



2022年第20期总343期

蔬菜育种专题

本期导读

► 学术文献

1. 芸苔属 (*Brassica campestris*, syn. *Brassica rapa*) ssp 基因组学开放获取平台
2. 提升CO₂浓度对十字花科植物物种和品种挥发物排放、光合特性和色素含量的影响
3. WRKY33介导的吲哚芥子油苷代谢途径赋予拟南芥和芸苔属作物对芸苔链格孢的抗性
4. 甘蓝类蔬菜中挥发性硫化物和S-甲基-L-半胱氨酸亚砷的形成
5. 植物对冷胁迫的反应：冷胁迫改变抽穗型泡菜白菜 (*Brassica rapa* L. ssp. *Pekinensis*) 的抗氧化代谢

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

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学术文献

1. Non-Heading Chinese Cabbage Database: An Open-Access Platform for the Genomics of *Brassica campestris* (syn. *Brassica rapa*) ssp. *chinensis* (芸苔属(*Brassica campestris*, syn. *Brassica rapa*) ssp基因组学开放获取平台)

简介: The availability of a high-quality genome sequence of *Brassica campestris* ssp. *chinensis* NHCC001 has paved the way for deep mining of genome data. We used the *B. campestris* NHCC001 draft genome to develop a comprehensive database, known as the non-heading Chinese cabbage database, which provides access to the *B. campestris* NHCC001 genome data. The database provides 127,347 SSR, from which 382,041 pairs of primers were designed. NHCCDB contains information on 105,360 genes, which were further classified into 63 transcription factor families. Furthermore, NHCCDB provides eight kinds of tools for biological or sequencing data analyses, including sequence alignment tools, functional genomics tools, comparative genomics tools, motif analysis tools, genome browser, primer design, and SSR analysis tools. In addition, eight kinds of graphs, including a box plot, Venn diagram, corrplot, Q-Q plot, Manhattan plot, seqLogo, volcano plot, and a heatmap, can be generated rapidly using NHCCDB. We have incorporated a search system for efficient mining of transcription factors and genes, along with an embedded data submit function in NHCCDB. We believe that the NHCCDB database will be a useful platform for non-heading Chinese cabbage research and breeding.

来源: Plants

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全文链接:

<http://agri.ckcest.cn/file1/M00/03/31/Csgk0YbTGTCAWHARADITXQu2Ppk843.pdf>

2. The Influence of Elevated CO₂ on Volatile Emissions, Photosynthetic Characteristics, and Pigment Content in Brassicaceae Plants Species and Varieties (提升CO₂浓度对十字花科植物物种和品种挥发物排放、光合特性和色素含量的影响)

简介: Climate change will determine a sharp increase in carbon dioxide in the following years. To study the influence of elevated carbon dioxide on plants, we grew 13 different species and varieties from the Brassicaceae family at three carbon dioxide concentrations: 400, 800, and 1200 ppmv. The photosynthetic parameters (assimilation rate and stomatal conductance to water vapor) increase for all species. The emission of monoterpenes increases for plants grown at elevated carbon dioxide while the total polyphenols and flavonoids content decrease. The chlorophyll content is affected only for some species (such as *Lipidium sativum*), while the β -carotene concentrations in the leaves were not affected by carbon dioxide.

来源: Plants

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<http://agri.ckcest.cn/file1/M00/10/03/Csgk0GJ8Y02AW3CuADWp4uE1vHQ038.pdf>

3. WRKY33-mediated indolic glucosinolate metabolic pathway confers resistance against *Alternaria brassicicola* in *Arabidopsis* and *Brassica* crops (WRKY33介导的吲哚芥子油苷代谢途径赋予拟南芥和芸苔属作物对芸苔链格孢的抗性)

