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Preface

Abstract Book of ICASB2026 & ICCBE2026 is composed of the abstracts of the 2026 7th International Conference on Agricultural Science and Biotechnology (ICASB2026) and 2026 7th International Conference on Chemical and Biological Engineering (ICCB2026). According to the similarity among the topics of ICASB2026 and ICCBE2026, ICASB2026 is held in conjunction with ICCBE2026 on August 16-18, 2026.

ICASB2026 and ICCBE2026 serve as an optimal platform for specialists, scholars and researchers in the field related to agricultural science, biotechnology, chemical engineering and biological engineering to facilitate academic communications and exchange ideas. These abstracts demonstrate the richness of interdisciplinary approaches, theories, models and applied research presented.

Major themes of the conferences include:

Agricultural Science: Agricultural Biotechnology, Agricultural Chemistry, Agricultural Diversification, Agricultural Education, Agricultural Economics, Agroecology, Agrophysics, Animal Breeding, Animal Husbandry, Animal Nutrition, Farm Management, etc.

Biotechnology: Industrial Biotechnology, Nanobiotechnology, Medical Biotechnology, Agro- and Food Biotechnology, Vector Technology, Imaging Technology, Single Cell Technology, Nanobiotechnology and Biomaterials, Omics Technology, Plant Biotechnology, Sequencing Technology, etc.

Chemical Engineering: Supramolecular Chemistry, Thermochemistry, Supramolecular and Nanoscale Chemistry, Computational and Modeling Chemistry, Crystallography and Physical Methods, Molecular Chemistry, Inorganic Materials and Polymers, Catalysis and Organometallic Chemistry, Medicinal and Bioinorganic Chemistry, Fundamental Chemistry, Applied Chemistry, etc.

Biological Engineering: Cell Engineering, Molecular Bioengineering, Nucleic Acid Engineering, Food Process Engineering, Physiological Engineering, Energy Systems Engineering, Soil and Water Engineering, Environmental Bioengineering, Bioresources and Biorefinery Engineering, Biomaterials and Tissue Engineering, Cell Culture Engineering, etc.

We thank all authors for their scientific contribution to ICASB2026 and ICCBE2026 and look forward to having the opportunity to showcase and disseminate your research.

Sincerely,

ICASB2026 and ICCBE2026 Organizing Committees

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The Nutritional Composition Analysis of Fermented Fruit Peels and Their Potential Use in Soil Fertilization

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Abstract

This study is based on a school project, aiming at the evaluation of using fermented fruit peel solution as soil fertiliser. This application, if proven to be successful, will be a potential way to improve the recycling of kitchen waste. In order to reach this goal, the bacteria content, pH value, nutrition and ethanol composition were analysed. The bacteria of the fermented solution may improve the bacterial diversity of the soil. The fermented fruit peels are known to be acidic and may be used to neutralise the alkaline soil in Tianjin. The nutrition analysis included nitrogen, potassium and phosphorus as these meet the main nutritional requirements of plants (Zhou X et al., 2014; Liu T, Lin Y et al., 2021). Ethanol content was also investigated because fermented solution is known to have ethanol content, but too much ethanol will disrupt the bacterial balance in the soil and also damage plant growth. Fermentation receipt is as follow, brown sugar : fruit peel : water = 1 : 3 : 10 (Zhou X et al., 2014). Fermentation happened in a closed container. The fermentation mixture was kept indoors, without direct sunlight. Test the pH value twice a week to monitor the change of acidity of the fermented mixture. Temperature was recorded on daily basis. First round fermentation lasted for 3 months. Second round fermentation lasted for 6 weeks. Nitrogen, potassium, phosphorus and ethanol detection were all carried out by students in the school chemistry lab. Nitrogen was detected by Kjeldahl Method. Phosphorus was tested by Mo-Sb-Ascorbic Acid Colorimetry. Potassium was analysed by Flame Photometry and ethanol was quantified by Hydrometry. The preliminary results are promising so far, with good nutritional content and tolerable ethanol content. Lactobacillus was detected in the fermented solution. The end pH value of fruit peel fermentation was between 3-4. The mild to medium acidic property is useful to neutralize the alkaline soil in Tianjin. Further studies are planned to be carried out to investigate the nutritional contents of other fruit and vegetable peels, and bio-assays should be carried out as well to investigate the effect of fermented mixture on plant growth.

Keywords

Kitchen Waste, Fruit Peel Fermentation, Nitrogen, Phosphorus and Potassium Content, pH Value, Microbial Analysis, Ethanol Content, Soil Fertilization

Effects of SMDT1 Knockout on Skeletal Muscle Development and Energy Metabolism in Mice

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Abstract

This study aimed to investigate the effects of SMDT1 knockout on skeletal muscle development and energy metabolism in mice. The SMDT1 heterozygous knockout (SMDT1^{+/-}) mouse model was successfully generated using CRISPR/Cas9 gene editing technology; breeding experiments revealed that homozygous knockout resulted in embryonic lethality. Body weight, glucose tolerance, insulin tolerance, and respiratory metabolic capacity were systematically evaluated in SMDT1^{+/-} and wild-type (WT) mice to assess the impact of SMDT1 deficiency on energy metabolism. The expression levels of myogenic differentiation marker genes and muscle fiber type-related genes in the soleus muscle were quantified by qRT-PCR. Furthermore, mRNA transcriptome sequencing was performed on soleus muscle tissues from SMDT1^{+/-} and WT mice to identify differentially expressed genes (DEGs). The results demonstrated that SMDT1^{+/-} mice exhibited significantly increased body weight, impaired glucose and insulin tolerance, and reduced oxygen consumption and CO₂ production, indicating diminished respiratory metabolic capacity compared with WT littermates. The expression levels of myogenic differentiation genes (*Myod*, *Myog*, *Myf5*, *Myhc*) and slow-twitch fiber marker genes (*Myh7*, *Myh2*) were markedly upregulated in the soleus muscle of SMDT1^{+/-} mice, whereas fast-twitch fiber marker genes (*Myh4*, *Myh1*) were significantly downregulated, suggesting that SMDT1 deficiency promotes myogenic differentiation and facilitates the transition from fast-twitch to slow-twitch muscle fibers. Transcriptome analysis identified 1,908 DEGs (942 upregulated and 966 downregulated), which were predominantly enriched in biological processes including skeletal muscle contraction, muscle cell development, glycolysis/gluconeogenesis, the PPAR signaling pathway, and the MAPK signaling pathway. In conclusion, SMDT1 plays a pivotal role in regulating skeletal muscle development and energy metabolism; its deletion transcriptionally reprograms myogenic differentiation and muscle fiber type switching while impairing systemic glucose homeostasis and metabolic capacity. These findings provide novel insights into the molecular mechanisms by which SMDT1 governs muscle growth and meat quality traits.

