收錄引用報

SCI·EI·ESI INDEX DATABASE

October.~December. 2025 No.44

黑龍江八一農墾大學

图书馆 咨询服务部

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2025.10.02-2025.11.26。

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

（2025.10.02-2025.11.26）

SCI 索引库共收录我校教师发表的 83 篇文献，图表后附录 83 篇文献详细题录信息。

RESEARCH FIELDS	研究领域	篇数
Agriculture	农业	15
Biochemistry & Molecular Biology	生物化学与分子生物学	6
Biotechnology & Applied Microbiology	生物工程学和应用微生物学	3
Computer Science	计算机科学	1
Chemistry	化学	8
Construction & Building Technology	施工和建筑技术	1
Energy & Fuels	能源和燃料	1
Engineering	工程	3
Environmental Sciences& Ecology	环境科学与生态学	2
Food Science & Technology	食品科学与技术	8
Immunology	免疫学	3
Life Sciences & Biomedicine - Other Topics	生命科学与生物医学-其他主题	1
Materials Science	材料科学	2
Parasitology	寄生物学	1
Pharmacology & Pharmacy	药理学和药剂学	1
Plant Sciences	植物科学	13
Reproductive Biology	生殖生物学	1
Science & Technology - Other Topics	科技与技术-其他主题	8
Spectroscopy	光谱学	1
Thermodynamics	热动力学	1

Veterinary Sciences	兽医学	**1**
Virology	病毒学	**2**

表 1　我校 22 个研究领域发文篇数及详细题录信息

Record 1

Title: A lightweight detection algorithm for cereal weed recognition based on deep learning

Author(s): Dong, XW (Dong, Xiao-Wei); Wang, LF (Wang, Lin-Feng); Zhang, XM (Zhang, Xi-Mu); Wang, M (Wang, Ming); Li, WK (Li, Wei-Kai)

Source: CROP PROTECTION **Volume:** 199 **Article Number:** 107451 **DOI:** 10.1016/j.cropro.2025.107451 **Published Date:** 2026 JAN

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Efficient and accurate identification of millet weeds enables weeding robots to perform precise pesticide application or mechanical weeding. To facilitate the effective deployment of the model on mobile devices with limited resources, a novel lightweight weed detection method, LRS-YOLOv8, is proposed in this research. The algorithm is composed of the Lightweight Shared Convolutional Group Normalization Head (LWSCGNH) detection head, the RepConv Lightweight Cross Stage Partial (RLWCSP) module, and the Inner Wise Shape-Intersection over Union (IWS-IoU) loss function. With the LWSCGNH, the model achieves better detection of small target weeds and retains its lightweight properties. The RLWCSP module is designed to enhance multi-scale feature extraction and gradient flow capabilities, while computation and storage costs are reduced. The IWS-IoU loss function improves bounding box regression performance and enhances the detection of small target weeds, while also addressing the weed occlusion problem. The experimental results indicate that, for the millet weed dataset collected in a field environment, compared to YOLOv8n, the improved model enhances the precision, recall, and mAP50 metrics by 4.5 %, 1.9 %, and 0.6 %, respectively. Moreover, the model achieves a 48.3 % reduction in parameters, a 38.7 % decrease in size, and a 44.4 % drop in floating-point operations per second. The detection speed reaches 203 FPS, satisfying the requirements for lightweight and real-time performance, and surpassing other comparable object detection methods. Model optimization and deployment were successfully implemented on the RK3588 mobile platform for efficient multi-target detection. It provides a reference for deploying millet weed detection models on resource-constrained mobile devices.

Accession Number: WOS:001607241000001

Document Type: Article

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Research Areas: Agriculture

Output Date: 2025-11-26

Record 2

Title: A lightweight hybrid model for accurate ammonia prediction in pig houses

Author(s): Musabimana, J (Musabimana, Jacqueline); Xie, QJ (Xie, Qiuju); Zhou, H (Zhou, Hong); Zheng, P (Zheng, Ping); Liu, HG (Liu, Honggui); Ma, TM (Ma, Tiemin); Liu, JM (Liu, Jiming)

Source: SMART AGRICULTURAL TECHNOLOGY **Volume:** 12 **Article Number:** 101266 **DOI:** 10.1016/j.atech.2025.101266 **Published Date:** 2025 DEC

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: In extensive pig farms, keeping good living conditions is crucial for pigs' good health, growth, and productivity, as ammonia (NH3) negatively impacts health and reproduction. Recently, deep learning techniques have proven potential in predicting ammonia concentration by capturing complex temporal dependencies. However, the standard transformer deep learning method relies heavily on self-attention, leading to high computational complexity and long training times, limiting its use in dynamic environments and real-time applications with limited resources. To overcome these issues, this study presents a novel, lightweight hybrid transformer model that combines Convolutional Neural Networks, Long Short-Term Memory, and Transformer (CNN-LSTMTransformer) for NH3 prediction. The model replaces feedforward networks with separable convolutional layers to capture local and spatial dependencies more efficiently, as well as reduce computational complexity. It also replaces positional encoding with global average pooling, simplifying the architecture and improving temporal feature aggregation. The outcomes indicated that, compared to the standard transformer, the proposed model reduces memory size by 21.1 % (4.9 MB vs. 6.21 MB) and training time by 29.7 % (5 min vs. 7.11 min). It also outperforms the standard transformer in accuracy and efficiency, with Root Mean Square Error (RMSE), Mean Absolute Percentage Error (MAPE), and coefficient of determination R2 of 0.3994, 0.0225, and 0.9260, respectively, compared to 0.4250, 0.0227, and 0.9162 for the standard model, reducing RMSE by 5.99 %, MAPE by 0.88 %, and increasing R2 by 1.08 %. The model improves accuracy compared to other state-of-the-art and ability for NH3 prediction.

Accession Number: WOS:001612421000004

Document Type: Article

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Research Areas: Agriculture

Output Date: 2025-11-26

Record 3

Title: Research Note: The influence of storage duration and short periods of incubation during egg storage on hatching performance of indigenous chickens

Author(s): Zhang, ZY (Zhang, Zhouying); Ge, CY (Ge, Caiyue); Ni, AX (Ni, Aixin); Yang, HH (Yang, Hanhan); Du, HF (Du, Hongfeng); Guo, JP (Guo, Jiangpeng); Li, YL (Li, Yunlei); Han, XT (Han, Xintong); Yuan, JW (Yuan, Jingwei); Chen, JL (Chen, Jilan); Sun, YY (Sun, Yanyan)

Source: POULTRY SCIENCE **Volume:** 104 **Issue:** 12 **Article Number:** 105950 **DOI:** 10.1016/j.psj.2025.105950 **Published Date:** 2025 DEC

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Extended duration of fertile eggs severely compromises hatchability and chick quality in poultry. This study evaluated the effect of short periods of incubation during egg storage (SPIDES) in mitigating hatching losses associated with storage for indigenous Beijing-You chickens. A total of 1,440 eggs were used across six treatments representing durations of egg storage (7, 14, and 21 days) and SPIDES treatment. Freshly collected eggs were stored in egg storage room at 16 degrees C and 65 % relative humidity. The eggs were subjected to a standard SPIDES procedure, which involved 1-h incubation at 35 degrees C and natural cooling to 28.8 degrees C. Following the cooling phase, the eggs were returned to the same storage room as the control eggs. SPIDES was performed at day 5, day 5 and 10, and day 5, 10, and 15 for eggs stored for 7 days, 14 days, and 21 days during storage, respectively. Results showed that prolonged storage significantly reduced the hatchability of fertile eggs (89.77 % for 7 days to 54.96 % for 21 days) and the percentage of normal day-old chicks (99.77 % to 78.07 %), and increased the percentage of mid-late-dead embryos (9-21 embryonic day) (4.69 % to 39.04 %).

SPIDES treatment dramatically reversed these effects on eggs stored for 21-day by improving hatchability of fertile eggs to 79.87 % ($P < 0.05$) and the percentage of normal day-old chicks to 89.50 % ($P < 0.05$), while reducing the percentage of mid-late-dead embryos to 17.09 % ($P < 0.05$). SPIDES also reduced early embryonic mortality and enhanced hatch synchrony by narrowing the hatch window. These results demonstrated that SPIDES effectively increase the hatching performance by reversing storage-induced embryonic damage. This confirms SPIDES as an essential intervention for maintaining hatching performance in eggs of indigenous chicken breeds subjected to prolonged storage.

Accession Number: WOS:001605775600002

Document Type: Article

Addresses: [Zhang, Zhouying; Ge, Caiyue; Ni, Aixin; Yang, Hanhan; Du, Hongfeng; Li, Yunlei; Han, Xintong; Yuan, Jingwei; Chen, Jilan; Sun, Yanyan] Chinese Acad Agr Sci, Inst Anim Sci, State Key Lab Anim Biotech Breeding, Beijing 100193, Peoples R China.
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Research Areas: Agriculture

Output Date: 2025-11-26

Record 4

Title: Corn protein hydrolysates as biostimulants: Effects on soybean physiology and rhizosphere microbial community in saline-alkali soil

Author(s): Jiang, CX (Jiang, Caixia); Liu, HD (Liu, Handong); Liu, XL (Liu, Xiaolan); Li, Y (Li, Yue); Wang, JT (Wang, Juntong); Zheng, XQ (Zheng, Xiqun)

Source: INDUSTRIAL CROPS AND PRODUCTS **Volume:** 236 **Article Number:** 122058 **DOI:** 10.1016/j.indcrop.2025.122058 **Published Date:** 2025 NOV 2

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Soil salinization poses a key challenge to global agriculture, and there is an urgent need for cost-effective amelioration measures. Microbial fermentation-derived proteases were employed to hydrolyze corn proteins, enriching the polypeptide fractions and enhancing their efficacy as biostimulants. This approach effectively promoted soybean seedling growth and improved tolerance to abiotic stresses. Results revealed that, compared with corn steep liquor, the contents of organic matter, small peptides, and amino acid nitrogen in fermented corn steep liquor increased significantly. Specifically, the proportion of protein components with a molecular weight < 1 kDa rose from 46.84 % to 62.34 %. After application, the phenotypic growth of soybean seedlings was significant, and the leaves' antioxidant and nitrogen metabolism-related enzyme activities were enhanced. The nutrient content and the abundance of beneficial microbial communities in the rhizosphere soil increased, with some bacteria exhibiting greater dominance in carbon and nitrogen cycling and energy metabolism. This study innovated a new pattern of resource utilization of corn processing by-products, aiming to promote synergistic greening of agriculture and the corn processing industry.

Accession Number: WOS:001593166900002

Document Type: Article

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Research Areas: Agriculture

Output Date: 2025-11-26

Record 5

Title: Analysis of Electrical Signals in Plant Physiological Responses: A Multi-Scale Adaptive Denoising Method Based on CEEMDAN-WST

Author(s): Liu, ZH (Liu, Zihan); Tian, FM (Tian, Fangming); Tan, F (Tan, Feng)

Source: AGRICULTURE-BASEL **Volume:** 15 **Issue:** 21 **Article Number:** 2269 **DOI:** 10.3390/agriculture15212269 **Published Date:** 2025 OCT 31

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Plant surface electrical signals are key representations for non-destructive monitoring of changes in cell membrane potential, enabling real-time reflection of physiological responses and regulatory processes under external stimuli. However, the low-frequency and weak-amplitude characteristics of these signals make them extremely susceptible to interference from multiple complex noise sources, such as environmental, power-line frequency, and inherent instrument noise. Existing denoising methods suffer from issues such as mode mixing and insufficient fidelity, hindering accurate extraction of genuine plant physiological information. This study proposes a novel denoising approach that integrates Complete Ensemble Empirical Mode Decomposition with Adaptive Noise (CEEMDAN) and Wavelet Soft Thresholding (WST). By decomposing and filtering noise components with adaptive thresholds based on the SURE criterion, the method achieves multi-scale decomposition and effective suppression of residual noise. Applied to surface electrical signals of maize leaves, the results demonstrated a 48% reduction in permutation entropy (PE) for the entire signal. In the resting potential segment, the root mean square (RMS) decreased by 28.91%, total energy dropped by 9.3%, and waveform stability improved. For the action potential segment, the full width at half maximum (FWHM) increased to 0.747, and although the peak amplitude slightly decreased, the waveform structure remained intact. Signal energy became more concentrated within the 0-2 Hz range, achieving efficient noise suppression and high signal fidelity. This method provides a reliable preprocessing technique for elucidating plant physiological mechanisms based on surface electrical signals and holds significant potential for real-time non-destructive monitoring and early warning systems in smart agriculture.

Accession Number: WOS:001612378300001

Document Type: Article

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Research Areas: Agriculture

Output Date: 2025-11-26

Record 6

Title: Effects of Straw Return on Soil Physicochemical Properties and Microbial Communities in a Cold-Region Alkaline Farmland

Author(s): Zhang, W (Zhang, Wei); Wang, JH (Wang, Jinghong); Khan, A (Khan, Aman); Shen, GN (Shen, Guinan); Wei, D (Wei, Dan); Wang, WD (Wang, Weidong)

Source: AGRONOMY-BASEL **Volume:** 15 **Issue:** 10 **Article Number:** 2433 **DOI:** 10.3390/agronomy15102433 **Published Date:** 2025 OCT 21

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Straw return is crucial for sustainable agriculture, but its efficiency is limited

by low temperatures in cold regions, especially in saline-alkali soils. This study investigates the degradation process of maize straw and the response of soil properties and microbial communities during the winter low-temperature period in the alkaline farmland of Anda, China. A two-year field experiment with straw return (SR) and no return (NR) treatments was conducted. Straw degradation rates and structural changes (as observed via scanning electron microscope, SEM) were monitored. Soil physicochemical properties and enzyme activities were analyzed. Microbial community composition was characterized using 16S rRNA and ITS sequencing. The cumulative straw degradation rate over two years reached 94.81%, with 18.33% occurring in the first winter freeze-thaw period. Freeze-thaw cycles significantly damaged the straw structure, facilitating microbial colonization. Straw return significantly improved soil properties after winter, increasing field water capacity (3.45%), content of large aggregates (6.57%), available nutrients (P 38.17 mg/kg, K 191.93 mg/kg), and organic carbon fractions compared to NR. Microbial analysis revealed that low temperatures filtered the community, enriching cold-tolerant taxa like Pseudogymnoascus, Penicillium, and Pedobacter, which are crucial for lignocellulose decomposition under cold conditions. The winter period plays a significant role in initiating straw degradation in cold regions. Straw return mitigates the adverse effects of winter freezing on soil quality and promotes the development of a cold-adapted microbial consortium, thereby enhancing the sustainability of alkaline farmland ecosystems in Northeast China.

Accession Number: WOS:001602233000001

Document Type: Article

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Forestry Sciences (BAAFS)

Research Areas: Agriculture; Plant Sciences

Output Date: 2025-11-26

Record 7

Title: The Establishment of a Geofencing Model for Automated Data Collection in Soybean Trial Plots

Author(s): Liang, JX (Liang, Jiaxin); Zhang, B (Zhang, Bo); Chen, CH (Chen, Changhai); Cui, HY (Cui, Haoyu); Ma, YC (Ma, Yongcai); Chen, B (Chen, Bin)

Source: AGRICULTURE-BASEL **Volume:** 15 **Issue:** 20 **Article Number:** 2169 **DOI:** 10.3390/agriculture15202169 **Published Date:** 2025 OCT 19

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Collecting crop growth data in field environments is crucial for breeding research. The team's current autonomous soybean phenotyping system requires manual control to start and stop data collection. To address the aforementioned issues, this study innovatively proposes an elliptical calibration rotating geofencing technique. Preprocess coordinates using Z-scores and mean fitting perform global error calibration via weighted least squares, calculate the inclination angle between the row direction and the relative standard direction by fitting a straight line to the same row of data, and establish a rotation model based on geometric feature alignment. Results show that the system achieves an average response time of 0.115 s for geofence entry, with perfect accuracy and Recall rates of 1, meeting the requirements for starting and stopping geographic fencing in soybean ridge trial plots. This technology provides the critical theoretical foundation for enabling a dynamic, on-demand automatic start-stop functionality in smart data collection devices for soybean field trial zones within precision agriculture.

Accession Number: WOS:001603163200001

Document Type: Article

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Research Areas: Agriculture

Output Date: 2025-11-26

Record 8

Title: Lipoxygenase ZmLOX3 Enhances Salt Tolerance of Maize Under the Regulation of ZmNAC032

Author(s): Che, XY (Che, Xinyang); Wei, YL (Wei, Yulei); Wang, XHY (Wang, Xueheyuan); Wang, XQ (Wang, Xinqi); Wu, ZX (Wu, Zixuan); Deng, J (Deng, Jie); Ge, SN (Ge, Shengnan); Liu, XY (Liu, Xinyu); Cai, ZC (Cai, Zhicheng); Zhang, HY (Zhang, Haiyang); He, L (He, Lin); Xu, JY (Xu, Jingyu)

Source: JOURNAL OF AGRICULTURAL AND FOOD CHEMISTRY **Volume:** 73 **Issue:** 42 **Pages:** 26516-26528 **DOI:** 10.1021/acs.jafc.5c02349 **Early Access Date:** OCT 2025 **Published Date:** 2025 OCT 22

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Lipoxygenase (LOX) plays a critical role in plant biotic and abiotic stress responses by mediating lipid peroxidation and the production of jasmonic acid (JA). In this study, maize ZmLOX3 was identified as a positive regulator in salt stress tolerance. Overexpression of ZmLOX3 enhanced the salt tolerance of Arabidopsis . When maize seedlings were subjected to salt stress, the ZmLOX3 OE lines exhibited a better growth phenotype than the control (B104) and the zmlox3 CR (CRISPR/Cas) knockout mutants. Overexpression of ZmLOX3 improved ROS scavenging, Na+/K+ homeostasis, and cell membrane stability. Transcriptome analyses revealed that ZmLOX3 OE triggered the expression of genes involved in both the JA synthesis and signaling pathways. A transcription factor ZmNAC032 was identified via Y1H screening and was able to bind to the C[A/G]CG[T/G] sequence in the ZmLOX3 promoter and activate its expression. These findings are helpful for deciphering the function and regulatory status of ZmLOX in improving salt tolerance.

Accession Number: WOS:001588856700001

Document Type: Article

Addresses: [Che, Xinyang; Wei, Yulei; Wang, Xueheyuan; Wang, Xinqi; Wu, Zixuan; Deng, Jie; Ge, Shengnan; Liu, Xinyu; Cai, Zhicheng; Zhang, Haiyang; He, Lin; Xu, Jingyu] Heilongjiang Bayi Agr Univ, Coll Agr, Key Lab Modern Agr Cultivat & Crop Germplasm Impro, Daqing 163319, Peoples R China.

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Affiliations: Heilongjiang Bayi Agricultural University

Research Areas: Agriculture; Chemistry; Food Science & Technology

Output Date: 2025-11-26

Record 9

Title: TGF- β 3-mediated phagocytosis protects mammary epithelial cells of ketotic dairy cows against metabolic stress-induced inflammatory damage

Author(s): Chang, RX (Chang, Renxu); Jia, HD (Jia, Hongdou); Chen, YY (Chen, Yuanyuan); Loor, JJ (Loor, Juan J.); Xu, QS (Xu, Qiushi); Ma, L (Ma, Li); Li, M (Li, Ming); Shen, TY (Shen, Taiyu); Li, XB (Li, Xiaobing); Xu, C (Xu, Chuang); Sun, XD (Sun, Xudong)

Source: JOURNAL OF DAIRY SCIENCE **Volume:** 108 **Issue:** 10 **Pages:** 11443-11462 **DOI:** 10.3168/jds.2025-26828 **Early Access Date:** SEP 2025 **Published Date:** 2025 OCT

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: The supraphysiological levels of free fatty acids (FFA) during early lactation led to an inflammatory response in the mammary gland of ketotic cows, which may be attributed to the untimely clearance of apoptotic cells (AC). Given the engulfment role of mammary epithelial cells for AC and the regulation of TGF-(33 on phagocytosis, we speculated that TGF-(33-mediated phagocytic function is closely related to inflammatory response in the mammary gland of ketotic cows. The objective of this study was to elucidate (1) the inflammatory state and phagocytic function of mammary epithelial cells and activity of the TGF-(33 pathway in mammary gland of ketotic cows, and (2) the role of TGF-(33-mediated phagocytosis on the inflammatory response of bovine mammary epithelial cells in response to exogenous FFA. In this study, excessive proliferation of AC, NF-kappa B/MAPKmediated inflammatory response, TLR4-mediated local natural immune dysfunction, phagocytic dysfunction of mammary epithelial cells, and activation of the TGF-(33 pathway were detected in the mammary gland of ketotic cows or in immortalized bovine mammary epithelial (MAC-T) cells in response to exogenous FFA. Knockdown of TLR4 attenuated the FFA-induced inflammatory response in MAC-T cells. Overexpression of TGF-(33 exacerbated FFA-induced TLR4-mediated local immune dysfunction and inflammatory response by aggravating phagocytic responses. Knockdown of TGF-(33 attenuated the overactivation of inflammation resulting from FFA challenge through inhibition of the TLR4 pathway, which improved phagocytic ability in MAC-T cells. Taken together, TGF-(33-mediated phagocytosis may be a promising therapeutic target for reducing the negative effect of FFA-induced inflammation in mammary gland of dairy cows with ketosis.

Accession Number: WOS:001585900800040

Document Type: Article

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Research Areas: Agriculture; Food Science & Technology

Output Date: 2025-11-26

Record 10

Title: Mitoquinone Can Effectively Improve the Quality of Thawed Boar Sperm

Author(s): Dong, YY (Dong, Yingying); Wang, Q (Wang, Qian); Wang, HC (Wang, Hechuan); Guo, Q (Guo, Qing); Li, YB (Li, Yanbing); Li, JC (Li, Jingchun)

Source: ANIMALS **Volume:** 15 **Issue:** 19 **Article Number:** 2808 **DOI:** 10.3390/ani15192808 **Published Date:** 2025 SEP 26

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Boar sperm is susceptible to damage by reactive oxygen species during in vitro preservation, leading to lipid peroxidation, which changes the sperm structure and affects its quality after thawing. Exogenous antioxidants play a vital role in preventing this damage. This research aimed to assess the impact of incorporating Mitoquinone into cryopreservation extenders on the quality and antioxidant capacity of boar sperm. Mitoquinone was added to the cryopreservation extender at varying concentrations, namely, 0, 50, 100, 150, and 200 nmol/L. Post-thawing, the sperm were examined for motility parameters, acrosome integrity, DNA integrity, mitochondrial activity, membrane integrity, and antioxidant enzyme activity. The results showed that compared with the control group, 150 nmol/L Mitoquinone could improve sperm viability after freezing and thawing and significantly reduce the malformation rate ($p < 0.05$). The addition of 150 nmol/L Mitoquinone led to a significant increase in the acrosome integrity, DNA integrity, mitochondrial activity, and membrane integrity of the boar sperm compared to the control group ($p < 0.05$). Moreover, it enhanced the antioxidant capacity of the sperm. This study demonstrated that the cryopreservation extender containing 150 nmol/L of Mitoquinone can enhance the effectiveness of semen cryopreservation.

Accession Number: WOS:001594517400001

Document Type: Article

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Research Areas: Agriculture; Veterinary Sciences; Zoology

Output Date: 2025-11-26

Record 11

Title: SLW-YOLO: A Hybrid Soybean Parent Phenotypic Consistency Detection Model Based on Deep Learning

Author(s): Yu, CT (Yu, Chuntao); Li, JY (Li, Jinyang); Shi, WQ (Shi, Wenqiang); Qi, LQ (Qi, Liqiang); Guan, ZY (Guan, Zheyun); Zhang, W (Zhang, Wei); Zhang, CB (Zhang, Chunbao)

Source: AGRICULTURE-BASEL **Volume:** 15 **Issue:** 19 **Article Number:** 2001 **DOI:** 10.3390/agriculture15192001 **Published Date:** 2025 SEP 25

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: During hybrid soybean seed production, the parents' phenotypic consistency is assessed by breeders to ensure the purity of soybean seeds. Detection traits encompass the hypocotyl, leaf, pubescence, and flower. To achieve the detection of hybrid soybean parents' phenotypic consistency in the field, a self-propelled image acquisition platform was used to obtain soybean plant image datasets. In this study, the Large Selective Kernel Network (LSKNet) attention mechanism module, the detection layer Small Network (SNet), dedicated to detecting small objects, and the Wise Intersection over Union v3 (WIoU v3) loss function were added into the YOLOv5s network to establish the hybrid soybean parent phenotypic consistency detection model SLW-YOLO. The SLW-YOLO achieved the following: F1 score: 92.3%; mAP: 94.8%; detection speed: 88.3 FPS; and model size: 45.1 MB. Compared to the YOLOv5s model, the SLW-YOLO model exhibited an improvement in F1 score by 6.1% and in mAP by 5.4%. There was a decrease in detection speed by 42.1 FPS, and an increase in model size by 31.4 MB. The parent phenotypic consistency detected by the SLW-YOLO model was 98.9%, consistent with manual evaluation. Therefore, this study demonstrates the potential of using deep learning technology to identify phenotypic consistency in the seed production of large-scale hybrid soybean varieties.

