



2023年第01期总376期

蔬菜育种专题

本期导读

▶ 前沿资讯

1. 巴斯夫与IUNU合作推进生菜数字表型分析

▶ 学术文献

1. 通过整合代谢组和全基因组转录组分析鉴定控制大白菜可溶性糖和芥子油苷生物合成的关键基因
2. 甘蓝型油菜开花时间基因型与环境相互作用的全基因组检测
3. 羽衣甘蓝 (*Brassica oleracea* var. *alboglabra* Bailey) 多汁茎发育的转录组学分析及其通过 RNA 测序合成的异源四倍体研究
4. 不同水分条件下油菜籽 (*Brassica napus* L.) 中多酚和抗氧化剂的比较分析和抗糖化活性分析

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➤ 前沿资讯

1. BASF's vegetable seeds business and IUNU partner to advance digital phenotyping for the elevation and breeding of hydroponic lettuce varieties (巴斯夫与IUNU合作推进生菜数字表型分析)

简介: 近日,巴斯夫蔬菜种子事业部宣布与美国计算机视觉技术公司IUNU合作,共同推进数字表型分析,助力水培生菜育种。IUNU作为计算机视觉和人工智能软件提供商,将人工智能纳入商业温室和室内农场的检测系统,通过机器学习和计算机视觉技术,实现对个体植株健康状况大规模的跟踪和预测。该服务基于一款名为“LUNA”的人工智能系统(LUNA AI),它是由计算机视觉和人工智能软件组成的先进数字表型平台,可生成有关水培生菜生长模式和性状的数据,这将使巴斯夫能够选择合适的生菜品种进行改良和育种,从而帮助种植者提高和扩大生产规模。

巴斯夫认为,为提供高质量的种子并满足不断增长的需求,育种必须由数据驱动。此次合作是巴斯夫数字化战略的一部分,旨在通过与合作伙伴的合作来改善数据驱动的决策。通过开发和应用具有额外表型的算法,将帮助育种者提高育种预测能力,判断哪些品系在特定情况下表现最佳。

来源: SeedQuest

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<http://agri.ckcest.cn/file1/M00/10/19/Csgk0G0s9nKAIh0FAAlceYQnpqs408.pdf>

➤ 学术文献

1. Identification of key genes controlling soluble sugar and glucosinolate biosynthesis in Chinese cabbage by integrating metabolome and genome-wide transcriptome analysis (通过整合代谢组和全基因组转录组分析鉴定控制大白菜可溶性糖和芥子油苷生物合成的关键基因)

简介: Introduction: Soluble sugar and glucosinolate are essential components that determine the flavor of Chinese cabbage and consumer preferences. However, the underlying regulatory networks that modulate the biosynthesis of soluble sugar and glucosinolate in Chinese cabbage remain largely unknown.

Methods: The glucosinolate and carotene content in yellow inner-leaf Chinese cabbage were observed, followed by the combination of metabolome and transcriptome analysis to explore the metabolic basis of glucosinolate and soluble sugar.

Results: This study observed high glucosinolate and carotene content in yellow inner-leaf Chinese cabbage, which showed a lower soluble sugar content. The differences between the yellow and the white inner-leaf Chinese cabbage were compared using the untargeted metabolomic and transcriptomic analyses in six cultivars of Chinese cabbage to explore the metabolic basis of glucosinolate and soluble sugar. Aliphatic glucosinolate and two soluble sugars (fructose and glucose) were the key metabolites that caused the difference in Chinese

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cabbage's glucosinolate and soluble sugar. By integrating soluble sugar and glucosinolate-associated metabolism and transcriptome data, we indicated BraA05gAOP1 and BraA04gAOP4, BraA03gHT7 and BraA01gHT4 were the glucosinolates and soluble sugar biosynthesis structural genes. Moreover, BraA01gCHR11 and BraA07gSCL1 were two vital transcription factors that regulate soluble sugar and glucosinolate biosynthesis.

Discussion: These findings provide novel insights into glucosinolate and soluble sugar biosynthesis and a possible explanation for the significant difference in nutrients between yellow and white inner-leaf Chinese cabbage. Moreover, it will facilitate genetic modification to improve the Chinese cabbage's nutritional and health values.

