SCHOLARLY PUBLICATIONS
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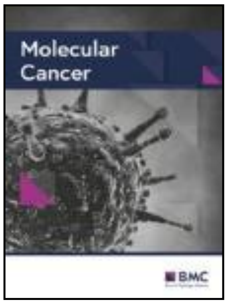
Journal Name: Molecular Cancer **IF: 33.9**

Title: Epithelial-to-mesenchymal transition (EMT) and cancer metastasis: the status quo of methods and experimental models 2025

Author: Allgayer H.; Mahapatra S.; Mishra B.; Swain B.; Saha S.; Khanra S.; Kumari K.; Panda V.K.; Malhotra D.; Patil N.S.; Leupold J.H.; Kundu G.C.

Details: Volume 24, Issue 1, December 2025, Article number 167

Abstract: Epithelial-to-mesenchymal transition (EMT) is a crucial cellular process for embryogenesis, wound healing, and cancer progression. It involves a shift in cell interactions, leading to the detachment of epithelial cells and activation of gene programs promoting a mesenchymal state. EMT plays a significant role in cancer metastasis triggering tumor initiation and stemness, and activates metastatic cascades resulting in resistance to therapy. Moreover, reversal of EMT contributes to the formation of metastatic lesions. Metastasis still needs to be better understood functionally in its major but complex steps of migration, invasion, intravasation, dissemination, which contributes to the establishment of minimal residual disease (MRD), extravasation, and successful seeding and growth of metastatic lesions at microenvironmentally heterogeneous sites. Therefore, the current review article intends to present, and discuss comprehensively, the status quo of experimental models able to investigate EMT and metastasis in vitro and in vivo, for researchers planning to enter the field. We emphasize various methods to understand EMT function and the major steps of metastasis, including diverse migration, invasion and matrix degradation assays, microfluidics, 3D co-culture models, spheroids, organoids, or latest spatial and imaging methods to analyze complex compartments. In vivo models such as the chorionallantoic membrane (CAM) assay, cell line-derived and patient-derived xenografts, syngeneic, genetically modified, and humanized mice, are presented as a promising arsenal of tools to analyze intravasation, site specific metastasis, and treatment response.



URL: https://molecular-cancer.biomedcentral.com/articles/10.1186/s12943-025-02338-2

SCHOLARLY PUBLICATIONS
School of Biotechnology
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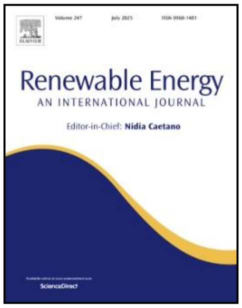
Journal Name: Renewable Energy **IF: 9.0**

Title: Biodiesel synthesis from Ricinus communis and Pongamia pinnata oil blends by injecting superheated methanol â€“ isopropanol mixtures: Optimization through CCD and ANN approaches

Author: Karmakar B.; Chakrabortty S.; Kumar R.; Halder G.

Details: Volume 249, 15 August 2025, 123223

Abstract: In the current study, blends of castor and karanja oils were subjected to uncatalysed alcoholysis with superheated mixtures of 2-propanol and methanol for their rapid conversion into fuel-grade esters. Optimizable ranges identified from batch studies for 6 parameters: alcohol preheat temperature, castor oil to karanja oil ratio, initial oil mass, methanol to 2-propanol ratio, reaction temperature and retention duration were fed into a spherical central composite design (CCD-S, used for identifying process conditions for optimal biodiesel yield. It was noted that a maximum biodiesel yield of 98.79 % could be obtained when 650g castor and karanja oil blend at a ratio of 2:1 was charged into the reactor. The alcohols at a ratio of 3:5 for methanol: 2-proanol had to be pre-heated to 140 °C to achieve desired energy, reactivity and flow. The reaction provided best results when allowed to occur at 260 °C for a duration of 8 min. The experimentally obtained data were verified for reliability through ANOVA studies and ANN was used to validate the data as well as develop a model capable of predicting output accurately, with a 6-10-1 algorithm giving an R^2 of 0.987, indicating high reliability.



URL:https://www.sciencedirect.com/science/article/pii/S0960148125008857?via%3Dihub

SCHOLARLY PUBLICATIONS
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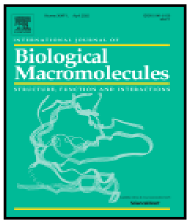
Journal Name: International Journal of Biological Macromolecules **IF: 7.7**

Title: Starch scavenges degradation products from protein solutions

Author: Gartia J.; Bopardikar M.; Dehury B.; Mishra S.; Mishra R.; Singh H.

