蔬菜育种专题

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➤ 学术文献

1．Growth, physiological, and temperature characteristics in chinese cabbage pakchoi as affected by Cd- stressed conditions and identifying its main controlling factors using PLS model（镉胁迫对小白菜生长、生理和温度特性的影响及其主要控制因素的PLS模型）

简介：Although hormesis induced by heavy metals is a well-known phenomenon, the involved biological mechanisms are not fully understood. Cadmium (Cd) is a prevalent heavy metal in the environment. Exposure of Cd, via intake or consumption of Cd-contaminated air or food, poses a huge threat to human health. Chinese cabbage pakchoi (Brassica chinensis L.) is widely planted and consumed as a popular vegetable in China. Therefore, study-ing the response of Chinese cabbage pakchoi to Cd- stressed conditions is critical to assess whether cabbage can accumulate Cd and serve as an important Cd exposure pathway to human beings. In this study, we investigated the influence of Cd stress on growth, photosynthetic physiology, antioxidant enzyme activities, nutritional quality, ana-tomical structure, and canopy temperature in Chinese cabbage pakchoi. A partial least squares (PLS) model was used to quantify the relationship between physical and chemical indicators with Cd accumulation in cabbage, and identify the main controlling factors.

Results showed that Cd stress significantly inhibited cabbage's growth and development. When Cd stress was increased, the phenotypic indicators were significantly reduced. Meanwhile, Cd stress significantly enhanced the oxidative stress response of cabbage, such as the activities of catalase (CAT), superoxide dismutase (SOD), peroxidase (POD), ascorbate peroxidase (APX), and the content of malondialdehyde (MDA) in leaves. Such a change tended to increase fenestrated tissues' thickness but decrease the thickness of leaf and spongy tissues. Moreover, Cd stress significantly increased soluble sugar, protein, and vitamin C contents in leaves as well as the temperature in the plant canopy. The PLS model analysis showed that the studied phenotypic and physicochemical indicators had good relationships with Cd accumulation in roots, shoots, and the whole plant of cabbage, with high coefficient of determi-nation (R^2) values of 0.891, 0.811, and 0.845, and low relative percent deviation (RPD) values of 3.052, 2.317, and 2.557, respectively. Furthermore, through analyzing each parameter's variable importance for projection (VIP) value, the SOD activity was identified as a key factor for indicating Cd accumulation in cabbage. Meanwhile, the effects of CAT on Cd accumulation in cabbage and the canopy mean temperature were also high.

Cd stress has significant inhibitory effects and can cause damage cabbage's growth and development, and the SOD activity may serve as a key factor to indicate Cd uptake and accumulation in cabbage.

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2．Comprehensive transcriptome analysis reveals heat-responsive genes in flowering Chinese cabbage (Brassica campestris L. ssp. chinensis) using RNA sequencing(利用 RNA 测序技术对开花大白菜 (Brassica campestris L. ssp. chinensis)热反应基因进行全转录组分析)

简介：Flowering Chinese cabbage (Brassica campestris L. ssp. chinensis var. utilis Tsen et Lee, 2n=20, AA) is a vegetable species in southern parts of China that faces high temperatures in the summer and winter seasons. While heat stress adversely impacts plant productivity and survival, the underlying molecular and biochemical causes are poorly understood. This study investigated the gene expression profiles of heat-sensitive (HS) '3T-6' and heat-tolerant (HT) 'Youlu-501' varieties of flowering Chinese cabbage in response to heat stress using RNA sequencing. Among the 37,958 genes expressed in leaves, 20,680 were differentially expressed genes (DEGs) at 1, 6, and 12 h, with 1,078 simultaneously expressed at all time points in both varieties. Hierarchical clustering analysis identified three clusters comprising 1,958, 556, and 591 down-regulated, up-regulated, and up-and/or down-regulated DEGs (3205 DEGs; 8.44%), which were significantly enriched in MAPK signaling, plant-pathogen interactions, plant hormone signal transduction, and brassinosteroid biosynthesis pathways and involved in stimulus, stress, growth, reproductive, and defense responses. Transcription factors, including MYB (12), NAC (13), WRKY (11), ERF (31), HSF (17), bHLH (16), and regulatory proteins such as PAL, CYP450, and photosystem II, played an essential role as effectors of homeostasis, kinases/phosphatases, and photosynthesis. Among 3205 DEGs, many previously reported genes underlying heat stress were also identified, e.g., BraWRKY25, BraHSP70, BraHSPB27, BraCYP71A23, BraPYL9, and BraA05g032350.3C. The genome-wide comparison of HS and HT provides a solid foundation for understanding the molecular mechanisms of heat tolerance in flowering Chinese cabbage.

