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MEDLIFE2026 & ICBLS2026

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Preface

Abstract Book of MEDLIFE2026 & ICBLS2026 is composed of the abstracts of the 2026 12th International Conference on Health, Medicine and Life Sciences (MEDLIFE2026) and 2026 13th International Conference on Biology and Life Sciences (ICBLS2026). According to the similarity among the topics of MEDLIFE2026 and ICBLS2026, MEDLIFE2026 is held in conjunction with ICBLS2026 on May 23-25, 2026.

MEDLIFE2026 and ICBLS2026 serve as an optimal platform for specialists, scholars and researchers in the field related to health, medicine, biology and life sciences 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:

Health: Health Science, Mental Health, Healthy Diet, Human Nutrition, Physical Exercise, Health Care, Epidemiology, Pharmacology, Medical Sociology, Applied Health Sciences, Biomedical Engineering, Public Health, etc.

Biology: Cell Biology, Biogeography, Aerobiology, Biochemistry, Biomechanics, Bioengineering, Bioinformatics, Molecular Biology, Biomedical Research, Environmental Biology, etc.

Life Sciences: Bioethics, Botany, Zoology, Genetics, Food Science, Biotechnology, Health Sciences, Bio-engineering, Microorganisms, Medicine, Biomedicine, etc.

Medical Sciences: Anatomy, Medical Ethics, Biology and Genetics, Microbiology, Biophisics and Physics, Neurology, Dentistry, Oncology, Dermatovenerology, Ophthalmology, Otolaryngology, etc.

We thank all authors for their scientific contribution to MEDLIFE2026 and ICBLS2026 and look forward to having the opportunity to showcase and disseminate your research.

Sincerely,

MEDLIFE2026 and ICBLS2026 Organizing Committees

Table of Contents

Spermidine Enhances Thymic Regeneration and Ameliorates Immunosenescence Through Autophagy Activation in Aged Mice

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Abstract

With advancing age, the progressive functional decline of the immune system—known as immune senescence—is a core factor contributing to increased susceptibility to infections, diminished vaccine responses, and chronic inflammatory states in older individuals. The thymus, as the primary lymphoid organ crucial for T cell development, undergoes progressive atrophy (thymic degeneration) with aging. This represents a hallmark event of immune senescence, directly leading to reduced output of naive T cells and disrupting the diversity and homeostasis of adaptive immunity. In recent years, cellular autophagy has been identified as playing a crucial role in maintaining tissue homeostasis and delaying aging. Its diminished activity is closely associated with the onset and progression of various age-related diseases. Consequently, exploring intervention strategies that can safely and effectively activate autophagy and specifically reverse aging in immune organs has become a frontier hotspot in anti-aging research.This study investigates how the natural polyamine spermidine enhances the aging immune system's capacity to rebuild adaptive immunity through autophagy mechanisms. In aged mice, spermidine treatment significantly mitigated age-related thymic atrophy, restored thymic architecture, and enhanced thymic function. This was manifested by increased thymic weight, elevated FOXN1 and AIRE protein expression in thymic epithelial cells, and enhanced output of naive T cells. These effects correlated with a remodeled peripheral T cell compartment, characterized by an increased proportion of naive T cells and a decreased proportion of memory T cells. Molecularly, spermidine enhances autophagic flux by activating the AMPK/mTOR signaling pathway. The critical role of autophagy was confirmed, as its pharmacological inhibition completely abolished spermidine-induced thymic regeneration and functional recovery. Furthermore, spermidine treatment demonstrated favorable safety in aged mice, with no significant hepatic or renal toxicity observed. This study confirms that spermidine primarily drives thymic regeneration and restores peripheral T-cell homeostasis by activating autophagy, offering a promising translational strategy for enhancing immune function in aging.

Keywords

Spermidine, Autophagy, Thymic Regeneration, Immunosenescence, Aging

From Natural Language to SQL Query: A Medical Knowledge Graph-Linked Text-to-SQL Semantic Disambiguation and Enhancement Framework

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Abstract

Background: In the medical domain, efficiently retrieving structured data from large-scale databases using natural language queries remains a significant challenge. While medical knowledge graphs offer rich, structured representations of biomedical concepts and their relationships, a substantial semantic gap persists between these graphs and the free-form expressions used in natural language queries. Traditional Text-to-SQL systems often struggle with the complexity and ambiguity of medical terminology, leading to inaccuracies in generated SQL queries and hindering effective data retrieval and knowledge discovery. To bridge this gap, there is a growing need for approaches that integrate domain-specific knowledge with advanced semantic parsing techniques, enabling more precise and reliable translation of natural language into structured queries. *Objective:* To address the semantic gap between medical knowledge graphs and natural language queries, this paper proposes a Text-to-SQL semantic disambiguation and enhancement framework based on medical knowledge graph linking. The framework aims to improve the accuracy and reliability of converting natural language into structured query language, thereby supporting efficient medical data retrieval and knowledge discovery. *Methods:* First, entity linking and relation mapping techniques are employed to align medical entities in natural language with concepts in the knowledge graph. Next, a context-aware disambiguation model is introduced to resolve issues of polysemy and term ambiguity. Finally, a graph embedding enhancement module is incorporated to leverage path and structural information from the knowledge graph, thereby completing query semantics. Based on the structured semantic information derived from the previous steps, the final SQL queries are generated under the guidance of template-based prompts. *Results:* In experiments comprising 30 PubMed literature retrieval tasks, the proposed framework demonstrated complete consistency with human experts in terms of semantic coverage — successfully identifying and mapping all key entities and relationships from natural language queries to the knowledge graph. This represents a 12.32% improvement over the baseline model (DeepSeek R1) on this core metric. Regarding time efficiency, the framework completed all retrieval tasks in approximately 5 minutes, significantly outperforming manual retrieval by domain experts, which averaged 62.55 minutes. *Conclusion:* By deeply integrating medical knowledge graphs with semantic parsing techniques, this framework significantly enhances the semantic understanding capability and query generation quality of Text-to-SQL systems. It provides a reliable solution for medical knowledge-driven data retrieval, with potential applications in supporting clinical decision-making and scientific research analysis.

Keywords

Medical Knowledge Graph, Large Language Model, Semantic Disambiguation, Entity Linking, Query Enhancement, Clinical Data Retrieval, Biomedical Natural Language Processing, Semantic Parsing

Prevalence of Overweight and Obesity, and Associated Complications in a Tertiary Hospital in Beijing

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† Yuxi Wang and Xun Cheng are co-first authors.

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Abstract

Aim: To assess the prevalence of overweight and obesity, as well as related complications, through a cross-sectional, single-center database in Beijing. *Materials and Methods:* Data were obtained from the physical examination center of our hospital via the Annual Health Examination System (Version 3.0). For the analysis of overweight and obesity, eligible participants were aged 30 years and older, had undergone routine examinations in 2024 (N=8,691), and had complete data on height, weight, gender, and unit. Additionally, the incidence of overweight and obesity-related complications, grouped by body mass index (BMI), was calculated using logistic regression. *Results:* In 2024, our hospital's health examination center conducted check-ups for 13,411 individuals. In the overweight and obesity study, a total of 8,691 eligible participants were included (median age 35 years; average BMI 24.8 kg/m^2; 79.80% male). According to the Chinese BMI classification, 45.58% were classified as overweight and 14.03% as obese. The growth trends across different age groups exhibited distinct characteristics in both males and females. Compared to participants with a normal BMI, those who were overweight or obese had a higher incidence of assessed complications (trend $P<0.05$). The most common complications among overweight and obese participants were fatty liver, hyperuricemia, and prediabetes (according to ADA criteria). *Conclusions:* Overweight and obesity, along with related complications, are highly prevalent in this population. These data provide insights into the health status of examined participants from the perspective of our medical center and can better inform management and prevention strategies for public health.

Keywords

Database Research, Diabetes Complications, Dyslipidaemia, Observational Study, Population Study, Real-world Evidence

Integrating Pretreatment CT Radiomics and Circulating Tumor Cells Using Machine Learning to Predict Survival After Immunoradiotherapy in Advanced Hepatocellular Carcinoma

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Abstract

Background This study aimed to evaluate the efficacy of adding PD-1 inhibitors to radiotherapy plus tyrosine kinase inhibitors (R+T+P) in advanced hepatocellular carcinoma (HCC) and to assess whether radiomics, circulating tumor cells (CTCs), and machine learning could improve outcome prediction. *Methods* A total of 295 patients with advanced HCC were included (R+T+P, n = 172; R+T, n = 123). For patients receiving R+T+P, predictive models were developed by integrating clinical variables, CT-based radiomic features, and CTC counts using machine learning algorithms. *Results* The R+T+P group achieved significantly longer median overall survival (mOS) and median progression-free survival (mPFS) than the R+T group (mOS: 27.8 vs. 20.1 months, P = 0.008; mPFS: 8.7 vs. 6.9 months, P = 0.014). Among the prognostic models, the Clinical – Radiomic – CTC nomogram outperformed the Clinical – Radiomic nomogram, showing a higher concordance index (0.789) and higher area under the receiver operating characteristic curves (AUCs) for 1-, 2-, and 3-year OS (0.889, 0.771, and 0.838, respectively). *Conclusion* PD-1 inhibitors combined with radiotherapy and TKIs significantly improved survival outcomes in patients with advanced HCC. Machine learning models integrating radiomics and CTCs provided robust individualized prognostic prediction, supporting risk stratification and clinical decision-making.

Keywords

Hepatocellular Carcinoma, Immunoradiotherapy, Radiomics; Circulating Tumor Cells, Machine Learning

Systematic Review of Psychological Resilience Assessment Tools for Stroke Patients Based on the COSMIN Guidelines

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Abstract

Background: Stroke has become a major public health issue, and psychological resilience is a key protective factor for improving prognosis. However, numerous tools for assessing psychological resilience in stroke patients exist both domestically and internationally, exhibiting considerable variation in applicability. There remains a lack of systematic integration and standardised evaluation of the measurement characteristics of these assessment tools. *Objective:* To conduct a systematic review of the methodological and psychometric properties of self-reported psychological resilience measurement tools for stroke patients, based on the COSMIN guidelines, thereby providing evidence for healthcare professionals to select high-quality assessment tools. *Methods:* We searched 10 databases (CNKI, Wanfang, VIP, SinoMed, PubMed, Embase, Web of Science, CINAHL, Cochrane, APA's PsycINFO) for studies on psychological resilience assessment tools for stroke patients, with the search date set to 21 November 2025. Two researchers independently screened and cross-checked the results, evaluating included studies according to the COSMIN guidelines and generating recommendations. *Results:* A total of four studies were included, encompassing five assessment tools. Four tools failed to report content validity, one tool did not report construct validity, and two tools omitted reporting of hypothesis tests for construct validity. All studies reported internal consistency. Evidence indicates that RSA, CD-RISC-10, CD-RISC-20, and CD-RISC-25 possess Grade B recommendation strength and demonstrate potential for practical application. RQSR was rated as Level C evidence and is not recommended for use. *Conclusion:* Compared to the other four instruments, the CD-RISC-10 demonstrates the most balanced psychometric properties. It exhibits good structural validity and internal consistency, with a high quality of evidence. Its concise item design makes it suitable for use in stroke patients and it can be temporarily recommended. However, its methodological quality and psychometric properties still require further improvement.

Keywords

Stroke, Psychological Resilience, Measurement Properties, COSMIN Guidelines, Systematic Review

Serum PLR Combined with CA125, HE4 and ROMA Index: A Novel Multi-marker Strategy for Diagnosis and Prognostic Evaluation in Ovarian Cancer

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Abstract

Background: Ovarian cancer (OC) is a highly lethal tumor of the female reproductive system. Early diagnosis is vital for improving patient survival rates. Recently, the platelet lymphocyte ratio has emerged as an important biomarker that indicates serum inflammation. Therefore, this study aims to investigate the potential of combining serum PLR with CA125, HE4, and ROMA for diagnosing and assessing the prognosis of ovarian cancer, especially in its early stages. *Methods*: We measured and analyzed CA125 and HE4 levels in 141 OC patients and 138 controls, using complete blood count (CBC) and enzyme-linked immunosorbent assay (ELISA). After validating the biomarker panel, we assessed the associations by comparing the expression levels of biomarkers in OC patients with varying clinical characteristics. We also collected two individual cohorts: a training cohort and a validation cohort. Multivariate Logistic regression model was constructed to screen the best combination, and the diagnostic efficacy of different combinations were compared by ROC curve, and the prognostic value was evaluated by Cox regression analysis and survival analysis. *Results*: PLR, CA125, HE4 and ROMA were significantly increased in OC patients. This elevation is particularly significant in patients with advanced disease, lymph node metastasis, and ascites. The combination of PLR, CA125, HE4 and ROMA improves the diagnostic efficiency of ovarian cancer. Furthermore, we discovered that combining PLR with CA125, HE4, and ROMA levels had considerable prognostic significance. *Conclusions*: Combining the PLR with CA125, HE4, and ROMA could improve the diagnosis of ovarian cancer. This combination may also enhance prognostic capabilities.

Keywords

Ovarian Cancer, the Platelet Lymphocyte Ratio, ROMA Index, Prognostic Maker

Overexpression of ESPL1 Is Associated with Progression and Poor Prognosis in Endometrial Cancer: A Study of Bioinformatics Analysis Combined with Experimental Research

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Abstract

Background: Endometrial cancer (EC) is one of the most prevalent malignant tumors affecting the female reproductive system and has a growing overall prevalence and a lack of effective treatments. Extra spindle pole bodies-like 1 (ESPL1), an isolated enzyme that can participate in mitosis, plays a role in developing several malignancies and influences prognosis. This study focuses on the role of ESPL1 in the progression, prognosis, and immunotherapeutic response of EC. *Methods:* In this study, we analyzed the expression of ESPL1 in EC from the Cancer Genome Atlas database (TCGA). We used bioinformatics tools to investigate the significance of ESPL1 expression in EC and its related functions. The ESPL1 was identified as a prognostic biomarker. Its expression and function were validated by clinical samples and in vitro experiments. The role of ESPL1 in DNA damage repair, chemotherapy resistance, immune cell infiltration, and its correlation with the signal transducer and activator of the transcription 3 (STAT3) pathway and immunotherapeutic response were also evaluated. *Results:* ESPL1 expression was significantly elevated in EC and was associated with clinical stage, menopausal status, and poor prognosis. In vitro experiments, overexpression of ESPL1 promoted EC cell proliferation, migration, and invasion, while knockdown reversed these effects. Mechanistically, ESPL1 potentially promotes EC growth by increasing phosphorylation of the STAT3 signaling pathway. ESPL1 may be associated with DNA damage repair and chemotherapy resistance. Low ESPL1 expression correlates with immune cell infiltration and improved response to immunotherapy. *Conclusion:* ESPL1 may serve as a promising prognostic biomarker and therapeutic target for EC.

