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蔬菜育种专题

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前沿资讯

1．A new regulator of vesicle trafficking in plants——Choline transporter regulates ion homeostasis and plant growth and development（研究发现胆碱可调控植物囊泡运输）

简介：《PLOS Biology》2017年12月28日发表了由中国上海生命科学研究院和美国加州大学伯克利分校共同完成的一项研究成果，揭示了拟南芥胆碱转运蛋白CTL1通过调控囊泡运输影响植物的生长发育及离子平衡的新机制，这也是首次有研究发现胆碱在生物体囊泡运输方面发挥重要作用。

胆碱转运蛋白CTL1之前被认为对调节植物韧皮部物质运输通道的筛板形成至关重要，但尚不清楚其功能机制以及是否还有其他作用。研究人员在筛选模式植物拟南芥体内控制离子平衡的基因时发现，CTL1在植株中无处不在，且在生长素浓度最高的地方含量最高，如生长锥、维管组织等。在细胞内部的反式高尔基体网状结构当中也发现了CTL1，而且它似乎控制着进出细胞质膜的物质运输。

研究表明，CTL1的缺失会扰乱多种蛋白质的分布，其中就包括一种植物生长素的转运蛋白。如果缺少CTL1，生长素转运蛋白就会失去方向，而植物就会出现生长素缺失的典型症状，如细胞不会伸长。研究还发现胆碱过多会抑制细胞的内吞作用，这和CTL1缺失时的影响相似，暗示CTL1的一个重要作用就是将胆碱汇集至核内体中。在该研究模型当中，CTL1的损失会提高胆碱水平，从而抑制磷脂酶D活性，改变囊泡中脂质的构成，并最终改变囊泡运输的目的地。这也就能解释CTL1变异所造成的后果，包括离子失衡、胞间连丝缺陷和生长素错位分布。

来源：AAAS

发布日期：2017-12-28

全文链接：

https://www.eurekalert.org/pub_releases/2017-12/p-anr122017.php

学术文献

1．An update on bioinformatics resources for plant genomics research（生物信息学资源在植物基因组学研究中的最新进展）

简介：Next-generation sequencing and traditional Sanger sequencing methods are of great significance in unraveling the complexity of plant genomes. These are constantly generating heaps of sequence data to be analyzed, annotated and stored. This has created a revolutionary demand for bioinformatics tools and software that can perform these functions. A large number of potentially useful bioinformatics tools and plant genome databases are created that have greatly simplified the analysis and storage of vast amounts of sequence data. The information garnered using the available bioinformatics methods have greatly helped in understanding the plant genome structure. Despite the availability of a good number of such tools, the information pouring from single gene-sequencing, and various whole-genome sequencing projects is overwhelming; thus, further innovations and improved methods are needed to sift through this sequence data, and assemble genomes. The current review focuses

on diverse bioinformatics approaches and methods developed to systematically analyze and store plant sequence data. Finally, it outlines the bottlenecks in plant genome analysis, and some possible solutions that could be utilized to overcome the problems associated with plant genome analysis.

来源：Current Plant Biology

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全文链接：

http://agri.ckcest.cn/ass/7c09cd12-94a6-4cfc-ae98-fc9b44373530.pdf

2. Molecular Diversity Analysis and Genetic Mapping of Pod Shatter Resistance Loci in Brassica carinata L.(甘蓝型油菜（Brassica carinata L）裂荚抗性位点的分子多样性分析与基因定位)

