



2023年第4期总379期

蔬菜育种专题

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► 学术文献

1. Marker-Assisted Pyramiding of CRa and CRd Genes to Improve the Clubroot Resistance of Brassica rapa (利用CRa 和 CRd 基因分子标记辅助聚合提高甘蓝根肿病抗性的研究)

简介: Clubroot, caused by *Plasmodiophora brassicae*, is an economically important soil-borne disease that threatens Brassicaceae crops worldwide. In recent years, the incidence area of Chinese cabbage (*Brassica rapa* ssp. *pekinensis*) clubroot disease has increased, which severely affects the yield and quality of Chinese cabbage. The resistance of varieties harboring the single clubroot-resistance (CR) gene is easily broken through by *P. brassicae* pathotypes. CRa and CRd, genetically identified in *B. rapa*, are CR genes known to be highly resistant to different *P. brassicae* pathotypes. In our study, we perform the gene pyramiding of CRa and CRd in Chinese cabbages through marker-assisted selection (MAS), and develop homozygous pyramided lines. The newly generated pyramided lines exhibit greater resistance to six different pathotypes than that of two parental lines carrying a single CR gene. This study provides new CR-gene-pyramided lines for the development of clubroot-resistant Brassica varieties for future breeding programs.

来源: Genes

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<http://agri.ckcest.cn/file1/M00/10/1B/Csgk0GPEqoSAFcZCAB2gax2RCJA776.pdf>

2. A high-efficiency PEG-Ca²⁺-mediated transient transformation system for broccoli protoplasts (高效 PEG-Ca²⁺ 介导的青花菜原生质体瞬时转化体系研究)

简介: Transient transformation of plant protoplasts is an important method for studying gene function, subcellular localization and plant morphological development. In this study, an efficient transient transformation system was established by optimizing the plasmid concentration, PEG4000 mass concentration and genotype selection, key factors that affect transformation efficiency. Meanwhile, an efficient and universal broccoli protoplast isolation system was established. Using 0.5% (w/v) cellulase R-10 and 0.1% (w/v) pectolyase Y-23 to hydrolyze broccoli cotyledons of three different genotypes for 3 h, the yield was more than 5×10^6 mL/g, and the viability was more than 95%, sufficient to meet the high standards for protoplasts to be used in various experiments. The average transformation efficiency of the two plasmid vectors PHG-eGFP and CP507-YFP in broccoli B1 protoplasts were 61.4% and 41.7%, respectively. Using this system, we successfully performed subcellular localization of the products of three target genes (the clubroot resistance gene CRa and two key genes regulated by glucosinolates, BoI029100 and BoI031350). The results showed that the products of all three genes were localized in the nucleus. The high-efficiency transient transformation system for broccoli protoplasts constructed in this study makes it possible to reliably acquire high-viability protoplasts in high yield. This research provides important technical support

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for international frontier research fields such as single-cell sequencing, spatial transcriptomics, plant somatic hybridization, gene function analysis and subcellular localization.

来源: Front Plant Sci

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<http://agri.ckcest.cn/file1/M00/03/49/Csgk0YgbX1qAPKucAi6WDj6nuTg085.pdf>

3. The analysis of lysine succinylation modification reveals the mechanism of oxybenzone damaging of pakchoi (*Brassica rapa* L. ssp. *chinensis*) (通过对赖氨酸琥珀酰化修饰的分析, 揭示了氧苯酮对小白菜的损伤机理)

简介: Oxybenzone (OBZ), one of a broad spectrum of ultraviolet (UV) absorbents, has been proven to be harmful to both plants and animals, while omics analysis of big data at the molecular level is still lacking. Lysine succinylation (Ksuc) is an important posttranslational modification of proteins that plays a crucial role in regulating the metabolic network in organisms under stress. Here, we report the changes in intracellular Ksuc modification in plants under OBZ stress. A total of 1276 succinylated sites on 507 proteins were identified. Among these sites, 181 modified proteins were hypersulfinylated/succinylated in OBZ-stressed pakchoi leaves. Differentially succinylated proteins (DSPs) are distributed mainly in the chloroplast, cytoplasm, and mitochondria and are distributed mainly in primary metabolic pathways, such as reactive oxygen species (ROS) scavenging, stress resistance, energy generation and transfer, photosynthetic carbon fixation, glycolysis, and the tricarboxylic acid (TCA) cycle. Comprehensive analysis shows that Ksuc mainly changes the carbon flow distribution, enhances the activity of the antioxidant system, affects the biosynthesis of amino acids, and increases the modification of histones. The results of this study first showed the profiling of the Ksuc map under OBZ treatment and proposed the adaptive mechanism of pakchoi in response to pollutants and other abiotic stresses at the posttranslational level, which revealed the importance of Ksuc in the regulation of various life activities and provides a reference dataset for future research on molecular function.