简介: The tryptophan (Trp)-derived plant secondary metabolites, including camalexin, 4-hydroxy-indole-3-carbonitrile, and indolic glucosinolate (IGS), show broad-spectrum antifungal activity. However, the distinct regulations of these metabolic pathways among different plant species in response to fungus infection are rarely studied. In this study, our results revealed that WRKY33 directly regulates IGS biosynthesis, notably the production of 4-methoxyindole-3-ylmethyl glucose-nolate (4MI3G), conferring resistance to *Alternaria brassicicola*, an important pathogen which causes black spot in Brassica crops. WRKY33 directly activates the expression of CYP81F2, IGMT1, and IGMT2 to drive side-chain modification of indole-3-ylmethyl glucose-nolate (I3G) to 4MI3G, in both *Arabidopsis* and Chinese kale (*Brassica oleracea* var. *alboglabra* Bailey). However, Chinese kale showed a more severe symptom than *Arabidopsis* when infected by *Alternaria brassicicola*. Comparative analyses of the origin and evolution of Trp metabolism indicate that the loss of camalexin biosynthesis in Brassica crops during evolution might attenuate the resistance of crops to *Alternaria brassicicola*. As a result, the IGS metabolic pathway mediated by WRKY33 becomes essential for Chinese kale to deter *Alternaria brassicicola*. Our results highlight the differential regulation of Trp-derived camalexin and IGS biosynthetic pathways in plant immunity between *Arabidopsis* and Brassica crops.

来源: Journal of Integrative Plant Biology

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<http://agri.ckcest.cn/file1/M00/03/31/Csgk0YbTFYeAAjHaAC80LntuZLw966.pdf>

4. Formation of volatile sulfur compounds and S-methyl-L-cysteine sulfoxide in *Brassica oleracea* vegetables (甘蓝类蔬菜中挥发性硫化物和S-甲基-L-半胱氨酸亚砜的形成)

简介: Besides glucosinolates, Brassica vegetables accumulate sulfur-containing (+)-S-methyl-L-cysteine sulfoxide (SMCSO, methiin), mainly known from Allium vegetables. Such (+)-S-alk(en)yl-L-cysteine sulfoxides can degrade to volatile organosulfur compounds (VOSCs), which have been linked to health beneficial effects. In the present study, the accumulation of SMCSO and the formation of VOSCs was investigated in Brassica oleracea vegetables. SMCSO content of commercially available white and red cabbages was monitored over a three-month period and linked with the formation of VOSCs. S-Methyl methanethiosulfinate was the main VOSC released from SMCSO. Upon heating, it degraded to dimethyltrisulfide and dimethyldisulfide, which were less abundant in fresh homogenates. SMCSO made up approximately 1% of the dry matter of cabbages and the overall contents

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were similar in white and red cabbages (3.2-10.2 and 3.9-10.3 $\mu\text{mol/g}$ fresh weight, respectively). Using proteome profiling it was shown that recovery of VOSCs correlated with abundance of two isoforms of cystine lyase.

来源: Food Chemistry

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http://agri.ckcest.cn/file1/M00/10/03/Csgk0GJ8Z2mAGpFqAC9c_iakzTI404.pdf

5. Plant Response to Cold Stress: Cold Stress Changes Antioxidant Metabolism in Heading Type Kimchi Cabbage (*Brassica rapa* L. ssp. *Pekinensis*) (植物对冷胁迫的反应: 冷胁迫改变抽穗型泡菜白菜 (*Brassica rapa* L. ssp. *Pekinensis*) 的抗氧化代谢)

简介: Cold stress is known as the important yield-limiting factor of heading type Kimchi cabbage (HtKc, *Brassica rapa* L. ssp. *pekinensis*), which is an economically important crop worldwide. However, the biochemical and molecular responses to cold stress in HtKc are largely unknown. In this study, we conducted transcriptome analyses on HtKc grown under normal versus cold conditions to investigate the molecular mechanism underlying HtKc responses to cold stress. A total of 2131 genes (936 up-regulated and 1195 down-regulated) were identified as differentially expressed genes and were significantly annotated in the category of “response to stimulus”. In addition, cold stress caused the accumulation of polyphenolic compounds, including p-coumaric, ferulic, and sinapic acids, in HtKc by inducing the phenylpropanoid pathway. The results of the chemical-based antioxidant assay indicated that the cold-induced polyphenolic compounds improved the free-radical scavenging activity and antioxidant capacity, suggesting that the phenylpropanoid pathway induced by cold stress contributes to resistance to cold-induced reactive oxygen species in HtKc. Taken together, our results will serve as an important base to improve the cold tolerance in plants via enhancing the antioxidant machinery.

来源: Antioxidants

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<http://agri.ckcest.cn/file1/M00/10/03/Csgk0GJ8aPuAVVI7ADgo15jKc1s055.pdf>