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目录

3 EI 收录情况

1 收录概况

为及时了解学校最新SCI、EI收录引用情况，图书馆推出信息参考《收录引用报》，呈现学校最新SCI、EI收录引用信息，收录内容为我校教师为第一作者和合著者被SCI、EI收录的文献信息。

《收录引用报》有关说明如下：

一、图书馆所提供信息全部来源于SCIE和EI数据库。

二、以机构“Heilongjiang Bayi Agricultural University”为检索条件，时间范围2025.04.17-2025.06.11。

三、本月报相关数据不保证100%的完整性，不做决策依据，仅做参考，如需了解详细情况，需做进一步查证、查询，请以官方网站信息为准。

2 SCI 收录情况

（2025.04.17-2025.06.11）

SCI 索引库共收录我校教师发表的 76 篇文献，图表后附录 76 篇文献详细题录信息。

RESEARCH FIELDS	研究领域	篇数
Infectious Diseases	传染病	1
Life Sciences & Biomedicine - Other	生命科学与生物医学-其他主题	1
Agriculture	农业	20
Biochemistry & Molecular Biology	生物化学与分子生物学	9
Biotechnology & Applied Microbiology	生物工程学和应用微生物学	2
Chemistry	化学	2
Computer Science	计算机科学	3
Environmental Sciences& Ecology	环境科学与生态学	5
Food Science & Technology	食品科学与技术	9
Geology	地质学	1
Immunology	免疫学	1
Mathematics	数学	1
Metallurgy & Metallurgical Engineering	冶金和冶金工程学	1
Microbiology	微生物学	1
Parasitology	寄生物学	1
Pharmacology & Pharmacy	药理学和药剂学	1
Plant Sciences	植物科学	11
Science & Technology - Other Topics	科技与技术-其他主题	5
Spectroscopy	光谱学	1

表 1　我校 23 个研究领域发文篇数及详细题录信息

Infectious Diseases

第 1 条

标题: Transformer-based deep learning enables improved B-cell epitope prediction in parasitic pathogens: A proof-of-concept study on Fasciola hepatica

作者: Hu, RS (Hu, Rui-Si); Gu, K (Gu, Kui); Ehsan, M (Ehsan, Muhammad); Raza, SHA (Raza, Sayed Haidar Abbas); Wang, CR (Wang, Chun-Ren)

来源出版物: PLOS NEGLECTED TROPICAL DISEASES **卷:** 19 **期:** 4
文献号: e0012985 **DOI:** 10.1371/journal.pntd.0012985
Published Date: 2025 APR

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摘要: Background The identification of B-cell epitopes (BCEs) is fundamental to advancing epitope-based vaccine design, therapeutic antibody development, and diagnostics, such as in neglected tropical diseases caused by parasitic pathogens. However, the structural complexity of parasite antigens and the high cost of experimental validation present certain challenges. Advances in Artificial Intelligence (AI)-driven protein engineering, particularly through machine learning and deep learning, offer efficient solutions to enhance prediction accuracy and reduce experimental costs.Methodology/Principal findings Here, we present deepBCE-Parasite, a Transformer-based deep learning model designed to predict linear BCEs from peptide sequences. By leveraging a state-of-the-art self-attention mechanism, the model achieved remarkable predictive performance, achieving an accuracy of approximately 81% and an AUC of 0.90 in both 10-fold cross-validation and independent testing. Comparative analyses against 12 handcrafted features and four conventional machine learning algorithms (GNB, SVM, RF, and LGBM) highlighted the superior predictive power of the model. As a case study, deepBCE-Parasite predicted eight BCEs from the leucine aminopeptidase (LAP) protein in Fasciola hepatica proteomic data. Dot-blot immunoassays confirmed the specific binding of seven synthetic peptides to positive sera, validating their IgG reactivity and demonstrating the model's efficacy in BCE prediction.Conclusions/Significance deepBCE-Parasite demonstrates excellent performance in predicting BCEs across diverse parasitic pathogens, offering a valuable tool for advancing the design of epitope-based vaccines, antibodies, and diagnostic applications in parasitology.

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研究方向: Infectious Diseases; Parasitology; Tropical Medicine

输出日期: 2025-06-11

Life Sciences & Biomedicine - Other Topics

第 **1** 条

标题: Epibrassinolide Induces Apoptosis and Inhibits the Migration of Gastric Cancer AGS Cells by Regulating Reactive Oxygen Species-Mediated Signaling Pathways

作者: Wang, C (Wang, Chang); Zhang, Z (Zhang, Zhi); Sun, W (Sun, Wei); Quan, Q (Quan, Quan); Hou, WS (Hou, Wenshuang); Jin, CH (Jin, Chenghao)

来源出版物: BIOCELL **卷:** 49 **期:** 3 **页:** 465-482
DOI: 10.32604/biocell.2025.062155 **Published Date:** 2025

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摘要: Objectives: Epibrassinolide (EBR) is a steroid hormone with anti-tumor properties. Nevertheless, its potential to inhibit gastric cancer (GC) cells remains unknown. The aim of this research was to examine the effects of EBR on GC cells and to investigate the specific mechanism of EBR. Methods: A cell counting kit-8 (CCK-8) assay was utilized to determine cell survival rates. The investigation of apoptosis, cell cycle progression, and reactive oxygen species (ROS) levels was performed using flow cytometry. To detect cell migration, a wound-healing assay was performed on AGS cells. Furthermore, western blotting assay was utilized to determine protein expression levels. Results: The CCK-8 assay demonstrated that EBR reduced the survival rates of AGS, KATO-3, and MKN-45 cells, while causing only minor toxicity to normal cells. The apoptosis assay indicated that EBR induced AGS cell apoptosis through a mitochondria-mediated pathway. Western blotting results demonstrated that EBR induced AGS cell apoptosis via mitogen-activated protein kinase (MAPK)/signal transducer and activator of transcription 3 (STAT3)/nuclear factor kappa B (NF-kappa B) signaling pathway. Further, after treating AGS cells with EBR, the accumulation of intracellular ROS markedly increased. EBR also induced G2/M phase cell cycle arrest in AGS cells by downregulating phospho-protein kinase B (p-AKT), cyclin-dependent kinase 1/2 (CDK1/2), and cyclin B1 expression levels, while simultaneously upregulating p21 and p27 expression levels. EBR inhibited AGS cell migration by downregulating p-AKT, phosphorylated-glycogen synthase kinase 3(3 (p-GSK-3(3), and beta-catenin expression levels and upregulating E-cadherin expression levels. However, these effects were reversed by pretreatment with N-acetylcysteine (NAC). Conclusion: EBR regulates AGS cells by inducing apoptosis and G2/M phase arrest, while also inhibiting cell migration, all of which are mediated through ROS-mediated signaling pathways. Ultimately, these effects suggest a significant role for EBR in regulating cellular processes within AGS cells.

入藏号: WOS:001465555200001

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研究方向: Life Sciences & Biomedicine - Other Topics

输出日期: 2025-06-11

Agriculture

第 1 条

标题: $CaCl^{2+}$chitosan treatment inhibits softening and quality decline in postharvest raspberry fruit during cold storage by regulating cell wall and antioxidation metabolisms

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作者: Sun, HJ (Sun, Huajun); Liu, Y (Liu, Ying); Cui, FZ (Cui, Fangzheng); Qian, LL (Qian, Lili); Zhu, SJ (Zhu, Sijing); Li, Y (Li, Yue)

来源出版物: POSTHARVEST BIOLOGY AND TECHNOLOGY **卷:** 227
文献号: 113604 **DOI:** 10.1016/j.postharvbio.2025.113604
Published Date: 2025 SEP

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被引频次合计: 0

摘要: The rapid quality decline in raspberry fruits significantly reduces their marketing potential. Herein, the effects of calcium chloride (CaCl2) and chitosan (CTS) composite coating on the softening and quality of raspberries were investigated. The firmness, titratable acid, soluble solid, total phenolic, and flavonoid contents of raspberry fruits treated with CaCl2+CTS were higher than those of untreated raspberry fruits. CaCl2+CTS delayed the degradation of cell wall components by reducing the activity of cell wall-modifying enzymes. The CaCl2+CTS treatment inhibited O2 center dot-, H2O2, and malondialdehyde accumulation by improving the superoxide dismutase, catalase, and ascorbate peroxidase activities, increased the total contents of antioxidant substances such as phenols, flavonoids, and anthocyanins, and mitigated oxidative damage during postharvest storage. CaCl2+CTS delays the softening and quality decline and extends the storage and shelf life of raspberry fruits by enhancing antioxidant capacity and maintaining cell wall integrity.

入藏号: WOS:001484418500001

文献类型: Article

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研究方向: Agriculture; Food Science & Technology

输出日期: 2025-06-11

第 2 条

标题: The regulatory effects of epigallocatechin gallate on growth performance, systemic antioxidant status, immune response, and gut microbiota structure in geese

作者: Liu, MY (Liu, Mengyu); Ge, YS (Ge, Yansong); Xu, ES (Xu, Enshuang); Zhu, TT (Zhu, Tingting); Ruan, HR (Ruan, Hongri); Zheng, JS (Zheng, Jiasan)

来源出版物: POULTRY SCIENCE **卷:** 104 **期:** 7 **文献号:** 105178
DOI: 10.1016/j.psj.2025.105178 **Published Date:** 2025 JUL

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摘要: The effects of dietary supplementation with epigallocatechin-3-gallate (EGCG) on growth performance, antioxidant capacity, immune function, and gut microbiota in geese were investigated. Seventy-two healthy 35-day-old male geese were randomly divided into a control group (basal diet) or an EGCG group (basal diet + 200 mg/kg EGCG), with 36 geese per group, which was further subdivided into 6 replicates (6 geese per replicate). The experiment lasted 21 days. Geese in the EGCG group exhibited significantly higher final body weight (2.93 kg vs. 2.28 kg, $P < 0.01$) and average daily gain (72.38 g/d vs. 41.4 g/d, $P < 0.01$) along with a 42.8 % reduction in the feed conversion ratio (3.95 vs. 6.91, $P < 0.01$) versus the control. Liver weights in the EGCG group were significantly elevated compared to the CON group on days 14 and 21 ($P < 0.05$) and a strong correlation between liver weight and body weight. EGCG significantly increased catalase, glutathione peroxidase, and superoxide dismutase activities, and the total antioxidant capacity in serum and jejunum while decreasing malondialdehyde (MDA) levels ($P < 0.05$). Immunological analyses revealed elevated serum immunoglobulin (Ig)A, IgG, and IgM and lysozyme in the EGCG group ($P < 0.05$), accompanied by a decrease in the pro-inflammatory cytokines interleukin-6 and interferon-gamma. Intestinal morphology demonstrated increased villus height-to-crypt depth ratios in the duodenum and ileum ($P < 0.05$). 16S rRNA sequencing indicated that EGCG increased the relative abundance of Akkermansia and Verrucomicrobiota ($P < 0.05$) in the cecal content and enriched microbial functions related to inorganic ion transport and metabolism. Correlation analysis revealed positive associations between Akkermansia and IgA, and between Firmicutes and oxidative damage markers (MDA). Overall, dietary supplementation with 200 mg/kg EGCG could improve growth performance, antioxidant capacity, immune response, and gut microbiota structure in geese, supporting its potential as a plant-based feed additive.

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文献类型: Article

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研究方向: Agriculture

输出日期: 2025-06-11

第 3 条

标题: Synergistic transcriptomic and metabolomic analyses in Zi geese ovaries with different clutch lengths

作者: Liu, SJ (Liu, Shengjun); Yin, JX (Yin, Jiaxin); Cong, KX (Cong, Kexin); Yue, S (Yue, Shan); Zhang, YL (Zhang, Yuanliang); Sun, JY (Sun, Jinyan); Ren, XF (Ren, Xiaofang); Jiang, K (Jiang, Ke); Liu, YN (Liu, Yunuo); Zhao, XH (Zhao, Xiuhua)

来源出版物: POULTRY SCIENCE **卷:** 104 **期:** 7 **文献号:** 105210
DOI: 10.1016/j.psj.2025.105210 **Published Date:** 2025 JUL

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摘要: The clutch is defined as consecutive days of oviposition. Clutch length is an index that reflects ovulation persistence, and is highly correlated with egg production in birds. To identify the genetic markers associated with clutch length in geese, two consecutive experiments were conducted. In the first experiment, 200 Zi geese were selected, all 230 days old, were selected from the same batch and raised individually in the same environment. Data of egg-laying and clutch traits were recorded. After the laying period, three geese with the longest clutch lengths were selected to form the length clutch group (LCG) and three geese with the shortest clutch lengths were formed the short clutch group (SCG). In the second experiment, the ovaries of six geese were collected for transcriptomic and metabolomic analyses. The results showed that large clutch length (LCL) and average clutch length (ACL) were positively correlated with egg number (EN) (P G 0.01; r = 0.63 and 0.60, respectively). Large clutch number (LCN) was significantly correlated with the peak egg number (PEN) (r = 0.58, P G 0.01) and EN (r = 0.60, P G 0.01). EN, LCN, LCL, and ACL showed significant differences (P G 0.01) between the two clutch length groups. Transcriptomic analysis identified 424 differentially expressed genes (DEGs). Functional enrichment analysis revealed that these DEGs were mainly involved in neuroactive ligand-receptor interactions, ovarian steroidogenesis, and calcium signaling pathways. Further, AVPR1A, FGF14, and LHCGR were predicted as the key genes regulating LCL. Metabolomic analysis identified 349 differential metabolites (DMs) in both the positive and negative ion modes. Pyruvate, isocitric acid, D/L-serine, 3-phospho-D-glycerate, succinate, glycine, and glutamic acid were identified as the key metabolites mainly enriched in the signaling pathways of the TCA cycle. Integration of transcriptomic and metabolomic data revealed critical gene-metabolite pairs, including ACSL4-phosphoenolpyruvate, implicated in LCL regulation. In summary, this study provides new insights into the genes and molecular markers affecting LCL in Zi geese.

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文献类型: Article

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研究方向: Agriculture

输出日期: 2025-06-11

第 4 条

标题: Integrated transcriptomic and metabolomic analysis of goose epididymis reveals molecular markers associated with sperm mobility

作者: Ren, XF (Ren, Xiaofang); Jiang, K (Jiang, Ke); Yin, JX (Yin, Jiaxin); Ma, ZG (Ma, Zhigang); Chen, ZF (Chen, Zhifeng); Yang, K (Yang, Kun); Liu, SJ (Liu, Shengjun)

来源出版物: POULTRY SCIENCE **卷:** 104 **期:** 7 **文献号:** 105180
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摘要: The low fertility of geese has long constrained the development of the geese industry. Sperm quality plays a critical role in fertility, and sperm mobility (SM) serves as a key indicator of sperm quality. However, the molecular mechanisms underlying SM remain largely unexplored. The objective of this study was to identify molecular markers associated with SM in the epididymis of Zi geese (Anser cygnoides L.). The SM of 40 one-year-old ganders was assessed. Based on SM values, six ganders were selected: three with the highest SM (H group: n = 3, SM = 0.43 +/- 0.02) and three with the lowest SM (L group: n = 3, SM = 0.10 +/- 0.01, P < 0.001). Semen quality parameters, fertility, and hormone levels were measured in both groups. Epididymal tissues from the six ganders were subjected to transcriptomic and metabolomic analyses. Results identified 438 differentially expressed genes (DEGs) between the groups, primarily associated with transmembrane transport of proteins and ions. These DEGs were enriched in pathways such as "alanine, aspartate and glutamate metabolism," "butanoate metabolism," and the "PPAR signaling pathway." Among these, ATP12A, ATP1B4, and CNDP1 were identified as key genes regulating SM. Additionally, 486 metabolites showed significant differences between the groups in both positive and negative ion modes. Integration of transcriptomic and metabolomic data revealed critical gene-metabolite pairs, including CNDP1-citric acid, implicated in SM regulation. Notably, the "arginine biosynthesis" pathway was significantly enriched by both DEGs and differential metabolites. In conclusion, this study provides novel insights into the molecular mechanisms regulating SM in the epididymis and lays a theoretical foundation for geese breeding programs.

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文献类型: Article

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研究方向: Agriculture

输出日期: 2025-06-11

第 5 条

标题: Isolation, identification, whole genome sequence analysis, and pathogenicity of a potential recombinant goose parvovirus

作者: Zhu, QH (Zhu, Qinghe); Li, HN (Li, Huinan); Li, HS (Li, Hansong); Bai, WF (Bai, Wenfei); Zhou, JX (Zhou, Jingxuan); Liu, M (Liu, Ming); Zhao, YY (Zhao, Yingying); Jiang, LM (Jiang, Limin); Sun, Y (Sun, Ying); Sun, J (Sun, Jia); Zhao, JJ (Zhao, Jingjing); Hu, J (Hu, Jia); Li, CQ (Li, Chunqiu); Xing, XX (Xing, Xiaoxu); Yang, D (Yang, Dan); Sun, DB (Sun, Dongbo)

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DOI: 10.1016/j.psj.2025.105231 **Published Date:** 2025 JUL

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摘要: Goose parvovirus (GPV) is the etiological agent responsible for gosling plague (GP), which is an acute hemorrhagic infectious disease affecting geese, posing significant economic challenges to the poultry industry. Furthermore, recent studies have identified that the novel goose parvovirus (NGPV), a recombinant variant of the classic GPV, is responsible for duck short beak dwarfism syndrome, which has significantly affected duck farm. Therefore, the infection and genetic evolution of GPV have attracted widespread attention of researchers in poultry disease. In order to clarify the prevalence and genetic evolution of clinically severe GPV in the Heilongjiang region, this study successfully isolated a strain of GPV HLJ2023 from goose embryos, which results in the mortality rate of 100 % after 5 generations. The electron microscope shows that the virus particles are spherical, with a diameter of approximately 28 nm, and HLJ2023 strain has a total genome length of 5048 nt. SimPlot analysis showed that HLJ2023 strain is closely related to duck parvovirus and NGPV in the VP3 gene region. Recombination analysis showed that the isolated strain is a potential recombinant of the NGPV JS191021 strain and the GMD (Goose parvovirus hosted by Muscovy duck) PT strain. the strong pathogenicity of HLJ2023 strain to goslings. 36 h after the challenge, the goslings were depressed and had a mortality rate up to 100 %. Autopsy revealed intestinal bleeding, thinning of the intestinal wall, and a large amount of fibrous clots and fragments in the intestinal cavity. This study isolated a highly pathogenic potential recombinant GPV, further expanding the genetic evolution and pathogenicity information of avian parvovirus. At the same time, the isolated strain provides a candidate strain for the development of biological products for treating GPV.

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文献类型: Article

地址: [Zhu, Qinghe; Li, Huinan; Li, Hansong; Bai, Wenfei; Zhou, Jingxuan; Liu, Ming; Zhao, Yingying; Jiang, Limin; Sun, Ying; Sun, Jia; Zhao, Jingjing; Hu, Jia; Li, Chunqiu; Xing, Xiaoxu; Yang, Dan; Sun, Dongbo] Heilongjiang Bayi Agr Univ, Coll Anim Sci & Vet Med, 5 Xinfeng Rd, Daqing 163319, Peoples R China.

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研究方向: Agriculture

输出日期: 2025-06-11

第 6 条

标题: Surface Defect and Malformation Characteristics Detection for Fresh Sweet Cherries Based on YOLOv8-DCPF Method

作者: Liu, YL (Liu, Yilin); Han, X (Han, Xiang); Ren, LL (Ren, Longlong); Ma, W (Ma, Wei); Liu, BY (Liu, Baoyou); Sheng, CR (Sheng, Changrong); Song, YP (Song, Yuepeng); Li, QD (Li, Qingda)

来源出版物: AGRONOMY-BASEL **卷:** 15 **期:** 5 **文献号:** 1234
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摘要: The damaged and deformed fruits of fresh berries severely restrict the economic value of produce, and accurate identification and grading methods have become a global research hotspot. To address the challenges of rapid and accurate defect detection in intelligent cherry sorting systems, this study proposes an enhanced YOLOv8n-based framework for sweet cherry defect identification. First, the dilation-wise residual (DWR) module replaces the conventional C2f structure, allowing for the adaptive capture of both local and global features through multi-scale convolution. This enhances the recognition accuracy of subtle surface defects and large-scale damages on cherries. Second, a channel attention feature fusion mechanism (CAFM) is incorporated at the front end of the detection head, which enhances the model's ability to identify fine defects on the cherry surface. Additionally, to improve bounding box regression accuracy, powerful-IoU (PIoU) replaces the traditional CIoU loss function. Finally, self-distillation technology is introduced to further improve the mode's generalization capability and detection accuracy through knowledge transfer. Experimental results show that the YOLOv8-DCPF model achieves precision, mAP, recall, and F1 score rates of 92.6%, 91.2%, 89.4%, and 89.0%, respectively, representing improvements of 6.9%, 5.6%, 6.1%, and 5.0% over the original YOLOv8n baseline network. The proposed model demonstrates high accuracy in cherry defect detection, providing an efficient and precise solution for intelligent cherry sorting in agricultural engineering applications.

