



2023年第3期总378期

蔬菜育种专题

本期导读

► 学术文献

1. 代谢组学分析揭示了芥菜茎发育过程中糖和酸的动态积累
2. 利用单细胞转录组测序, 揭示大白菜显性亚基因组表达和对热胁迫的转录反应
3. 干旱和盐碱胁迫下生育酚、水杨酸和抗坏血酸对甘蓝型油菜两个基因型农艺性状的交互作用
4. 甘蓝型油菜抗病基因同源序列拷贝数变异研究

► 科技图书

1. 抗非生物胁迫蔬菜作物的基因组设计

中国农业科学院农业信息研究所

联系人: 张晓静; 祁冉; 顾亮亮

联系电话: 010-51503648

邮箱: agri@ckcest.cn

2023年1月16日

更多资讯 尽在农业专业知识服务系统:<http://agri.ckcest.cn/>

学术文献

1. Metabolomics Analysis Reveals Dynamic Accumulation of Sugar and Acid during Stem Development of *Brassica juncea* (代谢组学分析揭示了芥菜茎发育过程中糖和酸的动态积累)

简介: The composition and content of sugar and acid are important indicators of organ development and the quality of horticultural products. *B. juncea* is an important vegetable in the cruciferous family, with a swollen fleshy stem as the edible organ. Elucidating the characteristics of sugar and acid accumulation during stem expansion of stem mustard and its regulatory mechanism could enhance stem quality. In this study, physiological indicators such as dry matter content, sugar-acid content and related enzyme activities were measured in eight stages of the tumorous stem. The results showed that the sugar and sucrose contents initially increased and then decreased during stem development: Sucrose exhibited a positive correlation with sucrose synthase and sucrose phosphate synthase, while acid content was highly positively correlated with malate dehydrogenase. Further analysis of the dynamic patterns of sugar and acid metabolite contents using metabolomics showed that 1097 metabolites were detected, including 229 organic acids and derivatives, 109 lipids, and other metabolites. Metabolic pathway enrichment analysis showed that metabolites were significantly enriched in organic acids, amino acids, glycolysis/gluconeogenesis, starch, and sucrose metabolism. Analysis of the sugar pathway and the tricarboxylic acid cycle revealed obvious differences in the content and type of metabolites, with most upregulated metabolites in S3 and S4. The expression patterns of enzyme genes associated with the biosynthesis and accumulation of sugar and acid metabolites were found based on differentially expressed genes at different developmental stages, and gene expression levels were verified by qPCR, which showed that the expression patterns of enzyme genes associated with this pathway were highly consistent with the metabolite accumulation. These results suggest that amino acids, sugars, and acids play a critical role in regulating the development of tumorous stems. Results of the present study offer a theoretical basis to improving the quality of mustard by using a metabolomics approach to determine the dynamics of metabolites and related regulatory enzymes during development and the correlation between these levels, which provides novel insights into the potential mechanisms underlying sugar and acid metabolism.

来源: Agronomy

发布日期: 2022-12-19

全文链接:

http://agri.ckcest.cn/file1/M00/10/1A/Csgk0GO_aU-AakEIAEeRTX8UxYY482.pdf

2. Single-cell transcriptome reveals dominant subgenome expression and transcriptional response to heat stress in Chinese cabbage (利用单细胞转录组测序, 揭示大白菜显性亚基因组表达和对热胁迫的转录反应)

简介: Chinese cabbage (*Brassica rapa* ssp. *pekinensis*) experienced a whole-genome

更多资讯 尽在农业专业知识服务系统: <http://agri.ckcest.cn/>

triplication event and thus has three subgenomes: least fractioned, medium fractioned, and most fractioned subgenome. Environmental changes affect leaf development, which in turn influence the yield. To improve the yield and resistance to different climate scenarios, a comprehensive understanding of leaf development is required including insights into the full diversity of cell types and transcriptional networks underlying their specificity.

Here, we generate the transcriptional landscape of Chinese cabbage leaf at single-cell resolution by performing single-cell RNA sequencing of 30,000 individual cells. We characterize seven major cell types with 19 transcriptionally distinct cell clusters based on the expression of the reported marker genes. We find that genes in the least fractioned subgenome are predominantly expressed compared with those in the medium and most fractioned subgenomes in different cell types. Moreover, we generate a single-cell transcriptional map of leaves in response to high temperature. We find that heat stress not only affects gene expression in a cell type-specific manner but also impacts subgenome dominance.

Our study highlights the transcriptional networks in different cell types and provides a better understanding of transcriptional regulation during leaf development and transcriptional response to heat stress in Chinese cabbage.

