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## 蔬菜育种专题

### 本期导读

#### ► 学术文献

1. 油菜中与亚油酸合成相关的OPR基因的克隆及功能验证
2. 油菜中十字花科疟原虫抗性相关的蛋白质组水平研究
3. 转录组分析揭示不结球白菜对缺铁胁迫的分子响应机制
4. 冬油菜 (*Brassica napus* L.) 基因型多样性的多维分析
5. 油菜籽对PEG-6000诱导的干旱胁迫的形态-生理-生化反应

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## 学术文献

### 1. Clone and Function Verification of the OPR gene in Brassica napus Related to Linoleic Acid Synthesis (油菜中与亚油酸合成相关的OPR基因的克隆及功能验证)

简介: Fatty acid composition and content affect rapeseed oil quality. Fatty acid synthesis-related genes in rapeseed have been studied globally by researchers. Nevertheless, rapeseed oil is mainly composed of seven different fatty acids (FA), and each fatty acid was regulated by different genes. Furthermore, different FA affect each other, which needs continuous and in-depth research to obtain more clear results in Brassica napus.

In this paper, broad-scale miRNA expression profiles were constructed and 21 differentially expressed miRNAs were detected. GO enrichment analysis showed that most up-regulated proteins were involved in transcription factor activity and catalytic activity. KEGG pathway enrichment analysis indicated that 20 pathways involving 36 target genes were enriched, of which the bna00592 pathway may be involved in fatty acid metabolism. The results were verified using a quantitative real-time PCR (RT-qPCR) analysis, we found that the target gene of bna-miR156b > c > g was the OPR (12-oxo-phytyldienoic acid reductase). Four copies of OPR gene were found, and the over-expression vectors (pCAMBIA1300-35 s-OPR and pCAMBIA1300-RNAi-OPR) were constructed to verify their functions. In T<sub>1</sub> and T<sub>2</sub> generation, the content of linoleic acid (LA) increased significantly in OE but decreased in OPRi.

This is the first study to provide four copies of the OPR gene that regulates LA metabolism, can be used for the molecular mechanism of LA and optimizing fatty acid profiles in oilseed for breeding programs.

来源: BMC Plant Biology

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全文链接:

<http://agri.ckcest.cn/file1/M00/03/30/Csgk0YbKOLWAb7foAEV-hHdbbuc545.pdf>

### 2. A Proteome-Level Investigation Into Plasmodiophora brassicae Resistance in Brassica napus Canola (油菜中十字花科疟原虫抗性相关的蛋白质组水平研究)

简介: Clubroot of Brassicaceae, an economically important soil borne disease, is caused by Plasmodiophora brassicae Woronin, an obligate, biotrophic protist. This disease poses a serious threat to canola and related crops in Canada and around the globe causing significant losses. The pathogen is continuously evolving and new pathotypes are emerging, which necessitates the development of novel resistant canola cultivars to manage the disease. Proteins play a crucial role in many biological functions and the identification of differentially abundant proteins (DAP) using proteomics is a suitable approach to understand plant-pathogen interactions to assist in the development of gene specific markers for developing clubroot resistant (CR) cultivars. In this study, P. brassicae pathotype 3 (P3H)

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was used to challenge CR and clubroot susceptible (CS) canola lines. Root samples were collected at three distinct stages of pathogenesis, 7-, 14-, and 21-days post inoculation (DPI), protein samples were isolated, digested with trypsin and subjected to liquid chromatography with tandem mass spectrometry (LC-MS/MS) analysis. A total of 937 proteins demonstrated a significant ( $q$ -value  $< 0.05$ ) change in abundance in at least in one of the time points when compared between control and inoculated CR-parent, CR-progeny, CS-parent, CS-progeny and 784 proteins were significantly ( $q < 0.05$ ) changed in abundance in at least in one of the time points when compared between the inoculated- CR and CS root proteomes of parent and progeny across the three time points tested. Functional annotation of differentially abundant proteins (DAPs) revealed several proteins related to calcium dependent signaling pathways. In addition, proteins related to reactive oxygen species (ROS) biochemistry, dehydrins, lignin, thaumatin, and phytohormones were identified. Among the DAPs, 73 putative proteins orthologous to CR proteins and quantitative trait loci (QTL) associated with eight CR loci in different chromosomes including chromosomes A3 and A8 were identified. Proteins including BnaA02T0335400WE, BnaA03T0374600WE, BnaA03T0262200WE, and BnaA03T0464700WE are orthologous to identified CR loci with possible roles in mediating clubroot responses. In conclusion, these results have contributed to an improved understanding of the mechanisms involved in mediating response to *P. brassicae* in canola at the protein level.