Accession Number: WOS:001593321300001

Document Type: Article

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Research Areas: Agriculture

Output Date: 2025-11-26

Record 12

Title: Effects of a Multi-Strain Lactic and Propionic Acid Bacteria Inoculant on Silage Quality, Methane Emissions, Milk Composition, and Rumen Microbiome

Author(s): Olorunlowu, S (Olorunlowu, Segun); Sidoruk, P (Sidoruk, Pola); Sznajder, J (Sznajder, Julia); Szczesny, J (Szczesny, Jakub); Lechniak, D (Lechniak, Dorota); Pawlak, P (Pawlak, Piotr); Ryczek, M (Ryczek, Marcin); Huang, HH (Huang, Haihao); Li, LY (Li, Lingyan); Irawan, A (Irawan, Agung); Komisarek, J (Komisarek, Jolanta); Szumacher-Strabel, M (Szumacher-Strabel, Malgorzata); Cieslak, A (Cieslak, Adam)

Source: ANIMALS **Volume:** 15 **Issue:** 18 **Article Number:** 2740 **DOI:** 10.3390/ani15182740 **Published Date:** 2025 SEP 19

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Total Times Cited: 0

Abstract: Ensiling grass with microbial inoculants is a promising strategy to enhance forage quality, animal performance, and environmental sustainability. This study evaluated the effects of a multi-strain inoculant (Lactobacillus plantarum, L. buchneri, Propionibacterium acidipropionici, and P. thoeni) on silage fermentation, nutrient digestibility, milk production, methane emissions, and rumen microbiota in dairy cows. In a 2 x 2 crossover design, 24 lactating Polish Holstein-Friesians were fed total mixed rations differing only in grass silage treated with or without inoculant. Inoculated silage had lower pH (4.56 vs. 5.06; $p = 0.02$) and higher crude protein (129 vs. 111 g/kgDM; $p < 0.05$). Cows fed inoculated silage showed higher ruminal propionate (28.3 vs. 26.3 mM; $p = 0.03$), reduced ammonia (7.61 vs. 8.67 mM; $p = 0.02$), and fewer protozoa (1.21 vs. 1.66 x 10(5)/mL; $p = 0.03$). Nutrient digestibility improved ($p < 0.05$), while methane emissions declined both per cow (368 vs. 397 g/d; $p = 0.01$) and per kgDMI (15.1 vs. 16.5; $p = 0.01$). Milk yield increased ($p = 0.04$), and the fatty acid profile improved. Our study revealed that cows fed inoculated silage had higher nutrient digestibility, lower methane emissions, and microbial shifts in the rumen detected by 16S rRNA sequencing ($p < 0.05$).

Accession Number: WOS:001581226600001

Document Type: Article

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Research Areas: Agriculture; Veterinary Sciences; Zoology

Output Date: 2025-11-26

Record 13

Title: Isolation and Identification of Antagonistic Bacteria with Common Bacterial Blight of Common Bean and Their Mechanism as Biological Control

Author(s): Liu, M (Liu, Ming); Cui, JR (Cui, Jiarui); Wang, X (Wang, Xin); Guo, YX (Guo, Yongxia)

Source: AGRONOMY-BASEL **Volume:** 15 **Issue:** 9 **Article Number:** 2176 **DOI:** 10.3390/agronomy15092176 **Published Date:** 2025 SEP 12

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Common bacterial blight (CBB), caused by Xanthomonas axonopodis pv.

phaseoli (Xap) and Xanthomonas fuscans subsp. fuscans (Xff), is a devastating disease threatening global common bean (Phaseolus vulgaris L.) production. Current reliance on copper-based chemicals has led to environmental toxicity and pathogen resistance, resulting in the need for sustainable alternatives. Here, we report the first biocontrol strain of Bacillus amyloliquefaciens (KY2) that is simultaneously effective against both Xap and Xff. Isolated from the rhizosphere of healthy common bean growing in a high-disease-incidence field, KY2 exhibited broad antagonism, with inhibition zones of 18.17 +/- 0.58 mm and 24.00 +/- 1.50 mm against Xap and Xff, respectively. Pot experiments revealed a 66.12% curative control efficacy against Xff, slightly lower than the chemical agent 12% Zhongshengmycin. Mechanistically, KY2 alleviated oxidative stress by enhancing antioxidant enzyme activity levels and reducing malondialdehyde accumulation. A transcriptome analysis further uncovered KY2-induced systemic resistance via phenylpropanoid biosynthesis and defense-related pathways. It also demonstrated adaptability to pH 4-8, 20-40 degrees C, and <= 6% NaCl. However, this study is limited to pot trials, necessitating future field validation to assess practical scalability. These findings establish KY2 as a novel, eco-friendly candidate for CBB management, advancing biocontrol strategies against CBB of bean.

Accession Number: WOS:001579476800001

Document Type: Article

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Research Areas: Agriculture; Plant Sciences

Output Date: 2025-11-26

Record 14

Title: miR-194-3 Regulates Proliferation and Apoptosis of Follicular Granulosa Cells by Targeting CHD4 in Zhedong White Geese

Author(s): Zheng, P (Zheng, Peng); Zang, ZY (Zang, Zhengyu); Wang, SZ (Wang, Size); Zeng, CC (Zeng, Chuicheng); Pan, Y (Pan, Yue); Zhang, YL (Zhang, Yuanliang); Yue, S (Yue, Shan); Liu, SJ (Liu, Shengjun); Huang, H (Huang, He);

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Source: ANIMALS **Volume:** 15 **Issue:** 18 **Article Number:** 2676 **DOI:** 10.3390/ani15182676 **Published Date:** 2025 SEP 12

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Total Times Cited: 0

Abstract: The dynamic balance between proliferation and apoptosis of follicular granulosa cells (GCs) is crucial for follicular development in poultry. microRNAs play important roles in ovarian development and follicular function. Previous transcriptome analyses showed that miR-194-3 was significantly differentially expressed in the ovaries of Zhedong white geese during the laying and brooding stages. Therefore, the aim of this study was to investigate the regulatory role and molecular mechanism of miR-194-3 on the proliferation and apoptosis of follicular GCs in Zhedong white geese. We first screened the target gene CHD4 of miR-194-3 and constructed the miR-194-3 mimic and inhibitor, a small interfering RNA of target gene CHD4. The experimental results showed that the overexpression of miR-194-3 significantly down-regulated the mRNA and protein expression of GC proliferation genes (PCNA, CDK-2, and CCND-1), reduced the proportion of EdU-labeled positive cells, blocked cell cycle progression, simultaneously up-regulated the mRNA and protein expression of Caspase-3 and Caspase-9, and significantly increased the rate of apoptosis. In contrast, the inhibition of miR-194-3 expression promoted the proliferation of goose follicular GCs, accelerated cell cycle progression, and decreased the apoptosis rate. Bioinformatics prediction combined with the results of the dual luciferase reporter assay confirmed that CHD4 was a direct target gene of miR-194-3. The knockdown of CHD4 expression resulted in the down-regulation of PCNA, CDK-2 and CCND-1 expression; blockage of cell cycle progression; attenuation of cell proliferation; an up-regulation of Caspase-3 and Caspase-9 expression and a significant increase in apoptotic cell death. In summary, both miR-194-3 overexpression and CHD4 knockdown produced similar effects on goose follicular GC proliferation and apoptosis, suggesting that CHD4 may partially mediate the regulatory effects of miR-194-3; however, additional targets or pathways cannot be excluded.

Accession Number: WOS:001579443000001

Document Type: Article

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Research Areas: Agriculture; Veterinary Sciences; Zoology

Output Date: 2025-11-26

Record 15

Title: Mechanism of mitofusin 2, mitochondria-associated membrane, and the mitochondrial pathway in alleviating oxidative stress and cell senescence in bovine mammary epithelial cells

Author(s): Hu, HJ (Hu, Huijie); Liu, JX (Liu, Juxiong); Yin, JX (Yin, Junxi); Hu, GQ (Hu, Guiqiu); Huang, BX (Huang, Bingxu); Tu, LQ (Tu, Liqun); Liu, XT (Liu, Xuanting); Xu, B (Xu, Bin); Cao, Y (Cao, Yu); Guo, WJ (Guo, Wenjin); Fu, SP (Fu, Shoupeng)

Source: JOURNAL OF DAIRY SCIENCE **Volume:** 108 **Issue:** 9 **Pages:** 10151-10172 **DOI:** 10.3168/jds.2025-26746 **Published Date:** 2025 SEP

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Total Times Cited: 0

Abstract: Bovine mastitis is a major challenge in the dairy industry, leading to persistent oxidative stress and mammary epithelial cell senescence, which impairs mammary gland function and hinders milk yield recovery. The mitochondria-associated membrane (MAM), a critical interface between mitochondria and the endoplasmic reticulum, plays an important role in redox balance and mitochondrial homeostasis. This study aimed to investigate the role of MAM in oxidative stress-induced cellular senescence in lactating Holstein dairy cows. We first examined oxidative stress markers and key proteins related to the MAM pathway in mammary tissues using Western blotting and commercial assay kits, and found that MAM pathway alterations were negatively correlated with oxidative stress. Transcriptome analysis further confirmed this association, with differentially expressed genes enriched in the mitochondria-endoplasmic reticulum network. Subsequently, an H2O2-induced oxidative stress model was established in bovine mammary epithelial cells. The results showed that oxidative stress inhibited MAM formation, promoted mitochondrial fission, and induced cellular senescence. In our previous experiments, we identified mitofusin 2 (MFN2) as a critical regulator in this process. Adenoviral overexpression of MFN2 enhanced MAM formation, alleviated oxidative stress, and delayed senescence. Further investigations revealed that MFN2 undergoes proteasomal degradation under oxidative stress. When the MAM structure was disrupted, MFN2 lost its antioxidative and antisenescence functions, indicating that MAM is essential for its activity. Based on this mechanism, we identified Gracilaria lemaneiformis polysaccharide (GLP) as a potential MFN2 activator. The GLP was found to upregulate MFN2 transcription, inhibit its ubiquitination, and enhance its protein stability. When combined with antibiotic therapy, GLP effectively reduced oxidative stress in mastitic cows, restored mammary gland function, and downregulated the expression of senescence-related markers. These findings suggest that oxidative stress-induced degradation of MFN2 impairs MAM formation, resulting in excessive mitochondrial fission and cellular senescence. Mitofusin 2 overexpression restores MAM integrity and mitigates oxidative stress. Activation of MFN2 by GLP offers a promising therapeutic strategy for mastitis, with potential to reduce recurrence and improve mammary gland health in dairy cows.

Accession Number: WOS:001583924000040

Document Type: Article

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Biochemistry & Molecular Biology

Record 1

Title: Mn2+ enhances phagocytosis of macrophages against Staphylococcus aureus by regulating autophagy

Author(s): Ma, JZ (Ma, Jinzhu); Ma, YX (Ma, Yixuan); Wei, SY (Wei, Shuyu); Wu, SS (Wu, Shuangshuang); Dong, YZ (Dong, Yazun); Liu, KY (Liu, Kaiyue); Liu, HY (Liu, Hongyan); Yu, SM (Yu, Simiao); Yu, LQ (Yu, Liquan); Wang, BY (Wang, Beiyan); Song, BF (Song, Baifen)

Source: INTERNATIONAL JOURNAL OF BIOCHEMISTRY & CELL BIOLOGY **Volume:** 190 **Article Number:** 106875 **DOI:** 10.1016/j.biocel.2025.106875 **Published Date:** 2026 JAN

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Mn2+ is an important trace nutrient element in the body. Macrophages act a significant role on resisting Staphylococcus aureus (S. aureus). Nowadays, it remains unclear whether Mn2+ can regulate the phagocytosis of macrophages against S. aureus through autophagy. Here, after the RAW264.7 cells transfected with the p3 x Flag-CMV10-ube2c plasmids were treated with Mn2+, subsequently infected with S. aureus, then these cells manifested that the expression levels of LC3-II and p62 proteins were significantly increased, and autophagosome formation was enhanced, and the expression level of RhoB phagocytosis-related protein also was significantly increased, the phosphorylation levels of mTOR, p38 and JNK were obviously decreased, while phosphorylation level of ERK was enhanced, the production levels of IL-6 and IL-2, IFN-beta, IFN-gamma, CAT and NO were significantly elevated, especially the phagocytosis against S. aureus was become obviously stronger. The data indicated that Mn2+ could promote the early autophagy activation and inhibit the degradation of autophagolysosomes in the late stage of autophagy of RAW264.7 cells infected with S. aureus through Ube2C, thereby enhancing the phagocytosis of macrophages against S. aureus. These data provide an important basis for a deeper understanding of the molecular mechanism by which Mn2+ enhances the phagocytosis of macrophages.

Accession Number: WOS:001612763700001

Document Type: Article

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Research Areas: Biochemistry & Molecular Biology; Cell Biology

Output Date: 2025-11-26

Record 2

Title: Role of the urokinase-type plasminogen activator system in viral infection and replication

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Source: MOLECULAR IMMUNOLOGY **Volume:** 188 **Pages:** 38-44 **DOI:** 10.1016/j.molimm.2025.10.012 **Published Date:** 2025 DEC

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Total Times Cited: 0

Abstract: The urokinase-type plasminogen activator system (uPAs) consists of the urokinase-type plasminogen activator (uPA), its receptor (uPA receptor, uPAR) and the plasminogen activator inhibitor (PAI). Recent studies have revealed that, beyond its well-established roles in promoting fibrinolysis and degrading extracellular matrix (ECM) proteins-thereby regulating tissue repair and tumor metastasis-this system also plays a significant role in viral infections. Specifically, the uPAs modulates viral infection processes by regulating the expression and activity of uPA and uPAR, which are involved in inflammatory response modulation, immune cell migration, and the infiltration of inflammatory cells during tissue repair in the context of viral infections. In this review, we summarize the roles of uPAs in various viral infections, aiming to deepen our understanding of the contributions of each uPA component and provide insights into potential strategies for inhibiting viral infection processes.

Accession Number: WOS:001612667600001

Document Type: Article

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Research Areas: Biochemistry & Molecular Biology; Immunology

Output Date: 2025-11-26

Record 3

Title: Madecassoside Induces Apoptosis and Inhibits Migration by Regulating ROS-Mediated Signaling Pathways in MDA-MB-231 Breast Cancer Cells

Author(s): Hou, WS (Hou, Wen-Shuang); Luo, YH (Luo, Ying-Hua); Wu, N (Wu, Nan); Tang, YJ (Tang, Yan-Jun); Liu, YZ (Liu, Yan-Zhi); Zhang, YL (Zhang, Yan-Liang); Jin, CH (Jin, Cheng-Hao)

Source: CHEMICAL BIOLOGY & DRUG DESIGN **Volume:** 106 **Issue:** 5 **Article Number:** e70197 **DOI:** 10.1111/cbdd.70197 **Published Date:** 2025 NOV 6

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Madecassoside (MC) is an anti-inflammatory and antibacterial active substance extracted from the traditional Chinese medicine Centella asiatica. Based on network pharmacology and experimental validation, this study assessed MC's anti-breast cancer (BC) actions and related molecular pathways. CCK-8, Trypan Blue, and Hoechst33342/PI assays showed that MC significantly reduced BC cell activity, but it had little inhibitory effects on normal cells. Network pharmacology analysis predicted 40 intersection targets between MC and BC, 291 GO-related biological processes, and 105 KEGG signaling pathways. The anti-breast cancer activity of MC is closely related to reactive oxygen species (ROS), AKT and MAPK signaling pathways. Through Annexin V-FITC/PI, flow cytometry, transwell, wound healing and western blotting experiments, it was found that MC induced mitochondria-dependent apoptosis, G2/M phase arrest and inhibited cell migration of MDA-MB-231 cells through MAPK/STAT3/NF-kappa B signaling pathway, PI3K/AKT signaling pathway and AKT/GSK-3 beta/beta-catenin signaling pathway, respectively. The induction and blocking effects were inhibited by the addition of ROS scavenger N-acetyl cysteine (NAC). Molecular docking showed that MC had significant binding ability with STAT3, CASP3, BCL2 and JUN targets in BC. In summary, MC induced apoptosis, cell cycle arrest, and migration inhibition via ROS-mediated MAPK/STAT3/NF-kappa B, PI3K/AKT, and AKT/GSK-3 beta/beta-catenin signaling pathways in MDA-MB-231 cells.

Accession Number: WOS:001608898500001

Document Type: Article

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Research Areas: Biochemistry & Molecular Biology; Pharmacology & Pharmacy

Output Date: 2025-11-26

Record 4

Title: Heating-homogenization synergistic preparation of soy protein isolate-sodium alginate composite particles and their performance study

Author(s): Zhou, L (Zhou, Lin); Liu, Q (Liu, Qian); Yue, XD (Yue, Xidian); Chen, HS (Chen, Hongsheng); Peng, XY (Peng, Xinyan)

Source: INTERNATIONAL JOURNAL OF BIOLOGICAL MACROMOLECULES **Volume:** 330 **Article Number:** 148285 **DOI:** 10.1016/j.ijbiomac.2025.148285 **Published Date:** 2025 NOV **Part:** 4

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: In this study, composite particles were prepared through the synergistic effect of heating and homogenization of soy protein isolate (SPI) and sodium alginate (SA), aiming to observe how different SA concentrations affect the structure and physicochemical quality of the composite particles. The composite particles were assessed using various methods such as turbidity analysis, Fourier infrared spectroscopy, and UV-visible absorption spectroscopy, and the results revealed that SA could considerably increase the composite particle stability. The particle size, turbidity, emulsifying properties, and foaming properties of the composite particles were significantly improved as the SA content increased, with the maximum protein solubility occurring at 1.0 wt% SA. Furthermore, Hydrophobic interactions and hydrogen bonding altered the structure of the composite particles. A theoretical foundation was established for the creation of new food emulsifiers and the enhancement of food stability.

Accession Number: WOS:001603129200009

Document Type: Article

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Research Areas: Biochemistry & Molecular Biology; Chemistry; Polymer Science

Output Date: 2025-11-26

Record 5

Title: Advances in CrRLK1L function in plant cell wall signaling during interaction with the environment and development

Author(s): Bawa, G (Bawa, George); Shen, Y (Shen, Yang); Sun, MZ (Sun, Mingzhe); Sun, XL (Sun, Xiaoli)

Source: STRESS BIOLOGY **Volume:** 5 **Issue:** 1 **Article Number:** 60 **DOI:** 10.1007/s44154-025-00231-y **Published Date:** 2025 OCT 16

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: As a barrier between the cell and its environment, the plant cell wall provides structural support during development and stress response. Plants are able to sense their surroundings and adjust their activities accordingly. A crucial mechanism involved in these adaptive changes is the cell wall integrity (CWI) maintenance mechanism, which monitors and maintains the integrity of cell walls via changes in cell and cell wall metabolism without destroying cell wall organization. Different abiotic stresses and changes in plant developmental phases disrupt CWI. However, emerging evidence has demonstrated the initiation of CWI signaling mechanisms as key in promoting plant growth in complex situations. This review discusses recent advances in the Catharanthus roseus receptor-like kinase 1-like (CrRLK1L) protein function in plant cell wall signaling during adaptation to changing environments and development. We conclude by highlighting how current spatially resolved transcriptomics may be used to advance the role of CrRLK1L members in plant cell wall signaling during development and stress response.

Accession Number: WOS:001595331200001

Document Type: Review

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Research Areas: Biochemistry & Molecular Biology

Output Date: 2025-11-26

Record 6

Title: Curcumin Alleviates HMGB1-Mediated Inflammation Through the Signaling Pathway of TLR2-NF-κB in Bovine Ovarian Granulosa Cells

Author(s): Liu, SQ (Liu, Siqi); Xie, YY (Xie, Yingying); Wang, L (Wang, Lei); Zhang, JY (Zhang, Jingyan); Chen, XL (Chen, Xiaoliang); Feng, XW (Feng, Xiaowei); Wang, JY (Wang, Junyan); Zhang, K (Zhang, Kang); Li, JX (Li, Jianxi)

Source: INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES **Volume:** 26 **Issue:** 18 **Article Number:** 9180 **DOI:** 10.3390/ijms26189180 **Published Date:** 2025 SEP 19

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Curcumin, the principal bioactive compound derived from turmeric, possesses a wide range of therapeutic properties such as anti-inflammatory, antioxidant, and wound-healing properties. Recent studies suggest that curcumin may alleviate HMGB1-mediated inflammation in ovarian cells. However, its role in modulating dysfunction in HMGB1-driven ovarian granulosa cells (OGCs) remains to be elucidated. In the present study, curcumin suppresses the HMGB1-induced overexpression of toll-like receptor 2 (TLR2) and ovulation-related factors such as EGFR, VEGF, STAR, and TIMP1/2 genes. Additionally, the elevated levels of TLR2, TLR1, TLR6, and phospho-NF-kappa B p65 proteins were significantly inhibited by curcumin. Further mechanistic analysis reveals that the interaction between HMGB1 and the TLR1-TLR2/TLR6 complex, as well as phospho-NF-kappa B p65, was restrained. This resulted in the suppression of the pro-inflammatory cytokine IL-6 production and the alleviation of the HMGB1-induced inflammation response in OGCs. Collectively, our findings demonstrate that curcumin modulates the upregulation of ovulation-related genes and pro-inflammatory cytokines in OGCs by inhibiting the TLR2-NF-kappa B pathway, providing a mechanistic basis for its potential application as a therapeutic agent against OGC inflammation.

Accession Number: WOS:001580139100001

Document Type: Article

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Research Areas: Biochemistry & Molecular Biology; Chemistry

Output Date: 2025-11-26

Biotechnology & Applied Microbiology

Record 1

Title: An α/β-Hydrolase GmABHD6 Controls Seed Oil Content and Yield in Soybean

Author(s): Yu, KX (Yu, Kaixin); Hu, LM (Hu, Limin); Sun, B (Sun, Bo); Chen, ZH (Chen, Zehao); Li, X (Li, Xu); Zhang, SY (Zhang, Shiyu); Tian, HL (Tian, Huilin); Zhang, WJ (Zhang, Wenjing); Ren, SM (Ren, Shimin); Han, X (Han, Xue); Xu, C (Xu, Chang); Wei, SM (Wei, Siming); Yang, ML (Yang, Mingliang); Kong, FJ (Kong, Fanjiang); Chen, QS (Chen, Qingshan); Qi, ZM (Qi, Zhaoming)

Source: PLANT BIOTECHNOLOGY JOURNAL **DOI:** 10.1111/pbi.70466 **Early Access Date:** NOV 2025 **Published Date:** 2025 NOV 17

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Seed oil content is a key trait in soybean, yet its genetic basis remains largely unresolved. Here, we identify GmABHD6, an alpha/beta-hydrolase domain-containing gene, as the causal gene underlying a major quantitative trait locus (QTL) for seed oil content on chromosome 16. Through fine-mapping in a chromosome segment substitution population derived from Glycine max (SN14) and wild Glycine soja (ZYD00006), we fine-mapped the QTL to a 150-kb interval. Functional analyses reveal that overexpression of GmABHD6 significantly reduces seed oil content, whereas gene editing to truncate GmABHD6 led to increased oil accumulation. These modifications also alter seed protein levels, seed size and 100-seed weight, indicating pleiotropic effects on seed composition and yield traits. Integrated transcriptomic and metabolomic profiling of transgenic lines highlighted widespread changes in lipid metabolism and energy pathways associated with GmABHD6 activity. Further functional characterisation indicates that the ERF transcription factor GmERF physically binds to the GmABHD6 promoter region to regulate its expression. Population genetic analyses show strong signatures of selection at the GmABHD6 locus, suggesting that favourable alleles are enriched during soybean domestication and improvement. Our findings establish GmABHD6 as a domestication-related gene that negatively regulates seed oil content and provide new insights into the genetic mechanisms driving soybean seed composition and evolution.

Accession Number: WOS:001615350300001

Document Type: Article; Early Access

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Research Areas: Biotechnology & Applied Microbiology; Plant Sciences

Output Date: 2025-11-26

Record 2

Title: Pepper root exudate attenuates snap bean root rot by mediating microbial community remodeling

Author(s): Li, Y (Li, Ying); Liu, L (Liu, Le); Teng, HY (Teng, Huaiyuan); Zhao, LQ (Zhao, Liqin); Fan, BW (Fan, Bowen); Yang, FJ (Yang, Fengjun)

Source: APPLIED AND ENVIRONMENTAL MICROBIOLOGY **Volume:** 91 **Issue:** 11 **DOI:** 10.1128/aem.01664-25 **Early Access Date:** OCT 2025 **Published Date:** 2025 NOV 19

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Intercropping, as a sustainable agricultural practice, has shown potential to reduce soil-borne diseases through rhizosphere microbial community remodeling. However, whether pepper (Capsicum annuum L.) confers this benefit to snap bean (Phaseolus vulgaris L.) remains unclear. This study investigated the disease-suppressive effects of exogenously applied pepper root exudates using pot experiments. In vitro assays were used to validate the biocontrol efficacy of antagonistic bacteria and a key flavonoid metabolite (Chrysin). High-throughput sequencing and untargeted metabolomics were combined to analyze changes in the

snap bean rhizosphere microbial community and root exudate profiles under pathogen stress. Compared to the treatment inoculated only with Fusarium solani (F. solani) (CKI), the treatment applying root exudates plus F. solani (REI) exhibited a substantial reduction in F. solani abundance, enhanced plant antioxidant enzyme activities, as well as markedly alleviated snap bean root rot symptoms. Furthermore, the REI treatment significantly altered rhizosphere microbial community composition by selectively enriching beneficial microbes (e.g., Actinobacteria, Ascomycota, Streptomyces, Saccharothrix), enhanced the complexity and stability of the bacterial-fungal cross-domain network, and formed a pathogen antagonism network centered on Streptomyces. Moreover, the REI treatment induced the secretion of flavone compounds (e.g., Chrysin) from snap bean roots, whose relative abundance demonstrated an essential positive correlation with Streptomyces and a significant negative correlation with Fusarium. The findings indicate that exogenous application of pepper root exudates mitigates the incidence of snap bean root rot by restructuring the rhizosphere microbial community and promoting the synthesis of endogenous flavone metabolites in the host plant. This study provides a basis for environmentally friendly vegetable disease management and supports the advancement of sustainable agricultural practices.IMPORTANCERoot rot induced by Fusarium solani poses a serious threat to snap bean production and the sustainable development of agriculture. Long-term continuous cropping intensifies the incidence of soilborne diseases. Conventional chemical control methods are frequently less effective against these diseases and may result in issues, such as the development of pathogen resistance, a decline in soil microbial diversity, and environmental contamination. Despite the fact that intercropping snap beans with peppers can reduce the incidence of snap bean root rot, the precise mechanisms through which pepper root exudates confer this protective effect remain inadequately understood. This study demonstrates that pepper root exudates can effectively reduce the occurrence of snap bean root rot by reshaping the microbial community and inducing the secretion of plant defense metabolites. The significance of this research lies in elucidating the key mechanisms and application potential of pepper root exudates in enhancing snap bean resistance to root rot, thereby providing essential theoretical foundations and practical guidance for the development of novel biological agents and the advancement of green agriculture.