Keywords

SMDT1, Skeletal Muscle Development, Muscle Fiber Type Switching, Energy Metabolism, CRISPR/Cas9

Heavy Metal Effects on Photosynthesis in *Scenedesmus Quadricauda*: Silver and Copper Comparison via OJIP Fluorescence

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Abstract

Heavy metal contamination critically threatens aquatic ecosystems. Microalgae serve as sensitive sentinel organisms, yet conventional growth and survival metrics only reflect ultimate outcomes rather than early cellular damage. This study investigated Ag^+ and Cu^{2+} toxicity to the photosynthetic apparatus of *Scenedesmus quadricauda* using the OJIP chlorophyll fluorescence test. Algal cultures were exposed to AgNO_3 (1–20 μM) and CuSO_4 (10–80 μM) for 2 and 18 hours. Results showed that both metals affected photosynthesis in a concentration- and time-dependent manner, but their toxicity profiles differed markedly. Silver induced rapid, pronounced alterations, with most damage occurring within 2 hours; extending exposure to 18 hours yielded minimal additional toxicity. This acute effect reflects Ag^+ binding to thiol groups, competitive substitution in plastocyanin disrupting electron transport, and oxidative stress induction. Conversely, copper exerted gradual, cumulative toxicity, with severe consequences emerging only after prolonged exposure. This delayed effect stems from Cu^{2+} redox cycling via Fenton-like reactions, generating hydroxyl radicals that cause primary cellular damage. Excess Cu also predisposes PSII to photoinhibition by inducing iron deficiency, reducing chlorophyll content and compromising photosynthetic integrity. For both ions, effects intensified with increasing concentration. These divergent kinetics carry important implications: silver's rapid action suggests acute contamination causes immediate, largely irreversible damage to primary producers, whereas copper's cumulative nature implies chronic low-level exposure leads to progressive ecosystem degradation through sustained photosynthetic impairment. The findings underscore the need for species-specific, time-resolved biomonitoring that integrates biophysical fluorescence parameters with traditional ecotoxicological endpoints, supporting mechanistic understanding of heavy metal–photosystem interactions and informing early-warning systems and evidence-based regulatory thresholds for freshwater ecosystems.

Keywords

Heavy Metals, *Scenedesmus Quadricauda*, Photosynthesis, Ojip Test, Chlorophyll Fluorescence

Variety and Environmental Factors Affecting Pru p 7 Level in Peach Fruit: Implications for Hypoallergenic Variety Selection

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Abstract

Peach allergy is a global food safety concern. Pru p 7, a gibberellin-regulated protein, has recently been recognized as a clinically relevant peach allergen capable of eliciting severe systemic reactions. However, comprehensive quantitative data on Pru p 7 content across diverse peach germplasm remain limited. Using a highly sensitive sELISA, we elucidated the distribution profile, variation and the expression determinants of Pru p 7 across 123 core peach accessions. Pru p 7 content varied greatly ranged from 0.03 – 51.89 µg/g and differed depending on varieties. It was predominantly accumulated in the pulp, and its levels were significantly associated with fruit type, quality, flesh color, and ripening date. Common horticultural practices including fruit bagging and post-harvest storage were observed to reduce Pru p 7 accumulation. Peach fruit natural ripening promoted allergen accumulation, particularly during the S3 to S4 developmental stages. Among the cultivars examined, white-fleshed and late-ripening peaches (most with high sugar content and mild aroma) tended to contain relatively low levels of Pru p 7. Combining immunofluorescence localization, and western blot, we identified two hypoallergenic candidates with favorable fruit quality traits: 'Da Xue Tao' and 'Yumyeong'. These findings provide practical strategies for the peach industry to mitigate allergen risks through variety selection and cultivation management, and offer science-based dietary recommendations for peach-allergic individuals.

Keywords

Peach, Pru p 7, Hypoallergenic Varieties, Protein Quantification, Environmental Factors

Validation of Vision-based Estrus Monitoring in Chongming White Goats: Behavioral Manifestations and Serum Hormone Correlations

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Abstract

Vision-based estrus monitoring for goats has matured rapidly, yet endocrine validation in indigenous breeds is largely missing. Here we tested whether behavioral estrus events captured by a machine vision pipeline reflect genuine reproductive endocrine transitions in Chongming white goats. Ten multiparous does were monitored continuously for 21 days under standard housing conditions; daily jugular samples yielded 206 paired serum measurements of estradiol (E2), FSH, LH, and progesterone (P4). Behavioral events were extracted from infrared video by a YOLOv8-seg + MMPose pipeline and cross-checked against teaser-buck confirmation. Hormone profiles differed markedly between estrus and non-estrus windows (all $p < 0.001$): estradiol rose from 14.81 ± 4.17 to 21.79 ± 2.10 ng/L, and progesterone fell from 2386.70 ± 466.93 to 1719.68 ± 157.52 pmol/L. Estrus status correlated moderately with E2 ($r = 0.459$), FSH ($r = 0.435$), and LH ($r = 0.446$), and inversely with P4 ($r = -0.406$); the E2/P4 ratio produced the most pronounced per-event peak and is proposed as a sensitive auxiliary indicator. Vision-based detection reached 86.9% accuracy. The data indicate that camera-derived behavioral markers track real physiological state changes in this breed, supporting the deployment of vision-based estrus screening as a first-pass tool, with hormone assays reserved for confirmation in commercial Chongming white goat herds.

Keywords

Chongming White Goat, Estrus, Reproductive Hormones, Vision-based Monitoring, Reproduction

Lactobacillus Salivarius Modulates Intestinal and Liver Functions in Poultry: From Gut Health to Hepatic Lipid Metabolism

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Abstract

The rising demand for antibiotic-free poultry production necessitates the development of effective probiotic alternatives that concurrently promote gut health and address metabolic disorders, such as fatty liver syndrome. This study explored the probiotic efficacy of *Lactobacillus salivarius* SNK-6, a strain derived from chickens, in modulating intestinal barrier function and hepatic lipid metabolism. In vitro analyses revealed that SNK-6 exhibits significant tolerance to acidic and bile salt conditions, possesses adhesive capabilities, and demonstrates antimicrobial activity against key poultry pathogens (e.g., *E. coli*, *Salmonella*) through the production of organic acids and bacteriocins. In vivo feeding trials indicated that SNK-6 enhances villus height and the villus-to-crypt ratio in the jejunum and ileum, upregulates tight junction protein expression, and alters the gut microbiota by increasing *Lactobacillus* populations while suppressing *E. coli*, thereby reducing diarrhea in pigeons. Notably, SNK-6 mitigated hepatic oxidative stress and lipid accumulation, decreased serum levels of AST, ALT, and triglycerides, and activated the miR-130a-5p/MBOAT2 and AMPK pathways in a non-alcoholic fatty liver disease model. Mechanistically, extracellular vesicles derived from SNK-6 (LsEVs) were internalized by hepatocytes, leading to the promotion of autophagy through the upregulation of Beclin-1 and LC3II/LC3I. Additionally, these vesicles restored the expression of intestinal claudin-1 and modulated the gut microbiota by increasing the abundance of *Lachnospira* and *Faecalibacterium*. Safety evaluations demonstrated the absence of mutagenicity, hemolytic activity, and reproductive toxicity. These findings underscore the potential of *L. salivarius* SNK-6 as an effective probiotic for sustainable poultry production, enhancing both intestinal integrity and liver health, with its extracellular vesicles playing a critical role in the communication between the gut and liver axis.

