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蔬菜育种专题

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2018年12月17日

➤ 前沿资讯

1. Researchers discover genes that give vegetables their shape (研究发现控制水果、蔬菜、谷物形状的遗传机制)

简介: 美国佐治亚大学的研究人员最近发现了一种能够控制水果、蔬菜、谷物形状的遗传机制, 文章发表于《Nature Communications》期刊。这一发现不仅对于植物育种人员来说十分重要, 对于更好地了解植物的演变和发育过程也十分关键。

科研人员发现在番茄、甜瓜、黄瓜、马铃薯甚至水稻中, 细胞会分成一列列或一排排, 这样就可以决定水果的形状。研究发现控制番茄形状和大小的基因序列控制着细胞分裂或细胞的大小。许多基因序列上的基因都决定着各自形成的水果形状。其中有些基因能在水果生长的后期, 即水果成熟前影响水果的大小和形状, 有些则早在开花前就能对大小和形状产生影响。

研究小组还分析调查了其他蔬菜水果的遗传机制和基因组, 以确定其他植物中类似基因组的具体位置。

该项目获得了美国农业部和国家科学基金的资助。下一步拟精确定位能够解释各种番茄形状和大小的基因。

来源: AgroPages

发布日期: 2018-11-14

全文链接:

<http://agri.ckcest.cn/file1/M00/02/9E/Csgk0FwEw8SAddCBAAmk6n99Fjg468.pdf>

➤ 学术文献

1. Precision genome engineering through adenine base editing in plants (植物腺嘌呤基编辑的精准基因组工程)

简介: The recent development of adenine base editors (ABEs) has enabled efficient and precise A-to-G base conversions in higher eukaryotic cells. Here, we show that plant-compatible ABE systems can be successfully applied to protoplasts of *Arabidopsis thaliana* and *Brassica napus* through transient transfection, and to individual plants through *Agrobacterium*-mediated transformation to obtain organisms with desired phenotypes. Targeted, precise A-to-G substitutions generated a single amino acid change in the FT protein or mis-splicing of the PDS3 RNA transcript, and we could thereby obtain transgenic plants with late-flowering and albino phenotypes, respectively. Our results provide ‘proof of concept’ for in planta ABE applications that can lead to induced neo-functionalization or altered mRNA splicing, opening up new avenues for plant genome engineering and biotechnology.

来源: Nature Plants

发布日期: 2018-06-04

全文链接:

<http://agri.ckcest.cn/file1/M00/02/9E/Csgk0FwEw0CAA0aMABnhLifE5bI100.pdf>

2. Effects of selenium on activity of glutathione peroxidase and expression of selenium metabolism-related genes in Brassica (硒对芸薹属植物谷胱甘肽过氧化物酶活性及硒代谢相关基因表达的影响)

简介: Inorganic selenium (Se) is absorbed and enriched by plants and converted into a stable and nutritionally important organic form, which subsequently when consumed by humans or animals results in increased Se tissue levels. Brassica is one of the most potent Se-enriched plants. The aim of this study was to compare differences in Se enrichment between two predominant Brassica plants namely Brassica rapa Linn L. and Brassica tumida Tsenet Lee L. on Se metabolic parameters. Plants exposed to soil Se levels (0, 0.5, 1, 2.5 or 5 mg/kg) were examined on the activity of glutathione peroxidase (GSH-Px), Se levels and expression of Se metabolism related genes using soil pots. Data showed that activities of GSH-Px in leaf and root of the two Brassica species were significantly increased in the presence of Se at 2.5 mg/kg. Se concentrations of leaf, stem and root in B. tumida Tsenet Lee L. and B. rapa Linn L. rose from 0.31 to 21.84-fold (leaf), 1.15 to 15.16-fold (stem) and 2.11 to 15.26-fold (root) in the presence of metal in a concentration-dependent manner. The highest expression levels of adenosine triphosphate (ATP), ATP sulfurylase (APS), selenocysteine methyltransferase (SMT), serine acetyltransferase (SAT), cysteine desulfurase (CysD) and S-adenosyl-L-Met:L-Met S-methyltransferase (MMT) in leaf of B. rapa Linn L. were found at 1 mg/kg Se. The highest expression levels of ATP, APS, SMT, SAT, CysD and MMT in leaf of B. tumida Tsenet Lee L. were observed at 2.5 mg/kg Se. The Se concentrations in leaf, stem and root of B. rapa Linn L. were higher than in B. tumida Tsenet Lee L. under the same soil Se level conditions. At the same Se level, differences in the expression of Se-related genes were observed between these two Brassica species. Our observations may be used to optimize the utilization of Brassica as a nutritional source of Se by growing this plant under certain soil conditions.