Details: Volume 306, May 2025

Abstract: The shelf life of proteins in-vitro is limited by their susceptibility to various degradation processes. This study demonstrates that starch can extend protein stability by selectively removing non-proteolytic degradation products. Using NMR spectroscopy, we show that starch effectively scavenges degraded protein impurities while preserving the native protein structure as indicated by nearly identical [^{15}N, ^{1}H]-HSQC spectra for fresh intact protein and degraded protein samples treated by starch. The interaction is primarily electrostatic, with starch exhibiting a strong affinity for positively charged amino acids such as arginine, lysine, and histidine. Molecular dynamics simulations further reveal that amylose stabilizes these amino acids through hydrogen bonding and charge-dipole interactions, reducing backbone flexibility. This low-cost, easy-to-implement approach holds promise for improved protein stability and has broad pharmaceutical applications.



URL: https://www.sciencedirect.com/science/article/pii/S0141813025019385?via%3Dihub

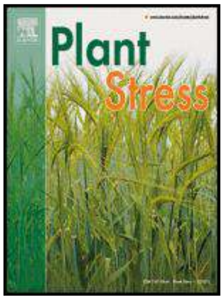
Journal Name: Plant Stress **IF: 6.8**

Title: Pearl millet WRKY transcription factor PgWRKY52 positively regulates salt stress tolerance through ABA-MeJA mediated transcriptional regulation

Author: Chanwala J.; Kumari K.; Jha D.K.; Giri M.K.; Dey N.

Details: Volume 16, June 2025, Article number 100814

Abstract: Environmental stresses adversely affect plant growth and development by disturbing physiological and metabolic equilibrium. Plants counteract these stresses through intricate genetic and biochemical pathways, which are largely mediated by signalling networks that involve key transcription factors (TFs). Among these, WRKY TFs are crucial in modulating plant responses to various stresses. In previous studies, WRKY TFs have been identified in millets. However, their functional characterization in millets remains vastly unexplored. Therefore, we have isolated and characterized PgWRKY52, a Group IIc WRKY TFs from pearl millet, along with its upstream promoter region to understand its functional regulatory role. Ectopic expression of PgWRKY52 in transgenic Arabidopsis improved seed germination under salt stress and phytohormonal treatments of abscisic acid (ABA) and methyl jasmonate (MeJA). Improved stress tolerance was linked to reduced reactive oxygen species (ROS) accumulation and upregulation of stress-responsive genes, indicating an enhanced defense system. Promoter analysis unveiled that the PgWRKY52 promoter was constitutively active across vegetative and reproductive tissues, with strong stress-inducible activity under salt, heat, and ABA treatments. Cis-regulatory element (CRE) analysis identified key stress-responsive elements, including ABRE, MYB, W-box and MYC, which were validated through mutational studies as essential for promoter activity. Additionally, PgWRKY52 exhibited W-box-dependent DNA-binding capability, a characteristic feature of WRKY TFs. These findings emphasize the important function of the PgWRKY52 promoter in driving stress-responsive transcription. Altogether, these findings establish PgWRKY52 as a stress-responsive TF that enhances salt stress tolerance through crosstalk of ABA-MeJA signalling pathways and the regulatory role of its promoter, presenting a promising tool for developing climate-resilient crops.



URL: https://www.sciencedirect.com/science/article/pii/S2667064X2500079X?via%3Dihub

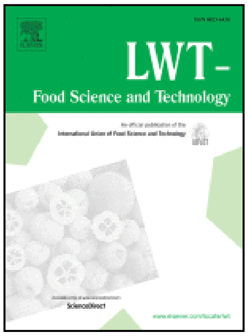
Journal Name: LWT **IF: 6.6**

Title: Formulation and characterization of ready-to-drink nutraceutical beverage from blood fruit (Haematocarpus validus)

Author: Sasikumar R.; Kumar T S.; Vivek K.; Panda S.K.; Jaiswal A.K.

