



UP-UK MICROCON 2026

21st Annual Conference of UP-UK Chapter of IAMM

Theme: Advances in Clinical Microbiology: Shaping Patient Care

Date : 6th & 7th February 2026



21ST ANNUAL CONFERENCE OF UP-UK CHAPTER OF
INDIAN ASSOCIATION OF MEDICAL MICROBIOLOGISTS

UP-UK MICROCON 2026



6th & 7th February 2026

Venue : Shruti Auditorium, SGPGIMS

Organised by :

Department of Microbiology

Sanjay Gandhi Postgraduate Institute of Medical Sciences, Lucknow

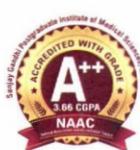


Prof. Radha Krishan Dhiman

MD, DM, FAMS, FACG, FRCP Edin., FRCP London,
FSGEI, FISG, FINASL, FAASLD, Master-ISG

Recipient of Padma Shri &
Dr. B. C. Roy National Award

Director, SGPGIMS
President, AIIMS, Patna



SANJAY GANDHI POSTGRADUATE INSTITUTE OF MEDICAL SCIENCES

RAEBARELI ROAD, LUCKNOW-226 014 (U. P.) INDIA



Message

It gives me immense pleasure to learn that the **Department of Microbiology, SGPGIMS, Lucknow** is organising the **21st Annual Conference of the UP-UK State Chapter of the Indian Association of Medical Microbiologists (UP-UK MICROCON 2026)** on **6th and 7th February 2026** at the **Shruti Auditorium and Library Complex, SGPGIMS, Lucknow**.

The theme of the conference, “**Advances in Clinical Microbiology: Shaping Patient Care,**” is both timely and forward-looking. In the face of emerging and re-emerging infections, increasing antimicrobial resistance, and rapidly evolving diagnostic technologies, clinical microbiology has assumed a central role in strengthening patient care, infection prevention, and public health preparedness. Conferences such as this are essential to align scientific progress with clinical and healthcare system needs.

SGPGIMS is forerunner in teaching, training and capacity building regarding medical care over state and India. In this regard, I find it appropriate for the inclusion of an extensive series of **Pre-Conference Workshops** reflects a comprehensive and pragmatic approach to capacity building. These workshops underscore the importance of precision diagnostics, biosafety, automation, and quality systems in delivering timely and reliable laboratory support for patient management.

I am confident that **UP-UK MICROCON 2026** will provide a vibrant platform for meaningful scientific deliberations, exchange of ideas, and collaborative networking among microbiologists, clinicians, researchers, and healthcare professionals from across the region and beyond. Such academic engagements are instrumental in fostering innovation, promoting translational research, and strengthening the laboratory-clinical interface for improved healthcare outcomes.

I commend the Organising Committee for their dedication and academic vision, and I extend a cordial invitation to all delegates who have come from all over Uttar Pradesh & Uttarakhand as well from other parts of India to participate actively in this conference. I also warmly welcome the participants to **Lucknow**, a city renowned for its rich cultural heritage, academic excellence and gracious hospitality.

I wish **UP-UK MICROCON 2026** every success and hope it serves as a catalyst for advancing clinical microbiology and patient care.

With best wishes,

Prof. Radha Krishna Dhiman

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Sanjay Gandhi Postgraduate Institute of Medical Sciences
Raebareli Road, Lucknow-226014, U. P. (India)



Prof. Shaleen Kumar, MD
Dean

Dean's Message

SGPGIMS is known for highest quality of patient care, teaching and research. In this regard, it is heartening to note that the **Department of Microbiology, SGPGIMS, Lucknow** is organising the **21st Annual Conference of the UP-UK State Chapter of the Indian Association of Medical Microbiologists (UP-UK MICROCON 2026)** on **6th and 7th February 2026** at the **Shruti Auditorium and Library Complex, SGPGIMS, Lucknow**. It is indeed a great honour and pleasure to invite the Microbiology fraternity to this prestigious academic gathering aimed at scholarly exchange and professional enrichment.

The chosen theme, **“Advances in Clinical Microbiology: Shaping Patient Care,”** resonates strongly with the evolving role of Microbiology as an indispensable pillar of modern medicine. Contemporary Clinical Microbiology extends far beyond diagnostic reporting to actively influence clinical decision-making, infection prevention and control strategies, antimicrobial stewardship programmes, and the strengthening of healthcare systems at large.

The carefully curated **Pre-Conference Workshops** encompassing **Bacteriology, Parasitology, Mycology, Tuberculosis, Serology, Virology, Infection Control and Bundle Care and Medical Education** reflect a thoughtful balance between technical competence, quality assurance, and pedagogical excellence. Such focused, hands-on academic initiatives are instrumental in fostering analytical thinking, skill refinement, and academic leadership, particularly among postgraduate trainees and early-career professionals.

I am confident that this conference will catalyse meaningful scientific dialogue, nurture interdisciplinary perspectives, and inspire innovation that ultimately translates into improved patient outcomes and safer healthcare practices. Academic forums of this nature play a vital role in sustaining excellence and relevance in medical education and research.

I congratulate the Organising Team for their academic vision and meticulous planning, and I extend a warm welcome to all delegates to engage in this enriching scientific endeavour at **Lucknow**, a city that seamlessly blends cultural heritage with intellectual vibrancy and academic tradition.

With best wishes for a successful and impactful conference.


Prof. Shaleen Kumar
Dean
SGPGIMS, Lucknow

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MESSAGE FROM THE PRESIDENT



Prof. Ragini Tilak
President

Dear Friend,
Greeting to all.

As the President of UP-UK Chapter of IAMM, I welcome you all to the XXI Annual Conference of UP-UK Chapter of IAMM organized by Department of Microbiology, SGPGI, Lucknow.

I hope all the delegates will find the meticulously designed scientific programme academically interesting and fruitful.

The conference is not just about attending workshops & lectures by stalwarts but also about opportunity of satsang with the wise & the learned & an occasion to collaborate with your peers. The beautiful campus of SGPGI provides an ideal ambience to learn, collaborate & a good time to make friends for a life time.

The conference theme 'Advances in Clinical Microbiology: Shaping Patient Care' is appropriate in the present times, when the microbiologists are no longer confined only to the laboratory. They are actively participating in the management of infections. The conference also includes eight workshops on various facets of microbiology & this will be quite helpful to the young & budding microbiologists who will deploy the practical skills & knowledge gained in these workshops for more accurate & faster diagnosis of infection & this will definitely translate into significant reduction in morbidity & mortality. Apart from this, they can use this knowledge for research in the field of Microbiology.

Numerous new diagnostic modalities are now available to a microbiologist. Artificial intelligence is knocking at our door step. We need to harness the available technology & the newer diagnostic modalities for the benefit of mankind. We also need to focus our attention on the emergence of new pathogens and re-emergence of disappeared pathogens.

Prof. Rungmei & her team is working very hard to make this conference a roaring success. On behalf of the Organizing Team, I once again welcome you to the 'City of Nawabs', known for its tehzeeb, mehmaan nawazi, rich history, culture & Awadhi Cuisine.

A handwritten signature in black ink that reads 'R. Tilak'.

Prof. Ragini Tilak
President
UP-UK Chapter of IAMM
IAMM

MESSAGE FROM THE SECRETARY



Dear esteemed members of UP-UK chapter of IAMM!

It gives me great pleasure to extend my warm greetings on the occasion of the 21st Annual Conference of UPUK chapter organized by SGPGIMS Lucknow on 6th-7th February 2026 on theme “Advances in Clinical Microbiology: Shaping Patient Care” and a Souvenir is also being published to commemorate the Conference.

This conference serves as an excellent platform for experienced faculty, young faculty, post graduate students and research scholars to come together and share knowledge, experiences, and recent advancements in the field of Medical Microbiology.

The scientific program of UPUK MICROCON 2026 has been meticulously curated to offer a rich blend of academic deliberations and eight skill-oriented training workshops on every aspect of microbiology. The inclusion of MICRO-ED NEXT, focusing on innovative teaching strategies in CBME, highlights the conference's forward-looking vision in medical education. I am sure that delegates will be immensely benefitted through this conference.

I sincerely appreciate the dedicated efforts of the organizing committee, faculty members, speakers, and volunteers whose hard work has made this conference possible. I am confident that the deliberations and discussions during the conference will be highly enriching and will contribute meaningfully to academic and clinico-diagnostic practice.

I wish the all the great success to entire organising committee of UP-UK MICROCON 2026 and hope that this will serve as a valuable event of the scientific endeavours.

With best wishes,

A handwritten signature in black ink, appearing to read 'Vineeta Mittal', written over a horizontal line.

Prof Vineeta Mittal
Secretary
UPUK Chapter
IAMM Association

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Raebareli Road, Lucknow- 226 014, UP (India)

Message from the Organizing Chairperson, UP-UK MICROCON 2026



It gives me immense pleasure and a deep sense of Honour to welcome all the distinguished faculty, eminent scientists, senior microbiologists, and enthusiastic young delegates to UP-UK MICROCON 2026, the 21st Annual Conference of the UP-UK Chapter of IAMM, being held at the Department of Microbiology, SGPGIMS, Lucknow from 6th–7th February 2026.

This conference has been envisioned as a vibrant academic platform that brings together renowned experts and budding microbiologists under one roof, fostering meaningful dialogue, exchange of ideas, and collaborative learning. The overwhelming response from faculty members, postgraduate students, and research scholars across the country truly reflects the collective commitment of our microbiology fraternity towards academic excellence, innovation, and professional growth.

We have curated a comprehensive scientific programme with keynote lectures, symposia, panel discussions, oral and poster presentations, designed to address contemporary challenges and emerging trends in clinical microbiology, antimicrobial resistance, diagnostics, infection prevention, and translational research. A defining strength of this conference is the inclusion of eight skill-oriented, hands-on workshops, carefully curated to bridge the gap between theory and real-world laboratory and clinical practice. I am confident that the scientific deliberations will not only enrich knowledge but also inspire young microbiologists to pursue excellence, curiosity, and ethical practice in their professional journeys.

Lucknow, with its unique blend of rich heritage, academic culture, and warm hospitality, provides the perfect backdrop for this academic congregation. On behalf of the Organizing Committee, I extend a heartfelt welcome to all our esteemed faculty and young delegates and wish you a stimulating, memorable, and fulfilling conference experience.

I look forward to your active participation and to the success of this academic celebration.

Warm regards,

Prof. (Dr.) Rungmei S. K. Marak
Organizing Chairperson
UP-UK MICROCON 2026
Vice President UP-UK IAMM
Professor & HOD
Department of Microbiology &
Department of Infectious Diseases.
SGPGIMS, Lucknow



Sanjay Gandhi Postgraduate Institute of Medical Sciences



Dr. Chinmoy Sahu
MD, DNB, PDCC
Professor
Department of Microbiology

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Message from the Organizing Secretary

Dear Esteemed Guests,

On behalf of the organizing committee, it is my immense pleasure to extend a heartfelt welcome to each one of you to the **21st Annual Conference of the UP-UK State Chapter of the Indian Association of Medical Microbiologists (UP-UK MICROCON 2026)** organized by **Department of Microbiology, Sanjay Gandhi Post Graduate Institute of Medical Sciences (SGPGIMS)** in the beautiful and vibrant city of Lucknow. Your presence adds immense value and we are thrilled to have you join us for this intellectual gathering.

Our team has worked diligently to ensure that every aspect of the conference enhances your experience, from the choice of venue to the selection of topics and the seamless organization of events. We are confident that you will find the conference both enlightening and enjoyable.

This conference is an essential forum for all stakeholders in clinical microbiology and infectious disease community. It seeks to re-energize our collaborative efforts and attract the next generation of clinical microbiologists and researchers dedicated to solving complex global health problems. The UP-UK Microcon 2026 is a premier event dedicated to the advancement of knowledge and innovation in the field of clinical microbiology and infectious diseases. It serves as a critical platform for the scientific community to collaborate, share research and address the most significant challenges in infection science.

Lucknow, with its rich history, cultural diversity, and modern charm, serves as the perfect backdrop for our conference. Beautiful monuments, lip-smacking awadhi cuisine and world-class medical institutions will offer you all, an experience of life-time.

Let us come together to make this conference a remarkable gathering of medical minds, where knowledge blossoms, collaborations thrive and friendships endure.

Thank you for being part of this prestigious event. We look forward to welcoming you to Lucknow. See you at UP-UK Microcon 2026 at SGPGIMS!

Warm regards,

Dr. Chinmoy Sahu

UP-UK CHAPTER OF IAMM

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SGPGIMS, Lucknow

NEWSLETTER UP-UK CHAPTER OF IAMM

NEWSLETTER IAMM - UP UK CHAPTER (DEC 10-JAN 24-25) Issue 3



NEWSLETTER
INDIAN ASSOCIATION OF MEDICAL
MICROBIOLOGISTS - UP UK STATE CHAPTER



Dr. Priyanka Shukla
Editor



Dr. Fareya Haider
Associate Professor
Assistant Editor

Editor's Desk...

As we welcome 2025, we, the editors, would like to extend our heartfelt wishes to all dedicated microbiologists. May this new year be filled with discoveries that deepen our understanding of the microbial world and motivate us to further explore the complexities of life.

The past year has been remarkable, showcasing significant progress in microbiology, from the development of new vaccines to cutting-edge diagnostic techniques. Looking ahead, let us continue our commitment to excellence in the pursuit of knowledge and its practical application to enhance human health.

