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蔬菜育种专题

本期导读

► 学术文献

1. 甘蓝型油菜BnaNTT1调节质体ATP稳态以维持代谢和生长
2. Hi-C 和 RNA-Seq 的综合分析揭示了白菜 (*Brassica rapa* ssp. *chinensis*) 同源多倍体生长优势的分子机制
3. BnKAT2通过调节生长素和细胞分裂素信号通路正向调控甘蓝型油菜的主花序长度和角果数量
4. 十字花科长基因间非编码RNA的鉴定和功能注释

► 科技图书

1. 植物胁迫缓解剂类型、技术和功能

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学术文献

1. **Brassica napus BnaNTT1 modulates ATP homeostasis in plastids to sustain metabolism and growth (甘蓝型油菜BnaNTT1调节质体ATP稳态以维持代谢和生长)**

简介: The plastid-localized nucleotide triphosphate transporter (NTT) transports cytosolic adenosine triphosphate (ATP) into plastid to satisfy the needs of biochemistry activities in plastid. Here, we investigate the key functions of two conserved BnaNTT1 genes, BnaC06.NTT1b and BnaA07.NTT1a, in Brassica napus. Binding assays and metabolic analysis indicate that BnaNTT1 binds ATP/adenosine diphosphate (ADP), transports cytosolic ATP into chloroplast, and exchanges ADP into cytoplasm. Thylakoid structures are abnormal and plant growth is retarded in CRISPR mutants of BnaC06.NTT1b and BnaA07.NTT1a. Both BnaC06.NTT1b and BnaA07.NTT1a play important roles in the regulation of ATP/ADP homeostasis in plastid. Manipulation of BnaC06.NTT1b and BnaA07.NTT1a causes significant changes in glycolysis and membrane lipid composition, suggesting that increased ATP in plastid fuels more seed-oil accumulation. Together, this study implicates the vital role of BnaC06.NTT1b and BnaA07.NTT1a in plant metabolism and growth in B. napus.

来源: CELL REPORTS

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全文链接:

<http://agri.ckcest.cn/file1/M00/03/3A/Csgk0YdIt22AeEk3ADLuFjcpy08125.pdf>

2. **Integrated Analysis of Hi-C and RNA-Seq Reveals the Molecular Mechanism of Autopolyploid Growth Advantages in Pak Choi (Brassica rapa ssp. chinensis) (Hi-C 和 RNA-Seq 的综合分析揭示了白菜 (Brassica rapa ssp. chinensis) 同源多倍体生长优势的分子机制)**

简介: Polyploids generated by the replication of a single genome (autopolyploid) or synthesis of two or more distinct genomes (allopolyploid) usually show significant advantages over their diploid progenitors in biological characteristics, including growth and development, nutrient accumulation, and plant resistance. Whereas, the impacts of genomic replication on transcription regulation and chromatin structure in pak choi have not been explored fully. In this study, we observed the transcriptional and genomic structural alterations between diploid B. rapa (AA) and artificial autotetraploid B. rapa (AAAA) using RNA-seq and Hi-C. RNA-seq revealed 1,786 differentially expressed genes (DEGs) between the diploids and autotetraploids, including 717 down-regulated and 1,069 up-regulated genes in autotetraploids. Of all the 1,786 DEGs, 23 DEGs (10 down-regulated DEGs in autotetraploids) were involved in Compartment A-B shifts, while 28 DEGs (20 up-regulated DEGs in autotetraploids) participated in Compartment B-A shifts. Moreover, there were 15 DEGs in activated topologically associating domains (TADs) (9 up-regulated DEGs in

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diploids) and 80 DEGs in repressed TADs (49 down-regulated DEGs in diploids). Subsequently, eight DEGs with genomic structural variants were selected as potential candidate genes, including four DEGs involved in photosynthesis (BraA01003143, BraA09002798, BraA04002224, and BraA08000594), three DEGs related to chloroplast (BraA05002974, BraA05001662, and BraA04001148), and one DEG associated with disease resistance (BraA09004451), which all showed high expression in autotetraploids. Overall, our results demonstrated that integrative RNA-seq and Hi-C analysis can identify related genes to phenotypic traits and also provided new insights into the molecular mechanism of the growth advantage of polyploids.