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3．Comparison of an Artificial Neural Network and a Response Surface Model during the Extraction of Selenium-Containing Protein from Selenium-Enriched Brassica napus L.(人工神经网络与响应面模型在富硒甘蓝型油菜富硒蛋白提取中的比较)

简介：n this study, the extraction conditions for selenium-enriched rape protein (SEP) were optimized by applying a response surface methodology (RSM) and artificial neural network (ANN) model, and then, the optimal conditions were obtained using a genetic algorithm (GA). Then, the antioxidant power of the SEP was examined by using the DPPH, ABTS, and CCK-8 (Cell Counting Kit-8), and its anticancer activities were explored by conducting a cell migration test. The results showed that compared with the RSM model, the ANN model was more accurate with a higher determination coefficient and fewer errors when it was applied to

optimize the extraction method. The data obtained for SEP using a GA were as follows: the extraction temperature was 59.4 ℃, the extraction time was 3.0 h, the alkaline concentration was 0.24 mol/L, the liquid-to-material ratio was 65.2 mL/g, and the predicted content of protein was 58.04 mg/g. The protein was extracted under the conditions obtained by the GA; the real content of protein was 57.69 mg/g, and the protein yield was 61.71%. Finally, as the concentration of the selenium-containing protein increased, it showed increased ability in scavenging free radicals and was influential in inhibiting the proliferation and migration of HepG2 cells.

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4．CRISPR/Cas9-mediated editing of double loci of BnFAD2 increased the seed oleic acid content of rapeseed (Brassica napus L.)(CRISPR/Cas9介导的 BnFAD2双基因座编辑提高了油菜种子油酸含量)

简介：Seed oleic acid is an important quality trait sought in rapeseed breeding programs. Many methods exist to increase seed oleic acid content, such as the CRISPR/Cas9-mediated genome editing system, yet there is no report on seed oleic acid content improvement via this system's precise editing of the double loci of BnFAD2. Here, a precise CRISPR/Cas9-mediated genome editing of the encoded double loci (A5 and C5) of BnFAD2 was established. The results demonstrated high efficiency of regeneration and transformation, with the rapeseed genotype screened in ratios of 20.18% and 85.46%, respectively. The total editing efficiency was 64.35%, whereas the single locus- and double locus-edited ratios were 21.58% and 78.42%, respectively. The relative proportion of oleic acid with other fatty acids in seed oil of mutants was significantly higher for those that underwent the editing on A5 copy than that on C5 copy, but it was still less than 80%. For double locus-edited mutants, their relative proportion of oleic acid was more than 85% in the T_1 and T_4 generations. A comparison of the sequences between the double locus-edited mutants and reference showed that no transgenic border sequences were detected from the transformed vector. Analysis of the BnFAD2 sequence on A5 and C5 at the mutated locus of double loci mutants uncovered evidence for base deletion and insertion, and combination. Further, no editing issue of FAD2 on the copy of A1 was detected on the three targeted editing regions. Seed yield, yield component, oil content, and relative proportion of oleic acid between one selected double loci-edited mutant and wild type were also compared. These results showed that although the number of siliques per plant of the wild type was significantly higher than those of the mutant, the differences in seed yield and oil content were not significant between them, albeit with the mutant having a markedly higher relative proportion of oleic acid. Altogether, our results confirmed that the established CRISPR/Cas9-mediated genome editing of double loci (A5 and C5) of the BnFAD2 can precisely edit the targeted genes, thereby enhancing the seed oleic acid content to a far greater extent than can a single locus-editing system.

5．Identification of a Leafy Head Formation Related Gene in Chinese Cabbage (Brassica rapa L. ssp. pekinensis)(大白菜（Brassica rapa L.ssp.pekinensis）叶头形成相关基因的鉴定)

简介：Leafy head formation is one of the most important characteristics of Chinese cabbage, and the process is regulated by a series of genes and environmental factors. In this study, a non-heading short leaf mutant slm was identified from an ethyl methane sulfonate mutagenesis (EMS) population of the heading Chinese cabbage line FT. The most significant phenotypic characteristics of slm was shortening leaves and increasing leaf numbers, which led to failure to form a leafy head. Genetic analysis showed that a single recessive gene Brslm was responsible for the mutant phenotype. Mutmap analysis suggested that Brslm was located on chromosome A07, and four candidate genes were predicted. KASP analysis demonstrated that BraA07g039390.3C was the target gene of the candidates. BraA07g039390.3C is a homologous to Arabidopsis CLV1 encoding receptor kinase with an extracellular leucine-rich domain. Sequencing analysis revealed that a single SNP from G to A occurred in 904th nucleotide of Brclv1, which resulted in the change of the 302nd amino acid from Asp to Asn. The SNP was co-segregated with the mutant phenotype in F_2 individuals and located on the conserved domains. These results indicated that BrCLV1 was the mutant gene for slm which led to shortening leaves and increasing leaf numbers, disrupting the leafy heading formation in FT. These findings contribute to revealing the BrCLV1 function in leafy head formation in Chinese cabbage.