We sincerely appreciate the invaluable contributions of all microbiologists that made the successful publication of our newsletters in 2024 possible. The continuous support and encouragement from esteemed Microbiologists have been crucial. This year, we will keep you updated through our newsletters, so stay tuned!

Thank you once again for being an integral part of this association. We wish you all a joyful and prosperous New Year.

Warm regards
Dr. Priyanka Shukla
Dr. Fareya Haider

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Role Of Biomarkers in Clinical Microbiology

NEWSLETTER IAMM - UP UK CHAPTER (Apr to June 25-26) Issue 1



NEWSLETTER
INDIAN ASSOCIATION OF MEDICAL
MICROBIOLOGISTS - UP UK STATE CHAPTER



Dr. Priyanka Shukla
Editor



Dr. Fareya Haider
Associate Professor
Assistant Editor

Editor's Desk...

We the Editor's would like to congratulate team Merat for the grand success of UP-UK MICROCON 2025. With over 500 participants (Delegates and faculty) from all over UP-UK, the conference success began with its impeccable organization. The conference had balanced comprehensive scientific content with meaningful engagement opportunities. In this first issue of newsletter we would like present published papers of Eminent Microbiologist on "Recent updates and insights on TB diagnostics and Treatment".

In an era marked by remarkable medical breakthroughs, one ancient disease continues to claim over 1.3 million lives annually (tuberculosis TB). For centuries, this airborne pathogen has exploited socioeconomic inequalities, crowded living conditions, and inadequate healthcare infrastructure to maintain its grim status as one deadliest infectious diseases. Yet recent years have witnessed a quiet revolution in TB diagnostics and treatment that may finally help us turn the tide against this persistent killer.

However, the landscape of TB management is undergoing significant transformation. The past few years have delivered remarkable updates in diagnostic capabilities and treatment protocols that may represent a genuine turning point in our global response to this enduring public health challenge.

The widespread implementation of Next-Generation Sequencing (NGS) represents one of the most significant updates in TB diagnosis. This advanced molecular test not only delivers results within hours but simultaneously detects rifampicin resistance, allowing for immediate treatment adjustments. Recent implementation studies show particularly impressive performance in previously challenging populations—children, people living with HIV, and those with extrapulmonary TB—where sensitivity has increased by up to 40% compared to conventional methods.

Warm regards
Dr. Priyanka Shukla
Dr. Fareya Haider

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Advancement in Tuberculosis Diagnosis

NEWSLETTER IAMM - UP UK CHAPTER (Oct. to Dec. 25-26) Issue 3



NEWSLETTER
INDIAN ASSOCIATION OF MEDICAL
MICROBIOLOGISTS - UP UK STATE CHAPTER



Dr. Priyanka Shukla
Editor



Dr. Fareya Haider
Associate Professor
Assistant Editor

Editor's Desk...

Dear Esteemed Members as our journey is nearing the end of this year, this is the last Newsletter of this eventful 2025. This year reminded us, once again, that microbes shape our world in ways both visible and hidden. We've witnessed the continued evolution of antimicrobial resistance, a challenge that grows more urgent with each passing year. The rise of multi-drug resistant pathogens is a threat which needs to be addressed at the earliest. Microbiologist all around world are working on phage therapies in clinical trials to AI-driven antibiotic discovery platforms. As we move into 2026, the invisible world reminds us of the essential truths that the collaboration across disciplines isn't optional but necessary, and sustained influence on the health of our planet and everything on it.

In this end of year Newsletter issue we have come up with an important theme: **The Preventing zoonoses together...One World One Health**. The "One Health, One World" remained important for 2025 for several interrelated reasons. The concept recognizes human, animal, and environmental health to be interconnected, and thus making a collaborative approach essential to improve surveillance, prevention and control of zoonotic diseases, like Avian influenza, Rabies, and Lyme's disease etc. This approach is vital for preventing future pandemics by breaking the cycle of disease transmission that crosses national and regional boundaries. In this context article titled "Preventing Zoonosis Together: One World, One Health" compiled by Dr. Vikas Gupta and another by Dr. Vikramjeet "Zoonosis: Focus on Leptospirosis" has been included.

Last but not the least we the editors would like to thank all our seniors, juniors and fellow microbiologist to make this Newsletter journey successful for the past 3 years.

Warm regards
Dr. Priyanka Shukla
Dr. Fareya Haider

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Zoonosis: One World One Health



UP-UK MICROCON 2026

21st Annual Conference of UP-UK

Chapter of Indian Association of Medical Microbiologists

Theme - Advances in Clinical Microbiology: Shaping Patient Care

Pre - Conference Workshop: Advanced fungal diagnostics; Molecular and Biomarker Diagnostics for Invasive fungal Infections & rare emerging opportunistic fungal pathogens

Date: 6th February 2026

Time: 09:00 AM to 04:30 PM

Venue: Seminar Room, Department of Neurology, II Floor, C-Block

Organising Department: Department of Microbiology, SGPGIMS, Lucknow

Course Coordinator: Dr. Rungmei S K Marak, Dr. Tasneem Siddiqui

Resource persons: Dr. Rungmei S K Marak, Dr. Ragini Tilak, Dr. Anupama Jyoti Kindo, Dr. Tasneem Siddiqui, Dr. Deepika Tyagi, Dr. Kanchan, Dr. Ajai Kumar Dixit

Mycology Team: Mr. Puspak Ghosh, Ms. Purnima Singh, Ms. Shikha Tripathi, Mr. Ashutosh Pandey

Target Participants: MD Microbiology Residents, Critical Care Residents (MD/DM, fellows), M.Sc. Microbiology, Ph.D. Students, Faculty members

Maximum number of participants: 20

Duration: One Day

Date: 06.02.2026

Venue: Mycology Laboratory, II Floor, New Diagnostic Block, Department of Microbiology, SGPGIMS, Lucknow

Workshop Overview & Key Highlights

- i. Demonstration of laboratory methods for identification of rare emerging opportunistic fungal pathogens in immunocompromised patients.
- ii. Practical demonstrations and hands-on training on MALDI TOF MS: Yeast and Mould identification
- iii. Practical demonstrations and hands-on training on fungal biomarkers: Beta D Glucan and Galactomannan assay.
- iv. Practical demonstrations and hands-on training on Real Time PCRs for *Aspergillus* and *Pneumocystis jirovecii* with DHPS mutation

Agenda: Advanced fungal diagnostics; Molecular and Biomarker Diagnostics for Invasive fungal Infections & rare emerging opportunistic fungal pathogens

Timing		Topic	Resource Faculty
08:00 AM - 08:45 AM	Registration		
08:45 AM - 09:00 AM	Introduction of Faculty/ Resource persons		
09:00 AM - 09:10 AM	Inaugural remarks Mycology workshop & Pre-Test		Dr. Rungmei S K Marak, Organizing Chairperson
Lectures/ Sessions			
09:30 AM - 09:50 AM		Identification of Molds	Dr. Anupma Jyoti Kindo
09:50 AM - 10:00 AM		Identification of Yeasts	Dr. Rungmei S K Marak
10:00 AM - 10:10 AM		MALDI-TOF MS principles and uses	Dr. Deepika Tyagi
10:10 AM - 10:30 AM		Fungal biomarkers	Dr. Ragini Tilak
10:30 AM - 10:40 AM		Real Time PCRs for fungi	Dr. Tasneem Siddiqui
10:40 AM - 11:40 PM		Hands-on Practical Session I PCR	Dr. Tasneem Siddiqui Ms. Purnima Singh Mr. Hemant Sharma (Pathonostics)
11:40 AM - 12:40 PM		Hands-on Practical Session II Fungal Biomarkers	Dr. Ragini Tilak Mr. Puspak Ghosh Mr. Pankaj Lavania (M/s Anand Brothers) Mr. Phaninder Koppula (M/s Immy)
12:40 PM - 01:30 PM		MALDI-TOF MS demonstration for identification of fungi (Batch A & B)	Dr. Deepika Tyagi Dr. Ajai Kumar Dixit Mr. Puspak Ghosh Mr. Utkarsh Gupta (BioMérieux)
01:30 PM - 02:00 PM	Lunch Break		
02:00 PM - 02:45 PM		Yeast Identification (Batch A)	Dr. Rungmei S K Marak Dr. Ragini Tilak Dr. Kanchan Dr. Ajai Dixit Ms. Shikha Tripathi
02:45 PM- 03:30 PM		Mold Identification (Batch B)	Dr. Anupma Jyoti Kindo Dr. Deepika Tyagi Mr. Puspak Ghosh
03:30 PM - 03:45 PM	Tea Break		
03:45 PM - 04:15 PM		Interpretation of PCR and result of Fungal Biomarker	Dr. Ragini Tilak Dr. Tasneem Siddiqui Mr. Puspak Ghosh Ms. Purnima Singh
04:15 PM - 04:30 PM	Post-Test & Feedback		Dr. Deepika Tyagi Dr. Kanchan
04:30 PM - 05:00 PM	Valedictory & Certificate distribution		Dr. Rungmei S K Marak Dr. Tasneem Siddiqui Dr. Kanchan



UP-UK MICROCON 2026

21st Annual Conference of UP-UK

Chapter of Indian Association of Medical Microbiologists

Theme - Advances in Clinical Microbiology: Shaping Patient Care

Pre - Conference Workshop

Workshop No.2: Advanced Tuberculosis Diagnostics & Best Laboratory Practices for Risk Group 3 Organisms

Organized by Division of Mycobacteriology, Department of Microbiology, SGPGIMS, Lucknow
Course Coordinator: Dr. Richa Mishra, Dr. Praveen Kumar Pachouri

Resource Faculty: Dr. Alok Nath, Dr. Zafar Neyaz, Dr. Vimal Kumar Paliwal, Dr. Sameer Mohindra,
Dr. Akshay Kumar Arya, Dr. Vikramjeet Singh

BSL-3 Lab Team: Dr. Sreya Deb, Mr. D.K Singh, Mr. Subhash, Ms. Anjali Yadav, Ms. Manu

Target Participants: Microbiologists, ID Consultants, Pulmonologists, Clinicians, Technologists,
Healthcare providers

Maximum number of participants: 20

Duration: One Day

Date: 06.02.2026

Venue: Biosafety Level 3 Tuberculosis Laboratory, II Floor, New Diagnostic Block, Department of
Microbiology, SGPGIMS, Lucknow

Learning objectives:

- Basic principles of Infection Prevention & Control for working in a Biosafety Level 3 tuberculosis facility
- Learn important definitions related to diagnosis and management of tuberculosis
- Recognize fundamental concepts of pulmonary and extrapulmonary tuberculosis
- Practical demonstrations of
 - Cultures (In-house LJ media preparation and colony morphology)
 - CBNAAT assay (both Xpert MTB/ RIF Ultra assay and XDR test)
 - Line probe assay for both MTBC and Non-tubercular Mycobacteria
 - MGIT culture and DST

Agenda: Advanced Tuberculosis Diagnostics & Best Laboratory Practices for Risk Group 3 Organisms

Timing		Topic	Resource Faculty
9:00 AM - 9:20AM	Registration		
9:20 AM – 9:30 AM	Pre-Test		
9:30 AM – 9:40 AM		Introduction to the workshop	Dr. Vikramjeet Singh
9:40 AM – 10:00 AM		Best IPC practices for BSL 3 facility	Dr. Praveen Kumar Pachouri
10:00 AM – 10:20 AM		Pulmonary tuberculosis: clinico-radiological perspective and treatment update	Dr. Alok Nath
10:20 AM – 10:40 AM		Radiological diagnosis and differentials of extrapulmonary tuberculosis	Dr. Zafar Neyaz
10:40 AM - 11:00 AM		Challenges in tubercular meningitis	Dr. Vimal Kumar Paliwal
11:00 AM – 11:20AM		Abdominal tuberculosis: tip of the iceberg	Dr. Sameer Mohindra
11:20 AM – 11:30 AM		Tea Break	
11:30 AM – 12:00 PM		Non-tuberculous Mycobacterial Infections: The Neglected Threat.	Dr. Richa Mishra
12:00 PM – 01:30 PM	Practical demonstrations in State-of-the-art BSL3 tuberculosis facility	Batch A <ul style="list-style-type: none"> • IPC Protocols in BSL3 facility • MGIT Culture and DST Batch B <ul style="list-style-type: none"> • Demonstration of CBNAAT assay- Ultra and XDR tests • Line probe assay for MTBC & NTM 	Dr. Richa Mishra Dr. Praveen Kumar Pachouri Dr Akshay Kumar Arya & BSL-3 Lab Team
01:30 PM – 02:00 PM		Lunch	
02:00 PM – 03:30 PM	Practical demonstrations in State-of-the-art BSL3 tuberculosis facility	Batch B <ul style="list-style-type: none"> • IPC Protocols in BSL3 facility • MGIT Culture and DST Batch A <ul style="list-style-type: none"> • Demonstration of CBNAAT assay- Ultra and XDR tests • Line probe assay for MTBC & NTM 	Dr. Richa Mishra Dr. Praveen Kumar Pachouri Dr Vikramjeet Singh & BSL-3 Lab Team
03:30 PM – 04:00 PM		Networking, Discussion and Troubleshooting	
		Round of Container BSL3 Lab	
04:00 PM – 04:10 PM		Post Test	
04:00 PM – 04:30 PM		Valedictory Function followed By High Tea	



UP-UK MICROCON 2026

21st Annual Conference of UP-UK

Chapter of Indian Association of Medical Microbiologists

Theme - Advances in Clinical Microbiology: Shaping Patient Care

Pre - Conference Workshop

Workshop No. 3: Diagnostic Bacteriology: Optimizing advanced laboratory methods for early diagnosis and management of sepsis

Date: 6th February 2025

Venue: Department of Microbiology, SGPGIMS, Lucknow

Maximum number of participants: 20

Workshop Overview

Bacteriology section of the Department of Microbiology of Sanjay Gandhi Postgraduate Institute of Medical Sciences (SGPGIMS), Lucknow is organizing a dedicated Pre-Conference Hands-on Workshop on “Optimizing advanced laboratory methods for early diagnosis and management of sepsis as part of UP-UK MICROCON 2026.”