Keywords

Endometrial Cancer, ESPL1, Biomarker, Prognosis, Immunoassay

Development of Vitamin-enriched Functional Curd Bars Using Cryogenic Grinding Technology and Comprehensive Quality Assessment

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Abstract

In the context of the increasing prevalence of diet-related disorders and micronutrient deficiencies, the development of food products aimed at improving the vitamin content and nutritional quality of the human diet is of particular relevance. This study explores the application of cryogenic grinding technology in the development of vitamin-enriched curd bars with functional properties. Cryogenic grinding enables the production of plant-based powders with high retention of thermolabile vitamins and amino acids, making this technology promising for use in preventive and functional nutrition. Cryogenically ground plant powders were incorporated into curd bar formulations at different concentrations as functional ingredients. Physicochemical, structural–mechanical, and sensory properties of the finished products were systematically evaluated using standard analytical techniques, including moisture content, protein and fat determination, pH measurement, texture analysis, and sensory assessment by expert panels. Additionally, the vitamin content, amino acid profile, and overall nutritional value of the curd bars were assessed. The results demonstrated that the inclusion of cryogenically processed plant raw materials led to an increase in vitamin content and improved the amino acid profile, while contributing to the formation of a stable product structure and maintaining acceptable texture and sensory characteristics. Optimal concentrations of cryopowders were identified, ensuring enhanced nutritional and functional value without deterioration of consumer acceptability. These findings confirm the feasibility of applying cryogenic grinding technology in the development of functional dairy products designed for the prevention of diet-related deficiencies and the improvement of overall nutritional quality.

Keywords

Cryogenic Grinding, Cryopowders, Vitamin Enrichment, Amino Acids, Functional Dairy Products, Curd Bars, Preventive Nutrition, Nutritional Quality

Fortified Gluten-free Extruded Snacks for Children with Celiac Disease: Advancing Sustainable Development Goal 3 in Kazakhstan

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Abstract

Celiac disease in children requires a strict gluten-free diet, which increases the risk of vitamin and mineral deficiencies in the absence of affordable domestic products. The aim of this study was to analyze the dynamics of celiac disease among children aged 0-14 years in Kazakhstan (2013-2024) and to develop fortified gluten-free extruded snacks as a potential solution to this problem. The epidemiological analysis revealed a steady increase in cases and a concentration of prevalence in the southern and western regions, as well as in major cities. The developed samples, based on corn flour with the addition of rice, buckwheat, or chickpea flour and fruit-berry powders, contained B vitamins, vitamin C, and antioxidants at levels consistent with functional food products. All formulations met safety requirements; pathogenic microflora and toxic elements were not detected. The findings confirm the feasibility of creating affordable domestic products for children with celiac disease, thereby contributing to the achievement of SDG 3 “Good Health and Well-Being.”

Keywords

Gluten-Free Snacks, Celiac Disease, Vitamin-enriched Food, Functional Nutrition, Children’s Health

Prospects of Using Safflower Oil in the Creation of Food Emulsion Products

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Abstract

The development of functional food products based on vegetable oils is one of the promising directions in modern food science and technology. Safflower oil (*Carthamus tinctorius* L.), distinguished by its high content of polyunsaturated fatty acids, tocopherols, and antioxidant compounds, was used as the main fat base in the creation of two emulsion functional products: high-calorie mayonnaise and a sauce with garlic and ginger. Experimental batches were produced under laboratory conditions using standard mixing and homogenizing equipment. Formulations were developed taking into account the optimal ratio of fat, protein, and carbohydrate components, and included natural additives with functional properties (garlic, ginger, ascorbic acid), which made it possible to enhance the nutritional and biological value of the products. For each variant, a technological scheme was developed to ensure emulsion stability and extended shelf life. Physico-chemical, rheological, and organoleptic characteristics were evaluated. Rheological studies revealed differences in the structural behavior of the products: mayonnaise exhibited pseudoplastic flow with high viscosity (2000–5000 mPa·s) and pronounced thixotropy, while the sauce was characterized by viscoplastic flow and moderate viscosity (800–1500 mPa·s). Physico-chemical analysis showed acceptable values of acid and peroxide numbers, confirming the stability of the fat phase. According to the results of sensory evaluation conducted by an expert panel of 20 specialists, both products received the “excellent” category, with the sauce containing ginger and garlic receiving the highest approval. Thus, the use of safflower oil in the development of emulsion products enables the creation of functional foods with high biological value, stable quality characteristics, and strong consumer appeal, confirming the feasibility of their industrial implementation.

Keywords

Safflower Oil, Functional Food Products, Mayonnaise, Sauce, Emulsion Systems, Physico-chemical Indicators, Rheological Properties, Organoleptic Evaluation

Development of Technology and Comprehensive Quality Assessment of Functional Structured Dairy Curd Products Enriched with Fruit and Vegetable Cryopowders

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Abstract

Modern trends in the food industry and preventive medicine prioritize the development of products with enhanced biological value, improved organoleptic characteristics, and functional properties. Structured dairy products enriched with fruit, berry, and vegetable cryopowders represent a significant area of interest within this context as potential components of dietary therapy. The objective of this study is to develop recipes and technological regimes for the production of structured dairy products using natural cryopowders obtained via freeze-drying. The research focuses on integrating these ingredients to enhance nutritional value while preserving natural vitamins, minerals, antioxidants, and bioactive compounds. The study involves the assessment of quality indicators to confirm safety, stability, and organoleptic properties, alongside the establishment of technological regimes to ensure process reproducibility and standardization. The results demonstrate that the addition of cryopowders improves the taste, color, and aroma of the final products without the need for artificial additives. Due to the high content of bioavailable micronutrients, the developed products are recommended for inclusion in therapeutic and preventive diets to support metabolic processes and prevent alimentary-dependent diseases. The scientific novelty of the work lies in the successful development of formulations that enrich the product with biologically active substances. Furthermore, the parameters ensuring structural stability and quality were justified, and a technological instruction adapted for the use of cryopowders in a dairy base was compiled. In conclusion, this research solves a critical scientific and practical task by creating a new generation of functional dairy products that meet the requirements of healthy nutrition, clinical dietetics, and modern technological standards, providing a regulatory basis for industrial scaling and increasing the competitiveness of domestic production.

Keywords

Functional Dairy Products, Healthy Nutrition, Fruit and Vegetable Cryopowders, Quality Assessment, Food Technology, Rheological Properties

Therapeutic Effects of Human Neural Progenitor Cells Derived from Placental Fibroblasts Induced by Small Molecule Compounds Under Normoxia on Parkinson's Disease Rat Models

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Abstract

Neural precursor cells (NPCs) can self-proliferate and have multi-directional differentiation potential, and chemically induced neural precursor cells (ciNPCs) derived from somatic cells have great potential for the treatment of neurological diseases. However, the single source and low number of endogenous neural precursor cells currently available for transplantation remains a major challenge in the effective treatment of central nervous system injury. Here, we present an effective method for reprogramming human fibroblasts into ciNPCs using a chemical cocktail of valproic acid, CHIR99021, and Repsox (VCR) under normoxia. In the two-step reprogramming of human placental fibroblasts (HPFs), intermediate compact cell colonies were first chemically induced in KSR medium containing VCR for 10 days under different oxygen conditions, followed by lineage-specific induction. Cells at each stage were analyzed by genome sequencing. A partial Parkinson's disease rat model was established using 6-OHDA with a brain stereotaxic apparatus. Two weeks post-lesion, successful modeling was confirmed by apomorphine-induced rotation. ciNPCs were labeled with CM-DiI and transplanted into the MFB region of the brain. At 2, 4, 8, and 12 weeks post-transplantation, motor behaviors were assessed to evaluate functional recovery. At 4, 8, and 20 weeks, brains were perfused and collected to examine ciNPC survival, migration, and differentiation in the PD microenvironment. After 10 days of induction with the VCR combination under varying oxygen conditions, the cells formed neurospheres following two days of suspension culture in low-adherence plates. Most of these cells stained positive for alkaline phosphatase and exhibited high expression of NPC-specific markers, as well as the astrocyte marker GFAP and the neuron-specific marker Tuj1. Following transplantation, ciNPCs survived and functioned in the MFB region of Parkinson's model rats for over 20 weeks and significantly improved motor behavioral deficits. Moreover, the grafted ciNPCs demonstrated long-term survival, migrated over long distances, and differentiated into various neural cell types in vivo. Our findings suggest that this chemical reprogramming approach, which generates ciNPCs directly from human fibroblasts without introducing exogenous genes, may provide a novel donor cell source for stem cell-based therapy in Parkinson's disease.

Keywords

Small Molecule Compounds, Neural Progenitor Cells, Cell Reprogramming, Parkinson's Disease, Cell Transplantation, Normoxia

The Current Situation and Influencing Factors of Adolescent Sexual Health Literacy: A Qualitative Study

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Abstract

Background There is relatively limited research in China on the current status and influencing factors of adolescents' sexual health literacy, and the findings are inconsistent. Quantitative studies struggle to provide an in-depth portrayal of the actual state of adolescents' sexual health literacy and are unable to thoroughly explore the primary factors influencing it. However, qualitative research offers unique advantages in this regard. *Objectives* Drawing on the socio-ecological model, this study employs semi-structured interviews to provide an in-depth interpretation and contextual understanding of quantitative research findings within the cultural context of China. It further explores influencing factors across five levels—individual, interpersonal, organizational, community, and policy—with the aim of providing a foundation for developing a multi-level intervention framework to promote sexual health among adolescents. *Methods* This study employed a descriptive qualitative research methodology, conducting semi-structured interviews with 16 adolescents using purposive sampling, and applying directed content analysis to identify themes. *Results* Following repeated analysis and organization of interview data from 16 adolescents, five main categories and 12 subcategories were identified. *Conclusions* Qualitative research has revealed that adolescents generally have low levels of holistic health literacy, which needs to be improved. Factors influencing adolescents' sexual health literacy include: sexual knowledge; proactive personality traits; the state of parent-child communication; family structure; peer influence; the content and format of school-based sex education; a lack of teacher training; ambiguous teaching methods and awkward teacher-student interactions; the absence of adolescent-friendly service providers and inadequate facilities; insufficient service promotion leading to information gaps; the attitude of service staff and lack of privacy protection during medical visits; and weak policy enforcement—specifically, the marginalization of sex education.

Keywords

Adolescents, Sexual Health Literacy, Factors Influencing, Qualitative Study

KDM2B Exacerbates Fibrosis After Myocardial Infarction by Regulating the Expression of GDF9 from Macrophage

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Abstract

In various cardiac pathologies, excessive fibrosis represents a central driver of adverse remodeling and dysfunction that culminates in heart failure. Histone methylation has been implicated in diverse pathophysiological processes, yet the contribution of histone methylation-modifying enzymes to pathological cardiac fibrosis remains incompletely understood. Here, we identify lysine-specific demethylase 2B, KDM2B, as a critical epigenetic regulator of pathological cardiac fibrosis. We generated KDM2B knockout mice via CRISPR-Cas9, established myocardial infarction models, assessed cardiac function, performed macrophage-fibroblast co-culture, used RNA-seq, qPCR, and western blot to validate KDM2B regulation of GDF9, and confirmed effects on fibroblast behavior via exogenous GDF9. KDM2B expression is upregulated in myocardial tissues under pathological stress, and its deficiency substantially attenuates cardiac fibrosis, preserves cardiac function, and prevents adverse remodeling following myocardial infarction. Genetic ablation or pharmacological inhibition of KDM2B restricts the differentiation of cardiac fibroblasts into fibrogenic myofibroblasts and suppresses the fibrotic response, while also promoting an endothelial-like phenotype and enhancing angiogenesis after myocardial injury. Mechanistically, KDM2B deficiency relieves repression of growth differentiation factor 9 in myeloid cells, thereby enhancing SMAD-dependent transforming growth factor-β signaling and the expression of fibrosis-promoting genes. Collectively, these findings establish KDM2B as a pathogenic driver of cardiac fibrosis and a potential therapeutic target for cardiac dysfunction and heart failure.

Keywords

Myocardial Infarction, Cardiac Fibrosis, KDM2B, Macrophage, GDF9

Immune-associated Cancer-associated Fibroblasts Define a Distinct Spatial Stromal State in Pancreatic Ductal Adenocarcinoma

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Abstract

Pancreatic ductal adenocarcinoma (PDAC) is characterized by a highly complex stromal microenvironment, in which cancer-associated fibroblasts (CAFs) constitute a major but heterogeneous component. However, the spatial organization, biological features, and potential clinical relevance of distinct CAF states remain incompletely understood. We performed an integrative analysis of PDAC centered on spatial transcriptomics, together with single-cell transcriptomic data, complementary molecular datasets, and clinical information. CAF populations were characterized according to their transcriptional features, spatial distribution, and microenvironmental context. Cross-platform integration was further used to evaluate immune-associated CAF states and prioritize candidate markers and related biological programs. We identified multiple CAF subtypes with distinct spatial and molecular characteristics in PDAC. These CAF states exhibited non-random spatial organization and were associated with different local microenvironmental contexts. Among them, an immune-associated CAF state was enriched in immune-related spatial regions. In a small exploratory cohort, this CAF state showed a trend toward favorable prognosis. Integrative analyses across spatial transcriptomics, single-cell data, molecular profiles, and clinical datasets further supported the robustness of this immune-associated CAF phenotype and identified candidate markers and pathways potentially related to this CAF state. Our findings support the existence of a spatially and biologically distinct immune-associated CAF state in PDAC. This CAF population may have prognostic relevance and warrants further mechanistic and clinical validation.

Keywords

Pancreatic Ductal Adenocarcinoma, Cancer-associated Fibroblasts, Spatial Transcriptomics, Tumor Microenvironment, Immune-associated CAFs

Integrative Chinese and Western Medicine Perspective on Cardiovascular Risk Prediction: Integration of TCM Macro-Phenotypes with Western Medical Indicators

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Abstract

Early risk assessment for cardiovascular disease is a key step in preventing cardiovascular events and reducing disease burden. However, existing assessment tools still face the issue of residual risk, as traditional models struggle to cover all risk dimensions. This paper systematically explores the integrative pathways and innovative applications of artificial intelligence in cardiovascular risk assessment from the perspective of integrating Chinese and Western medicine. Based on a review of mainstream technologies and research advances, it identifies limitations in current models, such as data source bias, insufficient interpretability, and single-dimensional risk evaluation. It further demonstrates the value of incorporating TCM macro-phenotypes, such as syndromes and body constitution, into cardiovascular risk assessment, and summarizes research progress in the digitization and objectification of the four diagnostic methods. The study suggests that methods such as association rule mining can significantly improve the integration efficiency, discovery of implicit relationships, and risk prediction performance between Western micro-level indicators and TCM macro-phenotypes, thereby effectively supporting clinical decision-making and enabling personalized risk assessment and early warning. Future efforts should focus on deepening multimodal data integration, advancing the development of high-quality databases that combine Chinese and Western medicine, and optimizing association rule mining methods. These steps will facilitate the standardization and personalization of cardiovascular risk assessment, promote the integration of Chinese and Western medicine, and provide important theoretical guidance and practical reference for empowering the "preventive treatment of disease" approach in cardiovascular care with AI.

