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Decoding biofilm tolerance in clinical infections: Matrixome architecture, metabolic zonation, and therapeutic implications

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A R T I C L E   I N F O

Keywords:
Biofilm tolerance
Persister cells
Heteroresistance
Matrixome architecture
Metabolic zonation
Phenotypic heterogeneity

A B S T R A C T

Biofilm-associated infections continue to pose a major challenge in clinical and public health due to their high tolerance to antimicrobial agents and host immune defences. Accounting for up to 80% of chronic human infections, unlike genetic resistance, biofilm tolerance is a reversible, phenotypic condition caused by the organised matrixome. Biofilm tolerance arises from structural protection conferred by the extracellular matrix and metabolic heterogeneity within the community. This review covers the structural and physiological factors of tolerance, emphasising metabolic zonation, stress-induced dormancy (persister cells), and transport-based protection through increased efflux systems. We explore emerging ideas such as tolerance memory, host-driven selective pressures, and the pharmacokinetic (PK) mismatch caused by spatial drug gradients within the biofilm structure. Despite advances in understanding mechanisms, a significant gap remains in translation due to the reliance on planktonic-based diagnostics and standard susceptibility measures (e.g., MIC) that do not reflect biofilm recalcitrance. We suggest shifting toward "biofilm-aware" clinical approaches that incorporate spatial transcriptomics, AI-driven predictive models, and matrix-disrupting adjunct therapies, including nanotechnology, phage therapy, and AI–guided interventions. To promote global equity in managing these infections, interdisciplinary collaboration and accessible diagnostics are essential. Eradicating pathogens through a tolerance-informed control strategy is crucial for sustainably managing chronic and recurrent infections.

1. Introduction

Biofilm-associated infections continue to pose clinical and public health challenges, despite advances in antimicrobial therapy. Biofilms are structured microbial communities that enable organisms to adhere to surfaces, exhibit environmental resilience, and antimicrobial tolerance, thereby contributing to chronic infections, particularly in medical devices and healthcare-related environments (Jandl et al., 2024; Yang et al., 2023). Pathogens such as *Staphylococcus aureus*, *Pseudomonas aeruginosa*, and *Escherichia coli* exhibit increased survival due to their ability to form resilient biofilms, complicating diagnosis and treatment (Ali et al., 2023; Thöming and Häussler, 2022).

A key feature of biofilm-associated microorganisms is their increased tolerance to antimicrobial agents, which is not just from genetic resistance but also from structural and metabolic adaptations (Luo et al., 2021). The extracellular polymeric substance (EPS) matrix acts as a barrier, limiting antimicrobial penetration and reducing treatment effectiveness. Within this biofilm environment, cells exist in diverse metabolic states, showcasing the adaptability of microbial communities and the challenges in addressing biofilm-related infections. Additionally, subpopulations of persister cells can survive antibiotic treatment, causing recurrent infections. Biofilms also impede host immune responses, contributing to antimicrobial resistance by increasing mutation rates and facilitating gene transfer (Ciofu et al., 2022; Singh et al., 2025).

Consequently, as traditional treatment strategies are ineffective against established biofilms, there is an urgent need for an understanding of biofilm tolerance mechanisms and new anti-biofilm

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Dose Dresponse evaluation of intravenous carbetocin for prevention of postpartum haemorrhage during elective caesarean delivery: A parallel-group randomised controlled trial

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Dose–response evaluation of intravenous carbetocin for prevention of postpartum haemorrhage during elective caesarean delivery: A parallel-group randomised controlled trial

Riya Abraham, Rajesh Prabu Chandrasekaran, Pradeesh Johny, Akshaya Manimaran, C L Sabu Kumar, Ezhilrajan Vaithiyalingam

Authors and Affiliations

Indian Journal of Anaesthesia 70(6):p 749-756, June 2026. | DOI: 10.4103/ija.ija_391_26

OPEN

Abstract

Background and Aims:

Postpartum haemorrhage (PPH) is a major cause of maternal morbidity and mortality. Although 100 µg intravenous carbetocin is commonly administered for uterotonic prophylaxis at caesarean delivery, the optimal dose remains uncertain. The primary objective was to evaluate the dose–response relationship of intravenous carbetocin in achieving adequate uterine tone during elective caesarean delivery.

Methods:

In this randomised, parallel-group, dose–response trial, 100 parturients scheduled for elective caesarean delivery were assigned into five groups to receive intravenous carbetocin at doses of 100 µg, 80 µg, 60 µg, 40 µg, or 20 µg (n = 20 per group) immediately after foetal delivery. The primary outcome was satisfactory uterine tone at 2, 5, and 10 minutes. Secondary outcomes included blood loss, requirement for additional uterotonics, PPH incidence, blood transfusion, haemodynamic variables, and adverse events. Trend analysis assessed dose–response relationships.