Accession Number: WOS:001605104800001

Document Type: Article

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Research Areas: Biotechnology & Applied Microbiology; Microbiology

Output Date: 2025-11-26

Record 3

Title: Research on the construction of degradation bacterial communities for Daqing Gulong Oilfield and their application effects

Author(s): Deng, S (Deng, Shuang); Wang, JB (Wang, Jiabin); Song, W (Song, Wei); Zhang, LJ (Zhang, Lijuan); Cao, D (Cao, Di); Li, LY (Li, Liyang)

Source: INTERNATIONAL BIODETERIORATION & BIODEGRADATION **Volume:** 206 **Article Number:** 106218 **DOI:** 10.1016/j.ibiod.2025.106218 **Early Access Date:** SEP 2025 **Published Date:** 2026 JAN 1

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Shale oil sludge, as a petroleum hydrocarbon pollutant, poses a serious threat to the environment. This study is the first to focus on the degradation of shale oil sludge from the Daqing Gulong Oilfield, aiming to establish an environmentally friendly, low-cost, and highly effective bioremediation method. This approach aims to reduce the cost of treating oil sludge, increase corporate profits, and achieve the goal of coordinated economic and environmental development. The experiment successfully constructed a composite bacterial consortium containing Acinetobacter calcoaceticus, Bacillus cereus, and Pseudomonas qingdaonensis. Under laboratory conditions, the degradation rate of petroleum hydrocarbons reached 91.47 %. The composite bacterial consortium can rapidly proliferate in shale oil sludge and become the dominant bacterial population, maintaining a stable microbial community structure in complex environments. In practical applications, it shows excellent degradation effects on shale oil sludge. The degradation rate of the composite bacterial strain can reach up to 59.9 % in practical applications. This research not only provides a new technical approach and bacterial resources for the remediation of shale oil sludge in the Daqing Gulong Oilfield but also holds significant theoretical and practical significance.

Accession Number: WOS:001576487400001

Document Type: Article

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Output Date: 2025-11-26

Computer Science

Record 1

Title: A Distributed Adaptive Differential Privacy Mechanism With Blockchain Integration for Edge Computing

Author(s): Sun, YH (Sun, Yuhan); Hou, SP (Hou, Suipeng); Zhao, J (Zhao, Jie); Ye, JH (Ye, Jinhua)

Source: SECURITY AND PRIVACY **Volume:** 8 **Issue:** 6 **Article Number:** e70143 **DOI:** 10.1002/spy2.70143 **Published Date:** 2025 NOV 12

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: With the proliferation of big data-driven healthcare, edge computing, and blockchain sharing, privacy protection for sensitive clinical data remains challenging. Conventional differential privacy (DP)-with fixed budgets, centralized noise injection, and no auditability-underperforms in distributed settings. We propose Distributed Adaptive Differential Privacy with Blockchain Integration (DADP-BI): each edge node dynamically allocates budgets by data sensitivity/query frequency, applies Kalman smoothing to local Laplace noise, and uses smart contracts for on-chain audit. Evaluated on the expanded UCI Heart Disease Dataset (920 samples, 14 attributes including high-sensitivity "cholesterol" and "fastingBS"): Privacy leakage dropped by 49.3% (21.7% -> 10.8% for "cholesterol") and 41.4% (15.2% -> 8.9% for "age"); Regression errors fell (MSE: 0.38 -> 0.22, MAE: 0.27 -> 0.16), and heart disease classification accuracy rose 7.2 percentage points (77.8% -> 85.0%); End-to-end runtime and blockchain latency decreased by 18.5%-19.8%, with CPU/memory usage down 31.8%/26.7%. DADP-BI offers a scalable solution for privacy-preserving data processing in decentralized edge big-data environments.

Accession Number: WOS:001612922700001

Document Type: Article

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Research Areas: Computer Science; Telecommunications

Output Date: 2025-11-26

Chemistry

Record 1

Title: A PSiO2/ZnO aptamer microarray chips based on "quenching-restoration" fluorescence strategy for multiple mycotoxin determination

Author(s): Chen, JY (Chen, Jiayu); Yao, BX (Yao, Boxiang); Yu, RZ (Yu, Runzhong); Zhang, LY (Zhang, Liyuan); Zhang, H (Zhang, Han)

Source: TALANTA **Volume:** 298 **Article Number:** 128989 **DOI:** 10.1016/j.talanta.2025.128989 **Published Date:** 2026 FEB 1 **Part:** B

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Co-contamination and co-exposure of mycotoxins in cereals threaten human life and health. And PSiO2/ZnO composite nanostructured substrates with signal amplification capability provide a versatile and more sensitive platform for high-throughput microarray chip detection. Therefore in this work a PSiO2/ZnO aptamer microarray chip for the detection of multiple mycotoxins in various cereals was developed and evaluated. The entire qualitative and quantitative process of the chip was primarily accomplished through a "quenching-restoration" fluorescence strategy. On the microarray immobilized with aptamers and complementary strands forming a double-stranded DNA structure. Fluorescence resonance energy transfer (FRET) caused fluorescence quenching on the chip surface. In this detection system, mycotoxins preferentially bound to the aptamers with high specificity. Consequently, the complementary strands were displaced, eliminating the quenching effect and allowing the fluorescence on the chip surface to recover. Finally, the changes of different fluorescence values in multiple channels were utilized. Thus, high-throughput and highly specific quantitative detection and analysis of multiple toxins have been completed. The results showed that the sensitivity of the method applied to the simultaneous detection of OTA, DON and ZEN in cereals was as low as 0.0137 ng/kg, 0.0185 ng/kg and 0.2730 ng/kg, respectively. In addition, the chip combined with the improved QuEChERS method enabled the detection of toxins in various cereals with good accuracy and stability at the same time. Based on the detection principle and adjustable characteristics of the chip, and the method is expected to be applied to the high-throughput detection of other small molecules.

Accession Number: WOS:001603102000003

Document Type: Article

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Research Areas: Chemistry

Output Date: 2025-11-26

Record 2

Title: Effects of geographical origin, processing and their interaction on stable isotopes in Pu-erh tea for traceability

Author(s): Li, YL (Li, Yanlong); Zou, HD (Zou, Hai-Dan); Wang, XL (Wang, Xiao-Li); Chen, MM (Chen, Ming-Ming); Zhang, BW (Zhang, Bo-Wen); Wang, WF (Wang, Wen-Fang); Li, J (Li, Jie); Jiang, HY (Jiang, He-Yuan); Qian, LL (Qian, Li-Li); Liu, HY (Liu, Hong-Yan)

Source: FOOD CHEMISTRY **Volume:** 496 **Article Number:** 146619 **DOI:** 10.1016/j.foodchem.2025.146619 **Published Date:** 2025 DEC 25 **Part:** 1

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: To establish a robust traceability model for Pu-erh tea, this study systematically investigated the effects of geographical origin, processing, and their interaction on the stable isotope ratios (13C, 15N, 2H, and 18O) in both tea and its caffeine monomer. Results revealed that the stable isotopic compositions in Pu-erh tea and caffeine significantly differed among regions, 2Htea, 13Ccaffeine, 2Hcaffeine and 18Ocaffeine were significantly influenced by processing, all the stable isotopes were significantly influenced by region-processing interaction, and region contributed most to the variation of each stable isotope. Among them, 13Ccaffeine, 13Ctea, 15Ntea, and 2Hcaffeine were identified as the key indicators for geographical discrimination. Furthermore, 97.2 % correct discrimination rate and good validation (Q2 = 0.775) were achieved by linear discriminant analysis and orthogonal partial least squares-discriminant analysis, respectively. Ultimately, this study confirms that tea and caffeine stable isotope signatures are capable for classifying the Pu-erh tea geographical origin even mixed with different processed samples.

Accession Number: WOS:001598148800008

Document Type: Article

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Research Areas: Chemistry; Food Science & Technology; Nutrition & Dietetics

Output Date: 2025-11-26

Record 3

Title: A near-infrared spectroscopy method for detecting corn starch content based on UVE-LightGBM feature selection

Author(s): Tong, J (Tong, Jie); Yang, DF (Yang, Dongfeng)

Source: JOURNAL OF FOOD COMPOSITION AND ANALYSIS **Volume:** 148 **Article Number:** 108421 **DOI:** 10.1016/j.jfca.2025.108421 **Published Date:** 2025 DEC **Part:** 3

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: This study introduces a feature selection methodology that uses Near-infrared spectroscopy (NIRS), combining Uniform Variable Elimination (UVE) with the LightGBM algorithm in Gradient Boosting Machines (GBMs) for the swift, non-destructive evaluation of maize starch content. The research initially employed various preprocessing methods on the original spectral data. It assessed their effectiveness by Partial Least Squares Regression (PLSR). The findings demonstrated that first derivative (1D) preprocessing was the most efficacious, yielding an R2 C of 0.9994, RMSEC of 0.0187, R2P of 0.9375, RMSEP of 0.2498, and RPD of 3.9985. UVE was subsequently utilized to identify essential wavelengths, while LightGBM further optimized the selection, markedly enhancing modeling efficiency and precision. Multiple feature selection techniques were employed for the comparison of regression models, including Ridge Regression (RR), Gaussian Process Regression (GPR), Multilayer Perceptron Regression (MLPR), and Random Forest (RF). The findings indicated that UVE-LightGBM modeling had a superior coefficient of determination and reduced root mean square error, with an R2P of 0.9972 and an RMSEP of 0.0470. The physical and chemical significance of specific wavelengths was clarified by SHapley Additive exPlanation (SHAP), validating their role in enhancing the model's predicted accuracy and interpretability.

Accession Number: WOS:001594466600003

Document Type: Article

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Research Areas: Chemistry; Food Science & Technology

Output Date: 2025-11-26

Record 4

Title: Enhancing the robustness of the 1-D CNN model through NIRS data augmentation based on sparse autoencoder and CARS feature selection for mango DMC determination

Author(s): Yang, DF (Yang, Dongfeng); Hu, J (Hu, Jun)

Source: JOURNAL OF FOOD COMPOSITION AND ANALYSIS **Volume:** 148 **Article Number:** 108380 **DOI:** 10.1016/j.jfca.2025.108380 **Published Date:** 2025 DEC **Part:** 3

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Accurate, rapid, and online determination of mango dry matter content (DMC) holds great significance for the mango industry. The integration of near-infrared spectroscopy and deep learning theory offers an opportunity to enhance determination accuracy. In this paper, we propose a spectral data augmentation method based on the sparse autoencoder and establish a one-dimensional convolutional model to predict mango DMC. The test results indicate that the model performs optimally when trained on a training set comprising 80 % of the augmented data. The root mean square error (RMSE) of the test set was 0.4073, and the coefficient of determination (R2) was 0.9782. The prediction accuracy of our model surpasses that of models such as Gaussian Process Regression, Support Vector Machines, and Partial Least Squares Regression. This study can assist in fruit quality inspection, processing optimization, variety selection, and breeding, as well as storage and preservation, and has a wide range of application potential and value. It also provides novel insights into data augmentation techniques for near-infrared spectral regression modeling.

Accession Number: WOS:001588683400001

Document Type: Article

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Research Areas: Chemistry; Food Science & Technology

Output Date: 2025-11-26

Record 5

Title: Prediction of maize crude fat content based on improved conditional mutual information maximization and SHAP analysis

Author(s): Zhou, HC (Zhou, Haichao); Ma, XD (Ma, Xiaodan); Guan, H (Guan, Haiou); Yang, J (Yang, Jiao); Wei, BX (Wei, Bingxue); Zhang, YF (Zhang, Yifei); Lu, YX (Lu, Yuxin)

Source: FOOD CHEMISTRY **Volume:** 493 **Article Number:** 146054 **DOI:** 10.1016/j.foodchem.2025.146054 **Published Date:** 2025 NOV 30 **Part:** 4

Times Cited in Web of Science Core Collection: 1

Total Times Cited: 1

Abstract: Traditional conditional mutual information maximization (CMIM) algorithms struggled to capture nonlinear dependencies in continuous near-infrared (NIR) spectral analysis. Therefore, this study proposed a novel framework combining improved CMIM with SHAP for rapid maize crude fat content prediction. Innovatively replacing discretization with continuous variable estimates and two-stage filter-wrapper feature selection. The CMIM_KDE method achieved R(2)p of 0.7618 and 0.7531 in the PLSR and SVR models, respectively, which was an average improvement of 6.18 % and 4.42 % over other improved strategies. In addition, SHAP revealed the screened feature wavenumbers around 5684 cm(-1) and 4312 cm(-1) were related to the C-H group of maize. The validity and generalizability of the method was validated on publicly available datasets. This study solved the applicability bottleneck of traditional CMIM method in NIR spectral analysis. It could provide technical support for the quality detection of other agricultural products as well as low-altitude remote sensing and real-time online prediction.

Accession Number: WOS:001578004600004

Document Type: Article

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Research Areas: Chemistry; Food Science & Technology; Nutrition & Dietetics

Output Date: 2025-11-26

Record 6

Title: Preparation and characterization on a dual-layer slow-release urea fertilizer coated using ethyl cellulose and phosphoric acid-carbamate di-esterified starch-based chitosan hydrogel

Author(s): Gu, SJ (Gu, Shijia); Zhang, WZ (Zhang, Wenzhi); Tan, XX (Tan, Xiaoxiao); Wang, P (Wang, Peng); Shi, ZC (Shi, Zhichun); Lv, J (Lv, Jun); Zhao, M (Zhao, Ming); Dong, GH (Dong, Guohua)

Source: CARBOHYDRATE POLYMERS **Volume:** 368 **Article Number:** 124212 **DOI:** 10.1016/j.carbpol.2025.124212 **Published Date:** 2025 NOV 15 **Part:** 2

Times Cited in Web of Science Core Collection: 1

Total Times Cited: 1

Abstract: The extensive utilization of natural starch (NS) in preparation of slow-release fertilizer (SRF) remains a crucial challenge owing to its undesirable defects such as poor solubility and mechanical properties. Herein, based on the preparation of di-esterified starch derivatives (PCDS) from NS with phosphoric acid and carbamate and synthesis of PCDS cross-linked chitosan (CS) hydrogels (PCDS-CSH), a dual-layer coated urea SRF (EC/PCDS-CSH/urea-SRF) was successfully developed utilizing ethyl cellulose (EC) and PCDS-CSH as the inner/outer coating. Due to the ameliorated properties of PCDS (viscosity and gelation temperature) compared to NS, the PCDS-CSH shows significantly improved swelling performance and water retention capacity. Importantly, the corresponding EC/PCDS-CSH/urea-SRF demonstrates superior nitrogen (N) nutrient slow-release behaviors, achieving cumulative release rates of 48.5 % (12h) and 61.3 % (48 h) in water together with 22.9 % (10 d) and 52.9 % (29 d) in soil, respectively. Kinetics fitting analysis reveals that N release in EC/PCDS-CSH/urea-SRF follows the Higuchi model (in water) and First-order kinetics (in soil), respectively, both of which belong to non-Fickian diffusion process. Furthermore, tomato seedling pot experiments demonstrate that the EC/PCDS-CSH/urea-SRF shows a significant promotion role toward the plant growth. Consequently, this study provides a novel route for developing biomass based SRFs utilizing modified NS derivatives.

Accession Number: WOS:001580947400002

Document Type: Article

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Research Areas: Chemistry; Polymer Science

Output Date: 2025-11-26

Record 7

Title: Differences in flavor profiles and meat quality of grass carp from China's jingpo lake across four thermal processing methods

Author(s): Pan, DY (Pan, De-yin); Ma, JM (Ma, Jin-ming); Li, CB (Li, Chang-bo); Du, HZ (Du, Hong-zhen); Diao, JJ (Diao, Jing-jing); Chen, HS (Chen, Hong-sheng)

Source: FOOD CHEMISTRY-X **Volume:** 31 **Article Number:** 103110 **DOI:** 10.1016/j.fochx.2025.103110 **Early Access Date:** OCT 2025 **Published Date:** 2025 OCT

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: This study examined the effects of four thermal processing methods (steaming, boiling, air frying, and roasting) on the flavor and meat quality of Grass Carp from Jingpo Lake, China (a natural water system). A total of 98 volatile substances were identified in Jingpo Lake Grass Carp (JPGC) meat after heat treatment. In the four treatments, the air frying could significantly decrease the content of unpleasant odor compounds (octanol, 1-octen-3-ol, 1-heptanol, hexanal, nonanal, and octanal). Electronic tongue analysis suggested a more appealing taste profile for air-fried samples compared to other groups. Sensory evaluation corroborated these findings. Additionally, air frying remarkably preserves polyunsaturated fatty acids. The correlation analysis indicated that the relative content of alcohols, aldehydes, and ketones were markedly correlated with fatty acids and free amino acids of the fish. In conclusion, air frying emerges as an optimal thermal processing method, offering consumers a pleasurable mouthfeel and appealing flavors.

Accession Number: WOS:001590501300001

Document Type: Article

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Research Areas: Chemistry; Food Science & Technology

Output Date: 2025-11-26

Record 8

Title: Untargeted metabolomics reveals phenolic compound dynamics during mung bean fermentation

Author(s): Lang, SJ (Lang, Shuangjing); Liu, LJ (Liu, Lijuan); Li, ZJ (Li, Zhenjiang); Liu, SL (Liu, Shilin); Liang, JX (Liang, Jiaxin); Lu, LL (Lu, Lele); Wang, LD (Wang, Lidong)

Source: FOOD CHEMISTRY-X **Volume:** 31 **Article Number:** 103189 **DOI:** 10.1016/j.fochx.2025.103189 **Published Date:** 2025 OCT

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: This study aimed to elucidate the changes and enrichment mechanisms of phenolic in mung beans subjected to solid-state fermentation by Aspergillus Niger. Whole mung bean seeds were fermented, the total phenolic, flavonoid content and antioxidant capacity were measured during fermentation. Phenolic at different fermentation stages was performed using UHPLC-FTMS. The results showed that fermentation significantly increased the total phenolic and flavonoid content, antioxidant capacity of mung beans ($P < 0.05$). A total of 61 phenolic differental metabolites were identified, the top 22 phenolic expression levels with significantly upregulated increased significantly with the time, the 32 phenolic esexpression was significantly positively correlated with antioxidant capacity. The composition and enrichment of phenolic compounds during fermentation were primarily influenced by the biosynthesis pathways associated with flavonoids, flavonols, isoflavones, phenylpropanoids, and other plant secondary metabolites. In conclusion, SSF with Aspergillus Niger is an effective strategy for improving the phenolic content and antioxidant capacity of mung beans.

Accession Number: WOS:001615188800002

Document Type: Article

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Research Areas: Chemistry; Food Science & Technology

Output Date: 2025-11-26

Construction & Building Technology

Record 1

Title: Experimental study on thermal properties of foamed concrete with expanded perlite aggregate particle size and gradation

Author(s): Liu, YD (Liu, Yandong); Ma, LY (Ma, Lingyonxg); Jiang, W (Jiang, Wei); Li, Q (Li, Qing); Qiao, M (Qiao, Ming); Fan, SJ (Fan, Shijie); Li, D (Li, Dong)

Source: JOURNAL OF BUILDING ENGINEERING **Volume:** 114 **Article Number:** 114338 **DOI:** 10.1016/j.jobe.2025.114338 **Published Date:** 2025 NOV 15

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: This study aimed to enhance the comprehensive properties of foamed concrete by using expanded perlite as the main aggregate. The study systematically examined the effects of water-cement ratio (0.6, 0.7, 0.8), single expanded perlite aggregate particle size (0.3-0.5 mm, 0.5-1 mm, 1-3 mm), and multi-particle size combinations (based on the Andreasen-Andersen equation, grading index q of 0.2, 0.3, 0.4). The effects of these factors on dry density, water absorption, compressive strength, thermal conductivity, and microstructure were evaluated against a conventional foamed concrete sample used as the control group. Experimental findings indicated that an elevated water-cement ratio notably decreased the dry density of the foamed concrete and increased water absorption, accompanied by a declining trend in compressive strength.Regarding mechanical strength, the 0.5-1 mm single expanded perlite aggregate achieved the highest compressive strength (9.12 MPa at w/c 0.6), while the 30:40:30 multi-particle size blend showed the second highest strength (8.06 MPa). For thermal performance, a low conductivity of 0.1194 W/(m-K) was obtained with a multi-particle size combination at a water-cement ratio of 0.8. This low conductivity was associated with a uniform vesicle distribution and dense pore structure.Incorporating expanded perlite aggregate significantly enhanced the dry density and compressive strength compared to control samples, while generally resulting in lower water absorption and higher thermal conductivity at the same water-cement ratio. Optimizing expanded perlite aggregate particle size and grading improves the mechanical strength of foamed concrete while maintaining its lightweight and thermal insulation properties.

Accession Number: WOS:001596613100001

Document Type: Article

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Research Areas: Construction & Building Technology; Engineering

Output Date: 2025-11-26

Energy & Fuels

Record 1

Title: Response surface optimization of high-voltage cold plasma for accelerating degradation of halloysite-sorghum straw biodegradable mulch films

Author(s): Li, J (Li, Juan); Zhang, Y (Zhang, Yuan); Wang, M (Wang, Miao); Zhang, ZT (Zhang, Zitong); Zhang, DJ (Zhang, Dongjie)

Source: CHEMICAL ENGINEERING AND PROCESSING-PROCESS INTENSIFICATION **Volume:** 219 **Article Number:** 110600 **DOI:** 10.1016/j.cep.2025.110600 **Published Date:** 2026 JAN

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Although agricultural plastic films enhance crop yields and water retention, they also generate substantial nonbiodegradable waste and microplastic pollution, posing ecological and health risks. To address the problems of persistent agricultural plastic waste and microplastic pollution, developing rapidly degrading, eco-friendly alternatives is imperative. To that end, this study engineered a waste-sourced composite mulch film from ultramicrocrushed sorghum straw, corn starch, halloysite nanotubes, polyvinyl alcohol, glycerol, and carbendazim. High-voltage electric-field cold plasma (HVEF-CP) treatment, optimized by response surface methodology (143.17 s, 122.54 kV, 112.82 Hz), was innovatively applied as a chemical-free degradation accelerator. Hence, 72.63 % weight loss was achieved after a 126-d soil burial process, significantly exceeding the weight loss of untreated controls ($p < 0.01$). Soil metagenomics confirmed concurrent promotion of biodegradation through enrichment of the hydrolytic genera (e.g., Actinobacteria and Streptomyces) and optimization of the functional diversity. Overall, this study presents a scalable, chemical-free strategy for accelerating the degradation of biodegradable mulch films while simultaneously reducing pesticide residues. These findings underscore the dual benefits of HVEF-CP treatment in addressing plastic waste and chemical pollution, offering a promising solution for sustainable agriculture.

Accession Number: WOS:001606306600003

Document Type: Article

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Research Areas: Energy & Fuels; Engineering

Output Date: 2025-11-26

Engineering

Record 1

Title: Metaheuristic-optimized LSSVM integrated with multi-modal sensing for intelligent nutrient monitoring in saline-alkali soils

Author(s): 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)

Source: JOURNAL OF ENVIRONMENTAL CHEMICAL ENGINEERING **Volume:** 13 **Issue:** 6 **Article Number:** 120088 **DOI:** 10.1016/j.jece.2025.120088 **Early Access Date:** DEC 2025 **Published Date:** 2025 DEC

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Insufficient sampling density remains a major obstacle in developing accurate fertilizer prescription maps for saline-alkali soils, mainly due to the costly and labor-intensive of conventional chemical detection methods. This study presents a machine learning-driven in-situ detection platform that integrates a modular chassis with multiphysical-field decoupled sensing. The system achieves +/- 2 % RH control through pulsed microdomain moisture replenishment. Coupling with a humidity-dependent cementation factor reduced conductivity errors by 63 % under low-humidity conditions (7-15 % RH). Improved Wild Horse Optimization - Least Squares Support Vector Machines (IWHO-LSSVM) achieved 58.3 % faster parameter-optimization rate, reducing training time from 70.3 s to 29.3 s. Validation results showed RMSEs of 15.29 mg/kg (N), 4.62 mg/kg (P) and 13.17 mg/kg (K), with R2 ranging from 0.88 to 0.92 and RPDs exceeding 2.0. Cross-regional and cross-seasonal generalization reduced prediction errors by 47.6-58.1 %, and all improvements were statistically significant. The platform enables costeffective sampling of 5000 points per day, supporting scalable nutrient monitoring in saline-alkali soils.

Accession Number: WOS:001613726800002

Document Type: Article

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Research Areas: Engineering

Output Date: 2025-11-26

Record 2

Title: Joint resource optimization for IRS-assisted solar-powered MEC with MAPPO

Author(s): Shi, CX (Shi, Chengxi); He, QH (He, Qiaohong); Song, L (Song, Lei); Fu, S (Fu, Shuang); Yang, L (Yang, Lin)

Source: PHYSICAL COMMUNICATION **Volume:** 73 **Article Number:** 102881 **DOI:** 10.1016/j.phycom.2025.102881 **Published Date:** 2025 DEC

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: With the rapid proliferation of Internet of Things (IoT) devices and the widespread adoption of edge computing, efficiently performing task offloading and resource scheduling in environments constrained by communication quality and energy availability has become a hot research topic. We focus on an intelligent reflecting surface (IRS)-assisted mobile edge computing (MEC) network and proposes a joint optimization model that integrates task allocation, solar energy harvesting, and IRS phase control. To tackle challenges such as the vast policy space and dynamically changing environment in multi-user, multi-resource collaborative optimization, the Multi-Agent Proximal Policy Optimization (MAPPO) algorithm is introduced, enabling devices to adaptively learn strategies in dynamic conditions. Simulation results demonstrate that the proposed optimization algorithm outperforms comparison algorithms in terms of delay and energy consumption, and also exhibits faster convergence and higher policy stability, validating the effectiveness and superiority of MAPPO in IRS-assisted MEC networks.

