



2018年第44期总104期

农业生物技术专题

本期导读

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1. 用于鉴定和富集包含位点特异性基因组修饰的细胞的方法和组合物
2. 高通量无损种子采样育种方法

➤ 学术文献

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2. PRC2抑制ABA诱导拟南芥衰老

➤ 前沿资讯

1. 华南农大利用代谢工程创制“赤晶米”新种质

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➤ 相关专利

1 . Methods and compositions for identifying and enriching for identifying and engriching foe cells aomprising site specific genomic modifications (用于鉴定和富集包含位点特异性基因组修饰的细胞的方法和组合物)

简介: The present invention relates to methods and compositions for modifying a target site in the genome of a plant cell. Such modifications include integration of a transgene and mutations. The present invention also relates to methods and compositions for identifying and enriching for cells which comprise a modified target site.

来源: 国家知识产权局

发布日期:2018-10-11

全文链接:

<http://agri.ckcest.cn/ass/ad660652-d0c3-458f-80b9-cdda876fb0a4.pdf>

2 . Methods Of Seed Breeding Using High Throughput Nondestructive Seed Sampling (高通量无损种子采样育种方法)

简介: A method is provided for use in a plant breeding program to generate a population having one or more desired traits. The method includes removing a tissue sample from each of one or more seeds using an automated seed sampler while preserving germination viability of the sampled seeds; analyzing the tissue samples for the presence or absence of a genetic sequence associated with at least one desired trait; based on the analysis of the tissue samples, cultivating plants from the sampled seeds that either possess or lack the genetic sequence associated with the at least one desired trait; creating a parental cross using at least one of the cultivated plants; and selecting seeds from the parental cross and cultivating offspring of the parental cross using the selected seeds.

来源: 国家知识产权局

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<http://agri.ckcest.cn/ass/a2ec135d-17bc-438c-b3b1-76ef555ea49e.pdf>

➤ 学术文献

1 . Sweet Sorghum Originated through Selection of Dry, a Plant-specific NAC Transcription Factor Gene (NAC转录因子调控甜高粱茎秆持汁特性)

简介: Sorghum (*Sorghum bicolor*) is the fifth most popular crop worldwide and a C4 model plant. Domesticated sorghum comes in many forms, including sweet cultivars with juicy stems and grain sorghum with dry, pithy stems at maturity. The Dry locus, which controls the pithy/juicy stem trait, was discovered over a century ago. Here, we found that Dry gene

encodes a plant-specific NAC transcription factor. Dry was either deleted or acquired loss-of-function mutations in sweet sorghum, resulting in cell collapse and altered secondary cell wall composition in the stem. Twenty-three Dry ancestral haplotypes, all with dry, pithy stems, were found amongst wild sorghum and wild sorghum relatives. Two of the haplotypes were detected in domesticated landraces, with four additional dry haplotypes with juicy stems detected in improved lines. These results imply that selection for Dry gene mutations was a major step leading to the origin of sweet sorghum. The Dry gene is conserved in major cereals; fine-tuning its regulatory network could provide a molecular tool to control crop stem texture.

来源: Plant Cell期刊

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全文链接:

<http://agri.ckcest.cn/ass/2ee21750-d11a-4634-b90a-c5148b946132.pdf>

2 .Polycomb repressive complex 2 attenuates ABA-induced senescence in Arabidopsis (PRC2抑制ABA诱导拟南芥衰老)

简介: The phytohormone abscisic acid (ABA)-induced leaf senescence facilitates nutrient reuse and potentially contributes to enhancing plant stress tolerance. However, excessive senescence causes serious reductions in crop yield, and the mechanism by which senescence is finely tuned at different levels is still insufficiently understood. Here, we found that the double mutant of core enzymes of the Polycomb repressive complex 2 (PRC2) is hypersensitive to ABA in *Arabidopsis thaliana*. To elucidate the interplay between ABA and senescence at the genome level, we extensively profiled the transcriptomic and epigenomic changes triggered by ABA. We observed that H3K27me3 preferentially targets ABA-induced senescence-associated genes (SAGs). In the double, but not single, mutant of PRC2 enzymes, these SAGs were de-repressed and could be more highly induced by ABA compared with the wild-type, suggesting a redundant role for the PRC2 enzymes in negatively regulating ABA-induced senescence. Contrary to the rapid transcriptomic changes triggered by ABA, the reduction of H3K27me3 at these SAGs falls far behind the induction of their expression, indicating that PRC2-mediated H3K27me3 contributed to long-term damping of ABA-induced senescence to prevent an over-sensitive response. The findings of this study may serve as a paradigm for a global understanding of the interplay between the rapid effects of a phytohormone such as ABA and the long-term effects of the epigenetic machinery in regulating plant senescence processes and environmental responses.

来源: 基因农业网

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全文链接:

<http://agri.ckcest.cn/ass/a2e40f98-c378-49a0-94b8-c0f94b3a6533.pdf>

▶ 前沿资讯

1. 华南农大利用代谢工程创制“赤晶米”新种质

简介: 记者从华南农业大学获悉,该校生命科学学院、亚热带农业生物资源保护与利用国家重点实验室刘耀光院士团队利用高效的多基因载体系统TGSII (TransGene Stacking II), 实现了在水稻胚乳特异合成虾青素的营养强化目标, 培育出世界首例胚乳富含虾青素的新型功能营养型水稻种质“aSTARice, 虾青素米”, 也称“赤晶米” 据介绍, 这是刘耀光院士团队继2017年率先创制富含花青素的功能营养型水稻种质“紫晶米”后, 又一重要科研成果。该系列成果为我国开发、储备了一批营养价值高、色彩丰富的水稻新种质, 极大地推动了植物合成生物学和作物生物强化研究领域的发展, 表明我校在植物多基因转化技术和复杂代谢途径的基因工程领域继续保持了国际领先水平。类胡萝卜素是一类重要的植物营养素, 而虾青素是一类橙红色类胡萝卜素, 为类胡萝卜素的最高级形式, 具有超强抗氧化活性。目前已在烟草、番茄、土豆、玉米、生菜等植物中实现了虾青素的合成。然而, 由于水稻胚乳中完全缺乏类胡萝卜素前体, 在水稻胚乳合成有效虾青素的研究仍未见报道。刘耀光院士团队通过分析水稻类胡萝卜素合成途径基因的表达模式, 发现大多数类胡萝卜素合成的相关基因在水稻胚乳中处于不表达或低表达状态。在此基础上, 结合对“黄金大米 (Golden Rice)”的分析, 确定了八氢番茄红素合成酶基因 (sZmPSY1)、八氢番茄红素脱氢酶基因 (sPaCrtI)、 β -胡萝卜素酮化酶基因 (sCrBKT) 和 β -胡萝卜素羟化酶基因 (sHpBHY) 四个类胡萝卜素合成途径的关键基因, 利用水稻胚乳特异性启动子和自主开发的高效多基因TGSII系统, 在水稻胚乳中重新构建了不同基因组合的类胡萝卜素/酮式胡萝卜素/虾青素的生物合成途径。

来源: 科学网

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<http://news.sciencenet.cn/htmlnews/2018/10/418680.shtm>