来源: Front. Plant Sci

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[http://agri.ckcest.cn/file1/M00/10/02/Csgk0GJzhrOACwTKAAq9\\_877j1E294.pdf](http://agri.ckcest.cn/file1/M00/10/02/Csgk0GJzhrOACwTKAAq9_877j1E294.pdf)

### **3. Transcriptome Analysis Revealed the Molecular Response Mechanism of Non-heading Chinese Cabbage to Iron Deficiency Stress (转录组分析揭示不结球白菜对缺铁胁迫的分子响应机制)**

简介: Iron is a trace metal that is found in animals, plants, and the human body. Human iron absorption is hampered by plant iron shortage, which leads to anemia. Leafy vegetables are one of the most direct and efficient sources of iron for humans. Despite the fact that ferrotrophic disorder is common in calcareous soil, however, non-heading Chinese cabbage performs a series of reactions in response to iron deficiency stress that help to preserve iron homeostasis in vivo. In this study, we discovered that iron deficiency stress caused leaf yellowing and impeded plant development in both iron-deficient and control treatments by viewing or measuring phenotypic, chlorophyll content, and  $Fe^{2+}$  content in both iron-deficient and control treatments. We found a total of 9213 differentially expressed genes (DEGs) in non-heading Chinese cabbage by comparing root and leaf transcriptome data with iron deficiency and control treatments. For instance, 1927 DEGs co-expressed in root and leaf, including 897 up-regulated and 1030 down-regulated genes, respectively. We selected some key antioxidant genes, hormone signal transduction, iron absorption and transport, chlorophyll metabolism, and transcription factors involved in the regulation of iron deficiency stress utilizing GO enrichment, KEGG enrichment, multiple types of functional annotation, and Weighted Gene Co-expression Network Analysis (WGCNA). This study

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identifies prospective genes for maintaining iron homeostasis under iron-deficient stress, offering a theoretical foundation for further research into the molecular mechanisms of greater adaptation to iron-deficient stress, and perhaps guiding the development of iron-tolerant varieties.

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<http://agri.ckcest.cn/file1/M00/10/02/Csgk0GJzh0yAHTPmAGmErCQr5Hc747.pdf>

#### **4. Multidimensional Analysis of Diversity in Genotypes of Winter Oilseed Rape (*Brassica napus* L.) (冬油菜 (*Brassica napus* L.) 基因型多样性的多维分析)**

简介: The effect of genotype, environment (year, location) and their interaction on seed yield and important breeding traits of 25 genotypes of winter oilseed rape were investigated under field conditions in Greater Poland. Multi-environmental field experiments were conducted in a randomized block design with four replications during three growing seasons in two locations. Five traits, such as the beginning of flowering, seed yield and its structure, the length of siliques, the number of seeds per silique and the weight of 1000 seeds were recorded. The tested *Brassica* genotypes showed significant differences in terms of yield and other investigated traits across harvesting years and growing locations. Analysis of variance indicated that the main effects of genotypes, locations and years as well as all interactions were significant for all traits of study. The correlation coefficient between the investigated traits displayed strong negative relationships between seed yield and the beginning of flowering (except E2). The use of multivariate statistical methods in this study allowed for the simultaneous characterization of 25 tested genotypes in terms of several traits. Visualization of the experimental results and finally the distribution of *Brassica* genotypes in space of two first canonical variates showed a variation between the cultivars, double low, resynthesized and lines with changed fatty acid content in terms of yield and its components, as well as the beginning of flowering.

来源: Agronomy

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[http://agri.ckcest.cn/file1/M00/03/30/Csgk0YbKNeOABf\\_NADLFEr9U-Ek078.pdf](http://agri.ckcest.cn/file1/M00/03/30/Csgk0YbKNeOABf_NADLFEr9U-Ek078.pdf)

#### **5. Rapeseed Morpho-Physio-Biochemical Responses to Drought Stress Induced by PEG-6000 (油菜籽对PEG-6000诱导的干旱胁迫的形态-生理-生化反应)**

简介: Rapeseed is a valuable oil crop due to its high nutritious value and ample oil content. The current study provides a comparative analysis of 24 cultivars to better understand the performance and predict the adaptative mechanisms of drought-tolerant and drought-sensitive cultivars based on germination and morphophysiological traits during the early seedling stage using PEG-6000 simulated drought conditions. JYZ 158 and FY 520 (tolerant cultivars) and

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YG 2009 and NZ 1838 (sensitive cultivars) were selected to further explore the role of osmolytes and enzymatic activity in improving drought tolerance. This investigation illustrated that drought stress negatively influenced all studied cultivars; however, the degree of influence was different for each cultivar, suggesting their different potential for drought tolerance. Moreover, enzymatic and osmoregulatory mechanisms were highly efficient in tolerant cultivars compared to sensitive cultivars. Additionally, tolerant cultivars showed higher chlorophyll and lower malondialdehyde (MDA) contents versus sensitive cultivars under drought stress conditions. Higher drought tolerance coincided with higher enzymatic activity and osmolyte content. This work showed that JYZ 158 and FY 520 cultivars had higher drought tolerance, and might be a significant germplasm resource for breeding programs developing drought-tolerant rapeseed.

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<http://agri.ckcest.cn/file1/M00/03/30/Csgk0YbKNUKAadcMADYJjF13upk219.pdf>