Accession Number: WOS:001599861200001

Document Type: Article

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Research Areas: Engineering; Telecommunications

Output Date: 2025-11-26

Record 3

Title: Synergistic integration of melatonin, copper nanoparticles, and Bacillus velezensis mitigates anthracnose and microplastic stress in chili: A novel eco-friendly strategy for sustainable crop protection

Author(s): Muhae-Ud-Din, G (Muhae-Ud-Din, Ghulam); Li, X (Li, Xiang); Zhong, FH (Zhong, Fuhan); Chen, DL (Chen, Delai); Nisa, ZU (Nisa, Zaib-un); Smagghe, G (Smagghe, Guy); Sun, MZ (Sun, Mingzhe)

Source: JOURNAL OF HAZARDOUS MATERIALS **Volume:** 498 **Article Number:** 139838 **DOI:** 10.1016/j.jhazmat.2025.139838 **Early Access Date:** SEP 2025 **Published Date:** 2025 OCT 15

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Anthracnose disease, caused by Colletotrichum capsici, severely reduces chili pepper growth and yield worldwide. Although melatonin (MT), copper nanoparticles (CuNPs), and Bacillus velezensis exhibit individual antifungal activity, their combined efficacy under environmental stress has not been explored. Here, we report for the first time the synergistic application of MT (100 mu M), CuNPs (75 mg/L), and B. velezensis (108 CFU/mL) (MCB) to suppress anthracnose under microplastic (MPs) stress, addressing both biotic and abiotic stress simultaneously. The MCB treatment significantly inhibited C. capsici by increasing fungal membrane permeability and reducing disease incidence. MPs and pathogen stress impaired plant morpho-physiological traits, while MT, CuNPs, and B. velezensis restored plant vigor. The MCB combination yielded the strongest improvements in photosynthetic capacity, chlorophyll content, hormonal balance, defense gene expression, antioxidant activity, and lignin accumulation, while reducing malondialdehyde and reactive oxygen species. Secondary metabolites and mineral contents, suppressed under stress, were also enhanced. This study presents a novel, integrative strategy combining biomolecule signaling, microbial biocontrol, and nanotechnology to mitigate fungal infection and MP stress simultaneously, offering a framework for resilient and sustainable crop protection in environmentally challenging agricultural systems.

Accession Number: WOS:001585523300002

Document Type: Article

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Research Areas: Engineering; Environmental Sciences & Ecology

Output Date: 2025-11-26

Environmental Sciences & Ecology

Record 1

Title: New insights into cadmium-modulated relationships of phosphorus-nitrogen functions under herbicide disturbance in cornfields

Author(s): Li, Y (Li, You); Wang, YL (Wang, Yonglu); Zhang, FS (Zhang, Fengsong); Liao, XY (Liao, Xiaoyong); Zhang, SQ (Zhang, Shaoqing); Fu, J (Fu, Jian); Yang, KJ (Yang, Kejun); Wei, Z (Wei, Zhuo); He, LX (He, Lixia); Zhu, SL (Zhu, Shiliang)

Source: ECOTOXICOLOGY AND ENVIRONMENTAL SAFETY **Volume:** 303 **Article Number:** 105556 **DOI:** 10.1016/j.jpain.2025.105556 **Published Date:** 2025 SEP 15

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Metallic micronutrients probably mediate the nutrient functions in soils with long-term herbicide application. However, will hazardous metal cadmium have a synergistic effect with herbicides, which amplifies the interference on soil nitrogen and phosphorus cycling functions? This study conducted a nationwide investigation to

characterize the accumulation patterns of two typical herbicides (atrazine and nicosulfuron), cadmium, and metal micronutrients (iron, manganese, copper, and zinc) in maize fields. It specifically elucidated the individual disruptive effects of herbicides, the interaction mechanisms between herbicides and metals (particularly cadmium), and the key pathways and drivers influencing soil nitrogen-phosphorus functional linkages. Results showed that nicosulfuron and atrazine residues were negatively correlated with nitrogen and phosphorus functional genes, while the cadmium content was positively correlated with these functional gene abundance. Additionally, cadmium acted antagonistically with atrazine in terms of nutrient cycling functions. This is further verified by the higher sensitivity values of functional genes in the north than those in the south. Moreover, the results of the structural equation model showed that the abundance of nirK and nirS genes was significantly correlated with the abundance of the phoC gene in maize fields and herbicides, cadmium, iron, and zinc affected the phoC gene by affecting the nirS and nirK genes. This study provides novel insights by demonstrating that soil cadmium, analogous to beneficial metal micronutrients, effectively alleviates herbicide-induced (especially atrazine) disruptions to the relationships between nitrogen and phosphorus cycling functions in maize fields.

Accession Number: WOS:001578435200001

Document Type: Article

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Research Areas: Environmental Sciences & Ecology; Toxicology

Output Date: 2025-11-26

Record 2

Title: Does Air pollution affect the green innovation of industrial enterprises? Insights from Urban Sewage Control Policies in China

Author(s): Zhang, XL (Zhang, Xilin); Li, D (Li, Ding); Yan, H (Yan, Han); Ma, SL (Ma, Shenglin)

Source: GLOBAL NEST JOURNAL **Volume:** 27 **Issue:** 6 **Article Number:** 07317 **DOI:** 10.30955/gnj.07317 **Published Date:** 2025 JUL

Times Cited in Web of Science Core Collection: 5

Total Times Cited: 5

Abstract: Environmental protection and technological innovation are key strategies for transforming economic development and have long been a focus of research. Environmental regulation plays a vital role in addressing the externalities of environmental governance and fostering corporate innovation. This study analyzes panel data from 28 manufacturing sectors in Shandong Province over the period from 2012 to 2023. It assesses the changes in environmental regulation levels that industrial firms face, focusing on pollution reduction initiatives under China's emission control policies from the 12th to the 14th Five-Year Plans. Using the System GMM method, the study investigates the impact and mechanisms of air pollution environmental regulation (APER) on the efficiency of green innovation (GIE) in industrial enterprises, while also considering the spatial and temporal dynamics of air pollution. The results show that WPER significantly enhances GIE at the 1% significance level. Threshold analysis reveals a notable double-threshold effect of industrial agglomeration on the influence of APER on green innovation efficiency. Specifically, when industrial agglomeration is below a certain threshold, APER promotes industrial innovation. However, when the industrial agglomeration surpasses another threshold, the positive effect of APER on GIE diminishes. This study provides valuable insights into the effectiveness of APER in tackling environmental pollution and offers policy recommendations for promoting corporate innovation and balanced environmental development.

Accession Number: WOS:001588004400007

Document Type: Article

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Research Areas: Environmental Sciences & Ecology

Output Date: 2025-11-26

Food Science & Technology

Record 1

Title: Preparation of mung bean antioxidant peptides and the mechanism by which they improve intestinal inflammation in Drosophila

Author(s): Wang, XC (Wang, Xiao Chun); Jiang, YJ (Jiang, Yingjun); Wang, CY (Wang, Changyuan)

Source: FOOD RESEARCH INTERNATIONAL **Volume:** 221 **Article Number:** 117283 **DOI:** 10.1016/j.foodres.2025.117283 **Early Access Date:** DEC 2025 **Published Date:** 2025 DEC **Part:** 1

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Intestinal inflammation is a complex chronic condition with an uncertain pathogenesis, and current pharmacological treatments are often associated with significant adverse effects and drug resistance. Owing to their high efficacy, bioactive peptides have emerged as promising candidates for intestinal inflammation regulation. Here, we aimed to explore the potential of mung bean peptides in alleviating intestinal inflammation. We prepared Neutrase-hydrolyzed mung bean peptides (NMP) and confirmed that these peptides were smaller in particle size and molecular weight than untreated mung bean protein. In vitro assays demonstrated the improved antioxidant activities of NMP. In an in vivo model of intestinal inflammation induced by dextran sulfate sodium (DSS), NMP treatment markedly increased survival rates and preserved the intestinal structure. Metabolomic analysis revealed that NMP significantly altered the metabolite profile of the DSS-induced inflammation model, specifically by modifying key metabolic processes, including amino acid and linoleic acid metabolism. This study provides a theoretical basis for the use of mung bean resources and the application of food-derived functional components in the treatment of intestinal inflammation.

Accession Number: WOS:001583182500038

Document Type: Article

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Research Areas: Food Science & Technology

Output Date: 2025-11-26

Record 2

Title: Dynamic regulation of mung bean globulin amyloid fibrillation by Gallic acid: Structural and functional insights

Author(s): Jiang, P (Jiang, Peng); Xu, QP (Xu, Qingpeng); Zhang, S (Zhang, Shu); Fu, TX (Fu, Tianxin); Diao, JJ (Diao, Jingjing); Li, ZJ (Li, Zhijiang); Wang, CY (Wang, Changyuan)

Source: FOOD RESEARCH INTERNATIONAL **Volume:** 221 **Article Number:** 117377 **DOI:** 10.1016/j.foodres.2025.117377 **Published Date:** 2025 DEC **Part:** 2

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Amyloid fibrils derived from plant proteins offer a novel strategy for constructing food systems with both structural and functional properties. However, the stage-specific effects of polyphenols on protein fibrillation remain unclear. In this study, gallic acid (GA) was introduced at the initial stage (MBGF0), the end of the lag phase (MBGF15), and the end of the growth phase (MBGF240) to investigate its regulatory effect on mung bean globulin fibrillation (MBGF). Results showed that GA addition at MBGF0 prolonged the lag phase, whereas GA addition at MBGF15 accelerated the fibrosis process. Moreover, GA addition at different fibrillation stages reduced Thioflavin T fluorescence intensity, beta-sheet content, and surface hydrophobicity, indicating that GA disrupted the ordered assembly of MBGF. Molecular dynamics simulations revealed that GA binding induced local conformational rearrangements of MBG, reduced conformational fluctuations, and enhanced structural stability. Functional analysis showed that GA improved the emulsifying properties of complexes at different fibrillation stages, with MBGF240-GA complex exhibiting the highest emulsifying activity index (23.50 m2/g) and emulsifying stability index (84.52 %), as well as excellent rheological properties. In summary, this study elucidates the dynamic regulatory effects of GA on mung bean globulin fibrillation and provides a theoretical basis for polyphenol-mediated modulation of protein structure and functionality.

Accession Number: WOS:001595352300008

Document Type: Article

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Research Areas: Food Science & Technology

Output Date: 2025-11-26

Record 3

Title: N-terminal modified coix seed peptides: enhanced transepithelial transport in Caco-2 cell monolayers and modulates key targets in T2DM

Author(s): Zhang, S (Zhang, Shu); Yu, SB (Yu, Shibo); Wang, X (Wang, Xuan); Zhang, LX (Zhang, Lixiang); Fu, TX (Fu, Tianxin); Li, ZJ (Li, Zhijiang); Wang, CY (Wang, Changyuan); Zhang, DJ (Zhang, Dongjie)

Source: JOURNAL OF FUNCTIONAL FOODS **Volume:** 135 **Article Number:** 107071 **DOI:** 10.1016/j.jff.2025.107071 **Published Date:** 2025 DEC

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: LPFYPN, a novel hypoglycaemic peptide found in Coix seeds, inhibits Dipeptidyl peptidase IV (DPP-IV). This study explored how N-terminal chemical modification impacts LPFYPN's inhibitory activity, type, mechanism, cellular bioavailability, degradation, absorption, and transport using simulated Caco-2 cell monolayer models. Results showed LPFYPN was fully absorbed and utilized by Caco-2 monolayers, but its permeability represented only 8.8 % of the initial concentration. LPFYPN was mainly degraded in the intestine, creating LPFYP, PFYPN, and PFYPD peptides, which facilitated transmembrane transport via paracellular diffusion. Multidrug-resistant proteins mediated PFYPD's efflux absorption. The primary reasons for the limited inhibitory activity of the LPFYPN are the weaker interaction between its degradation products and DPP-IV, as well as the reduction in tight binding sites with the enzyme. N-terminal modifications (Methoxy polyethylene glycol carboxyl - LPFYPN and Selenocysteine - LPFYPN,mPEG-LPFYPN and SeCys-LPFYPN) improved DPP-IV inhibitory activity, with IC50 values of 72.59 mu M and 57.29 mu M respectively. However, acetylated modified peptides (Ac-LPFYPN) decreased, with an IC50 value of 104.43 mu M. However, absorption of the three modified peptides improved significantly, with the apparent permeability coefficient (Papp) increasing by 1.15- to 2.53-fold, and better regulation of DPP-IV and GLP-1 protein levels. Ac-LPFYPN's transport mechanism mirrored parent peptides. SeCys-LPFYPN was involved in endocytosis as a transport pathway, and mPEG-LPFYPN's main transport mechanism was endocytosis-mediated, with P-glycoprotein mediating efflux.

Accession Number: WOS:001611903500002

Document Type: Article

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Research Areas: Food Science & Technology; Nutrition & Dietetics

Output Date: 2025-11-26

Record 4

Title: Metagenomics and binning analysis unveiled the diversity and transfer patterns of antibiotic resistance genes in traditional pickled vegetables

Author(s): Wang, H (Wang, Hui); Mu, XD (Mu, Xindi); Su, TT (Su, Tingting); Yang, XY (Yang, Xiyuan); Xu, L (Xu, Lei); Yao, D (Yao, Di); Li, LY (Li, Liangyu)

Source: FOOD BIOSCIENCE **Volume:** 73 **Article Number:** 107709 **DOI:** 10.1016/j.fbio.2025.107709 **Early Access Date:** NOV 2025 **Published Date:** 2025 NOV

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Antimicrobial resistance (AMR) is a public health problem of global concern. The presence of antibiotic resistance genes (ARGs) in food may aggravate the spread of AMR. Understanding the distribution and transfer of drug-resistant bacteria and ARGs in pickled vegetable foods was critical for food quality and safety. Therefore, this study used metagenomic sequencing, binning technology, and antibiotic susceptibility tests to explore the distribution and transfer of drug-resistant bacteria and ARGs in pickled vegetable foods. The results showed that Bacillota, Lactobacillus, and Salmonella were the dominant bacteria in all samples. A total of 12 ARG types and 52 ARG subtypes were identified. The abundance of bacitracin ARGs in high-salt samples (<2 %) was higher, and multidrug ARGs in low-salt samples (7 %-10 %) was higher. The most abundant ARG subtypes, baca and acrb, were associated with Salmonella. Furthermore, a total of 34 metagenome assembly genomes (MAGs) were obtained by metagenomic binning. MAG8 and MAG25, which carried the largest number of ARGs, virulence factors (VFs), and MGEs, were all derived from Vibrio. More importantly, horizontal gene transfer (HGT) could occur between microorganisms in pickled vegetable samples. In addition, most of the 25 isolates were resistant to bacitracin and multidrug antibiotics. Levilactobacillus brevis PNS3 carried a large number of multidrug ARG genes (patA, macB) and transposable MGE genes (recT, SadA). The results of the drug resistance phenotype were consistent with the results of the drug resistance genotype. These findings suggested that there was a risk of ARGs being carrying and spreading in pickled vegetable foods.

Accession Number: WOS:001594440400001

Document Type: Article

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Research Areas: Food Science & Technology

Output Date: 2025-11-26

Record 5

Title: Water-Assisted Microwave Processing: Rapid Detoxification and Antioxidant Enhancement in Colored Kidney Beans

Author(s): Yu, S (Yu, Song); Zhang, YT (Zhang, Yutao); Zhang, YF (Zhang, Yifei); Zhang, CY (Zhang, Chunyu); Liu, XR (Liu, Xinran); Wang, YJ (Wang, Yingjie); Meng, FD (Meng, Fandi); Yu, LH (Yu, Lihe)

Source: FOODS **Volume:** 14 **Issue:** 20 **Article Number:** 3557 **DOI:** 10.3390/foods14203557 **Published Date:** 2025 OCT 18

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: This study aimed to develop an industrially viable method for rapid detoxification of raw kidney beans (Phaseolus vulgaris L.) while enhancing nutritional properties. Through optimized 5 min water soaking combined with intermittent microwaving (500 W, 5 min), we achieved significant reductions in key antinutrients, namely phytic acid (43-49%), tannins (74-90%), and saponins (59-68%)-all below safety thresholds-concurrently elevating antioxidant capacity (e.g., Ferric Reducing Antioxidant Power: +66-115%) across four colored varieties. Metabolomic analysis of 412 identified metabolites revealed substantial accumulation of key antioxidants including glutathione and quercetin derivatives. Pathway analysis demonstrated dual mechanisms: (1) Detoxification via activated phenylpropanoid biosynthesis degrading tannin precursors and glutathione metabolism reducing phytate; (2) Nutrient enrichment through upregulated phenolic biosynthesis and color-specific flavonoid/betalain pathways. This integrated approach achieves comparable detoxification to 30 min boiling in just 5 min, establishing water-assisted microwave processing as an efficient strategy for industrial-scale production of safer, nutrient-enhanced legumes.

Accession Number: WOS:001602172100001

Document Type: Article

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Research Areas: Food Science & Technology

Output Date: 2025-11-26

Record 6

Title: Investigating the effect of MAG/(NaPO3)x on the physicochemical and structural properties of rice starch-protein rice and improving the mechanism in each zone during the extrusion process

Author(s): Wang, LS (Wang, Li-shuang); Jia-Sun (Jia-Sun); Jia, JH (Jia, Jin-hui); Huo, JJ (Huo, Jin-jie); Duan, YM (Duan, Yu-min); Na-Wang (Na-Wang); Yu, XS (Yu, Xiao-shuai); Xiao, ZG (Xiao, Zhi-gang); Wang, Y (Wang, Ying); Tian, XL (Tian, Xiao-ling)

Source: FOOD STRUCTURE-NETHERLANDS **Volume:** 46 **Article Number:** 100

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468 **DOI:** 10.1016/j.foostr.2025.100468 **Early Access Date:** SEP 2025 **Published Date:** 2025 OCT

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: The underlying mechanism of the interactions among rice starch (RS), glutelin (G), and texture improvement, during the formation, physicochemical, and structural properties of ternary reconstituted rice, has not been confirmed systematically. Herein, a comprehensive assessment was conducted to investigate the effects of monoacylglycerol (MAG) and composite phosphate (NaPO3)x on the characteristics and properties of reconstituted rice in each zone during extrusion processing. The results demonstrated that MAG and (NaPO3)x contributed to improving the hardness, chewiness, and springiness, while reducing the adhesiveness from 7.9 mJ to 1.07 mJ (for MAG-rice) and 1.6 mJ (for (NaPO3)x-rice), respectively. From the mixing zone to the extrudate zone, MAG acted as an embedded entity and was tightly bonded to rice starch-glutelin (RS/G) molecules via hydrogen bonding and hydrophobic interactions, which enhanced the tightness and flexibility of RS/G networks, reducing in a microstructure with smoother surface performance and fewer wrinkled protrusions. Meanwhile, (NaPO3)x interacted with RS/G by electrostatic interaction, beginning from the melting zone, promoting the formation of the (NaPO3)x-rice with a more solid and dense performance microstructure. In addition, compared with RS/G-rice, both MAG-rice and (NaPO3)x-rice exhibited higher viscosity coefficients, storage moduli (G'), and loss moduli (G ''), lower tans values (indicating more solid-like behavior), better thermal stability, and larger particle sizes. Furthermore, MAG-rice and (NaPO3)x-rice showed increased rapid viscosity, setback viscosity, and regularity of intermolecular arrangement. Among them, the improvement effect of MAG on RS/G was more prominent than that of (NaPO3)x. This study provides theoretical guidance for designing and producing reconstituted rice products with rice starch and glutelin as the skeletal structure.

Accession Number: WOS:001586847400001

Document Type: Article

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Research Areas: Food Science & Technology

Output Date: 2025-11-26

Record 7

Title: Lipidomic Analysis Reveals the Anti-Obesity and Hepatoprotective Effects of Flavonoid Mimetic Components in Adzuki Beans on High-Fat Diet-Induced Obese Mice

Author(s): Zhang, JY (Zhang, Jiayu); Jiang, XJ (Jiang, Xiujie); Xu, QP (Xu, Qingpeng); Li, WD (Li, Weidong); Zhang, DJ (Zhang, Dongjie)

Source: FOODS **Volume:** 14 **Issue:** 18 **Article Number:** 3191 **DOI:** 10.3390/foods14183191 **Published Date:** 2025 SEP 13

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Total Times Cited: 0

Abstract: Obesity and overweight have increasingly posed a serious challenge to public health security. This study systematically evaluated the reversal and regulatory effects of a composite flavonoid component mimicking the composition of adzuki bean flavonoids on high-fat diet (HFD)-induced obesity, related lipid metabolism disorders, and impaired liver function, based on lipid metabolomics and an HFD-induced obese mouse model. The results demonstrated that sustained HFD intake led to significant weight gain, increased adiposity index, dyslipidemia, and altered brown adipose tissue (BAT) cell status in mice, while also exerting adverse effects on hepatic lipid deposition and the lipid metabolic profile associated with liver fibrosis. Intervention with an adzuki bean flavonoid mimic (ABFM) effectively prevented further weight gain and ameliorated abnormal expression of serum lipid and liver function-related indicators. Furthermore, we found that ABFM alleviated HFD-induced liver damage and mitigated the whitening tendency of brown adipose tissue. Lipidomics analysis revealed that ABFM intake significantly improved abnormal hepatic lipid metabolic profiles, notably downregulating the expression levels of diacylglycerol (DG) and phosphatidylglycerol (PG), while markedly ameliorating sphingolipid metabolism disorders and ceramide (Cer) levels, which are highly associated with liver fibrosis. These findings further elucidate the mechanisms by which adzuki bean flavonoid components improve diet-induced obesity and associated liver injury, providing a theoretical basis for exploring safe and effective dietary intervention strategies based on plant flavonoids.

Accession Number: WOS:001580989200001

Document Type: Article

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Research Areas: Food Science & Technology

Output Date: 2025-11-26

Record 8

Title: Microwave treatment modulates in vitro dynamic gastrointestinal migration of sorghum polyphenols and influences gut microbiota metabolism

Author(s): Xu, L (Xu, Lei); Dai, LY (Dai, Lingyan); Yao, D (Yao, Di); Hu, YY (Hu, Yuyuan); Zhao, WH (Zhao, Wenhong); Song, XJ (Song, Xuejian); Li, ZJ (Li, Zhijiang)

Source: FOOD RESEARCH INTERNATIONAL **Volume:** 221 **Article Number:** 117278 **DOI:** 10.1016/j.foodres.2025.117278 **Early Access Date:** AUG 2025 **Published Date:** 2025 DEC **Part:** 2

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Gastrointestinal digestion is indispensable for the utilization of polyphenols from the diet. Polyphenol migration in the gastrointestinal tract, potential antioxidant activity, colonic accumulation, and regulation of short-chain fatty acids (SCFAs) by polyphenols were systematically explored in steamed sorghum (Nor-S) and microwaved steamed-sorghum (Mic-S). Relatively rapid gastric emptying and fragmented chyme of Mic-S liberated higher polyphenols (8.06 mg GAE/g DW) and antioxidant activity in the intestinal supernatant. Compared with the stomach, the bioaccessibility of intestinal polyphenols was significantly higher. Flavones, isoflavones, and flavanones were enriched in intestinal supernatant of Mic-S, while chyme was richer in phenolic acids and flavone glycosides (o-glucoside and c-glucoside). Moreover, fecal fermentation revealed higher bioaccessibility in Mic-S, which was attributed to the lower-size chyme that facilitated the extensive metabolism of Bifidobacterium, Megamonas, and Segatella. The hydroxybenzoic, hydroxycinnamic, and monomeric flavones enriched in the colon were correlated with

Bifidobacterium and Bacteroides. Additionally, these low-molecular polyphenols indirectly regulated the production of SCFAs through amino acid metabolism and glucose metabolism pathways. The above findings suggested the enhancing effect of microwave treatment on the gastrointestinal accessibility of foodderived polyphenols, and provided theoretical support for the development of grain foods related to precision nutrition and intestinal health.

Accession Number: WOS:001580993700005

Document Type: Article

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Research Areas: Food Science & Technology

Output Date: 2025-11-26

Immunology

Record 1

Title: Lipid nanoparticle encapsulated membrane-anchored E2 mRNA vaccine elicits cross-protective immune responses against bovine viral diarrhoea virus infection in calves

Author(s): Le, T (Le, Ting); Jia, B (Jia, Bin); Sun, C (Sun, Chao); Zhou, YF (Zhou, Yongfei); Qi, YL (Qi, Yinglin); Liu, H (Liu, Hao); Bian, HQ (Bian, Haiqiao); Tian, CY (Tian, Chongyu); Wang, J (Wang, Jun); Xue, F (Xue, Fei); Zhu, YM (Zhu, Yuanmao); Chang, JT (Chang, Jitao); Luan, YF (Luan, Yunfei); Zhang, ZX (Zhang, Zexin); Li, ZD (Li, Zhendong); Tai, WB (Tai, Wanbo); Jiang, ZG (Jiang, Zhigang); Yin, X (Yin, Xin)

Source: VACCINE **Volume:** 66 **Article Number:** 127841 **DOI:** 10.1016/j.vaccine.2025.127841 **Published Date:** 2025 NOV 14

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Bovine viral diarrhoea virus (BVDV) imposes significant economic burdens and biosecurity risks on the global animal trade and biological product industries. Addressing the challenges posed by the virus's complex subgenotypes requires the development of cross-protective vaccines. In this study, we evaluated the immunogenicity of two lipid nanoparticle-encapsulated mRNA (mRNA-LNP) vaccines: a full-length, membrane-anchored E2 (mE2) mRNA-LNP vaccine and a secretory, truncated E2 (tE2) mRNA-LNP vaccine, in both mice and calves. mE2 and tE2 mRNA-LNP induced robust E2-specific IgG antibodies and neutralising antibodies in mice. Neutralising antibody data further demonstrated that the mE2 mRNA-LNP exhibited superior immunogenicity compared with the tE2 mRNA-LNP in calves. Notably, administering two doses of the 100 mu g mE2 mRNA-LNP effectively protected calves against BVDV challenge. Furthermore, the mE2 mRNA-LNP elicited robust cross-neutralising antibodies against multiple BVDV-1 and BVDV-2 strains for up to six months and induced promising cross-reactive cellular immune responses. The safety of mE2 mRNA-LNP was confirmed through the administration of two high doses (500 mu g) in calves without adverse effects. Importantly, the rate of BVDV infection within the mE2 mRNALNP-vaccinated herd declined significantly, demonstrating that this vaccine effectively reduces BVDV transmission in field. In conclusion, this study comprehensively highlights the safety, efficacy, and broad crossimmune responses of the mE2 mRNA-LNP vaccine platform for preventing and controlling BVDV in calves.