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Expression and Methylation of Insulin-Like Growth Factor Binding Protein-1 Gene in Cord Blood of Intrauterine Growth Restricted Neonates


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Expression and Methylation of Insulin-Like Growth Factor Binding Protein-1 Gene in Cord Blood of Intrauterine Growth Restricted Neonates

Original Article | Published: 20 February 2026
Volume 93, pages 59–64 (2026) Cite this article

Indian Journal of Pediatrics

Aims and scope →
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Abstract

Objectives

To compare the insulin-like growth factor binding protein-1 (IGFBP-1) gene methylation and expression in the cord blood among intrauterine growth restricted (IUGR) and appropriate for gestational age (AGA) neonates and find their association with anthropometry at birth.

Methods

Cord blood samples from IUGR and AGA neonates were collected. Anthropometric measurements i.e., weight, length and head circumference of the infants were measured. RT-PCR was performed to examine IGFBP-1 gene expression and DNA methylation analysis by bisulfite sequencing PCR. The results were analysed by using Mann–Whitney U test and Pearson correlation

Results

IUGR neonates had significantly lower anthropometry (weight, length and head circumference) measurements at birth compared to AGA neonates. Gene expression analysis showed significantly higher IGFBP-1 gene expressions among IUGR compared to AGA neonates and gene expression level correlated with anthropometric measurements. There was no difference in IGFBP-1 gene methylation rate between the two groups of neonates and no correlation was observed with anthropometry

Conclusions

IGFBP-1 gene expression in cord blood was significantly higher among IUGR neonates and was associated with reduced birth weight, birth length and head circumference while the gene methylation was similar. This suggests involvement of multiple factors in occurrence of fetal growth restriction.

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Gut Microbiome in Neonatal Necrotizing Enterocolitis - A Comprehensive Review of Evidence

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Gut Microbiome in Neonatal Necrotizing Enterocolitis – A Comprehensive Review of Evidence

Review Article | Published: 13 July 2026

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Abstract

Necrotizing enterocolitis (NEC) is one of the most catastrophic gastrointestinal emergency occurring predominantly in preterm neonates. It contributes to substantial neonatal mortality and morbidity. Disturbances in the intestinal microbiome are crucial to disease pathogenesis. In preterm infants, an immature intestinal barrier, dysregulated immune responses, and environmental exposures altogether predispose to alterations in microbial colonization and intestinal inflammation. This review was done to present the current *evidence on gut microbiome* alterations associated with NEC in preterm infants. A systematic search of the MEDLINE and EMBASE databases was performed using search strategy related to prematurity, intestinal microbiota, and necrotizing enterocolitis. A total of 42 studies assessing microbial composition, microbial progression, or microbial functional patterns in relation to NEC were included. Across the included studies, NEC was consistently preceded by reduced microbial diversity, delayed maturation of anaerobic communities, and expansion of Proteobacteria, particularly Enterobacteriaceae family such as *Klebsiella* and *Escherichia*. Longitudinal studies further showed that these microbial changes may become evident days to weeks before clinical disease, suggesting a potential window for early risk identification. Functional analyses also showed alterations in microbial metabolic pathways, including short-chain fatty acids, tricarboxylic acid intermediates, volatile compounds, and viral signatures that may lead to epithelial injury and inflammatory signaling. Clinical and environmental factors including antibiotic exposure, mode of delivery, feeding practices, and NICU microbial ecosystem are important determinants of neonatal gut microbiome development. Thus, the current evidence supports a reproducible pattern of intestinal dysbiosis preceding NEC. Better understanding of microbiome dynamics may aid early risk stratification and support microbiome-targeted preventive strategies in vulnerable preterm populations.

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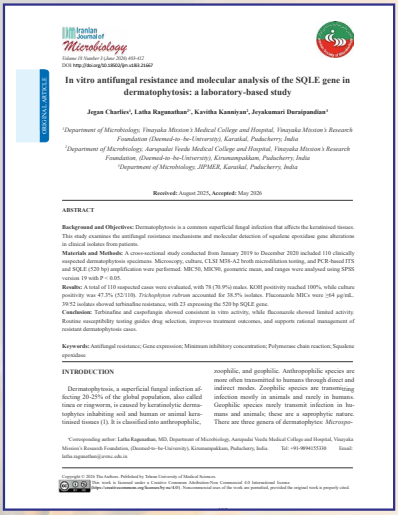
In vitro antifungal resistance and molecular analysis of the SQLE gene in dermatophytosis: a laboratory-based study



Iranian Journal of Microbiology

Volume 18 Number 3 June 2026: 400-412

DOI: http://doi.org/10.18502/ijm.v18i3.21667

ORIGINAL ARTICLE

In vitro antifungal resistance and molecular analysis of the SQLE gene in dermatophytosis: a laboratory-based study

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ABSTRACT

Background and Objectives: Dermatophytosis is a common superficial fungal infection that affects the keratinised tissues. This study examines the antifungal resistance mechanisms and molecular detection of squalene epoxidase gene alterations in clinical isolates from patients.