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文献类型: Article

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第 7 条

标题: Ergothioneine Improves the Quality of Boar Sperm During In Vitro Liquid Preservation by Regulating Mitochondrial Respiratory Chain

作者: Guo, Q (Guo, Qing); Liu, X (Liu, Xue); Li, Y (Li, Yang); Cheng, Y (Cheng, Ye); Li, JC (Li, Jingchun)

来源出版物: ANIMALS **卷:** 15 **期:** 10 **文献号:** 1450 **DOI:** 10.3390/ani15101450
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摘要: Porcine artificial insemination primarily utilizes liquid-preserved (17 degrees C) semen; however, the quality of sperm diminishes progressively with extended preservation time. Ergothioneine (EGT) is a mitochondria-targeting antioxidant. Therefore, this study aimed to analyze the effect of various concentrations of EGT (0, 0.15, 0.3, and 0.6 mM) on the quality of boar sperm during in vitro liquid preservation and elucidate the underlying mechanisms of the mitochondrial electron respiratory chain inhibitor ROT. The results demonstrated that the addition of 0.3 mM EGT to the modified Modena extender significantly improved sperm motility and kinetic parameters, as well as mitochondrial membrane potential (MMP), adenosine triphosphate (ATP), antioxidant capacity, and the integrity of both the sperm plasma membrane and acrosome. Additionally, ROT significantly inhibited sperm motility, kinetic parameters, MMP, ATP levels, antioxidant capacity, and sperm integrity of the plasma membrane and acrosome. However, these adverse effects could be partially mitigated by the addition of 0.3 mM EGT. In conclusion, the novel findings of this study indicated that EGT plays a crucial role in protecting sperm from oxidative damage by regulating the mitochondrial electron respiratory chain, suggesting that the use of EGT is a promising approach for enhancing the in vitro liquid preservation efficiency of boar semen at 17 degrees C.

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第 8 条

标题: Design and Implementation of an Intelligent Pest Status Monitoring System for Farmland

作者: Yuan, XY (Yuan, Xinyu); He, ZS (He, Zeshen); Huang, CJ (Huang, Caojun)

来源出版物: AGRONOMY-BASEL **卷:** 15 **期:** 5 **文献号:** 1214
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摘要: This study proposes an intelligent agricultural pest monitoring system that integrates mechanical control with deep learning to address issues in traditional systems, such as pest accumulation interference, image contrast degradation under complex lighting, and poor balance between model accuracy and real-time performance. A three-axis coordinated separation device is employed, achieving a 92.41% single-attempt separation rate and 98.12% after three retries. Image preprocessing combines the Multi-Scale Retinex with Color Preservation (MSRCP) algorithm and bilateral filtering to enhance illumination correction and reduce noise. For overlapping pest detection, EfficientNetv2-S replaces the YOLOv5s backbone and is combined with an Adaptive Feature Pyramid Network (AFPN), achieving 95.72%

detection accuracy, 94.04% mAP, and 127 FPS. For pest species recognition, the model incorporates a Squeeze-and-Excitation (SE) attention module and alpha-CIoU loss function, reaching 91.30% precision on 3428 field images. Deployed on an NVIDIA Jetson Nano, the system demonstrates a detection time of 0.3 s, 89.64% recall, 86.78% precision, and 1.136 s image transmission delay, offering a reliable solution for real-time pest monitoring in complex field environments.

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第 9 条

标题: Calibration and Experimental Validation of Discrete Element Parameters for Long-Grain Rice with Different Moisture Contents Based on Repose Angle

作者: Chen, ZF (Chen, Zhengfa); Che, G (Che, Gang); Wan, L (Wan, Lin); Wang, HC (Wang, Hongchao); Zhang, K (Zhang, Kun)

来源出版物: AGRICULTURE-BASEL **卷:** 15 **期:** 10 **文献号:** 1058
DOI: 10.3390/agriculture15101058 **Published Date:** 2025 MAY 14

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摘要: The accurate determination of discrete element parameters is crucial for ensuring reliable results in simulating the critical post-harvest stages of rice grain (processing, transportation, and storage) with different moisture contents. To determine the discrete element parameters, a physical model of rice grain was constructed by the multi-sphere (MS) modeling approach. Using the repose angle as the evaluation index, the discrete element parameters of rice grain were calibrated and optimized through the Plackett-Burman (PB) test, the steepest climbing test, and the Box-Behnken (BB) test using EDEM software. A moisture content-significance discrete element parameters model was further developed based on a moisture content-repose angle model (R2 = 0.992) and a repose angle-significance discrete element parameters model (R2 = 0.970). The calibration results showed that the relative error between the simulated and actual repose angle did not exceed 3.52%. Meanwhile, the cylinder lifting method and unloading mass flow rate verification were performed. And the results showed that the relative errors of the repose angle and mass flow rate of rice grain did not exceed 2.09% and 7.72%, respectively. The study provides a general and reliable method for determining the parameters of discrete element method simulation for rice grain with different moisture contents.

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第 10 条

标题: ATR Deficiency Impairs DNA Damage Repair and Accelerates Cellular Senescence in Bovine Mammary Epithelial Cells, Leading to Lactation Dysfunction

作者: Zhou, QJ (Zhou, Qijun); Geng, ZJ (Geng, Zijian); Lian, S (Lian, Shuai); Wang, JF (Wang, Jianfa); Wu, R (Wu, Rui)

来源出版物: ANIMALS **卷:** 15 **期:** 10 **文献号:** 1419 **DOI:** 10.3390/ani15101419
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摘要: Mammary glands in cows are highly dynamic, making genomic stability particularly crucial. Continuous lactation and self-renewal of these glands are primary contributors to genomic instability. Results: We employed transcriptomic and proteomic methods to analyze the expressional characteristics in the mammary glands of cows with varying levels of milk production. Our findings indicated differences in relevant pathways, including DNA damage repair and apoptosis, which are influenced by increasing parity. Notably, ATR protein levels in the mammary glands of low-yield dairy cows were reduced. Following in vitro silencing of ATR, beta-galactosidase content increased in aging mammary epithelial cells, with cell cycle arrest in the G2 and S phases. Secretory phenotypes associated with aging, including IL-6, IL-10, IL-1 beta, INF-gamma, and IL-2, were elevated, along with increased TNF-alpha content. The expressions of DNA repair-related proteins, including PIG3, PARP1, and Cleaved caspase3, were upregulated, and SP1 expression was decreased. Furthermore, the expressions of cytochrome C and BAK increased, and ATR silencing inhibited mTOR and STAT5 lactation signaling pathways, resulting in elevated STAT3 protein levels associated with mammary gland degeneration. Conclusions: This study emphasizes the significance of the ATR protein in the mammary glands of dairy cows, contributing valuable insights into maintaining their health and presenting a novel perspective on strategies to enhance their lifespan.

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研究方向: Agriculture; Veterinary Sciences; Zoology

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第 11 条

标题: Biochar Promotes Phosphorus Solubilization by Reconstructing Soil Organic Acid and Microorganism Networks

作者: Fan, BW (Fan, Bowen); Zhao, LQ (Zhao, Liqin); Yang, FJ (Yang, Fengjun); Zhao, CJ (Zhao, Changjiang); Li, ZT (Li, Zuotong)

来源出版物: AGRONOMY-BASEL **卷:** 15 **期:** 5 **文献号:** 1163
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摘要: Biochar has the ability to enhance the solubilization of phosphorus (P) in soil. Nonetheless, the role played by organic acid and microorganism in P solubilization under biochar application conditions remains unclear. In this study, we examined the relationship between soil organic acids and microorganisms, as well as P fractions, following the addition of biochar, utilizing foxtail millet, maize, soybean, and mung bean as materials. The results demonstrated that the addition of biochar increased the availability of P by increasing the content of the resin-P fraction and decreasing the content of the NaOH-Pi, NaOH-Po, and HCl-P fractions in the soil. In addition, resin-P fractions were elevated by 142.78%, 95.27%, 35.99%, and 21.55% in the soils of foxtail millet, maize, soybean, as well as mung bean, respectively. In the microorganisms, the addition of biochar promotes P conversion by increasing the number of labile-P-associated microorganisms and decreasing the number of moderate-labile-P- and non-labile-P-associated microorganisms. In the organic acids, biochar expanded the biological pathways for the solubilization of moderate-labile-P through organic acids. This study illustrates the potential mechanism of biochar to enhance soil P availability.

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研究方向: Agriculture; Plant Sciences

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第 12 条

标题: Serum Norepinephrine and Cholesterol Concentrations as Novel Diagnostic Biomarkers for Vitamin E Deficiency in Holstein Cows

作者: Song, YX (Song, Yuxi); Jiang, XJ (Jiang, Xuejie); Hao, Y (Hao, Yu); Sun, R (Sun, Rui); Bai, YL (Bai, Yunlong); Xu, C (Xu, Chuang); Xia, C (Xia, Cheng)

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摘要: Vitamin E deficiency (VED) represents a common micronutrient deficiency in dairy cows (DCs), leading to severe degenerative diseases, oxidative stress, immune dysfunction, and various health issues, ultimately causing significant economic losses for the global dairy sector. Accordingly, our objective was to explore the metabolic features of VED-afflicted cows by combining the untargeted gas chromatography-time-of-flight mass spectrometry (GC-TOF-MS) and targeted liquid chromatography-mass spectrometry (LC-MS) to identify effective serum VED biomarkers. Untargeted GC-TOF-MS analysis identified 31 differential metabolites (DMs): 20 were overexpressed and 11 were suppressed in the VED group compared to the healthy control group. These DMs were enriched in six major metabolic pathways: glycine, serine, and threonine; alanine, aspartate, and glutamate; cysteine and methionine; tyrosine; primary bile acid biosynthesis; and nitrogen metabolisms. These outcomes show that VED significantly disrupts amino acid/lipid/energy metabolism pathways in DCs. Further targeted LC-MS quantification revealed significant alterations in key metabolites, including increased levels of norepinephrine, glycine, cysteine, and L-glutamine, as well as a significant reduction in cholesterol concentrations. Binary logistic regression analysis identified norepinephrine and cholesterol as strong candidate biomarkers for VED. Receiver operating characteristic curve analysis established outstanding diagnostic accuracy for norepinephrine and cholesterol (for both $p < 0.001$, area under the curve = 0.980 and 0.990, correspondingly), with sensitivities and specificities of 90% and 100%, respectively. In conclusion, this study integrates untargeted and targeted metabolomics approaches to reveal VED-caused metabolic disruptions in DCs, particularly in amino acid/lipid/energy metabolism pathways. Norepinephrine and cholesterol were identified as highly accurate serum VED biomarkers with excellent diagnostic performance. Early detection and timely intervention using these biomarkers could promote disease treatment and cow health, as well as productivity, and decrease economic losses.

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输出日期: 2025-06-11

第 13 条

标题: Quantification and metabolic variations of mycotoxins in raw milk: Implications for dairy cow health and human safety

作者: Chen, YY (Chen, Yuanyuan); Cheng, JX (Cheng, Jiaxin); Wang, ZS (Wang, Zhuangshu); Liu, HL (Liu, Honglin); Xia, C (Xia, Cheng); Zhang, HF (Zhang, Haifeng); Zou, SQ (Zou, Siqi); Chang, QC (Chang, Qiaocheng); Xu, C (Xu, Chuang)

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摘要: This study established a method using ultra-performance liquid chromatography-tandem MS for the quantitative analysis of 9 harmful mycotoxins: zearalenone (ZEN), alpha-zearalanol, HT-2 toxin, T-2 toxin, ochratoxin A, fumonisin B1, deoxynivalenol, aflatoxin M1, and aflatoxin B1 in raw milk. The method exhibited good linearity, sensitivity, accuracy, and precision, making it suitable for trace analysis of these toxins in raw milk. We applied this method to analyze 200 raw milk samples from Heilongjiang Province, China, and found that they contained multiple mycotoxins, with a relatively high concentration of ZEN. To further explore the metabolism of these mycotoxins in dairy cows, we conducted a metabolic study on 12 lactating dairy cows. The results showed significant metabolic changes among the 9 mycotoxins, with ZEN demonstrating notably higher metabolic conversion rates compared with other mycotoxins in the transitions from feed to serum, from feed to milk, and from feed to feces. These findings provide new insights into the safety of raw milk and emphasize the importance of strict monitoring and regulation of these toxins in dairy products to protect human health. Simultaneously, we believe that future research should delve deeper into the metabolism of mycotoxins in dairy cows, which is crucial for ensuring public health safety.

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研究方向: Agriculture; Food Science & Technology

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第 14 条

标题: Deep Fertilization Is More Beneficial than Enhanced Efficiency Fertilizer on Crop Productivity and Environmental Cost: Evidence from a Global Meta-Analysis

作者: Wu, Q (Wu, Qi); Huang, H (Huang, Hua); Wang, QH (Wang, Qinhe); Liu, ZY (Liu, Zeyu); Pei, RZ (Pei, Runzhuo); Wen, GS (Wen, Guosheng); Feng, JH (Feng, Jinghui); Wang, H (Wang, Hao); Zhang, P (Zhang, Peng); Gao, ZQ (Gao, Zhiqiang); Wang, CY (Wang, Chuangyun); Wu, P (Wu, Peng)

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摘要: It is unclear whether enhanced efficiency fertilizer (EEF) or deep fertilization strategies (DF) can simultaneously improve crop productivity and reduce gaseous nitrogen losses. The DF strategy's investment cost is lower than that of EEF's, with more potential for large-scale promotion. However, there is still a need for a comprehensive comparison and evaluation of DF and EEF's effects on crop productivity and gaseous nitrogen losses. Here, we examine the effects of DF and EEF on crop yield, nitrogen use efficiency (NUE), and nitrous oxide (N2O) and ammonia (NH3) emissions by a meta-analysis of published studies. We collected peer-reviewed articles on EEF and DF published in recent decades and conducted a global meta-analysis, and explored their responses to different climatic, field management practices, and environmental factors. The results showed that compared with urea application on the surface, EEF and DF significantly increased yields by 7.52% and 13.88% and NUE by 25.84% and 36.27% and reduced N2O emissions by 37.98% and 34.18% and NH3 emissions by 42.37% and 69.68%, respectively. The DF strategy is superior to that of the EEF. Due to differences in climatic factors, soil properties, and management practices, the effects of DF and EEF in improving crop productivity and gaseous nitrogen loss vary. However, in most cases, DF is more beneficial than EEF. Compared with EEF, DF significantly increased the yield by 84.63% and reduced NH3 volatilization by 64.47%, yield-scaled N2O emission by 13.32%, and yield-scaled NH3 emission by 60.23%. Therefore, we emphasize that DF can achieve higher yields, nitrogen fertilizer utilization efficiency, lower emissions of gaseous nitrogen, and lower yield-scaled N2O and NH3 emissions than EEF, which is beneficial for the sustainable development of global agricultural ecosystems. The research results provide valuable information on crop productivity and environmental costs under an effective fertilizer type and fertilization strategy management.

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第 15 条

标题: Changes in Soil Properties, Content of Cd, and Cd-Resistant Bacterial Community with Biochar After One-Time Addition Under Soybean Continuous Cropping and Crop Rotation Patterns

作者: Yao, Q (Yao, Qin); He, GG (He, Gege); Yan, SB (Yan, Shubo); Song, J (Song, Jie); Zhang, YT (Zhang, Yuetong); Zhang, XY (Zhang, Xiaoyu); Sun, Y (Sun, Yan); Wang, YB (Wang, Yibo); Li, YJ (Li, Yongjuan); Tian, Y (Tian, Yu); Zhao, CJ (Zhao, Changjiang); Guo, YX (Guo, Yongxia)

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摘要: In recent years, Cadmium (Cd) pollution in soybean farmland is severe. Therefore, this study focused on whether biochar influences soil physiochemical properties, the Cd content in soil and soybean grains, and the abundance and community structure of the czcA gene. Four doses of rice husk biochar (0, 5, 15, and 25 t<middle dot>ha-1) were applied under continuous cropping and crop rotation systems, and soil samples were collected after four years of one-time addition. The results indicated that biochar addition significantly increased soil available nitrogen, phosphorus, and soil organic carbon contents under continuous cropping and rotation. Biochar application significantly reduced the total Cd content of soil samples and soybean grains. Additionally, biochar application reduced czcA gene abundance in soybean soils by 14.26-37.88% and 35.96-48.71%, respectively. Correlation analysis revealed that Cd content and the abundance of the czcA gene significantly correlated with soil nutrients and pH. High-throughput sequencing revealed that the relative abundances of several Cd-resistant microorganisms were decreased by biochar addition. In addition, adding biochar significantly affected the Cd-resistant microbial community structure and diversity by influencing soil properties and Cd content. Therefore, this study has important practical significance for improving the soil environment and ensuring the quality and safety of agricultural products.

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文献类型: Article

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研究方向: Agriculture; Plant Sciences

输出日期: 2025-06-11

第 16 条

标题: Nitrogen Fertiliser Reduction at Different Rice Growth Stages and Increased Density Improve Rice Yield and Quality in Northeast China

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来源出版物: AGRICULTURE-BASEL **卷:** 15 **期:** 8 **文献号:** 892
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摘要: Rice yield and quality decline due to excessive fertiliser use is problematic in China. To increase rice grain filling and improve rice yield and quality, a nitrogen reduction and density increase study in 2023 and 2024 was imposed on a long-term experimental field. The four treatments adopted for the study were normal nitrogen and normal density (CK), normal nitrogen and increased density (NN+ID), reduced nitrogen in panicle fertiliser and increased density (RPN+ID), and reduced nitrogen in basal fertiliser and increased density (RBN+ID). RPN+ID and RBN+ID, respectively, produced a 3.0% and 5.1% higher yield than CK in both years. The mean grain filling rate (Va) of superior grains in RBN+ID increased by 12.5%, while the mean grain filling rate (Va) of inferior grains in the RPN+ID treatment increased by 4.2% with respect to CK. RPN+ID caused 0.4%, 9.6%, and 13.3% decline in the brown rice rate, chalkiness degree, and chalkiness rate, respectively, while RBN+ID triggered 0.4%, 7.2%, and 11.0% decline in the brown rice rate, chalkiness degree, and chalkiness rate, respectively. RPN+ID stimulated 4.2% and 3.1% increases in flavour and straight-chain amylose values, respectively. Whereas a 20% reduction in basal nitrogen fertiliser and a 32% increase in density improved the yield and appearance quality of rice, a 20% reduction in nitrogen fertiliser at the panicle stage and a 32% increase in density promoted a higher steaming flavour quality. Therefore, an appropriate reduction in nitrogen fertiliser while simultaneously increasing rice density has a significant impact on rice quality, fertiliser pollution reduction, and is a theoretical basis for rice yield and quality improvement in Northeast China.

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研究方向: Agriculture

输出日期: 2025-06-11

第 17 条

标题: 16S amplicon sequencing and untargeted metabolomics reveal changes in rumen microorganisms and metabolic pathways involved in the reduction of methane by cordycepin

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来源出版物: JOURNAL OF INTEGRATIVE AGRICULTURE **卷:** 24 **期:** 4 **页:** 1310-1326 **DOI:** 10.1016/j.jia.2024.04.014 **Published Date:** 2025 APR

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摘要: As a major contributor to methane production in agriculture, there is a need for a suitable methane inhibitor to reduce ruminant methane emissions and minimize the impact on the climate. This work aimed to explore the influence of cordycepin on rumen fermentation, gas production, microbiome and their metabolites. A total of 0.00, 0.08, 0.16, 0.32, and 0.64 g L-1 cordycepin were added into fermentation bottles containing 2 g total mixed ration for in vitro ruminal fermentation, and then the gas produced and fermentation parameters were measured for each bottle. Samples from the 0 and 0.64 g L-1 cordycepin addition were selected for 16S rRNA gene sequencing and metabolome analysis. The result of this experiment indicated that the addition of cordycepin could linearly increase the concentration of total volatile fatty acid, ammonia nitrogen, the proportion of propionate, valerate, and isovalerate, and linearly reduce ruminal pH and methane, carbon dioxide, hydrogen and total gas production, as well as the methane proportion, carbon dioxide proportion and proportion of butyrate. In addition, there was a quadratic relationship between hydrogen and cordycepin addition. At the same time, the relative abundance of Succiniclasticum, Prevotella, Rikenellaceae_RC9_gut_group, NK4A214_group, Christensenellaceae_R_7_ group, unclassified_F082, Veillonellaceae_UCG_001, Dasytricha, Ophryoscolex, Isotricha, unclassified_Eukaryota, Methanobrevibacter, and Piromyces decreased significantly after adding the maximum dose of cordycepin. In contrast, the relative abundance of Succinivibrio, unclassified_Succinivibrionaceae, Prevotellaceae_UCG_001, unclassified_Lachnospiraceae, Lachnospira, Succinivibrionaceae_UCG_002, Pseudobutyrivibrio, Entodinium, Polyplastron, unclassified_Methanomethylophilaceae, Methanosphaera, and Candidatus_Methanomethylophilus increased significantly. Metabolic pathways such as biosynthesis of unsaturated fatty acids and purine metabolism and metabolites such as arachidonic acid, adenine, and 2"-deoxyguanosine were also affected by the addition of cordycepin. Based on this, we conclude that cordycepin is an effective methane emission inhibitor that can change the rumen metabolites and fermentation parameters by influencing the rumen microbiome, thus regulating rumen methane production. This experiment may provide a potential theoretical reference for developing Cordyceps byproduct or additives containing cordycepin as methane inhibitors.