Keywords

Artificial Intelligence, Cardiovascular Disease, Risk Assessment, Integration of Chinese and Western Medicine, Association Rule Mining, Preventive Treatment of Disease

Development of an Intervention Protocol for the Core Symptom Cluster in Postoperative Glioma Patients Receiving Chemotherapy Based on Symptom Management Theory

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Abstract

Objective: To construct an intervention protocol for the core symptom cluster in postoperative glioma patients receiving chemotherapy based on Symptom Management Theory, and to provide evidence for clinical nursing practice and future intervention studies.Methods: Under the guidance of Symptom Management Theory, the core symptom cluster in postoperative glioma patients receiving chemotherapy was identified using network analysis based on a previous cross-sectional study. Subsequently, an evidence-based approach was applied to retrieve relevant literature through the 6S evidence model in a top-down manner. Eighteen high-quality studies were included, and 38 items of intervention evidence were summarized. Based on these findings, a preliminary intervention protocol was drafted and further revised through two rounds of Delphi expert consultation.Results: After two rounds of Delphi consultation, consensus was achieved among 12 experts. The expert authority coefficient was 0.911, Kendall's coefficient of concordance was 0.187 ($P<0.05$), and the mean item coefficient of variation ranged from 0.100 to 0.136. The final protocol included six domains: target population, forms and settings of participation, organization and implementers, intervention content, evaluation time points, and outcome indicators.Conclusion: The intervention protocol developed in this study showed acceptable scientific rigor and reliability. It may serve as a reference for symptom cluster management in postoperative glioma patients receiving chemotherapy, although its effectiveness should be further validated in clinical practice.

Keywords

Glioma, Postoperative Chemotherapy, Symptom Cluster, Symptom Management Theory, Delphi Method, Intervention Protocol, Oncology Nursing

Research on Noise Reduction Behavior of Workers in Noisy Environments and Its Influencing Factors

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Abstract

Objective To analyze the noise reduction behavior of workers exposed to occupational noise and their influencing factors, providing a reference for developing health promotion programs and implementing intervention measures. *Methods* A cluster sampling method was used to select 449 workers exposed to noise from five enterprises within the jurisdiction. The basic information and occupational characteristics of the noise-exposed workers were collected. A scale for assessing noise reduction behaviors among noise-exposed workers was designed based on the Health Belief Model to investigate their noise reduction behavior patterns and influencing factors. *Results* There was correlation between noise exposure workers with different age and education level ($P<0.05$), with educational level demonstrating a positive correlation ($r_s=0.908$, $P=0.039$) and age showing a negative correlation ($r_s=-0.119$, $P=0.012$). There were statistically significant differences in perceived severity, social distance, behavioral barriers, self-efficacy and action benefit scores among workers exposed to noise reduction behavior types ($P<0.05$), and the self-rated health status ($r_s=0.109$, $P=0.021$), severity ($r_s= 0.185$, $P=0.001$), action benefit ($r_s= 0.108$, $P=0.022$) and self-efficacy ($r_s=0.373$, $P=0.001$) were positively correlated with noise reduction behaviors,while behavioral barriers ($r_s=-0.237$, $P=0.001$) was negatively correlated. *Conclusion* Based on the analysis of the results of the Health Belief Model, educational level, age, and health literacy significantly influence noise reduction behaviors among noise-exposed workers.Targeted occupational health education should be emphasized for workers with lower educational levels, younger age, and poorer health literacy to enhance their motivation and sustained engagement in proactive noise reduction behaviors.

Keywords

Occupational Noise Exposure, Noise-induced Damage, Health Literacy, Health Belief Model

LGALS3 Suppresses Colon Cancer Progression by Reprogramming TCA Cycle Metabolism Through the P53 Pathway

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Abstract

Colon cancer is a prevalent gastrointestinal malignancy with rising incidence. Tumor metabolic reprogramming, particularly involving the tricarboxylic acid (TCA) cycle, is a critical hallmark of cancer. While LGALS3 and the tumor suppressor P53 are known regulators of tumor metabolism, the specific mechanism by which LGALS3 mediates metabolic reprogramming via P53 in colon cancer remains unclear. This study aims to investigate the expression changes of LGALS3 under serum deprivation and elucidate its effects on colon cancer cell proliferation, TCA cycle metabolism, and the underlying molecular mechanisms. Subcellular fractionation and Western blotting were used to determine LGALS3 localization and expression changes under serum starvation. Using lentiviral-mediated knockdown and overexpression models in HCT116 (TP53+/+ and TP53-/-) cells, cell proliferation was assessed via CCK-8, colony formation, and EdU assays. Mechanisms were explored using immunofluorescence, protein stability assays with cycloheximide (CHX) and MG132, Seahorse mitochondrial stress tests, and ATP and α-ketoglutarate measurements. The regulatory relationship between LGALS3 and P53 was further validated by co-knockdown of Pirh2. The results show: LGALS3 was primarily localized in the mitochondria and nucleus, with its expression significantly upregulated under serum deprivation. Knockdown of LGALS3 significantly promoted colon cancer cell proliferation, whereas overexpression inhibited it. Mechanistically, LGALS3 co-localized with P53 in the nucleus and reduced P53 protein half-life by upregulating the E3 ubiquitin ligase Pirh2-mediated proteasomal degradation pathway; this effect was reversed by MG132 or Pirh2 co-knockdown. Furthermore, LGALS3 suppressed the cellular oxygen consumption rate, ATP production, and α-ketoglutarate accumulation. It specifically downregulated the expression of TCA cycle enzymes MDH2 and SDHA. Notably, the regulatory effects of LGALS3 on MDH2 and SDHA were completely abolished in TP53-/- cells. In conclusion LGALS3 inhibits colon cancer cell proliferation by destabilizing P53 protein via Pirh2, thereby regulating the TCA cycle and cell cycle through the P53 pathway. These findings provide a promising potential therapeutic target for colon cancer.

Keywords

Tricarboxylic Acid Cycle, Colon Cancer, LGALS3, P53, Mitochondrial Metabolism

Co-occurrence of Emotional Dysregulation and Impaired Functional Connectivity Between the Amygdala and Geschwind's Territory in the Dominant Hemisphere of Adolescents with Non-suicide Self-injury

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Abstract

Non-suicide self-injury (NSSI) is defined as a deliberate, self-inflicted damage to body tissue of a person in the absence of suicidal intent. Relative to the other populations, adolescents are more susceptible to NSSI. This study aims to explore the sociodemographic risk factors for NSSI and to investigate its underlying neural correlates. A total of 270 adolescents (12-18 years old) with major depressive symptoms were registered as the participants of this study. Among them, 154 reported engaging in NSSI (MDN), while the others denied such behavior (MD). Compared to the MD group, the MDN group had higher proportions of patients being females, grown in a single parent family, or having left-behind experience. Although the two groups exhibited the same scores of HAMD 24, the MDN persons presented lower levels of emotional understanding and experienced difficulties in impulse control and using emotion regulation strategies than MD group. When watching negative images under the three emotion regulation strategies of cognitive reappraisal, response inhibition, and neutral emotion, MDN group rated lower emotional valence than MD group. MDN group had lower P300 and LPP amplitudes recorded in the centroparietal zone，under all the three emotion regulation strategies. Furthermore, the functional connectivity between the left amygdala and the Geschwind area in the MDN group was significantly lower than that in the MD group. These data correlate emotional dysregulation to impaired functional connectivity between amygdala and Geschwind's territory in the dominant hemisphere of NSSI adolescents.

Keywords

Adolescents, Emotion Regulation Strategy, Event-related Potential, Nonsuicide Self-injury, Resting-state Functional Magnetic Resonance Imaging

Construction and Validation of a Novel Transdifferentiation Index Based on NOTCH1 and ADORA3 as a Prognostic Model for Glioblastoma

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Abstract

Background Glioblastoma (GBM) is an invasive primary brain tumor. Abnormal angiogenesis causes treatment resistance and unfavorable prognosis. Tumor stem cell-endothelial transdifferentiation is a vital angiogenic pathway; thus, discovering key molecular markers and building valid prognostic models is clinically valuable. *Methods* GBM clinical data were retrieved from CGGA, TCGA and Murat (GSE7696) datasets. Kaplan-Meier survival, univariate and multivariate Cox regression screened core genes from 12 transdifferentiation-related candidates. We constructed a GTN transdifferentiation index based on NOTCH1 and ADORA3, then established an integrated risk model and nomogram combined with clinical indicators. TCGA and Murat cohorts served as external validation sets. ROC curves and DCA evaluated predictive efficacy and clinical practicability. TIMER analyzed gene expression-immune infiltration correlations, while Western blot, tube formation and LDL uptake assays verified gene functions in vitro. *Results* NOTCH1 and ADORA3 were independent prognostic biomarkers for GBM. The GTN index and integrated risk model achieved robust predictive power across training and validation groups (AUC > 0.7), with higher risk scores corresponding to shorter overall survival. TIMER results indicated NOTCH1/ADORA3 expression correlated with CD4+ T cell and macrophage infiltration. Knockdown of either gene suppressed glioma cell tube formation and LDL uptake, impairing endothelial transdifferentiation capacity. *Conclusion* This study first validates NOTCH1 and ADORA3 as independent prognostic biomarkers for GBM and constructs a clinically applicable GTN index risk model for individualized survival evaluation. Their links to tumor immune microenvironment and transdifferentiation mechanism lay theoretical foundations for novel combined targeted therapies against GBM angiogenesis.

Keywords

Glioblastoma, Transdifferentiation of Tumor Cells, NOTCH1, ADORA3

PLA/HA Implant Materials Doped with Silver Nanoparticles for Bone Fixation

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Abstract

Bone implant materials were synthesized using the "solvent casting method", based on polylactide/hydroxyapatite and various organic-inorganic modifiers, such as MgF_2, CaF_2, $Mg_3(PO_4)_2$ and citric acid. The physicochemical properties of the materials were studied using modern analytical (FTIR, XRD, TGA, DTA, DSC, hardness and ect.) methods. IR spectroscopy showed that interactions occurred between PLA macromolecules and hydroxyapatite and other modifiers. By the X-ray diffraction method, it was found to have an average crystallinity of 50-90% after the extrusion. When the textural properties were examined using SEM analysis, it was found that the introduction of magnesium phosphate into the samples effected the formation of porous particles with dimensions of 100-250 μm. This in turn, leads to the improvement of metabolic processes when the samples are introduced into bone tissues. Microhardness was determined by the Vickers method and it was found to be close to the hardness of natural bone, i.e. 27-34 HV. *In vitro* resorbtion was also performed in simulated body fluids (SBF). Synthesized materials are shown non-toxicity for L929 cells. Resorbtion process was studied *in vivo* in the upper third of the femur of rabbits, it was found that the ossification process of the samples was about 90-95% after 75 days. Silver nanoparticles were synthesized using Lycium depressum berry extract using green synthesis. The resulting extract and nanoparticles were characterized physicochemically (TEM, SEM, thermal analysis, X-ray, etc.) and biologically (cytotoxicity, anticancer, antibacterial, antifungal, phytochemical composition, antioxidant properties, etc.). Silver nanoparticles were incorporated into the implant material at concentrations of 1%, 3%, and 5%. The resulting materials possessed antibacterial properties, which are highly desirable for implants.

Keywords

Poli-L-lactide, Hydroxyapatite, Femur, Fixation Materials, Physical-chemical and Antibacterial Properties, Ag-nanoparticles

AI-Optimized Machine Learning and Multi-omics Integration Identify ACADL as a Therapeutic Target in Pancreatic Cancer

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Abstract

Objective: Pancreatic cancer (PAAD) is characterized by poor prognosis and limited effective therapeutic options. Mitochondrial dysfunction plays a critical role in its progression. This study aimed to identify and validate the mitochondrial-related key gene ACADL using an artificial intelligence (AI)-driven integrative framework and to explore potential small-molecule inhibitors targeting ACADL. *Methods:* Transcriptomic data from TCGA, GTEx, and GEO databases were integrated to identify differentially expressed genes (DEGs) between tumor and normal tissues. Mitochondria-related genes were further screened through intersection analysis. Weighted gene co-expression network analysis (WGCNA) was applied to identify modules associated with tumor traits. Machine learning models, including LASSO and support vector machine (SVM), were constructed with cross-validation and hyperparameter tuning to identify robust hub genes. Cox regression and SHAP analysis were performed to evaluate the prognostic value and model contribution of ACADL. At the single-cell level, a large-scale pancreatic cancer single-cell atlas (~700,000 cells) was analyzed using the Seurat pipeline (SCT normalization, Harmony batch correction, UMAP dimensionality reduction, and clustering) to determine the cellular distribution of ACADL. Subsequently, approximately 500,000 compounds were subjected to virtual screening and molecular docking targeting ACADL. Molecular dynamics (MD) simulations were performed to assess the stability and interaction patterns of the protein–ligand complexes. *Results:* ACADL was significantly upregulated in pancreatic cancer tissues and was associated with advanced tumor stage and poor prognosis. WGCNA revealed that ACADL-associated modules were highly correlated with tumor progression and enriched in oxidative phosphorylation, energy metabolism, and hypoxia-related pathways. Machine learning models identified ACADL as a key predictive feature with strong diagnostic and prognostic performance (AUC > 0.85), which was further supported by SHAP analysis. Single-cell analysis demonstrated that ACADL was predominantly expressed in ductal/epithelial cells and showed elevated expression in specific stromal subpopulations. Virtual screening and molecular docking identified several candidate compounds, among which D001-lig_12580 exhibited strong binding affinity. MD simulations confirmed that D001-lig_12580 formed a stable complex with ACADL, characterized by favorable conformational stability and key hydrogen bond interactions. *Conclusion:* This AI-driven multi-omics and single-cell integrative study identifies ACADL as a critical regulator in pancreatic cancer and highlights D001-lig_12580 as a potential targeted inhibitor. These findings provide new insights into the molecular mechanisms of pancreatic cancer and offer promising directions for precision therapeutic development.