Details: Volume 2251, June 2025, Article number 117929

Abstract: Blood fruit (Haematocarpus validus) is a rich source of bioactive compounds with potential health benefits. This study aimed to develop and characterize a ready-to-drink (RTD) fermented nutraceutical beverage (FNB) using controlled fermentation at 20, 23, and 26 °C and to assess its biochemical composition, antioxidant potential, volatile profile, anti-nutritional factors, and sensory attributes. The beverage was analyzed using Fourier Transform Infrared (FTIR), Ultra Performance Liquid Chromatography (UPLC), High Performance Liquid Chromatography (HPLC), Gas Chromatography High Resolution Mass Spectrometry (GC-HRMS), and High-Resolution Liquid Chromatography with Mass Spectrometry (HR-LCMS), with key parameters such as total sugars, organic acids, total polyphenols, flavonoids, anthocyanins, and antioxidant activity determined. Fermentation at 26 °C resulted in the highest enrichment of total anthocyanins (411.7 ± 0.79 mg C3GE/100 mL), flavonoids (481.8 ± 0.49 mg RE/100 mL), and polyphenols (537.4 ± 0.84 mg GAE/100 mL). Antioxidant activity was significantly higher in the 26 °C fermented beverage, as indicated by 2,2-diphenyl-1-picrylhydrazyl or DPPH (2128 ± 2 μmol TE/100 mL), Oxygen Radical Absorbance Capacity or ORAC (2988 ± 3 μmol TE/100 mL), 2,2’-azino-bis(3-ethylbenzothiazoline-6-sulfonic acid or ABTS (1238 ± 2 μmol TE/100 mL), and Ferric Reducing Antioxidant Power or FRAP (3360 ± 2 μmol Fe^{2+}/100 mL). Volatile analysis identified 36 key compounds, contributing to sensory attributes.



URL: https://www.sciencedirect.com/science/article/pii/S0023643825006139?via%3Dihub

Journal Name: Journal of Industrial and Engineering Chemistry **IF: 5.9**

Title: A multi-approach study on CO2 absorption in packed beds: Theoretical, experimental, and CFD perspectives on gas phase pulsation

Author: Pattnaik C.; Kumar R.; Khan M.A.; Pahari P.; Banik A.; Jeon B.-H.; Banerjee S.; Chakrabortty S.; Tripathy S.K.

Details: Volume 146, Pages 641 – 655, 25 June 2025

Abstract: This work seeks to improve CO_2 absorption efficiency in packed bed columns by substituting amine-based solvents with sodium hydroxide and implementing gas phase pulsation to enhance mass transfer coefficients. Experimental analysis and computational fluid dynamics modeling were employed to investigate the impact of pulsation on absorption efficiency under various conditions. Essential parameters comprised superficial liquid velocity (1.2–4.6 cm/s), pulsation frequency (0–10 Hz), amplitude (0–20 mm), and NaOH concentration (0.25 N to 2 N), while maintaining a constant superficial gas velocity of 120 cm/s and a solute gas concentration of 13 %. Three packing materials—glass spheres, ceramic Raschig rings, and ceramic Pall rings—were evaluated. The results demonstrated that ceramic Pall rings exhibited the greatest efficiency. Pulsation, namely at 9.06 Hz and 20 mm amplitude, enhanced the volumetric mass transfer coefficient by as much as 4.53 times for Pall rings. Increased column diameters (from 7.00 cm to 11.5 cm) enhanced performance. The findings show advancement of more efficient CO_2 absorption (by switching from chemical absorption using amine based solvents to classical chemical absorption using aqueous NaOH solution) for industrial applications, aiding climate change mitigation initiatives.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URL: https://www.sciencedirect.com/science/article/pii/S1226086X24007858?via%3Dihub

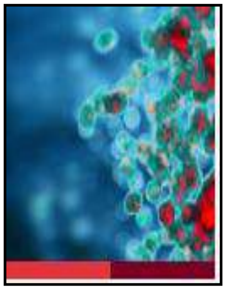
Journal Name: Frontiers in Immunology **IF: 5.7**

Title: Designing a potent multivalent epitope vaccine candidate against Orientia tsutsugamushi via reverse vaccinology technique - bioinformatics and immunoinformatic approach

Author: Panda S.; Swain S.K.; Sahu B.P.; Mahapatra S.R.; Dey J.; Sarangi R.; Ranade A.V.; Mishra N.