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文献类型: Article

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研究方向: Agriculture

输出日期: 2025-06-11

第 18 条

标题: Dual Melatonin Enhances Coordination Between Carbon and Nitrogen Assimilation in Soybean

作者: Wang, YH (Wang, Yanhong); Jin, XJ (Jin, Xijun); Zhang, YX (Zhang, Yuxian)

来源出版物: AGRICULTURE-BASEL **卷:** 15 **期:** 7 **文献号:** 681
DOI: 10.3390/agriculture15070681 **Published Date:** 2025 MAR 23

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摘要: Soybean production is currently insufficient to meet global demand, highlighting the need for strategies to enhance growth. Melatonin (MT) has emerged as a promising solution due to its growth-promoting properties. This study investigated the effects of a dual MT treatment-combining seed soaking and foliar spraying-on soybean carbon and nitrogen metabolism using metabolomics analysis. The results demonstrated that MT treatment significantly upregulated the TCA cycle, providing energy and precursors for amino acid and carbohydrate synthesis. Key amino acid pathways, including histidine and phenylalanine metabolism, were enhanced, with histidine metabolism stimulating purine synthesis to improve biological nitrogen fixation and phenylalanine metabolism promoting secondary metabolite production to support growth. Additionally, carbohydrate pathways such as starch and sucrose metabolism and glycolysis/gluconeogenesis were positively regulated, ensuring energy supply and carbon homeostasis. Overall, dual MT treatment enhanced soybean metabolic capacity by promoting amino acid and carbohydrate metabolism, stimulating purine and secondary metabolite production, and maintaining carbon and nitrogen balance. These findings underscore melatonin's regulatory role in soybean growth and provide insights for improving crop productivity.

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研究方向: Agriculture

输出日期: 2025-06-11

第 19 条

标题: Genome-Wide Discovery of Candidate Genes Associated with Cold Tolerance in Rice at Various Growth Stages

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来源出版物: RICE SCIENCE **卷:** 32 **期:** 2 **页:** 137-142
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研究方向: Agriculture; Plant Sciences

输出日期: 2025-06-11

第 20 条

标题: NF-kappaB is involved exclusively under inflammatory conditions in the regulation of cathelicidin 3 expression in bovine mammary glands through phosphorylation of p65

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来源出版物: JOURNAL OF ANIMAL SCIENCE **卷:** 103 **文献号:** skaf112
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摘要: Cathelicidin 3 (CATHL3), a member of the cathelicidin family, exhibits potent resistance against a spectrum of microorganisms. Despite its importance, the expression pattern and regulatory mechanisms of CATHL3 in inflamed dairy mammary glands remain elusive. For this purpose, healthy (n = 3) and inflamed (n = 3) mammary gland tissues were subjected to high-throughput transcriptome sequencing and RT-qPCR analysis. Our findings revealed significant differential expression of the CATHL3 gene and significantly higher nuclear factor kappa B (NF-kappa B) mRNA expression in inflamed tissues compared to healthy controls. Milk somatic cells from dairy cows with varying blood glucose concentrations were extracted and analyzed. In healthy cows, a decrease in blood glucose concentration was significantly associated with an increase in CATHL3 mRNA expression in milk somatic cells, while NF-kappa B mRNA expression significantly decreased. Conversely, in milk somatic cells from cows with subclinical and clinical mastitis, a decrease in blood glucose concentration still led to a significant increase in CATHL3 mRNA expression, but NF-kappa B mRNA expression paradoxically increased, contrasting with the healthy cow group. The in vitro experiments mirrored the findings of the in vivo experiments mentioned above by culturing dairy cow mammary epithelial cells under varying glucose concentrations, with or without lipopolysaccharides (LPS). Additionally, the effects of NF-kappa B inhibitor (BAY 11-7082, 10 mu mol/L) or NF-kappa B activator (NF-kappa B activator-1, 1 mu mol/L) on cultured dairy cow mammary epithelial cells were assessed. While the addition of NF-kappa B activator alone upregulated the mRNA expression level of NF-kappa B, it did not alter the p-p65/p65 ratio and CATHL3 mRNA expression compared to the blank control group. Notably, the co-addition of LPS and the NF-kappa B inhibitor significantly attenuated the stimulatory effects of LPS on NF-kappa B mRNA expression and the p-p65/p65 ratio and also weakened the stimulatory effect of LPS on CATHL3 mRNA expression. Our results suggest that mastitis stimulates CATHL3 gene expression in mammary gland with the NF-kappa B signaling pathway playing a regulatory role through the phosphorylation of p65 exclusively under inflammatory conditions. Additionally, decreased blood glucose concentration promotes CATHL3 mRNA expression. These findings provide novel insights into the molecular mechanisms of bovine mastitis and potential targets for therapeutic intervention.

This research highlights potential therapeutic targets for mastitis management in dairy cows.

This research explores how mastitis, a common dairy cow disease, affects the expression of cathelicidin 3 (CATHL3), an antimicrobial peptide. The study reveals that CATHL3, a key immune response factor, is more active in inflamed bovine mammary tissues, and the role of the nuclear factor kappa B (NF-kappa B) signaling pathway in regulating CATHL3 gene expression exclusively under inflammatory conditions in bovine mammary with a dependence on p65 phosphorylation.

Decreased blood glucose levels were associated with elevated CATHL3 mRNA expression.

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研究方向: Agriculture

输出日期: 2025-06-11

Biochemistry & Molecular Biology

第 1 条

标题: Trichothecenes toxicity in humans and animals: Unraveling the mechanisms and harnessing phytochemicals for prevention

作者: Zhang, JX (Zhang, Jiexing); Li, HY (Li, Haoyan); Zhang, EC (Zhang, Encheng); Lu, YH (Lu, Yuhan); Liu, BX (Liu, Bingxue); Yan, KX (Yan, Kexin); Yang, X (Yang, Xin); Lv, HM (Lv, Hongming)

来源出版物: COMPARATIVE BIOCHEMISTRY AND PHYSIOLOGY C-TOXICOLOGY & PHARMACOLOGY **卷:** 296 **文献号:** 110226

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摘要: Mycotoxins are the major widespread hazardous substances in feed and food and are widely distributed throughout the world. Mycotoxins are a major food safety concern since they can produce substantial toxic and carcinogenic consequences in human and animals when consumed. Trichothecenes (TCTs), a class of highly toxic mycotoxins mainly generated by Fusarium species, are among the most prevalent food pollutants. Deoxynivalenol (DON), largely biosynthesized by Fusarium graminearum and Fusarium culmorum, along with T-2 toxin generated chiefly by Fusarium langsethiae and Fusarium sporotrichioides, represent the most agriculturally significant TCT subtypes. There are still no effective control strategies. Furthermore, phytochemicals have received widespread attention as natural compounds with strong antioxidant, anti-inflammatory and detoxifying effects. Because of the powerful antioxidant effects of phytochemicals, researchers have begun to look at ways to counteract the intense toxicity of TCT. Focusing on the global challenge of TCTs, this comprehensive review systematically examines contamination patterns of DON and T-2 toxin, elucidates their multi-organ toxicity pathways, and critically evaluates emerging evidence on phytochemical-based interventions targeting DON and T-2 toxininduced health impairments. It concludes that These findings demonstrate that phytochemicals counteract DON and T-2 toxin toxicity by suppressing oxidative stress-mediated pathways, including pyroptosis, ferroptosis, apoptosis, and inflammatory responses. Accordingly, the direct addition of phytochemicals to food and feed is expected to be a promising prospect for the detoxification of DON and T-2 toxin, considering their safety, efficiency, and accessibility.

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文献类型: Review

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研究方向: Biochemistry & Molecular Biology; Endocrinology & Metabolism; Toxicology; Zoology

输出日期: 2025-06-11

第 2 条

标题: Identification and functional analysis of an LTR retrotransposon insertion in CsPHYB associated with early senescence in cucumber (Cucumis sativus L.)

作者: Liu, HQ (Liu, Hanqiang); Hu, KH (Hu, Kaihong); Ma, YX (Ma, Yuxuan); Fu, LT (Fu, Liting); Huang, ZQ (Huang, Zeqiang); Cheng, ZH (Cheng, Zhihui); Sheng, YY (Sheng, Yuyan); Li, DD (Li, Dandan); Pan, YP (Pan, Yupeng)

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摘要: Early senescence in plants significantly affects photosynthetic efficiency, crop yield, and overall plant vigor. In this study, we identified a spontaneous cucumber mutant, NW079, exhibiting premature leaf yellowing, reduced chlorophyll content, and impaired photosynthetic performance. To uncover the genetic basis of this phenotype, we generated F2mapping populations and employed bulked segregant analysis and fine mapping. These efforts led to the identification of a 5.5-kb long terminal repeat (LTR) retrotransposon insertion within the first exon of CsPHYB, a gene encoding phytochrome B. This insertion disrupted normal splicing and gave rise to two aberrant transcript variants: one containing a 261-bp LTR-derived sequence with premature stop codons, and the other harboring a 1,914-bp deletion due to exon skipping. Both variants are predicted to produce truncated, nonfunctional proteins. Functional analyses revealed that CsPHYB deficiency resulted in heightened sensitivity to varying light qualities and intensities, leading to pronounced leaf yellowing and reduced leaf area. RNA sequencing revealed widespread transcriptional reprogramming in NW079, with 580 differentially expressed genes (DEGs) implicated in heme metabolism, tetrapyrrole binding, and chloroplast development. These transcriptional disruptions were closely linked to the observed structural and functional abnormalities in chloroplasts. This study provides a molecular framework for understanding the early senescence in cucumber, offering valuable insights for breeding strategies aimed at improving crop resilience and productivity. Keymessage An LTR retrotransposon insertion in the first exon of CsPhyB disrupts its expression and splicing, leading to early leaf senescence in cucumber. This finding provides novel insights into the role of CsPHYB in chloroplast development and light signaling, offering valuable molecular markers and a target gene for cucumber breeding programs focused on enhancing yield and stress resilience.

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研究方向: Biochemistry & Molecular Biology; Plant Sciences

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第 3 条

标题: Investigation of the potential regulation of the CHYR E3 ligase genes on alfalfa response to drought and salt stresses

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来源出版物: INTERNATIONAL JOURNAL OF BIOLOGICAL MACROMOLECULES **卷:** 311 **文献号:** 143890 **DOI:** 10.1016/j.ijbiomac.2025.143890
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摘要: Plant CHYR family genes are key regulators of plant growth and development, as well as stress response. However, studies of CHYR genes in Medicago truncatula remain nebulous. In this study, we identified eight MtCHYR genes, which were phylogenetically grouped into three subfamilies. MtCHYR members from the same subfamily possessed similar intron-exon structure and conserved motif architecture. Cis-acting elements related to development and stress responses were identified in the promoter region of MtCHYRs. Expression analysis based on transcriptome data revealed that MtCHYR genes had different expression patterns in various organs and responded to salt, drought, cold and freezing stresses. qRT-PCR analysis showed the differential expression of MtCHYRs under abiotic stresses, especially a significant increase in MtCHYR3 expression under drought and salt stresses. Furthermore, MtCHYR3 was highly expressed in roots, and MtCHYR3-GFP proteins were localized in the cytoplasm and nucleus of plant cells. Ectopic expression of MtCHYR3 in Arabidopsis increased the drought and salt tolerance. These results will be beneficial for further revealing the biological functions of MtCHYRs and improving the drought and salt tolerance of alfalfa via molecular breeding.

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文献类型: Article

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研究方向: Biochemistry & Molecular Biology; Chemistry; Polymer Science

输出日期: 2025-06-11

第 **4** 条

标题: Cationic antimicrobial peptide CC34 potential anticancer and apoptotic induction on cancer cells

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来源出版物: AMINO ACIDS **卷:** 57 **期:** 1 **文献号:** 28

DOI: 10.1007/s00726-025-03458-1 **Published Date:** 2025 MAY 24

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摘要: To evaluate the potential of antimicrobial peptide CC34 for use as therapeutic agents for gastric cancer SGC-7901 and hepatocellular carcinoma HepG-2. In this study, the antibacterial activity and antibacterial mechanism were tested by the minimum inhibitory concentration (MIC) analysis, minimal bactericidal concentration (MBC) analysis, bacterial biofilm and NaCl permeability assays. Then, we assessed the hemolytic activity and cytotoxicity of CC34 for red blood cells and cancer cells, respectively. Apoptosis assay, cell cycle analysis, determination of intracellular ROS, western blot analysis caspase activity assay and ATP assay were further performed to investigate the mechanism of CC34 affected cancer cells. The novel peptide could inhibit Gram-negative and Gram-positive bacteria, with low hemolytic activity against mouse and chicken erythrocytes. Moreover, CC34 exhibited higher inhibitory activity against biofilm formation. In addition, our data showed that CC34 significantly suppressed cell proliferation, in a dose dependent manner. CC34 induced apoptosis, induced reactive oxygen species (ROS) generation, inhibited B-cell lymphoma-2 (Bcl-2) expression, increase B-cell lymphoma protein 2 associated X protein (Bax) expression, release of cytochrome c (Cyt C), promoted caspase-3 and - 9 activities and reduced cellular ATP levels in cancer cells. Our results indicate that CC34 with antimicrobial activity have a highly potent ability to induced apoptosis via mitochondrial-mediated apoptotic pathway in cancer cells.

入藏号: WOS:001494540300002

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研究方向: Biochemistry & Molecular Biology

输出日期: 2025-06-11

第 5 条

标题: Recent development in ozone-based starch modification: From generation methods to film applications

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来源出版物: INTERNATIONAL JOURNAL OF BIOLOGICAL MACROMOLECULES **卷:** 309 **文献号:** 142780 **DOI:** 10.1016/j.ijbiomac.2025.142780
Published Date: 2025 MAY **子辑:** 2

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摘要: Starch holds significant potential in food industry applications; however, its practical utility is hindered by several limitations, including freeze-thaw instability, shear sensitivity, insolubility in organic solvents, high retrogradation, and the instability of its gels and pastes. Ozonation, an eco-friendly modification technique, effectively addresses these challenges by oxidizing starch molecules, introducing carbonyl and carboxyl functional groups, and partially cleaving glycosidic bonds. These structural modifications enhance the functional, mechanical, and barrier properties of starch, making it a promising material for biodegradable food packaging films. Additionally, ozone treatment improves key physicochemical properties such as gelatinization behavior, pasting characteristics, crystallinity, solubility, and viscosity. This review explores the application of gaseous and aqueous ozone in modifying various starch sources, including cassava, wheat, rice, corn, sago, and potato starches. Furthermore, it delineates different ozone generation methods, such as corona discharge, dielectric barrier discharge, and microwave ultraviolet (UV) systems. The impact of ozonation on starch structure, its functionalization for packaging films, and the challenges associated with scaling up industrial ozonation processes are critically discussed. Finally, this review provides recommendations for optimizing ozone-based starch modification and advancing innovative ozone generation technologies to enhance industrial feasibility and sustainable packaging solutions.

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研究方向: Biochemistry & Molecular Biology; Chemistry; Polymer Science

输出日期: 2025-06-11

第 6 条

标题: Aldehyde-modified sodium alginate/gelatin-based bacteriophage-loaded multifunctional hydrogel for promoting the healing of multidrug-resistant bacterial-infected wounds

作者: Yuan, QX (Yuan, Qingxin); Zhao, ZP (Zhao, Zepeng); Wei, AB (Wei, Anbo); Fan, JP (Fan, Jiapeng); Wang, P (Wang, Pei); Pan, SY (Pan, Shunyuan); Gao, DY (Gao, Dongyang); Song, J (Song, Jun); Sun, DB (Sun, Dongbo)

来源出版物: INTERNATIONAL JOURNAL OF BIOLOGICAL MACROMOLECULES **卷:** 309 **文献号:** 142778 **DOI:** 10.1016/j.ijbiomac.2025.142778
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摘要: Multidrug-resistant bacterial infections in skin injuries are hard to repair. There is an urgent need to develop new antibacterials, antibiofilm formation, and immunomodulatory wound dressing. In this study, we produced a bacteriophage-loaded multifunctional hydrogel consisting of aldehyde-modified sodium alginate (ADA), gelatin (GEL), and carboxymethyl chitosan (CMCS) through a Schiff base reaction and borax complexation. These post-reactive ADA/GEL/CMCS/Phage (AGCP) hydrogels, particularly the AGCP3 hydrogel, boast a porous structure, high swelling rate, effective hemostasis, controlled degradation, good rheological properties, and strong antibacterial activity. Furthermore, the hydrogel developed in this study can sustainably release various bacteriophages targeting the bacteria responsible for major skin infections, thereby enhancing antibacterial activity and preventing bacterial biofilm formation. Besides, cytotoxicity and cell proliferation demonstrated that the hydrogel, comprising three polysaccharides, ADA, GEL, and CMCS, facilitates skin tissue regeneration by enhancing cellular proliferation and migration. The AGCP hydrogel enhanced healing and controlled inflammation in bacterial-infected wounds, as evidenced by wound closure, collagen deposition, and quantitative reverse transcription polymerase chain reaction results. In conclusion, the AGCP3 hydrogel exhibits strong antibacterial properties, excellent expands, biocompatibility, hemostatic properties, and a controlled release of bacteriophages, making it ideal for universal bacteriophage delivery systems and wound dressings for skin wounds infected with multidrug-resistant bacteria.

入藏号: WOS:001466430000001

文献类型: Article

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研究方向: Biochemistry & Molecular Biology; Chemistry; Polymer Science

输出日期: 2025-06-11

第 7 条

标题: Effects of Polyphenols on the Structure, Interfacial Properties, and Emulsion Stability of Pea Protein: Different Polyphenol Structures and Concentrations

作者: Tang, SY (Tang, Shiyao); Yang, XY (Yang, Xiyuan); Wang, C (Wang, Chang); Wang, CY (Wang, Changyuan)

来源出版物: MOLECULES **卷:** 30 **期:** 8 **文献号:** 1674
DOI: 10.3390/molecules30081674 **Published Date:** 2025 APR 8

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摘要: While protein-stabilized emulsions have demonstrated potential for various applications in food, their poor lipid oxidation remains a major challenge. The relationship between the architecture of polyphenolic compounds and their capacity to suppress lipid oxidation has not received extensive scrutiny. In this research, pea protein isolate (PPI)-polyphenol complexes were synthesized to examine their capability of maintaining emulsion stability and suppressing lipid oxidation. The collective evidence from fluorescence spectroscopy and molecular dynamics simulations pointed towards non-covalent and self-initiated interactions between the polyphenols and PPI. The presence of additional hydroxyl groups on the polyphenols could significantly boost the extent of these interactions. Specific clusters in PPI and polyphenols which might have formed hydrogen bonds and hydrophobic interactions. Polyphenols also reduced the interfacial tension and increased the surface hydrophobicity of the complex, thus driving more proteins to adsorb at the oil-water interface. The PPI-rosmarinic acid (RA)-stabilized emulsion had a smaller droplet size and higher electrostatic repulsion, enabling it to resist droplet aggregation. This emulsion stood out as having the most robust stability amongst all PPI-polyphenol emulsions and proved highly efficient in preventing lipid oxidation. This study bolsters the viability of employing polyphenol and pea protein-stabilized emulsions in developing new food products.

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研究方向: Biochemistry & Molecular Biology; Chemistry

输出日期: 2025-06-11

第 8 条

标题: Plant PAQR-like sensors activate heterotrimeric G proteins to confer resistance against multiple pathogens

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来源出版物: MOLECULAR PLANT **卷:** 18 **期:** 4 **页:** 639-650
DOI: 10.1016/j.molp.2025.02.006 **Published Date:** 2025 APR 7

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摘要: Human adiponectin receptors (AdipoRs) and membrane progestin receptors (mPRs, members of the progestin and adipoQ receptor [PAQR] family) are seven-transmembrane receptors involved in the regulation of metabolism and cancer development, which share structural similarities with G protein-coupled receptors. Plant PAQR-like sensors (PLSs) are homologous to human PAQRs but their molecular functions remain unclear. In this study, we found that PLSs associate with cell surface receptor-like kinases through KIN7 and positively regulate plant immune responses, stomatal defense, and disease resistance. Moreover, PLSs activate heterotrimeric G proteins (Gabg) to transduce immune signals and regulate the exchange of GDP for GTP on GPA1. Further analyses revealed that the immune function of PLSs is conserved in rice and soybean and contributes to resistance against multiple diseases. Notably, heterologous expression of human AdipoRs in Arabidopsis replicates the immune functions of PLSs. Collectively, our findings demonstrate that PLSs are key modulators of plant immunity via the G-protein pathway and highlight the potential application of human genes in enhancing plant disease resistance.

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文献类型: Article

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研究方向: Biochemistry & Molecular Biology; Plant Sciences

输出日期: 2025-06-11

第 9 条

标题: Identification and functional analysis of a novel single-transmembrane Na plus /H plus antiporter SATP1, in Pseudidiomarina sediminum: Characterization of its key Na plus binding site

作者: Han, L (Han, Lu); Yang, M (Yang, Ming); Xu, BB (Xu, Beibei); Dai, LY (Dai, Lingyan); Huang, YL (Huang, Yulan); Wang, WZ (Wang, Wenzhao); Pan, JX (Pan, Jingxuan); Abdel-motaal, H (Abdel-motaal, Heba); Wang, YH (Wang, Yanhong)

来源出版物: INTERNATIONAL JOURNAL OF BIOLOGICAL MACROMOLECULES **卷:** 308 **文献号:** 142670 **DOI:** 10.1016/j.ijbiomac.2025.142670
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Web of Science 核心合集中的 "被引频次": 0

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摘要: Halophilic microorganisms exhibit remarkable adaptability, enabling them to thrive in highly saline environments. This resilience is attributed to Na+/H+ antiporters, a specific class of transmembrane proteins that facilitate ion exchange and maintain cellular homeostasis under saline conditions. This study identified a novel Na+/H+ antiporter protein SATP1, from Pseudidiomarina sediminum c121T. SATP1 consists of 104 amino acids and has a unique single transmembrane region, setting it apart from other Na+/H+ antiporters. Functional assays demonstrated that SATP1 enhances the salt tolerance of Escherichia coli KNabc in environments containing 0.05 to 0.45 M NaCl at pH 8.5. We conducted structural and functional analyses to elucidate the molecular mechanisms underlying SATP1 is saline-alkaline tolerance. Our investigations revealed that aspartic acid at position 48 (D48) plays a critical role in SATP1 is activity. Through site-directed mutagenesis, we generated a D48A mutant and constructed a recombinant strain of E. coli KNabc pET-satp1 (D48A). Using isothermal titration calorimetry (ITC) and reverse membrane assays, we quantified the Na+/H+ antiporter activity of the mutant. The D48A mutant exhibited significantly reduced salt tolerance, with impaired Na+ binding and diminished Na+/H+ exchange functionality. These findings provide valuable insights into the molecular mechanisms that enable halophilic microorganisms to adapt to high-salt environments.