Keywords

Pancreatic Cancer, ACADL, Mitochondrial Dysfunction, Single-cell RNA Sequencing, Machine Learning, Multi-omics Integration, Molecular Docking, Molecular Dynamics

Development and Application of an Integrated Palliative Care Programme for Elderly Patients with Advanced Lung Cancer and Comorbidities

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Abstract

Objective: To develop an integrated palliative care programme for elderly patients with comorbidities and lung cancer, and to evaluate its effectiveness. *Methods:* Guided by the theory of supportive care, an integrated palliative care programme was developed through literature review and expert consultation. Using convenience sampling, elderly patients with advanced lung cancer and comorbidities admitted to the palliative care ward of a tertiary general hospital in Zhengzhou between January and February 2026 were selected as study subjects. The intervention group and control group each comprised 42 patients. The intervention group received an integrated palliative care intervention in addition to standard care, whilst the control group received standard care alone. Differences in scores for palliative care needs, quality of life, symptom burden, psychological distress, social support and sense of life's meaning were compared between the two groups before the intervention, two weeks after the intervention, and one month after the intervention. *Results:* A total of 11 experts completed two rounds of expert consultation, yielding an inter-rater reliability coefficient of 0.914. The response rates for valid questionnaires were 95.14% and 98.32%, respectively, with Kendall's coefficient of concordance at 0.098 and 0.260 ($P < 0.05$). The constructed integrated care program for palliative care encompasses four intervention themes: symptom management, comfort care, psychological and spiritual care, social and informational support, with a total of 38 specific intervention items. During the programme's implementation, four participants dropped out of the intervention group and three from the control group. Following the intervention, the intervention group's scores for quality of life, social support and sense of life's meaning were all significantly higher than those of the control group, with all differences being statistically significant ($P < 0.05$). Conversely, the intervention group's scores for palliative care needs, symptom burden and psychological distress were all significantly lower than those of the control group, with all differences being statistically significant ($P < 0.05$). *Conclusion:* The implementation of an integrated palliative care programme can meet the palliative care needs of elderly patients with advanced lung cancer and comorbidities, improve their quality of life, enhance their levels of social support and sense of life's meaning, and effectively reduce their symptom burden and psychological distress. This programme is scientifically sound, highly targeted and feasible, and can serve as a reference for healthcare professionals in the practice of palliative care.

Keywords

Advanced Lung Cancer, Comorbidities, Palliative Care Needs, Integrated Care

The Application of Microwave Ablation in Thyroid Microcarcinoma

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Abstract

Objective To compare the efficacy and safety of ultrasound-guided Microwave Ablation (MWA) with those of surgical resection for the treatment of papillary thyroid microcarcinoma (PTMC). *Methods* A retrospective analysis was performed on 92 patients with PTMC who underwent ultrasound-guided MWA.Additionally, 102 patients with PTMC who received surgical treatment during the same period were enrolled as the control group. In the ablation group, the volume reduction rate of the ablation zone was calculated over a 24-month follow-up period. The surgical group was monitored via conventional ultrasound examinations focusing on the thyroid gland and cervical lymph nodes. Outcomes including disease progression, operative duration, complication rates, and medical costs were compared between the two groups over a follow up period ranging from 12 to 42 months. *Result* Among the 92 patients in the ablation group, 70 presented with solitary nodules, while 22 exhibited multiple nodules. The mean volume reduction rate in the ablation group was 99%at 24months; one patient experienced local recurrence at 7months post-procedure and subsequently underwent secondary ablation. All 102patients in the surgical group achieved complete resection, although two cases showed residual intrathyroidal lesions without evidence of lymph node metastasis. Statistically significant differences were observed between the two groups regarding operative time, procedural cost, and complication rates ($P<0.05$). However, no significant difference was found in terms of disease progression ($P=0.60$). *Conclusions* Ultrasound-guided MWA is a viable treatment option for PTMC. Compared with surgical intervention, it demonstrates comparable efficacy and favorable safety profile, suggesting it as an effective alternative therapeutic approach.

Keywords

Thyroid, Papillary Thyroid Microcarcinoma, Microwave Ablation, Complication

Tortuosity of the Residual Cystic Duct is an Independent Risk Factor for Common Bile Duct Stones After Cholecystectomy: A Case-Control and Computational Study

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Abstract

Background & objective: Recurrent common bile duct (CBD) stones after cholecystectomy represent a significant clinical challenge, while the mechanism remains poorly understood. This study aimed to identify geometric characteristics of the bile duct associated with post-cholecystectomy CBD stones, elucidate and validate underlying mechanisms using computational fluid dynamics (CFD) and microfluidic experiments. *Methods*: This retrospective study enrolled 93 patients with post-cholecystectomy CBD stones and 81 without. Geometric parameters of the residual cystic duct (RCD), common hepatic duct (CHD), and CBD were measured on 3D reconstructions. Clinical data and biliary geometry were integrated into univariate and multivariate logistic regression analyses to identify independent risk factors. CFD with discrete phase model (DPM) was employed to observe bile flow and crystal behavior. Microfluidic chips were used to observe crystal aggregation in vitro. *Results*: Multivariate analysis identified RCD tortuosity, maximum RCD diameter, history of ERCP, and CBD angle as independent risk factors for post-cholecystectomy CBD stones. CFD simulations revealed that tortuous RCD geometry induced complex vortex structures and flow stagnation within the blind stump, leading to prolonged particle retention and reduced washout efficiency. Microfluidic experiments demonstrated that crystal aggregation was most pronounced in long and curved channels. *Conclusion*: RCD tortuosity is an independent risk factor for post-cholecystectomy CBD stones. The underlying mechanism involves disturbed bile flow dynamics within the tortuous blind stump, promoting crystal retention and aggregation. These findings provide a rationale for optimizing cholecystectomy procedure about the cystic duct stump, potentially reducing the incidence of postoperative CBD stones.

Keywords

Recurrent Cholangiolithiasis, Magnetic Resonance Cholangiopancreatography, Computed Fluid Dynamic, Discrete Phase Model, Microfluidic

Assessing Respiratory Function and Metabolic Response: The Importance of Cardiopulmonary Exercise Test (CPET) Parameters

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Abstract

Cardiopulmonary Exercise Test (CPET) is a method for assessing physical performance and aerobic capacity by examining the performance of the cardio-respiratory system, the musculoskeletal system and metabolism by monitoring parameters and reactions under the influence of dosed physical exertion. The following are examined: - ventilation and gas exchange parameters; and - cardiac activity parameters, which allow assessing the work metabolism, which is the basis of physical performance. For this purpose, it is necessary to use a spirometric system - open or closed and a load device that allows dosing physical work. The method was introduced in 1929 by Knipping and Brauer (Hollmann & Prinz, 1997). In CPET testing, loads involving the lower extremities are most often preferred, which can be dosed. The specificity of the sports discipline or the skills of the person being tested are also criteria for the type of load. Key CPET parameters offer valuable information about physiological function. Oxygen uptake (VO_2), particularly maximal oxygen consumption (VO_2 max), is considered the gold standard for assessing aerobic capacity and overall fitness. It reflects the efficiency of oxygen delivery and utilization by the body. Carbon dioxide production (VCO_2) and the respiratory exchange ratio (RER) help determine metabolic activity and substrate utilization, indicating whether energy is derived primarily from fats or carbohydrates during exercise. Ventilatory parameters such as minute ventilation (VE) and the VE/VCO_2 slope are critical for evaluating breathing efficiency. An elevated VE/VCO_2 slope may indicate ventilatory inefficiency and is often associated with cardiovascular and pulmonary diseases, including heart failure and pulmonary hypertension. The ventilatory threshold (VT), also referred to as the anaerobic threshold, marks the point at which lactate begins to accumulate in the blood. This parameter is especially useful for determining endurance capacity and prescribing individualized training intensities (Tsvetkova-Gaberska et al., 2023). Additional indicators, such as oxygen pulse (VO_2/HR), provide insight into cardiac function, particularly stroke volume and cardiovascular efficiency. Breathing reserve helps identify whether exercise limitation is due to pulmonary constraints. Together, these variables allow for a comprehensive assessment of exercise tolerance and the identification of limiting factors. Clinically, it supports early detection of cardiopulmonary and metabolic disorders, risk stratification, and evaluation of treatment outcomes. In sports

science, it aids in optimizing performance and monitoring training adaptations. Furthermore, it is widely used in rehabilitation and preoperative evaluations to assess functional capacity and predict patient outcomes. In conclusion, CPET-derived parameters provide a holistic and integrative view of human physiology under stress. Their ability to simultaneously assess multiple systems makes this method an indispensable tool in modern medicine and exercise science, contributing to improved diagnosis, personalized interventions, and enhanced performance outcomes.

Keywords

Cardiopulmonary Exercise Test (CPET), Gas Exchange, Respiratory Function, Metabolic Response

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Global Incidence, Prevalence, Mortality, and Burden of Pulmonary Arterial Hypertension: A 30-year Analysis and Future Projections

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Abstract

Background: Pulmonary arterial hypertension (PAH) is a progressive condition characterized by elevated pulmonary artery pressure, leading to substantial morbidity and healthcare burden globally. This study aimed to elucidate epidemiological trends and the global burden of PAH across diverse populations and regions, identifying knowledge gaps regarding its impact and risk factors. *Methods*: We analyzed data from the Global Burden of Disease 2021 study spanning 1990 to 2021, focusing on incidence, prevalence, mortality, disability-adjusted life years, age-standardized rates (ASRs), and average annual percentage change. Joinpoint regression was used to detect temporal shifts and calculate annual percentage change. All measures were stratified by sex, age, and sociodemographic index (SDI). Future trends were projected using the Bayesian age-period-cohort model. *Results*: Globally, the number of prevalent PAH cases increased from 105,703 in 1990 to 191,808 in 2021, although the age-standardized prevalence rate remained stable. PAH-related deaths rose from 14,842 to 22,021, while the age-standardized mortality rate (ASMR) declined, suggesting improvements in disease management. Males experienced greater reductions in ASMR and age-standardized death rate than females. Higher ASR were observed in low-SDI regions. Projections indicate that continued declines in ASMR through 2040, but a rising number of PAH cases, particularly among females. *Conclusions*: These findings highlight the importance of sustained surveillance and tailored public health strategies to reduce the burden of PAH and support efficient healthcare resource allocation in the face of evolving demographic and regional challenges.

Keywords

Pulmonary Arterial Hypertension, Global Burden of Disease, Epidemiological Trends and Burden, Disability-adjusted Life Years, Average Annual Percentage Change, Age-standardized Rates

Equity and Governance Mechanisms of Health Technical Personnel Allocation in Public Tibetan Hospitals from a Supply-side Reform Perspective

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Abstract

Background: Tibetan medicine is a unique component of China's healthcare system, and its human resource allocation is the core of supply-side reform in medical services. With the advancement of "Healthy Tibet," the hardware facilities of public Tibetan hospitals have significantly improved; however, the equity of health technical personnel allocation still restricts the governance efficiency of public hospitals. Objective: To support the formulation of the 15th Five-Year Plan for Tibetan medicine, this study aims to quantify the spatiotemporal evolution and sources of disparities in health technical personnel allocation across seven prefecture-level cities, explore deep-rooted governance bottlenecks, and provide local evidence for building an autonomous knowledge system of health policies with Chinese characteristics. Method: A mixed-methods approach was employed. Quantitatively, based on the Dagum Gini coefficient decomposition model and annual health commission data, the overall, intra-regional, and inter-regional differences, along with transvariation density, were calculated. Qualitatively, semi-structured interviews were conducted with managers and technicians in seven cities, and thematic analysis was utilized to extract key influencing factors. Result: From 2020 to 2024, the overall Gini coefficient showed a trend of initially rising and subsequently falling, peaking at 0.6599 in 2021 and dropping to 0.5894 in 2024, indicating a converging disparity that nevertheless remains at a high absolute level. Dagum decomposition revealed that inter-regional differences were the primary contradiction, with the Gini coefficient between the capital and extremely remote areas consistently exceeding 0.7. Transvariation density fluctuated downward, while intra-regional differences were relatively small and continuously decreasing. Qualitative analysis identified themes such as geographical and economic constraints, misalignment of medical insurance payment and performance mechanisms, and limited career development, revealing that the difficulty in attracting and retaining talent caused by high-altitude costs and lagging compensation is the core institutional cause of inter-regional disparities. Conclusion: The equity of health technical personnel allocation in public Tibetan hospitals in Tibet is generally improving, but inter-regional imbalance remains a bottleneck for supply-side reform. It is recommended that policy focus during the 15th Five-Year Plan period should shift to structural optimization, innovating public hospital governance and medical insurance performance mechanisms, and implementing precise compensation through targeted training and special allowances for high-altitude remote areas to narrow regional gaps and promote the equalization of Tibetan medicine services.

Keywords

Public Tibetan Hospitals, Health Technical Personnel, Allocation Equity, Dagum Gini Coefficient, Supply-side Reform

Analysis of Social Participation Attitudes and Behavioral Intentions of Patients with Spinal Cord Injury During the Rehabilitation Period

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Abstract

Objective To investigate the social participation experience of patients with spinal cord injury during rehabilitation, and to provide evidence for their early social participation and improvement of rehabilitation strategies. *Methods* Nine patients with spinal cord injury from three rehabilitation centers in Henan Province from December 2020 to June 2021 were selected by purpose sampling method. Semi-structured interviews were conducted, and data were analyzed by seven-part phenomenological analysis method. *Results* Three themes (cognition of social participation, loss of self-independence, coping with social participation) and six sub-themes were extracted from data analysis. *Conclusion* The social participation of patients with spinal cord injury is a complicated and tortuous process. Medical staff should formulate specific strategies according to the rehabilitation needs of patients in different periods to make psychological and physiological preparations for their final social participation.

Keywords

Spinal Cord Injury, Social Participation, Qualitative Research

A Qualitative Study on the Health Education and Supportive Care Needs of Patients with Lower Limb Lymphedema After LVA Surgery

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Abstract

Objective Understanding the health education and supportive care needs of patients with lower limb lymphedema following Lymphaticovenous Anastomosis (LVA) surgery. *Methods* Employing purposive sampling methodology,a semi-structured qualitative interview was conducted with 12 postoperative LVA patients hospitalized at the Department of Wound Repair Surgery, Affiliated First Hospital of Ningbo University. The Colaizzi 7-step analysis method was used to analyze the interview data and refine the themes. *Results* The health education and supportive care needs of patients after LVA surgery mainly include information needs(information needs related to diseases and operations; information needs regarding postoperative daily diet and follow-up examinations); Spiritual、psychological and emotional needs(lack of chronic disease thinking and high expectations postoperation; anxiety due to ineffectiveness of the operation or the recurrence of the disease; having a sense of uncertainty and want to know the real recovery situation postoperation; self-blame after the operation); Social need(expecting care and assistance from family members; expecting care and assistance from the medical staff; expecting care and assistance from fellow patients); Physical needs (management of early postoperative complications and discomforts); Practical needs (postoperative rehabilitation exercise and nursing skills). *Conclusion* When providing health education to patients after LVA surgery, it is necessary to understand and pay attention to the patients' supportive care needs. Providing targeted and comprehensive health education knowledge to patient.