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Document Type: Article

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Research Areas: Immunology; Research & Experimental Medicine

Output Date: 2025-11-26

Record 2

Title: Global Transmission, Prevention, Control, and Treatment of Mpox Virus in 2025: A Comprehensive Review from Infection Mechanisms to Vaccine Development

Author(s): Quan, Q (Quan, Quan); Wu, N (Wu, Nan); Luo, YH (Luo, Ying-Hua); Tang, YJ (Tang, Yan-Jun); Liu, YZ (Liu, Yan-Zhi); Huang, XC (Huang, Xi-Chun); Li, JH (Li, Jun-Hao); Ren, WX (Ren, Wan-Xia); Jin, CH (Jin, Cheng-Hao)

Source: VACCINES **Volume:** 13 **Issue:** 10 **Article Number:** 1071 **DOI:** 10.3390/vaccines13101071 **Published Date:** 2025 OCT 20

Times Cited in Web of Science Core Collection: 1

Total Times Cited: 1

Abstract: The World Health Organization (WHO) declared the mpox (MPX) outbreak a public health emergency of international concern (PHEIC) on 23 July 2022, and 14 August 2024, respectively, underscoring the confirmed and concerning global spread of the disease. A gap exists in our fundamental understanding of the mpox virus (MPXV), despite its genetic relatedness to the variola virus (VARV). This knowledge deficit is evident in the performance of current medical countermeasures; vaccines and antiviral therapies adapted from smallpox programs demonstrate only partial efficacy and are constrained by issues of safety and suboptimal effectiveness against MPXV. In this context, the development of MPX-specific vaccines and antiviral drugs has become a critical priority in the global effort to combat MPX. However, MPXV employs multiple strategies to evade host immune responses, such as producing specific and poxvirus homologous proteins that suppress both innate immunity (including the six principal innate immune signaling pathways and antiviral strategies, notably the interferon [IFN] pathway) and adaptive immunity, thereby complicating vaccine and drug development. Insights from research on vaccinia virus (VACV) and VARV may inform the investigation of MPXV pathogenesis and immune evasion mechanisms. Drawing on relevant scientific literature, this review systematically examines key aspects of MPX infection, pathogenicity, and immune evasion, as well as the coordination between innate and adaptive immune responses. Furthermore, this review elucidates the current application and deployment landscape of the three principal therapeutics and three major vaccines for MPX, aiming to provide a theoretical foundation for future research and development of vaccines and targeted antiviral agents.

Accession Number: WOS:001602753500001

Document Type: Review

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Research Areas: Immunology; Research & Experimental Medicine

Output Date: 2025-11-26

Record 3

Title: Pregnane X receptor activation attenuates intestinal inflammation: The role of pyroptosis and necroptosis inhibition

Author(s): Zheng, YW (Zheng, Yuwei); Qiao, CY (Qiao, Chunyu); Xiao, WZ (Xiao, Wanzhe); Liu, BX (Liu, Bingxue); Long, WY (Long, Wenyuan); Zhang, JX (Zhang, Jiexing); Lian, S (Lian, Shuai); Deng, XM (Deng, Xuming); Lv, HM (Lv, Hongming)

Source: INTERNATIONAL IMMUNOPHARMACOLOGY **Volume:** 166 **Article Number:** 115620 **DOI:** 10.1016/j.intimp.2025.115620 **Early Access Date:** OCT 2025 **Published Date:** 2025 DEC 3

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Intestinal inflammation compromises epithelial barrier integrity and disrupts immunological homeostasis, escalating the risk of severe gastrointestinal disorders. The Pregnane X Receptor (PXR), a xenobiotic-sensing nuclear receptor, is critical for maintaining intestinal structural integrity and suppressing inflammation, although its mechanistic underpinnings remain poorly characterized. In this study, we explored the therapeutic potential of PCN, a PXR agonist, in mitigating intestinal inflammation using two models: enterohaemorrhagic Escherichia coli O157:H7 (EHEC)-infected mice and lipopolysaccharide (LPS)-stimulated intestinal epithelial cells. PCN administration significantly improved survival rates in EHEC-challenged mice, alleviated intestinal mucosal damage, and restored tight junction protein (ZO-1 and occludin) expression. Concurrently, PCN attenuated Paneth cell dysfunction, macrophage hyperactivation, and pro-inflammatory mediator release (e.g., TNF-alpha, IL-6). In vitro, PCN counteracted LPS-induced barrier disruption and inflammation by suppressing the TLR4/NF-kappa B/MAPK axis and downstream pyroptotic (NLRP3/caspase-1/GSDMD), and necroptotic (RIPK1/ RIPK3/MLKL) signaling cascades. Interestingly, both EHEC infection and LPS stimulation impaired PCN-driven PXR activation. While PCN rescued EHEC-induced mortality, histological damage, and barrier dysfunction in wild-type mice, its protective effects were markedly diminished in PXR-knockout (PXR-/-) mice. Furthermore, PXR silencing in cultured cells abolished PCN-mediated inhibition of NF-kappa B, NLRP3 inflammasome, and necroptosis pathways. These results demonstrate that PXR activation coordinately blocks pyroptosis and necroptosis by modulating the TLR4/NF-kappa B/MAPK-NLRP3/caspase-1/GSDMD-RIPK1/RIPK3/MLKL axis, thereby preserving intestinal homeostasis. This dual-pathway targeting positions PXR as a promising therapeutic candidate for inflammatory bowel diseases.

Accession Number: WOS:001590348800001

Document Type: Article

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Research Areas: Immunology; Pharmacology & Pharmacy

Output Date: 2025-11-26

Record 1

Title: The Effects of p-Coumaric Acid on the Quality of Cryopreserved Boar Spermatozoa

Author(s): Li, H (Li, Han); Zhang, H (Zhang, Han); Dong, YY (Dong, Yingying); Li, YB (Li, Yanbing); Li, JC (Li, Jingchun)

Source: BIOLOGY-BASEL **Volume:** 14 **Issue:** 10 **Article Number:** 1406 **DOI:** 10.3390/biology14101406 **Published Date:** 2025 OCT 13

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: This research explored the effects of different concentrations of p-coumaric acid (PCA) on the quality of frozen-thawed boar semen. Boar sperm samples were pre-treated with different concentrations of PCA (0, 30, 60, 90, 120 mu g/mL) prior to the freezing process. Subsequently, multiple parameters were analyzed post-freeze-thawing, including sperm morphological and kinetic characteristics, acrosome and membrane integrity, mitochondrial function, DNA integrity, antioxidant enzyme activities, the expression levels of the BCL-2, BAX, and Caspase-3 proteins, the in vitro fertilization rate of porcine oocytes, and the embryo cleavage rate. The findings indicated that, compared with the control group, the addition of 90 mu g/mL PCA led to significant improvements in several key aspects. Sperm motility, average path velocity, straight-line velocity, curvilinear velocity, and beat cross frequency were all notably enhanced. Moreover, parameters related to sperm quality, such as acrosome integrity, plasma membrane integrity, mitochondrial activity, and DNA integrity, also showed significant increases (all $p < 0.05$). In terms of antioxidant capacity, the 90 mu g/mL PCA treatment significantly elevated the total antioxidant capacity, as well as the activities of superoxide dismutase, glutathione peroxidase, and catalase. Simultaneously, it caused a significant reduction in the contents of malondialdehyde and hydrogen peroxide ($p < 0.05$). Regarding protein expression, the addition of 90 mu g/mL PCA significantly upregulated the expression level of the BCL-2 protein, while downregulating the relative expression levels of BAX and Caspase-3 ($p < 0.05$). Additionally, this concentration of PCA significantly improved the in vitro fertilization rate of porcine oocytes and the embryo cleavage rate ($p < 0.05$). In conclusion, incorporating PCA into the semen extender can potentially be advantageous for the cryopreservation of boar sperm, with 90 mu g/mL being the optimal concentration.

Accession Number: WOS:001603797300001

Document Type: Article

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Research Areas: Life Sciences & Biomedicine - Other Topics

Output Date: 2025-11-26

Materials Science

Record 1

Title: Porosity, microstructure and performance control of laser metal deposition 17-4PH stainless steel components using laser shock forging method

Author(s): Gao, C (Gao, Chuang); Li, QD (Li, Qing-da); Song, YW (Song, Ya-wei); Zhang, XC (Zhang, Xiao-chen); Yao, J (Yao, Jun); Huan, PC (Huan, Peng-cheng); Wei, X (Wei, Xia); Wang, XN (Wang, Xiao-nan)

Source: MATERIALS LETTERS **Volume:** 403 **Article Number:** 139563 **DOI:** 10.1016/j.matlet.2025.139563 **Published Date:** 2026 JAN 15

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: This study introduces laser shock forging to perform in-situ peening on the molten pool and high-temperature solid phase zone during cladding, investigating porosity suppression and mechanical properties enhancement in 17-4PH stainless steel. The results demonstrate that laser shock forging effectively suppresses porosity defects and refines grains in the clad layer. The tensile strength of the clad layer increases from 865 MPa to 1067 MPa, which represents a 23 % enhancement. Fracture initiated at delta-ferrite and martensite interfaces where strain incompatibility induced stress concentration, forming crack nucleation sites that propagated to failure.

Accession Number: WOS:001585981900001

Document Type: Article

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Research Areas: Materials Science; Physics

Output Date: 2025-11-26

Record 2

Title: Entangled value: actor-network configurations and ESG pathways in China's textile value chain

Author(s): Ma, SL (Ma, Shenglin); Li, D (Li, Ding); Yan, H (Yan, Han)

Source: JOURNAL OF THE TEXTILE INSTITUTE **DOI:** 10.1080/00405000.2025.2587392 **Early Access Date:** NOV 2025 **Published Date:** 2025 NOV 9

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Environmental, Social, and Governance (ESG) is a critical criterion for evaluating corporate non-financial performance. For the textile sector, which is highly concentrated in global resource consumption and pollution emissions, the transition toward sustainable development presents particularly severe challenges. Traditional research primarily focuses on the linear effects of single factors, often failing to capture the non-linear interplay and complex causality among multiple influencing conditions. Based on corporate governance and market-driven perspectives, this study innovatively integrates Actor-Network Theory (ANT) to construct a multi-actor governance network. It then employs fuzzy-set Qualitative Comparative Analysis (fsQCA) to systematically explore the influence mechanism of multiple antecedent conditions (including external regulation, internal incentives, and market drive) on the ESG performance of China's A-share listed firms in the textile supply chain. The results indicate that no single factor (such as government regulation, social supervision, consumers, investors, the board of directors, or digital technology) is a necessary condition for achieving high ESG performance, thereby confirming the configurational complexity underlying high ESG outcomes. We identify two core sufficient paths leading to high performance: the 'internal-driven configuration,' centered on internal governance and digital technology, and the 'external supervision-market-driven configuration,' characterized by external governance and market drive. Furthermore, our findings reveal a significant asymmetry in the ESG performance of these textile firms. A group of firms, due to the absence of critical governance elements, follow an 'element-missing path,' resulting in persistently low ESG performance. This study not only enriches the configurational theory of ESG performance formation, particularly for the complex governance systems of highly polluting industries like textiles, but also addresses the limitations of traditional linear methods in revealing diverse driving pathways. Ultimately, it provides differentiated policy tools and practical references for promoting the green transition of the textile industry and its related value chain enterprises.

Accession Number: WOS:001616081000001

Document Type: Article; Early Access

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Research Areas: Materials Science

Output Date: 2025-11-26

Parasitology

Record 1

Title: Molecular characteristics and zoonotic potential of enteric protozoans in domestic small ruminants in Heilongjiang Province, Northeast China

Author(s): Hou, MR (Hou, Meiru); Liu, XW (Liu, Xuewei); Zhou, L (Zhou, Lu); Zhou, JW (Zhou, Jiawang); Zhang, YX (Zhang, Yuxi); Ma, TS (Ma, Tianshuai); Qiu, HY (Qiu, Hongyu); Wang, CR (Wang, Chunren); Gao, JF (Gao, Junfeng)

Source: FOOD AND WATERBORNE PARASITOLOGY **Volume:** 41 **Article Number:** e00296 **DOI:** 10.1016/j.fawpar.2025.e00296 **Published Date:** 2025 DEC

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Total Times Cited: 0

Abstract: Cryptosporidium spp., Giardia duodenalis, Enterocytozoon bieneusi, and Blastocystis sp. are four common zoonotic intestinal protozoa, that cause frequent foodborne and waterborne outbreaks worldwide. Despite their public health importance, epidemiological data remain scarce from Heilongjiang Province in China. Fecal samples were collected from 845 sheep and 166 goats across 13 regions of Heilongjiang Province, Northeast China. PCR-based methods were used to detect these pathogens and PCR products were sequenced to determine the species/genotypes. The overall infection rates for Cryptosporidium spp., G. duodenalis, E. bieneusi, and Blastocystis sp. were 4.15 % (42/1011), 2.67 % (27/1011), 12.15 % (127/1011), and 3.56 % (36/1011), respectively. The mixed infections with two or more protozoa occurred in 2.97 % (30/1011). The geographic location was a significant risk factor for the prevalence of Cryptosporidium spp., E. bieneusi, and Blastocystis sp. in domestic small ruminants. Four Cryptosporidium genotypes (C. xiaoi, C. ubiquitum, C. bovis, C. andersoni), seven E. bieneusi genotypes (BEB6, COS-I, CHS8, CHS7, CHG1, CHG3, J), two G. duodenalis assemblages (assemblage E, assemblage A), and six Blastocystis subtypes (ST10, ST14, ST26, ST5, ST15, ST30) were identified. This study provides critical data for developing control strategies with significant implications for zoonotic risk assessment in Heilongjiang Province.

Accession Number: WOS:001607936400001

Document Type: Article

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Research Areas: Parasitology; Veterinary Sciences

Output Date: 2025-11-26

Pharmacology & Pharmacy

Record 1

Title: Investigating the Potential Targets and Mechanisms of Action of Chinese Medicine for the Treatment of EIV Based on Network Pharmacology and Molecular Docking as Well as In Vitro

Author(s): Chen, NN (Chen, Nannan); Wang, JW (Wang, Jiewei); Han, H (Han, He); Chen, L (Chen, Liang); Liu, BC (Liu, Bochao); Wang, S (Wang, Shuang); Liu, Y (Liu, Yu); Qin, PW (Qin, Pingwei)

Source: PHARMACOGNOSY MAGAZINE **DOI:** 10.1177/09731296251371462 **Early Access Date:** NOV 2025 **Published Date:** 2025 NOV 7

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Background Equine influenza virus (EIV) can cause acute infections and outbreaks of epidemics in horses and donkeys. It is one of the most economically impactful pathogens in equine respiratory diseases globally, resulting in substantial financial losses within the farming industry. Utilizing targeted anti-viral drugs is an effective strategy.Purpose The present study analyzes the potential of herbal medicines for the treatment of equine influenza (EI) based on network pharmacology, molecular docking techniques, and in vitro anti-viral studies.Materials and Methods The construction of a "traditional Chinese medicine (TCM) component-target-disease" network was performed using Cytoscape 3.9.0. The protein-protein interaction (PPI) network is performed through the STRING system. Bioconductor software was employed to conduct gene ontology (GO) and Kyoto encyclopedia of genes and genomes (KEGG) functional enrichment analyses of biological processes (BPs).

Molecular docking techniques revealed the degree of binding of core components to key target genes. Characterization of the anti-EI effect of TCM by cytotoxicity and in vitro studies.Results Consequently, five core TCMs were screened, which had 79 core targets related to EI. PPI network analysis highlighted 10 significant targets. Molecular docking results analysis revealed binding interactions between the main core component, kaempferol, and the targets prostaglandin-endoperoxide synthase 2 (PTGS2), matrix metalloproteinase-9 (MMP9), and estimated glomerular filtration rate (EGFR), with binding energies of -9.1, -8.3, and -8.0 (kcal/mol), respectively. In vitro studies have demonstrated that the inhibitory effect of kaempferol on EI is mainly in the initial phase.Conclusion Through network pharmacology, molecular docking, and in vitro experiments, kaempferol was demonstrated to combat EI through key targets of PTGS2, MMP9, EGFR, AKT, tumor necrosis factor (TNF), and IL-6. This study provides a basis for treating EI with herbal medicine and for later drug development. Future research should integrate network pharmacology with clinical applications, focusing on large-scale clinical trials to evaluate the efficacy and safety of TCM in influenza treatment, thereby enhancing its potential role in treating the disease.

Accession Number: WOS:001610960300001

Document Type: Article; Early Access

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Research Areas: Pharmacology & Pharmacy

Output Date: 2025-11-26

Plant Sciences

Record 1

Title: SIMULATION OF WATER-NITROGEN MOVEMENT AND NITROGEN UTILIZATION RATE IN BLACK SOIL MAIZE FIELDS USING THE WHCNS MODEL

Author(s): Sun, X (Sun, Xin); Wei, D (Wei, Dan); Jin, L (Jin, Liang); Wang, L (Wang, Lei); Wang, P (Wang, Peng); Yin, DW (Yin, Dawei); Zou, GY (Zou, Guoyuan); Li, Y (Li, Yan); Ding, JL (Ding, Jian Li); Liang, LN (Liang, Lina); Zuo, Q (Zuo, Qiang); Xu, S (Xu, Sen); Sun, L (Sun, Lei); Wang, W (Wang, Wei); Shen, HB (Shen, Huibo); Wang, YX (Wang, Yuxian); Wang, JQ (Wang, Junqiang); Hui, HY (Hui, Hanye); Xu, KF (Xu, Kuifeng)

Source: PAKISTAN JOURNAL OF BOTANY **Volume:** 57 **Issue:** 6 **Pages:** 2059-2068 **DOI:** 10.30848/PJB2025-6(10) **Published Date:** 2025 DEC

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Straw returning is essential for soil conservation and mitigating wind erosion in semiarid regions bearing black soil areas. Quantitative studies on crop development and soil water-nitrogen dynamics processes under complete straw returning are fundamental for establishing a rational farmland management system. To model crop yields and soil profile water-nitrogen distribution under various fertilization treatments, we used the soil water heat carbon nitrogen simulator (WHCNS), namely CK (no fertilization), T1 (compound fertilizer), T2 (compound fertilizer + straw returning), and T3 (humic acid fertilizer + straw returning). We calibrated and evaluated the performance of the WHCNS model by using soil water content, nitrate nitrogen content, aboveground dry matter mass, and yield data collected from the Meilisi Daur District experimental farm in Qiqihar, Heilongjiang Province, in 2022. We also simulated the effects of different fertilization methods on spring maize field evapotranspiration, crop yield, and water-nitrogen use efficiency. The results indicate that the hydraulic parameters Qs and n significantly impacted the soil water content in the parameter sensitivity analysis. In contrast, SLAmax had the largest impact on soil nitrate nitrogen content among crop parameters, and Ts was the most influential factor on crop yield. The relative root mean square errors of simulated and observed soil water storage, nitrate nitrogen content, and aboveground dry matter mass were all lower than 32%. Consistency indices for the 0-60 cm and 60-100 cm soil layers were greater than or equal to 0.68 and 0.30, respectively. Finally, the Nash coefficients were within reasonable ranges. The evapotranspiration rate under the straw returning treatment (T2) was 6.33% lower than without straw returning (T1). T2 exhibited the highest water-nitrogen use efficiency among all treatments, and compared with T1 and T3, water-nitrogen use efficiency increased by 10.27%, 7.78%, 26.71%, and 48.15%, respectively. These findings suggest that straw returning can effectively reduce evapotranspiration and improve resource utilization efficiency. Overall, the calibrated WHCNS model can reliably simulate the dynamics of soil water-nitrogen movement and crop growth under straw returning in the semiarid regions of northeastern China.

Accession Number: WOS:001610680500042

Document Type: Article

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Research Areas: Plant Sciences

Output Date: 2025-11-26

Record 2

Title: Co-elevated atmospheric CO2 and temperature increase rice yield but degrade nutrient quality in a cold temperature region

Author(s): Zhang, CY (Zhang, Chunyu); Hu, YF (Hu, Yanfeng); Yu, ZH (Yu, Zhenhua); Zhang, JY (Zhang, Jinyuan); Hu, XJ (Hu, Xiaojing); Liu, JJ (Liu, Junjie); Wang, GH (Wang, Guanghua); Liu, XB (Liu, Xiaobing); Jin, J (Jin, Jian); Li, YS (Li, Yansheng)

Source: PLANT PHYSIOLOGY AND BIOCHEMISTRY **Volume:** 229 **Article Number:** 110504 **DOI:** 10.1016/j.plaphy.2025.110504 **Published Date:** 2025 DEC **Part:** B

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Abstract: The responses of three Japonica rice cultivars were investigated throughout a full growing season in computer-controlled open-top chambers under four treatments: control (CK), elevated CO2 (700 ppm, eC), elevated temperature (+2 degrees C, eT), and their combination (eCeT). To assess the impact of climate change factors, the present study performed comprehensive physiological measurements and flag leaf transcriptomic analysis to evaluate rice yield and quality. Both eC and eCeT synergistically upregulated genes related to photosystem II (PsbA) and photosystem I (PsaA/B/C), thereby enhancing photochemical efficiency (Phi PSII by +18% and 12%) through improved electron transport and ATP/NADPH synthesis. This molecular reprogramming, coupled with RBCL-mediated carbon assimilation and NEMDH-facilitated photorespiratory bypass, contributed to a 37% increase in net photosynthetic rate (P-n) under eC. eT alone activated phosphoenolpyruvate carboxylase (PEPC) while maintaining Phi PSII stability, supporting continued starch accumulation (+22% NPQ) without diminishing the CO2 fertilization effect. Although eCeT induced more synergistic gene regulation (32 differentially expressed genes vs. 22 under eC + eT), no significant interaction effect on P-n was observed ($p > 0.05$), suggesting maintenance of post-transcriptional homeostasis. Ultimately, eC significantly enhanced P-n and Phi PSII, resulting in a 24% yield increase that was not offset by warming. However, CO2-induced carbohydrate accumulation led to reductions in grain protein (-7.2%) and mineral contents (P, K, Mg, Mn), with elevated temperature only partially mitigating mineral losses. The identification of RBCL and NEMDH as key climate-resilience biomarkers, along with PEPC-mediated thermal adaptation, provides promising molecular targets for breeding nutrient-enriched rice cultivars suited to warming, high-latitude environments. These findings indicate that while warming helps sustain the yield benefits of elevated CO2 in cold regions, it exacerbates nutrient dilution, highlighting the need for strategies that jointly optimize both yield and nutritional quality under future climate scenarios.

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Document Type: Article

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Output Date: 2025-11-26

Record 3

Title: Protein elicitor AMEP412 suppressed rice blast caused by Magnaporthe oryzae through triggering plant immunity

Author(s): Qin, YZ (Qin, Yazhi); Guo, MJ (Guo, Meijun); Yang, JY (Yang, Junyan); Zheng, JY (Zheng, Jiayi); Wang, Q (Wang, Quan); Liu, Q (Liu, Quan)

Source: PHYSIOLOGICAL AND MOLECULAR PLANT PATHOLOGY **Volume:** 140 **Article Number:** 102968 **DOI:** 10.1016/j.pmpp.2025.102968 **Published Date:** 2025 NOV

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Abstract: AMEP412 is a protein elicitor secreted by Bacillus subtilis, exhibiting the ability to trigger plant immunity. In this study, we assessed how AMEP412 induced disease resistance in rice seedlings against rice blast caused by Magnaporthe oryzae. First, the pathogen inoculation assay confirmed that pre-treatment with AMEP412 significantly reduced the lesion areas on rice leaves. Subsequently, the inner response of rice seedlings to protein-eliciting and pathogen infection were analysed, respectively. At 12 h post treatment (hpt) with AMEP412, early defense response was successfully triggered in rice leaves, including obvious accumulation of reactive oxygen species and activity increase of antioxidant enzymes (superoxide dismutase, catalase, and peroxidase). Real-time quantitative polymerase chain reaction analysis also verified the upregulation of antioxidant related genes. After M. oryzae infection, rice leaves pre-treated with AMEP412 exhibited a quicker and stronger defense reaction than those in the control. At 6 h post infection (hpi), a series of early defense response pathways were activated, including phenylpropanoid biosynthesis, ascorbate and aldarate metabolism, and cutin, suberine, and wax biosynthesis. At 12 hpi, the downstream defense response pathways began to dominate, such as plant hormone signal transduction, mitogen-activated protein kinase signaling, and plant-pathogen interaction. Further RT-qPCR verification of key genes in these pathways showed that the plant immunity system was successfully activated. We confirmed that AMEP412 could rapidly and effectively trigger the rice immunity system, resulting in reduced disease symptoms in M. oryzae-infected leaves, thereby providing a novel option for the biocontrol of rice blast.

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Document Type: Article

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Research Areas: Plant Sciences

Output Date: 2025-11-26

Record 4

Title: Differential responses of two plant species with different ecological niches to long-term nitrogen and phosphorus addition in temperate meadow steppe

Author(s): Chen, L (Chen, Li); Zhao, D (Zhao, Dan); Yang, YR (Yang, Yunrui); Wei, Y (Wei, Yi); Wang, ZH (Wang, Zhihui); Wang, HY (Wang, Hongyi)

Source: FRONTIERS IN PLANT SCIENCE **Volume:** 16 **Article Number:** 1693163 **DOI:** 10.3389/fpls.2025.1693163 **Published Date:** 2025 OCT 27

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Abstract: Introduction Global nitrogen (N) and phosphorus (P) deposition are fundamentally altering soil nutrient availability and species interactions in grassland ecosystems. However, the long-term interplay between N and P in shaping ecological niche differentiation among co-existing plant species remains poorly understood.Methods Leveraging a decade-long nutrient addition experiment in a temperate meadow steppe, this study investigated the response strategies of the dominant upper-canopy grass Leymus chinensis and the subdominant lower-canopy forb Potentilla bifurca by analyzing their phenotypic and nutrient traits.Results We found that P. bifurca exhibited greater phenotypic plasticity than L. chinensis, a difference that was amplified under combined NP addition. Notably, the two nutrient regimes drove opposing niche dynamics: N addition alone exacerbated P limitation, reducing phenotypic trait differences between the species (niche distance decreased from 0.12 to 0.07) and leading to niche convergence. In contrast, combined NP addition alleviated P limitation, enhanced the plasticity of P. bifurca, and drove niche separation (distance increased to 0.16). Correlation and random forest analyses revealed that the aboveground biomass of L. chinensis was primarily associated with N-related traits, whereas that of P. bifurca was strongly associated with P-use efficiency traits.Conclusion Our results demonstrate that long-term N and P addition regulate interspecific competition by modulating soil N/P ratio and driving divergent trait responses, thereby shaping the niche partitioning between co-existing species.