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文献类型: Article

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研究方向: Biochemistry & Molecular Biology; Chemistry; Polymer Science

输出日期: 2025-06-11

Biotechnology & Applied Microbiology

第 1 条

标题: Preparation and inoculation of Bacillus spp. and Sinorhizobiummeliloti strains immobilized on biochar-humic acid improve potted soybean traits and soil parameters

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来源出版物: ENVIRONMENTAL TECHNOLOGY & INNOVATION **卷:** 38
文献号: 104210 **DOI:** 10.1016/j.eti.2025.104210 **Published Date:** 2025 MAY

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摘要: This study examines microbial carriers to enhance soil quality and promote crop development. A composite microbial consortium was developed, consisting of Bacillus velezensis HT-S1, Bacillus subtilis HT-S2, Bacillus megaterium HT-S3, and Sinorhizobium meliloti HT-S4, which were absorbed onto various carriers. The combination of biochar and humic acid was identified as the optimal carrier through characterization analysis and evaluation of its adsorption capacity. The conditions for adsorption were optimized (156 rpm, 1.22 hours, and pH 8.0), resulting in a bacterial adsorption capacity of 3.11 x 10 1 0 CFU & sdot;g-1 . Kinetic and thermodynamic models indicated that adsorption was a spontaneous exothermic process primarily driven by physical interactions, while desorption was an endothermic process increasing entropy. In pot experiments with soybeans, microbial agents significantly enhanced plant growth, increasing plant height (10.65-17.01 %), stem thickness (12.83-22.62 %), and dry weight (22.6-50.25 %). Soil quality also improved, with increases in ammonium nitrogen (8.49-25.32 %), nitrate nitrogen (10.45-22.28 %), inorganic phosphorus (11.69-20.11 %), quick-acting potassium (7.95-33.01 %), and enzyme activities (sucrase, urease, alkaline phosphatase, and catalase). These results demonstrate that Bacillus spp. and S. meliloti can be immobilized in a biochar-humic acid carrier and colonize soil. The findings provide a theoretical basis for developing microbial fertilizers to improve soil quality in arable land.

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文献类型: Article

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研究方向: Biotechnology & Applied Microbiology; Engineering; Environmental Sciences & Ecology

输出日期: 2025-06-11

第 **2** 条

标题: Genome-wide identification of the NAC family genes of adzuki bean and their roles in rust resistance through jasmonic acid signaling

作者: Shengmiao, L (Shengmiao, Liu); Xin, D (Xin, Ding); Yue, L (Yue, Li); Lihua, Y (Lihua, Yin); Xiwang, K (Xiwang, Ke); Yuhu, Z (Yuhu, Zuo)

来源出版物: BMC GENOMICS **卷:** 26 **期:** 1 **文献号:** 283
DOI: 10.1186/s12864-025-11478-0 **Published Date:** 2025 MAR 22

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摘要: BackgroundAdzuki bean (Vigna angularis) rust, caused by the fungus Uromyces vignae, is an important disease affecting adzuki bean yield and quality. Previously, several NAC transcription factors (TFs) were induced by rust infection in a resistant adzuki bean variety, suggesting that NAC TF members may play important roles in rust resistance.ResultsTo further explore the functions of NAC TFs in rust resistance and to provide a reference for resistant varietal breeding, 101 NAC TFs were identified from the adzuki bean genome. The synteny analysis revealed 25 pairs of VaNACs in the genome, which exhibited whole-genome/segmental duplication. Based on the phylogenetic relationships and conserved motif characteristics, the NAC TFs of V. angularis can be divided into 16 subfamilies. Previous transcriptome data showed that nine VaNACs are significantly induced by rust infection. Here, a cis-acting element analysis of these nine genes revealed that most contain hormone responsive elements, such as abscisic acid and methyl jasmonate (MeJA). The expression levels of these nine VaNACs were dynamically regulated in response to exogenous MeJA treatment, as revealed by quantitative real-time PCR analysis. Among them, seven VaNACs exhibited significantly upregulated expression, peaking at 12 h post treatment (hpt) and remaining significantly higher than that of the untreated control group for 48 hpt. These results suggest that these VaNACs are responsive to MeJA signaling and may play roles in the early and sustained transcriptional regulation of stress-related pathways. The exogenous MeJA decreased rust severity on adzuki bean leaves by 45.68%. Additionally, the expression levels of these nine genes in adzuki bean leaves in response to rust infection after pretreatment with MeJA were investigated. The expression of VaNAC002 rapidly peaked at 24 h post inoculation (hpi) and remained significantly higher than the control from 120 to 192 hpi. Subsequently, transient overexpression of VaNAC002 significantly enhanced the resistance of tobacco to Botrytis cinerea, indicating that VaNAC002 positively regulates plant disease resistance.ConclusionThese findings suggest that adzuki bean NAC family members may play important roles in disease resistance through JA signaling, with VaNAC002 having a positive regulatory role in plant immunity.

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文献类型: Article

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研究方向: Biotechnology & Applied Microbiology; Genetics & Heredity

输出日期: 2025-06-11

Chemistry

第 1 条

标题: Accuracy of near-infrared spectroscopy for prediction of amino acids in frozen mutton: Benchtop and handheld systems

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来源出版物: MICROCHEMICAL JOURNAL **卷:** 213 **文献号:** 113606 **DOI:** 10.1016/j.microc.2025.113606 **Published Date:** 2025 JUN

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摘要: Near-infrared spectroscopy (NIRS) is a promising nondestructive technique for rapidly analyzing meat quality. This study systematically evaluated the feasibility of benchtop and handheld NIR systems for measuring amino acids in frozen mutton. A total of 144 mutton samples obtained from three regions in China were analyzed using a benchtop spectrometer (1000-2500 nm) and a handheld device (900-1700 nm). Partial least squares regression models combined with competitive adaptive reweighted sampling were developed and used to predict 16 amino acids. The benchtop system accurately predicted amino acids at moderate to high concentrations (e.g., Glu: R2p = 0.69, RPD = 2.00; Ser: R2p = 0.77, RPD = 1.92), and feature wavelength selection improved model efficiency with minimal loss of performance. Although the handheld system had a narrower spectral range and lower sensitivity, it achieved moderate reliability for on-site applications (e.g., Ser: R2p = 0.71, RPD = 2.56; Gly: R2p = 0.58, and RPD = 2.33). Low-content amino acids (e.g., Met and His) exhibited low accuracy due to spectral noise and overlapping signals. This study highlights the potential of benchtop NIRS for laboratory-based quality control and handheld devices for real-time supply chain monitoring, advancing the application of NIRS in low-temperature food systems.

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文献类型: Article

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研究方向: Chemistry

输出日期: 2025-06-11

第 2 条

标题: Biopurification of functional soybean oligosaccharides from defatted soybean yellow pulp water fermented by yeast species: A process study

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来源出版物: FOOD CHEMISTRY-X **卷:** 27 **文献号:** 102522
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摘要: This study presents a biotechnological method for isolating highly functional soybean oligosaccharides (SBOS) from soybean yellow pulp water (YPW) using microbial fermentation and resin-based purification methods. Candida sake selectively metabolizes sucrose, enabling the enrichment of target oligosaccharides. Under optimized fermentation conditions (6 % w/v YPW, 4 % v/v inoculum, and 28 degrees C), an 8 h process achieved retention rates of 85.93 % for raffinose and 85.17 % for stachyose, preserving the functional oligosaccharides. Isoelectric precipitation at pH 4.6 removed 72.47 % of the protein, while sequential treatment with AB-8, 001 x 7, and D392 resins resulted in 72.47 % decolorization and 74.98 % desalination at a flow rate of 2 BV/h. The final product contained 74.98 % functional oligosaccharides, demonstrating the scalability of the proposed approach for YPW valorization. These findings contribute to the sustainable utilization of soybean-processing byproducts through targeted resource recovery strategies.

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文献类型: Article

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研究方向: Chemistry; Food Science & Technology

输出日期: 2025-06-11

第 1 条

标题: A coevolutionary algorithm for constrained multi-objective optimization with dynamic relaxation

作者: Li, YC (Li, Yongchao); Jia, HM (Jia, Heming); Li, HG (Li, Hongguang)

来源出版物: SWARM AND EVOLUTIONARY COMPUTATION **卷:** 95
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摘要: To effectively address constrained multi-objective problems, algorithms need to strike a balance between objectives and constraints. This article introduces a method that utilizes two separate populations to investigate the exploration of the constrained Pareto front (CPF) and the unconstrained Pareto front (UPF). The fitness of each population is evaluated based on the information entropy of their positions, and suitable evolutionary operators are employed to improve solution quality in terms of convergence and diversity. Moreover, by adaptively relaxing constraint conditions, the auxiliary population can traverse large infeasible domains, thereby enhancing solution diversity. In the initial stages, the auxiliary population evolves alongside the main population, bringing it close to the CPF and minimizing computational resource wastage. A tournament environment selection model based on a dynamic relaxation (DR) function is utilized in the later stages, helping the auxiliary population relax constraints, retain promising solutions, and augment diversity. In addition, an entropy selection evolutionary strategy was designed to address the problem of populations easily falling into local optima during the evolution process. By calculating the entropy information of the population, the current state of the population can be determined, and then appropriate operators can be selected to enable the population to effectively escape from local optimal solutions. Compared against seven state-of-theart algorithms, demonstrate that the proposed constrained multi-objective optimization evolutionary algorithm (CMOEA) surpasses the performance of existing CMOEAs.

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文献类型: Article

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研究方向**:** Computer Science

输出日期**:** 2025-06-11

第 **2** 条

标题**:** MSAFNet: a multi-scale data fusion-based drought recognition method for three-dimensional images of the soybean plant

作者**:** Xu, WK (Xu, Wenkang); Ma, XD (Ma, Xiaodan); Guan, HO (Guan, Haiou); Meng, Y (Meng, Yan); Zhang, X (Zhang, Xi)

来源出版物**:** EARTH SCIENCE INFORMATICS 卷**:** 18 期**:** 2 文献号**:** 391
DOI: 10.1007/s12145-025-01894-x **Published Date:** 2025 JUN

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摘要**:** Drought stress, as one of the key limiting factors affecting soybean reproductive development, frequently caused photosynthetic product obstruction and seed quality degradation. Deep learning-based crop high-throughput phenotyping techniques combined with image processing demonstrated significant potential in detecting crop biotic and abiotic stresses. Traditional drought recognition methods relying on deep learning models previously exhibited shortcomings such as inadequate three-dimensional feature extraction and fusion capabilities. To address these issues, this study innovatively proposed a drought stress detection method utilizing multi-scale feature fusion for soybean 3D canopy images. First, the ResNet50 network served as the backbone for feature extraction while integrating the SE attention mechanism to enhance feature representation and extract deep semantic features from soybean canopy images. Subsequently, a dedicated multi-scale feature fusion module (MSFM) was designed to effectively aggregate multi-view image features. Finally, the MSAFNet drought stress detection model for soybean 3D canopy images was constructed by mapping aggregated multi-view features to category probability distributions through a fully connected layer and Softmax function. During simulation tests, the model achieved 90.2% recognition accuracy, 91.3% F1-score, and 13.6 fps inference speed. Results demonstrated that the proposed MSAFNet enhanced inference speed while maintaining detection accuracy, providing an effective approach for rapid and precise drought stress identification in soybean cultivation.

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文献类型**:** Article

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研究方向: Computer Science; Geology

输出日期: 2025-06-11

第 3 条

标题: IMA-FLADRC-Based Electric-Driven High-Speed Maize Precision Seeding Control Strategy and System

作者: Wang, S (Wang, Song); Yi, SJ (Yi, Shujuan); Zhao, B (Zhao, Bin); Li, YF (Li, Yifei); Zhang, DM (Zhang, Dongming); Chen, T (Chen, Tao); Sun, WS (Sun, Wensheng)

来源出版物: IEEE ACCESS **卷:** 13 **页:** 85177-85195
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摘要: Under high-speed seeding conditions, the accuracy and synchronization of the guiding and seeding motors are critical to seed spacing uniformity. This study develops an electric-driven high-speed maize precision seeding control system, establishing kinematic models for the seeding and guiding motors relative to operating speed. An Improve Mayfly Algorithm-Fuzzy Linear Active Disturbance Rejection Control (IMA-FLADRC)-based control strategy is proposed, integrating a fuzzy algorithm to adaptively adjust the proportional coefficient of the Linear State Error Feedback (LSEF) and optimizing key parameters using an IMA, enhancing system adaptability and robustness. Simulation results show that the IMA-FLADRC-based guiding motor achieves no overshoot or static error, with an adjustment time of 1.121s, a maximum disturbance error of 12.016 r/min, and a disturbance recovery time of 0.008s, while the seeding motor exhibits no static error, minimal overshoot of 0.059%, an adjustment time of 0.374s, a maximum disturbance error of 2.563 r/min, and a disturbance recovery time of 0.003s, outperforming four other strategies. Speed accuracy tests confirm that at 12-16 km/h, the dual-motor speed deviation ratio remains below 1.54%. Bench tests under varying speeds and theoretical seed spacing conditions indicate that the IMA-FLADRC achieves an average seed spacing variation coefficient of 9.10%, with reductions of 2.35, 1.60, and 0.85 percentage points compared to LADRC, FLADRC, and MA-FLADRC, respectively. The average seed spacing deviation is 2.56 mm, the lowest among all strategies. These findings demonstrate that the IMA-FLADRC-based control system ensures highly synchronized dual-motor operation, significantly enhancing seeding uniformity.

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研究方向: Computer Science; Engineering; Telecommunications

输出日期: 2025-06-11

Environmental Sciences& Ecology

第 1 条

标题: Astaxanthin ameliorates Cr (VI) accumulation, antioxidant, digestive, apoptosis and inflammatory response

作者: Zhao, L (Zhao, Lei); Zhang, Y (Zhang, Ying); Yu, J (Yu, Jie); Liu, YH (Liu, Yi-Han); Cai, ZH (Cai, Zhi-Hao); Li, MY (Li, Mu-Yang); Liu, M (Liu, Ming)

来源出版物: REGIONAL STUDIES IN MARINE SCIENCE **卷:** 87
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摘要: Exposure to Cr (VI) can induce various adverse effects such as oxidative stress and inflammatory response in fish. Astaxanthin have been documented as a novel antioxidant and heavy metal antidote. This study was investigated potential protective effect of astaxanthin on Cr (VI) accumulation, antioxidant, digestive enzyme, glucocorticoid receptor (GR)-regulated inflammatory response and apoptosis in snakehead fish (Channa argus). In this study, 300 C. argus were randomly divided into three groups. The fish were exposed to waterborne Cr(VI) and/or dietary astaxanthin for 28 days. The results provided evidences that astaxanthin could inhibit Cr (VI) bioaccumulation, inflammatory response and apoptosis. Additionally, astaxanthin also exerted protective effects by increasing the activity of antioxidant, digestive enzymes and GR-related genes expression levels. Overall, our results suggest that administration of 100 mg/kg astaxanthin has the potential to combat Cr (VI) toxicity, antioxidant, digestive, anti-apoptosis.

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文献类型: Article

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研究方向: Environmental Sciences & Ecology; Marine & Freshwater Biology

输出日期: 2025-06-11

第 2 条

标题: CROP CANOPY SPECTRAL INFORMATION PREDICTION BASED ON EEMD AND CNN-LSTM

作者: Chen, H (Chen, H.); Yi, SJ (Yi, S. J.); Wang, X (Wang, X.); Li, W (Li, W.)

来源出版物: APPLIED ECOLOGY AND ENVIRONMENTAL RESEARCH
DOI: 10.15666/aeer/2303_49514966 **Early Access Date:** MAY 2025
Published Date: 2025 MAY 15

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摘要: The utilization of the Normalized Difference Vegetation Index (NDVI) derived from canopy spectral information during crop growth helps identify growth conditions in farmland areas and facilitates management zone establishment. Targeted fertilizer application is possible based on observed growth patterns. Accurate NDVI prediction from canopy spectral information is crucial for real-time zone delineation and precision fertilization. Long Short-Term Memory (LSTM) neural networks can predict NDVI time series, but have limitations in handling non-stationary signals. A prediction model integrating modal decomposition with Convolutional Neural Network and Long Short-Term Memory (CNN-LSTM) is proposed to address these issues. This model uses Ensemble Empirical Mode Decomposition (EEMD) to decompose NDVI data into Intrinsic Mode Functions (IMFs), Convolutional Neural Network (CNN) to extract spatial features from IMFs, and LSTM to predict NDVI. Evaluation against standalone CNN, CNN-LSTM, and EEMD-CNN models using MAPE, RMSE, and R-2 metrics showed the proposed CNNLSTM model with modal decomposition outperformed the others in prediction accuracy. For soybean and maize NDVI prediction, the model achieved MAPE of 2.111% and 2.425%, RMSE of 0.012, and R-2 of 0.971 and 0.968, respectively. This model provides a robust foundation for real-time management and precision fertilization, ensuring optimal crop growth and yield.

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文献类型: Article; Early Access

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研究方向: Environmental Sciences & Ecology

输出日期: 2025-06-11

第 **3** 条

标题: PARTITIONING OF FERTILIZATION MANAGEMENT ZONES FOR MAIZE BASED ON SOM-FCM

作者: Chen, H (Chen, H.); Yi, S (Yi, S. J.); Wang, X (Wang, X.); Li, W (Li, W.)

来源出版物: APPLIED ECOLOGY AND ENVIRONMENTAL RESEARCH
DOI: 10.15666/aeer/2303_58415857 **Early Access Date:** APR 2025
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摘要: At present, many clustering algorithms have been applied to the calculation of farmland fertilization management zoning, among which the fuzzy c-means (FCM) algorithm is the most widely used, but the FCM algorithm is sensitive to the initial clustering center, which affects the calculation efficiency. In order to improve the efficiency of clustering calculation, especially for the clustering calculation of large datasets such as normalized difference vegetation index (NDVI), an algorithm combining the self-organizing feature map neural network (SOM) and FCM is proposed. The algorithm first uses SOM for preliminary clustering to determine the cluster center, then applies it as the initial cluster center of the FCM, and finally uses the FCM to further cluster the data. This method effectively combines the advantages of SOM and the FCM algorithm, solves the problem of setting the initial clustering center in the FCM, and overcomes their respective limitations. The NDVI data of maize was obtained through the ground remote sensing detection system. The FCM algorithm and the SOM-FCM algorithm were used to partition the fertilization management zones of maize. The sum of squared errors (SSE) and silhouette coefficient (SC) were used to evaluate the effectiveness of partitioning the fertilization management zones. The experimental results show that the SOM-FCM algorithm is better than the FCM algorithm for different NDVI data volumes. The maximum SSE difference is 639, and the maximum difference of SC value is 0.048. As NDVI data volume continues to grow of NDVI data volume, SOM-FCM algorithm shows better performance than FCM algorithm.

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文献类型: Article; Early Access

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第 **4** 条

标题: EFFECT OF DIFFERENT IRRIGATION AMOUNT AND STRAW RETURNING AMOUNT ON GLOBAL WARMING POTENTIAL OF PADDY IN COLD REGIONS

作者: Lin, YY (Lin, Y. Y.); Yi, SJ (Yi, S. J.); Zheng, X (Zheng, X.); Liu, SD (Liu, S. D.)

来源出版物: APPLIED ECOLOGY AND ENVIRONMENTAL RESEARCH
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摘要: In order to explore the emission patterns and global warming potential (GWP) of CH4 and N2O from cold rice fields, the cold rice fields in Heilongjiang Province, China were selected as the research objects. The artificial static box method was used to comprehensively observe the CH4 and N2O gas emissions under three water management modes: controlled irrigation (CI), intermittent irrigation (II), and conventional flooding (CF), as well as three straw return management modes: no straw return amount (S0:0 t<middle dot>hm(-2)), low straw return amount (S1:t<middle dot>hm(-2)), and high straw return amount (S2:6t<middle dot>hm(-2)). The results showed that both irrigation amount and straw returning amount promoted the comprehensive warming potential of CH(4)and N2O. The effects of irrigation amount and straw returning amount on warming potential were as follows: irrigation amount>straw returning amount. At the same time, irrigation amount and straw returning amount also promoted each other. Based on comprehensive analysis, the optimization mode of cold rice field management aimed at reducing the comprehensive warming potential of CH(4)and N2O in cold rice fields should adopt controlled irrigation (CI) and low straw return treatment (S1:3t<middle dot>hm(-2)), which can facilitate the transformation of soil nutrients and effectively reduce the comprehensive warming of CH4 and N2O.