Keywords

Lactobacillus Salivarius, Gut-liver Axis, Poultry, Fatty Liver, Extracellular Vesicles, Autophagy

Study on the Physicochemical Quality, Active Ingredients, and Optimization of the Brewing Process for Eucommia Black Tea

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Abstract

This study aimed to explore the effects of *Eucommia ulmoides* blending ratio on black tea quality and optimize the brewing process. Three blending ratios were designed, and sensory evaluation confirmed that 1:4 was the optimal proportion for *Eucommia* black tea. *Eucommia* black tea, pure black tea and pure *Eucommia* tea were adopted as materials to compare their physicochemical properties and active components. Pure black tea had the highest water content ($0.96 \pm 0.10\%$) and water extract ($65.60 \pm 0.90\%$), while *Eucommia* black tea showed slightly lower values of $0.88 \pm 0.11\%$ and $62.60 \pm 1.11\%$ with good dissolution performance. It possessed higher tea polyphenols (82.03 ± 0.01 mg/g) and free amino acids (16.03 ± 0.28 mg/g) than pure black tea, compensating for fermentation-induced active substance loss and improving tea flavor. Although fermentation reduced its monomeric catechins, *Eucommia* blending diversified functional components. Brewing conditions significantly affected sensory quality and non-volatile constituents. High-temperature and long-time brewing degraded geniposidic acid and pinoresinol diglucoside and aggravated astringency, while insufficient brewing caused weak flavor. The optimal condition of 80°C for 7 minutes balanced sensory experience and component retention. This study proves *Eucommia* blending effectively improves black tea quality, providing technical support for the development of functional *Eucommia* black tea.

Keywords

Eucommia Black Tea, Blending Process, Physicochemical Quality, Active Ingredients, Sensory Characteristics

Funding

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Development of Scientific, Methodological and Practical Recommendations for the Creation of Organic Aquaculture Enterprises

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Abstract

Aquaculture represents a promising sector of agriculture. Recently, there has been a growing trend in agricultural production toward the use of environmentally friendly methods, including organic production technologies; this trend has extended to aquaculture as well. Successful examples of organic aquaculture development exist globally—in Europe, the USA, and Asian countries, including the People's Republic of China. The Republic of Kazakhstan has adopted a Fisheries Development Program for 2021–2030, which aims to increase the population's access to fish products and foster the development of fish farming (aquaculture). Achieving this goal requires addressing several tasks: increasing the volume of aquaculture production and processing; developing domestic fish feed production; ensuring scientific and workforce support for the industry; and providing state support for aquaculture development. Furthermore, the draft Law of the Republic of Kazakhstan "On Aquaculture" outlines the following state policy objectives: 1) ensuring national food security; 2) creating economic conditions for producing competitive aquaculture products and processed goods; and 3) fostering the production of organic aquaculture products in compliance with the Law of the Republic of Kazakhstan "On the Production and Circulation of Organic Products." However, there are currently no operational organic aquaculture enterprises in Kazakhstan; this study represents the only initiative of its kind. The authors selected the zander (pike-perch)—a highly valued species—as the primary subject of the study. The research aims to establish an experimental fish farm utilizing organic aquaculture technology. Specific objectives include adapting advanced organic fish production methods, determining optimal conditions for producing and rearing organic zander stocking material, and establishing optimal conditions for producing market-ready fish. Addressing these tasks will facilitate the creation of a functional enterprise for producing organic aquaculture products in Kazakhstan.

Keywords

Aquaculture, Fish Farming, Zander, Organic, Enterprise, Technology

Funding

Based on the materials of the IRN scientific project AP26104645 Development of scientific, methodological and practical recommendations for the creation of organic aquaculture enterprises funded by the Ministry of Science and Higher Education of the Republic of Kazakhstan.

Enhancement of Flavor Compounds in Umami Condiment Fermentation by Extruded Gluten Modification

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Abstract

Gluten is a widely available plant protein, yet its application in umami condiment fermentation is limited by its tendency to agglomerate and resist enzymatic hydrolysis. This study aimed to investigate the effects of twin-screw extrusion modification on the microstructure of gluten and its subsequent impact on fermentation efficiency and flavor metabolite formation. Gluten, blended with wheat starch and soy protein isolate (SPI) in varying ratios, was subjected to extrusion and utilized as raw material for *Aspergillus oryzae* koji and moromi fermentation over 150 days. The structural changes were analyzed using scanning electron microscopy (SEM), while flavor compounds were quantified via HPLC and GC-MS. Results demonstrated that extrusion significantly modified the gluten microstructure, transforming rough, irregular particles into smoother, porous structures. This physical alteration prevented the agglomeration observed in non-extruded control groups and facilitated the penetration of water and enzymes into the inner layers of the substrate. Consequently, the fermentation efficiency was markedly improved. The final amino acid nitrogen content in the extruded groups ranged from 0.80 g/100 mL to 1.05 g/100 mL. Furthermore, the extruded samples exhibited significantly higher levels of umami-enhancing substances, including glutamic acid, adenosine monophosphate (AMP), and guanosine monophosphate (GMP), along with increased concentrations of organic acids such as acetic and lactic acid. The addition of SPI further enriched the volatile profile of the condiment. In conclusion, extrusion modification effectively enhances the bio-utilization of gluten, accelerating fermentation and yielding a product with a superior sensory profile rich in umami and characteristic aromas. This research provides a promising strategy for the industrial production of high-quality gluten-based condiments.