Materials and Methods: A cross-sectional study conducted from January 2019 to December 2020 included 110 clinically suspected dermatophytosis specimens. Microscopy, culture, CLSI M38-A2 broth microdilution testing, and PCR-based ITS and SQLE (520 bp) amplification were performed. MIC50, MIC90, geometric mean, and ranges were analysed using SPSS version 19 with $P < 0.05$.

Results: A total of 110 suspected cases were evaluated, with 78 (70.9%) males. KOH positivity reached 100%, while culture positivity was 47.3% (52/110). *Trichophyton rubrum* accounted for 38.5% isolates. Fluconazole MICs were ≥64 µg/mL. 39/52 isolates showed terbinafine resistance, with 23 expressing the 520 bp SQLE gene.

Conclusion: Terbinafine and ciclopiroxlge showed consistent in vitro activity, while fluconazole showed limited activity. Routine susceptibility testing guides drug selection, improves treatment outcomes, and supports rational management of resistant dermatophytosis cases.

Keywords: Antifungal resistance; Gene expression; Minimum inhibitory concentration; Polymerase chain reaction; Squalene epoxidase

INTRODUCTION

Dermatophytosis, a superficial fungal infection affecting 20-25% of the global population, also called tinea or ringworm, is caused by keratinolytic dermatophytes inhabiting soil and human or animal keratinised tissues (1). It is classified into anthropophilic, zoophilic, and geophilic. Anthropophilic species are more often transmitted to humans through direct and indirect modes. Zoophilic species are transmitting infection mostly in animals and rarely in humans. Geophilic species rarely transmit infection in humans and animals; these are a saprophytic nature. There are three genera of dermatophytes: *Microspo-*

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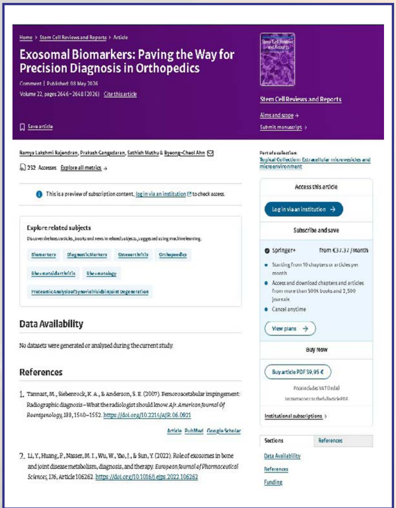
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No datasets were generated or analysed during the current study.

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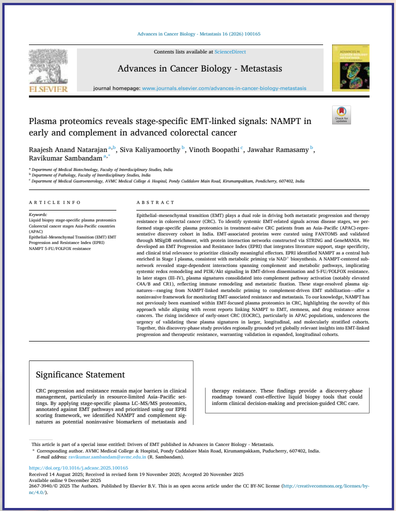
Plasma proteomics reveals stage-specific EMT-linked signals: NAMPT in early and complement in advanced colorectal cancer



Advances in Cancer Biology - Metastasis 16 (2026) 100165

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Plasma proteomics reveals stage-specific EMT-linked signals: NAMPT in early and complement in advanced colorectal cancer

Raajesh Anand Natarajan [a,b], Siva Kaliyamoorthy [b], Vinoth Boopathi [c], Jawahar Ramasamy [b], Ravikumar Sambandam [a,*]

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ARTICLE INFO

Keywords:
Liquid biopsy stage-specific plasma proteomics
Colorectal cancer stages Asia-Pacific countries (APAC)
Epithelial–Mesenchymal Transition (EMT) EMT Progression and Resistance Index (EPRI)
NAMPT 5-FU/FOLFOX resistance

ABSTRACT

Epithelial–mesenchymal transition (EMT) plays a dual role in driving both metastatic progression and therapy resistance in colorectal cancer (CRC). To identify systemic EMT-related signals across disease stages, we performed stage-specific plasma proteomics in treatment-naïve CRC patients from an Asia–Pacific (APAC)-representative discovery cohort in India. EMT-associated proteins were curated using FANTOM5 and validated through MSigDB enrichment, with protein interaction networks constructed via STRING and GeneMANIA. We developed an EMT Progression and Resistance Index (EPRI) that integrates literature support, stage specificity, and clinical trial relevance to prioritize clinically meaningful effectors. EPRI identified NAMPT as a central hub enriched in Stage I plasma, consistent with metabolic priming via NAD^+ biosynthesis. A NAMPT-centered subnetwork revealed stage-dependent interactions spanning complement and metabolic pathways, implicating systemic redox remodeling and PI3K/Akt signaling in EMT-driven dissemination and 5-FU/FOLFOX resistance. In later stages (III–IV), plasma signatures consolidated into complement pathway activation (notably elevated C4A/B and CR1), reflecting immune remodeling and metastatic fixation. These stage-resolved plasma signatures—ranging from NAMPT-linked metabolic priming to complement-driven EMT stabilization—offer a noninvasive framework for monitoring EMT-associated resistance and metastasis. To our knowledge, NAMPT has not previously been examined within EMT-focused plasma proteomics in CRC, highlighting the novelty of this approach while aligning with recent reports linking NAMPT to EMT, stemness, and drug resistance across cancers. The rising incidence of early-onset CRC (EOCRC), particularly in APAC populations, underscores the urgency of validating these plasma signatures in larger, longitudinal, and molecularly stratified cohorts. Together, this discovery-phase study provides regionally grounded yet globally relevant insights into EMT-linked progression and therapeutic resistance, warranting validation in expanded, longitudinal cohorts.