简介：Seed lost due to easy pod dehiscence at maturity (pod shatter) is a major problem in several members of Brassicaceae family. We investigated the level of pod shatter resistance in Ethiopian mustard (Brassica carinata) and identified quantitative trait loci (QTL) for targeted introgression of this trait in Ethiopian mustard and its close relatives of the genus Brassica. A set of 83 accessions of B. carinata, collected from the Australian Grains Genebank, was evaluated for pod shatter resistance based on pod rupture energy (RE). In comparison to B. napus (RE = 2.16 mJ), B. carinata accessions had higher RE values (2.53 to 20.82 mJ). A genetic linkage map of an F2 population from two contrasting B. carinata selections, BC73526 (shatter resistant with high RE) and BC73524 (shatter prone with low RE) comprising 300 individuals, was constructed using a set of 6,464 high quality DArTseq markers and subsequently used for QTL analysis. Genetic analysis of the F2 and F2:3 derived lines revealed five statistically significant QTL (LOD≥3) that are linked with pod shatter resistance on chromosomes B1, B3, B8, and C5. Herein, we report for the first time, identification of genetic loci associated with pod shatter resistance in B. carinata. These characterized accessions would be useful in Brassica breeding programs for introgression of pod shatter resistance alleles in to elite breeding lines. Molecular markers would assist marker-assisted selection for tracing the introgression of resistant alleles. Our results suggest that the value of the germplasm collections can be harnessed through genetic and genomics tools.

来源：Frontiers in Plant Science

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全文链接：

http://agri.ckcest.cn/ass/efb24393-1a99-4683-ba30-1e4a5e2d25b2.pdf

3. Assembly and comparison of two closely related Brassica napus genomes(两个密切相关的甘蓝型油菜基因组组合与分析)

简介：As an increasing number of plant genome sequences become available, it is clear that gene content varies between individuals, and the challenge arises to predict the gene content of a species. However, genome comparison is often confounded by variation in assembly and annotation. Differentiating between true gene absence and variation in assembly or

annotation is essential for the accurate identification of conserved and variable genes in a species. Here, we present the de novo assembly of the B. napus cultivar Tapidor and comparison with an improved assembly of the Brassica napus cultivar Darmor-bzh. Both cultivars were annotated using the same method to allow comparison of gene content. We identified genes unique to each cultivar and differentiate these from artefacts due to variation in the assembly and annotation. We demonstrate that using a common annotation pipeline can result in different gene predictions, even for closely related cultivars, and repeat regions which collapse during assembly impact whole genome comparison. After accounting for differences in assembly and annotation, we demonstrate that the genome of Darmor-bzh contains a greater number of genes than the genome of Tapidor. Our results are the first step towards comparison of the true differences between B. napus genomes and highlight the potential sources of error in future production of a B. napus pangenome.

来源： Plant Biotechnology Journal

发布日期： 2017-06-14

全文链接：

http://agri.ckcest.cn/ass/6c36f29d-63b9-486a-a964-05830db201ea.pdf

4．Construction and genetic analysis of anthocyanin-deficient mutants induced by T-DNA insertion in 'Tsuda' turnip (Brassica rapa)(在津田芜菁中通过T-DNA插入构建花青素缺陷型突变体及遗传分析)

简介： We previously showed that anthocyanin biosynthesis is specifically induced either by UV-A or co-irradiation with blue and UV-B, but not by monochromatic blue or UV-B light in the epidermis of the storage root of ‘Tsuda’ turnip (Brassica rapa L. subsp. rapa). To gain further molecular insights into the light signal transduction pathway of anthocyanin accumulation, over 10,000 germinated seeds of Tsuda turnip were sonicated and transformed using an improved Agrobacterium-mediated vacuum infiltration method. We obtained 17 anthocyanin-rich and 60 anthocyanin-deficient mutant lines from the mutant library. PCR identification, GFP assay and GUS staining showed that six anthocyanin-deficient mutants were generated by T-DNA insertion. Real-time qRT-PCR results demonstrated that expression of structural and regulatory genes of anthocyanin synthesis in the anthocyanin-deficient lines significantly decreased compared with wild type, which coincided with their anthocyanin levels in the epidermis of storage roots. In a genetic analysis of the F2 population of the mutants (g56w, g83w, g142w, and g143w) backcrossed with the wild type, the phenotypic proportions between the wild type and mutants were 3:1 following Mendelian segregation. Therefore, we speculated that the mutated trait of each mutant is controlled by a single recessive gene. This study provides a series of stable, homozygous and valuable mutant resources for elucidating the mechanisms of UV-A and blue+UV-B induced anthocyanin biosynthesis in higher plants.

来源： Plant Cell, Tissue and Organ Culture (PCTOC)

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全文链接：

http://agri.ckcest.cn/ass/ed652d3b-fda2-4557-aeee-d478b16b467b.pdf