This workshop aims to train students for optimizing conventional as well as advanced automated laboratory techniques for rapid diagnosis and optimum antibiotic reporting for sepsis.

Target Audience

This workshop is specifically designed for:

MD Microbiology faculty and Residents

Infectious Diseases faculty and residents (MD/DM/Fellows)

M.Sc. Microbiology students & Ph.D. Students

Key Highlights

1. Identification of bacterial isolates by Vitek using positive blood broth
2. Identification of bacterial isolates by MALDI TOF MS from positive blood broth
3. Rapid carbapenemase detection by tube and ICT method
4. Broth microdilution of latest antibiotics by automated MIC method
5. Procedure and interpretation of antibiotic susceptibility testing directly from positive blood broth

Course Coordinator: Dr Chinmoy Sahu, Professor, Microbiology, SGPGIMS, Lucknow.

Resource persons: 1. Prof Pradyot Praksh, Professor (Microbiology), IMS, BHU.

2. Dr. Sangram Singh Patel, Additional Professor (Microbiology), SGPGIMS, Lucknow.

3. Dr. Nidhi Tejan, Assistant Professor (Microbiology), SGPGIMS, Lucknow.

4. Dr. Akshay Arya, Assistant Professor (Microbiology), SGPGIMS, Lucknow.

5. Dr. Vikramjeet Singh, Assistant Professor (Microbiology), SGPGIMS, Lucknow.

6. Dr. Diksha Shukla, Senior Resident (Microbiology), SGPGIMS, Lucknow.

7. Dr. Ashutosh Pathak, Senior Research Fellow (Microbiology), SGPGIMS, Lucknow.

8. Ms. Nida, PhD student (Microbiology), SGPGIMS, Lucknow.

9. Mr. Tanuj Yadav, Laboratory Technician (Microbiology), SGPGIMS, Lucknow.

Agenda: Diagnostic Bacteriology: Optimizing advanced laboratory methods for early diagnosis and management of sepsis

Time	Topic	Resource Person
09:00 AM - 09:30 AM	Registration	
09:30 AM - 09:40 AM	Overview of workshop	Prof. Chinmoy Sahu
09:40 AM - 10:15 AM	Optimizing laboratory methods for early diagnosis of sepsis	Prof. Pradyot Prakash, IMS, BHU
Hands on session		
10:15 AM - 11:30 AM	Identification of bacterial isolates by Vitek using positive blood broth	Dr. Sangram Singh Patel Dr. Vikramjeet Singh Mr. Tanuj Yadav
11:30 AM - 01:00 PM	Identification of bacterial isolates by MALDI-TOF MS from positive blood broth	Dr. Chinmoy Sahu Dr. Nidhi Tejan Ms. Nida
01:00 PM - 02:00 PM	Lunch	
02:00 PM - 03:00 PM	Broth microdilution of antibiotics by automated MIC method	Dr. Akshay Arya Dr. Diksha Shukla Dr. Ashutosh Pathak Ms. Nida
03:00 PM - 04:00 PM	Procedure and interpretation of antibiotic susceptibility testing directly from positive blood broth	Dr. Chinmoy Sahu Dr. Sangram Singh Patel Dr. Akshay Arya Dr. Nidhi Tejan Ms. Nida
04:00 PM- 04:30 PM	Rapid carbapenemase detection by tube and ICT method	Dr. Vikramjeet Singh Dr. Diksha Shukla Dr. Ashutosh Pathak Mr. Tanuj Yadav
04:30 PM - 05:00 PM	Question-Answer session Valedictory & certificate distribution	Prof. Pradyot Prakash IMS, BHU, Varanasi



UP-UK MICROCON 2026

21st Annual Conference of UP-UK

Chapter of Indian Association of Medical Microbiologists

Theme - Advances in Clinical Microbiology: Shaping Patient Care

Pre - Conference Workshop

Workshop No. 4: Diagnostic virology: Basics to automated systems

Date: 6th February 2025

Venue: Department of Microbiology, SGPGIMS, Lucknow

Maximum number of participants: 20

Workshop Overview

The Department of Microbiology, SGPGIMS, Lucknow is organizing a dedicated hands-on workshop on Diagnostic virology: basics to automated systems as part of UP-UK MICROCON 2026. This workshop aims to exposure to post graduate students, Research scholars, and junior faculty members on classical as well as automated techniques used in Diagnostic virology.

Under the Aegis of IAMM UP-UK Chapter

This academic activity is being conducted **under the aegis of the Indian Association of Medical Microbiologists (IAMM), UP-UK Chapter**, as part of **UP-UK MICROCON 2026**, hosted by **Sanjay Gandhi Postgraduate Institute of Medical Sciences (SGPGI), Lucknow**.

Course Coordinator:

Dr. Atul Garg, Add. Professor, Department of Microbiology, SGPGIMS, Lucknow.

Resource persons:

1. Dr. Deepa Kailash Sharma, NPO (VPD Laboratory Network), WHO Country Office for India
2. Dr. Ankur Goyal, Professor and Head, Department of Microbiology, S N Medical college, Agra.
3. Dr. Dharam Veer Singh, Scientist B, Department of Microbiology, SGPGIMS, Lucknow.

Target Audience: This workshop is specifically designed for: MD Microbiology Residents, Ph. D Research Scholars, and Junior faculty Members

Tentative schedule

Sl. No.	Time	Schedule
1.	09:30 AM - 10:00 AM	Registration & Pre-Test
2.	10:00 AM - 01:00 PM	Cell culture media preparation and maintenance of cell lines Hands on Stool sample processing and cell inoculation for virus isolation, Cell splitting, counting and CPE observation Plaque Assay/ TCID-50
3.	01:00 PM - 02:00 PM	Lunch
4.	02:00 PM - 04:30 PM	Hands on Quantitative & Qualitative RT-PCR Cartridge based syndromic assays
5.	04:30 PM - 04:40 PM	Post Test
6.	04:40 PM - 05:00 PM	Valedictory Function followed by High Tea



UP-UK MICROCON 2026

21st Annual Conference of UP-UK

Chapter of Indian Association of Medical Microbiologists

Theme - Advances in Clinical Microbiology: Shaping Patient Care

Pre - Conference Workshop

Workshop No. 05: Emerging Technologies and Automation in Serological and Microbial Immunology: Translating Laboratory Efficiency into Clinical Excellence.

Organizing Department: Department of Microbiology, SGPGIMS, Lucknow

Course Coordinator: Dr. Rungmei S K Marak, Dr. Anju Dinkar, Dr. Nidhi Tejan

Resource persons: Dr. Rungmei S K Marak, Dr. Anju Dinkar, Dr. Nidhi Tejan,

Dr. Shampa Anupurba, Dr. Jaya Garg, Dr. Suruchi Shukla, Dr. Surbhi

Target Participants: MD Microbiology Residents, M.Sc. Microbiology, Ph.D. Students, Faculty members

Maximum number of participants: 20

Duration: One Day

Date: 06.02.2026

Venue: Seminar room, Department of Microbiology, SGPGIMS, Lucknow

Workshop Overview & Key Highlights

1. QuantiFERON-CMV Assay, a specialized Interferon-Gamma Release Assay (IGRA) to assess CMV-specific cell-mediated immunity, particularly in immunocompromised or transplant patients.
2. CLIA analyzer
3. Detection of IL-6 and IL-10 by Enzyme-Linked Immunosorbent Assay (ELISA)
4. MiniVidas platform for demonstration of new parameters
5. TPHA Testing and Interpretation
6. Brucella and Borrelia ELISA
7. Weil-Felix test for Rickettsial infections

Agenda: Emerging Technologies and Automation in Serological and Microbial Immunology: Translating Laboratory Efficiency into Clinical Excellence

Timing	Topic	Resource Faculty
08:00 AM - 08:45 AM	Registration	
08:45 AM - 09:00 AM	Registration & Pre-test	
09:00 AM - 09:10 AM	Inaugural remarks	Dr. Rungmei S K Marak Organizing Chairperson
09:10 AM - 09:30 AM	Recent update on HIV infection	Dr. Shampa Anupurba
09:30 AM - 09:50 AM	Role of Biomarkers in clinical infectious diseases	Dr. Jaya Garg
09:50 AM - 10:10 AM	Recent Advances in Immunodiagnosis	Dr. Suruchi Shukla
10:10 AM - 10 30 AM	Tea Break	
10:30 AM - 12:00 Noon	Hands-on Practical Session I (2 Batches)	Automation in Serology: ELFA & CLIA platforms
12:00 Noon - 01:30 PM	Hands-on Practical Session II (2 Batches)	QuantIFERON-CMV Assay, a specialized Interferon-Gamma Release Assay (IGRA) to assess CMV-specific cell-mediated immunity, particularly in immunocompromised or transplant patients
01:30 PM - 02:00 PM	Lunch Break	
02:00 PM - 02:30 PM	Hands-on Practical Session III (2 Batches)	Detection of IL-6 and IL-10 by Enzyme-Linked Immunosorbent Assay (ELISA)
02:30 PM - 03:00 PM	Hands-on Practical Session IV (2 Batches)	TPHA Testing and Interpretation
03:00 PM - 03.30 PM	Tea Break	
03.30 PM - 04.00 PM	Hands-on Practical Session V (2 Batches)	Brucella & Borrelia ELISA Testing and Interpretation
04.00 PM - 04.30 PM	Hands-on Practical Session VI (2 Batches)	Weil-Felix Reaction and Interpretation
04:30 PM - 04:40 PM	Post-test & Feedback	
04:40 PM - 05:00 PM	Valedictory & Certificate distribution	



UP-UK MICROCON 2026

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Chapter of Indian Association of Medical Microbiologists

Theme - Advances in Clinical Microbiology: Shaping Patient Care

Pre - Conference Workshop

Workshop No. 06: Conventional to Automation in diagnosis of Parasites

Course Chairperson: Prof. Rungmei S K Marak

Course Coordinator: Dr. Awadhesh Kumar

CONVENTIONAL METHODS

1. Microscopy

- Routine microscopy: Wet mount (Normal Saline and Iodine mount)
- Special stains: modified acid-fast stain, modified trichrome stain, Giemsa stain

2. Stool culture for Entero-pathogens

- Serology:** ELISA for detection of IgG *Entamoeba histolytica* and *Echinococcus granulosus*

AUTOMATION METHODS

- Automation in Parasitology:** AI based microscopy (AGAPE F-60)

- Molecular:** Multiplex PCR for identification of GI pathogens (Syndromic panels)

Resource Persons

External Faculty

Dr. Rakesh Singh, Professor, Department of Microbiology, JIPMER, Puducherry

Dr. Areena Hoda Siddiqui, Professor, Department of Microbiology, Autonomous Medical College, Amethi

Internal Faculty

Dr. Nidhi Tejan, Assistant Professor, Department of Microbiology, SGPGIMS

Agenda: Conventional to Automation in diagnosis of Parasites

Timing		Topic	Resource Faculty
08:00 AM - 08:45 AM	Registration		
08:45 AM - 09:00 AM	Registration & Pre-test		
09:00 AM - 09:10 AM	Inaugural remarks		Dr. Rungmei S K Marak Organizing Chairperson
09:10 AM - 09:30 AM		Conventional Parasitological Diagnosis: Scope & Limitations	Dr. Rakesh Singh
09:30 AM - 09:50 AM		Automation in Parasitology: AI-based platforms and multiplex PCR	Dr. Areena Hoda Siddiqui
10:00 AM - 10:20 AM	Tea Break		
10:20 AM - 10:40 AM		Staining methods in diagnosis of parasites	Dr. Awadhesh Kumar
10:40 AM - 11:10 AM		Diagnosis of <i>Clostridioides difficile</i> toxin	Dr. Nidhi Tejan
10:40 AM - 11:10 AM		Serological methods in diagnosis of parasitic infection	Dr. Diksha Shukla
11:10 AM - 01:30 PM		Hands-on Practical Session I (2 Batches)	Dr. Awadhesh Kumar
01:30 PM - 02:00 PM	Lunch Break		
02:00 PM - 03:30 PM		Hands-on Practical Session II (2 Batches)	Dr. Nidhi Tejan
03:30 PM - 03:45 PM	Tea Break		
03:45 PM - 04:15 PM		Hands-on Practical Session III (2 Batches)	Dr. Diksha Shukla
04:15 PM - 04:30 PM	Post-test & Feedback		
04:30 PM - 05:00 PM	Valedictory & Certificate distribution		



UP-UK MICROCON 2026

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Theme - Advances in Clinical Microbiology: Shaping Patient Care

Pre - Conference Workshop

Workshop No. 07: CLABSI BUNDLE CARE & VENTILATOR-ASSOCIATED EVENTS (VAE) BUNDLE CARE

Date: 6th February 2025

Venue: Department of Microbiology, RMLIMS, Lucknow

Maximum participants: 20

Under the Aegis of IAMM UP-UK Chapter

THEME: Towards Zero CLABSI & VAE: Transforming Patient Care Through Bundles

Workshop Overview: The Department of Microbiology, Dr. Ram Manohar Lohia Institute of Medical Sciences (RMLIMS), Lucknow is organizing a dedicated hands-on workshop on **CLABSI (Central Line–Associated Bloodstream Infection) Bundle Care** and **VAE (Ventilator-Associated Events) Bundle Care** as part of **UP-UK MICROCON 2026**. This workshop aims to strengthen evidence-based infection prevention practices in critical care settings, with special emphasis on surveillance, device care, bundle implementation, monitoring, and quality improvement.