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文献类型: Article; Early Access

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研究方向: Environmental Sciences & Ecology

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第 5 条

标题: PFOS exposure impairs porcine oocyte maturation and embryo development via mitochondria-dependent ferroptosis

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来源出版物: ENVIRONMENTAL POLLUTION **卷:** 374 **文献号:** 126185
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摘要: Perfluorooctane sulfonate (PFOS) is a widely utilized chemical known for its exceptional environmental stability over extended periods, its significant potential to bioaccumulate in living organisms, and its considerable risks to both health and the environment. Several studies have suggested that PFOS may pose reproductive risks in mammals; however, the exact mechanisms driving these effects are not well understood. In this study, we explored the possible mechanisms by which PFOS toxicity affects the maturation of mammalian oocytes and the embryonic development employing porcine oocytes as a model system. SMART-seq results suggested that PFOS may affect oocyte maturation through mechanisms involving ferroptosis, autophagy, and alterations in membrane structure. Our results suggest that PFOS exposure adversely affects mitochondrial function and structure, thereby influencing peroxisome biogenesis and contributing to oxidative stress. Most importantly, we found that exposure to PFOS significantly elevated Fe2+ levels, an indicator associated with ferroptosis in oocytes. Furthermore, malondialdehyde (MDA) levels in the PFOS group were significantly higher than those in the control group. Additionally, the mRNA expression levels of PCBP1 and PCBP2, which are related to ferroptosis, as well as the expression level of P53, were significantly reduced in the PFOS group. Overall, exposure to PFOS in vitro results in mitochondrial damage in porcine oocytes, which induces lipid peroxidation and subsequently leads to the occurrence of ferroptosis.

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研究方向: Environmental Sciences & Ecology

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Food Science & Technology

第 1 条

标题: Effects of organic acids on the physico-chemical and functional characteristics of mung bean globulin amyloid fibrils

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来源出版物: FOOD BIOSCIENCE **卷:** 69 **文献号:** 106837

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摘要: Amyloid fibers have valuable physicochemical properties for food and biomaterial applications, but research on their aggregation and fibrillation in different acidic environments is limited. This study integrated spectroscopic techniques, visual imaging, and molecular dynamic (MD) simulations to investigate the effect of different acidic environments on the structural transformation and fibrillation of mung bean globulin (MBG). The results indicated that acidic environments significantly affect the hydrolysis, self-assembly, and functional properties of MBG. Among them, mung bean protein amyloid fibrils (MBGF) formed from HCl exhibited the strongest fibrillation ability, with thioflavin T (ThT) fluorescence intensity 6 times higher than that induced by organic acids (lactic acid (LA), malic acid (MA), and citric acid (CA)). Transmission electron microscopy revealed that HCl-MBGF formed compact and uniform fibrils (similar to 5 nm in diameter), while organic acid-induced MBGF formed entangled fibrils with gel-like networks (similar to 20 nm in diameter). Functional analysis further showed that HCl-MBGF had the highest emulsifying activity index (EAI) of 17.25 +/- 0.13 m(2)/g, an increase of about 260 % compared to MBG (4.79 +/-

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0.23 m(2)/g), and enhanced rheological properties. In contrast, MBGF formed from organic acids exhibited weaker fibrillation abilities, but a rapid gelation process was promoted. MD simulations revealed that HCl disrupted the secondary structure of the protein, promoting the formation of beta-sheets, which were crucial for fibrillation. In contrast, organic acids (especially MA) facilitated protein unfolding and increased protein flexibility. This study highlights the impact of acidic conditions on MBG fibrillation and provides insights into its structural-functional design in food systems.

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文献类型: Article

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第 2 条

标题: Synthesis and characterization of a delivery system by combining cobalt (II) with soluble dietary fiber from Cyperus esculentus L. to regulate gut-derived neuroactive metabolite biosynthesis

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来源出版物: FOOD RESEARCH INTERNATIONAL **卷:** 211 **文献号:** 116356
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摘要: Cobalt (Co) deficiency significantly impacts vegetarians and individuals with malabsorption disorders. To enhance loading efficiency, safety, and bioavailability of Co, a novel organic delivery system, CESDF-Co (II), was constructed using soluble dietary fiber from Cyperus esculentus L. (CESDF) as an organic ligand, synthesized using a microwave-assisted solid-phase method. Comprehensive analyses were conducted to determine the structural characteristics of CESDF-Co (II) and evaluate its stability, targeted release efficiency, and potential to regulate the biosynthesis of gut-derived neuroactive metabolites. Results revealed the formation of a three-dimensional cross-linked network within the CESDF-Co (II) due to Co (II) coordination bridging, with a cobalt loading of 78.14 mg/g. This structure enhanced its thermal stability and surface hydrophobicity while retaining the intrinsic resistance of CESDF to gastrointestinal digestion, facilitating colon-targeted delivery of CESDF-Co (II). In vitro fermentation demonstrated that CESDF-Co (II) significantly increased neuroactive-related amino acid precursors (tryptophan, tyrosine, glutamic acid, and methionine by 2.04-, 2.92-, 2.33-, and 2.58-fold, respectively) and neurotransmitters (serotonin, gamma-aminobutyric acid, dopamine, and acetylcholine by 3.28-, 4.93-, 1.73-, and 1.54-fold, respectively). This enhancement positively correlated with increased production of total short-chain fatty acids (1.57-fold) and cobalt-dominated vitamin B12 synthesis (16.25-fold). These findings offer valuable insights for constructing secure colon-targeted, microbiota-triggered release delivery systems.

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第 3 条

标题: Dietary black soybean-whey blended protein prevents duodenal barrier damage via intestinal flora dysbiosis improvement, SCFA production and pyroptosis inhibition

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来源出版物: FOOD BIOSCIENCE **卷:** 68 **文献号:** 106738
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摘要: Background: The protective efficacy of black soybean-whey blended protein (B-WP) in preserving the integrity of the duodenal barrier has been established. Purpose: This study aimed to explore the effects of different doses of B-WP on duodenal intestinal contents, short-chain fatty acids (SCFAs) and pyroptosis. Method: A comprehensive investigation was conducted using 16 S rRNA sequencing, non-targeted metabolomics, Western blot, immunohistochemistry (IHC), and enzyme-linked immunosorbent assay (ELISA) to evaluate the impact of B-WP on intestinal microbiota composition, SCFAs levels and pyroptosis in the duodenum, aiming to elucidate its underlying mechanism of action. Result: The results showed that lipopolysaccharide (LPS) stimulated the proliferation of Proteobacteria and Streptococcus, while inhibiting Firmicutes, Ruminococcus, and Lactobacillus. Additionally, LPS induced pyroptosis and damaged the duodenal barrier. However, supplementation with low, medium, and high doses of B-WP enhanced the stability of the intestinal microbiota, with the medium dose yielding the most favorable outcome. Different doses of B-WP effectively suppressed pyroptosis, with the medium dose showing significant effects ($P < 0.01$). This was evidenced by a 40.00 % reduction in gasdermin-D (GSDMD) protein expression and decreases in mean optical density of 29.23 % for NOD-like receptor family pyrin domain-containing 3 (NLRP3) and 33.96 % for cysteinyl aspartate specific proteinase (caspase)-1, respectively. Moreover, IL-18 levels decreased by 33.77 %, while IL-33 levels increased by 42.62 %. Conclusion: These findings indicate that B-WP can mitigate duodenal barrier injury by modulating intestinal microbiota composition. Specifically, B-WP enhances the abundance of Firmicutes, Ruminococcus, and Lactobacillus, while reducing Proteobacteria and Streptococcus abundance. This modulation promotes the synthesis of SCFAs, thereby suppressing pyroptosis and contributing to the prevention of duodenal barrier damage.

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第 4 条

标题: Construction of a quercetin-kafirin nanodelivery system by ultrasound-treated: Synthesis and characterization

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摘要: Quercetin exhibits notable bioactivity, however, its poor solubility and stability result in rapid degradation and limited bioavailability. To solve this problem, kafirin was used to encapsulate quercetin, and an ultrasonicassisted anti-solvent precipitation method was employed to construct a nanoparticle delivery system. The results showed that kafirin-quercetin nanoparticles (KQN) subjected to ultrasonic treatment (600 W, 120 s) exhibited particle sizes ranging from 90.16 to 213.27 nm and achieved a maximum encapsulation efficiency of 81.36 % for quercetin. Spectral analysis and molecular docking identified van der Waals forces, hydrogen bonds, and other interactions between quercetin and kafirin, which enhanced nanoparticle stability. The nanoparticle system exhibited potent antioxidant and anti-inflammatory activities, as evidenced by DPPH, ABTS, FRAP, and inhibition of NO production. These findings establish a robust theoretical basis for enhancing the bioavailability of quercetin, fostering nanoparticle applications in the food industry, and expanding the potential uses of kafirin.

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研究方向: Food Science & Technology

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第 5 条

标题: Insight into the formation mechanism of umami taste in traditional Chinese soybean paste: A review

作者: Tong, JL (Tong, Jialu); Li, GL (Li, Guanlong); Liu, XL (Liu, Xiaolan); Zheng, XQ (Zheng, Xiqun)

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摘要: China boasts an extensive history of producing and consuming soybean paste. Soybean paste, as a typical fermented soybean product, is valued for its rich umami flavor and nutritional benefits. The distinctive taste of soybean paste is predominantly characterized by its umami taste. During soybean paste fermentation, the formation of umami compounds such as amino acids, nucleotides, organic acids and umami peptides is closely tied to microbial metabolism during fermentation. Therefore, it is crucial to elucidate the relationship between umami compounds and microbial diversity in soybean paste. At present, most of the research on the flavor of soybean paste focuses on volatile flavors, while there is relatively little research on its umami characteristics. There is still a lack of systematic reviews on the umami flavor of traditional Chinese soybean paste. This review synthesizes current research on umami compounds including amino acids, nucleotides, organic acids, and umami peptides, microbial diversity, and their interactions in soybean paste fermentation. It further explores detection methods and evaluation approaches of umami compounds, as well as the presentation mechanism of umami compounds. The objective is to provide insights into regulating umami compound formation during fermentation, supporting high-quality soybean paste production.

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第 6 条

标题: Comparative Analysis of Models for Identifying and Tracing Rice Flour Adulteration Using Raman Spectroscopy

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来源出版物: JOURNAL OF FOOD SCIENCE **卷:** 90 **期:** 5 **文献号:** e70272
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摘要: To address the issue of rice flour adulteration, where lower-cost rice flour is mixed with higher-grade varieties to reduce costs, this work proposes a rapid identification method using Raman spectroscopy. Rice varieties from Heilongjiang Province were selected for adulteration experiments, in which Longqingdao 8 (LQD) was mixed with Sanjiang 6, Longyang 16, Suijing 18, Longdao 18, and Daohuaxiang 2 in varying proportions. Six machine learning models were employed for classification, with four different preprocessing methods. The models' performance was evaluated using the receiver operating characteristic (ROC) curves, and key characteristic bands for each rice variety were identified. For Sanjiang 6, the optimal preprocessing method was standard normal transformation, and the best-performing model was the artificial neural network, which achieved an area under the curve (AUC) of 96.2% and an accuracy of 94.8%. For Daohuaxiang 2, smoothing forest and random forest yielded the best results, with an AUC of 92.4% and an accuracy of 94.8%. Similarly, for Longdao 18, standard normal transformation and artificial neural network provided the highest accuracy (99.6%) with an AUC of 99.3%. Longyang 16 also showed optimal results with standard normal transformation and artificial neural network, achieving an AUC of 93.7% and an accuracy of 96.6%. Finally, for Suijing 18, multivariate scattering correction and random forest were the most effective, with an AUC of 99.3% and an accuracy of 99.6%. This comparative analysis of traceability models demonstrates a promising approach to identifying rice flour adulteration. The identification of compounds influencing different rice varieties further enhances the traceability of rice types, providing a robust reference for future studies.

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研究方向: Food Science & Technology

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第 7 条

标题: Status of processing, nutritional and edible properties of rice after various degree of milling of brown rice

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摘要: This study examined the effect of bran degree (BD) ranging from to 0-10 % on the structural features, processing characteristics and edible quality of the Daohuaxiang paddy variety (Japonica variety). The results demonstrated that as BD decreased, the aleurone layer was destroyed, and the aleurone grains (AG) were flowed out and accumulated on the rice surface. With a decrease in BD, the defective kernels decreased from 33.15 % to 1.00 %, the yellow-colored kernels decreased from 4.50 % to 0.05 %, the fat, protein and fiber contents were reduced by 88.04 %, 15.54 % and 34.48 %, respectively. However, when BD was maintained at 5-10 %, the change in the whole kernels and broken kernels was not significant. When BD ranged from 0 to 7 %, the hardness and cohesiveness of cooked rice exhibited no significant difference, but elasticity and chewiness demonstrated different trends. The taste value of uncooked rice peaked at 4 % BD, whereas the decline in the taste value of cooked rice was more gradual between 2 and 6 % BD. These findings suggest that it is feasible to enhance the nutritional value and improve edible quality by controlling BD, which can provide theoretical support for the production of high value-added rice and reasonably well-milled rice.

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研究方向**:** Food Science & Technology

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第 **8** 条

标题**:** Integrated Volatile Compounds and Transcriptional Gene Analysis Elucidate the Deterioration Mechanism of Embryo Rice During Storage

作者**:** Yang, XY (Yang, Xiyuan); Su, TT (Su, Tingting); Ma, LX (Ma, Lixue); Mu, XD (Mu, Xindi); Wang, H (Wang, Hui); Xu, L (Xu, Lei); Wang, LD (Wang, Lidong); Wang, BJ (Wang, Baijun); Yao, D (Yao, Di); Wang, CY (Wang, Changyuan)

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摘要**:** Embryo rice, as a product of processing rice, improves palatability and retains the nutritional characteristics of brown rice. However, the storage period of embryo rice is only 30 d at room temperature. To delay the deterioration in the quality of embryo rice during storage, this study used polyethylene terephthalate/aluminum foil/polyethylene (PET/AL/PE) to vacuum-package embryo rice, and analyzed the quality changes under 25 or 4 degrees C storage conditions. At the same time, volatile compound analysis and transcriptomic analysis were integrated to explore the quality deterioration mechanism of embryo rice during storage. The electronic nose results showed that the odor of embryo rice changed significantly during different storage periods ($p < 0.05$). A total of 72 volatile compounds were identified by Headspace-Solid-Phase Micro-Extraction-Gas Chromatography-Mass Spectrometry (HS-SPME-GC-MS), with 2-pentylfuran, naphthalene, and styrene contributing the most in the early stage, and 2-hexenal, nonanal, trans-2-nonenal, and ethanol contributing more in the later stage. Correlation analysis showed that fatty acids, malondialdehyde (MDA), lipase, and ferric-reducing antioxidant power (FRAP) were positively correlated with aldehydes and acids ($p < 0.05$), while catalase (CAT) and 2,2-diphenyl-1-picrylhydrazyl (DPPH) were negatively correlated ($p < 0.05$). This was mainly because the oxidative decomposition of lipids and the weakening of antioxidant capacity would lead to the accumulation of aldehydes. In the Mantel test analysis, color had the strongest correlation with volatile compounds, followed by taste value, and finally texture. In transcriptomic analysis, lipid synthesis and metabolism were key pathways for the storage deterioration of embryo rice, and the LOX gene played an important regulatory role. These results can provide a theoretical basis for the evaluation of quality and selection of storage method of embryo rice.

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第 9 条

标题: Mung Bean Peptides Alleviate Dextran-Sulfate-Sodium-Induced Colitis Symptoms in Mice by Protecting the Intestinal Mechanical Barrier and Regulating Gut Microbiota

作者: Xu, C (Xu, Chong); Diao, JJ (Diao, Jingjing); Feng, YC (Feng, Yuchao); Zhang, S (Zhang, Shu); Sheng, YN (Sheng, Yanan); Wang, CY (Wang, Changyuan)

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摘要: Ulcerative colitis (UC), an idiopathic and recurrent ailment, substantially influences a patient's health. Mung bean peptides (MBPs) are bioactive substances derived from mung bean protein that possess notable anti-inflammatory properties. However, their efficacy and underlying mechanisms in UC treatment remain unclear. In this study, the structural characteristics of MBPs were examined by determining various parameters, such as amino acid composition, molecular weight distribution, and peptide sequences, thereby structurally demonstrating their anti-inflammatory potential. The therapeutic effectiveness of MBPs in UC treatment was evaluated by assessing its influence on colon length, histological damage to colonic tissue, and disease activity index of mice suffering from colitis induced by dextran sulfate sodium (DSS). Additionally, the study explored the potential mechanism of action of MBPs in

UC by analyzing the intestinal microbiota, inflammatory cytokines in serum, and tight junction (TJ) proteins in the colon tissue of mice. The results revealed that MBPs significantly increased colon length, reduced colonic tissue damage, and decreased the disease activity index in mice with UC. MBPs restored intestinal barrier function by upregulating the expression of ZO-1 and claudin-1 proteins within the colonic tissue of mice with DSS-induced colitis, thereby treating UC. MBPs exerted anti-inflammatory effects by downregulating the amplification of inflammatory cytokines in the serum, improving the gut microbiota structure in mice with colitis, and regulating immune-related signaling pathways. Therefore, there is an experimental basis for the potential use of MBPs as adjunctive therapy in UC.

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研究方向: Food Science & Technology

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Geology

第 1 条

标题: Ecological impact of rain splash erosion on saline-alkali grassland surfaces under photovoltaic panels

作者: Li, SY (Li, Siyu); Qu, SM (Qu, Shanmin); Zhang, DM (Zhang, Dongmei); Yang, WG (Yang, Weiguang); Liu, XP (Liu, Xiangping); Liu, JX (Liu, Jiaxin); Zhao, Y (Zhao, Yu); Jiang, W (Jiang, Wei)

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摘要: Photovoltaic panels (PVPs) in grasslands are arranged in such a way that they capture rainfall, which subsequently drips from the edges and causes splash erosion in the grassland, ultimately destroying the natural ecological environment. As such, PVPs can adversely affect fragile saline-alkali habitats, but the precise ecological impact of PVP-caused rainfall splash erosion on saline-alkali grassland has yet to be quantified. To explore the impact of splash erosion on the saline-alkali grassland under PVPs, an investigation was performed here on various surfaces commonly underneath PVPs. These surfaces were typical bare saline-alkali surface (B), Suaeda glauca surface (S) and Leymus chinensis surface (L), and all were positioned under PVPs in the Songnen Plain saline-alkali grassland. The soil splash erosion ditch morphology, the plant community status, and the field-measured soil properties of the three underlying surfaces were all analyzed as part of this investigation in accordance with the observed impact of splash erosion on the three underlying surface ecosystems. Ultimately, the splash erosion generated four ditches in the underlying surfaces, with the degree of soil loss ranked from greatest to smallest as B > S > L. According to the RDA results, vegetation coverage was the main factor affecting splash ditch morphology. The vegetation of the S. glauca surface was fragmented following splash erosion. Much of the S. glauca in the splash erosion ditch died, resulting in a 33.47 %-64.66 % reduction in coverage. In contrast, L. chinensis maintained a higher coverage, which means that it inhibited splash erosion more effectively. For the bare surface, the rainfall splash reduced pH and Ec, and S. glauca began to grow along the edge of the ditch. Collectively, our study quantified the impact of rain splash erosion under PVPs in a saline-alkali grassland ecosystem, comparing the difference in the degree of splash erosion among three different underlying surfaces.

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研究方向: Geology; Agriculture; Water Resources

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Immunology

第 1 条

标题: Human SLAM-adapted canine distemper virus can enter human peripheral blood mononuclear cells and replicate in mice expressing human SLAM and defective for STAT1 expression

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来源出版物: VIRULENCE **卷:** 16 **期:** 1 **文献号:** 2457967
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摘要: Canine distemper virus (CDV) is a member of the genus Morbillivirus with a worldwide distribution that causes fatal diseases in canids and marine mammals. In recent years, CDV has demonstrated the remarkable ability of pathogens to cross species barriers. The natural host range of CDV has expanded from Canidae to Primates, presumably attributed to ecological shifts and the emergence of viral variants. Therefore, it is important to investigate whether CDV can infect humans by adapting to the human signalling lymphocyte activation molecule (hSLAM) receptor to cross the species barrier. Through successive passaging and plaque cloning of a CDV wild-type strain (5804PeH) in Vero cells expressing hSLAM (Vero-hSLAM), we obtained an hSLAM adaptive strain, 5804PeH-VhS. The adapted CDV strain exhibited a D540G mutation within the receptor-binding domain (RBD) of the haemagglutinin (H) protein. The HD540G mutation has enhanced cell-cell fusion activity in Vero-hSLAM cells. This adaptation allowed the CDV strain to infect human peripheral blood mononuclear cells (PBMCs), particularly T lymphocytes and inhibited lymphocyte proliferation. Additionally, this strain could replicate in the lymphoid tissues of transgenic mice that express the hSLAM receptor, causing viraemia. However, the adapted strain did not spread to the epithelial cells or the central nervous system of the mice. While this adaptation indicates a potential risk, there is no definitive evidence that the virus can spread among humans.