来源: Front Plant Sci

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<http://agri.ckcest.cn/file1/M00/03/49/Csgk0YgbXiGAHfQBACbdBzT3nN4719.pdf>

4. A Comparative Study on the Nutrients, Mineral Elements, and Antioxidant Compounds in Different Types of Cruciferous Vegetables (不同类型十字花科蔬菜营养成分、矿质元素和抗氧化化合物的比较研究)

简介: Studies on the diversity within and among cabbage (*Brassica oleracea* L. var. *capitata* L.), cauliflower (*Brassica oleracea* var. *botrytis*), and Chinese cabbage (*Brassica rapa* L. ssp. *pekinensis*) variants are essential for the development of healthy diets. However, most studies

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on them have been limited to a single species, with little integrated analysis between them. In this study, the diversity within and among these species and varieties is assessed by determining the contents of 15 major characteristic nutrients, antioxidants, and minerals in 12 varieties of cabbage, 9 varieties of cauliflower, and 12 varieties of Chinese cabbage cultivated under the same conditions. The results show that there are significant differences in the compositional distributions of cabbage, cauliflower, and Chinese cabbage. Cabbage has the highest contents of soluble sugars ($27.73 \text{ mg} \cdot \text{kg}^{-1} \text{ FW}$), flavonoids ($5.90 \text{ mg} \cdot \text{g}^{-1} \text{ FW}$), and Fe ($46.90 \text{ mg} \cdot \text{kg}^{-1} \text{ DW}$). Cauliflower is an ideal source of soluble protein ($603.04 \text{ mg} \cdot \text{kg}^{-1} \text{ FW}$), polyphenols ($1.53 \text{ mg} \cdot \text{g}^{-1} \text{ FW}$), glucosinolates ($25.27 \mu\text{mol} \cdot \text{g}^{-1} \text{ FW}$), and Cu ($4.25 \text{ mg} \cdot \text{kg}^{-1} \text{ DW}$). Chinese cabbage is rich in vitamin C ($0.45 \text{ mg} \cdot \text{g}^{-1} \text{ FW}$) and minerals (K, Ca, Mg, P, Mn, and Zn, at $9206.67 \text{ mg} \cdot \text{kg}^{-1} \text{ DW}$, $3297.00 \text{ mg} \cdot \text{kg}^{-1} \text{ DW}$, $3322.79 \text{ mg} \cdot \text{kg}^{-1} \text{ DW}$, $5614.78 \text{ mg} \cdot \text{kg}^{-1} \text{ DW}$, $15.36 \text{ mg} \cdot \text{kg}^{-1} \text{ DW}$, and $21.87 \text{ mg} \cdot \text{kg}^{-1} \text{ DW}$, respectively). There is a correlation between the quality, antioxidant properties, and minerals of the three species. In principal component analysis, a wide distribution of cabbage varieties and a high degree of overlap with the confidence ellipse of cauliflower are observed, indicating that certain cabbage varieties share compositional characteristics with cauliflower. These findings provide a reference for selecting varieties with higher nutritional value and antioxidant properties, as well as breeding new varieties.

来源: Agronomy

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<http://agri.ckcest.cn/file1/M00/03/49/Csgk0YgbXJAbW-dABa82SWJn9Y494.pdf>

5. Genome-Wide Identification and Expression Analysis of BrATGs and Their Different Roles in Response to Abiotic Stresses in Chinese Cabbage (大白菜BrATGs的全基因组鉴定和表达分析及其在非生物胁迫反应中的不同作用)

简介: Autophagy is an important degradation pathway that maintains cellular homeostasis in living organisms and plays a key role in plant fitness and immunity. To date, more than 30 autophagy-related genes (ATGs) have been identified in model plants such as Arabidopsis. However, autophagy in Chinese cabbage, the largest cultivated vegetable crop in China, has scarcely been studied. We identified 64 Chinese cabbage autophagy-associated genes, named BrATGs, at the genome-wide level. The majority of the BrATGs were highly conserved over a long evolutionary period, and the expression patterns indicated that BrATGs were most highly expressed in the healing tissues and flowers. Furthermore, BrATGs responded to the stresses of the heavy metal Cd, drought, salt, and low and high temperatures to varying degrees. Among them, BrATG8c/8j was specifically induced in response to drastic temperature changes; BrATG4c was upregulated only in response to drought and salt stress; and BrATG8f/10/VTI12C was highly expressed only in response to Cd stress. This work will advance the understanding of the molecular mechanisms underlying the abiotic stress response in Chinese cabbage.

来源: Agronomy

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