Under the Aegis of IAMM UP-UK Chapter

This academic activity is being conducted **under the aegis of the Indian Association of Medical Microbiologists (IAMM), UP-UK Chapter**, as part of **UP-UK MICROCON 2026**, hosted by **Sanjay Gandhi Postgraduate Institute of Medical Sciences (SGPGIMS), Lucknow**.

Target Audience: This workshop is specifically designed for:

- **MD Microbiology Residents**
- **Critical Care Residents (MD/DM/Fellows)**
- **Infection Prevention & Control (IPC) Team Members**

Key Highlights

- Principles and components of CLABSI and VAE bundles
- Practical demonstrations and hands-on training
- Device insertion & maintenance safety protocols
- Surveillance definitions (CDC/NHSN based) and case studies
- Audit tools, monitoring checklists & performance indicators
- Root-cause analysis and prevention strategies for outbreaks
- Multidisciplinary implementation approaches in ICUs

Chairperson: Prof. Jyotsna Agarwal

Organizing Secretary: Prof. Manodeep Sen

Co-organizing Secretary: Prof. Fatima Khan

Scientific Advisor: Prof. Anupam Das

Resource person: Dr SS Nath, Dr. Rimjhim, Dr. Mohd. Saquib, Dr. Anuragini, Dr. Akanksha Gupta, Dr Shiva Verma

Agenda: CLABSI & VAE Bundle Care: From Bench to Bedside

Time	Session / Topic	Resource Faculty
08:00 AM - 09:00	Registration	—
09:00 - 09:15	Pre-Workshop Assessment	Dr. Akanksha Gupta, Dr. Shiva Verma
09:15 AM - 09:25	Welcome & Workshop Overview	Dr. Jyotsna Agarwal
09:25 AM - 09:40	Device-Associated Infections: Clinical Impact & Real-World Data	Dr. Jyotsna Agarwal
09:40 AM - 09:55	Evidence-Based Care Bundles: From Guidelines to Bedside	Dr. Manodeep Sen
09:55 AM - 10:15 AM	CLABSI: Principles & Components	Dr. Fatima Khan
10:15 AM - 10:55 AM	CLABSI Insertion & Maintenance Demonstration	Dr. S. S. Nath, Dr. Anupam Das, Prof. Fatima Khan, Dr. Mohd. Saquib, Dr. Shiva Verma, Dr. Anuragini
10:55 AM - 11:15 AM	CLABSI Surveillance (CDC/NHSN)	Dr. Mohd. Saquib
11:15 AM - 11:35 AM	Group Activity: Spot the Error	Dr. Fatima Khan, Dr. Shiva Verma
11:35 AM - 11:55 AM	Inauguration & Hi-Tea	Chair & Co-Chairs
11:55 AM - 12:15 PM	VAE/VAP Principles & Bundle Components	Dr. S. S. Nath
12:15 PM- 12:55 PM	VAE Maintenance – Practical Session	Dr. S. S. Nath, Dr. Manodeep Sen, Dr. Rimjhim, Dr. Akanksha
12:55 PM - 13:15 PM	VAE Surveillance (CDC/NHSN)	Dr. Rimjhim
13:15 PM - 13:35 PM	Group Activity: Build-the-Bundle Challenge	Dr. Anuragini, Dr. Shiva Verma, Dr. Akanksha
13:35 PM - 14:00 PM	Audits, Checklists & Root-Cause Analysis	Faculty Team
14:00 PM - 14:15 PM	Post-Workshop Assessment	Dr. Akanksha Gupta, Dr. Shiva Verma
14:15 PM onwards	Valedictory & High-Tea	Organising Team



UP-UK MICROCON 2026

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Chapter of Indian Association of Medical Microbiologists

Theme - Advances in Clinical Microbiology: Shaping Patient Care

Pre - Conference Workshop

Workshop No.08: MICRO-ED NEXT: *Future-Ready Teaching through SDL and Gamification*

Organizing Department: Department of Microbiology, King George's Medical University, Lucknow

Course Directors: Prof. Vimala Venkatesh, Dr. Parul Jain

Target Participants: Faculty members, Senior Residents and Junior Residents

Maximum number of participants: 30

Duration: One Day

Date: 06.02.2026

Venue: Room no 309, Kalam center, KGMU, Lucknow

Learning Objectives of the workshop:

At the end of this workshop, the participants will be able to:

1. Explain the principles and importance of Self-Directed Learning (SDL) in Competency-Based Medical Education.
2. Identify suitable topics in Microbiology for implementing SDL and gamification.
3. Design a structured SDL module including learning objectives, activities and assessment.
4. Describe the concept and educational value of gamification in medical education.
5. Develop simple gamified teaching-learning resources for Microbiology topics.
6. Integrate SDL and gamification strategies into the undergraduate and postgraduate Microbiology curriculum.
7. Apply appropriate assessment and feedback methods for SDL and gamified learning.

Agenda: MICRO-ED NEXT: *Future-Ready Teaching through SDL and Gamification*

Timing	Topic	Teaching-Learning Method	Resource Faculty
09:00 AM - 09:30 AM	Registration & Pre-test		
09:30 AM - 10:00 AM	Inaugural session		
10:00 AM - 11:00 AM	Foundations of Self-Directed Learning (SDL) in Medical Education	Interactive lecture	Prof. R. K. Dixit
11:00 AM - 11:15 AM	Tea Break		
11:15 AM - 01:00 PM	Designing SDL Modules in Microbiology	Group work & discussion	Dr. Suyog Sindhu Dr. Parul Jain
01:00 PM - 01:30 PM	Introduction to Gamification in Medical Education	Demonstration & interaction	Prof. Vimala Venkatesh
01:30 PM - 02:00 PM	Lunch Break		
02:00 PM - 03:30 PM	Gamification Strategies in Microbiology	Hands-on workshop	Dr. Parul Jain Dr. Suyog Sindhu
03:30 PM - 03:45 PM	Tea break		
03:45 PM - 04:15 PM	Integrating SDL & Gamification in CBME	Panel discussion	Prof. Vimala Venkatesh Prof. RK Dixit Prof. Jyoti Chopra Prof. Sarika Gupta
04:15 PM - 04:30 PM	Post-test & Feedback		
04:30 PM - 05:00 PM	Valedictory		



EMINENT AWARDS of UP-UK Chapter of IAMM

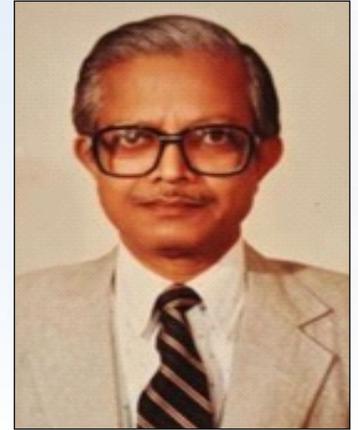


Prof. U.C. Chaturvedi Oration Award

Instituted in 2008 in honour of Prof. U.C. Chaturvedi, an eminent microbiologist and former Professor & Head, Department of Microbiology, KGMU. He has actively used experimental animal models to study the pathogenesis of diseases and then translated them in human clinical presentations, such as immunological cardiac injury and dengue haemorrhagic fever (DHF). This prestigious 30-minute oration celebrates outstanding scientific contributions to Microbiology. The award comprises a gold medal, plaque, citation, and a ceremonial shawl, presented during the inaugural function by the Chief Guest during the Annual UP-UK Conference. Senior life members of the UP-UK Chapter are invited to apply.



EMINENT AWARDS of UP-UK Chapter of IAMM



Prof. P.C. Sen Best Junior Scientist Award (Best Oral Paper)

This award commemorates Prof. Provas Chandra Sen, a visionary microbiologist who played a foundational role in establishing Microbiology at Banaras Hindu University and contributed profoundly to research, AIDS surveillance, vaccine potency testing, and national scientific committees. The award includes a gold medal and certificate. Abstracts and full-length papers of original, unpublished work are invited from registered delegates and has to be submitted to Organizing Secretary, IAMM UP-UK Chapter. The presenting author must belong to Uttar Pradesh or Uttarakhand.

Names of shortlisted candidates:

Sl. No.	Name of the Presenter	Title of Presentation
1.	Dr Diksha Shukla	Diagnostic performance of an automated AI Based Stool Microscopy System compared with conventional manual microscopy: A cross-sectional analysis of 150 cases
2.	Dr Dharamveer Singh	Development of an in-house multiplex RT-PCR for detection of common respiratory viruses and its comparative evaluation with QIAstat Respiratory Panel
3.	Dr Pratima Rawat	NMR Based Serum Metabolomics reveals distinct metabolic signatures of Human Parvovirus B19 infection

1. Diagnostic performance of an Automated AI-Based Stool Microscopy System compared with conventional manual microscopy: A cross-sectional analysis of 150 cases

Author: Diksha Shukla

Introduction: Automated image-based stool analysis systems are increasingly promoted to support parasitology screening. However, their real-world diagnostic performance remains uncertain. This study compared AI-driven stool microscopy platform with conventional manual microscopy (gold standard) at tertiary care center in North India.

Materials & Methods: A total of 150 consecutive stool samples were evaluated. Manual microscopy recorded stool color, consistency, presence of RBC/pus cells and parasitological findings. The AI system reported stool characteristics and parasite identification. Diagnostic agreement, sensitivity, specificity, predictive values, kappa statistics, and chi-square analysis were performed.

Results: Manual microscopy detected parasites in 38% (57/150) of cases, predominantly *Entamoeba histolytica* (25.3%) and *Giardia lamblia* (15.3%). The AI system identified parasites in only 18.7% (28/150). Sensitivity for detecting any parasite was 28.1%, while specificity was 87.1%. AI performance varied markedly by organism: detection was high for *Giardia* (60.9%) but extremely poor for *E. histolytica* (15.8%). Agreement between AI and manual microscopy was low ($\kappa = 0.136$). McNemar's test confirmed significant discordance, driven by a high false-negative rate ($p < 0.001$). AI performed significantly better in yellow stools ($p = 0.047$) typically associated with giardiasis.

Conclusion: The AI stool microscopy system demonstrated acceptable specificity but unacceptably low sensitivity, missing nearly three-quarters of true parasitic infections—especially *E. histolytica*. In its current form, the system is unsuitable as a standalone diagnostic tool. Manual microscopy remains essential, and AI-negative results must not be used for clinical exclusion of parasitic disease.

2. Development of an in-house multiplex RT-PCR for detection of common respiratory viruses and its comparative evaluation with QIAstat Respiratory Panel

Author: Dharam Veer Singh

Introduction: Rapid and accurate diagnosis of respiratory viral infections is essential for optimal patient management and infection control. Automated syndromic platforms such as the QIAstat Respiratory Panel provide broad pathogen detection but are costly and less adaptable for routine use in resource-limited settings. This study aimed to develop and evaluate an in-house multiplex real-time RT-PCR assay for common respiratory viruses and compare its performance with the QIAstat system.

Materials & Methods: A two-tube in-house multiplex real-time RT-PCR assay targeting six major respiratory viruses—Influenza A, Influenza B, SARS-CoV-2, Respiratory Syncytial Virus (RSV), Adenovirus (ADV), and Human Metapneumovirus (hMPV)—was developed. A total of 930 nasopharyngeal/throat swab samples were tested using the QIAstat Respiratory Panel, and all samples were subsequently analyzed in parallel using the in-house assay. Diagnostic performance was assessed in terms of sensitivity, specificity, concordance, turnaround time, and cost-effectiveness.

Results: The QIAstat Respiratory Panel detected 222 positive samples (23.87%). Among these, 148 samples (15.91%) were positive for the six major respiratory viruses, including Influenza A (43.9%), SARS-CoV-2 (16.89%), RSV (18.9%), Influenza B (12.16%), hMPV (6.75%), and Adenovirus (1.35%). The remaining 74 samples (7.95%) were positive for other respiratory viruses. The in-house multiplex RT-PCR assay demonstrated complete concordance with the automated platform for the six targeted viruses, achieving 100% sensitivity and specificity.

Conclusion: The in-house multiplex real-time RT-PCR assay is a reliable and cost-effective alternative to automated syndromic testing for respiratory viruses, particularly suited for high-volume laboratories and resource-limited settings, while automated platforms remain valuable for rapid, comprehensive diagnostics.