Accession Number: WOS:001615131900001

Document Type: Article

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Output Date: 2025-11-26

Record 5

Title: Foliar spray of prohexadione-calcium improves the adaptability of mung bean to saline-alkali stress

Author(s): Liang, XL (Liang, Xilong); Dong, YL (Dong, Yanlei); Jiang, QY (Jiang, Qiuyu); Hou, X (Hou, Xue); Song, Y (Song, Yang); Zhao, FZ (Zhao, Fengzhou); Sun, Y (Sun, Yu); Jiang, HP (Jiang, Haipeng); Fang, SM (Fang, Shumei); Wang, QY (Wang, Qingyan)

Source: FRONTIERS IN PLANT SCIENCE **Volume:** 16 **Article Number:** 1681992 **DOI:** 10.3389/fpls.2025.1681992 **Published Date:** 2025 OCT 24

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Total Times Cited: 0

Abstract: Introduction Saline-alkali soils are a major constraint to mung bean cultivation and extension, and prohexadione-calcium (Pro-Ca) can enhance plant tolerance to saline-alkali stress.Methods In order to explore the regulatory effect and mechanism of Pro-Ca on mung bean growth under saline-alkali stress, the morphology, ultrastructure, physiological indicators, and gene expression were measured in this study.Results The results indicate that Pro-Ca can improve the adaptability of mung bean to saline-alkali stress. Specifically, it manifests as increasing dry matter accumulation, protecting the structural integrity and quantity of organelles such as chloroplasts and mitochondria, enhancing photosynthetic capacity, increasing antioxidant enzyme activity and the content of osmoregulatory substances. These changes may be related to the enhanced expression of calcium signal transmission and the synthesis of nitric oxide (NO), polyamines and jasmonic acid in the root system under saline-alkali stress.Discussion Our findings partially explain the physiological and molecular mechanisms by which Pro-Ca enhances the tolerance and adaptability of mung bean plants to saline-alkali stress. This may become an effective strategy for the utilization of saline-alkali soil.

Accession Number: WOS:001609105000001

Document Type: Article

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Research Areas: Plant Sciences

Output Date: 2025-11-26

Record 6

Title: Identification and genome insights into Pyrenochaeta nobilis, a novel endophytic fungus isolated from Astragalus membranaceus with gray mold-control activity

Author(s): Yang, F (Yang, Fan); Wang, S (Wang, Shuang); Jiang, XF (Jiang, Xifeng); Du, HR (Du, Hongrui); Liu, Y (Liu, Yu); Zhou, YY (Zhou, Yuanyuan); Liu, CL (Liu, Chunlai)

Source: FRONTIERS IN PLANT SCIENCE **Volume:** 16 **Article Number:** 1610287 **DOI:** 10.3389/fpls.2025.1610287 **Published Date:** 2025 OCT 16

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Abstract: Introduction Gray mold, caused by the necrotrophic fungus Botrytis cinerea, is a significant threat to agricultural production, especially under low temperature and high humidity conditions. This disease can cause substantial yield losses in various crops, including tomatoes. To address this issue, the search for novel biocontrol agents has become a priority. In this study, we explored the potential of endophytic fungi isolated from wild medicinal plants in the southern foothills of the Daxing'an Mountains in China as biocontrol resources against B. cinerea.Methods Endophytic fungi were isolated from the roots of Astragalus membranaceus, a wild medicinal plant native to the study area. Among the isolates, Pyrenochaeta nobilis strain SFJ12-R-5 (CGMCC No.17766) was selected for its significant antagonistic activity against B. cinerea. The inhibitory effects of P. nobilis on B. cinerea were evaluated through in vitro assays, including mycelial growth inhibition tests and lesion inhibition tests on tomato leaves and fruits. Additionally, the genome of P. nobilis SFJ12-R-5 was sequenced using a combination of next-generation and third-generation sequencing techniques, followed by systematic annotation and identification of key gene families, such as carbohydrate-active enzymes (CAZymes) and phage-related (Phi) genes.Results P. nobilis strain SFJ12-R-5 exhibited strong inhibitory effects on B. cinerea, with a mycelial growth inhibition rate of 66.67 +/- 3.15% and a large inhibition zone of 20.83 +/- 3.78 mm. The fresh fermentation filtrate of P. nobilis, even at a 10-fold dilution, completely inhibited the growth of pathogenic hyphae. In vitro tests on tomato leaves and fruits showed lesion inhibition rates of 87.21% and 100%, respectively. Furthermore, plants co-treated with B. cinerea and the P. nobilis filtrate had a significantly lower gray mold disease severity (28.57%)

compared to those inoculated solely with B. cinerea (75.34%), indicating a disease reduction rate of 62.08%. The genome of P. nobilis SFJ12-R-5 was successfully assembled and annotated, revealing the presence of CAZymes and Phi genes that may contribute to its biocontrol potential.Discussion Our findings provide the first evidence that P. nobilis could serve as a promising natural antagonist against B. cinerea, particularly in integrated disease management systems for tomato production in greenhouses. The high-quality genome sequence and the identification of key gene families lay a solid foundation for future research on the molecular mechanisms underlying the inhibitory activity of Pyrenochaeta spp. against B. cinerea. Further studies are needed to explore the practical application of P. nobilis in agricultural settings and to elucidate its mode of action at the molecular level.

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Document Type: Article

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Research Areas: Plant Sciences

Output Date: 2025-11-26

Record 7

Title: Physiological and Transcriptional Responses of Sorghum Seedlings Under Alkali Stress

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Source: PLANTS-BASEL **Volume:** 14 **Issue:** 19 **Article Number:** 3106 **DOI:** 10.3390/plants14193106 **Published Date:** 2025 OCT 9

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Abstract: Saline-alkali stress seriously affects the growth and development of crops. Sorghum bicolor (L.), a C4 plant, is an important cereal crop in the world, and its growth and geographical distribution are limited by alkali conditions. In this study, sorghum genotypes with different alkaline resistance (alkaline-sensitive Z1 and alkaline-tolerant Z14) were used as experimental materials to explore the effects of alkali on sorghum seedlings. RNA-seq technology was used to examine the differentially expressed genes (DEGs) in alkali-tolerant Z14 to reveal the molecular mechanism of sorghum response to alkali stress. The results showed that plant height, root length, and biomass of both cultivars decreased with time under 80 mM NaHCO3 treatment, but Z14 showed better water retention abilities. The photosynthetic fluorescence parameters and chlorophyll content also decreased, but the Fv/Fm, ETH, Phi PSII, and chlorophyll content of Z14 were significantly higher than those of Z1. The level of reactive oxygen species (ROS) increased in both sorghum varieties under alkali stress, while the enzyme activities of SOD, POD, CAT, and APX were also significantly increased, especially in Z14, resulting in lower ROS compared with Z1. Transcriptome analysis revealed around 6000 DEGs in Z14 sorghum seedlings under alkali stress, among which 267 DEGs were expressed in all comparison groups. KEGG pathways were enriched in the MAPK signaling pathway, plant hormone signal transduction, and RNA transport. bHLHs, ERFs, NACs, MYBs, and other transcription factor families are actively involved in the response to alkali stress. A large number of genes involved in photosynthesis and the antioxidant system were found to be significantly activated under alkali stress. In the stress signal transduction cascades, Ca2+ signal transduction pathway-related genes were activated, about 23 PP2Cs in ABA signaling were upregulated, and multiple MAPK and other kinase-related genes were triggered by alkali stress. These findings will help decipher the response mechanism of sorghum to alkali stress and improve its alkali tolerance.

Accession Number: WOS:001593535300001

Document Type: Article

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Research Areas: Plant Sciences

Output Date: 2025-11-26

Record 8

Title: Computer vision-based steering path visualization of headlands in soybean fields

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Total Times Cited: 0

Abstract: Introduction To address the insufficient accuracy of autonomous steering in soybean headland areas, this study proposes a dynamic navigation line visualization method based on deep learning and feature detection fusion, enhancing path planning capability for autopilot systems during the soybean V3-V8 stage.Methods First, the improved lightweight YOLO-PFL model was used for efficient headland detection (precision, 94.100%; recall, 92.700%; mAP@0.5, 95.600%), with 1.974 M parameters and 4.816 GFLOPs, meeting embedded deployment requirements for agricultural machines. A 3D positioning model was built using binocular stereo vision; distance error was controlled within 2.000%, 4.000%, and 6.000% for ranges of 0.000-3.000 m, 3.000-7.000 m, and 7.000-10.000 m, respectively. Second, interference-resistant crop row centerlines (average orientation angle error, -0.473 degrees, indicating a small systematic leftward bias; mean absolute error, 3.309 degrees) were obtained by enhancing contours through HSV color space conversion and morphological operations, followed by fitting feature points extracted from ROIs and the crop row intersection area using the least squares method. This approach solved centerline offset issues caused by straws, weeds, changes in illumination, and the presence of holes or sticking areas. Finally, 3D positioning and orientation parameters were fused to generate circular arc paths in the world coordinate system, which were dynamically projected across the coordinate system to visualize navigation lines on the image plane.Results and discussion Experiments demonstrated that the method generates real-time steering paths with acceptable errors, providing a navigation reference for automatic wheeled machines in soybean fields and technical support for the advancement of intelligent precision agriculture equipment.

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Document Type: Article

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Research Areas: Plant Sciences

Output Date: 2025-11-26

Record 9

Title: Effects of Different Nitrogen Fertilizer Rates on Spring Maize Yield and Soil Nitrogen Balance Under Straw Returning Conditions of Cold Regions

Author(s): Ji, JH (Ji, Jinghong); Liu, SQ (Liu, Shuangquan); Hao, XY (Hao, Xiaoyu); Zheng, Y (Zheng, Yu); Zhao, Y (Zhao, Yue); Xia, YQ (Xia, Yuqi); Xing, ZQ (Xing, Zhanqiang); Guo, W (Guo, Wei)

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Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Under the condition of straw returning to the field, appropriate nitrogen fertilizer application is one of the key factors used to improve crop yield and ensure environmental safety. Therefore, an experiment with different rates of nitrogen fertilization was conducted with a randomized block design in Harbin, China. The straw was deeply plowed back into the field after harvest in the autumn. The nitrogen application rates were 0, 75, 150, 180, 225, and 300 kgha-1. The purpose of this study is to clarify the appropriate amount of nitrogen fertilizer under the condition of straw returning to the field and to provide technical support for high-yield and high-efficiency maize in cold regions. The results indicated that the yield of maize first increased and then stabilized as the amount of nitrogen fertilizer increased, while the economic benefits first increased and then decreased. When the nitrogen application rate exceeds 225 kgha-1 or is lower than 150 kgha-1, the economic benefits significantly decrease. When high-nitrogen fertilizer rates of 225 kgha-1 and 300 kgha-1 were applied, the residual nitrate nitrogen in the soil was increased by 2.1 times and 2.3 times, respectively, compared to before sowing. With the increase in the nitrogen application rate, the nitrogen fertilizer utilization efficiency and agronomic efficiency decreased, and the apparent nitrogen loss and nitrogen surplus significantly increased. Comprehensively considering the maize yield, benefits, and environmental risk factors the suitable nitrogen application rate was in a range of 170.2 kgha-1 to 178.2 kgha-1 in the first year and 150.0 kgha-1 to 171.3 kgha-1 in the second year. This work provides a theoretical basis and technical support for the rational application of nitrogen fertilizer and high-yield and high-efficiency spring maize under the condition of straw returning to the field.

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Document Type: Article

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Research Areas: Plant Sciences

Output Date: 2025-11-26

Record 10

Title: Exogenous tryptophan increases soybean yield by enhancing sucrose-starch metabolism in leaves and seeds at the R6 stage under salt-alkali stress

Author(s): Wang, WY (Wang, Weiyu); Feng, RQ (Feng, Ruiqi); Zhu, JX (Zhu, Jixing); Cao, Y (Cao, Yu); Feng, J (Feng, Jing); Zhao, YL (Zhao, Yanlin); Du, JD (Du, Jidao); Du, YL (Du, Yanli)

Source: BMC PLANT BIOLOGY **Volume:** 25 **Issue:** 1 **Article Number:** 1274 **DOI:** 10.1186/s12870-025-07277-0 **Published Date:** 2025 OCT 1

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Background Saline-alkali stress (SA) can significantly limit the growth and yield of soybean. The grain filling stage (R6) is a crucial growth period that determines the yield of soybeans and is also the most complex stage of sucrose-starch metabolism. Tryptophan (Trp) is an essential amino acid for protein synthesis and also an important signaling molecule in plants, plays an important role in maintaining osmotic regulation in plants and resisting adverse external environments. However, the mechanism of Trp regulation on sucrose-starch metabolism in R6-stage soybean leaves and seeds under SA is still unclear. This study investigated the effects of different Trp concentrations (100mgL-1,200mgL-1 and 300mgL-1) on sucrose-starch metabolism in soybean under SA (NaCl: Na2SO4: Na2CO3: NaHCO3 = 1:9:1:9).Results The results showed that exogenous tryptophan alleviated the growth inhibition of R6 soybean under SA treatment. Exogenous Trp could enhance the photosynthetic capacity of soybean by increasing photosynthetic pigment content, net photosynthetic rate (Pn), intercellular carbon dioxide concentration (Ci), stomatal conductance (Gs), and the transpiration rate (Tr) of soybean leaves under SA. Exogenous Trp affected the balance of sucrose-starch metabolism in soybean leaves and seeds under SA by changing the activities of key enzymes in sucrose metabolism(SPS, SuSy, A-INV and N-INV) and expression levels of related genes. Meanwhile, exogenous Trp promoted the transport of sucrose equivalents from the source to the sink by increasing sucrose transport-related genes (GmSUC2, GmSWEET6, and GmSWEET15) under SA.Conclusions These results showed that exogenous Trp could improve the photosynthesis of leaves, regulate the metabolic balance of starch-sucrose, and increase the node number, pod number, and seed number, ultimately affecting high soybean yield at maturity and enhancing the saline-alkali tolerance of plants. These results can provide a new direction and theoretical basis for improving saline-alkali soil and tolerant crop breeding.

Accession Number: WOS:001586616400009

Document Type: Article

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Research Areas: Plant Sciences

Output Date: 2025-11-26

Record 11

Title: CsAPRR2 regulates cucumber immature fruit color by coordinating chloroplast biogenesis and photosynthesis-related gene expression

Author(s): Liu, HQ (Liu, Hanqiang); Cui, MM (Cui, Mingming); Hu, KH (Hu, Kaihong); Tan, JY (Tan, Junyi); Weng, YQ (Weng, Yiqun); Ma, YX (Ma, Yuxuan); Li, J (Li, Ju); Huang, ZQ (Huang, Zeqiang); Chen, BR (Chen, Birong); Meng, HW (Meng, Huanwen); Pan, YP (Pan, Yupeng); Cheng, ZH (Cheng, Zhihui)

Source: PLANT JOURNAL **Volume:** 123 **Issue:** 6 **Article Number:** e70496 **DOI:** 10.1111/tpj.70496 **Published Date:** 2025 SEP 27

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Immature fruit color (IFC) of cucumber (Cucumis sativus L.) is an important marketability trait affecting consumer preferences. We previously identified a single-base insertion (-/G) in CsAPRR2 that introduces a premature stop codon, leading to loss of the conserved C-terminal GCT box that is essential for protein-protein interactions. This mutation is strongly associated with reduced CsAPRR2 expression and white IFC. RNA interference (RNAi) and transgenic overexpression confirmed the critical role of CsAPRR2 in regulating IFC. Chromatin immunoprecipitation sequencing analysis and transcriptome profiling identified 225 candidate targets of CsAPRR2, many of which encode thylakoid membrane proteins or key enzymes in chlorophyll biosynthesis. Knockdown of CsAPRR2 expression in RNAi plants significantly reduced the expression of these genes, resulting in impaired thylakoid development, lower chloroplast numbers, and reduced pigment content. CsAPRR2 physically interacts with transcription factors CsTCP15 and CsTCP20B in a GCT box-dependent manner, supporting a model in which these interactions contribute to CsAPRR2-mediated regulation of chloroplast development. Notably, a CsTCP20B variant identified in a wild cucumber with light green immature skin and white mature skin supports its involvement in skin color regulation. Together, this work establishes CsAPRR2 as a central regulator of chloroplast biogenesis and immature fruit pigmentation in cucumber and underscores the importance of transcription factor interactions in modulating photosynthesis-related gene expression.

Accession Number: WOS:001581889900001

Document Type: Article

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Research Areas: Plant Sciences

Output Date: 2025-11-26

Record 12

Title: Integrated Transcriptome-Metabolome Analysis Reveals the Flavonoids Metabolism Mechanism of Maize Radicle in Response to Low Temperature

Author(s): Dou, Y (Dou, Yi); Luo, WQ (Luo, Wenqi); Zhang, YF (Zhang, Yifei); Li, WS (Li, Wangshu); Zhang, CY (Zhang, Chunyu); Lv, YJ (Lv, Yanjie); Liu, XR (Liu, Xinran); Yu, S (Yu, Song)

Source: PLANTS-BASEL **Volume:** 14 **Issue:** 19 **Article Number:** 2988 **DOI:** 10.3390/plants14192988 **Published Date:** 2025 SEP 26

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: The Northeast region in China is a major maize-producing area; however, low-temperature stress (TS) limits maize (Zea mays L.) seed germination, affecting population establishment and yield. In order to systematically explore the regulation mechanism of maize radicle which is highly sensitive to low-temperature environment response to TS, seeds of ZD958 and DMY1 were used to investigate germination responses under 15 degrees C (control) and 5 degrees C (TS) conditions. Phenotypic, physiological, transcriptomic, and metabolomic analyses were conducted on the radicles after 48 h of TS treatment. TS caused reactive oxygen species (ROS) imbalance and oxidative damage in radicle cells, inhibiting growth and triggering antioxidant defenses. Integrated transcriptomic and metabolomic analyses revealed that flavonoid metabolism may play a pivotal role in radicle responses to TS. Compared with the control treatment, ZD958 and DMY1 under TS treatment significantly increased ($p < 0.01$) the total flavonoid content, total antioxidant capacity, 4-coumarate-CoA ligase activity, and dihydroflavonol 4-reductase activity by 15.99% and 16.01%, 18.41% and 18.54%, 63.54% and 31.16%, and 5.09% and 7.68%, respectively. Despite genotypic differences, both followed a shared regulatory logic of "low-temperature signal-driven-antioxidant redirection-functional synergy." This

enabled ROS scavenging, redox balance, and antioxidant barrier formation, ensuring basal metabolism and radicle development.

Accession Number: WOS:001594805800001

Document Type: Article

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Research Areas: Plant Sciences

Output Date: 2025-11-26

Record 13

Title: Multi-Scale Remote-Sensing Phenomics Integrated with Multi-Omics: Advances in Crop Drought-Heat Stress Tolerance Mechanisms and Perspectives for Climate-Smart Agriculture

Author(s): Liang, XW (Liang, Xiongwei); Yu, SP (Yu, Shaopeng); Ju, YF (Ju, Yongfu); Wang, YN (Wang, Yingning); Yin, DW (Yin, Dawei)

Source: PLANTS-BASEL **Volume:** 14 **Issue:** 18 **Article Number:** 2829 **DOI:** 10.3390/plants14182829 **Published Date:** 2025 SEP 10

Times Cited in Web of Science Core Collection: 1

Total Times Cited: 1

Abstract: Climate change is intensifying the co-occurrence of drought and heat stresses, which substantially constrain global crop yields and threaten food security. Developing climate-resilient crop varieties requires a comprehensive understanding of the physiological and molecular mechanisms underlying combined drought-heat stress tolerance. This review systematically summarizes recent advances in integrating multi-scale remote-sensing phenomics with multi-omics approaches-genomics, transcriptomics, proteomics, and metabolomics-to elucidate stress response pathways and identify adaptive traits. High-throughput phenotyping platforms, including satellites, UAVs, and ground-based sensors, enable non-invasive assessment of key stress indicators such as canopy temperature, vegetation indices, and chlorophyll fluorescence. Concurrently, omics studies have revealed central regulatory networks, including the ABA-SnRK2 signaling cascade, HSF-HSP chaperone systems, and ROS-scavenging pathways. Emerging frameworks integrating genotype x environment x phenotype (G x E x P) interactions, powered by machine learning and deep learning algorithms, are facilitating the discovery of functional genes and predictive phenotypes. This "pixels-to-proteins" paradigm bridges field-scale phenotypes with molecular responses, offering actionable insights for breeding, precision management, and the development of digital twin systems for climate-smart agriculture. We highlight current challenges, including data standardization and cross-platform integration, and propose future research directions to accelerate the deployment of resilient crop varieties.

Accession Number: WOS:001579868100001

Document Type: Review

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Research Areas: Plant Sciences

Output Date: 2025-11-26

Reproductive Biology

Record 1

Title: 13-cis-retinoic acid modulates porcine ovarian granulosa cell differentiation via retinoic acid signaling-FoxA1 axis: Implications for ovarian follicular development and luteinization

Author(s): Zhang, HL (Zhang, Hong-Liang); Wang, HB (Wang, Hua-Biao); Mi, YX (Mi, Yi-Xuan); Wu, XM (Wu, Xia-Meng); Bao, L (Bao, Li); Zhao, M (Zhao, Ming); Ma, L (Ma, Li); Wang, SL (Wang, Shui-Lian)

Source: THERIOGENOLOGY **Volume:** 250 **Article Number:** 117682 **DOI:** 10.1016/j.theriogenology.2025.117682 **Published Date:** 2026 JAN 15

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: 13-cis-Retinoic acid (13cRA), a vitamin A derivative clinically employed in cancer therapy, demonstrates novel regulatory effects on ovarian follicular development and luteinization through granulosa cell proliferation and differentiation in this study. Our murine model revealed that 13cRA administration significantly increased the number of primary follicle and corpus luteum by ovarian sectioning and follicle counting, indicating accelerated follicular maturation and ovulation competence. In porcine ovarian granulosa cell cultures, 13cRA treatment induced cell cycle progression (G1-S phase transition), and promoted cell proliferation while up-regulating differentiation markers luteinizing hormone receptor (LHR) and progesterone receptor (PGR). Cellular retinoic acid-binding protein CRABP2-mediated mechanisms were identified as pivotal through gain/loss-of-function experiments. Overexpression of CRABP2 amplified 13cRA-induced LHR and PGR expression, while knockdown of CRABP2 by specific siRNA resulted in the opposite effect. The retinoid acid signaling axis was further delineated through receptor-specific modulation. 13cRA promoted RAR(3/RXR(3 receptor heterodimer formation, with pharmacological activation (Adapalene) potentiating LHR and PGR expression and receptor knockdown diminishing their expression. RA metabolic regulation studies revealed that CRABP1 and CYP26 isoforms (CYP26A1 and CYP26B1) as functional antagonists of 13cRA activity were demonstrated through siRNA silencing or CYP26 inhibitor R115866 treatment experiments. Notably, we identified that FoxA1, as a negative regulator of granulosa cell proliferation and differentiation, mediated the effect of 13cRA on granulosa cell differentiation through siRNA transfection and FoxA1 recombinant protein treatment experiments. 13cRA-mediated FoxA1 expression suppression occurred through CRABP2-dependent nuclear shuttling and RAR(3/RXR(3 receptor heterodimer activating, with combinatorial modulation of CRABP1/CYP26 system components (CYP26A1 and CYP26B1) significantly altering FoxA1 regulatory dynamics. Finally, we conclude that 13cRA can inhibit FoxA1 expression through RA signaling molecules (CRABP2, RAR(3/RXR(3 heterodimer, CRABP1, CYP26A1 and CYP26B1) and thus promote the differentiation of porcine ovarian granulosa cells.

Accession Number: WOS:001587183000001

Document Type: Article

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Research Areas: Reproductive Biology; Veterinary Sciences

Science & Technology - Other Topics

Record 1

Title: Modeling and analysis of active thermal regulation in segmented PCM wall systems for optimizing energy efficiency in severe cold regions

Author(s): Li, JW (Li, Jingwei); Han, ZH (Han, Zhonghong); Luo, D (Luo, Dan); Xue, T (Xue, Ting); Jia, JJ (Jia, Jiaojio); An, S (An, Shuai); Li, D (Li, Dong); Cheng, YJ (Cheng, Yujing); Li, Q (Li, Qing); Jiang, W (Jiang, Wei)

Source: SUSTAINABLE ENERGY TECHNOLOGIES AND ASSESSMENTS **Volume:** 84 **Article Number:** 104690 **DOI:** 10.1016/j.seta.2025.104690 **Published Date:** 2025 DEC

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: This study investigates rural residential buildings in severely cold regions and develops a segmented phase change material (PCM) wall integrated with an active solar-assisted heating system. The PCM layer, 50 mm thick, is evenly divided into three sections along the inner sides of the east and west exterior walls. The solar collector provides a solar energy contribution rate of 33.01 %, while using a heat pump as an auxiliary source achieves a primary energy saving rate of 66.5 %. Numerical simulations compare the melting rate, wall surface temperature, and heat flux between segmented and concentrated PCM walls, revealing that the segmented design shortens complete melting time by 16.7 %, increases indoor heating capacity by 15.5 %, and reduces outdoor heat loss by 23.8 %. Orthogonal experiments further show that optimal performance occurs at a phase change temperature of 28 degrees C, an inlet temperature of 50 degrees C, and a pipe diameter of DN25.

Accession Number: WOS:001614788500001

Document Type: Article

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Research Areas: Science & Technology - Other Topics; Energy & Fuels

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Output Date: 2025-11-26

Record 2

Title: Can data assetization drive high-quality enterprise development?-Evidence from China's "Specialized, refined, unique, and innovative" SMEs

Author(s): Li, L (Li, Lin); Zhu, JL (Zhu, Jiulin)

Source: PLOS ONE **Volume:** 20 **Issue:** 11 **Article Number:** e0335903 **DOI:** 10.1371/journal.pone.0335903 **Published Date:** 2025 NOV 7

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Data assetization empowers the high-quality development of "Specialized, Refined, Distinctive, and Innovative" (SRDI) small and medium-sized enterprises (SMEs) by enhancing organizational performance and driving innovation. Based on this, this study selects SRDI SMEs in China from 2013 to 2023 as samples. It constructs a keyword graph spectrum based on enterprise annual report texts to quantitatively assess the level of data assetization and investigates whether data assetization can facilitate the high-quality development of these SMEs. The research findings indicate that: (1) data assetization significantly contributes to the high-quality development of SRDI SMEs, primarily through two mechanisms-enhancing strategic differentiation and improving resource allocation efficiency; (2) the robustness of these findings is confirmed through a series of tests, including alternative specifications of dependent variables, inclusion of additional control variables, subsample analyses, and the exclusion of potential confounding factors; (3) further analysis grounded in the TOE (Technology-Organization-Environment) framework demonstrates that the positive impact of data assetization is amplified by firm-level innovation capacity, customer relationship strength, regional characteristics, and the extent of enterprise digital finance development. This study contributes to advancing the understanding of how data assetization influences the high-quality development of SRDI SMEs, offering a theoretical foundation for future research in this domain.