Keywords

Lower Limb Lymphedema, Lymph Venous Anastomosis, Health Education, Supportive Care, Needs, Qualitative Study

Decreasing Surgical Site Infections Through Methicillin-Resistant Staphylococcus Aureus Pre-screening

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Abstract

Surgical site infections (SSIs) are a known and preventable adverse event for the surgical population. The project site noted an increase in SSI rates, specifically, methicillin-resistant staphylococcus aureus (MRSA) and determined the need to use an evidencebased preoperative screening tool. The purpose of this quantitative quasi-experimental quality improvement project was to determine if or to what degree the translation of Saraswat et al.'s research on a methicillin-resistant staphylococcus aureus prescreening would impact surgical site infection rates among adult elective surgical patients. The project was implemented in an acute care hospital in California over four weeks. Marilyn Ann Ray's bureaucratic caring theory and Deming's plan-do-study-act change theory were the theoretical underpinnings of the project. The total sample size was 108, n = 23 in the comparative group and n = 85 in the implementation group. Data were extrapolated from the facility's electronic health record. To analyze the comparison and implementation group data, a chi-square test was used, and showed no statistically significant decrease in MRSA X 2 (1, N= 108) = 3.79, p =.052. Despite the lack of statistical significance, there is clinical significance as SSIs reduced from 8.7% in the comparative group to 1.2% in the implementation group. Therefore, the implementation of an MRSA prescreening may prevent SSIs in this population. Recommendations are to sustain the MRSA prescreening and further data analysis is conducted over six months. Keywords: methicillin-resistant staphylococcus aureus screening, surgical site infections, bureaucratic caring theory, evidence-based practice, SSI, prevention of SSI, the plan-do-study-act change theory (PDSA).

Keywords

Methicillin-resistant Staphylococcus Aureus Screening, Surgical Site Infections, Bureaucratic Caring Theory, Evidence-based Practice, SSI, Prevention of SSI, the Plan-do-study-act Change Theory (PDSA)

The Interaction Between High-Altitude Hypoxia and COVID-19 Injury: Dissociation of Ventilatory Efficiency and Oxygen Uptake

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Abstract

Background: Both high-altitude hypoxia and COVID-19 can independently induce cardiopulmonary dysfunction, with multiple pathophysiological intersections theoretically existing between the two. *Methods*: This cross-sectional study recruited 290 Han Chinese residents living in Lhasa, comprising 89 COVID-19 convalescents (COVID group) and 201 non-infected controls (N-COVID group). All participants underwent standardized cardiopulmonary exercise testing (CPET), muscle strength assessment, and completed the FACIT-Fatigue, IPAQ, and Pittsburgh Sleep Quality Index questionnaires. *Results*: No significant differences were observed between the COVID and N-COVID groups in age, height, body weight, BMI, duration of high-altitude residence, FACIT-Fatigue score, IPAQ score, or Pittsburgh Sleep Quality Index score ($P > 0.05$). Additionally, no significant between-group differences were found in FVC, FEV_1, VO_2peak, or VO_2peak/kg ($P > 0.05$). However, the COVID group demonstrated significantly elevated VE/VCO_2 (43.66±4.49VS40.92±4.40), VE/VCO_2 slope (43.18±5.95VS40.47±5.49), and RER (1.08±0.046VS1.06±0.046) compared to the N-COVID group ($P < 0.05$). Furthermore, the N-COVID group exhibited significantly better grip strength and balance performance than the COVID group ($P < 0.05$). *Conclusions*: Ventilatory efficiency may serve as a more specific indicator for evaluating cardiopulmonary function in this population. Clinical assessment should not rely solely on traditional metrics such as VO_2peak. For rehabilitation, interventions targeting respiratory pattern training to improve ventilatory efficiency and proprioceptive training to enhance neuromuscular control are recommended.

Keywords

High-altitude Hypoxia, Covid-19, Cardiopulmonary Exercise Testing, Ventilatory Efficiency, Oxygen Uptake

The Independent Association Between Dietary Protein Energy Ratio and Sleep Quality Among Chinese Patients with Type 2 Diabetes

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Abstract

Background Current clinical evidence regarding the association between protein intake and sleep quality remains limited and inconsistent. *Objective* To investigate the association between dietary protein energy ratio with sleep quality among Chinese patients with type 2 diabetes (T2DM). *Methods* A cross-sectional study was conducted among 193 T2DM patients recruited by convenience sampling. Twenty-four-hour dietary recall questionnaire was used to evaluate the energy contribution of dietary macronutrients. Pittsburgh Sleep Quality Index (PSQI) was adopted to assess sleep quality. Restricted cubic spline (RCS) regression was applied to test nonlinear relationships, while binary logistic regression was used to verify the independent correlation between protein energy ratio and sleep quality. Receiver operating characteristic (ROC) curve analysis was further performed to determine the optimal cut-off value of dietary protein energy contribution for predicting poor sleep status. *Results* The prevalence of clinically significant sleep disturbance was 56.5%. RCS analyses indicated no obvious nonlinear associations of protein energy proportion with sleep quality. Binary logistic regression revealed that higher dietary protein energy contribution was an independent protective factor against sleep disturbance (OR=0.93, 95%CI 0.89– 0.98). A cut-off value of 19.6% dietary protein energy contribution ($p < 0.001$, AUC 0.65, standard error 0.04) predicted poor sleep quality risk. Addiotnally, a higher dietary protein proportion served as a protective factor against poor sleep quality, especially among male patients, those aged ≥ 60 years and individuals with BMI < 24 kg/m^2. *Conclusions* A dietary protein energy contribution below 19.6% was associated with elevated risk of sleep disturbance among individuals with T2DM. Rational regulation of dietary protein intake should be highlighted, especilly for male patients aged ≥ 60 years with BMI < 24 kg/m^2, to optimize their sleep quality.

Keywords

Macronutrients, Sleep Quality, Type 2 Diabetes

Transcutaneous Auricular Vagus Nerve Stimulation Exerts Antidepressant Effects by Inhibiting Hippocampal Cell Ferroptosis and Enhancing Neuroplasticity via NRF2 Mediation

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Abstract

Depression is a severe mental disorder characterized by complex pathophysiological changes. Although transcutaneous auricular vagus nerve stimulation (taVNS) has shown therapeutic effects, the underlying mechanisms related to hippocampal oxidative stress and iron dyshomeostasis are still not well understood. This study aimed to investigate whether taVNS exerts antidepressant-like effects by regulating Nrf2-related signaling to inhibit iron dyshomeostasis and enhance hippocampal neuroplasticity. Adolescent rats were randomly divided into control, model, taVNS, taVNS+DMSO, taVNS+ML385 (Nrf2 inhibitor), and taVNS+EX527 (Sirt1 inhibitor) groups. Except for the control group, the remaining rats were subjected to chronic unpredictable mild stress (CUMS). The intervention groups received 21-day taVNS treatment and were intraperitoneally injected with inhibitors prior to each stimulation session. Behavioral assessments (SPT, OFT, EPM) were carried out both before and after the intervention. Hippocampal tissues were collected at PND 80 for Western blot (WB) and immunofluorescence (IF) analysis. Our results showed that CUMS induced significant depressive and anxiety-like behaviors. taVNS significantly alleviated these behavioral abnormalities, and there was no significant difference between the taVNS and taVNS+DMSO groups. However, ML385 or EX527 significantly blocked these therapeutic effects. At the molecular level, taVNS upregulated the expression of Sirt1, Nrf2 and GPX4, while downregulating the expression of Keap1 and GSDMD. These regulatory effects were consistent between the taVNS and taVNS+DMSO groups, yet were significantly reversed by ML385 or EX527. Immunofluorescence results indicated that taVNS reduced the number of Iba-1-positive cells and the fluorescence intensity of 4-hydroxynonenal (4-HNE), while increasing the signals of NeuN, PSD95, MAP2, BDNF, and TREM2 in the CA1, CA3, and DG regions. Similarly, these histological improvements were consistent between the taVNS and taVNS+DMSO groups but were significantly blocked by ML385 or EX527. In conclusion, these findings imply that taVNS exerts antidepressant-like effects by inhibiting hippocampal iron dyshomeostasis, alleviating neuroimmune dysregulation, and enhancing neuroplasticity, a process predominantly mediated by the Nrf2 signaling pathway.

Keywords

Transcutaneous Auricular Vagus Nerve Stimulation, Depression, Ferroptosis, NRF2, Hippocampus

Advances in Machine Learning-Based Prediction for Personalized Tacrolimus Therapy in Liver Transplant Recipients

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Abstract

Objective Tacrolimus is a cornerstone immunosuppressant following liver transplantation, characterized by a narrow therapeutic window and significant interindividual pharmacokinetic variability, which necessitates routine therapeutic drug monitoring. This study systematically reviews the application of machine learning algorithms in the personalized tacrolimus therapy for liver transplant patients, aiming to provide evidence-based guidance for the individualized clinical use of tacrolimus. *Methods* A systematic literature search was performed in 4 English databases (PubMed, Web of Science, Scopus, and Embase) and 3 Chinese databases (China National Knowledge Infrastructure, Wanfang Database, and *China Science and Technology Journal Database*) to identify studies on machine learning approaches in tacrolimus therapy for liver transplant patients. Original research focusing on machine learning models for the individualized application of tacrolimus in this population was included. Data including sample characteristics, variable selection methods, included predictors, and model predictive performance were extracted from the eligible literature, and the advantages and limitations of existing models were systematically summarized. *Results* A total of 10 studies were included, comprising 2 in pediatric and 8 in adult liver transplantation populations. The majority employed single-center retrospective study designs, with sample sizes ranging from 32 to 443 participants. Stepwise regression was the most frequently used method for variable selection, and commonly included predictors comprised demographic characteristics, postoperative time, genetic polymorphism, and concomitant medication. Among machine learning algorithms, extreme gradient boosting (XGBoost), gradient boosting decision tree (GBDT), and random forest (RF) were the most widely applied. The XGBoost model demonstrated the optimal predictive performance, with coefficient of determination (R^2) ranging from 0.82 to 0.91 and root mean square error (RMSE) of 0.90 to 2.0 ng/mL, substantially outperforming traditional pharmacokinetic models. Time-series models, particularly long short-term memory (LSTM) networks, exhibited notable advantages in handling high-dimensional data and dynamic changes in tacrolimus concentrations, achieving goodness-of-fit values exceeding 0.89. Regarding model validation, internal cross-validation predominated in early studies, whereas external multicenter validation has been increasingly adopted in recent years. Most models achieved prediction accuracy exceeding 80% within ±20% of the measured drug concentration, confirming their generalizability. However, currently established machine learning models generally lack calibration performance evaluation and external validation, and face limitations including low interpretability and limited reproducibility. *Conclusion* Machine learning-based prediction models demonstrate favorable accuracy and potential clinical utility in guiding personalized tacrolimus therapy for liver transplant recipients. Nevertheless, current models are constrained by

inherent biases of retrospective studies, insufficient investigation on special populations, inadequate calibration assessment, limited interpretability, and poor reproducibility, warranting further investigation.

Keywords

Tacrolimus, Machine Learning, Individualized Medication

GPR110-Dependent Macrophage Polarization Mediates the Therapeutic Effect of V-N_3P Single-Atom Catalyst in Septic Intestinal Injurys

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Abstract

Background: Sepsis-induced intestinal injury involves complex pathological processes, including dysregulated macrophage polarization, gut microbiota dysbiosis, and metabolic disturbances. Vanadium-based single-atom catalysts (SACs) with defined coordination structures show promise for inflammatory diseases, but their role and mechanisms in septic intestinal injury remain unclear. *Methods*: Two coordination-defined SACs, V-N_4 and V-N_3P, were synthesized and evaluated. Density functional theory calculations analyzed their electronic structure and catalytic activity. Sepsis models were established using cecal ligation and puncture in mice and pigs, with in vitro validation using LPS-stimulated RAW264.7 macrophages. Techniques including immunofluorescence, Western blot, RNA sequencing, 16S rRNA gene sequencing, and metabolomics were employed to investigate the effects on intestinal barrier, macrophage polarization, gut microbiota, host metabolism, and underlying mechanisms. *Results*: V-N_3P exhibited superior reactive oxygen species scavenging ability over V-N_4, attributed to phosphorus-induced charge delocalization. In septic mice, V-N_3P significantly improved survival, restored intestinal mucosal integrity, upregulated tight junction proteins (ZO-1, occludin) and MUC2, and reduced pro-inflammatory cytokine levels. V-N_3P promoted a shift from M1 to M2 macrophage polarization, which was reversible by a GPR110 agonist, identifying GPR110 as a key target. Mechanistically, V-N_3P downregulated GPR110, suppressed the JNK/NF-κB/ERK pro-inflammatory axis, and activated the A20/STAT3 anti-inflammatory pathway. Furthermore, V-N_3P restored gut microbiota α-diversity, enriched beneficial bacteria, and remodeled host metabolic profiles. *Conclusion*: The V-N_3P single-atom catalyst alleviates septic intestinal injury by targeting GPR110 to rebalance macrophage polarization and regulate the microbiota-metabolism network. This study provides a novel therapeutic strategy and theoretical basis for SAC-based "catalytic medicine" in treating inflammatory diseases.

Keywords

Vanadium-based Single-atom Catalysts, Sepsis, Intestinal Injury, GPR110, Macrophage Polarization

Optimizing Low-Dose Post-Emergence Tank Mixtures for Weed Control in Alfalfa

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Abstract

Alfalfa (*Medicago sativa*), a globally important perennial forage legume, is widely cultivated in China, where effective weed management remains essential for sustainable production. Chemical control, primarily relying on the herbicide imazethapyr, is the most common strategy. However, the continuous and exclusive use of imazethapyr exerts strong selection pressure on weed populations, promoting herbicide resistance and often necessitating increased application rates. To address this challenge, a two-year field study (2022–2023) was conducted to reduce chemical inputs and delay resistance by evaluating post-emergence herbicide alternatives and tank mixtures. Initial screening identified imazethapyr, prometryn, imazapic, and 2,4-DB as safe and effective against broadleaf weeds (*Chenopodiaceae album* and *Amaranthus retroflexus*). Haloxyfop-R-methyl and quizalofop-P-ethyl were highly selective against grasses, providing 100% and >98.4% control, respectively, but were less effective on broadleaf weeds (<35%). To broaden the control spectrum and reduce total herbicide use, haloxyfop-R-methyl was tank-mixed with each of the four broadleaf-active herbicides. The combinations haloxyfop-R-methyl + imazethapyr (36.5 + 56.26 g ai ha^{-1}) and haloxyfop-R-methyl + 2,4-DB (36.5 + 506.25 g ai ha^{-1}) maintained >90% control of *C. album*, *A. retroflexus*, and grasses while allowing a 25% reduction in total active ingredient compared to standard solo applications. Crucially, the mixtures haloxyfop-R-methyl + imazethapyr (36.5 + 56.25 g a.i. ha^{-1}) and haloxyfop-R-methyl + 2,4-DB (36.5 + 506.25 g a.i. ha^{-1}) delivered broad-spectrum weed control without compromising—and in some growth parameters even enhancing—alfalfa performance. These mixtures represent promising, sustainable options for integrated weed management in alfalfa production systems.