3. NMR-Based Serum Metabolomics reveals distinct metabolic signatures of Human Parvovirus B19 infection

Author: Pratima Rawat

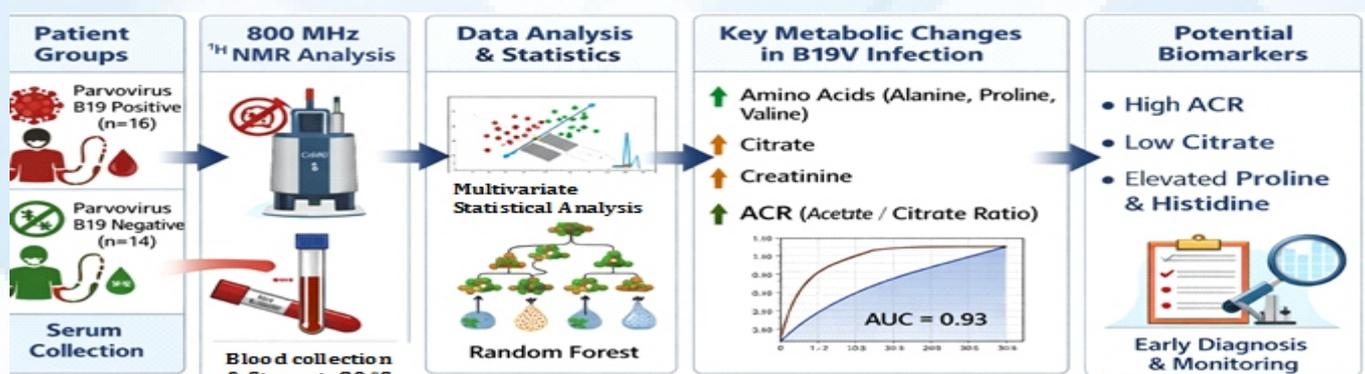
Introduction: Human Parvovirus B19 is an important etiological agent of diverse hematological disorders; however, its impact on host systemic metabolism remains poorly characterized.

Materials & Methods: In this study, we employed high-field 800 MHz ^1H Nuclear Magnetic Resonance (NMR)-based serum metabolomics to elucidate metabolic perturbations associated with B19V infection. Serum samples from Parvovirus B19 - positive patients (n = 16) and Parvovirus-negative controls (n = 14), confirmed by IgM ELISA, were analysed using 1D ^1H CPMG NMR spectroscopy. Metabolite identification and quantification were performed using CHENOMX NMR Suite, followed by multivariate and Univariate statistical analyses.

Results: Over 30 metabolites were identified. Multivariate analyses (PCA, PLS-DA, and Random Forest) showed clear metabolic differences between infected and non-infected groups. B19V-infected patients exhibited changes in amino acids (histidine, proline, valine, alanine), energy metabolism (citrate, fumarate), and lipids. Key discriminatory metabolites included ACR, citrate, histidine, and proline. ROC analysis indicated strong diagnostic potential for ACR (AUC=0.93) and citrate (AUC=0.90), suggesting their use as non-invasive biomarkers.

Conclusion: This study identifies a serum metabolic fingerprint linked to Parvovirus B19 infection, showing disruptions in amino acid and energy metabolism. These findings offer new insights into B19V pathophysiology and highlight NMR-based metabolomics as a helpful diagnostic and monitoring tool in clinical microbiology.

Graphical Abstract:





EMINENT AWARDS of UP-UK Chapter of IAMM



Prof. Archana Ayyagari Best Junior Scientist Award in Antimicrobial Resistance (Best Oral Paper)



Dedicated to Prof. Archana Ayyagari, a pioneering microbiologist, former HOD and Dean of SGPGIMS, and a distinguished ICMR scientist, with over 200 scientific publications and a legacy of initiating MD, PhD, and PDCC (Infectious Diseases) programs at SGPGI, she remains a towering figure in Indian Microbiology. This award honours exceptional work in Antimicrobial Resistance (AMR) and carries a gold medal and certificate. The abstract along with full length paper for oral presentation-UPUK-IAMM Junior Scientist award is to be submitted for screening to Organizing Secretary, IAMM UP-UK Chapter. Presenting authors must be from UP or Uttarakhand.

Names of shortlisted candidates:

S. No.	Name of the Presenter	Title of Presentation
1.	Dr. Huma Jamal	Antimicrobial Susceptibility Profile of <i>Corynebacterium diphtheriae</i> in Uttar Pradesh
2.	Dr. Anu Aravindh	Precision in your palm: Use your mobile to get rapid Antimicrobial Susceptibility Testing
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1. Antimicrobial Susceptibility profile of *Corynebacterium diphtheriae* in Uttar Pradesh

Author: Huma Jamal

Introduction: Diphtheria remains a significant public health problem in India despite widespread immunization, with continued morbidity and mortality reported from several states. Timely laboratory confirmation and updated antimicrobial susceptibility data are essential for effective clinical management and outbreak control. However, contemporary data on antimicrobial resistance patterns of *Corynebacterium diphtheriae* in India are limited.

Objectives:

To perform phenotypic and genotypic identification of *Corynebacterium diphtheriae*, determine toxigenicity, evaluate antimicrobial susceptibility patterns, and detect antimicrobial resistance (AMR) genes in confirmed isolates.

Materials & Methods: A total of 1,640 throat swab samples were collected from clinically suspected diphtheria cases across Uttar Pradesh. Of these, 153 samples were received from the Department of Paediatrics, KGMU, Lucknow, while the remaining samples were obtained through WHO-supported diphtheria surveillance from multiple districts of Uttar Pradesh. All samples were cultured, and isolates were confirmed by multiplex real-time PCR targeting the *rpoB* and *toxA* genes. Toxigenicity was assessed using the modified Elek's gel precipitation test. Antimicrobial susceptibility testing was performed using E-test methodology on Mueller–Hinton agar supplemented with 5% sheep blood and interpreted according to CLSI M45, 3rd edition guidelines. Whole genome sequencing data were analyzed for AMR determinants using the Comprehensive Antibiotic Resistance Database (CARD).

Results: Antimicrobial susceptibility testing was performed on 136 confirmed *Corynebacterium diphtheriae* isolates. All isolates were susceptible to Vancomycin, Daptomycin, Rifampicin, Gentamicin, Doxycycline, and Linezolid. Reduced susceptibility was observed to Penicillin, Macrolides, and Tetracyclines, while Trimethoprim–sulfamethoxazole showed poor activity (11% susceptible) and all isolates were resistant to Ciprofloxacin. CARD analysis identified AMR genes associated with Sulfonamide and glycopeptide resistance; however, phenotypic susceptibility to vancomycin was preserved.

Conclusion: This study provides updated phenotypic and genomic antimicrobial resistance data for toxigenic *Corynebacterium diphtheriae* isolates from Uttar Pradesh, highlighting emerging resistance to first-line agents and emphasizing the importance of integrated phenotypic and genomic surveillance.

Keywords:

Diphtheria; *Corynebacterium diphtheriae*; antimicrobial resistance; CARD; toxigenicity

2. Precision in your palm: Use your mobile to get rapid Antimicrobial Susceptibility Testing

Author: Anu Aravindh

Introduction: Antimicrobial Resistance (AMR) is a global public health challenge driven by the rapid emergence of multidrug-resistant pathogens. Timely and accurate Antimicrobial Susceptibility Testing (AST) is the key to effective antibiotic stewardship. The Kirby–Bauer disc diffusion (KBDD) method remains the most widely used AST technique; however, manual measurement of Zones of Inhibition (ZOI) is prone to inter-observer variability and requires time-consuming cross-referencing with updated CLSI guidelines. Advances in smartphone technology provides an opportunity to digitize AST without the need for expensive hardware. This study aimed to develop and validate a custom, pocket-sized, semi-automated Android-based application for ZOI measurement and interpretation and to evaluate its clinical accuracy and diagnostic reliability compared with the manual method.

Materials & Methods: This prospective cross-sectional validation study utilized an in-house developed application created using an AI-assisted coding workflow for algorithm optimization and debugging, without third-party commercial involvement. The application uses a digital calibration algorithm converting pixel measurements to milli metres and functions entirely offline, making it suitable for resource-limited settings. AST was performed on Mueller–Hinton agar using the KBDD method as described in CLSI M100, 35th edition (2025). ZOI was measured manually with a ruler and interpreted using CLSI tables, followed by analysis of the same plates using the smartphone application.

Results: The smartphone-based AST application provides a reliable interpretation of disk diffusion AST, with high categorical agreement and excellent detection of resistant isolates when compared with the manual reference method. The very low, very major error and the low major error rates highlight the safety of the application for resistance detection.

Conclusion: This semi-automated smartphone-based application reliably supports disk diffusion AST interpretation with high agreement to manual reading. By combining digital measurement with user-guided verification, it reduces interpretation time and inter-observer variability. This user-friendly, cost-effective tool offers a high-precision solution that integrates seamlessly into routine workflows, particularly in resource-limited laboratories.

3. Pattern of carbapenemase producing genes in E. coli and Klebsiella pneumoniae isolated in a tertiary care superspeciality hospital of U.P.

Author: Kumari Richa

Introduction: The emergence of carbapenem resistance in Enterobacteriaceae particularly E. coli and Klebsiella pneumoniae is a growing public health concern worldwide because of their increasing prevalence, multidrug resistance profile and rapid dissemination of resistance to other organisms. CDC and WHO has categorized carbapenem resistant Enterobacteriaceae (CRE) as “critical priority pathogens” requiring urgent attention. One major cause is the production of carbapenem hydrolyzing carbapenemase enzymes, which are highly transmissible. This study is planned to assess the molecular characteristics and pattern of genes causing carbapenem resistance in clinical isolates of E. coli and Klebsiella pneumoniae.

Materials & Methods: A single centric prospective study in 227 culture isolates of E. coli and Klebsiella pneumoniae showing carbapenem resistance detected by Vitek2 automated system. The isolates were analyzed by open system real-time PCR assay (3B Black Bio Biotech) using carbapenem resistance detection kit for detection of blaKPC, blaIMP, blaNDM, blaOXA-48 & blaVIM.

Results: Only NDM was found in 6.2% & only OXA-48 in 5.7% but these two coexist in 79.7% isolates, either exclusively together or along with other genes like VIM or IMP or both; whereas none of the isolates had KPC gene. 8.4% cases were negative for any carbapenemase genes suggesting some other mechanism of resistance.

Conclusion: The increasing resistance with co-occurrence of metallo-beta-lactamase and class D beta-lactamase is a major concern due to limited therapeutic options, necessitating urgent need for surveillance, isolation protocols, antibiotic stewardship practices and utilization of molecular assay in large scale for early detection & trend analysis.



Abstracts of Invited Speakers

AI in Clinical Microbiology: Transforming Diagnostics and Laboratory Practice

Dr. Vikas Manchanda

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Artificial intelligence (AI) and machine learning (ML) are revolutionizing clinical microbiology by enhancing diagnostic accuracy, significantly reducing turnaround times (TAT), and optimizing workflows in clinical laboratories.

AI-enhanced MALDI-TOF mass spectrometry achieves over 95% accuracy in organism identification along with reducing TAT to few minutes. Direct antimicrobial resistance (AMR) prediction using mass spectra achieves over 93% accuracy with results available in 2-3 hours. Deep Colony and automated plate reading systems demonstrate > 99% agreement with manual interpretation. Negative culture automated release reduces TAT by 75% (24-48 hours to 4-6 hours) enabling earlier clinical decision-making.

Integration of AI with laboratory automation achieves significant operational gains. When implemented, it has led to 43% reduction in plate handling time per specimen, 52% reduction in specimen "touches," enhancing biosafety and reducing errors, 60% faster organism identification and AST reporting and 60% reduction in technologist biosafety exposure.

Machine learning enables integration of clinical data, laboratory biomarkers, imaging, and genomic information for disease-specific diagnosis. Multi-omics approaches integrate bacterial, fungal, and viral profiles simultaneously, enabling personalized antimicrobial stewardship.

Emerging technologies include culture-free rapid pathogen detection, point-of-care integrated devices, real-time genomic analysis during diagnostic tests, and AI-guided outbreak prediction. Clinical virology is being transformed through deep learning for viral inclusion detection, rapid identification, and antiviral resistance prediction.

Successful AI integration requires validated applications, comprehensive staff training, regulatory compliance, and continuous quality assurance. The augmented microbiology laboratory represents the future - AI handles routine cases while expert microbiologists focus on complex diagnostics, ensuring enhanced accuracy and improved patient outcomes through targeted, evidence-based therapy. Thus, future of clinical microbiologists with AI is bright and more relevant than ever before.

Integrated Diagnostic and Antibiotic Stewardship approach in ICU patients

Dr. Jyotsna Agarwal

Professor & HOD

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Integrated diagnostic and antibiotic stewardship is a multidisciplinary approach that combines correct diagnostic strategies with appropriate antibiotic therapy to optimize patient care and reduce antibiotic resistance. The Intensive Care Unit (ICU) is a high-risk environment where patients are more susceptible to infections, and antibiotic resistance is a growing concern along with all the other co-morbidities that patient might have.

What does Integrated Diagnostic and Antibiotic Stewardship approach include: 1. Rapid and accurate diagnostics: Utilizing appropriate and where possible advanced diagnostic tools, such as molecular tests and biomarkers, to quickly and correctly identify the cause of infection. 2. Antimicrobial stewardship: Implementing evidence-based guidelines for antibiotic use, including selection, dosing, and duration of therapy. 3. Collaboration and communication: Fostering a team-based approach among clinicians, microbiologists, pharmacists, and infection control specialists to ensure optimal patient care.

Why is it needed in the ICU: 1. To reduce antibiotic resistance: Overuse and misuse of antibiotics contribute to selection pressure and emergence of resistant in bacteria. 2. Better patient outcomes: Timely and targeted antibiotic therapy can reduce morbidity, mortality, and length of stay. 3. Minimize adverse events: Antibiotic-related adverse events, such as *Clostridioides difficile* infection, can be reduced. 4. Optimize resource utilization: reduce healthcare costs in treatment and diagnostics.