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研究方向: Immunology; Infectious Diseases; Microbiology

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Mathematics

第 1 条

标题: Coevolutionary Algorithm with Bayes Theorem for Constrained Multiobjective Optimization

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来源出版物: MATHEMATICS **卷:** 13 **期:** 7 **文献号:** 1191
DOI: 10.3390/math13071191 **Published Date:** 2025 APR 4

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摘要: The effective resolution of constrained multi-objective optimization problems (CMOPs) requires a delicate balance between maximizing objectives and satisfying constraints. Previous studies have demonstrated that multi-swarm optimization models exhibit robust performance in CMOPs; however, their high computational resource demands can hinder convergence efficiency. This article proposes an environment selection model based on Bayes' theorem, leveraging the advantages of dual populations. The model constructs prior knowledge using objective function values and constraint violation values, and then, it integrates this information to enhance selection processes. By dynamically adjusting the selection of the auxiliary population based on prior knowledge, the algorithm significantly improves its adaptability to various CMOPs. Additionally, a population size adjustment strategy is introduced to mitigate the computational burden of dual populations. By utilizing past prior knowledge to estimate the probability of function value changes, offspring allocation is dynamically adjusted, optimizing resource utilization. This adaptive adjustment prevents unnecessary computational waste during evolution, thereby enhancing both convergence and diversity. To validate the effectiveness of the proposed algorithm, comparative experiments were performed against seven constrained multi-objective optimization algorithms (CMOEAs) across three benchmark test sets and 12 real-world problems. The results show that the proposed algorithm outperforms the others in both convergence and diversity.

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研究方向: Mathematics

输出日期: 2025-06-11

Metallurgy & Metallurgical Engineering

第 1 条

标题: Effect of Carburizing and Carbonitriding Temperatures on the Microstructure and Wear Resistance of 18Cr2Ni4WA Steel with Carburizing-Carbonitriding Heat Treatment

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来源出版物: STEEL RESEARCH INTERNATIONAL
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摘要: This study systematically investigates the effects of carburizing and carbonitriding temperatures on the microstructural evolution and wear resistance of 18Cr2Ni4WA steel. The surface layer after carburizing-carbonitriding treatment comprises acicular/lath martensite, residual austenite, and dispersed carbides, with microstructural gradients dependent on processing parameters. Elevated carburizing temperatures (930-970 degrees C with 850 degrees C carbonitriding) marginally reduce surface microhardness and harden layer depth, while increasing carbonitriding temperature to 880 degrees C (930 degrees C carburizing) significantly decreases hardness and accelerates softening at depth. Microstructural analysis reveals that higher carbonitriding temperature (880 degrees C) promotes grain coarsening, reduces carbide fraction, and increases residual austenite content, attributed to altered carbon/nitrogen diffusion kinetics and solute supersaturation. Wear resistance correlates strongly with carbide dispersion and grain refinement, and the 930 degrees C carburizing and 850 degrees C carbonitriding sample exhibiting the lowest wear rate, 61.5% lower than conventional carburized specimens, due to optimized nitrogen-containing martensite and dislocation pinning by fine carbides. These findings demonstrate that synergistic control of carburizing and carbonitriding temperatures enables tailored surface engineering, achieving enhanced wear resistance through nanoscale carbide distribution and stabilized martensitic matrices, offering critical insights for manufacturing high-performance gears and aerospace components.

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输出日期: 2025-06-11

Microbiology

第 1 条

标题: Differential impact of spotted fever group rickettsia and anaplasmosis on tick microbial ecology: evidence from multi-species comparative microbiome analysis

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来源出版物: FRONTIERS IN MICROBIOLOGY **卷:** 16 **文献号:** 1589263
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摘要: Tick-borne diseases (TBDs) pose a significant public health challenge, as their incidence is increasing due to the effects of climate change and ecological shifts. The interplay between tick-borne pathogens and the host microbiome is an emerging area of research that may elucidate the mechanisms underlying disease susceptibility and severity. To investigate the diversity of microbial communities in ticks infected with vertebrate pathogens, we analyzed the microbiomes of 142 tick specimens. The presence of Rickettsia and Anaplasma pathogens in individual samples was detected through PCR. Our study aimed to elucidate the composition and variation of microbial communities associated with three tick species, which are known vectors for various pathogens affecting both wildlife and humans. We employed high-throughput sequencing techniques to characterize the microbial diversity and conducted statistical analyses to assess the correlation between the presence of specific pathogens and the overall microbial community structure. Pathogen screening revealed an overall positivity rate of 51.9% for Anaplasma and 44.6% for spotted fever group rickettsia (SFGR). Among the three tick species (Dermacentor silvarum, Haemaphysalis concinna, and Haemaphysalis japonica) analyzed, D. silvarum (the predominant species) exhibited the highest pathogen prevalence. The results indicate significant variation in microbial diversity between tick samples, with the presence of Anaplasma and SFGR associated with distinct changes in the microbial community composition. These findings underscore the complex interactions between ticks and their microbial inhabitants, enriching our understanding of tick-borne diseases.

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研究方向: Microbiology

输出日期: 2025-06-11

第 **1** 条

标题: Prevalence and risk factors of Babesia species in domestic herbivores in China: A systematic review and meta-analysis

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来源出版物: ACTA TROPICA **卷: 265** **文献号:** 107614
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摘要: Babesia species are tick-transmitted hemoprotozoa that infect mammals, birds, and humans, posing a significant global threat to veterinary medicine threat. In this study, the authors systematically retrieved articles on the occurrence of Babesia species in domestic herbivores in China, including ovine, bovine, and equine species, through a search in the following six databases from their inception to 4 November 2024: PubMed, Web of Science, ScienceDirect, Chinese National Knowledge Infrastructure, Wanfang Data, and VIP Chinese Journal Database. A total of 94 studies (54 high-quality studies, 40 medium-quality studies) from 28 provinces were included. The pooled prevalence of Babesia infection was 11 % in ovines, 12 % in bovines, and 18 % in equines, with significant differences observed across subgroups, including, region, species, longitude, temperature, and season. Infection prevalence was higher in East and Central China, particularly in Hunan, Fujian, and Ningxia, as well as in regions characterized by lower altitude, higher temperature, and higher humidity. Longitude and season were significantly associated with Babesia infection in equines ($p < 0.05$), while temperature analysis indicated a significant difference ($p < 0.05$) in Babesia infection in bovines. In addition, infection rates were higher in female animals than in male animals; rates were also higher in 2013 or before in comparison to later sampling years. Moreover, the infection rates of different Babesia species varied significantly in bovines. These findings highlight key epidemiological patterns and potential risk factors, including regional and environmental influences associated with Babesia infection in domestic herbivores in China; thus, the findings of this study provide a solid foundation for developing targeted prevention and control strategies that can aim to mitigate the impact of babesiosis in domestic herbivores.

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Pharmacology & Pharmacy

第 1 条

标题: Design and evaluation of methionine based sulfonium lipid for nucleic acid delivery

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来源出版物: JOURNAL OF DRUG DELIVERY SCIENCE AND TECHNOLOGY **卷:** 108 **文献号:** 106956 **DOI:** 10.1016/j.jddst.2025.106956 **Published Date:** 2025 JUN

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摘要: Sulfonium is a potential structure with multiple bioactivities and has attracted extensive attention recently. It contains cationic charge that can interact with the phosphate anion of nucleic acid and can be used as vector for gene delivery. We developed a group of sulfonium lipids (SLs) based on methionine structure and tested their gene carrier abilities. The SLs were synthesized in three steps by linking oleoyl or lauryl group via ester or amide bond, and attaching short alkyl group on thioether to form sulfonium. The gene delivery capacity of these SLs were evaluated by testing the gene binding ability, cytotoxicity and measuring the particle size, zeta potential, cellular uptake and transfection ability of SL/eGFP nanoparticles on HepG2 cells. The results showed that all the SLs can fully encapsulate nucleic acids at S/P ratio of 4/1. The formed nanoparticles had sizes in range of 161 similar to 224 nm and the zeta potentials in range of +40 similar to 49 mV. SLs presented low toxicity on HepG2 cell when concentration was lower than 2.5 mu M. SL/eGFP nanoparticles were observed to have strong cellular uptake ability, some of the particles presented stronger gene transfection to cells than lipo2000. SLs are a kind of new cationic lipid for gene delivery as well as other biological studies.

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研究方向: Pharmacology & Pharmacy

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Plant Sciences

第 1 条

标题: Starch-sucrose metabolic homeostasis in germinating soybean reserve mobilization with different levels of salt stress

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摘要: Salt stress is one of the abiotic factors limiting crop growth. However, the mechanisms regulating starch-sucrose metabolism in the mobilization of soybean (Glycine max L.) reserves at different levels of salt stress during germination remain unknown. This study evaluated the effects of different levels of salt stress [0 mmol L-1 NaCl (CK), 75 mmol L-1 NaCl (S), and 150 mmol L-1 NaCl (SS)] on germinating seeds of three soybean varieties. Salt stress, especially the SS treatment, significantly reduced the radicle length, radicle fresh weight, and total fresh weight. Salt stress had different effects on the starch accumulation of cotyledons and radicles, while significantly increased the sucrose accumulation through several mechanisms. The regulatory mechanisms governing starch-sucrose metabolism in cotyledon and radicle during the germination stage exhibit distinct differences. In cotyledons, the decrease of starch content under S and SS treatment was due to the decrease of sucrose decomposition, which inhibited the metabolic cycle of starch. The up-regulated expression of GmSWEET6/15 under different levels of salt stress can promote the accumulation of sucrose in radicles. However, different salt stress levels have different response mechanisms to sucrose and starch metabolism in radicles. The activities of sucrose-metabolizing enzymes sucrose synthase (cleavage) and invertase in the radicle of S treatment were significantly reduced, while SS treatment could activate the sucrose metabolic cycle and increase the efficiency of starch-sucrose conversion. Compared with S treatment, the accumulation of starch content in SS treatment was due to the increase of SSS, alpha-amylase and beta-amylase activities and the up-regulation of GmAMY3 and GmBAM1 expression levels. Based on the results of this study, in order to promote soybean germination in saline soils, rationalized soybean seed compositions can be designed according to the degree of salinity in each region, which can provide a reference to the future breeding of salt-tolerant soybeans.

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文献类型: Article

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研究方向: Plant Sciences

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第 2 条

标题: QTL-based dissection of three key quality attributes in maize using double haploid populations

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摘要: Introduction Maize is a crucial source of nutrition, and the quality traits such as starch content, oil content, and lysine content are essential for meeting the demands of modern agricultural development. Understanding the genetic basis of these quality traits significantly contributes to improving maize yield and optimizing end-use quality.

While previous studies have explored the genetic basis of these traits, further investigation into the quantitative trait loci (QTL) responsible for variations in starch content, oil content, and lysine content still requires additional attention.Methods Double haploid (DH) populations were developed via a nested association mapping (NAM) design. Phenotypic data for starch, oil, and lysine content were collected using near-infrared spectroscopy and analyzed via ANOVA. Genotyping employed a 3K SNP panel, and genetic maps were constructed using QTL IciMapping. QTL analysis integrated single linkage mapping (SLM) and NAM approaches, with candidate genes identified via maizeGDB annotation and transcriptome data.Results The broad-sense heritability of the populations with a range of 63.98-80.72% indicated the majority of starch content, oil content and lysine content variations were largely controlled by genetic factors. The genetic maps were constructed and a total of 47 QTLs were identified. The phenotypic variation explained (PVE) of the three traits is in a range of 2.60-17.24% which suggested that the genetic component of starch content, oil content and lysine content was controlled by many small effect QTLs. Five genes encoding key enzymes in regulation of starch, oil and lysine synthesis and metabolism located within QTLs were proposed as candidate genes in this study.Discussion The information presented herein will establish a foundation for the investigation of candidate genes that regulate quality traits in maize kernels. These QTLs will prove beneficial for marker-assisted selection and gene pyramiding in breeding programs aimed at developing high-quality maize varieties.

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Academy of Agricultural Sciences

研究方向: Plant Sciences

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第 3 条

标题: Integrated metabolomics and transcriptomics unravel the biosynthZaesis mechanism of anthocyanin in postharvest red raspberry (<i>Rubus idaeus</i> L.)

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摘要: Introduction Anthocyanins are crucial secondary metabolites that are responsible for pigment deposition in fruits. Raspberry fruit color shifts from white to red during natural or postharvest ripening. However, the precise mechanisms and biosynthetic pathways of anthocyanins in postharvest raspberries remain unclear.Methods This study used metabolomic and transcriptomic analyses to explore anthocyanin biosynthesis in postharvest raspberries at various color stages: white (RBT-1), white-to-pink (RBT-2), pink (RBT-3), red (RBT-4), and deep red (RBT-5).Results We identified 43 key metabolites, and 13,239 DEGs linked to anthocyanin biosynthesis in postharvest raspberry colour development, including cyanidin-3-O-sophoroside and cyanidin-3-O-glucoside. The key DAMs in colored raspberries were gentiobioside, pelargonidin-3,5-O-diglucoside, cyanidin-3-O-sambubioside, and pelargonidin-3-O-sambubioside. Transcriptome analysis revealed 32 differentially expressed structural genes linked to anthocyanin and flavonoid synthesis, with significant upregulation of PAL, CHS, F3H, C4H, F3'H, DFR, ANS, CHI, and UFGT genes, which promote anthocyanin synthesis and pigment accumulation. Integrated analysis showed that cyanidin-3-O-sophoroside was correlated with 9 structural genes involved in anthocyanin biosynthesis, 19 transcription factors (TFs), and 14 hormone signaling-related genes.Discussion This study explored the regulatory mechanisms of MYB, WRKY, bHLH, and NAC transcription factors, as well as structural genes and phytohormone-related genes, in modulating anthocyanin metabolism during postharvest color changes in raspberries. The findings provide valuable insights for optimizing postharvest fruit storage conditions and enhancing fruit quality.

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文献类型: Article

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研究方向: Plant Sciences

输出日期: 2025-06-11

第 4 条

标题: Effects of rot-promoting bacteria on decomposition characteristics of corn straw and spring soybean yield in Saline-alkali Land

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摘要: Understanding the relationship between microbial inoculants and straw decomposition is crucial for achieving a high soybean yield in northern China's cold region. This study investigated the effects of different microbial inoculants on nutrient release characteristics and extracellular enzyme activities. A pot experiment was conducted over two growing seasons (2023 and 2024) using the soybean (Glycine max L. Merrill) cultivar Nongqing 28, the saline-alkali soil as the test soil, and corn straw as the test straw. The microbial inoculants tested were Bacillus sp. ND1 and Bacillus sp. ND2. The following treatments were employed: straw with no microbial agent application (CK), straw with Bacillus sp. ND1 application (T1), straw with Bacillus sp. ND2 application (T2), and straw with a 1:1 application of Bacillus sp. ND1 and Bacillus sp. ND2 compound bacteria (T3).The two-year results showed that the T1, T2, and T3 treatments significantly increased the rate of straw decomposition, reduced the lignocellulose content, and progressively released nitrogen, phosphorus, and potassium from the straw compared to the CK. During both years, the T3 treatment exhibited the highest straw decomposition rate and enzyme activity at R2(Full Bloom period), R4(Full Pod period), R6(Full Seed period) and R8(Full Maturity period) periods, which ultimately increased soybean yield by 24.00%-28.00% ($P<0.05$). These findings indicate that microbial inoculants have significant potential for application in straw management and provide an important basis for optimizing straw return and crop yield. In summary, T3 treatment can accelerate straw decomposition and nutrient release rates, increase soybean yield, and provide a theoretical basis for optimizing the straw decomposition effect and rational utilization of organic resources by promoting the activity of extracellular enzymes and the degradation of straw cellulose, hemicellulose, and lignin.

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研究方向: Plant Sciences

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第 5 条

标题: Proline-Nitrogen Metabolic Coordination Mediates Cold Priming-Induced Freezing Tolerance in Maize

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摘要: Cold stress critically restricts maize seedling growth in Northeast China, yet the mechanism by which cold priming (CP) enhances cold tolerance through proline-nitrogen metabolic networks remains unclear. This study systematically investigated CP's synergistic regulation in cold-tolerant (Heyu27) and cold-sensitive (Dunyu213) maize using a two-phase temperature regime (priming induction/stress response) with physiological and multivariate analyses. CP alleviated cold-induced photosynthetic inhibition while maintaining a higher chlorophyll and **photosynthetic** rate, though biomass responses showed varietal specificity, with Heyu27 minimizing growth loss through optimized carbon-nitrogen allocation. Antioxidant enzymes such as superoxide dismutase (SOD), peroxidase (POD), and catalase (CAT) were pre-activated during early stress, effectively scavenging reactive oxygen species (ROS) and reducing malondialdehyde (MDA) accumulation, with Heyu27 showing superior redox homeostasis. CP enhanced proline accumulation via bidirectional enzyme regulation (upregulating triangle 1-pyrroline-5-carboxylate

synthase/reductase [P5CS/P5CR], inhibiting proline dehydrogenase [ProDH]) and reprogrammed nitrogen metabolism through glutamate dehydrogenase/isocitrate dehydrogenase (GDH/ICDH)-mediated ammonium conversion to glutamate, alleviating nitrogen dysregulation while supplying proline precursors. Principal component analysis revealed divergent strategies: Heyu27 prioritized proline-antioxidant synergy, whereas Dunyu213 emphasized photosynthetic adjustments. These findings demonstrate that CP establishes "metabolic memory" through optimized proline-nitrogen coordination, synergistically enhancing osmoregulation, reactive oxygen species (ROS) scavenging, and nitrogen utilization. This study elucidates C4-specific cold adaptation mechanisms, advancing cold-resistant breeding and stress-resilient agronomy.

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研究方向: Plant Sciences

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第 6 条

标题: Melatonin Mitigates Cd-Induced Growth Repression and RNA m⁶A Hypermethylation by Triggering MMR-Mediated DNA Damage Response

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摘要: Melatonin (MT) has been found to mitigate cadmium (Cd) toxicity with negligible environmental risks. It remains poorly understood as to how MT mitigates Cd-induced growth repression and regulates RNA m(6)A methylation. We aimed to elucidate the effect of MT on growth repression and RNA m(6)A methylation in Arabidopsis (Arabidopsis thaliana) exposed to Cd stress. MT mitigated, on average, 13.96% and 8.42% of growth repression resulting from Cd and mismatch repair (MMR) deficiency. The ameliorative effect on Cd stress was reduced by 70.56% and 34.23% in msh2 and msh6 mutants, respectively. With distinct dose-effect relationships, m(6)A hypermethylation responded to Cd stress rather than Cu stress, which was further elevated in MMR-deficient seedlings. MT reduced m(6)A levels by 22.98% even without stress induction, whereas the depressed m(6)A levels in MMR-deficient seedlings, greatly exceeding those in the WT. The "writer" and "eraser" gene expression responsible for m(6)A methylation was reduced with the concentration of stresses due to MT, but VIR and ALKBH9B no longer responded to Cd stress in msh2 and msh6. Despite the remarkable repression, MMR gene expression was regularly promoted by MT under Cd and Cu stress. Our study provides novel insights into the molecular mechanisms underlying the restorative effects of MT on growth repression and m(6)A methylation regulation, which shed light on Cd phytoremediation.

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研究方向: Plant Sciences

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第 7 条

标题: 2,4-Epibrassinolide Alleviates cd Toxicity in Vigna angularis by Boosting Antioxidant Defense, Detoxification, and Genome Stability

作者: Tang, ZH (Tang, Zihan); Wang, HT (Wang, Hetong); Chen, SY (Chen, Suyu); Wang, XP (Wang, Xianpeng); Hou, JL (Hou, Jialin); Zhang, YX (Zhang, Yuxian); Zhao, Q (Zhao, Qiang)

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摘要: Cadmium is one of the most toxic heavy metal pollutants in the world, seriously affecting crop growth and human health. 2,4-Epibrassinolide (BRs) has been proven to promote plant growth, enhance abiotic stress resistance and improve crop quality and yield. In this study, adzuki bean (V. angularis) cultivar 'Zhen Zhuhong' was grown hydroponically in 1/2 Hoagland nutrient solution with 0, 1, and 2 mg L-1 cadmium chloride (CdCl2), and then treated with 0 or 1 mu M BR at the V1 stage. Compared with Cd stress, ascorbic acid content, peroxidase (POD, EC 1.11.1.7), catalase (CAT, EC 1.11.1.6) and superoxide dismutase (SOD, EC1.15.1.1) activities in adzuki Cd-stressed bean roots under BR treatment were increased by 30.63%, 41.83%, 51.49%, and 29.48%, which alleviated intracellular ROS accumulation and DNA oxidative damage. In addition, proline content and free amino acid content in BR-treated adzuki bean seedling roots under Cd stress increased by 30.37% and 35.96%, which was conducive to maintaining cell membrane homeostasis and improving root activity. RNA-seq and real-time quantitative reverse transcription PCR analyses revealed that BR treatment regulates the absorption, transport, and accumulation processes of Cd2+ in adzuki bean seedling roots, reducing the nonspecific accumulation of Cd2+ within cells and alleviating the toxic effects of Cd on root cells. BR treatment enhances the DNA damage repair in the roots of adzuki beans under Cd stress by reducing the extent of DNA oxidative damage, and effectively promoting the transition of cells from the G1 phase to the S phase.

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研究方向: Plant Sciences

输出日期: 2025-06-11

第 8 条

标题: Functional analysis of the strawberry FaPR1 gene in response to Colletotrichum gloeosporioides infection

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摘要: Currently, the PR1 gene in strawberry has not been reported yet. Therefore, in this study, the FaPR1 gene sequence was obtained and cloned based on the transcriptome data of strawberry in response to anthracnose infection. The characteristics of FaPR1-related sequences were analyzed using bioinformatics methods. Moreover, the potential interacting proteins of FaPR1 were predicted using the interaction pairs included in the STRING database, and the interaction between them was verified by the yeast two-hybrid method. In addition, the phenotypic and physiological changes of strawberry materials with overexpressed FaPR1 gene after infection by Colletotrichum gloeosporioides (Penz.) Sacc. were analyzed to provide reference genes and a theoretical basis for molecular breeding for anthracnose resistance. The main results were as follows: (1) The FaPR1 gene encodes a protein containing 162 amino acid residues with an isoelectric point of 5.52; (2) The FaPR1 protein is closely related to Rosa chinensis Jacq. PR1 (RcPR1) protein and Rosa hugonis Hemsl. PR1 (RhPR1) protein; (3) There is an interaction between FaPR1 and the strawberry thaumatin-like protein 1 (FaTLP1); (4) The FaPR1 gene plays an important role in strawberry resistance to anthracnose, and overexpression of the FaPR1 gene can enhance strawberry resistance to this disease.

