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1. 提高大豆转化效率的方法

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▶ 前沿资讯

1. 联合国会议同意限制基因驱动

简介: 11月29日，在埃及沙姆沙伊赫举行的联合国生物多样性公约（CBD）会议上，各国否决了一项暂时禁止释放携带基因驱动生物体的提议。基因驱动是一种基因工程技术，旨在目标群体内迅速传播突变。尽管许多环保组织和活动人士支持这项提议，但几十名科学家反对暂停研究。面对生物技术友好型国家的反对，基因驱动的暂停是不可能成功的，因为对CBD的改变必须由近200个缔约方达成共识来实现。相反，在为期两周的会议上，代表们同意对条约进行修改，但这些修改非常模糊，以至于基因驱动技术的支持者和怀疑者都在鼓吹胜利。CBD的签署国同意有必要在个案基础上评估基因驱动释放的风险，并应咨询可能受这种释放影响的当地社区和土著群体。该条约已得到世界上大多数国家的批准。英国伦敦帝国理工学院进化遗传学家Austin Burt在给媒体的一封电子邮件中表示：“这里的最终协议承认了基因驱动研究代表的巨大机遇，以及确保其负责任地发展所必需的保障措施。”Burt领导的目标疟疾项目打算最早于2024年在撒哈拉以南非洲测试携带了被修改基因的蚊子。但加拿大渥太华环保组织ETC Group的联合主管Jim Thomas持不同看法。“这是一个关于基因驱动的非非常谨慎的决定。”他说，“文中没有提到基因驱动的所谓益处，而只有风险。这不是一个正式的禁令，但已经非常接近了。”Thomas指出，条约将权力交还给社区，让它们决定是否在自己的土地上进行基因驱动试验。美国北卡罗来纳州立大学生物技术政策专家Todd Kuiken所在专家小组就基因驱动向CBD提出建议。他表示，该文本必须由最终批准基因驱动的国家来解释，因此争论不会很快结束。

来源: 科学网

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全文链接:

<http://news.sciencenet.cn/htmlnews/2018/12/420623.shtm>

▶ 学术文献

1. Structure Studies of the CRISPR-Csm Complex Reveal Mechanism of Co-transcriptional Interference (CRISPR-Csm复合物的结构研究揭示了共转录干扰机制)

简介: Csm, a type III-A CRISPR-Cas interference complex, is a CRISPR RNA (crRNA)-guided RNase that also possesses target RNA-dependent DNase and cyclic oligoadenylate (cOA) synthetase activities. However, the structural features allowing target RNA-binding-dependent activation of DNA cleavage and cOA generation remain unknown. Here, we report the structure of Csm in complex with crRNA together with structures of cognate or non-cognate target RNA bound Csm complexes. We show that depending on complementarity with the 5' tag of crRNA, the 3' anti-tag region of target RNA binds at two distinct sites of the Csm complex. Importantly, the interaction between the non-complementary anti-tag region of cognate target RNA and Csm1 induces a conformational change at the Csm1 subunit that allosterically activates DNA cleavage and

cOA generation. Together, our structural studies provide crucial insights into the mechanistic processes required for crRNA-mediated sequence-specific RNA cleavage, RNA target-dependent non-specific DNA cleavage, and cOA generation.

来源: Cell期刊

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全文链接:

<http://agri.ckcest.cn/file1/M00/02/9E/Csgk0FwEoS0AT4bzAMlusqa32pc299.pdf>

2. Maize multi-omics reveal roles for autophagic recycling in proteome remodelling and lipid turnover (玉米多组学揭示了自噬循环在蛋白质组重组和脂质代谢中的作用)

简介: The turnover of cytoplasmic material by autophagic encapsulation and delivery to vacuoles is essential for recycling cellular constituents, especially under nutrient-limiting conditions. To determine how cells/tissues rely on autophagy, we applied in-depth multi-omic analyses to study maize (*Zea mays*) autophagy mutants grown under nitrogen-replete and -starvation conditions. Broad alterations in the leaf metabolome were evident in plants missing the core autophagy component ATG12, even in the absence of stress, particularly affecting products of lipid turnover and secondary metabolites, which were underpinned by substantial changes in the transcriptome and/or proteome. Cross-comparison of messenger RNA and protein abundances allowed for the identification of organelles, protein complexes and individual proteins targeted for selective autophagic clearance, and revealed several processes controlled by this catabolism. Collectively, we describe a facile multi-omic strategy to survey autophagic substrates, and show that autophagy has a remarkable influence in sculpting eukaryotic proteomes and membranes both before and during nutrient stress.

来源: Nature Plants期刊

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全文链接:

<http://agri.ckcest.cn/file1/M00/02/9E/Csgk0FwEmNqAS4xcAD51rVc6fDE683.pdf>

3. NRT1.1B Improves Selenium Concentrations in Rice Grains by Facilitating Selenomethionone Translocation (NRT1.1B通过促进亚硒酮易位提高了水稻籽粒中的硒浓度)

简介: Selenium (Se) is an essential trace element for humans and other animals, yet approximately one billion people worldwide suffer from Se deficiency. Rice is a staple food for over half of the world's population that is a major dietary source of Se. In paddy soils, rice roots mainly take up selenite. Se speciation analysis indicated that most of the selenite absorbed by rice is predominantly transformed into selenomethionone (SeMet) and retained in roots. However, the mechanism by which SeMet is transported in plants remains largely unknown. In this study, SeMet uptake was found to be an energy - dependent symport process involving H⁺ transport, with neutral amino acids strongly inhibiting SeMet uptake. We further revealed that NRT1.1B, a member of rice peptide transporter (PTR) family which

plays an important role in nitrate uptake and transport in rice, displays SeMet transport activity in yeast and *Xenopus* oocyte. The uptake rate of SeMet in the roots and its accumulation rate in the shoots of *nrt1.1b* mutant were significantly repressed. Conversely, the overexpression of NRT1.1B in rice significantly promoted SeMet translocation from roots to shoots, resulting in increased Se concentrations in shoots and rice grains. With vascular - specific expression of NRT1.1B, the grain Se concentration was 1.83 - fold higher than that of wild type. These results strongly demonstrate that NRT1.1B holds great potential for the improvement of Se concentrations in grains by facilitating SeMet translocation, and the findings provide novel insight into breeding of Se - enriched rice varieties.

来源: Plant Biotechnology Journal期刊

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http://agri.ckcest.cn/file1/M00/02/9E/Csgk0FwEhmeAMqLPAAoSOG_ntto729.pdf

➤ 相关专利

1. Method for improving transformation efficiency of soybean (提高大豆转化效率的方法)

简介: Provided is a method for improving the transformation efficiency of soybean, the method comprising: transforming plant cells by using a recombinant vector containing a target gene and a gene encoding a sulfonyleurea-type herbicide hydrolase; selectively cultivating the transformed plant cells by externally applying an ALS inhibitor, with the gene encoding the sulfonyleurea-type herbicide hydrolase acting as a selective marker; and selecting plant cells which are not killed and/or not inhibited. By adding a selection agent into a proliferation medium and a differential medium by externally applying same in the plant transformation process, the effective screening concentration range of the selection agent is optimized, such that the transformation efficiency and the proportion of positive plants obtained by the progeny thereof are significantly improved; in addition, transgenic plants obtained by means of transformation with the sulfonyleurea-type herbicide hydrolase gene acting as the selective marker in the present invention have good resistance and genetic stability.

来源: 国家知识产权局

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全文链接:

<http://agri.ckcest.cn/file1/M00/00/00/Csgk0VwF21iAKOr8ACXhb5uC2h4265.pdf>