Significance Statement

CRC progression and resistance remain major barriers in clinical management, particularly in resource-limited Asia–Pacific settings. By applying stage-specific plasma LC–MS/MS proteomics, annotated against EMT pathways and prioritized using our EPRI scoring framework, we identified NAMPT and complement signatures as potential noninvasive biomarkers of metastasis and therapy resistance. These findings provide a discovery-phase roadmap toward cost-effective liquid biopsy tools that could inform clinical decision-making and precision-guided CRC care.

This article is part of a special issue entitled: Drivers of EMT published in Advances in Cancer Biology - Metastasis.

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Abstract

Single nucleotide polymorphisms (SNPs) of the CD40 gene are expressed in normal B lymphocytes and endothelial cells and have been associated with susceptibility to rheumatoid arthritis (RA). Anti-cyclic citrullinated peptide (anti-CCP) antibodies are useful biomarkers for the early detection of RA, particularly in resource-limited settings. This study aimed to evaluate the association between anti-CCP antibodies and CD40 gene polymorphisms in patients with and without RA. This cross-sectional study included 160 patients presenting with symmetrical joint pain and swelling, particularly in the small joints. Serum samples were tested for rheumatoid factor (RF), high-sensitivity C-reactive protein (hsCRP) and anti-CCP antibodies according to the manufacturer's instructions. Genomic DNA was extracted from EDTA blood samples for analysis of the CD40 gene.

Among 160 patients, males were predominant. Anti-CCP antibodies were detected 26 (32.5%) in RF-positive and 19 (23.75%) negative patients. CD40 gene positivity was observed in 47.5% of RF-positive patients and 25% of RF-negative patients. A statistically significant association was observed between anti-CCP antibodies and the CD40 gene ($p < 0.05$). Anti-CCP antibodies and CD40 gene polymorphisms may play an important role in the early prediction of RA.

Keywords: Rheumatoid Arthritis, Cyclic citrullinated peptide, Rheumatoid Factor, IgG ELISA, Autoantibody.

Introduction

Early intervention of Rheumatoid arthritis (RA) is often crucial as well as challenging due its chronic and non–organ-specific autoimmune diseases. In which it primarily affects multiple, small joints and it impacts with other conditions such as obesity, morning stiffness etc.[1,2] It reduces the life span by average of 5-10 years by both hereditary as well as environmental factors that significantly decrease the mobility of the joints[3,4]. Early prediction of this disease helps to prevent joint destruction, disease dissemination and their complications[1]. The modern medicine has solved by detection of RA in early stages through various sensitive and specific diagnostic tests like Rheumatoid factor, anti-CCP antibodies etc.[3]

In general, female is the most predominant than male for this disease. Autoantibodies against the citrullinated peptides are highly specific for the diagnosis of RA and are also slightly higher sensitive than RF IgM antibody. Other subclasses of anti-CCP are measured in patient serum by using Enzyme linked immunosorbent assay (ELISA)[1]. It also suggested being a promising biomarker for the serodiagnosis of RA[1-6].

A single nucleotide polymorphism or SNP is an alteration at a single position in DNA sequence among individuals. These SNPs act as a marker for detection of genetic disorders. Numerous polymorphisms in non-HLA genes increased the susceptibility for the development of the RA. Clustered Differentiation 40 gene is a type 1 transmembrane protein, a member of TNF receptor class with 277 amino acids producing autoantigens which encode proteins involved in the immune cell activation, differentiation, proliferation and apoptosis of the immune system mechanisms[7]. More than 100 genomic loci have been found from various genetic association studies on different populations and these loci accounted for about 15% of the variance[6,8].

Recently, CD40 tends to stimulate monocytic phagocytes to produce angiogenic factors such as fibroblast growth factor (FGF) and vascular endothelial growth factor (VEGF)[6]. The primary objective of this study is to correlate Anti-CCP autoantibody levels with CD40 gene in patients with or without Rheumatoid arthritis in Coimbatore population.