来源: Front Plant Sci

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<http://agri.ckcest.cn/file1/M00/03/3A/Csgk0YdIxkiAe0c8ADPtRIiMJsY260.pdf>

3. BnKAT2 Positively Regulates the Main Inflorescence Length and Silique Number in Brassica napus by Regulating the Auxin and Cytokinin Signaling Pathways (BnKAT2通过调节生长素和细胞分裂素信号通路正向调控甘蓝型油菜的主花序长度和角果数量)

简介: Brassica napus is the dominant oil crop cultivated in China for its high quality and high yield. The length of the main inflorescence and the number of siliques produced are important traits contributing to rapeseed yield. Therefore, studying genes related to main inflorescence and silique number is beneficial to increase rapeseed yield. Herein, we focused on the effects of BnKAT2 on the main inflorescence length and silique number in B. napus. We explored the mechanism of BnKAT2 increasing the effective length of main inflorescence and the number of siliques through bioinformatics analysis, transgenic technology, and transcriptome sequencing analysis. The full BnKAT2(BnaA01g09060D) sequence is 3674 bp, while its open reading frame is 2055 bp, and the encoded protein comprises 684 amino acids. BnKAT2 is predicted to possess two structural domains, namely KHA and cNMP-binding domains. The overexpression of BnKAT2 effectively increased the length of the main inflorescence and the number of siliques in B. napus, as well as in transgenic Arabidopsis thaliana. The type-A Arabidopsis response regulator (A-ARR), negative regulators of the cytokinin, are downregulated in the BnKAT2-overexpressing lines. The Aux/IAA, key genes in auxin signaling pathways, are downregulated in the BnKAT2-overexpressing lines. These results indicate that BnKAT2 might regulate the effective length of the main inflorescence and the number of siliques through the auxin and cytokinin signaling pathways. Our study provides a new potential function gene responsible for improvement of main inflorescence length and silique number, as well as a candidate gene for developing markers used in MAS (marker-assisted selection) breeding to improve rapeseed yield.

来源: Plants

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4. Identification and functional annotation of long intergenic non-coding RNAs in Brassicaceae (十字花科长基因间非编码RNA的鉴定和功能注释)

简介: Long intergenic noncoding RNAs (lincRNAs) are a large yet enigmatic class of eukaryotic transcripts that can have critical biological functions. The wealth of RNA-sequencing (RNA-seq) data available for plants provides the opportunity to implement a harmonized identification and annotation effort for lincRNAs that enables cross-species functional and genomic comparisons as well as prioritization of functional candidates. In this study, we processed >24 Tera base pairs of RNA-seq data from >16,000 experiments to identify ~130,000 lincRNAs in four Brassicaceae: *Arabidopsis thaliana*, *Camelina sativa*, *Brassica rapa*, and *Eutrema salsugineum*. We used nanopore RNA-seq, transcriptome-wide structural information, peptide data, and epigenomic data to characterize these lincRNAs and identify conserved motifs. We then used comparative genomic and transcriptomic approaches to highlight lincRNAs in our data set with sequence or transcriptional conservation. Finally, we used guilt-by-association analyses to assign putative functions to lincRNAs within our data set. We tested this approach on a subset of lincRNAs associated with germination and seed development, observing germination defects for *Arabidopsis* lines harboring T-DNA insertions at these loci. LincRNAs with Brassicaceae-conserved putative miRNA binding motifs, small open reading frames, or abiotic-stress modulated expression are a few of the annotations that will guide functional analyses into this cryptic portion of the transcriptome.

来源: The Plant Cell

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<http://agri.ckcest.cn/file1/M00/10/0C/Csgk0GLyFmuAWAYTAF9mtYJnpzI726.pdf>

➤ 科技图书

1. Plant Stress Mitigators - Types, Techniques and Functions (植物胁迫缓解剂类型、技术和功能)

简介: Plant Stress Mitigators: Types, Techniques and Functions presents a detailed contextual discussion of various stressors on plant health and yield, with accompanying insights into options for limiting impacts using chemical elicitors, bio-stimulants, breeding techniques and agronomical techniques such as seed priming, cold plasma treatment, and nanotechnology, amongst others. The book explores the various action mechanisms for enhancing plant growth and stress tolerance capacity, including nutrient solubilizing and mobilizing, biocontrol activity against plant pathogens, phytohormone production, soil conditioners, and many more unrevealed mechanisms. This book combines research, methods, opinion, perspectives and reviews, dissecting the stress alleviation action of different plant stress mitigators on crops grown under optimal and sub-optimal growing conditions (abiotic and biotic stresses).

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