Keywords

Weed Management, Post-emergence Herbicide, *Medicago Sativa*, Dose Reduction, Imazethapyr

Applying Artificial Intelligence to Predict Mosquito Microbiome–Mediated Resistance: A Proposed Framework for Next-Generation Vector Control

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Abstract

Mosquito-borne diseases continue to impose a significant global health burden, causing millions of infections and deaths annually, and control efforts are increasingly compromised by the rapid emergence of insecticide resistance. While genetic mutuations contributing to resistance have been extensively studied, emerging evidence suggests that the mosquito microbiome plays a substantial yet underexplored role in modulating insecticide tolerance through mechanisms such as detoxification, metabolic regulation, and immune modulation. The high diversity and complexity of microbial communities, coupled with their interactions with environmental and physiological factors, make traditional analytical approaches insufficient to capture patterns predictive of resistance. This study proposes the development of an artifical intelligence (AI) based framework to predict microbiome-mediated insecticide resistance in mosquito populations. High-throughput sequencing will be employed to comprehensively profile bacterial communities from both field-collected and laboratory-reared mosquitoes exhibiting varying resistance phenotypes. Machine learning algorithms, including random forests, support vector machines, and neural network, will be used to indentify microbial signatures associated with resistance. Feature selection and model interpretability techniques will highlight key microbial taxa and functional pathways potentially contributing to tolerance, while environmental and physiological covariates such as breeding habitat, mosquito age, and microclimatic variables will be integrated to improve predictive accuracy. The anticipated outcomes include the indetification of specific microbial taxa and community patterns predictive of resistance, and the development of an AI-driven diagnostic tool capable of rapid classification of mosquito populations based on microbiome profiles. By bridging high-resolution microbiome profiling with AI analytics, this approach aims to provide objective, scalable, and data-driven tools for early detection of emerging insecticide resistance. The expected impact includes informing precision vector management strategies, guiding sustainable interventions, and contributing to the global effort to mitigate the burden of mosquito-borne diseases through innovative, integrative approaches that combine microbiome science, computational analytics, and applied vector control.

Keywords

Mosquito-borne Diseases, Insecticide Resistance, Mosquito Microbiome, Artificial Intelligence, Machine Learning, Microbial Community Profiling, Vector Control, Predictive Diagnostics

Research Progress on the Intervention of Callicarpa Nudiflora in Methamphetamine-induced Neurotoxicity and its Forensic Toxicological Significance

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Abstract

The abuse of methamphetamine (METH) remains a critical global health concern due to its profound neurotoxicity and associated mortality. Extensive experimental evidence has demonstrated that oxidative stress and neuroinflammation constitute the central pathophysiological mechanisms underlying METH-induced neuronal injury. Excessive reactive oxygen species production, mitochondrial dysfunction, blood–brain barrier disruption, and activation of microglial-mediated inflammatory cascades collectively contribute to progressive neurodegeneration. Despite advances in understanding these mechanisms, effective mechanism-targeted interventions remain limited. Callicarpa nudiflora (CN), a traditional medicinal herb widely used in Li ethnomedicine of Hainan, has attracted increasing attention due to its well-characterized phytochemical profile, particularly flavonoids and phenylethanol glycosides. Pharmacological studies have demonstrated that these constituents exert potent antioxidant and anti-inflammatory effects through modulation of the Nrf2/ARE signaling pathway and suppression of NF-κB–mediated inflammatory responses. Notably, these signaling pathways overlap substantially with the molecular networks implicated in METH-induced neurotoxicity. This review systematically summarizes the current phytochemical characterization and pharmacological evidence of CN, with particular emphasis on its regulatory effects on oxidative and inflammatory signaling pathways. Furthermore, the potential mechanistic intersections between CN bioactive compounds and METH-induced neurotoxic cascades are critically analyzed. By integrating evidence from toxicological, pharmacological, and molecular studies, this review provides a mechanistic framework for evaluating CN as a potential modulatory agent against METH-induced neurotoxicity and highlights future directions for experimental validation.

Keywords

Callicarpa Nudiflora, Methamphetamine, Neurotoxicity, Oxidative Stress, Neuroinflammation, Forensic Toxicology, Neuroprotection

Cellular Mechanisms of Chiral Enantiomer Toxicity Differences and Their Significance in Forensic Toxicology of Novel Psychoactive Substances

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Abstract

The proliferation of new psychoactive substances (NPS) presents a significant challenge to global forensic toxicological analysis. A substantial number of NPS are chiral compounds, whose different enantiomers often exhibit distinct pharmacological and toxicological profiles *in vivo*. However, current forensic analytical standards frequently report racemic mixtures as single entities, overlooking enantioselective toxicity, which may lead to substantial misinterpretation in the forensic assessment of intoxication cases. This review aims to systematically elucidate the key cellular mechanisms responsible for the toxicity differences of chiral NPS enantiomers and discuss their transformative implications for forensic toxicology practice. The core discussion focuses on stereoselective interactions at the cellular level. The differences in the affinity and efficacy of enantiomers when binding to specific molecular targets directly trigger divergent cellular signal transduction and functional responses. Their variations in cellular uptake, metabolic activation, and transport processes significantly influence their intracellular exposure kinetics and the generation of active metabolites, forming the basis of stereoselective toxicokinetics. These stereoselective interactions, amplified through intracellular signal transduction cascades, can induce multidimensional cellular stress responses, including mitochondrial dysfunction, excessive reactive oxygen species generation, endoplasmic reticulum stress, and calcium homeostasis disruption, subsequently selectively activating programmed cell death pathways such as apoptosis, necroptosis, or autophagy. Integrating the toxicological understanding of enantioselective mechanisms into forensic practice is essential for enhancing the scientific rigor of analytical conclusions. This paradigm shift necessitates the development and application of highly selective analytical techniques, such as chiral chromatography-mass spectrometry, and mandates that enantiomeric composition be incorporated as a critical variable in toxicological evaluations and cause-of-death determinations. A comprehensive elucidation of these mechanisms not only provides a theoretical foundation for constructing precise risk prediction models for novel psychoactive substances but also establishes a robust molecular basis for forensic identifications involving complex chiral compounds, thereby propelling the field towards greater precision and standardization.

Keywords

Chiral Enantiomers, Stereoselective Toxicity, New Psychoactive Substances (NPS), Forensic Toxicology, Cellular Mechanisms, Toxicokinetics, Enantiomer Separation and Analysis

Engineering Cas12j3 for Enhanced Trans-Cleavage Activity Toward Sensitive Nucleic Acid Detection

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Abstract

The trans-cleavage activity of CRISPR nucleases is critical for the development of highly sensitive nucleic acid detection platforms. Among compact effectors, Cas12j3 shows promising programmability but relatively limited trans-cleavage efficiency, which restricts its diagnostic potential. To address this limitation, we report a directed evolution strategy to enhance Cas12j3 activity using a two-stage screening workflow that integrates GFP-based primary screening and Cell-Free Protein Synthesis (CFPS)-based functional validation.In the first stage, a mutagenesis library of Cas12j3 variants was generated and expressed in a fluorescence-based screening system. A GFP-linked cleavage reporter enabled rapid identification of mutants with enhanced cis-cleavage activity. Variants showing increased GFP signal reduction were selected as candidates for further evaluation.In the second stage, these selected mutants were quantitatively assessed for trans-cleavage activity in a CFPS system. Fluorescence reporter assays were performed to compare the catalytic performance of evolved variants with the wild-type enzyme. This two-step strategy allows rapid enrichment of functionally improved variants while minimizing false positives due to expression variability. The evolved Cas12j3 variants exhibited significantly enhanced trans-cleavage activity, demonstrating the effectiveness of this approach. Overall, this platform provides a generalizable strategy for protein engineering of compact CRISPR nucleases and advances the development of future nucleic acid detection platforms with improved sensitivity and diagnostic potential.

Keywords

Cas12j3, Trans-Cleavage Activity, GFP-Based Screening, Nucleic Acid Detection

Application of Next-Generation Sequencing in Monitoring Ribosome Display Selection Against Doxorubicin

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Abstract

The selection of peptide ligands for small molecule drugs presents unique challenges due to their limited structural epitopes and the prevalence of non-specific interactions during screening. This study employs ribosome display coupled with next-generation sequencing (NGS) to investigate the enrichment trajectory of a random 50-amino acid peptide library against the small molecule chemotherapeutic agent doxorubicin. The library was subjected to five rounds of selection using doxorubicin-coated magnetic beads, with mRNA recovery and NGS analysis performed after each round to monitor sequence convergence and population dynamics. NGS data revealed progressive library enrichment across successive selection rounds, indicating effective selection pressure. The most highly enriched peptide candidates were synthesized and evaluated for binding affinity to doxorubicin using isothermal titration calorimetry (ITC). However, no detectable binding was observed under the tested conditions. These findings demonstrate that while NGS provides valuable insights into library evolution during ribosome display selections, sequence enrichment alone does not guarantee specific target binding, particularly for small molecule targets. The observed discrepancy between NGS data and biophysical validation underscores the importance of incorporating counter-selection strategies and orthogonal validation methods in screening workflows. This study contributes to the methodological understanding of peptide library screening against small molecules and offers practical considerations for optimizing future selection campaigns.

Keywords

Ribosome Display, Next-generation Sequencing, Peptide Library, Doxorubicin, Small Molecule

Assessing Tagging and Chemical Marking as Monitoring Tools for the Marbled Octopus (*Amphioctopus aegina* Gray, 1849)

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Abstract

Tagging and marking are widely used techniques for tracking individual cephalopods in natural environments, enabling investigations of growth, survival, and individual trajectories in wild populations. However, the effectiveness of these approaches varies considerably among species due to their soft–bodied morphology and complex behavioral responses to external manipulation. This study evaluated and practical application the suitability of external physical tagging and chemical marking techniques for monitoring the Marbled octopus (*Amphioctopus aegina* Gray, 1849). A total of 28 individuals were used, comprising 21 octopuses subjected to external tagging using medical–grade PE silk and 7 octopuses treated with chemical marking using Alizarin Red S administered via enriched prey. The chemical marking was administered in three pulses at 7–day intervals. Tag retention, survival, and behavioral responses were monitored throughout the experimental period. Subsequently, beak structures were examined under fluorescence microscopy to detect distinct fluorescent bands produced by each marking pulse. These bands served as permanent internal reference marks, allowing retrospective identification of marked individuals and reconstruction of growth chronology over time. Results showed that all tagged individuals removed the external tags within 36–48 hours, and tag rejection was consistently associated with tissue damage and subsequent mortality during the observation period. Therefore, the high rate of tag rejection rendered physical tagging ineffective for long–term tracking. In contrast, the chemical marking group resulted in high survival and produced clearly distinguishable fluorescent bands in the beaks, confirming successful incorporation of the marker and enabling reliable long–term individual identification and growth tracking. These findings demonstrate that external physical tagging is unsuitable for *A. aegina* due to high tag rejection and associated injury, whereas chemical marking using Alizarin Red S provides an effective, minimally invasive, and biologically stable alternative for long–term monitoring and individual–based studies in this species.

Keywords

Marbled Octopus, *Amphioctopus aegina*, Chemical Marking, Alizarin Red S, Physical Tagging

An Antimicrobial Protein with Broad-Spectrum Activity Against Drug-Resistant Bacteria: The Phage-Derived Holin

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Abstract

Objective: This study aims to investigate the lytic activity against host bacteria, fundamental biological characteristics, and antimicrobial activity against other clinical strains of the holin protein HolKpV318, which is derived from *Klebsiella pneumoniae* phage vB_Kp_XP4. *Methods*: Bioinformatics analysis was performed on the gene and amino acid sequence of HolKpV318. The recombinant plasmid pET-28a(+)-HolKpV318 was constructed using homologous recombination and transformed into *Escherichia coli* BL21 for induced expression. The minimum inhibitory concentration (MIC), antimicrobial and anti-biofilm activities, morphological effects on the host bacteria, and tolerance to temperature and pH stability of the protein were evaluated. Additionally, the antimicrobial spectrum against non-host bacteria was determined using the spot assay. *Results*: The HolKpV318 gene is 252 bp in length and encodes a protein consisting of 83 amino acid residues, which belongs to the phage Holin family, with a predicted molecular weight of approximately 9 kDa. HolKpV318 exhibited concentration- and time-dependent antimicrobial effects, with a minimum inhibitory concentration (MIC) of approximately 4 μg/mL. When combined with HolKpV318, the MIC of sulfamethazine decreased to 1/256 of its value when used alone. The optimal anti-biofilm effect of HolKpV318 was observed at a concentration of 12 μg/mL. Treatment with this protein significantly increased the permeability of the host bacterial cell membrane, ultimately leading to cell lysis. HolKpV318 exhibited the highest antimicrobial activity at 50°C and effectively inhibited host bacterial growth within a pH range of 3–10. Furthermore, HolKpV318 demonstrated lytic activity against a variety of clinical pathogenic bacteria, including *Klebsiella pneumoniae, Klebsiella pasteurii*, *Klebsiella grimontii*, *Enterobacter hormaechei*, and *Raoultella planticola*. Notably, it exhibited robust lytic capability against *Klebsiella pneumoniae* strains carrying carbapenemase genes (such as KPC-2, NDM-1, and NDM-5) and those of different ST and K types, including hypervirulent strains. *Conclusion*: The holin HolKpV318 derived from phage vB_Kp_XP4 exhibits potent broad-spectrum antibacterial activity, effectively lyses various drug-resistant strains, inhibits biofilm formation, and demonstrates favorable stability under varying pH and temperature conditions. These characteristics highlight its promising potential for clinical translation and its viability for the development of novel antimicrobial agents.

Keywords

Holin, *Klebsiella Pneumonia*, Endolysin, Antibacterial Activity, Biofilm

Ophiostomatoid Fungi Associated with Dendroctonus Micans (Coleoptera: Curculionidae) in a Resort Area (Bakhmaro) of Western Georgia

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Abstract

Dendroctonus micans is a widely distributed beetle that pest coniferous plants and spreed phytopatogenic fungi in coniferous forest of in Europe and Asia; however, as a vector of phytopathogenic fungi have been poorly studied in Georgia. Therefore, our aim was to study diversity and spread of ophiostomatoid fungi associated with D. micans in the western Georgia, forest ecosystem of Bakhmaro. This study recorded the diversity and distribution of ophiostomatoid fungi associated with D. micans collected from forest of Bakhmaro resort, during 2024–2025. Bark beetle specimens were sampled from four localities (Adjara Street, Leknari I, Leknari II, and Chokhatauri–Bakhmaro road). Fungal isolates were obtained under laboratory conditions and identified using morphological characteristics and molecular analyses.Four fungal taxa were detected: Ophiostoma piceae, Ophiostoma sp., Leptographium sp., and Graphilbum sp. In 2024, Graphilbum sp. and Ophiostoma spp. were widely distributed across sampling sites, with the highest frequencies recorded at Adjara Street (20 and 15 isolates, respectively). Leptographium sp. occurred at lower frequencies, while no fungi were detected from the Chokhatauri–Bakhmaro road samples that year. In contrast, collections from 2025 showed a shift in species composition, with Ophiostoma sp. becoming dominant, particularly at Leknari II and Chokhatauri–Bakhmaro road (18 and 28 isolates, respectively), whereas Graphilbum sp. was not recovered. The preliminary results recorded diversity of ophiostomatoid fungi associated with D. micans, in forest ecosistem of bakhmaro, Western Georgia.This research contributes to understanding pest–pathogen interactions in coniferous forest ecosystems and provide a basis for future forest health monitoring and management studies.

