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➤ 相关专利

1. 一种用于预测羽衣甘蓝内叶颜色的分子标记及应用

中国农业科学院农业信息研究所

联系人：王爱玲;李凌云;顾亮亮

联系电话：010-51503648

邮箱：agri@ckcest.cn

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▶ 前沿资讯

1. 研究发现水稻转座子受驯化选择和抗病抗逆中的调节功能

简介: 6月19日, Molecular Plant 杂志在线发表了中国科学院分子植物科学卓越创新中心/植物生理生态研究所何祖华研究组题为Elimination of a retrotransposon for quenching genome instability in modern rice 的研究论文。该项研究发现自然条件下一个活跃的反转录转座子HU0 (“活”), 该转座子广泛存在于野生稻基因组中, 部分存在于考古水稻样本和农家种中, 但在现代栽培稻中丢失。研究揭示HU0通过表观遗传学途径影响基因组水平的功能基因, 激活基因组的不稳定性/防卫反应, 这些都有利于野生稻适应复杂多变的自然环境。但由于HU0的存在不利于对栽培稻高产稳产的需求, 该转座子在水稻驯化和育种过程中被逐步选择性删除。该研究首次提出转座子元件也可以像功能基因一样, 在物种驯化过程中被选择, 拓展了人们对转座子功能和物种驯化机理的认识。

来源: 中国科学院

发布日期:2019-06-25

全文链接:

http://agri.ckcest.cn/file1/M00/06/81/Csgk0F0TFt0AegcLAAv_J5sk8X0691.pdf

2. Scientists unearth green treasure -- albeit rusty -- in the soil (科学家发现有机物中天然磷释放新机制)

简介: 磷是一种有限的资源, 但在农业中, 经常将磷与氮一起施用到作物上, 以改善土壤健康, 促进作物生长。对于种植农作物的农民来说, 从开采无机磷矿中获得的磷肥是一种日益减少的资源。一旦耗尽, 它就消失了。

如果能了解土壤中这些自然过程的分子机制, 以及这些过程可能被植物和细菌利用的方式, 我们就能帮助环境, 阻止农田氮磷径流进入河流和湖泊, 或许还能防止附近水域的藻类繁殖。

康奈尔大学的工程师们已经迈出了一步, 他们阐明了土壤中的铁是如何释放有机物中天然磷的机制。这种磷可以用于肥料中, 这样农民有一天就可以减少施用到农田中的化学肥料的数量。现在可以利用有机物释放磷酸盐的自然土壤机制, 减少对开采磷矿的依赖, 减少因农田或草坪开采磷矿粉。

生物与环境工程副教授Ludmilla Aristilde表示, 人们对自然的干扰越少越好。磷循环过程的这一组成部分在很大程度上被忽视了, 但他们正在研究土壤矿物对环境有益的磷循环机制, 探索目前未知的磷循环途径, 进而避免更多的化学磷的开采与投入。

该项研究由美国国家粮食和农业研究所和美国能源部支持。

来源: ScienceDaily

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/81/Csgk0F0TJEGAZIRPAA08eb26ZUQ705.pdf>

学术文献

1. Proteomic Analysis and Functional Validation of a *Brassica oleracea* Endochitinase Involved in Resistance to *Xanthomonas campestris* (甘蓝抗野油菜黄单胞菌内切酶的蛋白质组学分析及功能验证)

简介: Black rot is a severe disease caused by the bacterium *Xanthomonas campestris* pv. *campestris* (Xcc), which can lead to substantial losses in cruciferous vegetable production worldwide. Although the use of resistant cultivars is the main strategy to control this disease, there are limited sources of resistance. In this study, we used the LC-MS/MS technique to analyze young cabbage leaves and chloroplast-enriched samples at 24 h after infection by Xcc, using both susceptible (Veloce) and resistant (Astrus) cultivars. A comparison between susceptible Xcc-inoculated plants and the control condition, as well as between resistant Xcc-inoculated plants with the control was performed and more than 300 differentially abundant proteins were identified in each comparison. The chloroplast enriched samples contributed with the identification of 600 additional protein species in the resistant interaction and 900 in the susceptible one, which were not detected in total leaf sample. We further determined the expression levels for 30 genes encoding the identified differential proteins by qRT-PCR. CHI-B4 like gene, encoding an endochitinase showing a high increased abundance in resistant Xcc-inoculated leaves, was selected for functional validation by overexpression in *Arabidopsis thaliana*. Compared to the wild type (Col-0), transgenic plants were highly resistant to Xcc indicating that CHI-B4 like gene could be an interesting candidate to be used in genetic breeding programs aiming at black rot resistance.