Keywords

Gluten, Extrusion, Fermentation, Umami Condiment, Flavor Compounds, *Aspergillus Oryza*

Liquid–liquid Phase Separation of Designer EF-hand Peptides for Selective and Enhanced Recovery of Rare Earth Elements

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Abstract

The sustainable and selective separation of rare earth elements (REEs) remains a pressing challenge owing to their nearly identical chemical properties. Despite the widespread adoption of liquid-liquid extraction, the method entails considerable reliance on organic solvents, thereby posing substantial environmental burdens. Here, we develop a bioinspired liquid–liquid phase separation (LLPS) system based on engineered EF-hand peptides, which enables highly efficient and selective recovery of REEs through a fully aqueous, green, and low-cost separation process. By incorporating a hydrophobic self-assembling Nap-FF motif, these peptides undergo rapid coacervation upon REE binding, forming dense liquid-like condensates. Remarkably, the LLPS platform enhances REE binding capacity by over 30 %, significantly outperforming conventional immobilization approaches. Moreover, the system achieves efficient separation of adjacent light REEs (Nd/Ce) with a separation factor exceeding 2.8 at pH 5.6, surpassing most reported liquid–liquid extraction systems. With excellent reusability, broad pH tolerance, and strong resistance to competing ions, this LLPS strategy provides a sustainable and efficient route for the selective recovery and enrichment of REEs.

Keywords

Rare Earth Elements, Liquid–liquid Phase Separation, Engineered EF-hand Peptides, Enhanced Recovery, Selective Separation

Subnanowires-driven Polymer Composite Systems: Systematic Exploration from Interfacial Interaction Mechanisms to Trans-scenario Applications

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Abstract

Subnanowires (SNWs), with sub-1 nm size, polymer-like flexibility, and ultrahigh specific surface area, emerge as ideal fillers to address critical challenges in inorganic/organic composites, including poor interfacial compatibility, discontinuous interfacial interactions, and difficult synergistic performance optimization. This report presents systematic explorations on SNW/polymer composite systems, verifying their universal performance enhancement and multi-scenario applications: (1) GdOOH SNWs-based elastomers exhibit high elasticity, impact resistance, and excellent triboelectric performance for efficient energy harvesting from human motion, water droplets, and ocean waves. (2) Ca-POM SNWs-based flexible hydrogels exhibit high fracture stress and toughness for wearable sensors and piezoelectric sensors, and achieve 100% accurate human motion recognition when integrated into smart insoles with machine learning. (3) Sr-POM SNWs-based bioactive piezoelectric films exhibit high output voltage, toughness, antibacterial activity, and capabilities to induce dental pulp stem cell differentiation and continuous mineralization, successfully applied in dentin regeneration via the piezoelectric microenvironment and sustained stimulation. These studies demonstrate that the size matching between SNWs and polymer chains enables molecular-level entanglement and continuous interfacial interactions, solving the synergistic optimization challenge of mechanical strength, functional activity, and environmental stability in composites, and providing a universal strategy for designing next-generation flexible electronics, biomedical materials, and energy devices.

Keywords

Subnanowires, Polymer Composites, Multi-performance Enhancement, Energy Harvesting, Biomedical Applications

Lattice-fringed Supramolecular Assemblies with Inflammation Microenvironment-specific Antibacterial Enhancement for Periodontitis Therapy

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Abstract

Acidic inflammatory microenvironment emerges as a pivotal pathological feature of periodontitis, but it is largely neglected. Due to the lack of specific distinguishment to this microenvironment, the current therapeutics usually cannot realize the targeted treatment. Herein, a supramolecular strategy is adopted to construct co-assemblies that can specifically respond to the inflammatory microenvironment while concurrently exerting antibacterial, biofilm elimination, and anti-inflammatory effects. By combined thermodynamic and microscopic structure characterization, sodium dodecyl benzene sulfonate (SDBS) is screened from a panel of anionic amphiphiles as the optimal candidate for co-assembly with chitoooligosaccharide (COS). The multiple noncovalent interactions drive the formation of nanospheres with ordered lattice fringes. Strikingly, SDBS/COS assembly remains inert under physiological condition of pH 7.4 to minimize oral irritation and side effects, while it becomes activated in acidic lesion sites of pH 6.5 to exert high antibacterial/anti-biofilm activity. Moreover, the assemblies effectively ameliorate inflammatory by scavenging reactive oxygen species (ROS) and modulating the Nrf2/NF- κ B pathway. *In vivo* evaluation demonstrates that this strategy achieves a comparable therapeutic effect to the clinical gold standard for periodontitis, without inducing systemic toxicity. This work establishes a facile and intelligent method for enhancing localized antibacterial activity, offering a new avenue for the comprehensive management of periodontitis.

Keywords

Hierarchical Assembly, Antibacterial Nanospheres, Multi-layered Structure, Microenvironment-responsiveness, Dental Plaque

Transition Metal-doped Ceria Nanozymes: Enhancement of Enzyme-like Activity and Their Applications

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Abstract

The precise detection of excessive heavy metal ions, oxyanion pollutants, and other contaminants in the environment is of great significance for ensuring ecological safety. However, existing detection methods often suffer from limitations such as heavy reliance on instruments, complex operation, and poor anti-interference ability. Due to their tunable catalytic activity and good stability, ceria nanozymes have become important materials for constructing novel sensing platforms. Nevertheless, their selectivity, sensitivity, and anti-interference ability in the detection of complex real samples still need to be improved. To address these issues, the synergistic strategies combining transition metal doping and surface functionalization are employed to precisely regulate the electronic structure and surface properties of ceria nanozymes, thereby constructing nanozyme systems with significantly enhanced enzyme-like activity. Manganese-doped CeO_2 nanoparticles and cobalt/manganese dual-metal co-doped CeO_2 nanoparticles were prepared, leading to a significant improvement in phosphatase-like activity than CeO_2 nanoparticles without doping. The metal-doping-enabled modulation of the surface electronic structure considerably elevated both the oxygen vacancy concentration and the Ce^{4+} fraction, thereby serving as a key function of the substantially enhanced phosphatase-like activity. Utilizing the inhibitory effect of environmental pollutants on the enzyme-like activity of nanoparticles, these systems achieved highly sensitive and specific detection of Al^{3+} , and environmental oxyanion pollutants (PO_4^{3-} , MoO_4^{2-} , WO_4^{2-}), respectively. The proposed nanozyme-based sensing platforms both exhibited outstanding analytical performance, including high detection accuracy, long-term operational stability, and strong anti-interference capability, even when applied to complex environmental matrices such as real water samples and simulated wastewater containing diverse coexisting substances. These favorable features underscore their significant potential for practical applications in real-world environmental monitoring and pollution control.