Material and Methods

This case control study was carried out after getting approval from our Institutional Human Ethics Committee (EC/2020/0411/CR/85), for the period of one year from April 2023 to April 2024. Patients attended with complaints of joint pain especially small joints, symmetric pain, swelling in the joints in various private clinics as well as laboratories from Coimbatore district. After obtained consent from 160

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Recent advances in chitosan-derived carbon aerogels for supercapacitor applications: A review

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Highlights

- Chitosan-derived aerogels are promising electrodes for supercapacitors.
- High surface area, porosity, and good wettability helps in efficient charge storage.
- Nitrogen-rich chitosan enables self N-doping, improving electrical conductivity.

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An Uncommon Culprit: Leclercia Adecarboxylata Causing Native Mitral Valve Infective Endocarditis in an Immunocompromised Host

JK SCIENCE pISSN: 0972-1177

CASE REPORT

An Uncommon Culprit: *Leclercia Adecarboxylata* Causing Native Mitral Valve Infective Endocarditis in an Immunocompromised Host

Gerard Rakesh J, Suresh Kumar D, Anushakarunsagar*, Mathai D, Jayaprasanthi S, Rajan S**, Margaret Theresa J***

Abstract

Leclercia adecarboxylata is an uncomon pathogen causing infective endocarditis, with limited number of infections reported in the literature. A literature review showed only three case of infective endocarditis caused by L. adecarboxylata had been reported up to 2022, highlighting the organism's rarity as a cause of endocarditis in clinical practice. We report a unique case of native mitral valve infective endocarditis in a 69-year-old woman with long-standing diabetes mellitus and hypertrophic non-obstructive cardiomyopathy. Although initial blood cultures yielded methicillin-sensitive Staphylococcus epidermidis, definitive diagnosis was established intraoperatively when purulent material and excised mitral valve tissue grew pan-sensitive *Leclercia adecarboxylata*, fulfilling a major criterion of the 2023 Duke–ISCVID infective endocarditis guidelines. This case illustrates the emerging role of uncommon pathogens in infective endocarditis and reinforces the diagnostic significance of valve tissue cultures and intraoperative evidence in modern clinical practice.

Key Words

Leclercia Adecarboxylata, Infective Endocarditis, Native Mitral Valve, Opportunistic Infection, Immunocompromised Host

Introduction

Leclercia adecarboxylata is a Gram-negative bacterium first described by H. Leclerc in 1962.[1] L. adecarboxylata is considered as an opportunistic pathogen. Human infections are rare, predominantly affecting immunocompromised individuals, with diabetes mellitus, malignancy, or receiving long-term immunosuppressive therapy.[2,3] A 2025 literature review showed 227 cases of L. adecarboxylata infection involving various organ systems have been reported worldwide, with the highest incidence in Asia.[4] However only three case of infective endocarditis caused by L. adecarboxylata had been reported up to2022, highlighting the organism's rarity as a cause of endocarditis in clinical practice. [5]

Here, we report a rare case of native mitral valve infective endocarditis caused by L. adecarboxylata. This case underscores the emerging pathogenic potential of

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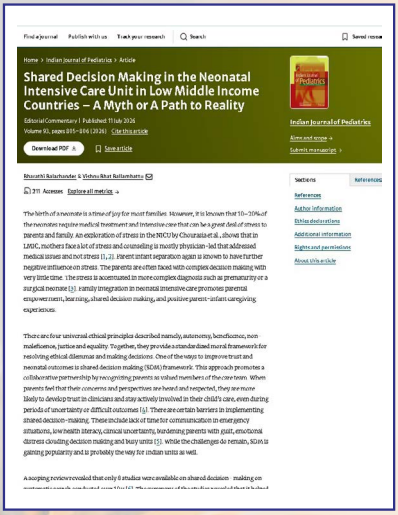
Shared Decision Making in the Neonatal Intensive Care Unit in Low Middle Income Countries - A Myth or A Path to Reality


Shared Decision Making in the Neonatal Intensive Care Unit in Low Middle Income Countries – A Myth or A Path to Reality

Indian Journal of Pediatrics

Bharathi Balachandar · Vishnu Bhat Ballambattu

The birth of a neonate is a time of joy for most families. However, it is known that 10–20% of the neonates require medical treatment and intensive care that can be a great deal of stress to parents and family. An exploration of stress in the NICU by Chouraiala et al., shows that in LMIC, mothers face a lot of stress and counseling is mostly physician-led that addressed medical issues and not stress [1, 2]. Parent infant separation again is known to have further negative influence on stress. The parents are often faced with complex decision making with very little time. The stress is accentuated in more complex diagnosis such as prematurity or a surgical neonate [3]. Family integration in neonatal intensive care promotes parental empowerment, learning, shared decision making, and positive parent–infant caregiving experiences.

