



2017年第48期总110期

蔬菜育种专题

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► 前沿资讯

1. New bioresources for plant peptide hormones using gene editing technology (基因编辑技术为植物肽激素研究增添新生物资源)

简介: 肽激素是在生物体中起着重要作用的生长调节剂。编码肽激素基因的重要性已被广泛认知,然而大多数肽的功能特征尚未被解释。利用基因组编辑技术,日本熊本大学的研究人员敲除CLE多肽编码基因后产生了一个新的植物遗传资源。CLE肽是一组在细胞信号传导中发挥作用并受CLE基因调控的植物特异性肽激素。这一成果将有助于有关肽类激素在植物中的作用机理研究。

近年来,通过基因组编辑敲除或修改特定基因的技术一直备受瞩目。自2013年发明“CRISPR/Cas9”方法以来,在动物、植物、酵母和许多其他生物体上都有了成功的基因组编辑案例。在CRISPR/Cas9之前,基因组编辑的程序很复杂,因此在针对多个定向基因的研究中并不常用;CRISPR/Cas9方法建立之后,因其高效率、高特异性和简便性而使基因组编辑取得了巨大进步。研究人员因此也获得了研究基因功能的方法,比如,在敲除特定基因后分析对生物体和/或细胞的影响。

植物科学的最新进展已经发现,肽激素在植物生命周期中的多个领域中提供有价值的信息,例如确定细胞的数量和组织大小、控制授粉、对气候变化和病害的响应等。尽管肽激素编码基因的研究很难,但它们仍可为将来的研究创造丰富的遗传资源。

熊本大学研究团队尝试利用CRISPR/Cas9技术加速植物肽激素的研究。他们选择了含有32个CLE肽编码基因的模式植物拟南芥,并创造了一组与32个基因相对应的基因敲除工具。通过建立拟南芥的突变系,使得研究每个基因的功能变得更加容易。

为了评估基因敲除的有效性,研究团队选择了CLE肽中研究较多的CLV3,已知其在茎的生长点具有抑制细胞分裂的作用。正如所料,拟南芥植物的CLV3突变体由于细胞数目增加而形成不规则形状的果实。

此外,研究人员还利用这些突变植物完成了被认为是CLE44基因生物相关性的第一份报告。尽管推测CLE44基因参与调节维管束中的细胞数目,但由于生物资源不足,对该假设的研究尚未进行。在他们新开发的突变植物系的帮助下,熊本大学的研究人员观察到CLE44突变体植物中维管束细胞数量的减少,从而证实了其在维管束发育中的作用。

该研究成果2017年9月25日在线发表于《植物与细胞生理学》。

来源: AAAS

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全文链接:

https://www.eurekalert.org/pub_releases/2017-11/ku-nbf110817.php

► 学术文献

1. DNA methylation alteration is a major consequence of genome doubling in autotetraploid *Brassica rapa* (DNA甲基化变化是同源四倍体芜菁基因组加倍的主要结果)

简介: Polyploids are typically classified as autopolyploids or allopolyploids based on the origin of their chromosome sets. Autopolyploidy is much more common than traditionally

believed. Allopolyploidization, accompanied by genomic and transcriptomic changes, has been well investigated. In this study, genetic, DNA methylation and gene expression changes in autotetraploid *Brassica rapa* were investigated. No genetic alteration was detected using an amplified fragment length polymorphism (AFLP) approach. Using a cDNA-AFLP approach, approximately 0.58% of fragments showed changes in gene expression in autotetraploid *B. rapa*. The methylation-sensitive amplification polymorphism (MSAP) analysis showed that approximately 1.7% of the fragments underwent DNA methylation changes upon genome doubling, with hypermethylation and demethylation changes equally affected. Fragments displaying changes in gene expression and methylation status were isolated and then sequenced and characterized, respectively. This study showed that variation in cytosine methylation is a major consequence of genome doubling in autotetraploid *Brassica rapa*.

来源: Archives of Biological Sciences

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全文链接:

<http://agri.ckcest.cn/ass/4a024031-917a-48c0-ba84-c8539fc91019.pdf>

2. BrEXL6, a GDSL lipase gene of *Brassica rapa*, functions in pollen development (一种GDSL脂肪酶基因BrEXL6在芜菁花粉发育中的作用)

简介: Multiple allele-inherited male sterility has been widely used by breeders of *Brassica rapa* L. ssp. *pekinensis*, but the molecular mechanisms of male sterility are not yet clear. In this study, we isolated the full-length cDNA of a new gene (not included in the *Brassica* database). This gene, comprising 1 054 bp, encodes a 39.99 kDa protein with a Gly-Asp-Ser-Leu (GDSL)-lipase domain that is a member of the lipolytic protein GDSL family. The sequence of candidate gene is the most similar to extracellular lipase 6 (EXL6) of *Arabidopsis* and was therefore designated BrEXL6 and submitted to NCBI (accession No. JX131630.1). Reverse transcription semi-quantitative PCR and Western blot analysis showed that BrEXL6 and its encoded protein were significantly more expressed in fertile buds than in sterile buds. Quantitative PCR and in situ hybridization showed that BrEXL6 was highly expressed in the anthers of fertile buds, especially anthers at the pollen-development stages, but only weakly expressed in other tissues and floral organs of fertile plants and whole sterile plants. These results suggest that BrEXL6 is a pollen development-related gene. The results of this study provide clues for understanding the mechanisms underlying multiple allele-inherited male sterility.

来源: Biologia Plantarum

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<http://agri.ckcest.cn/ass/a8cee3f2-d76c-4adc-b53a-42831a3fde6c.pdf>

3. Isolation and expression analyses of KLUH gene in developing seeds and enhanced seed oil in KLUH overexpressing *Brassica juncea* transgenics (在过量表达KLUH基因的转基因芥菜种子发育和种子油量方面KLUH基因的分离和表达分析)

简介: Improving oil yield of Indian mustard (*Brassica juncea*) is exigent as it is a major oilseed crop of Indian subcontinent, which has severe shortage of vegetable oil production in the world. Some of the regulators of seed development have been shown to improve oil yield in *Arabidopsis*. *Arabidopsis* KLUH (*AtKLUH*), a maternal regulator of seed size, has been shown to control seed oil content. In this study, we identified three homologs of *AtKLUH* in *B. juncea*, *BjKLUH1*, *BjKLUH2-1* and *BjKLUH2-2*. We observed that *BjKLUH1* differentially expresses in developing seeds in *B. juncea* accessions with varying seed size and oil content. Further, analyses for seed oil content in *B. juncea* transgenics carrying *AtKLUH* demonstrated an increase in seed oil up to 8.3% compared to wild-type plants. The results of this study suggest that KLUH may have a role in seed development and is a good candidate for engineering seed oil accumulation in *B. juncea*.

来源: *Biologia*

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<http://agri.ckcest.cn/ass/dd910c55-d099-4f81-84df-efb1850d9cdb.pdf>

4. Synteny analysis of genes and distribution of loci controlling oil content and fatty acid profile based on QTL alignment map in *Brassica napus* (在甘蓝型油菜中基于QTL定位图方法对控制含油量和脂肪酸组成的基因及分布位点进行同线分析)

简介: Background: Deciphering the genetic architecture of a species is a good way to understand its evolutionary history, but also to tailor its profile for breeding elite cultivars with desirable traits. Aligning QTLs from diverse population in one map and utilizing it for comparison, but also as a basis for multiple analyses assure a stronger evidence to understand the genetic system related to a given phenotype.

Results: In this study, 439 genes involved in fatty acid (FA) and triacylglycerol (TAG) biosyntheses were identified in *Brassica napus*. *B. napus* genome showed mixed gene loss and insertion compared to *B. rapa* and *B. oleracea*, and C genome had more inserted genes. Identified QTLs for oil (OC-QTLs) and fatty acids (FA-QTLs) from nine reported populations were projected on the physical map of the reference genome “Darmor-bzh” to generate a map. Thus, 335 FA-QTLs and OC-QTLs could be highlighted and 82 QTLs were overlapping. Chromosome C3 contained 22 overlapping QTLs with all trait studied except for C18:3. In total, 218 candidate genes which were potentially involved in FA and TAG were identified in 162 QTLs confidence intervals and some of them might affect many traits. Also, 76 among these candidate genes were found inside 57 overlapping QTLs, and candidate genes for oil content were in majority (61/76 genes). Then, sixteen genes were found in overlapping QTLs involving three populations, and the remaining 60 genes were found in overlapping QTLs of two populations. Interaction network and pathway analysis of these candidate genes indicated ten genes that might have strong influence over the other genes that control fatty acids and oil formation.

Conclusion: The present results provided new information for genetic basis of FA and TAG formation in *B. napus*. A map including QTLs from numerous populations was built, which

could serve as reference to study the genome profile of *B. napus*, and new potential genes emerged which might affect seed oil. New useful tracks were showed for the selection of population or/and selection of interesting genes for breeding improvement purpose.

来源: BMC Genomics

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全文链接:

<http://agri.ckcest.cn/ass/a7dbf115-b2f4-4210-ad87-8b0a237d8667.pdf>