Keywords

Bark Beetles, Ophiostomatoid Fungi, Insect-fungus Interactions

The Role of Corin in Regulating Sweat Excretion in Eccrine Sweat Glands

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Abstract

In humans, sweating via the eccrine sweat glands is essential in thermoregulation that prevents the body from overheating. Corin is a serine protease highly expressed in the heart, where it activates atrial natriuretic peptide (ANP), a hormone that promotes renal sodium and water excretion. Previous studies reported corin expression in mouse dermal papilla, where it regulated coat color in an agouti-dependent mechanism. Constantly, we also detected corin expression in human hair follicles. However, there is no evidence to indicate that corin regulates hair color in humans. Unexpectedly, we found corin expression in secretory and ductal epithelial cells of human eccrine sweat glands by immune staining. In the secretory coil, corin was expressed in the luminal epithelial cells but not the peripheral myoepithelial cells. Similar expression patterns of ANP and natriuretic peptide receptor-A (NPR-A) were also found in human eccrine sweat glands. We confirmed the expression of corin, ANP and NPR-A in the eccrine sweat glands in mouse footpads. These data suggest that corin and ANP may act in the eccrine sweat glands to promote sodium excretion, thereby regulating electrolyte homeostasis in thermoregulation. We tested this hypothesis in wild-type (WT) and corin knockout (KO) mice in a sweat assay. Paws from anesthetized mice were wiped clean and coated with a layer of iodine/starch mixture. Pilocarpine, a sweat-stimulant, was injected in the paw. Photos were taken before and after (2 and 5 min) the injection. Sweat responses were indicated by the number and size of black dots, which were quantified by image software. The results showed that compared to WT mice, corin KO mice had a markedly reduced sweat response, as indicated by less black staining in footpads. In controls, we found no apparent differences in sweat gland numbers and morphology between WT and corin KO mice. These results indicate that sodium and water excretion is reduced in the sweat glands in corin KO mice, suggesting a physiological role of corin in promoting sweat secretion. Together, our findings have uncovered a novel function of corin in regulating sodium and water excretion in the eccrine sweat glands that are essential in thermoregulation.

Keywords

Corin, Sweat Glands, Sweat Secretion

Expression and Function of the Protease Corin in Sebaceous Glands

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Abstract

Sebaceous glands are vital skin appendages that regulate sebum production and maintain the skin barrier system. Dysregulated sebaceous metabolism is implicated in the pathogenesis of inflammatory skin diseases; however, the precise molecular mechanisms controlling sebum secretion remain largely unclear. Corin, a serine protease primarily identified in the heart, activates atrial natriuretic peptide (ANP) to modulate blood pressure and cardiac function. In skin and lipid metabolism, Corin is known to influence hair pigmentation and lipid secretion via the Agouti/AGRP-MC1R signaling pathway. However, the expression, function and molecular mechanisms of corin in human sebaceous glands remain unclear. This study aims to employ an integrative approach combining bioinformatics, cell biology, molecular biology, and in vivo animal studies. The goal is to identify and validate the molecular mechanisms by which Corin regulates sebum secretion, and to investigate its potential involvement in the pathogenesis of inflammatory skin diseases through modulating sebaceous gland function. Our research is expected to provide novel insights into the regulatory function of Corin in sebaceous gland biology. By clarifying its molecular mechanism in sebum secretion, this work may reveal a previously unrecogned link between Corin signaling and the pathophysiology of inflammatory skin conditions such as acne and seborrheic dermatitis. The findings could establish Corin as a potential new therapeutic target, thereby offering a fresh conceptual framework and theoretical basis for the prevention and treatment of skin inflammatory diseases associated with abnormal sebum metabolism.

Keywords

Corin, Sebaceous Glands, Sebum Secretion

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Digital Health Needs and Self-Management Barriers in Women with Polycystic Ovary Syndrome: A Qualitative Study to Inform Intervention Design

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Abstract

Objective: Polycystic ovary syndrome (PCOS) is a prevalent chronic endocrine–metabolic disorder that significantly affects women's reproductive, metabolic, and psychosocial health. Long-term self-management of lifestyle behaviors is critical for improving outcomes. Despite increasing use of digital health technologies in chronic disease management, limited research has explored the lived experiences, behavioral challenges, and digital health needs of women with PCOS. This study aimed to examine these aspects and provide evidence to inform targeted digital health interventions.Methods:A descriptive qualitative design was employed. Fifteen women aged 20–33 years with clinically diagnosed PCOS participated in semi-structured interviews. Topics included disease understanding, self-management practices, perceived barriers, emotional experiences, and engagement with digital health tools. Data were analyzed using thematic content analysis to identify key themes and domains related to self-management and digital health needs.Results:Analysis identified two overarching domains: (1) barriers to effective self-management, including insufficient disease knowledge, difficulty maintaining consistent health behaviors, and emotional stress; (2) digital health support needs, including (a) personalized guidance and behavioral reminders, (b) user-friendly interfaces with integrated self-monitoring for diet, activity, and symptom tracking, and (c) motivational features and peer/community support to enhance adherence and engagement. Findings highlight the complex interplay of cognitive, behavioral, and psychosocial factors in PCOS self-management.Conclusion: Women with PCOS face multidimensional challenges to self-management. Digital health interventions integrating personalized guidance with social and community support may improve adherence to healthy behaviors and long-term outcomes. These insights provide practical guidance for developing patient-centered digital health tools and evidence-based health promotion strategies tailored to women with PCOS.

Keywords

Digital Health, Polycystic Ovary Syndrome, Health Behavior, Self-Management, Qualitative Study

Cholesterol Metabolism Orchestrates Epigenetic Remodeling to Facilitate Neuronal Gene Activation During Direct Neuronal Reprogramming

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Abstract

Direct neuronal reprogramming via attenuation of polypyrimidine tract-binding protein 1 (PTBP1) has emerged as a candidate regenerative approach to replace neurons lost in neurodegenerative disorders, offering potential for functional restoration. Although emerging evidence confirm that *PTBP1* deficiency drives transdifferentiation of somatic cells into functional neurons, whether concurrent metabolic remodeling actively instructs this cell fate conversion or merely occurs as a non-functional epiphenomenon remains to be elucidated. Given the brain's status as the most cholesterol-enriched organ, it relies on sterol homeostasis for neuronal architecture synaptic transmission and myelin integrity. We also considered the role of acetyl-CoA as a metabolic intermediate linking cellular bioenergetics to epigenetic regulation. Thus, we investigated the hierarchical relationship between PTBP1-mediated reprogramming and coordinated metabolic-epigenetic remodeling. Then, we used a well-established fibroblast-to-neuron transdifferentiation model and employed an integrated multi-omics approach (metabolomics, transcriptomics, and epigenomics) to map dynamic network changes during *PTBP1* knockdown-induced transdifferentiation. Our findings demonstrate that *PTBP1* knockdown in human dermal fibroblasts effectively drives neuronal conversion. It is accompanied by global transcriptional downregulation of cholesterol biosynthesis pathways and intracellular accumulation of acetyl-CoA. Mechanistically, PTBP1 maintains cholesterol homeostasis by directly mediating the alternative splicing of core cholesterol enzymes and a key transcription factor. The accumulated acetyl-CoA subsequently fuels histone acetylation, driving genome-wide chromatin remodeling. This sequential metabolic-epigenetic cascade is required to activate the neurodevelopmental transcriptional programs essential to neuronal fate specification. Inhibition of cholesterol synthesis by statins enhances transdifferentiation efficiency, whereas mevalonate supplementation reversed this effect, demonstrating a functional requirement of cholesterol metabolic remodeling for *PTBP1*-mediated neuronal transdifferentiation. Multi-omic profiling further corroborates that statin treatment amplifies the open chromatin landscape and reinforces neuron-specific gene expression signatures. Collectively, these findings identify cholesterol metabolism as an instructive node functionally coupling *PTBP1*-mediated neuronal reprogramming to epigenetic remodeling, revealing a hierarchical mechanism wherein metabolic rewiring actively orchestrates the epigenetic and transcriptional execution of cell fate conversion, with direct implications for regenerative therapeutics.

Keywords

PTBP1, Direct Neuronal Reprogramming, Epigenetic Remodeling, Cholesterol Synthesis, Metabolic Rewiring

Optimization of Fermentation Culture Conditions for Salt-Tolerant *Azotobacter chroococcum* Strain A4 from the Rhizosphere of *Lycium ruthenicum* Using AI-Assisted Design

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Abstract

Xinjiang has a vast area of saline-alkali soil, accounting for one-third of China's total saline-alkali land, and soil salinization severely restricts sustainable agricultural development. *Lycium ruthenicum*Murr., a pioneer plant in Xinjiang's saline-alkali regions, exhibits strong salt tolerance and medicinal value, but its growth is still limited by nitrogen availability. *Azotobacter chroococcum*, an aerobic free-living nitrogen-fixing bacterium, can convert atmospheric N_2 into plant-available nitrogen, secrete plant growth regulators, and solubilize insoluble soil nutrients, making it a promising candidate for saline-alkali soil improvement and crop yield enhancement. A salt-tolerant *Azotobacter chroococcum*strain A4 isolated from the rhizosphere of *Lycium ruthenicum*shows excellent salt tolerance and nitrogen-fixing ability, but its unoptimized fermentation conditions limit large-scale application. This study combined AI-assisted design with single-factor experiments and response surface methodology to optimize the fermentation medium for strain A4, aiming to improve its biomass and nitrogenase activity, and provide theoretical and technical support for the development of nitrogen-fixing microbial agents dedicated to saline-alkali lands.

Keywords

Lycium ruthenicumMurr, *Azotobacter chroococcum*, Fermentation Condition Optimization, Response Surface Methodology, Cost-benefit Analysis

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The Integration of Nanomedicine and Bioinformatics: A New Frontier of Accurate Diagnosis and Treatment

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Abstract

The deep integration of nanomedicine and bioinformatics is reshaping the pattern of precision medicine. With their adjustable physicochemical properties, nanodrugs have shown unique advantages in the fields of targeted delivery, gene therapy and diagnostic imaging, but their clinical transformation has long been trapped in the challenges of complex nano-biological interactions, batch differences and safety prediction. Bioinformatics provides systematic solutions to the above problems by integrating multi-group data, molecular simulation and artificial intelligence algorithms. This article is trying to explore new learning and development directions. This article systematically reviews the latest progress in this cross-field: at the level of drug design, molecular dynamics simulation and machine learning models can accurately predict the transfection efficiency, protein crown formation and cell uptake behavior of lipid nanoparticles (LNPs); in the optimization of targeting strategies, bioinformatics tools can explore tumor characteristics Heterosexual biomarkers (such as FOLH1) are combined with molecular docking to guide the surface functional modification of nanocarriers and significantly improve their active targeting ability. In addition, the AI drive platform represented by NanoForge is realizing the rational design and high-throughput screening of nanodelivery systems through closed-loop iteration of dry and wet experiments. Although data standardization, in vivo and external correlation and regulatory framework still need to be improved, nanoinformatics, as an emerging interdisciplinary discipline, is promoting nanomedicine from "experiential exploration" to "predictive design" by integrating multimodal data and advanced computing models, providing complex indications such as cancer, genetic diseases and pediatric diseases. A safer and more efficient personalized treatment strategy.

Keywords

Nanodrugs, Bioinformatics, Artificial Intelligence, Drug Delivery, Targeted Therapy, Nanoinformatics

Targeted Thrombolytic Therapy Enabled by Near-Infrared Light-Responsive Microcapsules with Controlled Release Behavior

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Abstract

Venous thromboembolism (VTE) represents a major global health burden. Conventional thrombolytic drugs are severely constrained in clinical practice due to their short half-life, limited targeting specificity, and high bleeding risk. In recent years, photothermal therapy (PTT) has emerged as a promising thrombolytic strategy, which employs near-infrared (NIR) light to convert photon energy into localized heat for thrombus dissolution. Nevertheless, conventional metallic nanomaterials, despite their high photothermal conversion efficiency, are associated with potential biosafety issues that limit their translational potential. In comparison, melanin or polydopamine (PDA) nanoparticles exhibit outstanding biocompatibility and biodegradability, thus representing safer alternatives for photothermal applications. Meanwhile, nitric oxide (NO) possesses distinctive antithrombotic effects and shows great potential as an adjuvant for thrombolytic therapy. Among various NO donors, S-nitrosoglutathione (GSNO) is highly favorable owing to its superior stability and biocompatibility. In this work, two types of microcapsules were successfully fabricated via layer-by-layer (LBL) self-assembly, with NIR light acting as an external trigger for on-demand thrombolytic therapy. These microcapsules were tailored for the treatment of femoral vein thrombosis and pulmonary embolism, and displayed high drug-loading efficiency, stable photothermal performance, and controllable NO release profiles. Moreover, with the targeting capability of fucoidan, the microcapsules could be precisely delivered to thrombotic lesions. In vivo results confirmed that this microcapsule-based thrombolytic system achieved therapeutic efficacy comparable to traditional thrombolytics, while markedly alleviating the associated bleeding risk. Collectively, this study establishes a novel, precise, efficient and safe therapeutic platform for thrombus management, providing important implications for further research and clinical translation in thrombotic diseases.

Keywords

Near-Infrared Light, Microcapsules, Thrombolytic Therapy, Thrombus Targeting

Multi-Omics Integration Combined with Deep Learning Predicts High-Density Growth Regulatory Genes in *Saccharomyces cerevisiae*

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Abstract

Saccharomyces cerevisiae is the most widely used eukaryotic model chassis and core industrial workhorse in the fields of synthetic biology, metabolic engineering and green biomanufacturing. For industrial-scale bioproduction, high-density fermentation of this yeast is the core prerequisite for the large-scale manufacturing of bio-based chemicals, recombinant proteins and biofuels. Its high-density growth performance is the core trait that directly determines the upper limit of fermentation titer, production efficiency and comprehensive manufacturing cost of the yeast cell factories. However, traditional experimental screening and validation of high-density growth regulatory genes face inherent bottlenecks: long research cycles, high experimental costs, heavy dependence on prior knowledge, and low hit rate of functional targets, which severely restrict the rapid directed optimization of industrial yeast chassis. To address these gaps, this study aims to develop an efficient and accurate prediction method for high-density growth regulatory genes in *Saccharomyces cerevisiae* through multi-omics integration and deep learning, as multi-omics data can comprehensively cover the multi-dimensional information of genes from sequence to expression and function, while deep learning can effectively mine the hidden nonlinear regulatory relationships in high-dimensional omics data to make up for the shortcomings of traditional analysis methods. We integrated whole-genome, transcriptomic, proteomic and phenomic data to build a multi-dimensional panoramic gene feature set, and constructed a deep learning prediction model embedded with an attention mechanism to increase the acccuracy and identify high-confidence regulatory genes links to yeast high-density growth. This study provides a low-cost, high-efficiency research strategy and a high-value candidate target library for the directed modification and performance optimization of industrial *Saccharomyces cerevisiae* chassis.