There are four universal ethical principles described namely, autonomy, beneficence, non-maleficence, justice and equality. Together, they provide a standardised moral framework for resolving ethical dilemmas and making decisions. One of the ways to improve trust and neonatal outcomes is shared decision making (SDM) framework. This approach promotes a collaborative partnership by recognizing parents as valued members of the care team. When parents feel that their concerns and perspectives are heard and respected, they are more likely to develop trust in clinicians and stay actively involved in their child's care, even during periods of uncertainty or difficult outcomes [4]. There are certain barriers in implementing shared decision-making. These include lack of time for communication in emergency situations, low health literacy, clinical uncertainty, burdening parents with guilt, emotional distress clouding decision making and busy units [5]. While the challenges do remain, SDM is gaining popularity and is probably the way for Indian units as well.

A scoping review revealed that only 8 studies were available on shared decision - making on

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Cannabis and Liver Health: Exploring the Gut-Liver Axis and the Role of the Gut Microbiota

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Role of Whole-Body Magnetic Resonance Imaging in Detecting Metastasis in Patients With Known Cancer

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Role of Whole-Body Magnetic Resonance Imaging in Detecting Metastasis in Patients With Known Cancer

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Abstract

Background: Cancer continues to impose a significant global health burden, with metastatic disease being the leading cause of cancer-related mortality. Accurate detection and staging of metastases are essential for prognostication and treatment planning. Conventional imaging modalities, including contrast-enhanced computed tomography (CECT), have limitations in detecting early or subtle metastatic lesions. Whole-body magnetic resonance imaging (WB-MRI), particularly with diffusion-weighted imaging (DWI), has emerged as a radiation-free technique that enables comprehensive evaluation with high soft-tissue contrast. Therefore, this study aimed to evaluate the diagnostic performance of WB-MRI, including DWI, in detecting nodal, skeletal, and visceral metastases in patients with known malignancies and to compare its performance with CECT on a patient-based analysis.

Methodology: This analytical cross-sectional study was conducted in the Department of Radiodiagnosis at Aarupadai Veedu Medical College and Hospital, Puducherry, over a period of six months. Eighty patients aged 18-60 years with histopathologically confirmed malignancy were included. All participants underwent CECT of the neck, thorax, and abdomen, followed by WB-MRI using a 1.5-T system with diffusion-weighted sequences. Imaging findings were documented and, wherever feasible, correlated with histopathology or cytology. Data were analyzed using descriptive statistics and the chi-square test in Statistical Package for the Social Sciences, version 26.0 (IBM Corp., Armonk, NY; 2019). A p value of <0.05 was considered statistically significant.

Results: The mean age of the participants was 53.39 ± 8.16 years, with a slight female predominance. Carcinoma of the cervix and breast carcinoma were the most common primary malignancies. WB-MRI demonstrated significantly higher sensitivity and specificity than CT in detecting nodal, skeletal, and visceral metastases. It showed excellent performance in detecting skeletal metastases and superior accuracy in identifying nodal and visceral involvement, with statistically significant differences compared to CT.

Conclusion: WB-MRI outperforms CT in the comprehensive detection of metastatic disease across multiple organ systems. Its high diagnostic accuracy, absence of ionizing radiation, and ability to detect early metastatic changes support its role as a reliable imaging modality for staging and follow-up in oncology.

Categories: Radiology, Radiation Oncology
Keywords: cancer staging, computed tomography, diffusion-weighted imaging, metastasis, whole-body mri

Introduction

Cancer remains a major global health burden, contributing substantially to morbidity and mortality worldwide. Despite advances in early detection and targeted therapies, metastatic disease continues to account for nearly 90% of cancer-related deaths [1]. Global estimates indicate a steady rise in both incidence and mortality, with approximately 19.3 million new cases and over 10 million deaths reported in 2020. In India, cancer incidence is projected to increase by nearly 12% over five years, with reported cases rising from approximately 1.16 million in 2018 to 1.39 million in 2020, along with a corresponding increase in mortality [2,3].

Metastasis involves the dissemination of malignant cells from a primary tumor to distant organs, often following characteristic patterns, such as skeletal involvement in breast and prostate cancers and visceral spread to the liver and lungs. Accurate detection and staging of metastatic disease are critical, as the extent and distribution of metastases strongly influence prognosis and therapeutic decision-making [4].

Imaging plays a central role in staging, treatment planning, and follow-up. Conventional approaches utilize multiple modalities, including radiography, ultrasonography, bone scintigraphy, computed tomography (CT), positron emission tomography/computed tomography (PET/CT), and regional magnetic resonance imaging (MRI), each with inherent limitations [5]. Whole-body magnetic resonance imaging (WB-MRI) has

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The Role of Indian Diabetic Risk Score In Predicting Metabolic Dysfunction Associated Steatotic Liver Diease In Non-Diabetic Population

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The Role Of Indian Diabetic Risk Score In Predicting Metabolic Dysfunction Associated Steatotic Liver Diease In Non-Diabetic Population

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Abstract

Background: Metabolic Dysfunction–Associated Steatotic Liver Disease (MASLD) represents a continuum of hepatic involvement ranging from uncomplicated fat accumulation to inflammatory injury, progressive fibrosis, cirrhosis, and ultimately hepatocellular carcinoma. In many non-diabetic individuals, MASLD remains clinically silent and is often driven by metabolic derangements such as abdominal adiposity, insulin resistance, and lipid abnormalities. Identifying individuals at risk at an early stage is essential to halt disease progression and reduce long-term hepatic and cardiovascular morbidity. The Indian Diabetes Risk Score (IDRS), a simple and validated screening instrument for diabetes, may also reflect underlying metabolic risk and thereby serve as a potential indicator for MASLD.