来源: *Frontiers in Plant Science*

发布日期: 2019-04-12

全文链接:

<http://agri.ckcest.cn/file1/M00/06/81/Csgk0F0TGv-AB6cfAEKxzP-IS90094.pdf>

2. Early Brassica Crops Responses to Salinity Stress: A Comparative Analysis Between Chinese Cabbage, White Cabbage, and Kale (大白菜、白菜和羽衣甘蓝对盐胁迫反应的比较分析)

简介: Soil salinity is severely affecting crop productivity in many countries, particularly in the Mediterranean area. To evaluate early plant responses to increased salinity and characterize tolerance markers, three important Brassica crops Chinese cabbage (*Brassica rapa* ssp. *pekinensis*), white cabbage (*B. oleracea* var. *capitata*) and kale (*B. oleracea* var. *acephala*) were subjected to short-term (24 h) salt stress by exposing them to NaCl at concentrations of 50, 100, or 200 mM. Physiological (root growth, photosynthetic performance parameters, and Na⁺/K⁺ ratio) and biochemical parameters (proline content and lipid peroxidation as indicated by malondialdehyde, MDA, levels) in the plants' roots and leaves were then measured. Photosynthetic parameters such as the total performance index PI_{total} (describing the overall efficiency of PSI, PSII and the intersystem electron transport

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chain) appeared to be the most salinity-sensitive parameter and informative stress marker. This parameter was decreased more strongly in Chinese cabbage than in white cabbage and kale. It indicated that salinity reduced the capacity of the photosynthetic system for efficient energy conversion, particularly in Chinese cabbage. In parallel with the photosynthetic impairments, the Na⁺/K⁺ ratio was highest in Chinese cabbage leaves and lowest in kale leaves while kale root is able to keep high Na⁺/K⁺ ratio without a significant increase in MDA. Thus Na⁺/K⁺ ratio, high in root and low in leaves accompanying with low MDA level is an informative marker of salinity tolerance. The crops' tolerance was positively correlated with levels of the stress hormone abscisic acid (ABA) and negatively correlated with levels of jasmonic acid (JA), and jasmonoyl-L-isoleucine (JA-Ile). Furthermore, salinity induced contrasting changes in levels of the growth-promoting hormones brassinosteroids (BRs). The crop's tolerance was positively correlated with levels of BR precursor typhasterol while negatively with the active BR brassinolide. Principal Component Analysis revealed correlations in observed changes in phytohormones, biochemical, and physiological parameters. Overall, the results show that kale is the most tolerant of the three species and Chinese cabbage the most sensitive to salt stress, and provide holistic indications of the spectrum of tolerance mechanisms involved.

来源: Frontiers in Plant Science

发布日期: 2019-04-11

全文链接:

<http://agri.ckcest.cn/file1/M00/06/81/Csgk0F0TG7SAEZgTAJz4hP4pkOM101.pdf>

3. Silicon supply affects the root transcriptome of *Brassica napus* L. (硅供应对甘蓝型油菜根转录组的影响)

简介: **Main conclusion** Modulation of gene expression in roots of *Brassica napus* by silicon (Si) supply could allow plants to cope with future stresses.