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文献类型: Article; Early Access

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研究方向: Plant Sciences

输出日期: 2025-06-11

第 9 条

标题: Selection of Optimal Diagnostic Positions for Early Nutrient Deficiency in Cucumber Leaves Based on Spatial Distribution of Raman Spectra

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摘要: Accurate diagnosis of crop nutritional status is critical for optimizing yield and quality in modern agriculture. This study enhances the accuracy of Raman spectroscopy-based nutrient diagnosis, improving its application in precision agriculture. We propose a method to identify optimal diagnostic positions on cucumber leaves for early detection of nitrogen (N), phosphorus (P), and potassium (K) deficiencies, thereby providing a robust scientific basis for high-throughput phenotyping using Raman spectroscopy (RS). Using a dot-matrix approach, we collected RS data across different leaf positions and explored the selection of diagnostic positions through spectral cosine similarity analysis. These results provide critical insights for developing rapid, non-destructive methods for nutrient stress monitoring in crops. Results show that spectral similarity across positions exhibits higher instability during the early developmental stages of leaves or under short-term (24 h) nutrient stress, with significant differences in the stability of spectral data among treatment groups. However, visual analysis of the spatial distribution of positions with lower similarity values reveals consistent spectral similarity distribution patterns across different treatment groups, with the lower similarity values predominantly observed at the leaf margins, near the main veins, and at the leaf base. Excluding low-similarity data significantly improved model performance for early (24 h) nutrient deficiency diagnosis, resulting in higher precision, recall, and F1 scores. Based on these results, the efficacy of the proposed method for selecting diagnostic positions has been validated. It is recommended to avoid collecting RS data from

areas near the leaf margins, main veins, and the leaf base when diagnosing early nutrient deficiencies in plants to enhance diagnostic accuracy.

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研究方向: Plant Sciences

输出日期: 2025-06-11

第 10 条

标题: Real-time detection of Chinese cabbage seedlings in the field based on YOLO11-CGB

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摘要: Introduction Accurate application of pesticides at the seedling stage is the key to effective control of Chinese cabbage pests and diseases, which necessitates rapid and accurate detection of the seedlings. However, the similarity between the characteristics of Chinese cabbage seedlings and some weeds is a great challenge for accurate detection.Methods This study introduces an enhanced detection method for Chinese cabbage seedlings, employing a modified version of YOLO11n, termed YOLO11-CGB. The YOLO11n framework has been augmented by integrating a Convolutional Attention Module (CBAM) into its backbone network. This module focuses on the distinctive features of Chinese cabbage seedlings. Additionally, a simplified Bidirectional Feature Pyramid Network (BiFPN) is incorporated into the neck network to bolster feature fusion efficiency. This synergy between CBAM and BiFPN markedly elevates the model's accuracy in identifying Chinese cabbage seedlings, particularly for distant subjects in wide-angle imagery. To mitigate the increased computational load from these enhancements, the network's convolution module has been replaced with a more efficient GhostConv. This change, in conjunction with the simplified neck network, effectively reduces the model's size and computational requirements. The model's outputs are visualized using a heat map, and an Average Temperature Weight (ATW) metric is introduced to quantify the heat map's effectiveness.Results and discussion Comparative analysis reveals that YOLO11-CGB outperforms established object detection models like Faster R-CNN, YOLOv4, YOLOv5, YOLOv8 and the original YOLO11 in detecting Chinese cabbage seedlings across varied heights, angles, and complex settings. The model achieves precision, recall, and mean Average Precision of 94.7%, 93.0%, and 97.0%, respectively, significantly reducing false negatives and false positives. With a file size of 3.2 MB, 4.1 GFLOPs, and a frame rate of 143 FPS, YOLO11-CGB model is designed to meet the operational demands of edge devices, offering a robust solution for precision spraying technology in agriculture.

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文献类型: Article

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第 11 条

标题: Effects of phospholipase C inhibition on the regulation of membrane lipid metabolism in maize leaves

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摘要: Introduction Phospholipase C (PLC) is an enzyme that catalyzes the hydrolysis of glycerophospholipids and can be classified as phospholipase-specific PLC (PI-PLC) and non-specific PLC (NPC) depending on its specific substrate.Methods In this study, neomycin sulfate (NS, 100 mM) was used to inhibit the activity of phospholipase C in maize seedlings, and the effect of phospholipase C on lipid metabolism was investigated by combined analysis of transcriptome and lipidome.Results Lipidomic analysis showed that when PLC was inhibited, the content of phospholipids showed more than 10% increase due to the elevated accumulation of PC and PE. At the same time, transcriptomic data suggested an activation of the de novo biosynthesis of PC and PE from choline and ethanolamine via upregulated CCT and PECT, respectively. Thus, the inhibition of phospholipid hydrolysis and the enhancement of de novo synthesis together contribute to the increase in the total phospholipids. Glycolipids account for around 60% of the total lipids in leaves. Under NS treatment, MGDG decreased significantly, while DGDG increased.Discussion Our results indicate that NS treatment may cause damage to photosynthetic membrane lipids, whereas the increase in bilayer lipid DGDG may provide a kind of protection to maintain the stability of chloroplasts. These findings suggest that phospholipase C plays a key role in plasma membrane metabolism.

入藏号: WOS:001466530500001

文献类型: Article

地址: [Wei, Yulei; Cai, Zhicheng; Che, Zhiyuan; Guo, Xu; Ge, Shengnan; Che, Xinyang; Deng, Jie; Zhang, Haiyang; He, Lin; Xu, Jingyu] Heilongjiang Bayi Agr Univ, Coll Agr, Key Lab Modern Agr Cultivat & Crop Germplasm Impro, Daqing, Peoples R China.

通讯作者地址: He, L; Xu, JY (通讯作者)，Heilongjiang Bayi Agr Univ, Coll Agr, Key Lab Modern Agr Cultivat & Crop Germplasm Impro, Daqing, Peoples R China.

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Affiliations: Heilongjiang Bayi Agricultural University

研究方向: Plant Sciences

输出日期: 2025-06-11

Science & Technology - Other Topics

第 1 条

标题: Temporal and spatial dynamics of carbon emissions in animal husbandry and their influencing factors: A case study of three provinces in Northeast China

作者: Wei, CB (Wei, Chunbo); Li, JQ (Li, Jiaqi); Xu, W (Xu, Wei); Sha, YY (Sha, Yanyu); Qu, YL (Qu, Yongli)

来源出版物: JOURNAL OF CLEANER PRODUCTION **卷:** 508 **文献号:** 145418

DOI: 10.1016/j.jclepro.2025.145418 **Published Date:** 2025 MAY 25

Web of Science 核心合集中的 "被引频次": 0

被引频次合计: 0

摘要: There is a significant correlation between the development of animal husbandry and the spatial clustering distribution of carbon emissions. Employing the IPCC methodology, we accurately estimated carbon emissions from animal husbandry across 36 prefecture-level cities in the three northeastern provinces of China. We further integrated a spatial correlation model with the Tapio decoupling model to explore the relationship between the spatial clustering of animal husbandry development and carbon emissions, utilizing the Log-Mean Divisia Index (LMDI) decomposition model for analyzing the decoupling relationship. Our findings indicate that from 2004 to 2021, carbon emissions from animal husbandry in these provinces exhibited a fluctuating trend, decreasing from 48.241 million tonnes of CO2-eq in 2004 to 41.574 million tonnes of CO2-eq in 2021, a reduction of 13.82 %. Additionally, during the study period, the average annual GDP output in low-cluster areas declined by 0.34 %, while average annual CO2 emissions increased by 8.11 % compared to high-cluster areas. The enhancement of production efficiency emerges as a potent means to mitigate the conflict between economic development and carbon emissions and to curb the rise in emissions. In conclusion, this study elucidates the similarity in spatial aggregation and decoupling of animal husbandry development on a regional scale, providing crucial insights for government strategies aimed at relocating animal husbandry to optimally suited areas and refining the industrial structure.

入藏号: WOS:001482279000001

文献类型: Article

地址: [Wei, Chunbo; Li, Jiaqi; Xu, Wei; Sha, Yanyu; Qu, Yongli] Heilongjiang Bayi Agr Univ, Coll Anim Sci & Vet Med, Dept Anim Sci, Daqing 163316, Peoples R China.
[Wei, Chunbo; Li, Jiaqi; Xu, Wei; Sha, Yanyu; Qu, Yongli] Minist Agr & Rural Affairs, Key Lab Low Carbon Green Agr Northeastern China, Beijing 100125, Peoples R China.

通讯作者地址: Wei, CB (通讯作者)，Heilongjiang Bayi Agr Univ, Coll Anim Sci & Vet Med, Dept Anim Sci, Daqing 163316, Peoples R China.
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研究方向: Science & Technology - Other Topics; Engineering; Environmental Sciences & Ecology

输出日期: 2025-06-11

第 2 条

标题: Punicalagin relieves hepatic injury by antioxidation and enhancement of autophagy in diet-induced nonalcoholic steatohepatitis

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作者: Ma, L (Ma, Li); Sun, HB (Sun, Hanbing); Xiang, N (Xiang, Nian); Xu, QS (Xu, Qiushi)

来源出版物: SCIENTIFIC REPORTS **卷:** 15 **期:** 1 **文献号:** 14516 **DOI:** 10.1038/s41598-025-98044-6 **Published Date:** 2025 APR 25

Web of Science 核心合集中的 "被引频次": 0

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摘要: Hepatic injury induced by many factors play a central role in the pathogenesis of liver diseases. Punicalagin (PUN) is a major antioxidant polyphenolic compound extracted from pomegranates. The aim of this study was to investigate the potential role of PUN on liver injury induced by nonalcoholic steatohepatitis (NASH). Therefore, the effects and mechanistic action of PUN on NASH mouse model induced by choline-deficient, L-amino acid- defined, high-fat (CDAAH) diet were investigated in vivo. Wild-type or nuclear erythroid 2-related factor 2 (Nrf2) KO mice were fed with CDAAH diet to induce NASH and then treated with PUN (100, 300 or 500 mg kg- 1 day- 1) by gavage for 12 weeks. Blood and liver samples were collected to assess liver function, oxidative stress, inflammation, and autophagy pathological status. The results showed that 300 mg/kg PUN was the optimal concentration for relieving hepatic injury in NASH, characterized by decreased activities of serum alanine transaminase, aspartate aminotransferase, and liver lactate dehydrogenase activity and histopathological structural damage, and showed a hepatoprotective effect against NASH. PUN significantly reduced the level of liver inflammation and Txnip-NLRP3 signaling pathway in NASH mice. PUN reduced oxidative stress by reducing liver malondialdehyde levels and the accumulation of reactive oxygen species (ROS) and increasing liver superoxide dismutase and glutathione peroxidase activity. PUN may also attenuate oxidative stress and induce autophagy through the p62/Nrf2 and AMPK/mTOR/ULK1 pathway. More importantly, we found that these protective effects of PUN were attributed to enhanced antioxidant, anti-inflammatory and autophagy activity, which was mediated by the activation of the Nrf2 pathway using Nrf2 KO mice. In summary, the present results indicate that PUN successfully relieved NASH-induced liver damage by upregulating Nrf2 signaling and autophagy.

入藏号: WOS:001476772500048

文献类型: Article

地址: [Ma, Li; Sun, Hanbing; Xiang, Nian; Xu, Qiushi] Heilongjiang Bayi Agr Univ, Coll Anim Sci & Vet Med, Xinfeng Rd 5, Daqing 163319, Peoples R China.

通讯作者地址: Xu, QS (通讯作者)，Heilongjiang Bayi Agr Univ, Coll Anim Sci & Vet Med, Xinfeng Rd 5, Daqing 163319, Peoples R China.

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研究方向: Science & Technology - Other Topics

输出日期: 2025-06-11

第 3 条

标题: Research progress of nano drug delivery systems in the anti-tumor treatment of traditional Chinese medicine monomers

作者: Song, BC (Song, Bocui); Shuang, L (Shuang, Li); Zhang, S (Zhang, Shuang); Tong, CY (Tong, Chunyu); Chen, Q (Chen, Qian); Li, YQ (Li, Yuqi); Hao, MH (Hao, Meihan); Niu, WQ (Niu, Wenqi); Jin, CH (Jin, Cheng-Hao)

来源出版物: PEERJ **卷:** 13 **文献号:** e19332 **DOI:** 10.7717/peerj.19332
Published Date: 2025 APR 24

Web of Science 核心合集中的 "被引频次": 0

被引频次合计: 0

摘要: Tumors pose a serious threat to global public health and are usually treated from two aspects: tumor cells and tumor microenvironment. Compared with traditional chemotherapy drugs, traditional Chinese medicine (TCM) monomers have advantages in tumor treatment, such as multiple targets, multiple levels and synergistic intervention. However, most TCM active ingredients have disadvantages such as poor water solubility and stability, which restrict their clinical application. Nano drug delivery systems have the functions of improving the bioavailability of TCM anti-tumor active ingredients, enhancing tissue targeting, achieving controlled drug release, and inhibiting tumor multidrug resistance. Compared with free monomers, they have higher therapeutic effects and fewer side effects. This article summarizes five commonly used anti-tumor TCM monomer nanocarriers, including lipid nanomaterials, exosomes, polymer micelles, carbon nanotubes, and dendrimers, and explains their anti-tumor mechanisms after combining with TCM, such as inhibiting tumor cell proliferation and metastasis, regulating tumor microenvironment, etc. At the same time, the potential of nano drug delivery systems combined with radiotherapy and immunotherapy is discussed, as well as the current problems of potential toxicity, long-term stability, and complex amplification process, as well as future development directions, aiming to provide a reference for promoting the clinical application of nano drug delivery systems for TCM anti-tumor active ingredients.

入藏号: WOS:001478571800001

文献类型: Article

地址: [Song, Bocui; Shuang, Li; Tong, Chunyu; Chen, Qian; Li, Yuqi; Hao, Meihan; Niu, Wenqi; Jin, Cheng-Hao] Heilongjiang Bayi Agr Univ, Coll Life Sci & Technol, Daqing, Heilongjiang, Peoples R China.
[Zhang, Shuang] Comprehens Serv Ctr, Yongji Econ Dev Zone, Jilin, Jilin, Peoples R China.
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通讯作者地址: Song, BC; Jin, CH (通讯作者)，Heilongjiang Bayi Agr Univ, Coll Life Sci & Technol, Daqing, Heilongjiang, Peoples R China.
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Affiliations: Heilongjiang Bayi Agricultural University

研究方向: Science & Technology - Other Topics

输出日期: 2025-06-11

第 4 条

标题: The NADC30-like PRRSV activates the integrin V subunit to facilitate its entry into Marc-145 cells

作者: Li, CL (Li, Chunlin); Cui, J (Cui, Jin); Zheng, H (Zheng, Hui); Sha, Z (Sha, Zhou); Wei, R (Wei, Rong); Wu, R (Wu, Rui); Ni, B (Ni, Bo)

来源出版物: PLOS ONE **卷:** 20 **期:** 3 **文献号:** e0316239
DOI: 10.1371/journal.pone.0316239 **Published Date:** 2025 MAR 27

Web of Science 核心合集中的 "被引频次": 0

被引频次合计: 0

摘要: Porcine reproductive and respiratory syndrome virus (PRRSV) is a highly contagious virus that poses a significant threat to the global pig farming industry, resulting in substantial economic losses. However, owing to the high variability of PRRSV and unclear mechanisms of infection, there are currently no effective vaccines or drugs available for its prevention and control. Our previous report revealed that highly pathogenic PRRSV (HP-PRRSV) requires the FAK-PI3K-AKT signaling pathway to facilitate its entry into cells. In this study, we further investigated whether the integrin subunit was involved in the entry process of NADC30-like PRRSV. First, the integrin subunits in Marc-145 cells were characterized by RT-PCR, and 11 of these subunits were identified, nearly all of which interacted with the integrin alpha V and beta 1 subunits to form heterodimers. Western blot analysis revealed that the integrin alpha V subunit was highly expressed in Marc-145 cells, and blocking this subunit with a functional antibody or siRNA significantly attenuated NADC30-like PRRSV entry without affecting virus binding. Moreover, in Marc-145 cells, NADC30-like PRRSV could activate the FAK-PI3K-AKT signaling pathway through the integrin alpha V subunit. Blocking the alpha V subunit significantly inhibited signal transduction and virus entry, and treatment of cells with the PI3K activator greatly reversed this inhibitory effect. Furthermore, the alpha V subunit activator manganese could also enhance NADC30-like PRRSV entry and signal transduction. In conclusion, our results revealed that NADC30-like PRRSV could activate the integrin alpha V subunit and subsequently transduce signals to the FAK-PI3K-AKT signaling pathway to facilitate entry into Marc-145 cells.

入藏号: WOS:001456748400038

文献类型: Article

地址: [Li, Chunlin; Cui, Jin; Zheng, Hui; Sha, Zhou; Wei, Rong; Ni, Bo] China Anim Hlth & Epidemiol Ctr, Qingdao, Peoples R China.
[Li, Chunlin; Wu, Rui] Heilongjiang Bayi Agr Univ, Daqing, Peoples R China.
[Cui, Jin; Sha, Zhou; Ni, Bo] Minist Agr & Rural Affairs, Key Lab Anim Biosafety Risk Prevent & Control Sout, Qingdao, Peoples R China.
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Affiliations: China Animal Health & Epidemiology Center; Heilongjiang Bayi Agricultural University; Ministry of Agriculture & Rural Affairs; Jiamusi University

研究方向: Science & Technology - Other Topics

输出日期: 2025-06-11

第 **5** 条

标题: Integrating genomics and transcriptomics reveals candidate genes affecting loin muscle area in Huaxi cattle

作者: Xue, QQ (Xue, Qingqing); Du, LL (Du, Lili); Deng, TY (Deng, Tianyu); Liang, M (Liang, Mang); Li, KN (Li, Keanning); Qian, L (Qian, Li); Qiu, SY (Qiu, Shiyuan); Chen, Y (Chen, Yan); Gao, X (Gao, Xue); Xu, LY (Xu, Lingyang); Wang, ZZ (Wang, Zezhao); Zheng, CH (Zheng, Caihong); Zhang, LP (Zhang, Lupei); Li, JY (Li, Junya); Gao, HJ (Gao, Huijiang)

来源出版物: PLOS ONE **卷:** 20 **期:** 5 **文献号:** e0322026
DOI: 10.1371/journal.pone.0322026 **Published Date:** 2025

Web of Science 核心合集中的 "被引频次": 0

被引频次合计: 0

摘要: Loin muscle area (LMA) is an indicator of carcass composition and is related to weight gain, animal musculature and meat quality traits. Therefore, integrating multi-omics data to reveal candidate genes affecting LMA has attracted extensive attention. We used the combined analysis method of GWAS and RNA-seq to find the candidate genes that affect the size of LMA. The association of 770K SNPs with the LMA captured four significant SNPs within or near three genes. Additionally, seven overlapping genes regarding LMA were determined via the analysis of differentially expressed genes (DEGs) and weighted gene co-expression network analysis (WGCNA). There is an overlapping gene (CD93) between the results of GWAS and DEGs. Through functional enrichment analysis of the above genes, candidate genes were identified as THBD, CD93, RIMS2, PLP1, SNCA, and NDUFS8, and it was found that they mainly affected the size of LMA by affecting muscle fiber diameter, muscle cell development, differentiation, and function. The findings provide valuable molecular insights into the mechanisms that influence LMA content in beef cattle.

入藏号: WOS:001488720800047

文献类型: Article

地址: [Xue, Qingqing] Heilongjiang Bayi Agr Univ, Dept Coll Anim Sci & Vet Med, Daqing, Heilongjiang, Peoples R China.
[Xue, Qingqing; Du, Lili; Deng, Tianyu; Liang, Mang; Li, Keanning; Qian, Li; Qiu, Shiyuan; Chen, Yan; Gao, Xue; Xu, Lingyang; Wang, Zezhao; Zheng, Caihong; Zhang, Lupei; Li, Junya; Gao, Huijiang] Chinese Acad Agr Sci, Dept Inst Anim Sci, Beijing, Peoples R China.

通讯作者地址: Gao, HJ (通讯作者)，Chinese Acad Agr Sci, Dept Inst Anim Sci, Beijing, Peoples R China.