来源: Toxicological & Environmental Chemistry

发布日期: 2018-09-04

全文链接:

<http://agri.ckcest.cn/file1/M00/02/9E/Csgk0FwEwkeASXjIACA99ozuQnY017.pdf>

3. Highly preserved roles of Brassica MIR172 in polyploid Brassicas: ectopic expression of variants of Brassica MIR172 accelerates floral transition (芸薹属植物MIR172变异体的异位表达促进花转变)

简介: Functional characterization of regulatory genes governing flowering time is a research priority for breeding earliness in crop Brassicas. Highly polyploid genomes of Brassicas pose challenges in unraveling homeolog gene function. In Arabidopsis, five MIR172 paralogs control flowering time and floral organ identity by down-regulating AP2 and AP2-like genes. The impact of homeolog diversification on MIR172 loci, however, needs to be examined in morphologically diverse Brassicas. Herein, we analyze fractionation status and phylogeny of MIR172 and target AP2 from Brassicas and compare functionality of MIR172 variants representing distinct sub-genomes and progenitor genomes. Copy number analysis revealed higher retention of MIR172 loci relative to AP2 in diploid and amphi-diploid Brassica

species. Dendrogram of 87 MIR172 sequences from Brassicaceae showed five major clusters corresponding to MIR172a-MIR172e which further separated into sub-genome and progenitor genome specific clades. Similar groupings were observed in the phylogeny of 11 Brassica AP2 and AP2-like genes. Over-expression of a pair of natural variants for each of MIR172b, MIR172d and MIR172e representing sub-genomes, progenitor genomes and species of Brassicas displayed floral acceleration in all transgenic lines indicating a strong selection pressure on MIR172. All gain-of-function lines, except 35S::MIR172e and 35S::MIR172e' displayed floral organ defects implying altered target spectrum of MIR172e relative to MIR172b and MIR172d. Expression of MIR172e caused marginal earliness in flowering time in *B. juncea*. In conclusion, this study demonstrates tightly preserved role of homeologs and natural variants of MIR172 family in mediating flowering in Brassicas and suggests their deployment for introgression of early flowering trait.

来源: Molecular Genetics and Genomics

发布日期:2018-05-11

全文链接:

<http://agri.ckcest.cn/file1/M00/02/9E/Csgk0FwEozqAXA19ADGU8ed4KLM207.pdf>

4. Genome-wide survey, characterization, and expression analysis of RING finger protein genes in Brassica oleracea and their syntenic comparison to Brassica rapa and Arabidopsis thaliana (甘蓝环指蛋白基因的全基因组调查、鉴定、表达分析及其与油菜和拟南芥的同源比较)

简介: The ubiquitin-mediated post-translational regulatory pathway regulates a broad range of cell functions in all eukaryotes. It requires the involvement of a large number of E3 ligases, of which more than one third belongs to the RING protein family as in *Arabidopsis thaliana*. In this study, a total of 756 RING domains in 734 predicted proteins were identified in *Brassica oleracea*. Their encoding genes were characterized by RING domain type, additional domain, and expression pattern, and mapped on the nine chromosomes of *B. oleracea*. Comparison of these results with *B. rapa* and *A. thaliana* revealed some common as well as species-specific features. Our results showed that the differential gene loss following the whole genome triplication has largely contributed to the RING protein gene number variation among these species, although other factors such as tandem duplication, RING domain loss, or modification had also contributed to this variation. Analysis of RNA-seq data showed that these RING protein genes were functionally diversified and involved in all the stages of plant growth and development, and that the triplicated members were also diverged in expression with one member often more dominantly expressed over the two others in the majority of cases. Our study lays the foundation for further functional determination of each RING protein gene among species of the genus *Brassica*.

来源: Genome

发布日期:2018-08-03

全文链接:

<http://agri.ckcest.cn/file1/M00/02/9E/Csgk0FwEon0AaLhFALjobf5Ps9M240.pdf>