Keywords

Nanozyme, Enzyme-like Activity, Sensor

Traditional Gold-labeled and Nanozyme-enhanced Immunochromatographic Test Systems for Fluoroquinolone Detection in Food

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Abstract

Antibiotic residues, particularly fluoroquinolones, are among the major food-safety concerns because of their widespread use in animal husbandry and their serious public health effects. Rapid, highly sensitive, and selective detection methods are therefore essential to prevent antibiotic contamination of food products and minimize human exposure. In this study, we present a set of advanced immunochromatographic assay (ICA) technologies for the detection of fluoroquinolone antibiotics, specifically gatifloxacin (GAT) and two enantiomeric forms of ofloxacin (OFL), in various food matrices. Both traditional and nanozyme-enhanced ICAs using gold nanoparticles and catalytically active bimetallic nanoparticles (Au@Pd and Au@Ag) as labels were developed. The nanozyme-based platforms exploit peroxidase-mimicking signal amplification, yielding instrumental limits of detection as low as 0.8 pg/mL for GAT and 1.4 pg/mL for S-OFL. Sensitivity was thereby improved by up to 625-fold compared with traditional AuNP-based ICAs. For the first time, a multiplexed double ICA was developed for the simultaneous enantioselective detection of S- and R-ofloxacin isomers using a universal polyclonal antibody and distinct coating conjugates, with LODs of 0.001 ng/mL and 0.007 ng/mL, respectively, and negligible cross-reactivity. This approach enables integrated monitoring of pharmaceutical components that differ in biological activity. All developed test systems enable assays to be completed within 25 min and require only minimal sample preparation, making them suitable for on-site screening. Validation in milk and raw meat samples demonstrated recoveries of 77-115% and confirmed analytical performance consistent with reference HPLC and ELISA methods. The presented approaches provide powerful tools for robust, sensitive, specific, and stereospecific monitoring of antibiotic residues, directly supporting food safety and regulatory compliance. This study was supported by the Russian Science Foundation (grant no. 24-46-00026).

Keywords

Fluoroquinolone Antibiotics, Immunochromatographic Assay, Gold Nanoparticles, Bimetallic Nanozymes, Nanozyme-enhanced Detection, Stereospecific Analysis, Food Safety

AI-empowered Precise Structural Regulation and Multidimensional Directed Evolution of Industrial Enzymes

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Abstract

The directed evolution of industrial enzymes holds significant strategic value in green biomanufacturing. However, traditional engineering methods face critical bottlenecks. These include the vast sequence space and the challenge of synergistically optimizing multidimensional properties such as activity and stability. To overcome these limitations, we developed a highly efficient closed-loop system integrating rational protein design with artificial intelligence (AI)-assisted computation. To elucidate poorly understood structure-function relationships, we combined molecular docking, molecular dynamics simulations, and density functional theory (DFT) calculations. By incorporating deep learning tools such as RFDiffusion, we accurately characterized the catalytic mechanisms and active site conformations of complex enzymes including 3-OST and TbSMT. Furthermore, to address the low efficiency of monomeric stability engineering, we established a multi-energy filtered stability screening strategy (MEFS Pipeline) alongside a high-precision thermal stability prediction model. This pipeline computationally prioritized high-potential mutants and seamlessly bridged *in silico* predictions and wet-lab validations. It directly guided downstream experiments including protein expression, purification, and catalytic kinetics assays. For instance, the W59R mutant of 3-OST was designed by remodeling its spatial electrostatic distribution. This mutation significantly increased the overall electrostatic potential of the protein from 9,109.99 kT/e to 24,320.46 kT/e. Consequently, it enhanced the long-range electrostatic guidance and substrate capture of negatively charged polysaccharides. Additionally, our thermal stability prediction model (SMRC-Net) achieved an R^2 of 0.89 and an RMSE of 0.79. It also demonstrated 90% accuracy in predicting the direction of stability changes for independently designed mutants. To further enable the synergistic evolution of multiple enzyme attributes, we constructed a multimodal machine learning framework. This framework integrated pre-trained protein language models with topological descriptors such as persistent Laplacians. In turn, it successfully facilitated the co-optimization of protein solubility and thermal stability. Tightly coupling computational prescreening with rigorous wet-lab experimentation drastically reduces the costs associated with blind trial and error. Ultimately, this study demonstrates that AI-driven computational design substantially empowers rational macromolecular engineering. It provides a reliable framework to accelerate the transition of enzymes from natural states to industrially customized functions.

Keywords

Directed Evolution of Enzymes, Rational Protein Design, AI-assisted Computation, Multidimensional Property Optimization, Conformational Stability

Remodeling of Photosynthetic Membrane Lipids in Plants: Insights from *Perilla Frutescens* and Tomato

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Abstract

Lipid metabolism plays a central role in plant stress tolerance and developmental programming, with direct implications for crop productivity and nutritional quality. This study integrated lipidomic approaches to investigate glycerolipid remodeling in two contexts: exogenous melatonin (MT) alleviation of cadmium (Cd) stress in tomato, and polar lipid dynamics during oil biosynthesis in developing *Perilla frutescens* cotyledons. In Cd-stressed tomato, MT application significantly improved growth and photosynthetic performance. Glycerolipidomic analysis revealed that MT counteracted Cd-induced declines in key lipids, including monogalactosyldiacylglycerol (MGDG), digalactosyldiacylglycerol (DGDG), sulfoquinovosyldiacylglycerol (SQDG), phosphatidylcholine (PC), and phosphatidylglycerol (PG). Notably, MT elevated the unsaturation index of total lipids and individual classes, increased the DGDG/MGDG and PC/PE ratios, and reduced Cd accumulation in leaves and roots. These changes preserved thylakoid membrane integrity and fluidity, thereby sustaining photosynthetic electron transport under Cd stress. In *Perilla frutescens*, a lipidomic analysis of developing perilla cotyledons (5, 15, and 25 days after anthesis) identified 147 molecular species across 10 polar lipid classes. During cotyledon maturation, total lipid and polar lipid contents declined, with PC showing the most pronounced decrease (65.8%), while lysophosphatidic acid (LPA) increased by 62.4% at the late stage. Major species such as MGDG C36:6 and DGDG C36:6 decreased significantly, and the unsaturation index of most polar lipids dropped, indicating a metabolic shift from membrane biogenesis to triacylglycerol (TAG) accumulation. Collectively, these findings highlight that targeted glycerolipid remodeling—whether induced by melatonin under heavy metal stress or occurring naturally during seed development—is a conserved strategy for optimizing membrane function and carbon partitioning. Understanding these lipid regulatory networks provides a foundation for enhancing stress resilience and oil quality in nutritionally important crops.