来源: Genome Biology

发布日期: 2022-12-19

全文链接:

<http://agri.ckcest.cn/file1/M00/03/48/Csgk0YgWHLsAdNZzAHm0mNrr5JE226.pdf>

3. Interactive Effect of Tocopherol, Salicylic Acid and Ascorbic Acid on Agronomic Characters of Two Genotypes of Brassica napus L. Under Induced Drought and Salinity Stresses (干旱和盐碱胁迫下生育酚、水杨酸和抗坏血酸对甘蓝型油菜两个基因型农艺性状的交互作用)

简介: Several agricultural systems are vulnerable to the harmful effects of climate change in today's increasingly vulnerable world. Drought and salinity are two major factors in climate change that can severely slow down the development of many crops. This study determined the influence of induced drought and salinity on growth of two varieties of Brassica napus L. (Shiralee and Vanguard), after priming with salicylic acid, ascorbic acid and tocopherol. Seed priming significantly promoted seed germination and reduced the normal germination time of seeds under both induced stressors. Significant increase in shoot length, shoot and root fresh weight, dry shoot weight of seedling was found for all the primed seeds as compared to non-primed seeds of both cultivars. Results showed that absolute growth rate of both varieties were remarkably influenced by the imposed drought as compared to salinity treatments. Relative growth rate, net assimilation rate, seed germination index, Timson germination index were negatively affected by 150 mM NaCl concentration for the vanguard cultivar. According to results of scanning electron microscope (SEM), osmoprimed seeds increased stomatal physiology and epidermal vigor of both cultivars significantly by boosting the water potential. Response of both B. napus cultivars was found different under induced drought and

更多资讯 尽在农业专业知识服务系统: <http://agri.ckcest.cn/>

salinity treatments. It has been concluded from the results that, seed priming with growth regulators such as tocopherol, ascorbic acid and salicylic acid is considered as useful technique for enhancing the germination and growth responses of *B. napus* under drought and salinity stresses.

来源: Gesunde Pflanzen

发布日期:2022-12-15

全文链接:

<http://agri.ckcest.cn/file1/M00/03/48/Csgk0YgWHj6AJ1BhADahbpA-k3M606.pdf>

4. Copy Number Variation among Resistance Genes Analogues in *Brassica napus* (甘蓝型油菜抗病基因同源序列拷贝数变异研究)

简介: Copy number variations (CNVs) are defined as deletions, duplications and insertions among individuals of a species. There is growing evidence that CNV is a major factor underlining various autoimmune disorders and diseases in humans; however, in plants, especially oilseed crops, the role of CNVs in disease resistance is not well studied. Here, we investigate the genome-wide diversity and genetic properties of CNVs in resistance gene analogues (RGAs) across eight *Brassica napus* lines. A total of 1137 CNV events (704 deletions and 433 duplications) were detected across 563 RGAs. The results show CNVs are more likely to occur across clustered RGAs compared to singletons. In addition, 112 RGAs were linked to a blackleg resistance QTL, of which 25 were affected by CNV. Overall, we show that the presence and abundance of CNVs differ between lines, suggesting that in *B. napus*, the distribution of CNVs depends on genetic background. Our findings advance the understanding of CNV as an important type of genomic structural variation in *B. napus* and provide a resource to support breeding of advanced canola lines.

来源: Genes

发布日期:2022-11-04

全文链接:

http://agri.ckcest.cn/file1/M00/10/1A/Csgk0GO_ZxmAEvVJABrGH6RdMd0782.pdf

科技图书

1. Genomic Designing for Abiotic Stress Resistant Vegetable Crops (抗非生物胁迫蔬菜作物的基因组设计)

简介: This book presents deliberations on molecular and genomic mechanisms underlying the interactions of crop plants to the abiotic stresses caused by heat, cold, drought, flooding, submergence, salinity, acidity, etc., important to develop resistant crop varieties. Knowledge on the advanced genetic and genomic crop improvement strategies including molecular breeding, transgenics, genomic-assisted breeding, and the recently emerging genome editing for developing resistant varieties in vegetable crops is imperative for addressing FHNEE (food, health, nutrition, energy, and environment) security. Whole genome sequencing of these crops followed by genotyping-by-sequencing has provided precise information

更多资讯 尽在农业专业知识服务系统:<http://agri.ckcest.cn/>

regarding the genes conferring resistance useful for gene discovery, allele mining, and shuttle breeding which in turn opened up the scope for 'designing' crop genomes with resistance to abiotic stresses.

来源: Springer

发布日期: 2022-08-21

全文链接:

http://agri.ckcest.cn/file1/M00/10/1A/Csgk0GO_b0-AShnaAASiVpBBB4023.pdf