I will be discussing it further as case-based approach to emphasize on role of integrated diagnostic and antibiotic stewardship. This approach requires a multidisciplinary effort, education, and a commitment to quality improvement.

Role of Syndromic Multiplex RT-PCR in Diagnostic Virology.

Dr. Atul Garg

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Syndromic multiplex reverse transcription polymerase chain reaction (RT-PCR) has become a cornerstone of modern diagnostic virology, offering rapid, sensitive, and simultaneous detection of multiple viral pathogens associated with a common clinical syndrome. Traditional diagnostic approaches based on viral culture, serology or single-plex molecular assays are often time-consuming and limited in scope, particularly in clinical settings where several viral agents may present with overlapping symptoms. Syndromic multiplex RT-PCR overcomes these limitations by integrating numerous pathogen-specific targets into a single assay, enabling comprehensive etiological diagnosis from a single clinical specimen.

In clinical virology, syndromic panels are most widely applied in respiratory tract infections, Tropical fever, gastrointestinal illness and central nervous system infections. Multiple studies have demonstrated that multiplex RT-PCR panels exhibit high analytical sensitivity and specificity, often exceeding 90% for common respiratory viruses such as influenza A/B, respiratory syncytial virus, rhinovirus, and endemic human coronaviruses¹⁻². The ability to detect viral co-infections, which may influence disease severity and clinical outcomes, represents a significant advantage over conventional diagnostic strategies³. During the COVID-19 pandemic, syndromic respiratory panels played a critical role in differentiating SARS-CoV-2 infection from other viral respiratory illnesses, supporting patient triage and infection control practices⁴.

Beyond diagnostic accuracy, syndromic multiplex RT-PCR has a measurable impact on patient management and antimicrobial stewardship. Rapid identification of viral aetiologies has been associated with reduced unnecessary antibiotic use, shorter hospital stays, and earlier implementation of appropriate isolation measures^{5,6}.

Despite its advantages, syndromic multiplex RT-PCR is not without limitations. Fixed panel design restricts detection to predefined pathogens, and positive results do not necessarily indicate active disease. Additionally, higher costs and lack of antimicrobial susceptibility data for bacterial targets necessitate judicious use within well-defined clinical algorithms². Nevertheless, ongoing technological advancements, including expanded panels, point-of-care platforms, and integration with digital surveillance systems, continue to enhance the clinical utility of syndromic testing.

In conclusion, syndromic multiplex RT-PCR represents a paradigm shift in diagnostic virology, providing rapid, comprehensive, and clinically actionable results. When applied appropriately, it significantly improves diagnostic yield, optimizes patient management, and supports antimicrobial stewardship, reinforcing its growing role in contemporary clinical and public health virology.

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Stop Neglecting Fungi

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Among the four disciplines under microbiology, fungus is considered human friendly, as it plays substantial role in food production, bioremediation, sustainability of products, medicine development and in industry¹. The same fungus, which feeds us, heals us and reveals the secret of universe, has become global threat for human, animal, plant and ecosystem in recent years. It comprises of the highest threat of extinction of 72% animal and 64% plant species². In human it has rapidly evolved as a formidable challenge due to growing number of cases, new species emerges causing infection, outbreaks and epidemic in recent years. At the same time diagnosis and management of invasive fungal infections are difficult. The journal 'Nature Microbiology' in its editorial on July 25, 2017 cautioned as 'Stop neglecting fungi'³. WHO mentioned 'despite posing growing threat to human health, fungal infections receive very little attention and resources globally' and they identified 19 fungal pathogens as priority agents⁴. The recent global outbreaks due to antifungal resistant *Candida auris* and COVID-19 associated mucormycosis have caused panic in population at large^{5, 6}. The recent pandemic due to drug resistant *Trichophyton indotineae* has baffled the dermatologists⁷. Humans are now facing the challenge of rapid rise and change in epidemiology of fungal diseases. In the world over a million eyes go blind due to fungal keratitis, nearly a billion people have fungal infections of skin, 6.5 million suffer from invasive fungal infections annually and around 3.8 million die due to fungal infections, which is more than malaria and tuberculosis death toll^{3, 8}. India is contributing 30% of those global candidemia cases, 12% of invasive aspergillosis and 92% mucormycosis cases⁹. It was believed that invasive fungal infections (IFIs) occur only in immunosuppressed hosts. Presently, change is noted in all three determinants (host, agent, and environment) of epidemiology. New susceptible hosts (patients with chronic obstructive lung disease, liver and renal disease, respiratory viral infections, diabetes, tuberculosis etc.), new agents (*C. auris*, *C. vulturna*, *C. blankii*, *C. africana*, *C. viswanathii*, *Emergomyces* spp., *Blastomyces helicus*, *Rhizopus homothallicus* etc.) and natural disasters in environment play important role in this formidable global challenge of fungal infections^{1, 8}. The challenge is more acute in developing countries due to tropical environment where fungi thrive easily, compromise in healthcare, misuse and abuse of antibiotics and steroids. The challenge is difficult to handle in this country due to lack of awareness among healthcare workers, limited number of diagnostic mycology laboratories, and poor affordability for expensive diagnostics and antifungal drugs among patients. A sustained advocacy with the slogan 'Stop neglecting fungi' is seriously needed to draw the attention of administrator, funding agencies and public at large.

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Effective Hand Hygiene: Adherence to Guidelines for Hand Hygiene in Health-Care Settings

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Hand hygiene is the primary measure which has been proven to be effective in preventing Health Care Associated Infection (HAIs) and preventing spread of antimicrobial resistance. Contaminated hands are the commonest route of transmission of HAIs. On comparing alcohol based handrub (ABHR) use versus handwashing, it has been observed that overall compliance of ABHR is better than handwashing except against soiled hands as well as against *C. difficile*. Surgical hand scrubbing is performed with scrubbing agents and alcohol-based antiseptic agents to inhibit the growth of residual microorganisms. In Europe, the in-vivo efficacy of products for surgical hand disinfection is tested -European Standard EN 12791 in comparison with that of a standardized reference disinfection procedure in which 60% v/v propan-1-ol is applied for 3 min. As per CDC guidelines in 2002, for routine hand hygiene- alcohol based hand rub (ABHR) -containing either isopropyl alcohol, ethanol or a combination of both, in concentrations between 65% and 95% is recommended. For surgical antisepsis-ABHR with 0.5%-1% chlorhexidine gluconate is recommended for Persistent activity while for Maximum Persistent activity 2%-4% chlorhexidine gluconate formulations are recommended. Recent research using EN 1500 (hygienic hand disinfection) it has been observed that most alcohol-based hand gels are significantly less effective than the reference alcohol (2-propanol 60%). Chlorhexidine too has limitations being- pH dependent, reduced in the presence of organic matter, unable to penetrate biofilm, residual activity of chlorhexidine gluconate on hands being destroyed by using an anionic soap which neutralizes residual chlorhexidine gluconate and having no sporicidal activity. Propanol-based product has been found to be significantly more effective against routine test organisms than ethanol-based product in quantitative suspension tests. Mecertronium ethylsulfate (MES) is a detergent and belongs to the group of surface-active ingredients. MES along with propan-2-ol and propan-1-ol is an ingredient of rub-in hand disinfectants. European standards certifying microbiological efficacy of hand hygiene are as follows- EN13727 (Bactericidal), EN14348 (Mycobactericidal), EN13624 (*Candida albicans*), Virucidal (> 4 log reduction in viruses within 5 min(surface) at temperature 4-30°C in clean/dirty conditions), EN14476, EN 1500 (hygienic hand disinfection); EN 12791(surgical hand disinfection); certificates of ISO 9001 : 2015 :QMS; ISO 13485 : 2016 :QMS-Medical devices/related services; WHO-GMP/GMP for safe and efficient health care Biocidal product ,CE Certified in accordance to Medical Devices Directive-93/42/EEC & Biocidal Products Directive -98/8/EC. The presentation cited a study entitled "Effectiveness of Alcohol-based Solution for Hand Hygiene" by Yanamandra Sushma conducted at BJMC, Pune in which healthcare workers' fingerprints were taken before and after using ABHR-(Zuvagard16 Hand Rub containing 2-Propanol I.P 45% w/w, 1-Propanol - 30% w/w, Mecertronium Ethylsulphate-0.2 % w/w., Zuverlasse Hygiene India Pvt. Ltd., India) .It was cultured on blood agar plates and Significant reduction in bacterial colony counts was observed post-ABHR use.

Conventional Parasitological Diagnosis: Scope & Limitations

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Parasitic infections affect nearly one fourth of the world's population, exert a substantial toll on public health, yet are often overlooked, particularly in tropical and subtropical regions. Of the 20 Neglected Tropical Diseases listed by the World Health Organization, more than 50% are parasitic infections. In the context of increasing global risk of parasitic diseases, accurate and timely diagnosis is critical for effective treatment, disease control, and improved patient outcomes. Reliable diagnostic strategies enable appropriate therapy, help limit the emergence of drug resistance, and support surveillance programmes, thereby playing a pivotal role in reducing the overall burden of parasitic diseases.

Microscopy enables direct visualization of the parasites that were previously invisible to the naked eye. Earlier, parasitic diseases were poorly understood, with clinical manifestations often attributed to supernatural causes or imbalances in bodily humors. Microscopy provided the scientific foundation for identifying parasites as etiological agents of disease, fundamentally altering diagnostic and therapeutic approaches.

Early parasitological studies relied on simple microscopes, allowed observation of relatively large parasites and their basic morphological features. These instruments typically provided magnification in the range of 10X to 40X, sufficient to demonstrate the general form and external characteristics of protozoa, helminths, and arthropods. However, their limited resolving power restricted visualization of finer internal structures. Despite these limitations, simple light microscopy laid the groundwork for the systematic classification of parasites and facilitated the early understanding of their morphology and life cycles.

Over time, light microscopy became the cornerstone of routine parasitological diagnosis and remains widely used, particularly in resource-limited settings. It is extensively employed for the examination of stool, blood, and other clinical specimens, provided personnel are adequately trained. In stool microscopy, staining plays a crucial role in differentiating parasites from background debris. Both fresh and preserved specimens are examined using a variety of mounts and stains. Blood parasites are routinely identified using Giemsa or Wright's stain. Giemsa staining requires prior fixation with absolute methanol, and thick blood films often necessitate dehemoglobinization to enhance parasite visualization.

In stool, alternative mount techniques have also been evaluated to improve routine diagnostic yield. Studies by Parija and Prabhakar demonstrated the effectiveness of lactophenol cotton blue (LPCB) staining for wet mount preparation of stool samples. LPCB was shown to clearly highlight trophozoites, cysts, and helminthic ova, facilitating easy detection and identification through routine microscopy. Based on these findings, LPCB was recommended for routine use in parasitology laboratories. Microscopic techniques are recently combined with artificial intelligence which improves the diagnostic yield and reduces the requirement of expert microscopist.

Nevertheless, conventional stool microscopy has inherent limitations. Sensitivity is often low, requiring examination of multiple serial samples and a high level of technical expertise. Now serological and molecular tests are available which will complement microscopy technique in parasitological diagnosis.

In summary, conventional microscopy—particularly light microscopy—remains a fundamental tool in parasitology. Despite advances in molecular and imaging technologies, it continues to play a vital role in diagnosis, education, and research, especially in endemic and resource-constrained regions. Its historical significance, practical utility, and adaptability ensure its continued relevance in the evolving landscape of parasitic disease investigation.

Automation in Parasitology : AI-Based Platforms and Multiplex PCR

Dr. Areena Hoda Siddiqui

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Parasitic infections pose a significant challenge worldwide. Their prevalence is more in tropical and subtropical regions. Around 25% of the global population suffer from one or more parasitic infections, of which food- and vector-borne parasitic zoonotic diseases are a major concern. Out of 20 neglected tropical diseases (NTDs) listed by the World Health Organization (WHO) and the Centres for Disease Control and Prevention (CDC), 13 diseases are of parasitic origin.

Timely and appropriate diagnosis of these parasitic infections is very critical for early treatment and prevention of transmission of infection. Consequently the patients suffer from malnutrition anemia and various other health issues. The routine diagnostic methods include Microscopy, staining techniques, antigen antibody detection, RDT. These were associated with limitations which include low sensitivity, cross reactivity, trained personnel.

With the advent of automated methods the field of parasitic diagnostics, it has gone by leaps and bounds. These include polymerase chain reaction (PCR), multiplex assays, and next-generation sequencing with improve sensitivity and specificity in detecting parasites. These methods are beneficial in identifying mixed infections with syndromic approach. Techniques such as PCR and LAMP are pivotal in areas where RDTs fail due to genetic deletions in the parasite. The challenges to molecular diagnosis include infrastructure and cost, standardisation, trained staff. Newer technology in the field of multiplex PCR is also available where closed-system, cartridge-based platform automates nucleic acid extraction, amplification, and detection with minimum hands on and less turn around time.

In the era of automation AI has taken lead . With the application of AI, the detection and classification of parasites from microscopic images has become easy . It has reduced human error and detection time, leading to improved patient outcomes. Few examples include YOLOV5, DAPI, Mispa F60. Available literature suggest that these AI methods have better sensitivity when compared to manual microscopy and have also detected missed parasites. These AI methods are scalable to remote/endemic areas and can aid in achieving NTD goals 2030.