Keywords

Lipidomics, Melatonin, Cadmium Stress, *Perilla Frutescens*, Tomato, Glycerolipid Remodeling, Oil Biosynthesis

Flax: A Promising Oilseed for Functional Food Innovation

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Abstract

This report examines the chemical composition of flax phospholipids and evaluates their fundamental potential for practical application. While flaxseed oil is rich in essential alpha-linolenic acid (omega-3), evaluated varieties like Snow White, LM 97, and Norlin fail to meet the health dietary ratios of omega-6 to omega-3 PUFAs recommended by the FITZ Nutrition of the Russian Federation due to an extreme imbalance. However, flaxseed phospholipids exhibit an ideal 1:1 omega-6 to omega-3 ratio, offering higher absorption and bioavailability compared to triglycerides. Due to their amphiphilic properties, these phospholipids spontaneously form nanostructures called liposomes in aqueous media, which serve as versatile vehicles for nutrient encapsulation and drug delivery. Characterization of the investigated flax lecithin sample showed 43.8% of acetone-insoluble substances, predominantly consisting of phosphatidylcholine (45%), followed by phosphatidylinositol (28.7%), phosphatidylethanolamine (22.7%), and phosphatidic acids (3.6%). Given its high phosphatidylcholine content, flaxseed lecithin was utilized to synthesize liposomes via ultrasonic homogenization, using resveratrol as a model encapsulation compound. A comparative analysis with conventional soy lecithin formulations using dynamic light scattering revealed comparable colloidal parameters: a hydrodynamic diameter of 58.64 ± 0.34 nm, a polydispersity index below 0.3, and a zeta potential of approximately -30 mV. Crucially, flaxseed lecithin achieved a maximum encapsulation efficiency of 58%, outperforming soy counterparts due to increased bilayer capacity and greater membrane fluidity provided by omega-3 acids. Consequently, liposomes from flax phosphatide concentrate demonstrate optimal colloidal properties and encapsulation efficiency, establishing flaxseed lecithin as a highly promising, functional alternative to soy lecithin for advanced liposomal delivery systems.

Keywords

Flaxseed Lecithin, Phospholipids, Liposomes, Encapsulation Efficiency, Phosphatidylcholine, Omega-3 Fatty Acids, Drug Delivery Systems

Rational Design of Ni-Mo₂N Nitrogen Carriers for Chemical Looping Ammonia Synthesis

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Abstract

Chemical looping ammonia synthesis (CLAS) has emerged as a promising green ammonia production technology, demonstrating significant potential in the field of decentralized ammonia synthesis. Although early transition metal-based nitrogen carriers have shown encouraging prospects in CLAS, their practical application has been persistently constrained by the inherent limitations of lattice nitrogen conversion and insufficient NH₃ selectivity. Herein, we design an efficient Ni-Mo₂N composite nitrogen carrier synthesized via a one-step pyrolysis strategy. The optimized 25% Ni-Mo₂N (molar ratio) system achieves an outstanding lattice nitrogen conversion of 76%. Ni-Mo₂N exhibits a remarkable initial ammonia yield of 9,050 $\mu\text{mol}\cdot\text{g}^{-1}\cdot\text{h}^{-1}$, three times higher than that of pristine Mo₂N. Critically, the incorporation of Ni effectively suppresses the formation of the inactive Mo₂C phase during pyrolysis, ensuring that the Mo species exist exclusively as metallic Mo and the active Mo₂N phase. This structural integrity endows the catalyst with excellent stability over 10 consecutive cycles, delivering an average ammonia production rate of 451 $\mu\text{mol}\cdot\text{g}^{-1}\cdot\text{h}^{-1}$, a 4.5-fold enhancement compared with pristine Mo₂N. Systematic characterization combined with density functional theory (DFT) calculations elucidates the CLAS reaction pathway on the Ni-Mo₂N surface and reveals a pronounced synergistic interaction between Ni clusters and Mo₂N. Specifically, Ni sites act as hydrogen activation centers, adsorbing and dissociating H₂ into reactive H* species, which subsequently undergo spontaneous spillover onto adjacent Mo₂N surfaces and cooperatively activate lattice nitrogen species for efficient ammonia formation. Collectively, this work establishes a solid foundation for the rational design of advanced transition-metal nitrogen carriers and offers fresh theoretical and methodological perspectives for developing high-performance CLAS systems.

Keywords

Chemical Looping, Ni-Mo₂N, Nitrogen Carrier, Lattice Nitrogen Conversion, Ammonia Synthesis, Transition Metal Nitride

Dual-functional Pd Metallene for Boosted Photocatalytic H₂ Evolution Coupled with Lactic Acid Oxidation over ZnCdS

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Abstract

Constructing highly efficient active sites is fundamental to advancing photocatalytic performance. However, the fabrication of stable bifunctional catalytic interfaces capable of sustaining concurrent redox reactions remains a significant challenge. Herein, we rationally design Pd metallene-decorated ZnCdS photocatalysts (PZCS) featuring electronic metal-support interaction (EMSI) interfacial architecture, which enables the synchronous photocatalytic H₂ evolution and selective lactic acid (LA) oxidation. Owing to the dynamically modulated interfacial electronic environment and the optimized adsorption configurations for H₂O and LA substrates, the optimal 10PZCS catalyst achieves an H₂ evolution rate of 22.4 mmol g⁻¹ h⁻¹ and a LA-to-pyruvic acid conversion rate of 6.7 mmol g⁻¹ h⁻¹, substantially outperforming pristine ZnCdS. A synergistic combination of comprehensive spectroscopic characterizations, photoelectrochemical measurements, and density functional theory (DFT) calculations unravels the origins of the markedly enhanced dual-redox activity, which are attributed to the spatially coupled yet functionally differentiated Pd metallene active sites. Specifically, Pd sites reinforce H₂O adsorption, disrupt the rigid hydrogen-bonding network on ZnCdS surface, and lower the dissociation energy barrier of H₂O. Meanwhile, the reversible Pd²⁺/Pd⁰ redox cycle ensures continuous regeneration of active centers, thereby accelerating the reduction half-reaction toward efficient H₂ generation. Driven by the EMSI effect, photogenerated electrons spontaneously migrate from ZnCdS to Pd metallene, substantially suppressing charge-carrier recombination, while the hole-enriched ZnCdS selectively oxidizes the adsorbed LA into high-value pyruvic acid with negligible over-oxidation. This work not only elucidates the atomic-scale kinetic mechanism underlying the bifunctionality of Pd metallene cocatalysts in integrated photocatalytic water splitting and organic valorization, but also offers a versatile interfacial engineering paradigm for development of high-performance sulfide-based photocatalysts toward synergistic clean H₂ production and value-added chemical synthesis.

Keywords

Pd Metallene, Photocatalytic, ZnCdS, EMSI, LA Oxidation, H₂ Evolution

Effect of Activated Carbon Modification on the Performance of Adsorption Arsenic Removal Catalyst

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Abstract

The activated carbon (AC) was chemically modified by K_2CO_3 , and the specific surface area, pore volume and pore size of the AC after modification were investigated. As the mass ratio of K_2CO_3 to AC (alkali-carbon ratio) increased, the specific surface area of the modified AC shows a trend of increasing first and then decreasing. When the ratio of alkali to carbon was 6, the specific surface area of the modified AC increased from the initial $653.3\text{m}^2/\text{g}$ to $1333.6\text{m}^2/\text{g}$. The modified AC was then used as the support to prepare an adsorption catalyst for arsenic removal, which exhibits excellent arsenic adsorption owing to the multi-level pore channels composed of micropore-mesopores. The micropore ensured the catalyst with a large specific surface area, so the active components can be efficiently dispersed on it, while the mesopore allowed the macromolecular arsenide to fully contact and react with the active metal components, and thus improved arsenic removal efficiency.