The origin of the beneficial effects of silicon (Si) in plants, especially when they are subject to stress, remains poorly understood. Some authors have shown that Si alleviates plant stress and consider that this is mainly due to a mechanical effect on the cell wall. In addition, the other studies have shown that Si can also affect gene expression and modulate a number of metabolic pathways, especially in plants cultivated under stress conditions. Previously, Haddad et al. (Front Plant Sci 9:5-16, 2018) showed that a pretreatment of *Brassica napus* plants with Si (1.7 mM) for 1 week alleviated the stress induced by N privation. These results suggest that this improved resistance in Si-treated plants might be due to the establishment of defense mechanisms prior to exposure to the N stress. The aim of the current work was to test this assumption in *Brassica napus* roots (where Si is mainly stored) using a transcriptomic approach via the RNA sequencing. Our results indicated that the Si supply leads to a modulation of the expression of genes in *Brassica napus* roots. Functional categorization of the differentially expressed genes demonstrated that numerous genes are involved in different metabolic pathways and especially in cell wall synthesis, phytohormone metabolism, and stress responses. All these results show that Si modifies the root metabolism of *B. napus*, which could allow a better adaptation to future stresses.

来源: Planta

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<http://agri.ckcest.cn/file1/M00/06/81/Csgk0F0THCqADTm0ABP6vC33Tsg911.pdf>

4. Genome-wide analysis of the Chinese cabbage IQD gene family and the response of BrIQD5 in drought resistance (大白菜IQD基因家族的全基因组分析及BrIQD5对抗旱性的响应)

简介: Key message Thirty-five IQD genes were identified and analysed in Chinese cabbage and BrIQD5 transgenic plants enhanced the drought resistance of plants.

The IQD (IQ67-domain) family plays an important role in various abiotic stress responses in plant species. However, the roles of IQD genes in the Chinese cabbage response to abiotic stress remain unclear. Here, 35 IQD genes, from BrIQD1 to BrIQD35, were identified in Chinese cabbage (*Brassica rapa* ssp. *pekinensis*). Based on the phylogenetic analysis, these genes were clustered into three subfamilies (I-III), and members within the same subfamilies shared conserved exon-intron distribution and motif composition. The 35 BrIQD genes were unevenly distributed on 9 of the 10 chromosomes with 4 segmental duplication events. Ka/Ks ratios showed that the duplicated BrIQDs had mainly experienced strong purifying selection. Quantitative real-time polymerase chain reaction of 35 BrIQDs under PEG6000 indicated that BrIQD5 was significantly induced by PEG6000. To verify BrIQD5 function, BrIQD5 was heterologously overexpressed in tobacco and was silenced in Chinese cabbage. BrIQD5-overexpressed plants showed more tolerance to drought stress than wild-type plants, while BrIQD5-silenced plants in Chinese cabbage showed decreased drought tolerance. Additionally, six BrIQD5 potential interactive proteins were isolated by the yeast two-hybrid assay, including BrCaMa, BrCaMb and four other stress-related proteins. Motif IQ1 of BrIQD5 is important for the interaction with BrCaMa and BrCaMb, and the isoleucine in motif IQ1 is an essential amino acid for calmodulin binding to BrIQD5. The identification and cloning of the new Chinese cabbage drought tolerance genes will promote the drought-resistant breeding of Chinese cabbage and help to better understand the mechanism of IQD involved in the drought tolerance of plants.

来源: Plant Molecular Biology

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<http://agri.ckcest.cn/file1/M00/06/81/Csgk0F0TF1-ANABjAFHHm8dr8sA045.pdf>

5. Comparative transcriptomics analysis uncovers alternative splicing events and molecular markers in cabbage (*Brassica oleracea* L.) (比较转录组分析揭示甘蓝 (*Brassica oleracea* L.) 的选择性剪接事件和分子标记)

简介: Main conclusion Alternative splicing (AS) events were identified and verified in cabbage by comparative transcriptome analysis. The corresponding markers were developed and the germplasm resources were identified.

