



2018年第23期总137期

蔬菜育种专题

本期导读

▶ 前沿资讯

1. 研究发现触发植物开花的蛋白质

▶ 学术文献

1. 甘蓝型油菜种子脂肪酸成分的无条件和有条件QTL分析
2. 通过高通量测序找到两种白菜型冬油菜中可对冷胁迫做出反应的miRNAs
3. 种子品质育种对油菜发芽的隐性影响
4. 转录组与生理学分析揭示AM1作为一种脱落酸(ABA)模拟配体可提高油菜抗旱能力

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▶ 前沿资讯

1. Researchers identify the cells that trigger flowering (研究发现触发植物开花的蛋白质)

简介: 到目前为止, 还不确定哪些细胞会产生被称为开花基因座 (FT) 的小蛋白质。康奈尔大学研究人员进行的一项新研究揭示了关键蛋白在触发植物开花前的具体形成位置, 同时指出FT的产生受到细胞间信号系统的调控。研究结果发表在《美国国家科学院院刊》(PANS) 上。许多植物的开花始于叶子感知日照的长度。此前已知, 长日照会开启拟南芥叶片合成和传递FT到植物维管组织的过程。FT被运输到茎尖、新叶顶点, 在这些部位促进花的形成。开花过程的调控很复杂, 因为FT的释放受到相互作用级联中的30多种蛋白质控制。由于叶脉非常小且被富含叶绿素的光合细胞覆盖, 因此很难识别产生FT的细胞。研究人员借助荧光蛋白来找出产生FT的韧皮部 (叶脉) 细胞。研究发现, 一种烟草的韧皮部中同样产生了FT。当这些伴胞被杀死后, 会延迟拟南芥和烟草的开花。通过对成花路径更加细致的研究, 发现杀死这些伴胞停止了FT的下游过程, 而不是上游, 证实FT起源于这些细胞, 并且FT的合成受一个大范围的细胞间信号系统调控。

来源: AAAS

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https://www.eurekalert.org/pub_releases/2018-04/cu-rit040518.php

▶ 学术文献

1. Unconditional and conditional QTL analyses of seed fatty acid composition in *Brassica napus* L. (甘蓝型油菜种子脂肪酸成分的无条件条件和有条件QTL分析)

简介: Background: The fatty acid composition of *B. napus*' seeds determines the oil's nutritional and industrial values, and affects seed germination. Many studies have reported correlations among C16:0, C18:0, C18:1, C18:2 and C18:3 based on phenotypic data; however, the genetic basis of the fatty acid composition in *B. napus* is still not well understood.

Results: In this study, unconditional and conditional quantitative trait locus (QTL) mapping analyses were conducted using a recombinant inbred line in six environments. In total, 21 consensus QTLs each for C16:0, C18:0 and C18:2, 16 for C18:1 and 22 for C18:3 were detected by unconditional mapping. The QTLs with overlapping confidence intervals were integrated into 71 pleiotropically unique QTLs by meta-analysis. Two major QTLs, uuqA5-6 and uuqA5-7, simultaneously affected the fatty acids, except C18:0, in most of environments, with the homologous genes fatty acid desaturase 2 (FAD2) and glycerol-3-phosphate sn-2-acyltransferase 5 (GPAT5) occurring in the confidence interval of uuqA5-6, while phosphatidic acid phosphohydrolase 1 (PAH1) was assigned to uuqA5-7. Moreover, 49, 30, 48, 60 and 45 consensus QTLs were detected for C16:0, C18:0, C18:1, C18:2 and C18:3, respectively, by the conditional mapping analysis. In total, 128 unique QTLs were

subsequently integrated from the 232 conditional consensus QTLs. A comparative analysis revealed that 63 unique QTLs could be identified by both mapping methodologies, and 65 additional unique QTLs were only identified in conditional mapping.

Conclusions: Thus, conditional QTL mapping for fatty acids may uncover numerous additional QTLs that were inhibited by the effects of other traits. These findings provide useful information for better understanding the genetic relationships among fatty acids at the QTL level.

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<http://agri.ckcest.cn/ass/2f65f1d5-1a6a-47e2-8326-0920783a9ce6.pdf>

2. Identification of cold stress responsive microRNAs in two winter turnip rape (*Brassica rapa* L.) by high throughput sequencing (通过高通量测序找到两种白菜型冬油菜中可对冷胁迫做出反应的miRNAs)

简介: Background: Low temperature is a major abiotic stress affecting the production of rapeseed in China by impeding plant growth and development. A comprehensive knowledge of small-RNA expression pattern in *Brassica rapa* under cold stress could improve our knowledge of microRNA-mediated stress responses.