Accession Number: WOS:001611683000037

Document Type: Article

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Research Areas: Science & Technology - Other Topics

Output Date: 2025-11-26

Record 3

Title: Spatiotemporal evolution regional differences and decoupling effects of greenhouse gas emissions from animal husbandry in Henan Province

Author(s): Sha, YY (Sha, Yanyu); Li, JQ (Li, Jiaqi); Zhang, HB (Zhang, Hongbo); Wei, CB (Wei, Chunbo)

Source: SCIENTIFIC REPORTS **Volume:** 15 **Issue:** 1 Article **Number:** 38421 **DOI:** 10.1038/s41598-025-22285-8 **Published Date:** 2025 NOV 3

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: As global warming intensifies, the livestock industry has become one of the largest contributors to greenhouse gas (GHG) emissions, with its environmental impact increasingly drawing attention. Henan Province is a major contributor to these emissions, prompting this study to systematically investigate GHG emissions from the livestock industry in Henan Province. This study utilises panel data from 2001 to 2021 and employs the Life Cycle Assessment (LCA) method to estimate GHG emissions from the livestock industry, revealing their spatiotemporal changes and regional characteristics. Spatial analysis of GHG emissions from the livestock industry is conducted using the Theil index, the Tapio decoupling model, and Markov chains. The findings are as follows: (1) The total GHG emissions from the livestock industry exhibit a fluctuating downward trend, gradually forming a main GHG emission belt extending from the northwest to the southeast. (2) The Theil index shows an overall 'declining trend,' with inter-regional differences being the primary source of overall variation. (3) The overall decoupling state is primarily characterised by weak and strong decoupling, indicating that environmental protection and economic development in Henan Province are gradually moving toward coordination. (4) Regional GHG emission changes are constrained by their original emission types and reserves, exhibiting growth inertia and path dependence, with neighbouring types significantly influencing the transition of regional GHG emission types. Henan Province should formulate differentiated emission reduction policies and optimise the spatial layout of the livestock industry, which holds certain implications for other regions in achieving GHG emission reductions and livestock industry development.

Accession Number: WOS:001608129300012

Document Type: Article

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Research Areas: Science & Technology - Other Topics

Output Date: 2025-11-26

Record 4

Title: Wind-induced response analysis of flat-elliptical pipe skeleton plastic greenhouse considering dynamic wind effects

Author(s): Xie, HY (Xie, Hengyan); Wei, CX (Wei, Cunxing); Zheng, X (Zheng, Xin); Xu, WB (Xu, Wenbao)

Source: SCIENTIFIC REPORTS **Volume:** 15 **Issue:** 1 **Article Number:** 37024 **DOI:** 10.1038/s41598-025-19888-6 **Published Date:** 2025 OCT 23

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Existing codes for agricultural structures, such as greenhouses, primarily account for the mean wind load, neglecting the impact of fluctuating wind. This study investigated the dynamic response of flat-elliptical pipe skeleton plastic greenhouses(FEPG) under fluctuating wind loads. Using ABAQUS software, a model of the greenhouse with film was established. The fluctuating wind speeds were simulated through the Linear Filtering Method. The greenhouse was subjected to full dynamic and mean wind loads, with the resulting displacement and stress distributions of the skeleton analyzed. The results revealed the significant effects of fluctuating wind on the greenhouse structure. Displacement and stress were unevenly distributed, with the larger displacement observed at the windward and leeward shoulders, and peak stress occurring on the windward side. Under dynamic loads, displacement and stress increased by 2.57 and 1.53 times, respectively, compared to mean wind loads. For areas subjected to lower loads, maximum displacement and Mises stress under dynamic wind were only slightly higher (1.05 and 1.02 times) than under mean wind loads. These results highlight the need to account for the adverse effects of fluctuating wind in the design of greenhouse structures to enhance their wind resistance.

Accession Number: WOS:001600537100042

Document Type: Article

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Research Areas: Science & Technology - Other Topics

Output Date: 2025-11-26

Record 5

Title: SUMOylation modulates the dual functions of Krüppel homolog 1 in transcriptional regulation of Broad-Complex expression

Author(s): He, QY (He, Qianyu); Chen, JX (Chen, Jinxia); Chen, SS (Chen, Shanshan); Gao, XY (Gao, Xinyu)

Source: JOURNAL OF ADVANCED RESEARCH **Volume:** 75 **Pages:** 123-135 **DOI:** 10.1016/j.jare.2025.07.032 **Published Date:** 2025 SEP

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Introduction: Insects undergo intricate metamorphosis processes governed by hormonal regulatory mechanisms, exemplified by the antagonistic actions of 20-hydroxyecdysone (20E) and juvenile hormone (JH). Kr & uuml;ppel homolog 1 (Kr-h1) is a key transcription factor mediating JH's antagonistic effects on 20E. Previous studies have shown that Kr-h1 plays dual roles in regulating the 20E signaling gene BroadComplex (Br-C), repressing it in larvae and activating it during pupation. However, the mechanisms underlying this dual functionality remain elusive. Objectives: This study aimed to determine whether SUMOylation, a post-translational modification, functions as part of a molecular switch mechanism for Kr-h1's stage-specific transcriptional roles. Methods: Using Drosophila melanogaster, we analyzed Kr-h1 SUMOylation dynamics via Western blot, immunoprecipitation combined with Drosophila genetics. Immunostaining, RT-qPCR, and luciferase reporter assays were performed to investigate the impact of SUMOylation on the bidirectional transcriptional regulation of Kr-h1 on Br-C. SUMOylation sites were identified through mutagenesis and bioinformatics. Coimmunoprecipitation and mass spectrometry explored Kr-h1 interactors. Hormonal effects on regulation of Kr-h1 SUMOylation were tested using JH mimic (methoprene) and 20E treatments. Results: Kr-h1 undergoes stage-specific SUMOylation: it is highly SUMOylatedin early third-instar larvae, enabling interaction with the histone methyltransferase SmydA-8 to repress Br-C. Conversely, at the white prepupal stage, deSUMOylation disrupts the Kr-h1- SmydA-8 interaction, thereby activating Br-C expression. K113 was identified as the primary SUMOylation site in Kr-h1. JH stimulated Kr-h1 SUMOylation by enhancing its interaction with the SUMO-conjugating enzyme Ubc9. Conversely, 20E promotedKr-h1 deSUMOylation via increased association with the deSUMOylating enzyme ubiquitinlike protease 1 (Ulp1). Co-stimulation with JH and 20E synergistically amplified deSUMOylation. Conclusion: SUMOylation of Kr-h1 serves as a molecular switch governing its dual regulatory functions in Br-C expression. JH and 20E an lishes SUMOylation as a critical regulator of Kr-h1's stage-specific activity, revealing how it orchestrates crosstalk between JH and 20E signaling during insect development. These findings provide a mechanistic framework for understanding how post-translational modifications confer functional plasticity to transcription factors at pivotal developmental transitions. Moreover, identifying SUMOylation as a central node in JH/20E crosstalk opens new avenues for targeting this pathway in insect growth regulators for pest management. tagonistically control this post-translational modification. Our study estab

Accession Number: WOS:001584293800016

Document Type: Article

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Research Areas: Science & Technology - Other Topics

Output Date: 2025-11-26

Record 6

Title: Study on the influence of rice straw ash cement mortar finish on the temperature pattern of sunning water pool in cold regions

Author(s): Wang, FC (Wang, Fu-cheng); Wang, W (Wang, Wei); Wen, JM (Wen, Jia-mei); Tian, JB (Tian, Jia-bing); Zhao, JQ (Zhao, Jin-qi); Majeed, Y (Majeed, Yaqoob)

Source: GREEN ENERGY AND RESOURCES **Volume:** 3 **Issue:** 3 **Article Number:** 100142 **DOI:** 10.1016/j.gerr.2025.100142 **Published Date:** 2025 SEP

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: To investigate the warming effect of rice straw ash (RSA) cement mortar facing on sunning water pools, this study focuses on a sunning water pool with a 5% substitution rate of RSA in its cement mortar facing. A temperature control test was conducted to compare it with a conventional cement mortar-faced sunning water pool. Additionally, finite element software was employed to create models for both the RSA and conventional cement mortar-faced sunning water pools, facilitating an analysis of the variations in water temperature within these systems.The results indicate that the RSA cement mortar facing can enhance the daily average water temperature of the sunning water pools by 0.1-0.6 degrees C compared to those featuring conventional cement mortar facing. Simulation data reveal that the water temperature in the sunning water pool utilizing RSA cement mortar facing is approximately 0.46 degrees C higher than that observed in its counterpart with standard cement mortar facing. The trends identified through theoretical calculations, experimental data, and simulation results are largely consistent, suggesting that RSA cement mortar facing effectively improves the thermal performance of sunning water pools.These findings provide valuable theoretical support for implementing RSA cement mortar in agricultural facilities.

Accession Number: WOS:001583126100001

Document Type: Article

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Research Areas: Science & Technology - Other Topics; Energy & Fuels

Output Date: 2025-11-26

Record 7

Title: Potato-onion intercropping enhances tomato yield and quality and modifies soil microbial diversity

Author(s): He, XJ (He, Xingjia); Zhang, AJ (Zhang, Aijia); Sha, CM (Sha, Chenning); Wu, FZ (Wu, Fengzhi); Yang, KJ (Yang, Kejun)

Source: SCIENTIFIC REPORTS **Volume:** 15 **Issue:** 1 **Article Number:** 30573 **DOI:** 10.1038/s41598-025-15045-1 **Published Date:** 2025 AUG 20

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Intercropping can promote sustainable agricultural development and increase economic benefits by enhancing ecosystem stability, soil health, and resource use efficiency. In this study, we analyzed the effects of tomato monoculture and tomato/potato-onion intercropping on tomato root distribution and bacterial and fungal communities in tomato rhizosphere by stratified subsection excavation method, quantitative PCR, and Illumina MiSeq sequencing. The results indicated that the root system of monoculture tomato farming did not exhibit significant displacement, whereas the tomato root system in intercropping exhibited spatial adjustments to avoid competition. Intercropping increased soil pH, nitrate nitrogen (NO3--N), available phosphorus (AP), and available potassium (AK), but decreased soil electrical conductivity (EC). Intercropping increased tomato biomass, yield, and quality, but reduced the number of diseased fruits caused by tomato blossom-end rot. Additionally, intercropping increased alpha-diversity and altered the composition and structure of bacterial and fungal communities, as well as the abundance of potentially beneficial bacteria (e.g., Bacillus spp. and Pseudomonas spp.). Redundancy analysis (RDA) based on the euclidean distance were used to evaluate the relationship between bacterial and fungal community structures and various factors. The results indicated that soil bacterial and fungal communities in tomato/potato-onion system were significantly positively correlated with AP, NO3--N, pH, and yield, while EC in monoculture system was significantly positively correlated with bacterial communities, but negatively correlated with fungal communities. Microbial co-occurrence network analysis showed that, compared with the monoculture tomato farming, the tomato rhizosphere bacterial community in the intercropping system exhibited significantly enhanced network connectivity. This was manifested by a substantial increase in degree and graph density, alongside reduced modularity. Conversely, the fungal community network connectivity in the intercropped tomato rhizosphere was significantly weakened, characterized by decreased degree and graph density, with a concurrent increase in modularity. Overall, our study demonstrated that intercropping with potato-onion changed tomato root distribution, increased soil microbial community diversity and changed community structure, and improved the soil environment, which may be the key factors to promote the growth of tomato and improve the yield and quality of tomato.

Accession Number: WOS:001577164900026

Document Type: Article

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Research Areas: Science & Technology - Other Topics

Output Date: 2025-11-26

Record 8

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

Author(s): 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)

Source: PLOS ONE **Volume:** 20 **Issue:** 5 **Article Number:** e0322026 **DOI:** 10.1371/journal.pone.0322026 **Published Date:** 2025

Times Cited in Web of Science Core Collection: 2

Total Times Cited: 2

Abstract: 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.

Accession Number: WOS:001488720800047

Document Type: Article

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[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.

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Research Areas: Science & Technology - Other Topics

Output Date: 2025-11-26

Spectroscopy

Record 1

Title: Early Detection of Northern Corn Leaf Blight Using Hyperspectral Images Combined With One-Dimensional Convolutional Neural Networks

Author(s): Lu, Y (Lu, Yang); Gu, FQ (Gu, Fu-qian); Gu, NN (Gu, Ninh-nan); Xu, SY (Xu, Si-yuan); Wang, P (Wang, Peng)

Source: SPECTROSCOPY AND SPECTRAL ANALYSIS **Volume:** 45 **Issue:** 8 **Pages:** 2302-2310 **DOI:** 10.3964/j.issn.1000-0593(2025)08-2302-09 **Published Dat**

e: 2025 AUG

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: Northern corn leaf blight (NCLB) occurs in major maize producing regions globally, leading to a reduction in both maize quality and yield. Disease identification typically occurs when lesions are more obvious, making it challenging to prevent And control the disease promptly. This study proposes a one-dimensional convolutional neural network (IDCNN) model for early disease detection using hyperspectral imaging. In this research, NCLB was selected as the target disease. After manual poculation, maize leaves at the silking stage were used for experiments, when lesions had just begun to appear, but the disease ould not yet be visually identified. First, hyperspectral images were captured using the SOC710E spectrometer, and spectral data of both healthy and NCLB-infected maize leaves were obtained by selecting regions of interest. Four spectral preprocessing methods Savitzky-Golay smoothing (SG), multiplicative scatter correction (MSC), standard normal variate transformation (SNV), and detrending (DT) were applied to remove noise from the spectral data. Supervised learning algorithms, random forest (RF) and K-nearest neighbors (KNN), were employed for hyperspectral image classification, with accuracy as the Evaluation metric. The results indicated that MSC was the optimal preprocessing method. achieving prediction accuracies of88. 13% and 86.26% for the RF and KNN models, respectively. Next. a competitive adaptive reweighted sampling (CARS) algorithm was applied to extract characteristic wavenumbers from the maize leaf spectral data, reducing the original 260 wavenumbers to 48 selected features, Finally, a 1DCNN deep learning model was developed for classification, achieving an Accuracy of 99.61%. Compared with traditional classification models such as KNN, RF, partial least squares discriminant analysis (PLS-DA), backpropagation neural network (BP), and support vector machines (SVM), the proposed model improved recognition accuracy by 5.94%, 6.88%, 6.48%, 8.27%, 12.12%, respectively. These findings demonstrate that combining Lyperspectral technology with deep learning models provides a new approach and method for early detection of maize diseases, enhancing the accuracy and timeliness of disease recognition.

Accession Number: WOS:001578696700001

Document Type: Article

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Research Areas: Spectroscopy

Output Date: 2025-11-26

Thermodynamics

Record 1

Title: Material removal mechanism based on scratched surface and abrasive chips in ultrasonic-assisted grinding of SiCp/Al composites

Author(s): Wang, M (Wang, Ming); Gao, YP (Gao, YanPeng); Li, ZA (Li, ZhenAo); Dong, XW (Dong, XiaoWei)

Source: ADVANCES IN MECHANICAL ENGINEERING **Volume:** 17 **Issue:** 10 **Article Number:** 16878132251384823 **DOI:** 10.1177/16878132251384823 **Published Date:** 2025 OCT

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: To thoroughly investigate the influence of ultrasonic vibration on the removal process and the removal mechanism, scratching experiments are conducted, and chip shape characteristics are examined. The application of ultrasonic vibration produces a protective shielding effect on the material's surface cracks, thereby effectively reducing the risk of surface damage to the work piece. Additionally, the critical cutting depth in dynamic conditions can be increased, leading to enhanced plastic removal and reduced occurrence of surface fracture and fragmentation. The aluminum matrix interacts with the reinforcement particles, leading to their removal through plastic deformation. Moreover, certain portions of the substrate material undergo a phenomenon known as substrate coating. The elimination of SiC particles is achieved through the synergistic interaction between brittleness and plasticity, which arises from the continuous variation in the instantaneous cutting depth ap(t) of the abrasive on the tool within a specific amplitude range. This process involves phenomena such as particle displacement, detachment, and extraction.

Accession Number: WOS:001589364300001

Document Type: Article

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Research Areas: Thermodynamics; Engineering

Output Date: 2025-11-26

Veterinary Sciences

Record 1

Title: LGG/LAC-MMT combination mitigates AFB1-induced liver and intestinal injury in mice based on intestinal microbiota modulation

Author(s): Cheng, JX (Cheng, Jiaxin); Gao, Y (Gao, Ying); Lv, HM (Lv, Hongming); Li, J (Li, Jing); Sun, XD (Sun, Xudong); An, TH (An, Tianhui); Liu, HL (Liu, Honglin); Wang, JQ (Wang, Junqi); Zhang, HF (Zhang, Haifeng); Wang, HY (Wang, Haiyan); Zou, SQ (Zou, Siqi); Fan, Z (Fan, Zhao); Chen, YY (Chen, Yuanyuan)

Source: FRONTIERS IN VETERINARY SCIENCE **Volume:** 12 **Article Number:** 1654294 **DOI:** 10.3389/fvets.2025.1654294 **Published Date:** 2025 OCT 21

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: AFB1 induces hepatotoxicity and enterotoxicity. Lactobacillus acidophilus (LAC) and Lactobacillus rhamnosus (LGG), both belonging to LAB, have strong binding affinity for AFB1. Montmorillonite (MMT) not only adsorbs AFB1 but also serves as a carrier for LAB, thereby enhancing their colonization ability and prolonging their survival. Despite the unclear effects of LGG/LAC-MMT combination on AFB1-induced tissue injury and intestinal microbiota disruption, this study aimed to determine whether it could effectively alleviate tissue damage from AFB1 exposure and enhance LAB colonization capacity in mouse intestines. Separately, LGG (2 x 109 cfu/mL) and LAC (2 x 109 cfu/mL) were combined with MMT (0.5 mg/kg), and the AFB1-intoxicated mice were gavaged with the mixtures for 4 weeks. Findings suggested that LGG, LAC, and MMT supplementation restored oxidative stress and inflammatory caused by AFB1 to some degree. Furthermore, they altered the intestinal microbiota structure, enhancing the colonization ability of LABs, thereby alleviating liver and intestinal injury. The combination of LGG/LAC-MMT was more effective, especially LAC-MMT. Overall, LGG/LAC-MMT exhibits a synergistic effect and can effectively ameliorate AFB1-induced tissue injury and intestinal microbiota disorder.

Accession Number: WOS:001607624500001

Document Type: Article

Addresses: [Cheng, Jiaxin; Gao, Ying; Lv, Hongming; Sun, Xudong; An, Tianhui; Liu, Honglin; Wang, Junqi; Zhang, Haifeng; Wang, Haiyan; Zou, Siqi; Fan, Zhao; Chen, Yuanyuan] Heilongjiang Bayi Agr Univ, Coll Anim Sci & Vet Med, Daqing Hightech Ind Dev Zone, Daqing, Peoples R China.

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Research Areas: Veterinary Sciences

Output Date: 2025-11-26

Virology

Record 1

Title: Polyvalent phage GSP004 recognizes O-antigen polysaccharide receptors in Salmonella and Escherichia coli through tail fiber protein ORF208

Author(s): Gao, DY (Gao, Dongyang); Pang, SY (Pang, Shenyu); Zhao, YH (Zhao, Yuanhang); Pan, SY (Pan, Shunyuan); Kong, XY (Kong, Xiangyu); Song, J (Song, Jun); Sun, DB (Sun, Dongbo)

Source: JOURNAL OF VIROLOGY **DOI:** 10.1128/jvi.00810-25 **Early Access Date:** NOV 2025 **Published Date:** 2025 NOV 18

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: The majority of phages are capable of lysing only specific bacterial strains within a single species, and polyvalent phages with cross-genus lytic capability are relatively rare. In this study, we isolated a polyvalent phage, GSP004, from swine farm wastewater, which exhibited cross-genus lytic activity against multiple Salmonella serovars and Escherichia coli (E. coli) O157:H7. Morphological classification assigns GSP004 to the family Myoviridae within the order Caudovirales, while phylogenetic analysis of its genome identifies it as a member of the genus Kuttervirus in the family Ackermannviridae. The periodate/proteinase K assays confirmed bacterial surface polysaccharides as the host receptor targeted by GSP004. Combined with lipopolysaccharide (LPS) competitive adsorption assays, gene knockout strain spot/adsorption/dynamic lysis assays, and phage nucleic acid release experiments, we demonstrated that the O-antigen of LPS was the sole receptor for GSP004 to infect Salmonella and E. coli O157:H7, respectively. Subsequent characterization via protein competition adsorption, antibody blocking, and fluorescent labeling experiments identified the tail protein ORF208 as the receptor-binding protein (RBP) recognizing LPS O-antigens. Further studies revealed that phage GSP004 employs its tail protein ORF208 to recognize and bind to the LPS O-antigen of Salmonella and E. coli through distinct molecular mechanisms, thereby mediating cross-genus infection. This finding provides critical molecular insights into the interaction between polyvalent phages and their bacterial hosts.IMPORTANCEElucidating the molecular mechanism of cross-genus host recognition in polyvalent phages will provide a critical theoretical foundation for the rational design of broad-host-range phages. However, research on the cross-genus host recognition mechanisms of polyvalent phages remains scarce. Here, we isolated a polyvalent phage GSP004, which serves as an exemplary model for investigating the interaction mechanisms between such polyvalent phages and their bacterial hosts. Our study elucidates the molecular basis underlying the capability of GSP004 to simultaneously infect Salmonella and E. coli O157:H7 across genera. This study provides crucial molecular evidence for understanding the evolutionary strategies by which phages expand their cross-genus host range and establishes a theoretical foundation for the rational design of broad-host-range phage therapeutics.

Accession Number: WOS:001616413700001

Document Type: Article; Early Access

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Research Areas: Virology

Output Date: 2025-11-26

Record 2

Title: A glycoprotein D-targeted lipid nanoparticle-encapsulated mRNA vaccine elicits strong protective immunity against pseudorabies virus

Author(s): Sun, Y (Sun, Yue); Xu, SJ (Xu, Shi-Jia); Zhou, YF (Zhou, Yongfei); Zhang, YH (Zhang, Yanhe); Zhang, HL (Zhang, Hongliang); Le, T (Le, Ting); Bai, YZ (Bai, Yuan-Zhe); Rao, CH (Rao, Cui-Hong); Huo, SS (Huo, Shanshan); Zhou, TC (Zhou, Tianceng); An, TQ (An, Tong-Qing); Yin, X (Yin, Xin); Yu, F (Yu, Fei); Cai, XH (Cai, Xue-Hui); Tang, YD (Tang, Yan-Dong)

Source: JOURNAL OF VIROLOGY **DOI:** 10.1128/jvi.01472-25 **Early Access Date:** NOV 2025 **Published Date:** 2025 NOV 6

Times Cited in Web of Science Core Collection: 0

Total Times Cited: 0

Abstract: The pseudorabies virus (PRV), a highly contagious pathogen with zoonotic potential, continues to threaten swine production and public health due to the emergence of virulent variants and insufficient protection conferred by conventional live attenuated vaccines. Although commercial vaccines are safe for pigs, their residual pathogenicity in other susceptible species underscores the demand for universally safe alternatives. Here, we engineered a lipid nanoparticle-encapsulated mRNA vaccine (mRNA-LNPs) expressing PRV glycoprotein D (gD) and evaluated its efficacy in murine and porcine models. In mice, vaccination with gD mRNA-LNPs elicited potent neutralizing antibodies and provided complete protection against lethal PRV challenge. In piglets, immunization induced rapid humoral immune responses, significantly reduced viral loads in tissues and viral shedding post-challenge, and alleviated histopathological damage. Mechanistically, except for its ability to elicit neutralizing antibodies, the vaccine also stimulated antigen-specific CD3+CD4+ T-cell and CD3+CD8+ T-cell proliferation and enhanced IFN-gamma production, demonstrating robust activation of both humoral and cellular immunity. These findings establish gD mRNA-LNPs as a safe, effective, and broadly applicable vaccine candidate for PRV control across susceptible species, with advantages in scalability and biosafety over traditional platforms.IMPORTANCEThe emergence of virulent pseudorabies virus (PRV) variants and the insufficient cross-species protection conferred by conventional live attenuated vaccines pose significant challenges to global swine production and zoonotic biosecurity. Here, we developed a lipid nanoparticle-encapsulated mRNA vaccine (gD mRNA-LNPs) targeting PRV glycoprotein D (gD), a critical mediator of viral entry. This vaccine elicits robust neutralizing antibodies and potent T-cell responses, providing complete protection against lethal PRV challenge in both murine and porcine models. Unlike traditional vaccines, gD mRNA-LNPs eliminates residual pathogenicity risks and demonstrates broad efficacy against diverse PRV strains, including emerging variants. Its scalable production platform and ability to differentiate vaccinated from infected animals via serological diagnostics align with One Health strategies for PRV eradication. This study establishes mRNA-LNPs technology as a versatile, safe, and effective solution for combating PRV, with implications for improving livestock health and reducing zoonotic spillover threats.