Details: Volume 16, 2025, Article number 1513245

Abstract: Scrub typhus is a life-threatening, undifferentiated febrile illness caused by a gram-negative bacterium, Orientia tsutsugamushi. The bacterial strain is a global health concern that should be considered. Despite several years of effort for the development of an effective immunogenic vaccine, no successful licensed vaccine is available. The aim of the study is to construct an epitope response using a reverse vaccinology approach. The TSA56 and ScaA proteins combined can be the most promising subunit vaccine candidates against O. tsutsugamushi. B-cell, CTL, and HTL epitopes were predicted, and subsequently, all the epitopes were linked by KK, AAY, and GPGPG linkers, respectively, along with an adjuvant at the N-terminal region. Furthermore, molecular docking and MD simulations were performed that exhibited a higher affinity towards TLR-2. A total of 16 linear B-cells, 6 CTL, and 2 HTL epitopes were identified and validated. The final vaccine construct showed high antigenicity, stability, and solubility. Molecular docking and MD simulations indicated strong binding interactions with TLR-2 and a stable vaccine-receptor complex. The expression of the vaccine in pET28a (+) vector was successfully implemented via in silico cloning as well as significant results from immune simulation demonstrated the efficacy of the vaccine in the immune cell interaction during the innate and adaptive immune responses immune simulation. In conclusion, the outcome suggested that the newly developed vaccine will be a promising candidate for controlling and providing definitive preventive measures against scrub typhus if further investigation is conducted experimentally.



URL:https://www.frontiersin.org/journals/immunology/articles/10.3389/fimmu.2025.1513245/full

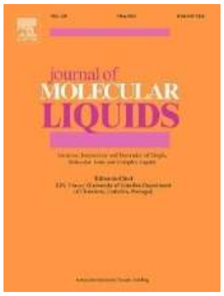
Journal Name: Journal of Molecular Liquids **IF: 5.3**

Title: Unravelling pair-wise interactions in viral proteins: Quasielastic light scattering, in-silico molecular docking and coarse-grained simulation

Author: Mohanty M.; Manoswini M.; Tripathy G.; Siddhabhatti M.; Mohanty P.S.

Details: Volume 426, 15 May 2025, Article number 127237

Abstract: Understanding protein–protein interactions is vital for studying protein association and aggregation, with size and shape adding complexity. While low molecular weight proteins (5–20 kDa) have been widely studied, larger, anisotropic proteins require further exploration at the pair-wise interaction level. This study focuses on pair-wise interactions of the well-characterized Salmonella phage P22 Tailspike protein, analyzed using quasielastic light scattering, molecular docking, and residue-level coarse-grained simulations. Chosen for its role in protein folding and aggregation, Tailspike was studied in dilute solutions, revealing bimodal size distributions with hydrodynamic radii of 7 nm and 50 nm, corresponding to its trimer and higher-order structures. The presence of higher-order structures, even at low concentrations, suggests strong pair-wise interactions, leading to larger aggregates. Molecular docking using ClusPro revealed that hydrophobic interactions dominate these interactions, while coarse-grained simulations using Complexes++ highlighted the significant role of van der Waals forces. The bound conformations observed in simulations also demonstrate how proteins adjust their shapes for optimal interactions. Our study emphasizes the importance of hydrophobic and van der Waals forces, along with structural complementarity, in the pair-wise interactions of P22 Tailspike trimers, offering valuable insights into the mechanisms driving protein folding and aggregation in large, anisotropic proteins.



URL: https://www.sciencedirect.com/science/article/pii/S0167732225004040?via%3Dihub

Journal Name: Materials Advances **IF: 4.7**

Title: Chitosan-acrylic acid biomaterial with an antimicrobial nature supports biomineralization and is suitable for bone tissue regeneration

Author: Agarwal S.; Singh A.; Kumar S.; Rokade T.P.; Goswami C.; Goswami L.

Details: 23 May 2025, Article number d4ma01178c

Abstract: Rapid increases in different pathophysiologies in mineralized tissues have imposed demands on biomaterials of natural origin to act as a surface for the regeneration of fully functional tissue. It has been reported that chitosan-based biomaterials are biocompatible, biodegradable, nontoxic, and also have antibacterial properties. However, due to the insoluble nature of chitosan, for biomaterial synthesis it needs to be dissolved in an acidic medium followed by pH neutralization. The objective of this study was to synthesize a chitosan-based biomaterial without the use of any acidic medium, followed by modification with acrylic acid in different w/v ratios. The synthesized biomaterial, i.e. chitosan-acrylic acid (chitosan-AA) shows uniform dispersion in water. It was further characterized for various physicochemical properties. The obtained results indicate successful modification of the polymer, exhibiting a porous nature with a high swelling index. It shows biocompatibility against different osteogenic cell lines and supports biomineralization by osteoblasts under osteo-inductive conditions. No hemolytic effect was observed in response to the biomaterial even after prolonged exposure to blood cells. We also show that the synthesized material can be used for controlled drug release. This work demonstrates that the biomaterial can be used as a suitable surface for the adhesion and proliferation of bone cells in vitro.