Results: A total of 353 cold-responsive miRNAs, 84 putative novel and 269 conserved miRNAs, were identified from the leaves and roots of two winter turnip rape varieties 'Longyou 7' (cold-tolerant) and 'Tianyou 4' (cold-sensitive), which were stressed under -4°C for 8h. Eight conserved (miR166h-3p-1, miR398b-3p, miR398b-3p-1, miR408d, miR156a-5p, miR396h, miR845a-1, miR166u) and two novel miRNAs (Bra-novel-miR3153-5p and Bra-novel-miR3172-5p) were differentially expressed in leaves of 'Longyou 7' under cold stress. Bra-novel-miR3936-5p was up-regulated in roots of 'Longyou 7' under cold stress. Four and five conserved miRNAs were differentially expressed in leaves and roots of 'Tianyou 4' after cold stress. Besides, we found two conserved miRNAs (miR319e and miR166m-2) were down-regulated in non-stressed roots of 'Longyou 7' compared with 'Tianyou 4'. After cold stress, we found two and eight miRNAs were differentially expressed in leaves and roots of 'Longyou 7' compared with 'Tianyou 4'. The differentially expressed miRNAs between two cultivars under cold stress include novel miRNAs and the members of the miR166 and miR319 families. A total of 211 target genes for 15 known miRNAs and two novel miRNAs were predicted by bioinformatic analysis, mainly involved in metabolic processes and stress responses. Five differentially expressed miRNAs and predicted target genes were confirmed by quantitative reverse transcription PCR, and the expressional changes of target genes were negatively correlated to differentially expressed miRNAs. Our data indicated that some candidate miRNAs (e.g., miR166e, miR319, and Bra-novel-miR3936-5p) may play important roles in plant response to cold stress.

Conclusions: Our work indicates that miRNA and putative target genes mediated metabolic processes and stress responses are significant to cold tolerance in *B. rapa*.

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<http://agri.ckcest.cn/ass/ce643e44-c648-4258-9c88-62322f98b9d7.pdf>

3. Hidden Effects of Seed Quality Breeding on Germination in Oilseed Rape (*Brassica napus* L.) (种子品质育种对油菜发芽的隐性影响)

简介: Intense selection for specific seed qualities in winter oilseed rape breeding has had an inadvertent negative influence on seed germination performance. In a panel of 215 diverse winter oilseed rape varieties spanning over 50 years of breeding progress in winter-type rapeseed, we found that low seed erucic acid content and reduced seed glucosinolate content were significantly related with prolonged germination time. Genome-wide association mapping revealed that this relationship is caused by linkage drag between important loci for seed quality and germination traits. One QTL for mean germination time on chromosome A09 co-localized with significant but minor QTL for both seed erucic acid and seed glucosinolate content. This suggested either potential pleiotropy or close linkage of minor factors influencing all three traits. Therefore, a reduction in germination performance may be due to inadvertent co-selection of genetic variants associated with 00 seed quality that have a negative influence on germination. Our results suggest that marker-assisted selection of positive alleles for mean germination time within the modern quality pool can help breeders to maintain maximal germination capacity in new 00-quality oilseed rape cultivars.

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<http://agri.ckcest.cn/ass/1540b519-c941-42e3-bd00-ca92728bd0b4.pdf>

4. Transcriptome and physiological analyses reveal that AM1 as an ABA-mimicking ligand improves drought resistance in *Brassica napus* (转录组与生理学分析揭示AM1作为一种脱落酸 (ABA) 模拟配体可提高油菜抗旱能力)

简介: Abscisic acid (ABA) is the most important stress hormone in the regulation of plant adaptation to drought. Owing to the chemical instability and rapid catabolism of ABA, ABA mimic 1 (AM1) is frequently applied to enhance drought resistance in plants, but the molecular mechanisms governed by AM1 on improving drought resistance in *Brassica napus* are not entirely understood. To investigate the effect of AM1 on drought resistance at the physiological and molecular levels, exogenous ABA and AM1 were applied to the leaves of two *B. napus* genotypes (Q2 and Qinyou 8) given progressive drought stress. The results showed that the leaves of 50 μM ABA- and AM1-treated plants shared over 60% differential expressed genes and 90% of the enriched functional pathways in Qinyou 8 under drought. AM1 affected the expression of the genes involved in ABA signaling; they down-regulated pyrabactin resistance/PYR1-like (PYR/PYLs), up-regulated type 2C protein phosphatases

(PP2Cs), partially up-regulated sucrose non-fermenting 1-related protein kinase 2s (SnRK2s), and down-regulated ABA-responsive element (ABRE)-binding protein/ABRE-binding factors (AREB/ABFs). Additionally, AM1 treatment repressed the expression of photosynthesis-related genes, those mainly associated with the light reaction process. Moreover, AM1 decreased the stomatal conductance, the net photosynthetic rate, and the transpiration rate, but increased the relative water content in leaves and increased survival rates of two genotypes under drought stress. Our findings suggest that AM1 has a potential to improve drought resistance in *B. napus* by triggering molecular and physiological responses to reduce water loss and impair growth, leading to increased survival rates.

来源: Plant Growth Regulation

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<http://agri.ckcest.cn/ass/71285ac6-b6cd-4b7e-8aa9-e28850336216.pdf>