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<http://agri.ckcest.cn/file1/M00/10/19/Csgk0G0s8nqAT5rrAQKBPuowY-Y178.pdf>

2. Genome-wide detection of genotype environment interactions for flowering time in Brassica napus (甘蓝型油菜开花时间基因型与环境相互作用的全基因组检测)

简介: Flowering time is strongly related to the environment, while the genotype-by-environment interaction study for flowering time is lacking in Brassica napus. Here, a total of 11,700,689 single nucleotide polymorphisms in 490 B. napus accessions were used to associate with the flowering time and related climatic index in eight environments using a compressed variance-component mixed model, 3VmrMLM. As a result, 19 stable main-effect quantitative trait nucleotides (QTNs) and 32 QTN-by-environment interactions (QEIs) for flowering time were detected. Four windows of daily average temperature and precipitation were found to be climatic factors highly correlated with flowering time. Ten main-effect QTNs were found to be associated with these flowering-time-related climatic indexes. Using differentially expressed gene (DEG) analysis in semi-winter and spring oilseed rapes, 5,850 and 5,511 DEGs were found to be significantly expressed before and after vernalization. Twelve and 14 DEGs, including 7 and 9 known homologs in Arabidopsis, were found to be candidate genes for stable QTNs and QEIs for flowering time, respectively. Five DEGs were found to be candidate genes for main-effect QTNs for flowering-time-related climatic index. These candidate genes, such as BnaFLCs, BnaFTs, BnaA02.VIN3, and BnaC09.PRR7, were further validated by the haplotype, selective sweep, and co-expression networks analysis. The candidate genes identified in this study will be helpful to breed B. napus varieties adapted to particular environments with optimized flowering time.

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<http://agri.ckcest.cn/file1/M00/10/19/Csgk0G0s9E2AUy9PAKYXBq5aT2o154.pdf>

3. Transcriptomic analysis of succulent stem development of Chinese

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kale (*Brassica oleracea* var. *alboglabra* Bailey) and its synthetic allotetraploid via RNA sequencing (羽衣甘蓝 (*Brassica oleracea* var. *alboglabra* Bailey) 多汁茎发育的转录组学分析及其通过 RNA 测序合成的异源四倍体研究)

简介: Chinese kale (*Brassica oleracea* var. *alboglabra* Bailey, CC) is a succulent stem vegetable in the Brassica family. Its allotetraploid (AACC) vegetable germplasm, which was synthesized via distant hybridization with the colloquially named ‘yellow turnip’ (*B. rapa* L. ssp. *rapifera* Matzg., AA), has a swelling stem similar to CC. To address the molecular mechanism of stem development for CC and AACC, RNA sequencing (RNA-seq) was used to investigate transcriptional regulation of their stem development at three key stages including 28 days, 42 days and the bolting stage (BS) after sowing. As a result, 32,642, 32,665, 33,816, 32,147, 32,293 and 32,275 genes were identified in six corresponding cDNA libraries. Among them, 25,459 genes were co-expressed, while 7,183, 7,206, 8,357, 6,688, 6,834 and 6,814 genes were specifically expressed. Additionally, a total of 29,222 differentially expressed genes (DEGs) were found for functional enrichment as well as many genes involved in plant hormones including gibberellin (GA), abscisic acid (ABA), cytokinin (CTK) and auxin (AUX). Based on gene expression consistency between CC and AACC, the gene families including DELLA, GID, PYR/PYL, PP2C, A-ARR and AUX/IAA might be related to stem development. Among these, eight genes including Bo00834s040, Bo5g093140, Bo6g086770, Bo9g070200, Bo7g116570, Bo3g054410, Bo7g093470 and Bo5g136600 may play important roles in stem development based on their remarkable expression levels as confirmed by qRT-PCR. These findings provide a new theoretical basis for understanding the molecular mechanism of stem development in Brassica vegetable stem breeding.

来源: Front Plant Sci

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http://agri.ckcest.cn/file1/M00/03/47/Csgk0YgDp2SAfj_tASF7h0c26mI348.pdf

4. Comparative profiling of polyphenols and antioxidants and analysis of antiglycation activities in rapeseed (*Brassica napus* L.) under different moisture regimes (不同水分条件下油菜籽 (*Brassica napus* L.) 中多酚和抗氧化剂的比较分析和抗糖化活性分析)

简介: Genotype, growth stages, and moisture regimes affect polyphenols as beneficial compounds in rapeseed with edible and medicinal properties. The aims of this study were to assess the effects of tissue, genotype background and moisture on growth, pigment composition, phenolic acids, flavonoids, antioxidant, and antiglycation activities in rapeseed. Treatments included two moisture regimes (10% field capacity as drought-treated and 30% field capacity as control), tissue (leaf, flower and seed), and 12 rapeseed genotypes. The range of loss in growth traits under drought compared with control was between 23% and 47%. Drought reduced number of leaves, leaf area, fresh and dry weights by 23%, 31%, 37%,

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and 36%, respectively whilst increased chlorophylls, carotenoids, total pigment, phenolic compounds, flavonoids, and antioxidant activities. Analysis for antiglycation properties in two genotypes (G01 and G08) which accumulated higher phenolic compounds showed that higher anti-glycation property was associated with higher epicatechin, and caffeic, and syringic acids. Flower extracts showed higher phenolics than leaf and seed suggesting flowering stage is a preferred timing to harvest a higher polyphenols from rapeseed. Overall, our results demonstrated role of specific polyphenols in antiglycation activities and the importance of growth stage and genotype in attaining higher polyphenols and antioxidants that affect edible and medicinal values of rapeseed under water limited conditions.

来源: Food Chemistry

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