Keywords

Activated Carbon, Modification by Potassium Carbonate (K_2CO_3), Adsorption, Support, Catalyst

Prediction of Transcriptional Regulatory Network for Suspension Adaptation of Vero Cells Via Multi-omics Integration

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Abstract

Adherent Vero cells are widely used for viral vaccine production, while suspension culture is the key strategy for large-scale industrial manufacturing. Nevertheless, the transcriptional and translational molecular reprogramming that enables Vero cells to resist anoikis after detachment from extracellular matrix remains poorly characterized by single-omics analysis. This study aims to systematically screen core regulatory genes and transcription factors governing suspension adaptation and construct a reliable bidirectional regulatory model through multi-omics integration and multi-layer cross-verification. RNA-seq transcriptome and TMT quantitative proteomics data from adherent and suspension-adapted Vero cells were collected. Genes with significant synchronous mRNA and protein changes were filtered under unified thresholds of $|\log_2FC| > 1$ and adjusted $P < 0.05$, and an equal-weighted comprehensive scoring model was established to rank top 20 hub genes. GSEA revealed global suppression of ribosome biogenesis, mitochondrial translation and MYC/E2F-mediated G2/M cell cycle pathways in suspension cells. Four-dimensional radar profiling, DepMap CRISPR dependency data and two independent transcription factor activity enrichment pipelines jointly verified two regulatory cascades. Stress-responsive TFs EPAS1, CEBPD, IRF1 and SMAD3 were activated to upregulate MMP1/MMP9 for ECM degradation and anoikis resistance, whereas MYC, E2F and LEF1 were suppressed to inhibit metabolism and cell proliferation and reduce matrix dependence. This multi-computational analysis constructs a predictive molecular network of Vero suspension adaptation and provides a credible candidate library for subsequent wet-lab functional validation and genetic engineering of high-yield suspension cell lines.

Keywords

Vero Cells, Suspension Adaptation, Multi-omics Integration, Transcription Factor, Anoikis Resistance, Bioinformatic Analysis

Transcriptomic Analysis of Vero Cell Adaptation to Suspension Cultivation and Its Association with Viral Receptor Expression

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Abstract

Vero cells represent an indispensable continuous cell lineage for large-scale viral vaccine manufacturing. To facilitate high-density industrial bioprocessing and overcome the spatial limitations of traditional adherent monolayers, transitioning these cells to suspension cultivation in bioreactors is a fundamental and highly sought-after strategy. However, the systemic transcriptomic alterations underlying this drastic physical and physiological adaptation process—particularly concerning their potential collateral impact on viral entry receptor expression and subsequent viral susceptibility—remain incompletely characterized. In this study, we performed comprehensive bulk RNA-sequencing to systematically delineate the global transcriptomic landscape of adherent and suspension-adapted Vero cells. Principal Component Analysis (PCA) and rigorous differential expression analysis ($|\log_2\text{FoldChange}| \geq 1$, adjusted $P < 0.05$) revealed a massive global transcriptomic reprogramming upon suspension adaptation, characterized by the widespread dysregulation of thousands of genes. To uncover the functional implications of these variations, comprehensive pathway analyses, including Gene Ontology (GO) and KEGG enrichment, were conducted. The results indicate that the differentially expressed genes are predominantly driven by cellular structural reorganization and extracellular matrix (ECM) interactions. Furthermore, Gene Set Variation Analysis (GSVA) and Gene Set Enrichment Analysis (GSEA) identified significant directional shifts. Most notably, we observed a pronounced repression in the Focal adhesion hallmark, perfectly mirroring the physical detachment from culture substrates, alongside distinct metabolic reprogramming characterized by significantly enhanced glycolysis to meet new energetic demands in suspension. Crucially, absolute expression quantification and Pearson correlation analysis demonstrated that this physiological adaptation concurrently and divergently modulates the expression landscape of key viral entry receptors. While receptors such as CD46 were significantly upregulated, others including ACE2, AXL, and PVR exhibited pronounced downregulation. These receptors established a robust co-expression matrix with core cellular adaptation signatures, implying a tightly linked regulatory environment. Overall, this study provides compelling evidence that the structural and metabolic reprogramming requisite for Vero cell suspension growth intrinsically alters their viral susceptibility profiles. These findings offer valuable molecular insights that can inform rational cell line engineering and targeted bioprocess optimization strategies, ultimately facilitating the efficient production of diverse viral vaccines.

Keywords

Vero Cells, Transcriptomics, Suspension Adaptation, Viral Entry Receptors, Vaccine Biomanufacturing

Whole-genome Resequencing Identifies Candidate Genes Regulating Tail Fat Deposition in Two Indigenous Sheep Breeds

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Abstract

Excessive tail fat buildup will lower feed utilization efficiency, disrupt insulin sensitivity and weaken reproductive performance of sheep. The hidden genetic drivers that create distinct tail fat phenotypes between long-fat-tailed local sheep breeds and short-fat-tailed counterparts still lack systematic clarification. This research intends to screen vital genes regulating tail fat lipid metabolism via phenotype contrast between Lanzhou fat-tailed sheep with long fat tails and Hu sheep featuring short fat tails. We selected 15 healthy adult sheep individuals from each breed to conduct whole-genome resequencing. Three mainstream selection signal detection metrics including fixation index, cross-population extended haplotype homozygosity and cross-population composite likelihood ratio were jointly adopted to pinpoint differentiated genome segments, followed by GO functional annotation and KEGG pathway enrichment analysis. Seventy-five genome regions with notable selection pressure were screened out, eight candidate genes were repeatedly detected across all three analytical pipelines. Among these candidates, DAB1 and GPC5 had prominent enrichment on lipid metabolism biological processes. Existing functional research confirms DAB1 accelerates adipocyte differentiation relying on the PI3K-AKT signaling pathway, while GPC5 restricts lipid accumulation through suppressing the Wnt/ β -catenin pathway; the two genes collaboratively shape breed-specific tail fat fatness differences. The two screened core genes supply reliable molecular markers for indigenous sheep germplasm preservation and marker-assisted selective breeding practice.