Aim: To assess the utility of the Indian Diabetes Risk Score as a predictor of MASLD in adults without diabetes.

Materials and Methods: A hospital-based cross-sectional study was carried out over an 18-month period at Aarupadai Veedu Medical College and Hospital, enrolling 93 non-diabetic adults aged 18–65 years. All participants were evaluated using the IDRS, along with detailed anthropometric measurements and biochemical investigations including fasting blood sugar, HbA1c, lipid profile, and liver function tests. Abdominal ultrasonography was performed to detect and grade hepatic steatosis. Statistical analysis involved chi-square testing and Pearson's correlation, with statistical significance defined as $p<0.05$.

Results: The mean age of the study cohort was 42.76 ± 14.46 years, with females comprising 62.4% of participants. Higher IDRS categories showed a significant association with ultrasonographic evidence of fatty liver ($\chi^2 = 30.16$, $p = 0.01$), with most high-risk individuals demonstrating grade 1 or grade 2 steatosis. IDRS scores exhibited significant positive correlations with age ($r = 0.587$), fasting blood sugar ($r = 0.440$), HbA1c ($r = 0.573$), body mass index ($r = 0.545$), and waist circumference ($r = 0.451$). In addition, ultrasonographic abnormalities were significantly linked to advancing age and elevated fasting glucose levels.

Conclusion: The Indian Diabetes Risk Score emerges as a practical, non-invasive, and cost-effective tool for identifying non-diabetic individuals at increased risk of MASLD. Its use in routine clinical settings may facilitate early recognition and prompt lifestyle-based interventions, thereby helping to prevent progression to advanced liver disease and related metabolic complications.

Keywords: MASLD, IDRS, Ultrasonography, Non-Diabetic, Obesity, Metabolic Risk

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P177 Adolescent skincare practices in the era of social media: implications for self-perception and body image

ORIGINAL ARTICLE

P177 Adolescent skincare practices in the era of social media: implications for self-perception and body image

Sushmitha Dharani Sankar

British Journal of Dermatology, Volume 195, Issue Supplement_1, June 2026, ljag086.204, https://doi.org/10.1093/bjd/ljag086.204
Published: 26 June 2026

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Volume 195, Issue Supplement_1, June 2026

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Abstract

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Abstract

Adolescence is a formative period for self-identity, during which appearance-related concerns and skincare behaviours are increasingly shaped by social media. Continuous exposure to idealised beauty standards may influence skincare practices, self-perception and body image, with potential implications for psychological wellbeing. The aims of this study were to assess skincare knowledge, attitudes and practices among adolescents; to evaluate social media influence and to examine associations with self-perception and body image. A cross-sectional study was conducted among 413 adolescents (age 13–17 years). Data on routine steps, product choices, side effects and information sources were collected using a structured questionnaire. Body image and internalization of beauty ideals were assessed using the Perceptions of Beauty Standards Scale (PBSS) and the Body Esteem Scale for Adults and Adolescents (BESAA). Multivariable analysis examined predictors of poor body image adjusting for age, sex and socioeconomic status (SES). Knowledge was moderate (shown by 67% of respondents), but only 34% followed evidence-based routines. Cleansing (92%) and moisturizing (58%) were common, while sunscreen use remained low (27%). Social media was the primary source of information for 82%. Side effects were reported by 32%. Higher PBSS scores correlated with increased social media exposure ($P < 0.05$), and elevated PBSS was associated with lower BESAA ($P < 0.05$). Higher Social Media Engagement Scale for Adolescents scores were associated with increased PBSS scores and lower BESAA ($P < 0.05$). After adjustment for confounders, adolescents across groups showed similar body-image patterns, reflecting high exposure to beauty-driven online content. SES differences were modest: adolescents with lower SES reported greater dissatisfaction due to limited access to trending products, while those with higher SES showed more experimentation yet increased comparison-driven dissatisfaction. Female respondents demonstrated lower BESAA than male, although social media remained the dominant influence among groups. Social media significantly shapes adolescent skincare behaviours and body image. Strengthening media and advertising regulations, alongside targeted education and media-literacy initiatives, is essential to promote safe skincare practices and healthy self-perception.