URL: https://pubs.rsc.org/en/content/articlelanding/2025/ma/d4ma01178c

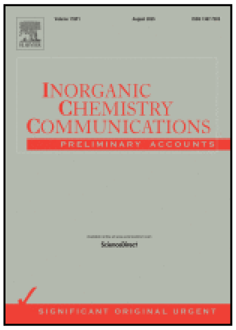
Journal Name: Inorganic Chemistry Communications **IF: 4.4**

Title: Bio-synthesized cerium oxide nano-particles for efficient adsorption of fluoride ion from aqueous solution

Author: Hansdah S.; Das J.; Mandal D.; Parhi P.K.

Details: Volume 178, Part 2, August 2025, 114583

Abstract: Cerium oxide (CeO_2) nanoparticles (NPs) were successfully synthesized via a facile biosynthesis route, utilizing a cost-effective and environmentally friendly bio-extract derived from fenugreek seeds, for the effective removal of fluoride ions from contaminated water. The synthesized CeO_2 NPs were characterized using UV, FTIR, XRD and SEM to determine the phase, purity, and size, revealing an average size of approximately 17.4 nm. The fluoride sorption behavior and mechanism on to the ceria NPs phase was confirmed through kinetics, isotherm, and thermodynamics investigations. The sorption affinity of fluoride ion with ceria NPs appears to be effective at solution pH 2.0. The fluoride sorption rate onto the nano-ceria phase was observed to follow a pseudo-second order kinetic model along with intra-particle diffusion. Among the three sorption adopted isotherm models; Langmuir, Freundlich and Temkin, the fluoride adsorption behavior revealed to follow Langmuir Isotherm with high regression coefficient value (R^2 = 0.993). The maximum fluoride adsorption loading capacity of CeO_2 NPs was determined to be 123.6 mg/g at the temp. 293 K. The fluoride ion adsorption with CeO_2 NPs is observed to be spontaneous and endothermic in nature which was strongly supported by the thermodynamics results; ΔH= 13.789 KJ/mol, and ΔS= +62.799. The phase transformation due to the sorption of fluoride onto the homogeneous ceria phase was ascertained isotherm results and EDX analysis resulted of fluoride ion loaded Ceria NPs.



URL: https://www.sciencedirect.com/science/article/pii/S1387700325006999?via%3Dihub

SCHOLARLY PUBLICATIONS
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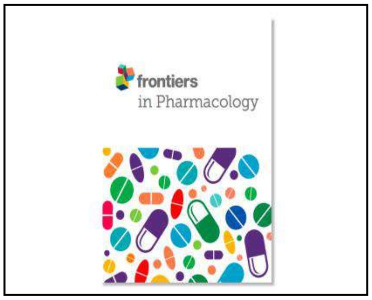
Journal Name: Frontiers in Pharmacology **IF: 4.4**

Title: Editorial: Emerging and reemerging neglected tropical diseases: epidemiology, transmission, mitigation, and vaccines and chemotherapy advancements

Author: Mohapatra R.K.; Mishra S.; Kandi V.; Sirka C.S.; Tuglo L.S.

Details: Volume 16, 2025, Article number 1545801

Abstract: Neglected tropical diseases (NTDs) are infectious diseases caused by bacteria, viruses, fungi and parasites, including ectoparasites like mites and fleas (Mohapatra et al., 2024; Kutikuppala et al., 2023; WHO, 2024). NTDs are an ongoing challenge to global public healthcare and community health. The main reason why such diseases remain collectively neglected is that they are considered "diseases of the poor", primarily people in low- and middle-income countries (LMICs) with modest purchasing capacity. As a result of this, the commercial diagnostic, therapeutic and prophylactic efforts by the pharmaceutical companies are only skeletal as they do not envision a profitable market. Thus, although treatable, these diseases ultimately manifest as terminal diseases of the have-nots. The World Health Organisation (WHO) has compiled a list of the world's most prevalent NTDs and updates it from time to time. Currently, there are 21 aetiologically, epidemiologically and clinically unique diseases (or groups of diseases) listed as NTDs by the WHO (Malecela and Ducker, 2021). The WHO has devised public health strategies and proposed a roadmap to eliminate NTDs by 2030 (WHO, 2021). However, as the majority of the NTD-affected subjects live in financially constrained third-world countries, this seems to be an uphill task and achieving it is by no means easy. Lack of NTD-related awareness and limited diagnostic resources in these regions severely affect their foolproof identification. This is evidenced by the constantly increasing number of diseases that fit into the WHO criteria for NTDs. Various NTDs re-emerged in the wake of the coronavirus disease 2019 (COVID-19) pandemic by the severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), which hit the healthcare infrastructure hard worldwide and exposed its underbelly.