Keywords

Tail Fat Deposition, Whole-genome Resequencing, Selection Signature, Lipid Metabolism, Dab1, Gpc5

Inhibition of EMCV Replication in BHK-21 Cells by Regulating ROS Microenvironment Based on Novel Hydrogen Sulfide Sustained-release Nanomaterials

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Abstract

Background: Encephalomyocarditis virus (EMCV) infection often induces excessive reactive oxygen species (ROS) production in host cells. (ROS), destroy redox homeostasis and promote viral replication. Mitochondria are cell energy centers and immune signal hubs, and their dysfunction is closely related to viral pathogenicity. Hydrogen sulfide (H₂S), as an endogenous gas signal molecule, has significant antioxidant and mitochondrial protection potential, but its short half-life and lack of targeting limit its clinical application. Recent studies have shown that the use of nanomaterials to achieve precise delivery of H₂S and microenvironment regulation of ROS has become a new strategy against viral infection. The purpose of this study was to construct a ROS-responsive H₂S sustained-release nanosystem and to explore its synergistic antiviral effect and mechanism on EMCV-infected BHK-21 cells. **Methods :** H₂S donor nanomaterials and superoxide dismutases with ROS response characteristics were prepared. (SOD) nanozyme. The EMCV infected BHK-21 cell model was established, and the biocompatibility was evaluated by CCK-8 method. The viral load was determined by qRT-PCR and plaque assay. The intracellular ROS level and mitochondrial membrane potential were detected by fluorescent probe. The expression of key proteins in NRF2 antioxidant pathway and type I interferon signaling axis was analyzed by Western Blot. **Results :** Experiments showed that the nanomaterial effectively removed the peak of intracellular ROS in the early stage of infection, maintained the integrity of mitochondrial function, and blocked the path of virus using oxidative stress signal to promote replication. The combined treatment group showed a significant synergistic effect, and the virus titer was reduced by more than one order of magnitude compared with the control group. Mechanistically, the precise release of H₂S enhances NRF2-mediated antioxidant defense and up-regulates the expression of interferon-stimulated genes (ISGs), reshaping the host microenvironment that is not conducive to virus propagation. **Conclusion :** This study confirmed that the H₂S / ROS synergistic regulation strategy based on new materials can effectively inhibit EMCV replication by reshaping the host redox microenvironment. This strategy avoids the shortcomings of traditional direct antiviral drugs that are prone to drug resistance, and provides a new paradigm for the development of broad-spectrum nanomedicines for positive-strand RNA viruses. In the future, its efficacy and safety in vivo models will be further evaluated to promote clinical transformation.

Keywords

Encephalomyocarditis Virus (EMCV), BHK-21 Cells, Hydrogen Sulfide (H₂S), Reactive Oxygen Species (ROS), Nanomaterials, Oxidative Stress

The Protective Effect of L-fucose on HSF Cells and the Anti-inflammatory Mechanism of THP-1 Macrophages

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Abstract

Skin oxidative stress injury and local chronic inflammation are important core causes of skin barrier damage and inflammatory skin diseases. It is of great research value to find safe and efficient natural active substances to repair skin damage and regulate inflammation. The purpose of this study was to investigate the anti-apoptotic protective effect of L-fucose on human skin fibroblasts (HSF), and its anti-inflammatory effect and molecular mechanism on PMA-induced differentiated THP-1 macrophages. In the experiment, HSF cells cultured in vitro were used to construct an oxidative damage model, and the protective effect of L-fucose on cells was verified by detecting cell viability, apoptosis level and Caspase family apoptosis-related protein expression. At the same time, PMA-induced THP-1 monocytes were used to differentiate into mature macrophages to construct an in vitro inflammatory model, and the secretion of pro-inflammatory factors and the expression of key proteins in the inflammatory pathway were detected. The results showed that L-fucose could significantly up-regulate the activity of HSF cells, effectively inhibit the activation of Caspase apoptosis pathway, reduce the apoptosis damage of human skin fibroblasts, and had good cell protection effect. At the same time, it can significantly inhibit the excessive inflammatory response of THP-1 macrophages, effectively reduce the release of pro-inflammatory factors such as TNF- α , IL-6, and IL-1 β , and inhibit the abnormal activation of inflammatory signaling pathways. In summary, L-fucose can not only effectively protect skin cells and reduce apoptosis, but also significantly inhibit the inflammatory response of immune cells, and can simultaneously regulate apoptosis and inflammatory response, which provides an important experimental theoretical basis for its application in skin inflammatory injury repair and functional skin care raw materials development.

Keywords

L-fucose, hSF Cells, Caspase, tHP-1 Macrophages, Cell Apoptosis, Anti-inflammatory

Study on Microglial Immune Response and Neuronal Regulatory Mechanisms Mediated by EMCV Infection

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Abstract

Encephalomyocarditis virus (EMCV) infection can trigger central nervous system (CNS) immune inflammation and neuronal dysfunction, yet the underlying mechanism by which EMCV modulates microglial immune responses and subsequent neuronal functional regulation remains poorly elucidated. This study established a consistent viral titer infection paradigm with a standardized 150 TCID (converted to corresponding PFU via the classical conversion coefficient of 0.69) to conduct integrated in vivo and in vitro experiments. For the in vivo assay, 2–3-month-old mice were subjected to intracranial EMCV injection to induce CNS infection. We dynamically observed the activation state, phenotypic characteristics, and cytokine secretion profile of microglia post infection, and further explored the functional regulatory effect of activated microglia on cerebral neurons. Meanwhile, kidney tissues were collected as a peripheral organ reference to comparatively analyze the differential immune responses between central and peripheral systems upon EMCV infection. For the in vitro assay, RAW264.7 macrophages were infected with the same TCID viral titer to monitor cellular phenotypic changes and immune activation characteristics, which assisted in verifying the microglia-mediated immune response pattern induced by EMCV. By virtue of the unified TCID infection dosage bridging in vivo and in vitro models, this study focuses on clarifying the cascade mechanism of EMCV directly triggering microglial immune activation, releasing inflammatory cytokines, and further regulating neuronal functions. The findings are expected to provide new experimental evidence and mechanistic insights for understanding EMCV-induced neuroinflammation and CNS immune injury.

Keywords

EMCV, Microglia, Neuroinflammation, Neuronal Dysfunction, Immune Activation

Reutilize a Metalorganic Mineral Under Aqueous Micro-environment

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Abstract

A salt-less inorganic mineral was discovered, which was origin from the soil and metallic inorganic under high pressure to form a crystal mineral. From the efficiency spectroscopy discover and categorized, the salt-inorganic might belong to the face center cubic (FCC). And after the reaction, which can be transformed from FCC to body center cubic (BCC), MOF-(Cao) n and MOF- [Ca(OH)₂] n. The reaction on the mineral was a kind of artificial modification which let the exo-site of the inorganic could bear the different kinds of storage also like “surface heterogeneity”. Except the construction of the MOFs, which, the radiant characters from the mineral were influenced the diversity of agriculture’s inherent mutation. The concept of the internal radiation could be analyzed by the Fermi- Dirac cone, synchrotron- spread of average electro waves; the type of the distant was achieved on 6.4×10^7 nm length, through the distant on the radiant of interference dissemination, the utilize on the mineral could be improved.

Keywords

MOFs, Surface Heterogeneity, Metalloid, Radiant Dosage, Pump U



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