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研究方向: Science & Technology - Other Topics

输出日期: 2025-06-11

Spectroscopy

第 1 条

标题: CWBLS network and its application in portable spectral measurement

作者: Sui, YT (Sui, Yutong); Zhao, XY (Zhao, Xiaoyu); Liu, C (Liu, Cheng); Zhao, Y (Zhao, Yue); Cai, LJ (Cai, Lijing); Tong, YC (Tong, Yuchen)

来源出版物: SPECTROCHIMICA ACTA PART A-MOLECULAR AND BIOMOLECULAR SPECTROSCOPY **卷:** 340 **文献号:** 126329
DOI: 10.1016/j.saa.2025.126329 **Published Date:** 2025 NOV 5

Web of Science 核心合集中的 "被引频次": 0

被引频次合计: 0

摘要: The research presents a novel approach called the D-CWBLS network to address the challenges of poor accuracy and stability in regression models caused by low-signal-to-noise-ratio and low reproducibility data in portable near-infrared spectroscopy. The D-CWBLS network improves upon the BLS network in three key aspects. Firstly, it expands the network structure by incorporating Near-Infrared characteristic spectral band data, thereby emphasizing important information and enhancing accuracy. Secondly, it deepens the network by adding a Dropout layer vertically, optimizing the structure, eliminating redundant information, and improving robustness. Lastly, it combines optimized feature node weight matrices and enhanced node weight matrices to eliminate uncertainty resulting from randomness during network training, subsequently improving robustness. In tests examining model reproducibility, accuracy, and robustness, the D-CWBLS model demonstrated superior performance compared to traditional machine learning models (PLSR, BP-ANN, and ELM), as well as deep learning models (MLP, CNN, and RNN), and even basic BLS and CWBLS models. This highlights the significant progress made by the D-CWBLS model in addressing the challenges associated with using portable near-infrared spectroscopy devices in outdoor settings, exhibiting higher reliability and applicability.

入藏号: WOS:001490595900002

文献类型: Article

地址: [Sui, Yutong; Zhao, Xiaoyu; Zhao, Yue; Cai, Lijing] Heilongjiang Bayi Agr Univ, Coll Informat & Elect Engn, Daqing 163319, Heilongjiang, Peoples R China.
[Liu, Cheng] Heilongjiang Beifeng Agr Prod Means Ltd Co Grp, Harbin 150028, Heilongjiang, Peoples R China.
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通讯作者地址: Zhao, XY (通讯作者)，Heilongjiang Bayi Agr Univ, Coll Informat & Elect Engn, Daqing 163319, Heilongjiang, Peoples R China.

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研究方向: Spectroscopy

输出日期: 2025-06-11

3 EI 收录情况

（2025.04.17-2025.06.11）

3.1 EI Compendex

EI 索引库共收录我校教师发表的 41 篇文献，文献详细题录信息如下。

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1. Global comprehensive evaluation shows that green manure enhances crop productivity while mitigating gaseous nitrogen losses

Huang, Hua (College of Agriculture, Shanxi Agricultural University, Shanxi, Taigu; 030801, China); Zhang, Zihui; Wu, Qi; Liu, Zeyu; Wang, Qinghe; Ying, Yuhang; Zhang, Zechao; Zhang, Huijuan; Wang, Yifan; Zhang, Guangxin; Bangura, Kemoh; Liu, Enke; Xue, Jianfu; Gao, Zhiqiang; Cai, Tie; Zhang, Peng; Wu, Peng

Source: Resources, Conservation and Recycling, v 220, June 30, 2025

Database: Compendex

Data Provider: Engineering Village

Compilation and indexing terms, Copyright 2025 Elsevier Inc.

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2. Rapid grading prediction of mould in rice grains based on factorisation and partial least squares algorithm

Zuo, Feng (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Hao, Zhenyu; Zhang, Caidong; Dong, Zhihao; Qian, Lili; Zhang, Tao; Liu, Xingquan; Zhou, Guoxin

Source: Nongye Gongcheng Xuebao/Transactions of the Chinese Society of Agricultural Engineering, v 41, n 4, p 299-308, February 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

Compilation and indexing terms, Copyright 2025 Elsevier Inc.

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3. Biopurification of functional soybean oligosaccharides from defatted soybean yellow pulp water fermented by yeast species: A process study

Li, Zhenjiang (College of Food Science, Heilongjiang Bayi Agricultural University, Heilongjiang, Daqing; 163319, China); Liang, Jiaxin; Liu, Shilin; Hu, Xin; wang, Lidong; Wang, Changyuan

Source: Food Chemistry: X, v 27, April 2025

Database: Compendex

Data Provider: Engineering Village

Compilation and indexing terms, Copyright 2025 Elsevier Inc.

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4. Preparation and inoculation of Bacillus spp. and Sinorhizobium meliloti strains immobilized on biochar-humic acid improve potted soybean traits and soil parameters

Hao, Ziyu (Heilongjiang Provincial Key Laboratory of Environmental Microbiology and Recycling of Argo-Waste in Cold Region, College of Life Science and Biotechnology, Heilongjiang Bayi Agricultural University, Heilongjiang, Daqing; 163319, China); Zhang, Shuang; Shao, Yaxu; Pan, Zi; Meng, Tingting; Liu, Tao; Yan, Lei

Source: Environmental Technology and Innovation, v 38, May 2025

Database: Compendex

Data Provider: Engineering Village

Compilation and indexing terms, Copyright 2025 Elsevier Inc.

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5. Recent development in ozone-based starch modification: From generation methods to film applications

Lang, Shuangjing (College of Life Science and Technology, Heilongjiang BayiAgricultural University, Heilongjiang, Daqing; 163319, China); Sui, Chunguang; Wang, Lidong

Source: International Journal of Biological Macromolecules, v 309, May 2025

Database: Compendex

Data Provider: Engineering Village

Compilation and indexing terms, Copyright 2025 Elsevier Inc.

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6. Construction of a quercetin-kafirin nanodelivery system by ultrasound-treated: Synthesis and characterization

Song, Xuejian (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Wang, Xinhui; Dai, Lingyan; Zhang, Dongjie; Li, Zhijiang; Ruan, Changqing; Zhang, Hongwei; Cao, Rongan

Source: LWT, v 224, May 15, 2025

Database: Compendex

Data Provider: Engineering Village

Compilation and indexing terms, Copyright 2025 Elsevier Inc.

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7. Effects of Citrus Fiber and Inulin Addition on the Lamb Protein Structure and Mince Quality

Ma, Kexin (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Xiang, Haiqiao; Yu, Xiao; Pan, Deyin; Li, Changbo; Chen, Hongsheng; Diao, Jingjing

Source: Science and Technology of Food Industry, v 46, n 8, p 43-51, April 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

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8. Investigation of the potential regulation of the CHYR E3 ligase genes on alfalfa response to drought and salt stresses

Jin, Jun (Crop Stress Molecular Biology Laboratory, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Sheng, Jiaxun; Jia, Bowei; Mu, Naize; Li, Wanhong; Wang, Jia; Bawa, George; Shen, Yang; Sun, Xiaoli; Liu, Xiangping; Sun, Mingzhe

Source: International Journal of Biological Macromolecules, v 311, June 2025

Database: Compendex

Data Provider: Engineering Village

Compilation and indexing terms, Copyright 2025 Elsevier Inc.

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9. DESIGN AND EXPERIMENTAL STUDY OF A CONTROL SYSTEM FOR SYNCHRONIZED CORN SEEDING AND HOLE FERTILIZATION

WANG, Ziyu (College of Information and Electrical Engineering, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); WANG, Hongchao; LIANG, Chunying; ZHAO, Naichen

Source: INMATEH - Agricultural Engineering, v 75, n 1, p 1097-1112, 2025

Database: Compendex

Data Provider: Engineering Village

Compilation and indexing terms, Copyright 2025 Elsevier Inc.

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10. Synthesis and characterization of a delivery system by combining cobalt (II) with soluble dietary fiber from Cyperus esculentus L. to regulate gut-derived neuroactive metabolite biosynthesis

Wang, Weihao (College of Forestry, Northeast Forestry University, Harbin, China); Kou, Fang; Quan, Zhigang; Sun, Jiajia; Zhang, Zhi

Source: Food Research International, v 211, June 2025

Database: Compendex

Data Provider: Engineering Village

Compilation and indexing terms, Copyright 2025 Elsevier Inc.

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11. Exploration and Optimization of a Deep Reinforcement Learning-based Model for the Creation of Children's Literature

Yue, Jianing (College of Humanities and Social Sciences, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Liu, Bing

Source: Engineering Intelligent Systems, v 32, n 6, p 605-612, November 2024

Database: Compendex

Data Provider: Engineering Village

Compilation and indexing terms, Copyright 2025 Elsevier Inc.

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12. Effect of Degree of Milling on the Nutrition and Eating Quality of Brown Rice

Li, Jinling (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Leng, Haijing; Cao, Rongan; Wang, Changyuan; Diao, Jingjing

Source: Science and Technology of Food Industry, v 46, n 8, p 85-94, April 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

Compilation and indexing terms, Copyright 2025 Elsevier Inc.

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13. DESIGN AND OPTIMIZATION OF AIR-ASSISTED SPIRAL SEED-SUPPLY DEVICE FOR HIGH-SPEED DENSE PLANTING MAIZE SEEDER

SUN, Wen-sheng (College of Engineering, Heilongjiang Bayi Agricultural University, Daqing, China); YI, Shu-juan; QI, Hailong; LI, Yi-fei; DAI, Zhi-bo; ZHANG, Yu-peng; YUAN, Jia-sha; WANG, Song

Source: INMATEH - Agricultural Engineering, v 75, n 1, p 13-25, 2025

Database: Compendex

Data Provider: Engineering Village

Compilation and indexing terms, Copyright 2025 Elsevier Inc.

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14. A coevolutionary algorithm for constrained multi-objective optimization with dynamic relaxation

Li, Yongchao (School of Information and Electrical Engineering, Heilongjiang Bayi Agricultural University, Heilongjiang, Daqing; 163000, China); Jia, Heming; Li, Hongguang

Source: Swarm and Evolutionary Computation, v 95, June 2025

Database: Compendex

Data Provider: Engineering Village

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15. Insight into the Stabilization Mechanism of Rice Protein Amyloid Fibrils Modification on Soy Protein Gels: Gel Properties, Microstructure, and Molecular Conformation

Ma, Jinming (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Wang, Lishuang; Pan, Deyin; Wang, Kexin; Huo, Jinjie; Ma, Xiaoqi; Lu, Baoxin; Yu, Xiaoshuai; Xiao, Zhigang

Source: SSRN, April 8, 2025

Database: Compendex

Data Provider: Engineering Village

Compilation and indexing terms, Copyright 2025 Elsevier Inc.

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16. PFOS exposure impairs porcine oocyte maturation and embryo development via mitochondria dependent ferroptosis

Sun, Xiaoqing (Jilin Agricultural University, Xincheng Street 2888, Changchun; 130118, China); Teng, Ran; Xu, Ning; Sun, Yutong; Zhang, Enbo; Chen, Xingfu; Guo, Qing; Li, Suo

Source: Environmental Pollution, v 374, June 1, 2025

Database: Compendex

Data Provider: Engineering Village

Compilation and indexing terms, Copyright 2025 Elsevier Inc.

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17. WORKING MECHANISM ANALYSIS AND EXPERIMENTAL STUDY OF GRASS CRUSHER

CHEN, Tao (College of Engineering, Heilongjiang Bayi Agricultural University, Daqing, China); YI, Shu-juan; WANG, Song; SUN, Wen-sheng

Source: INMATEH - Agricultural Engineering, v 75, n 1, p 334-345, 2025

Database: Compendex

Data Provider: Engineering Village

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18. High Precision Visual Simulation and Verification of Flood Flooding Range Based on Ue$_5$

Lu, Jiajie (College of Civil Engineering and Water Conservancy, Heilongjiang Bayi Agricultural Reclamation University, Heilongjiang, Daqing; 163319, China); Liu, Shaodong; Lin, Yanyu; Xu, Jiayang; Feng, Ji; Zhang, Zejian; Kong, Pengfei

Source: SSRN, April 8, 2025

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19. NUMERICAL SIMULATION AND PARAMETER OPTIMIZATION OF COMBINED CUTTING AND CRUSHING FORAGE CRUSHER

Chen, Tao (College of Engineering, Heilongjiang Bayi Agricultural University, Daqing, China); Yi, Shu-juan; Wang, Song; Sun, Wen-sheng

Source: INMATEH - Agricultural Engineering, v 75, n 1, p 95-109, 2025

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20. Temporal and spatial dynamics of carbon emissions in animal husbandry and their influencing factors: A case study of three provinces in Northeast China

Wei, Chunbo (Department of Animal Science, College of Animal Science and Veterinary Medicine, Heilongjiang Bayi Agricultural University, Daqing; 163316, China); Li, Jiaqi; Xu, Wei; Sha, Yanyu; Qu, Yongli

Source: Journal of Cleaner Production, v 508, May 25, 2025

Database: Compendex

Data Provider: Engineering Village

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21. Triple ERA Rapid Detection Method for Pathogens in Refrigerated Meat Products

Yang, Yange (Key Laboratory of Food Quality and Safety for State Market Regulation, Chinese Academy of Inspection and Quarantine, Beijing; 100176, China); Wu, Zhanwen; Liu, Tong; Wang, Shuai; Wei, Ying; Zhao, Jiansong; Li, Hongna; Li, Tao; Zhang, Feng

Source: Huanan Ligong Daxue Xuebao/Journal of South China University of Technology (Natural Science), v 53, n 4, p 135-146, April 2025

Language: Chinese

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22. DESIGN AND SIMULATION ANALYSIS OF KEY COMPONENTS OF GRASS CRUSHER

Chen, Tao (College of Engineering, Heilongjiang Bayi Agricultural University, PR, Daqing, China); Yi, Shu-Juan; Wang, Song; Sun, Wen-Sheng

Source: INMATEH - Agricultural Engineering, v 75, n 1, p 560-570, 2025

Database: Compendex

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23. Effect of novel carburizing-carbonitriding heat treatment on the microstructure, surface hardness, and wear resistance of 18Cr2Ni4WA steel

Wang, Xiao-nan (School of Iron and Steel, Soochow University, Suzhou; 215021, China); Chen, Ke; Li, Qing-da; Chen, Qi-yuan; Li, Zhen-xing; Liu, Zhen-guang; Zhang, Qing-yu; Yuan, Yue-dong; Wu, Ze-hua

Source: Materials Today Communications, v 46, June 2025

Database: Compendex

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24. Fast identification of maize varieties with small samples using near-infrared spectral feature selection and improved stacked sparse autoencoder deep learning

Yang, Dongfeng (College of Information and Electrical Engineering, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Hu, Jun

Source: Expert Systems with Applications, v 288, September 1, 2025

Database: Compendex

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25. Generalized model for the quantitative moisture analysis of maize grains during filling stage based on near-infrared spectroscopy

Wang, Xue (College of Information and Electrical Engineering, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Zhang, Guangyue; Ma, Tiemin; Zhao, Xiaoyu; Liu, Jinming; Yi, Shujuan

Source: Nongye Gongcheng Xuebao/Transactions of the Chinese Society of Agricultural Engineering, v 41, n 8, p 291-300, April 2025

Language: Chinese

Database: Compendex

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26. IMA-FLADRC-Based Electric-Driven High-Speed Maize Precision Seeding Control Strategy and System

Wang, Song (Heilongjiang Bayi Agricultural University, College of Engineering, Daqing; 163319, China); Yi, Shujuan; Zhao, Bin; Li, Yifei; Zhang, Dongming; Chen, Tao; Sun, Wensheng

Source: IEEE Access, v 13, p 85177-85195, 2025

Database: Compendex

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27. Construction of Multi-dimensional Teaching Resource System in Higher Education under the Blended Teaching Model

Chen, Zhengguang (College of Information and Electrical Engineering, Heilongjiang Bayi Agricultural University, Heilongjiang, Daqing, China); Liu, Shuo; Wang, Xue; Ma, Tiemin

Source: Proceedings of 2024 3rd International Conference on Artificial Intelligence and Education, ICAIE 2024, p 190-195, April 29, 2025, Proceedings of 2024 3rd International Conference on Artificial Intelligence and Education, ICAIE 2024

Database: Compendex

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28. Microbial conversion of crop straw: From bioenergy to bio-based materials

Zheng, Anwang (Heilongjiang Provincial Key Laboratory of Environmental Microbiology and Recycling of Argo-Waste in Cold Region, College of Life Science and Biotechnology, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Ji, Xinyue; Liu, Tao; Zhao, Dan; Zhang, Shuang; Yan, Lei

Source: Process Safety and Environmental Protection, v 200, August 2025

Database: Compendex

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29. Preparation, Structure and in Vitro Activity Analysis of Selenopolysaccharide from Auricularia 黑木耳

Shen, Qin (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Lu, Lele; Pan, Piao; Yue, Shibo; Cao, Dongmei

Source: Science and Technology of Food Industry, v 46, n 10, p 250-259, May 2025

Language: Chinese

Database: Compendex

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30. CWBLS network and its application in portable spectral measurement

Sui, Yutong (Heilongjiang Bayi Agricultural University, College of Information and Electrical Engineering, Heilongjiang, Daqing; 163319, China); Zhao, Xiaoyu; Liu, Cheng; Zhao, Yue; Cai, Lijing; Tong, Yuchen

Source: Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy, v 340, November 5, 2025

Database: Compendex

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31. Discrimination of Different Varieties of Rice in Wuchang Area Based on E-Nose and Hs-Spme-Gc-O-Ms

Qian, Lili (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Chen, Mingming; Song, Yan; Zhang, Tao; Liu, Xingquan; Zhou, Guoxin; Liu, Hongyan; Zuo, Feng

Source: SSRN, April 28, 2025

Database: Compendex

Data Provider: Engineering Village

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32. Establishment and Application of a Quality Evaluation System for Commercial Flavored Extruded Noodles

Zhao, Xue (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Cong, Zhongxiao; Sun, Huajun; Zang, Yanqing; Li, Changsheng; Zhou, Xuan; Qian, Lili

Source: Shipin Kexue/Food Science, v 46, n 8, p 25-33, April 25, 2025

Language: Chinese

Database: Compendex

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33. Insight into the formation mechanism of umami taste in traditional Chinese soybean paste: A review (*Open Access*)

Tong, Jialu (Heilongjiang Provincial Key Laboratory of Corn Deep Processing Theory and Technology, College of Food and Bioengineering, Qiqihar University, Qiqihar; 161006, China); Li, Guanlong; Liu, Xiaolan; Zheng, Xiqun

Source: LWT, v 224, May 15, 2025

Open Access type(s): All Open Access, Gold

Database: Compendex

Data Provider: Engineering Village

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34. Properties, Physiological Functions and Applications of Starch-Lipid Complexes

Zhao, Xinying (College of Food Science, Heilongjiang Bayi Agricultural University, National Coarse Cereals Engineering Research Center, Heilongjiang Engineering Research Center for Coarse Cereals Processing and Quality Safety, Daqing; 163319, China); Ruan, Changqing; Li, Zhijiang; Tang, Huacheng; Wang, Changyuan

Source: Science and Technology of Food Industry, v 46, n 10, p 12-20, May 2025

Language: Chinese

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35. Exploration of Feature Engineering Teaching Based on Max-Relevance Min-Redundancy

Chen, Zhengguang (College of Information and Electrical Engineering, Heilongjiang Bayi Agricultural University, Heilongjiang, Daqing, China); Ma, Xiaohui; Liu, Shuo; Feng, Huiyan; Yin, Shuxin; Xu, Nan

Source: Proceedings of 2024 3rd International Conference on Artificial Intelligence and Education, ICAIE 2024, p 292-296, April 29, 2025, Proceedings of 2024 3rd International Conference on Artificial Intelligence and Education, ICAIE 2024

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36. Effects of Soybean Oligosaccharides Extracted from Defatted Soybean Meal on Gut Microbiota and Metabolites during in Vitro Fermentation Process

Su, Tingting (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Yang, Xiyuan; Yu, Qiaoru; Wu, Mengna; Xu, Lei; Wang, Hui; Mu, Xindi; Yao, Di; Wang, Changyuan

Source: Shipin Kexue/Food Science, v 46, n 11, p 164-179, June 15, 2025

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37. Study on regulation of kidney bean and haskap composite fermentation broth on gut microbiota via in vitro fermentation model

Wang, Jia (College of Food, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Wang, Xi; Zhou, Fang; An, Yu; Zhang, Zhihui; Li, Sinan; Xu, Kaiyuan; Yuan, Peng; Wang, Ying; Zhang, Lu

Source: Food and Fermentation Industries, v 51, n 8, p 211-218, April 25, 2025

Language: Chinese

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38. Optimization of the Fermentation Enrichment Method for Oat Non-starch Polysaccharides and Study of Their Immunostimulatory Activity

Gao, Ruohan (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Ma, Nan; Yang, Mingzhe; Cao, Jiabao; Wang, Xia; Lu, Baoxin

Source: Science and Technology of Food Industry, v 46, n 10, p 21-32, May 2025

Database: Compendex

Data Provider: Engineering Village

39. A Thermodynamics-Based Carbon Accounting Model for Carbon Emissions: A Multi-Objective Coupling Analysis of Energy Conservation and Cost Accounting

Geng, Xiaoyuan (College of Economics and Management, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Su, Xuefei; Gao, Wangsheng

Source: International Journal of Heat and Technology, v 43, n 2, p 403-414, April 2025

Database: Compendex

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40. Design and Experiment of Seed Orientation Correction Element for High-speed Belt-type Soybean Seeding Device

Yi, Shujuan (College of Engineering, Heilongjiang Bayi Agrieultural Vniversity, Daqing; 163319, China); Wang, Guangyu; Li, Yifei; Wang, Song; Li, Shuaifei; Wei, Ruiyong

Source: Nongye Jixie Xuebao/Transactions of the Chinese Society for Agricultural Machinery, v 56, n 5, p 268-278 and 424, May 2025

Language: Chinese

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41. Effect of Degree of Milling on the Quality of Daohuaxiang Rice and Physicochemical Properties of Instant Rice

Lu, Lele (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Shen, Qin; Lang, Shuangjing; Yao, Di; Wang, Lidong; Wang, Changyuan

Source: Science and Technology of Food Industry, v 46, n 10, p 220-227, May 2025

Language: Chinese

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