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2	Dr. Malvika Himalayan Institute of Medical Sciences, Jolly Grant, Dehradun.	Comparative Analysis of Antimicrobial Resistance Trends in Neonatal Sepsis: A Two-Year Retrospective Study (2024–2025).
3	Dr. Shweta Singh AIIMS, Raebareli, U.P.	Genomic analysis and formulation of a cost-effective combination method for early detection of CRE isolates at a tertiary level set up of North India.
4	Dr. Ashish Kumar Sarojini Naidu Medical College, Agra.	Enhancing the Diagnostic Accuracy of Human Brucellosis Using a Combined Serological Approach.
5	Dr. Ishleen Pahwa Kasturba Medical College, Manipal.	Bloodstream Infections in Surgical Inpatients: Aetiology, Laboratory Predictors, Source Concordance, and Clinical Outcomes.
6	Dr. Mukesh Singh Rohilkhand Medical College, Bareilly, U.P.	<i>Chryseobacterium indologenes</i> infection in newborn: A case report.
7	Dr. Reena Yadav KGMU, Lucknow.	Etiology of atypical pathogens in adult community-acquired pneumonia: interim findings from an ongoing observational study.
8	Dr. Jasmin Kaur, GMCH Chandigarh.	PCR – Based Clinico-microbiological Analysis of Bacterial and Viral Sexually transmitted infections.
9	Dr. Ishan Singh Hind Institute of Medical Sciences, Mau, Ataria, Sitapur.	Prevalence of <i>mecA</i> & <i>mecC</i> Gene in Methicillin Resistant <i>Staphylococcus aureus</i> (MRSA) Isolated from Various Clinical Sample from Patients of a Tertiary Care Hospital.
10	Somya Shukla Santosh Medical College, Ghaziabad.	Characterisation of uropathogenic <i>E.coli</i> by detecting virulence factors and its drug resistance pattern in tertiary care hospital.
11	Dr. Kartikeya Dixit GIMS, Greater Noida.	Bacterial Profile and Antibiogram of Various Clinical Samples at a Tertiary Care Hospital in Greater Noida, Uttar Pradesh.
12	Dr. Abhipsa Pal Department of Microbiology, IMS, BHU, Varanasi, India.	Importance of clinical correlation in ‘Resistance to all applied antibiotics’ culture reports: A pre-interventional analysis.
13	Urvashi Kumari RMLIMS, Lucknow.	Detection of Amp C β -Lactamase Production in Uropathogenic <i>Escherichia coli</i> .
14	Dr. Nidhi Rana Government Doon Medical College, Dehradun, Uttarakhand.	Clinical and microbiological profiling of skin and soft tissue infections in diabetic patients at a tertiary care centre in Dehradun, Uttarakhand.
15	Aditya Singh Dr. Ram Manohar Lohia Institute of Medical Sciences, Lucknow.	Comparative Evaluation of Colistin Susceptibility Testing Methods in Carbapenem-Resistant <i>Pseudomonas aeruginosa</i> : A Validation of Alternative Methodologies.
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18	Dr. Tanya Pandey Autonomous state medical college, Auraiya.	Comparative Analysis of Procalcitonin and C-Reactive Protein in Bloodstream Infections Among Febrile Neutropenic Pediatric Cancer Patients.
19	Prachi Paul Institute of Medical Sciences, BHU.	Nested PCR vs Real-time PCR for detection of <i>Orientia tsutsugamushi</i> among Suspected cases of Scrub Typhus from Eastern Uttar Pradesh, India.
20	Dr. Nidhi Bhatnagar Hind Institute of Medical Sciences, Safedabad, Uttar Pradesh.	Epidemiology of multidrug resistant uropathogens over three years period at a tertiary care centre: a retrospective observational study.
21	Dr. Pratibha Rathaur Hind Institute of Medical Sciences, Safedabad, Uttar Pradesh.	Detection of <i>Neisseria Gonorrhoeae</i> and <i>Chlamydia Trachomatis</i> by Nucleic acid amplification test in Genitourinary samples of Females in Reproduction Age Attending Obstetrics and Gynaecology OPD at a Tertiary Care Hospital.
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27	Dr. Kirti Yadav Shri Ram Murti Smarak Institute of Medical Sciences, Bareilly.	A study on bacteriological profile and its correlation with CRP in neonatal sepsis in tertiary teaching hospital.
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Bacteriology Abstracts

1. Molecular Characterization of *Enterobacteriales* in a Tertiary Care Hospital, Eastern Uttar Pradesh

Author: Dr. Satyendra Chaudhary

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Introduction: Antimicrobial resistance among Enterobacteriales has emerged as a major global and national public health concern, particularly in tertiary care hospitals. The rapid spread of extended-spectrum β -lactamase and carbapenemase-producing strains, mediated by transferable genetic elements, has significantly limited therapeutic options. Molecular characterization of resistance genes is essential for understanding resistance mechanisms, monitoring local epidemiology, and guiding effective antimicrobial stewardship and infection control strategies.

Objectives: To determine the mechanisms of carbapenem resistance in clinical isolates of enterobacteriaceae by phenotypic and molecular methods.

To determine the risk factors associated with carbapenem resistance.

To compare the outcome of patients harbouring carbapenem resistant isolates

Materials & Methods: A hospital-based cross-sectional study was conducted in a tertiary care hospital of Eastern Uttar Pradesh. Non-duplicate Enterobacteriales isolates from various clinical specimens were identified by standard microbiological methods. Antimicrobial susceptibility testing was performed using the Kirby–Bauer disc diffusion method as per CLSI guidelines. Molecular characterization of resistance genes using polymerase chain reaction.

Results: This study highlights a high burden of carbapenem-resistant Enterobacteriaceae (22.31%) in a tertiary care hospital in Eastern Uttar Pradesh. *Escherichia coli* and *Klebsiella pneumoniae* were the predominant CRE pathogens. Among CRE isolates, bla NDM was the most prevalent carbapenemase gene, detected in all isolates. Bla VIM was identified in 17.10% isolates, while blaOXA-23 and blaOXA-48 were found in 6.57% and 2.63% isolates, respectively. Important risk factors identified for CRE acquisition included prolonged hospital stay, prior antibiotic exposure, ICU admission, diabetes mellitus, and the presence of indwelling medical devices. Clinical outcomes were significantly better when definitive therapy was guided by susceptibility testing, indicating the importance of rapid diagnostics and appropriate combination-based treatment strategies.

Conclusion: Our findings demonstrate a significant burden of genetically mediated antimicrobial resistance among Enterobacteriales in a tertiary care setting. Molecular characterization enabled precise identification of resistance mechanisms beyond routine phenotypic methods, highlighting its critical role in early detection, targeted therapy, and prevention of the spread of multidrug-resistant organisms. Continuous molecular surveillance is essential to strengthen antimicrobial stewardship and infection control practices.

2. Comparative Analysis of Antimicrobial Resistance Trends in Neonatal Sepsis: A Two-Year Retrospective Study (2024 -2025)

Author: Malvika Singh

Co-Authors: Rajendra Singh, Chinmay Chetan, Garima Mittal, Arpana Singh, Aarti Kotwal

Institute: Himalayan Institute of Medical Sciences, Jollygrant, Dehradun

Introduction: Neonatal sepsis remains a major cause of morbidity and mortality, particularly in low-middle income countries. The growing burden of antimicrobial resistance among neonatal pathogens complicates effective treatment, underscoring the need for continuous surveillance to guide empirical therapy and infection control strategies. The study was conducted to compare the distribution of bacteria and antimicrobial resistance trends in clinically suspected neonatal sepsis over a two-year period and to identify emerging organisms and resistance patterns.

Materials & Methods: Retrospective analysis was performed on culture-positive blood sample from neonates in a tertiary care hospital during 2024 (n = 154) and 2025 (n = 199). Bacterial isolates and antimicrobial susceptibility profiles were compared between two years. Fisher's exact test was used for statistical analysis, $p < 0.05$ considered significant.

Results: A total of 821 and 1,092 blood samples were received from the neonatal intensive care unit in 2024 and 2025, respectively. Culture positivity rates were 18.3% and 19.0%. A significant reduction in coagulase-negative Staphylococci was observed (30.51% to 19.1%, $p = 0.018$). Whereas, *Enterobacter cloacae* increased markedly from 3.24% to 20.1% ($p = 0.001$), indicating its emergence. No significant changes were seen in *Escherichia coli*, *Klebsiella pneumoniae*, *Staphylococcus aureus*, or *Enterococcus* species. Increased resistance in *E. coli* to amoxicillin-clavulanate, piperacillin-tazobactam, and gentamicin, while *E. cloacae* showed multi drug resistance to carbapenems. Reduced resistance to imipenem and colistin was observed in *K. pneumoniae*.

Conclusion: Evolving microbial landscape, particularly emergence of multidrug-resistant *Enterobacter cloacae*, highlights the importance of ongoing surveillance and regular revision of empirical antibiotic policies in NICUs.

3. Genomic analysis and formulation of a cost-effective combination method for early detection of CRE isolates at a tertiary level set up of North India.

Author: Sweta Singh

Co-Authors: Niraj Kumari, Shefali Gupta, Niraj Kumar Srivastava, Kali Charan Das, Manu Sharma

Institute: AIIMS, Raebareli, U.P

Introduction: Carbapenem group of antibiotics are amongst the most effective antibacterial agents for the treatment of multidrug-resistant bacterial infections. Their widespread use has led to the emergence of carbapenem-resistant Enterobacteriaceae (CRE) which has become a serious threat to public health. A variety of methods for the rapid detection of CRE: phenotypic and genotypic have been developed for use in clinical microbiology laboratories.

Materials & Methods: Clinical samples were cultured on routine media and various Phenotypic tests were done for carbapenemase detection; namely Chromogenic media culture, Carbapenemase inhibition method (CIM), Modified CIM (m CIM), Rapid card test. This was followed by Genotypic testing in the form of Real time and Conventional PCR for various Carbapenemase genes. Finally sequencing of the CRE strains for prevalent resistance genes was done.

Results: 1000 positive samples with Enterobacteriaceae growth were studied. Out of which 292 came out positive for CRE; giving the prevalence rates of 28.7%. NDM was the most prevalent gene (87%), followed by OXA (14%). Chromogenic agar, CIM and m CIM showed concordance of results in 87% of the isolates. Rapid card test showed sensitivity of 98% and specificity of 92 % for the CRE isolates. Multiplex Real time as well as conventional PCR showed maximum positivity for NDM genes, which was followed by sequencing of the gene.

Conclusion: Formulating a combination of phenotypic and genotypic tests for early detection of CREs is crucial for every health set-up. Knowledge about the resistance mechanisms responsible for the carbapenem resistance in the particular hospital setting will help to build a strong antibiotic stewardship program. This will help in early detection as well as better patient outcome, in terms of mortality and morbidity.

4. Enhancing the Diagnostic Accuracy of Human Brucellosis Using a Combined Serological Approach

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Co-Authors: Dr. Ankur Goyal, Dr. Vikas Kumar

Institute: Sarojini Naidu Medical College, Agra

Introduction: Human brucellosis is an important yet underdiagnosed zoonotic infection in endemic regions due to its nonspecific clinical presentation and overlap with other febrile illnesses. Serological assays remain the mainstay of diagnosis in resource-limited settings; however, variability in antibody responses and test performance at different stages of disease often leads to diagnostic uncertainty. This study aims to assess the diagnostic utility of a combined serological approach for improved detection of human brucellosis.

Materials& Methods: This prospective cross-sectional study is being conducted at S.N. Medical College, Agra, over a period of three months. A total of 50 patients aged 1–80 years with clinical features suggestive of brucellosis, including undulant fever, arthralgia, and hepatosplenomegaly, are being enrolled. Venous blood samples from all participants will be tested using the Rose Bengal Plate Test (RBPT), Serum Agglutination Test (SAT), and enzyme-linked immunosorbent assay (ELISA) for detection of anti-*Brucella* IgM and IgG antibodies. Patients who have received brucellosis-specific antimicrobial therapy within the preceding four weeks are being excluded.

Results: Preliminary observations indicate that RBPT and SAT serve as effective screening tools, particularly in acute presentations, while ELISA facilitates differentiation between IgM and IgG antibodies, aiding in the interpretation of acute and chronic infections. The combined application of these serological tests is expected to improve overall diagnostic accuracy compared to individual assays.

Conclusion: An integrated serological testing strategy using RBPT, SAT, and ELISA offers a practical and reliable approach for the diagnosis of human brucellosis in endemic and resource-limited settings. This approach has the potential to support early diagnosis, guide appropriate management, and strengthen disease surveillance.

5. Bloodstream Infections in Surgical Inpatients: Aetiology, Laboratory Predictors, Source Concordance, and Clinical Outcomes

Author: Dr. Ishleen Pahwa

Co-Authors: Dr. Vandana K.E, Dr. Dinesh B.V

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Introduction: Bloodstream infections (BSIs) cause significant morbidity and mortality among surgical inpatients and present diagnostic challenges due to variable clinical features. Early recognition using laboratory predictors and assessing concordance between bloodstream isolates and suspected anatomical sources are important. Data from tertiary-care centers in India remain limited. This study evaluated BSI etiology, laboratory predictors, bloodstream- source concordance, antimicrobial susceptibility, and clinical outcomes in adult surgical inpatients.

