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蔬菜育种专题

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▶ 前沿资讯

1. The origin of flower-making genes (日本科学家探究成花基因)

简介: 开花植物由无花植物进化而来。人们已知一些叫做MADS盒蛋白基因的基因负责产生花朵特有的组成部分,如雄蕊、雌蕊和花瓣。苔藓、蕨类和绿藻等不开花的植物中也有MADS盒蛋白基因,但MADS盒蛋白基因是如何在无花植物中起作用的,目前还不得而知。因此,为了弄清楚花朵的进化机制,就必须弄明白MADS盒蛋白基因在无花植物中的作用机理。

日本国家基础生物学研究所的长谷部光泰教授领导的研究团队对小立碗藓 (*Physcomitrella patens*) 的研究表明, MADS盒蛋白基因控制配子托茎部的细胞伸长、细胞分裂和精子活力。小立碗藓中有六个MADS盒蛋白基因,研究团队分解了这六个基因,分析它们的功能,发现在失去全部MADS盒蛋白基因的苔藓中,精子鞭毛几乎不活动。MADS盒蛋白基因在以下两方面影响授精:一是提供充足的水让精子能够游动,二是产生活动的鞭毛。

研究人员认为,开花植物适应了陆地的干旱环境之后,配子托和精子鞭毛就在进化过程中消失了,而在配子托和精子鞭毛中起作用的MADS盒蛋白基因也就无关紧要了,但花朵在进行过程中也许利用了这些基因的其他功能。有趣的是,植物生长发育的基因调控网络在不同谱系中也不相同,而在动物中却相对保守。

该研究结果于1月3日发表在《自然植物》(Nature Plants)杂志上。

来源: AAAS

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全文链接:

https://www.eurekalert.org/pub_releases/2018-01/nion-too011018.php

▶ 学术文献

1. Cytogenetics and germplasm enrichment in Brassica allopolyploids in China (中国芸苔属植物异源多倍体具有丰富的细胞遗传学和种质资源)

简介: This paper reviews research advances in cytogenetics and germplasm innovation in Brassica allopolyploids, particularly oilseed rape (*Brassica napus*), in China. Three naturally evolved Brassica allotetraploid species are cytologically stable but tend to preferentially lose several chromosomes from one subgenome when induced by alien chromosome elimination. A-subgenome is extracted from *B. napus*, and the ancestral Brassica rapa was restituted after the total loss of C-subgenome chromosomes. Genome-wide genetic and epigenetic alterations were observed in both natural and synthetic Brassica allotetraploids. *B. napus* was subjected to extensive interspecific hybridization with landraces of *B. rapa* and *Brassica juncea*, which exhibit abundant phenotype variations, to widen the genetic diversity in breeding and select numerous elite germplasm resources and cultivars; these cultivars include the representative Zhongyou 821, which also parented numerous other varieties. Novel *B. napus* genotypes were obtained using Brassica trigeneric hybrids and allohexaploids ($2n=54$, AABBCC) by

combining subgenomes from extant allotetraploids and diploids as bridge. Alien additions, substitutions, and translocations of the *B. napus* genome were developed by intergeneric/intertribal sexual and somatic hybridizations with several crucifers. Furthermore, mitochondrial DNA recombination promoted the production of novel cytoplasmic male sterile lines.

来源: Journal of Integrative Agriculture

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<http://agri.ckcest.cn/ass/01e5c480-fccd-403c-ae6d-5f3777714b88.pdf>

2. TDZ-induced plant regeneration in *Brassica oleracea* L. var. botrytis: effect of antioxidative enzyme activity and genetic stability in regenerated plantlets (TDZ诱导的甘蓝型油菜植株再生: 抗氧化酶活性的影响和再生植株的遗传稳定性)