Alternative splicing (AS) is a central regulatory mechanism that greatly contributes to plant

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gene expression and transcriptome diversity. A large body of evidence has shown that AS complexity is relevant for plant development, evolution, complexity, and adaptation. Both insertion/deletion (InDel) and single nucleotide polymorphism (SNP) are typically co-dominant inheritance markers and have abundant polymorphisms. These have been widely used for marker-assisted selection, genetic mapping, and germplasm identification in plants. However, little is known about the molecular mechanisms underlying AS events and the development of markers including SNP and InDel from the cabbage transcriptome. In this study, three cabbage transcriptome datasets were collected and aligned to the cabbage reference genome to analyze AS events and marker development. 31,524 AS events were identified from three cabbage genotypes, accounting for 20.8% of the total cabbage genes. Alternative 3' splice site donor (A3SS) was the most frequent type of the four main AS events in cabbage. 70,475 InDels and 706,269 SNPs were identified with average frequencies of 1 InDel/6.9 kb and 1 SNP/0.7 kb, respectively. 71,942 potential SSRs were identified in 53,129 assembled unigenes with a density of 1 SSR/6.8 kb. The ratio of SNPs with synonymous/non-synonymous mutations was 1:0.65. 142 InDels and 36 SNPs were randomly selected and validated via Sanger sequencing and polymorphism was found among 66.2% of the InDels and 78.6% of the SNPs. Furthermore, 35 informative InDel markers were successfully used for genetic diversity analysis on 36 cabbage accessions. These results facilitate understanding of the molecular regulation mechanism underlying AS events in cabbage. They also provide molecular marker resource data for genetic mapping construction and germplasm identification, and facilitate the genetic improvement of cabbage via breeding.

来源: Planta

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/81/Csgk0F0TH0qAFR5dAErrgK-tCWg607.pdf>

6. Independent activation of the BoMYB2 gene leading to purple traits in Brassica oleracea (BoMYB2基因的独立激活导致甘蓝紫色性状的研究)

简介: **Key message** Transposon insertion and point mutation independently activated the BoMYB2 gene in three purple cultivars of Brassica oleracea including kale, kohlrabi, and cabbage.

Abstract Several varieties of *B. oleracea* have both green and purple cultivars. In this study, the causal genes for the purple traits in kale, kohlrabi and cabbage were cloned using map-based cloning approach. The purple traits in all three varieties were mapped to the same locus as the BoMYB2 gene in cauliflower. Surprisingly, the insertion of Harbinger transposon of BoMYB2 in cauliflower was not found in purple kale, kohlrabi and cabbage. Sequencing of the BoMYB2 gene in purple kale and purple kohlrabi discovered a 7606 bp CACTA-like transposon in its promoter region. Transient assay and promoter activity study showed that the insertion upregulated the expression of the BoMYB2 gene. On the other hand, the activation of the BoMYB2 gene in purple cabbage was caused by point mutation

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and/or 1-bp insertion in its promoter region. Sequence analysis of the BoMYB2 gene in different varieties suggested that the activating events most likely occurred independently after the divergence of cabbage, cauliflower, and kale/kohlrabi. Our results not only contribute to a better understanding of anthocyanin inheritance in *B. oleracea*, but also provide useful information for future hybrid breeding of purple cultivars through combination of different functional alleles of the BoMYB2 gene.

来源: Theoretical and Applied Genetics

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/81/Csgk0F0TGXCAQru8AC0hK8475YY748.pdf>

➤ 相关专利

1. 一种用于预测羽衣甘蓝内叶颜色的分子标记及应用

简介: 本发明涉及一种用于预测羽衣甘蓝内叶颜色的分子标记及应用, 所述分子标记具有SEQ ID NO: 5和SEQ ID NO: 6所示的核苷酸序列, 所述分子标记预测羽衣甘蓝内叶颜色的应用方法包括如下步骤: (1) 提取叶片基因组DNA; (2) PCR扩增, 扩增引物为所述分子标记; (3) 琼脂糖凝胶电泳检测; 本发明建立了一种应用分子标记在不受温度影响的情况下, 早期预测羽衣甘蓝内叶颜色的方法, 为羽衣甘蓝内叶颜色鉴定与新品种选育具有重要的科学指导意义。

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全文链接:

<http://agri.ckcest.cn/file1/M00/06/81/Csgk0F0TIu-AduyRAAWNEYmXYP8532.pdf>