to increasing agricultural productivity.

来源: Nature 期刊

发布日期: 2018-10-24

全文链接:

http://agri.ckcest.cn/file1/M00/00/08/Csgk0FvX1SWAce6gAPHe9e_2hwM017.pdf