简介: The effects of various combinations of plant growth regulators on regeneration potential from seedling-derived leaf tissues of *Brassica oleracea* L. var. botrytis were evaluated. Callus was induced from 2-wk-old leaf explants. The explants were incubated on Gamborg's (MSB5) medium. The maximum frequency of callus induction (85.56%) was recorded on MSB5 medium supplemented with 9.1 μM thidiazuron (TDZ) and 0.5 μM α -naphthaleneacetic acid (NAA). Optimum shoot induction (54.44%) was obtained on MSB5 medium supplemented with 4.5 μM TDZ and 0.5 μM NAA. The maximum number of shoots per explant (5.33) was recorded on MSB5 medium with 4.5 μM TDZ and 0.5 μM NAA, whereas the maximum shoot length (4.86 cm) was recorded for shoots cultured on MSB5 medium supplemented with 4.5 μM TDZ and 5.7 μM gibberellic acid (GA3). However, optimum root induction (71.11%) occurred on half-strength Murashige and Skoog basal medium supplemented with 4.9 μM indole-3 butyric acid (IBA). Studies on the antioxidant activity of superoxide dismutase, ascorbate peroxidase, and peroxidase in seedlings, callus, regenerated shoots, and regenerated plantlets cultured on 4.5 μM TDZ and 0.5 μM NAA medium revealed the roles of these key antioxidative enzymes in callus induction and regeneration. The genetic stability of the regenerated plantlets was assessed using inter simple sequence repeat primers. The monomorphic amplification products confirmed true-to-type in vitro regenerated plants. This in vitro regeneration method can be useful in the large-scale production of genetically uniform plants, for genetic transformation, and conservation of elite germplasm of plant species.

来源: In Vitro Cellular & Developmental Biology - Plant

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<http://agri.ckcest.cn/ass/66d44b42-3d44-4ae8-b0e8-7c8a5e09656d.pdf>

3. BnDGAT1s Function Similarly in Oil Deposition and Are Expressed with Uniform Patterns in Tissues of *Brassica napus* (BnDGAT1s功能同样存在于油脂沉积中且在甘蓝型油菜组织中)

均匀表达)

简介: As an allotetraploid oilcrop, *Brassica napus* contains four duplicated AcylCoA: diacylglycerol acyltransferase 1 (DGAT1) genes, which catalyze one of the ratelimiting steps in triacylglycerol (TAG) biosynthesis in plants. While all four BnDGAT1s have been expressed functionally in yeast, their expression patterns in different germplasms and tissues and also consequent contribution to seed oil accumulation in planta remain to be elucidated. In this study, the coding regions of the four BnDGAT1s were expressed in an *Arabidopsis dgat1* mutant. All four BnDGAT1s showed similar effects on oil content and fatty acid composition, a result which is different from that observed in previous studies of their expression in yeast. Expression patterns of BnDGAT1s were analyzed in developing seeds of 34 *B. napus* inbred lines and in different tissues of 14 lines. Different expression patterns were observed for the four BnDGAT1s, which suggests that they express independently or randomly in different germplasm sources. Higher expression of BnDGAT1s was correlated with higher seed oil content lines. Tissue-specific analyses showed that the BnDGAT1s were expressed in a uniform pattern in different tissues. Our results suggest that it is important to maintain expression of the four BnDGAT1s for maximum return on oil content.

来源: *Frontiers in Plant Science*

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<http://agri.ckcest.cn/ass/77bbd368-3356-46ac-89bb-f50c9c0ffffb.pdf>

4. 'Ogura'-based 'CMS' lines with different nuclear backgrounds of cabbage revealed substantial diversity at morphological and molecular levels (具有不同细胞核背景且以Ogura为基础的不育系在形态和分子水平上都表现出巨大的多样性)

简介: A comprehensive study on characterization and genetic diversity analysis was carried out in 16 'Ogura'-based 'CMS' lines of cabbage using 14 agro-morphological traits and 29 SSR markers. Agro-morphological characterization depicted considerable variations for diferent horticultural traits studied. The genotype, ZHA-2, performed better for most of the economically important quantitative traits. Further, gross head weight (0.76), head length (0.60) and head width (0.83) revealed significant positive correlation with net head weight. Dendrogram based on 10 quantitative traits exhibited considerable diversity among diferent CMS lines and principle component analysis (PCA) indicated that net and gross head weight, and head length and width are the main components of divergence between 16 CMS lines of cabbage. In molecular study, a total of 58 alleles were amplified by 29 SSR primers, averaging to 2.0 alleles in each locus. High mean values of Shannon's Information index (0.62), expected (0.45) and observed (0.32) heterozygosity and polymorphic information content (0.35) depicted substantial polymorphism. Dendrogram based on Jaccard's similarity coefcient constructed two major groups and eight sub-groups, which revealed substantial diversity among diferent CMS lines. In overall, based on agro-morphological and molecular studies genotype RRMA, ZHA-2 and RCA were found most divergent. Hence, they have immense potential in future breeding programs for the high-yielding hybrid development in

cabbage.

来源：3 Biotech

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全文链接：

<http://agri.ckcest.cn/ass/51196f2a-0d63-4ae1-b753-a4cfbabd722b.pdf>