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Quercetin and Carvacrol Act Synergistically to Inhibit *Candida albicans* Biofilms In Vitro via Membrane Disruption and Oxidative Stress

Suganya Kannan[1], Jeyakumar Balakrishnan[1], Ananta Priya[2], Satyavani Kaliamurthi[3], Gurudeeban Selvaraj[3], Prithiviraj Nagarajan[2]

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Highlights

- Quercetin–carvacrol combination exhibited potent synergistic activity against *C. albicans* (FICI = 0.13).
- Combination treatment disrupted membrane integrity and enhanced intracellular leakage.
- ROS-mediated apoptosis-like death was associated with metacaspase activation and chromatin condensation.
- Key biofilm and virulence genes (*ALS1*, *HWP1*, *ECE1*, *LIP3*, *CAP1*, and *SOD1*) were significantly downregulated.
- Molecular docking supported multitarget interactions with virulence-associated proteins.

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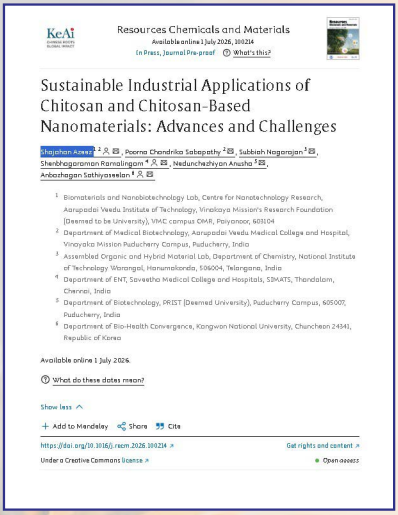

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Original Article

A Novel Ruthenium(II) Complex and its Synergistic Anti-Leukemia Activity with GidA Protein via Dual-Pathway Apoptosis

Antony K. T. Infanta S[1], Thandeeswaran Murugesan[2], Anand Raj Dhanapal[3], Palaniswamy Muthuswamy[4], Angayarkanni Jayaraman[1]

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ABSTRACT

This study demonstrates the effective anticancer activity of a semi-synthetic complex integrating the GidA protein and the ruthenium(II) complex against K562 human leukemia cells. Monotherapy evaluation revealed exceptional cytotoxicity, with half-maximal inhibitory concentration values of 0.058 µg/mL for GidA (a novel topoisomerase II inhibitor) and 14.1 µg/mL for Ru(II). Subsequently, isobologram analysis of six combination ratios identified profound synergy in formulations with elevated Ru(II) concentrations (combinations 4 and 5; sum of the fractional inhibitory concentration = 0.17–0.86). All these synergistic complexes induced up to 73.91 % apoptosis, exceeding single-agent efficacy ($p < 0.01$), while minimizing necrosis (< 20 %). Besides, mechanistic studies revealed dual pathways: Ru(II) triggered reactive oxygen species-dependent apoptosis (2.8-fold reactive oxygen species surge at 30 min; $p < 0.01$), while GidA operated via reactive oxygen species-independent mechanisms. This semi-synthetic complex may involve Ru(II), potentially mediated by transferrin receptor overexpression for targeted uptake. Also, combination 5 (4 × Ru(II):1 × GidA) emerged as the lead candidate, reducing effective doses and potentially mitigating resistance. Overall, these findings establish GidA–Ru(II) complexes as first-in-class dual-mechanism agents with high translational potential for refractory leukemia, offering a strategic solution to chemotherapy limitations through rational synergy.

Keywords anticancer drugs, biopharmaceuticals, cancer pharmacology, drug research

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Abbreviations

TopoII	Topoisomerase
Ru	Ruthenium
ROS	Reactive Oxygen Species
TfR1	Transferrin Receptor
IC_{50}	Half-Maximal Inhibitory Concentration
FIC	Fractional Inhibitory Concentration
DMSO	Dimethyl Sulfoxide
SYN	Synergistic
ADD	Additive

Introduction

Over the last five decades, cytotoxic chemotherapy and radiation therapy have formed the cornerstone of cancer treatment. While yielding profound benefits for hematological malignancies and certain solid tumors (e.g., germ cell and childhood cancers), these approaches have shown limited efficacy against the most prevalent malignancies.[1,2] Dose escalation strategies have offered only marginal improvements, failing to constitute an effective therapeutic breakthrough.

The effectiveness of conventional cytotoxic treatments is inherently constrained by their deleterious side effects on normal tissues. Although supportive measures (e.g., bone marrow rescue, antibiotics, and growth factors) have mitigated some toxicities, limitations to cancer therapy persist.[3,4] Simultaneously, advances in understanding cellular growth regulation, stress responses, and the mechanisms of cytotoxic agents provide a conceptual framework for developing more targeted chemotherapies at the molecular level.[5]

A pivotal shift occurred with the discovery that many chemotherapeutic agents induce cancer cell death via apoptosis. Landmark studies demonstrated that etoposide, a topoisomerase II (Topo II) inhibitor, triggers internucleosomal DNA fragmentation characteristics of apoptosis.[6,7] This finding expanded to include diverse agents like cisplatin, cyclophosphamide, cytosine arabinoside, and 4'-(9-acridinylamino)methanesulfon-m-anisidide, which induce apoptotic cell death in various solid tumors and leukemia, both in experimental models and patients.[8] Apoptosis is recognized as a critical mechanism underlying successful chemotherapy.[9]

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