Accession Number: WOS:001608665900001

Document Type: Article; Early Access

Addresses: [Sun, Yue; Xu, Shi-Jia; Zhang, Yanhe; Zhang, Hongliang; Le, Ting; Bai, Yuan-Zhe; Rao, Cui-Hong; An, Tong-Qing; Yin, Xin; Cai, Xue-Hui; Tang, Yan-Dong] Chinese Acad Agr Sci, Harbin Vet Res Inst, State Key Lab Anim Dis Control & Prevent, Harbin, Peoples R China.
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Research Areas: Virology

Output Date: 2025-11-26

3 EI 收录情况

（2025.10.02-2025.11.26）

3.1 EI Compendex

EI 索引库共收录我校教师发表的 52 篇文献，文献详细题录信息如下。

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1. Experimental study on thermal properties of foamed concrete with expanded perlite aggregate particle size and gradation

Liu, Yandong (School of Civil Engineering and Architecture, Northeast Petroleum University, Fazhan Lu Street, Daqing; 163318, China); Ma, Lingyonxg; Jiang, Wei; Li, Qing; Qiao, Ming; Fan, Shijie; Li, Dong

Source: Journal of Building Engineering, v 114, November 15, 2025

Database: Compendex

Data Provider: Engineering Village

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2. Design of a Herd Health Identification System Based on YOLOv11

(*Open Access*)

Zhu, Jun (School of Information and Electrical Engineering, Heilongjiang Bayi Agricultural University, Daqing, China)

Source: Advances in Transdisciplinary Engineering, v 74, p 1134-1143, August 28, 2025, Moving Integrated Product Development to Service Clouds in the Global Economy - Proceedings of the 21st ISPE Inc. International Conference on Concurrent Engineering, CE 2014

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

Database: Compendex

Data Provider: Engineering Village

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3. Effects of Ultrasonic Assisted Autoclave Modification on the Structure, Physicochemical Properties and Digestibility of Corn Starch (超声辅助压热改性对玉米淀粉结构、理化性质及消化特性的影响)

Li, Huimin (College of Food Sciences, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Ruan, Changqing; Song, Xuejian; Li, Zhijiang; Tang, Huacheng; Wang, Changyuan

Source: Science and Technology of Food Industry, v 46, n 20, p 1-8, October 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

Compilation and indexing terms, Copyright 2025 Elsevier Inc.

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4. Study on the Rheological Properties, Aeration Performance, and Flavor Quality of Whipping Cream With Different Lipid Composition (不同脂质组成的搅打奶油的流变学特性&充气性能及风味品质研究)

Hou, Yi-Fei (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Liang, Chao; Cao, Hong-Fang; Li, Feng; Lu, Jia-Ping; Pang, Xiao-Yang; Zhang, Shu-Wen; Xie, Ning; Li, Xu; Wang, Xiao-Dan; Du, Xin-Yu; Liu, Yan-Yan; Wang, Yun-Na

Source: Guang Pu Xue Yu Guang Pu Fen Xi/Spectroscopy and Spectral Analysis, v 45, n 10, p 2968-2977, October 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

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5. Effects of Shh Signal on the Proliferation and Differentiation of Follicular Granulosa Cells in Dairy Cows (Shh 信号对奶牛卵泡颗粒细胞增殖与分化的影响)

Sun, Han-Bing (College of Animal Science and Technology, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Xiang, Nian; Fang, Xin-Xin; Yue, Jun-Xiu; Xu, Qiu-Shi; Ma, Li

Source: Biotechnology Bulletin, v 41, n 9, p 326-334, September 26, 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

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6. Effect of Konjac Glucomannan Combined with Tea Polyphenols on Freeze-thawed Carp Surimi (魔芋葡甘聚糖联合茶多酚对冻融鲤鱼鱼糜蛋白的保护作用)

Li, Jia (College of Food, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Li, Yanqing; Li, Bo; Zhang, Jinghao

Source: Science and Technology of Food Industry, v 46, n 20, p 349-357, October 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

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7. PREPARATION OF BIOMASS SEEDLING TRAYS USING LIGNIN BONDING PROPERTIES AND DESIGN OF HEATING COMPRESSION FORMING MOLD (基于木质素粘结特性的生物质育苗盘制备及热压成型模具设计)

Li, Jin-Yang (College of Information and Electrical Engineering, Heilongjiang Bayi Agricultural University, Daqing, China); Zhang, Wei; Yu, Chun-Tao; Qi, Li-Qiang; Zhang, Bo

Source: INMATEH - Agricultural Engineering, v 76, n 2, p 900-909, 2025

Database: Compendex

Data Provider: Engineering Village

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8. DESIGN AND EXPERIMENT OF AN AIR-ASSISTED, GUIDED-GROOVE MAIZE SEED-GUIDING DEVICE BASED ON THE BRACHISTOCHRONE CURVE (基于最速降线的气辅-导槽式玉米导种装置设计与试验)

Sun, Wen-Sheng (College of Engineering, Heilongjiang Bayi Agricultural University, Daqing, China); Yi, Shu-Juan; Qi, Hai-Long; Li, Yi-Fei; Zhang, Yu-Peng; Yuan, Jia-Sha; Wang, Song

Source: INMATEH - Agricultural Engineering, v 76, n 2, p 210-222, 2025

Database: Compendex

Data Provider: Engineering Village

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9. A novel phage cocktail effectively control carbapenem-resistant Klebsiella pneumoniae in food production chain

Kong, Xiangyu (College of Animal Science and Veterinary Medicine, Heilongjiang Bayi Agricultural University, No. 5 Xinfeng Road, Daqing; 163319, China); Wei, Anbo; Pan, Shunyuan; Yuan, Qingxin; Chen, Qibai; Wang, Jintao; Li, He; Gao, Dongyang; Song, Jun

Source: SSRN, August 28, 2025

Database: Compendex

Data Provider: Engineering Village

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10. STABILITY ANALYSIS OF FLAT-ELLIPTICAL GREENHOUSE SKELETON CONSIDERING INITIAL GEOMETRICAL IMPERFECTIONS (考虑初始几何缺陷的平椭圆管大棚骨架稳定性分析)

Xie, Hengyan (College of Civil Engineering and Water Conservancy, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Wei, Cunxing; Zheng, Xin; Xu, Wenbao

Source: INMATEH - Agricultural Engineering, v 76, n 2, p 369-379, 2025

Database: Compendex

Data Provider: Engineering Village

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11. Corn protein hydrolysates as biostimulants: Effects on soybean physiology and rhizosphere microbial community in saline-alkali soil

Jiang, Caixia (National Coarse Cereals Engineering Research Center, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Liu, Handong; Liu, Xiaolan; Li, Yue; Wang, Juntong; Zheng, Xiqun

Source: Industrial Crops and Products, v 236, November 2, 2025

Database: Compendex

Data Provider: Engineering Village

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12. Differences in flavor profiles and meat quality of grass carp from China's jingpo lake across four thermal processing methods

Pan, De-yin (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing, China); Ma, Jin-ming; Li, Chang-bo; Du, Hong-zhen; Diao, Jing-jing; Chen, Hong-sheng

Source: Food Chemistry: X, v 31, October 2025

Database: Compendex

Data Provider: Engineering Village

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13. DESIGN AND EXPERIMENTAL STUDY OF A SHAFTLESS DOUBLE-SCREW FERTILIZER SPREADER FOR RICE (无轴双螺旋式水稻排肥器的设计与试验研究)

Wang, Ziyu (College of Information and Electrical Engineering, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Hong, Deyu; Wang, Hongchao; Liu, Chengyang; Ma, Zanfeng; Liu, Xingkang; Li, Wentao

Source: INMATEH - Agricultural Engineering, v 76, n 2, p 1177-1189, 2025

Database: Compendex

Data Provider: Engineering Village

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14. EXPERIMENTAL STUDY ON VARIABLE TEMPERATURE DRYING P ROCESS OF PADDY BASED ON GLASS TRANSITION (基于玻璃化转变的稻谷变温干燥工艺及试验研究)

Wang, Hongchao (College of Engineering, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Wang, Jing; Wang, Ziyu; Wan, Lin; Che, Gang; Wang, Shuo; Chen, Zhengfa

Source: INMATEH - Agricultural Engineering, v 76, n 2, p 1030-1041, 2025

Database: Compendex

Data Provider: Engineering Village

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15. Quantitative determination of multiple illegal additives in flour based on near-infrared spectroscopy

Wu, Siting (College of Information and Electrical Engineering, Heilongjiang Bayi Agricultural University, Daqing, China); Jian, Minghe; Wang, Chunqi; Liu, Jinming

Source: Journal of Computational Methods in Sciences and Engineering, 2025 Article in Press

Database: Compendex

Data Provider: Engineering Village

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16. Eugenol-Mung Bean Protein Hydrolysate Cleavage Interaction an d Intercropping Functional Activity and Structural Characterization (丁香酚-绿豆蛋白酶解物相互作用及互作物功能活性与结构表征)

Leng, Haijing (College of Food, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Shen, Yan; Zheng, Huaijun; Li, Jinling; Chen, Hongsheng; Cao, Rong'an; Diao, Jingjing

Source: Science and Technology of Food Industry, v 46, n 20, p 48-56, October 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

17. ELECTRIC RED BEAN PRECISION SEEDING CONTROL SYSTEM BASED ON IHBA-LADRC (基于IHBA-LADRC的电驱动红豆精量播种控制系统)

Li, Yi-Fei (College of Engineering, Heilongjiang Bayi Agricultural University, Heilongjiang, Daqing, China); Wang, Guang-Yu; Zhao, Lin; Yi, Shu-Juan

Source: INMATEH - Agricultural Engineering, v 76, n 2, p 1140-1154, 2025

Database: Compendex

Data Provider: Engineering Village

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18. Effects of Compound Bacteria Fermentation on Physicochemical Properties of Fresh Waxy Cornmeal Batter and Its Cake Quality (复合菌发酵对鲜食糯玉米面糊理化性质及其糕点品质的影响)

Liu, Yamei (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Zhu, Libin; Ma, Jing; Wang, Na; Zhu, Dan; Wei, Wenyi; Niu, Guangcai

Source: Science and Technology of Food Industry, v 46, n 20, p 21-30, October 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

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19. RESEARCH ON A DETECTION ALGORITHM FOR DRY-DIRECT SEEDED RICE BASED ON YOLOv11N-DF (基于YOLOv11N-DF的旱直播水稻检测算法研究)

Li, Mingyang (College of Engineering, Heilongjiang Bayi Agricultural University, Daqing, China); Zhao, Bin; Wang, Song; Wang, Di

Source: INMATEH - Agricultural Engineering, v 76, n 2, p 531-540, 2025

Database: Compendex

Data Provider: Engineering Village

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20. PADDY RICE POROSITY PREDICTION BASED ON SNAKE ALGORITHM OPTIMIZED SUPPORT VECTOR REGRESSION (基于蛇算法优化支持向量回归的稻谷孔隙率预测)

Zhang, Zhi-Qi (College of Engineering, Heilongjiang Bayi Agricultural University, Daqing, China); Wan, Lin; Che, Gang; Wang, Hong-Chao; Pan, Heng; Wang, Shuo

Source: INMATEH - Agricultural Engineering, v 76, n 2, p 723-734, 2025

Database: Compendex

Data Provider: Engineering Village

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21. Heating-homogenization synergistic preparation of soy protein isolate-sodium alginate composite particles and their performance study

Zhou, Lin (College of Life Science, Yantai University, Shandong, Yantai; 264005, China); Liu, Qian; Yue, Xidian; Chen, Hongsheng; Peng, Xinyan

Source: International Journal of Biological Macromolecules, v 330, November 2025

Database: Compendex

Data Provider: Engineering Village

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22. Joint resource optimization for IRS-assisted solar-powered MEC with MAPPO

Shi, Chengxi (School of Information and Electrical Engineering, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); He, Qiaohong; Song, Lei; Fu, Shuang; Yang, Lin

Source: Physical Communication, v 73, December 2025

Database: Compendex

Data Provider: Engineering Village

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23. CsAPRR2 regulates cucumber immature fruit color by coordinating chloroplast biogenesis and photosynthesis-related gene expression

Liu, Hanqiang (Hainan Institute of Northwest A&F University, Hainan, Sanya; 572024, China); Cui, Mingming; Hu, Kaihong; Tan, Junyi; Weng, Yiqun; Ma, Yuxuan; Li, Ju; Huang, Zeqiang; Chen, Birong; Meng, Huanwen; Pan, Yupeng; Cheng, Zhihui

Source: Plant Journal, v 123, n 6, September 2025

Database: Compendex

Data Provider: Engineering Village

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24. Cold-region Dry Direct-seeded Rice Plant Detection Method Based on Improved YOLO v11n (基于改进 YOLO v11n 的寒地旱直播水稻植株检测方法研究)

Zhao, Bin (College of Engineering, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Li, Mingyang; Wang, Song; Wang, Di; Sun, Bo; Xiao, Yanwei; Chen, Xiucheng

Source: Nongye Jixie Xuebao/Transactions of the Chinese Society for Agricultural Machinery, v 56, n 9, p 585-595, 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

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25. Genistein supplementation alleviates bone damage by regulating gut microbiota composition and metabolism in obesity and estrogen decline

Jin, Shengzi (College of Veterinary Medicine, Northeast Agricultural University, Harbin; 150030, China); Liu, Xingyao; Zheng, Yingce; Zhu, Tingting; Tong, Danning; Zhang, Runxiang; Liu, Yun

Source: Food and Function, v 16, n 19, p 7900-7918, September 29, 2025

Database: Compendex

Data Provider: Engineering Village

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26. Porosity, microstructure and performance control of laser metal deposition 17-4PH stainless steel components using laser shock forging method

Gao, Chuang (School of Engineering, Heilongjiang Bayi Agricultural University, Heilongjiang, Daqing; 163711, China); Li, Qing-da; Song, Ya-wei; Zhang, Xiao-chen; Yao, Jun; Huan, Peng-cheng; Wei, Xia; Wang, Xiao-nan

Source: Materials Letters, v 403, January 15, 2026

Database: Compendex

Data Provider: Engineering Village

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27. Effects of geographical origin, processing and their interaction on stable isotopes in Pu-erh tea for traceability

Li, Yanlong (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing, China); Zou, Hai-Dan; Wang, Xiao-Li; Chen, Ming-Ming; Zhang, Bo-Wen; Wang, Wen-Fang; Li, Jie; Jiang, He-Yuan; Qian, Li-Li; Liu, Hong-Yan

Source: Food Chemistry, v 496, December 25, 2025

Database: Compendex

Data Provider: Engineering Village

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28. ESTABLISHMENT AND VALIDATION OF A THEORETICAL MODEL FOR SINGLE LONGITUDINAL AXIAL FLOW THRESHING AND SEPARATION OF MILLET (谷子单纵轴流脱粒分离理论模型的建立与验证)

Zhang, Jun-Hui (College of Engineering, Heilongjiang Bayi Agricultural University, Daqing, China); Zhao, Lin; Yi, Shu-Juan; Zhang, Dong-Ming; Zhang, Xin

Source: INMATEH - Agricultural Engineering, v 76, n 2, p 100-110, 2025

Database: Compendex

Data Provider: Engineering Village

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29. SAFF-YOLO-BASED LIGHTWEIGHT DETECTION METHOD FOR THE DIAMONDBACK MOTH (基于 SAFF-YOLO 的白菜小菜蛾轻量化检测方法)

Wu, Miao (College of Engineering, Heilongjiang Bayi Agricultural University, Daqing, China); Shi, Hang; Liu, Changxi; Zhang, Hui; Li, Yufei; Bao, Derui; Hu, Jun

Source: INMATEH - Agricultural Engineering, v 76, n 2, p 142-155, 2025

Database: Compendex

Data Provider: Engineering Village

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30. RESEARCH ON THE TRAY CONVEYING AND OUTPUT DEVICE OF AN AUTOMATIC TRAY PLACEMENT MACHINE FOR MULTI-ROW RI

GID RICE SEEDLING TRAYS (多行水稻硬质育秧盘全自动摆盘机送盘与出盘装置研究)

Liu, Cheng-Long (College of Engineering, Heilongjiang Bayi Agricultural University, Daqing, China); Yi, Shu-Juan; Li, Yi-Fei; Wang, Song

Source: INMATEH - Agricultural Engineering, v 76, n 2, p 517-530, 2025

Database: Compendex

Data Provider: Engineering Village

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31. Preparation and Performance Analysis of Slow-release Antimicrobial Films Containing Oregano Essential Oil-loaded Rice Straw Cellulose-based Halloysite Nanotubes (稻草秸秆纤维素基埃洛石纳米管负载牛至精油缓释抗菌膜的制备与性能分析)

Zhang, Zitong (College of Food, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Zhang, Yuan; Wang, Miao; Li, Juan; Zhang, Dongjie

Source: Science and Technology of Food Industry, v 46, n 20, p 290-299, October 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

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32. Response surface optimization of high-voltage cold plasma for accelerating degradation of halloysite-sorghum straw biodegradable mulch films

Li, Juan (College of Food, Heilongjiang Bayi Agricultural University, Daqing, China); Zhang, Yuan; Wang, Miao; Zhang, Zitong; Zhang, Dongjie

Source: Chemical Engineering and Processing - Process Intensification, v 219, January 2026

Database: Compendex

Data Provider: Engineering Village

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33. Lipoxygenase ZmLOX3 Enhances Salt Tolerance of Maize Under the Regulation of ZmNAC032

Che, Xinyang (Key Lab of Modern Agricultural Cultivation and Crop Germplasm Improvement of Heilongjiang Province, College of Agriculture, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Wei, Yulei; Wang, Xueheyuan; Wang, Xinqi; Wu, Zixuan; Deng, Jie; Ge, Shengnan; Liu, Xinyu; Cai, Zhicheng; Zhang, Haiyang; He, Lin; Xu, Jingyu

Source: Journal of Agricultural and Food Chemistry, v 73, n 42, p 26516-26528, October 22, 2025

Database: Compendex

Data Provider: Engineering Village

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34. Rapid and Non-destructive Identification of Wuchang Daohuaxiang Rice Using Near-Infrared Spectroscopy and t-Distributed Stochastic Neighbor Embedding

Sun, Xinyue (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Li, Yanlong; Chen, Mingming; Song, Yan; Qian, Lili; Zuo, Feng; Guan, Hai'Ou; Zhang, Tao; Liu, Xingquan; Zhou, Guoxin Source: Shipin Kexue/Food Science, v 46, n 20, p 318-326, October 25, 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

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35. DESIGN AND TESTING OF A WINGED SUBSOILER SHOVEL FOR STRIP MINIMUM-TILLAGE DEEP LOOSENING FERTILISER MACHINE (条带少耕深松施肥机带翼式深松铲设计与试验)

Xu, Shi-Cheng (College of Engineering, Heilongjiang Bayi Agricultural University, Daqing, China); Tao, Gui-Xiang; Yi, Shu-Juan; Wang, Song; San, Yu-Hang

Source: INMATEH - Agricultural Engineering, v 76, n 2, p 910-922, 2025

Database: Compendex

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36. A Privacy Protection Method for Trustworthy Traceability of Rice Supply Chain Based on Blockchain and Multilayer Encryption

Yu, Runzhong (College of Computer Science and Technology, Harbin Engineering University, Harbin, China); Yang, Wu; Zhang, Liyuan

Source: Concurrency and Computation: Practice and Experience, v 37, n 27-28, December 25, 2025

Database: Compendex

Data Provider: Engineering Village

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37. Untargeted metabolomics reveals phenolic compound dynamics during mung bean fermentation

Lang, Shuangjing (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Liu, Lijuan; Li, Zhenjiang; Liu, Shilin; Liang, Jiaxin; Lu, Lele; Wang, Lidong

Source: Food Chemistry: X, v 31, October 2025

Database: Compendex

Data Provider: Engineering Village

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38. Effects of Synergistic Addition of Corn Steep Liquor Hydrolysate and Amino Acids on the Synthesis of Ergothioneine by Fermentation of Pleurotus ostreatus (玉米浆水解液和氨基酸协同添加对糙皮侧耳发酵合成麦角硫因的影响)

Li, Lin (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Li, Jing; Liu, Xiaolan; Jiang, Caixia; Wang, Juntong; Zheng, Xiqun

Source: Science and Technology of Food Industry, v 46, n 22, p 247-255, November 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

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39. Effect of Exogenous Antioxidant Peptides on Quality and Oxidation Characteristics of Cantonese Sausage during Processing (外源性抗氧化肽对广式腊肠加工过程中品质及氧化特性的影响)

Bao, Wei (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Li, Yuchen; Guo, Tingyu; Han, Qi; Li, He

Source: Science and Technology of Food Industry, v 46, n 21, p 48-57, November 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

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40. A PSiO2/ZnO aptamer microarray chips based on "quenching-restoration" fluorescence strategy for multiple mycotoxin determination

Chen, Jiayu (College of Food Science, Heilongjiang Bayi Agricultural University, 5 Xinfeng Road, Daqing; 163319, China); Yao, Boxiang; Yu, Runzhong; Zhang, Liyuan; Zhang, Han

Source: Talanta, v 298, February 1, 2026

Database: Compendex

Data Provider: Engineering Village

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41. Effect of Lactic Acid Bacteria Fermentation on the Main Components and Antioxidant Activity of Cranberry Juice (乳酸菌发酵对蔓越莓汁主要成分及抗氧化活性的影响)

Zhao, Chenyu (Food College, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Zhu, Libin; Zhu, Dan; Yang, Tianyou; Niu, Guangcai; Wei, Wenyi; Ma, Jing

Source: Science and Technology of Food Industry, v 46, n 21, p 187-195, November 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

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42. Protective Effect of British Red Kidney Bean Peptide Fractions on Ethanol-induced Gastric Mucosal Epithelial Cell Injury (英国红芸豆多肽组分对乙醇诱导的胃黏膜上皮细胞损伤的保护作用)

Zhang, Yajuan (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Dong, Zhihao; Zu, Lijia; Wang, Kun; Li, Dan; Zuo, Feng

Source: Science and Technology of Food Industry, v 46, n 21, p 425-435, November 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

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43. Effects of Catechins on Structure and Antioxidant Activity of Coix Seed Protein (儿茶素对薏米蛋白结构及抗氧化活性的影响)

Yu, Wenjing (College of Food, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Zhang, Yiwei; Diao, Jingjing; Zhang, Dongjie

Source: Science and Technology of Food Industry, v 46, n 22, p 124-134, November 2025

Language: Chinese

Database: Compendex

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44. Mitoquinone Mesylate Enhances Bovine Oocyte In Vitro Maturation Efficiency by Modulating Oxidative Stress and Enhancing Mitochondrial Function

Li, Yongxin (College of Animal Science and Technology, Heilongjiang Bayi Agricultural University, Heilongjiang, Daqing, China); Li, Mengman'; Wang, Hongtao'; Chen, Xiaoxin; Luan, Hu'; Lv, Junwei'; Li, Xintao'; Li, Jingchun'; Zhang, Lichun

Source: SSRN, October 19, 2025

Database: Compendex

Data Provider: Engineering Village

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45. A Distributed Adaptive Differential Privacy Mechanism With Blockchain Integration for Edge Computing

Sun, Yuhan (College of Science, Heilongjiang Bayi Agricultural University, Daqing, China); Hou, Suipeng; Zhao, Jie; Ye, Jinhua

Source: Security and Privacy, v 8, n 6, November/December 2025

Database: Compendex

Data Provider: Engineering Village

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46. A Multimodal Recommendation Algorithm Integrating Project Text and Image Information

Li, Tian-Hao (Heilongjiang Bayi Agricultural University, College of Information and Electrical Engineering, Daqing, China); Ma, Tie-Min; Wang, Xue

Source: 2025 International Conference on Electrical Engineering, Automation and Information Science, EEAIS 2025, p 191-195, 2025, 2025 International Conference on Electrical Engineering, Automation and Information Science, EEAIS 2025

Database: Compendex

Data Provider: Engineering Village

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47. Modeling and analysis of active thermal regulation in segmented PCM wall systems for optimizing energy efficiency in severe cold regions

Li, Jingwei (School of Architecture and Civil Engineering, Northeast Petroleum University, Daqing; 163318, China); Han, Zhonghong; Luo, Dan; Xue, Ting; Jia, Jiaojio; An, Shuai; Li, Dong; Cheng, Yujing; Li, Qing; Jiang, Wei

Source: Sustainable Energy Technologies and Assessments, v 84, December 2025

Database: Compendex

Data Provider: Engineering Village

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48. Adipose stem cells attenuate apoptosis by regulating C/EBP-homologous protein transcriptional activity in canines with acute pancreatitis

Ge, Yansong (College of Animal Science and Veterinary Medicine, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Chen, Mingzhen; Ding, Ruxin; Wan, Zhiying; Xu, Enshuang; Zheng, Jiasan

Source: International Journal of Biological Macromolecules, v 334, December 2025

Database: Compendex

Data Provider: Engineering Village

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49. Effects of Modification Methods on Structure and Physicochemical Properties of Insoluble Dietary Fiber in Oat Bran (改性方法对燕麦麸皮不溶性膳食纤维结构及理化特性的影响)

Yu, Wenting (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Zhang, Shu; Fu, Tianxin; Wang, Changyuan

Source: Science and Technology of Food Industry, v 46, n 22, p 61-70, November 2025

Language: Chinese

Database: Compendex

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50. Effect of phosphoric acid-microbial agent on ammonia emission reduction in liquid slurry (磷酸-微生物菌剂对生猪粪水氨气减排效果的影响)

Zou, Hongyu (Institute of Energy and Environmental Protection, Academy of Agricultural Planning and Engineering, MARA, Beijing; 100121, China); Zhang, Pengyue; Hou, Shance; Zhou, Haibin; Shen, Yujun; Xu, Pengxiang; Qin, Yiwei; Ding, Jingtao

Source: Nongye Gongcheng Xuebao/Transactions of the Chinese Society of Agricultural Engineering, v 41, n 8, p 253-260, September 2025

Language: Chinese

Database: Compendex

Data Provider: Engineering Village

51. Outlier Identification Method Based on Multi-Model Weighted Consensus in Conjunction With Monte Carlo Cross-Validation

Wang, Yujing (Heilongjiang Bayi Agricultural University, College of Information and Electrical Engineering, Daqing; 163319, China); Chen, Zhengguang; Liu, Jinming; Wang, He

Source: Journal of AOAC International, v 108, n 6, p 818-827, November 1, 2025

Database: Compendex

Data Provider: Engineering Village

52. Physicochemical Properties and Immunomodulatory Activity of Exopolysaccharide Produced by Lactic Acid Bacteria in Fermented Mung Bean Porridge (发酵绿豆粥中乳酸菌胞外多糖的理化特性及免疫调节活性研究)

Li, Silu (College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China); Wang, Kun; Pan, Yuxi; Tai, Mengdie; Zhao, Jing; Qian, Lili; Zuo, Feng

Source: Science and Technology of Food Industry, v 46, n 21, p 78-90, November 2025

Language: Chinese

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