Keywords

Saccharomyces Cerevisiae, High-density Growth, Growth Regulatory Genes, Multi-omics Integration, Deep Learning

Intelligent Construction and Biomechanical Optimization of Post Space for Maxillary Anterior Teeth Restoration

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Abstract

Background: Trauma to maxillary anterior teeth frequently results in crown-root fractures. Post-core crown restoration serves as the primary treatment following root canal therapy. Conventional post space preparation is associated with insufficient cutting accuracy, high operator dependence, poor repeatability, and uncontrollable biomechanical performance, which may lead to complications such as post loosening, root fracture, and root perforation. *Objective*: To address these clinical challenges, this study established a digitally intelligent design and biomechanical optimization system for post space preparation. *Methods*: CBCT data were collected from 50 patients with traumatized maxillary anterior teeth. The nnU-Net framework was applied to achieve pixel-level segmentation of dental hard tissues and root canals, with automatic extraction of anatomical parameters. Optimal post space parameters were output and a guiding model was generated via Abaqus finite element analysis, XGBoost machine learning, and genetic algorithm-based multi-objective optimization. *Results*: The segmentation accuracy of dental anatomical structures exceeded 96.2%. After optimization, the maximum dentin stress was reduced by 25.7%, the stress distribution peak coefficient decreased by 25.8%, and the amount of preserved tooth tissue increased by 15.6%. *Conclusions*: Driven by anatomy and mechanics, this study enables personalized and precise design of post space and optimizes the mechanical distribution of the post space. It is expected to further improve the safety and long-term outcomes of anterior teeth post-core crown restoration, providing an AI-enhanced novel approach for digital post crown restoration in dentistry.

Keywords

Post Crown Restoration, Post Space, Intelligent Design, Biomechanical Optimization, Machine Learning

Comparative Transcriptomic Analysis Reveals Morphotype Associated Differences in Immune Responses to *Ichthyophthirius multifiliis* Exposure in Goldfish (*Carassius auratus*)

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Abstract

Ichthyophthirius multifiliis (Ich) is a highly invasive protozoan parasite that causes massive disease outbreaks in freshwater fish, posing a significant threat to global aquaculture. Despite its impact, the molecular basis of differential host response to *I. multifiliis* exposure in goldfish (*Carassius auratus*) remain poorly understood. This study addressed this gap by comparing the transcriptome profiles of single-tail (S) and twin-tail (T) goldfish following parasite exposure to identify the genetic basis of host responses. RNA-seq analysis identified 9,408 differentially expressed genes (DEGs) between the two morphotypes, with 4,387 genes up-regulated and 5,021 down-regulated in the S group compared to the T group. Functional enrichment and KEGG analysis revealed that these DEGs were primarily involved in cellular and metabolic processes, as well as key immune signaling pathways, including NOD-like receptor, RIG-I-like receptor, C-type lectin receptor, chemokine, NF-κB, and JAK-STAT signaling. Among 92 genes associated with Ich responses across 10 immune pathways, 15 candidate genes were prioritized for further functional investigation. Quantitative RT-PCR validation of five key immune genes (*GIMAP4, TRIM25, GFAP, C-type lectin*, and *CHRNA3*) confirmed the reliability of the RNA-seq data. These results provide insight into morphotype-associated differences in transcriptomic immune responses to *I. multifiliis* exposure in goldfish and identify candidate pathways and genes for future functional studies.

Keywords

Twin-tail Goldfish, *Carassius Auratus*, *Ichthyophthirius Multifiliis*, Transcriptome Analysis, Immune Response, Parasite Exposure

Structural Basis of TRA16-Mediated Inhibition of TR4 Transcriptional Activation in Diabetes

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Abstract

Diabetes mellitus is a prevalent metabolic disorder worldwide, in which the nuclear receptor TR4 promotes disease progression by transcriptionally activating key genes such as *PEPCK* and *SCD1*. The associated protein TRA16 has been shown to specifically inhibit TR4; however, its precise molecular mechanism remains unclear. In this study, we successfully expressed and purified full-length TR4, TRA16, and their complex through optimization of fusion tags, host strains, and induction conditions. Crystallization of the TRA16–TR4 complex was achieved using the hanging-drop vapor diffusion method, yielding diffraction data at approximately 3.8 Å resolution, from which the three-dimensional structure was determined. In parallel, the structure of TRA16 was predicted using AlphaFold3 and further analyzed through molecular docking and molecular dynamics simulations. The results suggest that TRA16 inhibits TR4 by directly interacting with either the DNA-binding domain (DBD) or the ligand-binding domain (LBD) of TR4, with high model fitting scores supporting the reliability of the interaction modes. This study elucidates the structural basis and molecular mechanism by which TRA16 suppresses TR4-mediated transcriptional activation, providing new insights into TR4 regulation in diabetes. The resolved complex structure and identified key interaction sites offer a critical framework for the rational design of small-molecule or peptide-based TR4 inhibitors, with significant potential for precise therapeutic intervention and reduced side effects.

Keywords

Diabetes Mellitus, Nuclear Receptor TR4, TRA16, Transcriptional Regulation, Complex Structure, Molecular Docking and Dynamics Simulation

Acknowledgments

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Construction of Chlorogenic Acid-Functionalized Stimuli-Responsive Hydrogel and Its Promoting Effect on Diabetic Wound Healing

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Abstract

Diabetic chronic wounds are often characterized by delayed healing, dysregulated inflammation, and excessive oxidative stress, and there is still a lack of safe and effective therapeutic strategies in clinical practice. In this study, a stimuli-responsive hydrogel loaded with chlorogenic acid (CGA) was designed and constructed. Through material structure optimization and regulation of biological activities, the hydrogel was endowed with synergistic antioxidant, anti-inflammatory, and pro-healing effects targeting the wound microenvironment. Systematic characterization results showed that the hydrogel possessed a three-dimensional interconnected porous structure, good swelling properties, and mechanical stability, and enabled sustained and stable release of chlorogenic acid. In vitro cell experiments demonstrated that the hydrogel extract exhibited no significant cytotoxicity against mouse embryonic fibroblasts (L929), indicating excellent biocompatibility. In a streptozotocin-induced diabetic mouse model with full-thickness excisional wounds, CGA-functionalized hydrogel significantly accelerated wound closure, with a healing rate of ~98% at day 14 post-surgery, outperforming blank controls, blank hydrogels, and commercial wound dressings. Moreover, this hydrogel significantly reduced local reactive oxygen species (ROS) levels and the expression of inflammatory cytokines (TNF-α, IL-6) at the wound site, promoted angiogenesis and the polarization of macrophages from the M1 toward the M2 phenotype, thereby remodeling the wound immune microenvironment and accelerating tissue regeneration and repair. In summary, the chlorogenic acid-functionalized hydrogel constructed in this study possesses good biocompatibility, antioxidant and anti-inflammatory capabilities, and efficient wound healing performance. It provides a safe, simple, and effective new material and strategy for the treatment of chronic refractory diabetic wounds, showing promising clinical translation prospects in the fields of skin tissue engineering and wound repair.

Keywords

Stimuli-responsive Hydrogel, Chlorogenic Acid, Diabetic Wound, Antioxidant, Wound Healing

Mechanism Underlying Heat Stress-induced Anther Abortion in Wheat at the Tetrad Stage

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Abstract

Climate change has increased the frequency of extreme high-temperature events during the booting stage of wheat, coinciding with the tetrad stage—a critical window for floret development. Heat stress during this stage disrupts anther tissues, particularly the tapetum, thereby reducing grain number and causing substantial yield losses. In this study, two wheat cultivars differing in thermotolerance, Huaimai 33 (HM33, heat-tolerant) and Fanmai 5 (FM5, heat-sensitive), were subjected to heat stress at the tetrad stage. HM33 exhibited markedly higher anther fertility than FM5, which was attributable to lower accumulation of reactive oxygen species (ROS) and attenuated programmed cell death (PCD) in the anthers. Scanning and transmission electron microscopy, TUNEL assays, and physiological analyses revealed that heat stress damaged chloroplasts and mitochondria in the endothecium and tapetum, elevated Caspase-9 and Caspase-3 activities, and thereby exacerbated PCD, ultimately leading to severe degradation of the tapetum and adjacent tissues. Toluidine blue and periodic acid–Schiff (PAS) staining further demonstrated that structural damage to the endothecium and tapetum blocked carbohydrate transport to microspores, resulting in insufficient polysaccharide accumulation and a pronounced decline in pollen viability. Collectively, heat stress triggers ROS over-accumulation and intensified PCD, disrupts anther architecture and sugar translocation, and consequently increases anther abortion, reduces grain number per spike, and causes significant yield losses. These findings provide a theoretical basis for breeding heat-tolerant wheat cultivars and developing mitigation strategies against heat stress during the booting stage.

Keywords

Tetrad Stage, Heat Stress, Anther Abortion, Reactive Oxygen Species, Programmed Cell Death

Phenylboronic Acid-based Composite Hydrogel Microneedles for Multifunctional Glucose-responsive Transdermal Insulin Delivery

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Abstract

Poor compliance with conventional insulin injection therapy has driven interest in microneedle-mediated transdermal delivery, which combines the advantages of percutaneous and injectable administration. However, long-term application of microneedles can induce localized tissue damage, including infection, oxidative stress, and inflammation. To address these challenges, this study integrates skin-repair biomaterials with glucose-responsive microneedle technology. A phenylboronic acid-based composite glucose-sensitive microneedle system was developed by blending phenylboronic acid-modified quaternized chitosan (QCS-FPBA) with polyvinylpyrrolidone (PVP), polyvinyl alcohol (PVA), epigallocatechin gallate (EGCG), and insulin (INS). This integrated system simultaneously confers antibacterial, antioxidant, anti-inflammatory, and skin-regenerative functionalities. The hydrogel microneedles were comprehensively evaluated through systematic physicochemical characterization, *in vitro* biological assays, and *in vivo* pharmacodynamic studies to assess their morphology, biological effects, and glucose-responsive performance. Experimental results demonstrated that the three composite hydrogels constructed with QCS-FPBA as the core component all formed dynamic and reversible crosslinked networks. Notably, the QCS-FPBA-25-PVP-PVA-EGCG hydrogel exhibited optimal glucose sensitivity, and the fabricated microneedles exhibited uniform morphology and robust mechanical strength. The synergistic antioxidant, anti-inflammatory, and antibacterial efficacy of the system, arising from the cooperative action of boronate ester bonds, quaternized chitosan, and EGCG, was validated through DPPH radical scavenging assays, fluorescent probe analysis, ELISA, and antimicrobial testing. Preliminary biocompatibility was established *via* CCK-8 cytotoxicity assays, hemolysis tests, and histological staining. *In vivo* pharmacodynamic studies demonstrated that the microneedles enabled sustained and dynamic glycemic regulation under the "three-meal-per-day" mode. Collectively, this phenylboronic acid-based composite glucose-sensitive hydrogel microneedle system integrates exceptional glucose-responsive drug release with robust antioxidant, anti-inflammatory, and antibacterial functionalities, effectively mitigating localized adverse reactions associated with long-term transdermal microneedle application, and holds substantial promise for intelligent transdermal drug delivery in diabetes management.

Keywords

Glucose-sensitive Microneedles, Phenylboronic Acid Hydrogel, Intelligent Insulin Delivery, Antioxidant, Anti-inflammatory

Effects of Rice-*Sphagnum* Intercropping on Rice Growth and Soil Bcaterial Community Structure

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Abstract

Sphagnum is an ecologically important peat-forming moss with substantial value in carbon sequestration, wetland restoration, and horticultural applications. Rice-*Sphagnum* intercropping has the potential to couple agricultural production with the cultivation of this high-value peat moss resource. To evaluate the ecological feasibility of rice-*Sphagnum* intercropping, field experiments were conducted to compare intercropping with conventional rice monoculture by examining rice growth, soil physicochemical properties, enzyme activities, and soil bacterial communities. Differences in intercropping performance were also assessed between low- and high-altitude sites at 100 and 800 m, respectively. The results indicated that rice-*Sphagnum* intercropping enhanced rice vegetative growth, while grain yield remained unaffected. Moreover, this intercropping system mitigated oxidative stress in rice, as evidenced by reduced malondialdehyde accumulation and stable superoxide dismutase activity. Altitude exerted contrasting effects on rice and *Sphagnum*: lower altitude favored rice growth and grain yield, whereas higher altitude promoted *Sphagnum* growth, biomass accumulation, and nutrient retention. In terms of soil properties, intercropping slightly reduced soil pH but did not significantly affect soil nutrient supply capacity in paddy fields. It moderately reduced the activities of soil oxidative enzymes, including phenol oxidase and peroxidase, thereby slowing the oxidative decomposition of organic matter and altering key biochemical processes related to soil carbon sequestration and nutrient cycling. Furthermore, the intercropping system reshaped soil bacterial community structure and increased the complexity of bacterial co-occurrence networks. Variations in bacterial communities were mainly associated with soil pH, carbon fractions, total nitrogen, and available phosphorus. Overall, rice–*Sphagnum* intercropping represents a promising cultivation strategy for integrating paddy production with the utilization of *Sphagnum* as an ecological resource. Further studies are needed to optimize establishment methods and field management practices in order to better balance *Sphagnum* cultivation with stable rice production.

Keywords

Sphagnum, *R*ice-*Sphagnum* Intercropping, Altitude, Soil Bacterial Community

Identifying *Pyricularia Orizae* on the Head Smut of Fonio (*Digitaria Exilis*) in Bauchi Nigeria

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Abstract

During the rainy cropping season of 2003 in Bauchi, Nigeria, involving *nakusni* variety of *acha*, the local names for the cereal crop fonio (*Digitaria exilis* Stapf.), smutted heads of black sooty spores were observed at harvest on many of the 3 replication plots. Replacement of panicles by the smutted heads is a complete loss of grain yield, and undesirable. Smutted heads from each replication were sampled and surface sterilized using 70% alcohol. They were cultured in triplicate on potato dextrose agar plates which were placed on the laboratory table at 27 ± 2°C for 7 days and observed daily. Greyish brown or ash colonies of mycelia were noted between 4-7 days on all the plates. Microscopic observation at magnification 10 and 40 of the mycelial strands, after having been scrapped off aseptically using an inoculating needle and placed on a sterile glass slide containing 3 drops of lactophenol cotton blue solution revealed hypopodia, septate hyphae, single conidia that is obclavate to lop shape which appeared 3-celled, the typical features for *Pyricularia orizae* Cav., a fungus known to be pathogenic for leaf spot and blight on several grasses including *Digitaria* species. Its identification here is quite unusual though not surprising, as 3 new smut species of Chinese rice blast isolates (*Pyricularia orizae* Cav.) have been reported by Lin Guo (Mycosystema 6: 51-55, 1993). This observation and the referred, strongly suggest its new potential for influencing smut pathogenesis in grasses, a detrimental process to grain yield. Genetic mutation in this pathogen, resulting from high environmental temperature prevalent during the growing season, is suspected to have accentuated this transformation. It is also the first such report on fonio, from Bauchi Nigeria.

Keywords

Digitaria, Fonio, Pyricularia, Smut

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