URL:https://www.frontiersin.org/journals/pharmacology/articles/10.3389/fphar.2025.1545801/full

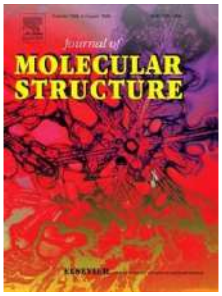
Journal Name: Journal of Molecular Structure **IF: 4.0**

Title: Antimicrobial activities of novel substituted spiropyrrolidine based heterocycles synthesized by multicomponent reaction against Bacillus subtilis and Pseudomonas aeruginosa

Author: Suresh Babu A.R.; Rani S.; Singh S.P.; Khera A.; Alajangi H.K.; Parandaman S.; Raj A.R.N.; Gavaskar D.; Gartia J.; Pandey A.; Yadav V.K.; Singh G.; Barnwal R.P.

Details: Volume 1339, 5 September 2025, Article number 142373

Abstract: The growing resistance of bacteria to antimicrobial agents has intensified the need for novel strategies to combat bacterial infections, particularly those associated with biofilm formation. Biofilms enhance bacterial resilience against hostile environments, immune responses, and antimicrobial treatments. The ability of biofilms to influence bacterial pathogenesis underscores the critical need for new antibacterial agents with anti-biofilm activity. This research aims to synthesize cost-effective, structurally diverse, chemical compounds with the biological significance of disrupting biofilm formation. Here, we report a facile sequential reaction for one-pot, four-component synthesis of spiropyrrolidine heterocycles with 1,3-dipolar cycloaddition of azomethine ylide. The multicomponent reaction (MCR) provides high yield and regioselectivity of the desired product, under mild reaction conditions. Preliminary screening for these novel compounds involves biofilm assays, which assess the developmental processes of biofilms, providing insights into the compounds' biological potential. Subsequent in vitro experiments assessed their antibacterial potential against B. subtilis and P. aeruginosa using the minimum inhibitory concentration (MIC) assay. A cell culture assay evaluated toxicity of these compounds in MDA-MB-231 cell lines. All these investigations cumulatively highlight the potential of these molecules as antibacterial agents for B. subtilis and P. aeruginosa.



URL: https://www.sciencedirect.com/science/article/pii/S0022286025010531?via%3Dihub

Journal Name: Scientific Reports **IF: 3.9**

Title: Novel endophytic actinomycetes species Streptomyces panacea of Panax sokpayensis produce antimicrobial compounds against multidrug resistant Staphylococcus aureus

Author: Rai S.; Singh L.S.; Liriina K.; Jeyaram K.; Parija T.; Sahoo D.

Details: Volume 15, Issue 1, December 2025, Article number 19863

Abstract: Endophytic actinomycetes of medicinal plants have recently been in focus for developing novel antimicrobial compounds to combat multidrug-resistant pathogens. In this study, we isolated and characterised endophytic actinomycetes of Panax sokpayensis rhizome traditionally used as medicine in Sikkim-Himalayan region and assessed their antimicrobial activity against multidrug-resistant (MDR) clinical isolates of Staphylococcus aureus. Saccharopolyspora dominated as the endophytic actinomycetes of P. sokpayensis rhizome. However, a novel actinomycete strain PSRA5^T belongs to the genus Streptomyces, with the highest genome sequence similarity of 91.54% with its closest relative Streptomyces niveus NCIMB 11891 has shown an effective inhibition of six clinical isolates of MDR S. aureus during disc diffusion assay. Further comparative analysis of cellular fatty acids composition and phenotypic and biochemical characteristics of strain PSRA5^T with its phylogenetically closely related strain of S. niveus, classified as representing a novel species of the genus Streptomyces, for which the name Streptomyces panacea sp. nov. is proposed here with type strain PSRA5^T (= MCC5238^T). The minimum inhibition concentration of ethyl acetate crude extract of PSRA5^T culture supernatant against MDR S. aureus isolates was 5.5 to 13.5 µg/mL. Further correlation between biosynthetic gene clusters identified by genome search with LC-MS analysis-based chemical profiling of PSRA5^T culture extract and antibacterial activity of the representative compounds detected several compounds of aminoglycosides and polyketides with antimicrobial activity against MDR S. aureus isolates.

URL: https://www.nature.com/articles/s41598-025-05333-1