Materials & Methods: In this prospective study (May 2023- May 2024), adult surgical inpatients with suspected BSI were enrolled. Blood cultures were collected before initiation or escalation of therapy. Pathogens were identified using MALDI-TOF, and susceptibility testing was performed using VITEK-2 per CLSI guidelines. Samples from suspected sources were obtained when feasible. Independent predictors of bacteremia were identified using multivariate logistic regression.

Results: Of 199 patients, 39 (19.6%) had confirmed BSIs. Gram-negative bacilli predominated (82%), mainly *Escherichia coli* (28.2%) and *Klebsiella pneumoniae* (25.6%). Source concordance was seen in 64.1%, mostly from surgical drains and wound exudates. BSI-positive patients had higher ICU admissions (66.6% vs. 6.9%; $p<0.001$) and prolonged hospitalization (>10 days; $p=0.009$). Elevated procalcitonin (AOR 1.15; 95% CI 1.05-1.26; $p=0.002$) and hypoalbuminemia (AOR 1.88; 95% CI 1.23-2.87; $p=0.003$) predicted bacteremia. Carbapenem resistance occurred in 80% of *K. pneumoniae*; *Acinetobacter baumannii* and *Pseudomonas aeruginosa* were extensively drug-resistant. Mortality was 35.8%, with 71.4% of deaths in patients with multidrug or extensively drug-resistant organisms.

Conclusion: BSIs show substantial bloodstream- source concordance, highlighting targeted sampling. Laboratory predictors enable early risk stratification, while antimicrobial susceptibility guides empirical therapy decisions.

6. *Chryseobacterium indologenes* infection in newborn: A case report

Author: Dr. Mukesh Singh

Institute: ROHILKHAND MEDICAL COLLEGE BAREILLY UP

Introduction: *Chryseobacterium indologenes* is an aerobic, non-motile, Gram-negative bacilli, non-lactose fermenting bacteria. It is widely distributed in hospital environment and is an emerging nosocomial pathogen which is inherently resistant to wide range of antibiotics. It has been identified as the causative agent of bacteremia, pneumonia and indwelling device associated infections and resulting in high mortality. A few number of *C. indologenes* cases have been reported from India. In this report, we describe a rare case of meningitis due to *C. indologenes* in a preterm neonate.

Case report: (Materials and Methods & Result): A preterm neonate was referred to NICU of our hospital with severe respiratory distress and shock. Baby was put on ventilator support and inotropic drugs. Baby had episodes of seizure and CSF sample was sent to Microbiology lab for culture and sensitivity. Culture showed growth of yellow pigmented beta hemolytic colonies. Isolate was identified as *Chryseobacterium indologenes* by using standard biochemical tests and BD Phoenix automated system. Antimicrobial susceptibility testing showed susceptibility only to fluoroquinolones and co-trimoxazole. On the basis of susceptibility report, co-trimoxazole was started and neonate showed substantial improvement and was discharged within 10 days.

Conclusion: *C. indologenes* is a rare causative agent of hospital acquired infections causing neonatal sepsis and meningitis in neonates with indwelling invasive devices. The management of this infection requires strict vigilance and prompt diagnosis to prevent mortality in newborns. Moreover, transmission of this nosocomial pathogen can be curtailed by effective infection control practices and environmental surveillance.

7. Etiology of atypical pathogens in adult community-acquired pneumonia: interim findings from an ongoing observational study

Author: Dr. Reena Yadav

Co-Authors: Prof. Prashant Gupta, Prof. Vimala Venkatesh, Prof. RK Kalyan, Dr. Sheetal Verma, Dr. Anand Srivastav

Institute: King George's medical college

Introduction: Community-acquired pneumonia (CAP) is a major cause of morbidity among adults. Atypical pathogens such as *Chlamydia pneumoniae*, *Mycoplasma pneumoniae*, and *Legionella pneumophila* contribute significantly to CAP but are often underdiagnosed due to nonspecific clinical features and limitations of conventional diagnostic methods. Molecular assays, particularly in-house multiplex real-time PCR, enable rapid and sensitive detection of these organisms. This ongoing study aims to evaluate the etiological role of atypical pathogens in adult CAP using molecular diagnostic techniques.

Material & methods: This ongoing observational study is being conducted at tertiary care center and includes 137 adult patients clinically and radiologically diagnosed with CAP. Urine antigen testing for *Legionella pneumophila* was performed in 75 patients using an immunochromatographic assay. Respiratory samples from 29 patients were tested by in-house multiplex real-time PCR for detection of *Chlamydia pneumoniae*, *Mycoplasma pneumoniae*, and *Legionella pneumophila*. The study was approved by the Institutional Ethics Committee, and informed consent was obtained from all participants.

Results: All 75 urine samples tested negative for *Legionella pneumophila* antigen. Among 29 respiratory samples tested by multiplex PCR, atypical pathogens were detected in 7 cases (24.1%). *Legionella pneumophila* was identified in 5 samples (17.2%), while *Chlamydia pneumoniae* was detected in 2 samples (6.9%). All samples were negative for *Mycoplasma pneumoniae*.

Conclusion: Interim findings of this ongoing study suggest notable presence of atypical pathogens, particularly *Legionella pneumophila* and *Chlamydia pneumoniae*, among adult CAP patients. In-house multiplex real-time PCR appears to enhance etiological detection in tested subset. Completion of study will help define true burden of atypical pathogens in adult community-acquired pneumonia.

8. PCR – Based Clinico-microbiological Analysis of Bacterial and Viral Sexually transmitted infections

Author: Kaur J

Co-Authors: Gupta V, Goel B

Institute: GMCH CHANDIGARH

Introduction: STI caused by bacteria and Viruses are a major public health concern. Conventional diagnostic methods have limited sensitivity and longer turnaround times. The DIAGSure STI PCR Kit enables rapid, sensitive detection of these pathogens. His study evaluates the Clinico-microbiological profile of STIs and correlates PCR findings with clinical presentation

Materials & Methods: A Prospective cross-sectional study was conducted on 50 Clinical specimens from adults suspected of STIs between April 2024 to June 2025. Blood, urogenital swabs and wart tissue was analyzed using the DIAGSure STI PCR Kit for simultaneous detection of bacterial and viral STI pathogens. PCR results were correlated with clinical findings to perform a clinic-microbiological analysis.

Results: Among 50 clinical specimens analyzed by PCR, 14 were Positive for at least one STI Pathogen. *Neisseria gonorrhoeae* was positive in 3 samples, *Chlamydia Trachomatis* 1sample and none were Positive for *Mycoplasma genitalium* and *Treponema pallidum*. In Viral panel, HSV-1 was positive in 4 samples, HSV 2 in 1 sample, HPV -16 In 6 samples and HPV-18 in 4 samples. All PCR positive cases showed clinically significant pathogen loads associated with symptoms.

Conclusion: PCR based molecular diagnosis proved to be reliable and sensitive method for the detection of viral and bacterial STIs. The standardized PCR assay demonstrated consistent performance across the study period, enabling accurate identification of STI pathogens.

9. Prevalence Of *mecA* & *mecC* Gene in Methicillin Resistant *Staphylococcus aureus* (MRSA) Isolated from Various Clinical Sample from Patients of a Tertiary Care Hospital

Author: Dr. Ishan Sing

Co-Authors: Dr. Razia Khatoon, Dr. Divakar Srivastava, Dr. Mohd Shahid Khan

Institute: Hind Institute of Medical Sciences, Mau, Ataria, Sitapur

Introduction: MRSA is a major cause of hospital and community-acquired infections, presenting significant therapeutic challenges due to its multidrug resistance. Continuous surveillance of antimicrobial susceptibility patterns and resistance mechanisms is essential for effective patient management and infection control.

Materials & Methods: This prospective observational study analyzed 87 non-duplicate *Staphylococcus aureus* isolates recovered from clinical specimens collected between 2024 and 2025 at a tertiary care hospital. AST was performed using the Kirby–Bauer disc diffusion method in accordance with CLSI guidelines. Methicillin resistance was determined by cefoxitin disc testing, and the presence of *mecA* and *mecC* genes was confirmed by molecular detection.

Results: All isolates were confirmed as MRSA, showing 100% resistance to penicillin and cefoxitin (100%). High resistance was observed to ciprofloxacin (85.1%), levofloxacin (83.9%), erythromycin (81.6%), azithromycin (79.3%), moxifloxacin (80.5%), and clindamycin (77%). Moderate susceptibility was noted for gentamicin (59.8%), tetracycline (56.3%), doxycycline (62.1%), and trimethoprim–sulfamethoxazole (66.7%), while vancomycin and linezolid showed complete susceptibility (100%). The *mecA* gene was detected in (86.2%), *mecC* in (5.7%), and *mecA* and *mecC* in (2.3%). A female predominance was observed for *mecA* (69.3%), and the highest departmental contributions were from ENT (32%) and Obstetrics (28%). Pus samples were the most common source (60%), followed by high vaginal swabs (13.3%) and respiratory samples (10.7%), indicating skin and soft tissue infections as the primary clinical presentation.

Conclusion: The study reveals a high burden of multidrug-resistant MRSA, with preserved susceptibility to vancomycin and linezolid, underscoring the need for sustained antimicrobial surveillance and strict infection control measures.

10. Characterisation of uropathogenic E. coli by detecting virulence factor and drug resistance pattern in tertiary care hospital

Author: Somya Shukla

Institute: Santosh medical college, Ghaziabad

Introduction: E. coli is the most common pathogen identified from urinary tract infections (UTIs), which are among the most common nosocomial and community-acquired bacterial illnesses in people. The idea that UPEC is associated with urinary pathogenicity is further supported by the presence of virulence factors in UPEC strains, including as biofilm formation, ESBL production, and hemolysin

Materials & Methods: Study period-between June 2025-november 2025

Study design – cross sectional

Study population-160 urinary isolates Method of analysis;

Detection of biofilm by congo red agar

ESBL testing by double disc synergy test

Haemolysis to be seen on blood agar

Antibiotic sensitivity testing by Kirby bauer disc diffusion method

Results: 160 E. coli from urinary isolates were collected from patients of urinary tract infection out of which 84 (52%) showed biofilm production. ESBL were seen in 77 isolates i.e 48%. Also haemolysin were in 38 isolates i.e 23%. Most isolates obtained were resistant to beta-lactam antibiotics but showed high sensitivity towards antibiotic like chloramphenicol, meropenem, amikacin, imipenem and nitrofurantoin.

Conclusion: The common virulence factors associated with UTI were ESBL producers, haemolysin production, biofilm production. Because of the emerging drug resistance among UPEC, therapy should be advocated as far as possible after obtaining the culture and sensitivity results to determine exact aetiology and susceptibility patterns.

11. Bacterial Profile and Antibigram of Various Clinical Samples at a Tertiary Care Hospital in Greater Noida, Uttar Pradesh

Author: Kartikeya Dixit

Co-Authors: Harmesh Manocha, Ajay Kumar Sahni

Institute: GIMS, Greater Noida

Introduction: Present study determines the bacterial profile and antibiogram of bacteria isolated from various clinical samples of patients visiting Tertiary Care Hospital, Greater Noida, Uttar Pradesh.

Materials & Methods: A retrospective cross-sectional study was carried out in the Department of Microbiology of a Tertiary Care Hospital in Greater Noida, Uttar Pradesh. Various clinical samples such as blood, urine, pus, sputum and other samples received during the study period May 2025 to October 2025 (6 Months) were processed as per standard microbiological procedures. Organism identification and antimicrobial susceptibility testing were performed by conventional as well as VITEK 2 compact automated system. Antimicrobial susceptibility patterns were interpreted and cumulative antibiogram was prepared as per CLSI guidelines.

Results: A total of 1,135 culture-positive samples were included in the study, comprising of 604 body fluid samples (pus and sputum), 366 urine samples, 152 blood samples, and rest 13 samples including stool, ear swab, and cerebrospinal fluid (CSF). Among the 1,134 culture-positive isolates, the predominant Gram-negative bacteria were *Escherichia coli* (41.97%), *Klebsiella pneumoniae* (14.99%), *Pseudomonas aeruginosa* (9.78%), and *Acinetobacter baumannii* (6.79%). The major Gram-positive isolates included *Staphylococcus aureus* (2.82%), coagulase-negative staphylococci (CoNS) (2.11%), *Enterococcus faecium* (1.32%), and *Enterococcus faecalis* (1.05%). In body fluid samples (pus and sputum), *Escherichia coli* followed by *Klebsiella pneumoniae* were the predominant isolates. In urine samples, *Escherichia coli* whereas in blood samples, *Klebsiella pneumoniae* was the dominant isolate.

Conclusion: The cumulative antibiogram indicated that Gentamicin and Amikacin had the highest susceptibility rates, Rifaximin demonstrated moderate susceptibility, whereas Ampicillin showed the lowest susceptibility among the tested antimicrobials.

12. Importance of clinical correlation in ‘Resistance to all applied antibiotics’ culture reports: A pre-interventional analysis

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Introduction: With escalation in antimicrobial resistance, the clinical microbiological laboratory is often challenged with reports of organisms ‘Resistant to all applied antibiotics’ (RAA). This is seen commonly with multidrug-resistant priority pathogens. However, several factors contribute.

Objective: To analyse the factors of RAA (pre-intervention) with emphasis on differentiation of colonization from infection.

Materials & Methods: This was a cross-sectional study. A total of 150 cases of RAA reports were traced from laboratory to hospital from August to November 2025. Cases were analysed based on sample selection, quality, method of collection, indication for culture, type and susceptibility of organisms.

Results: Of the total, 74 (49.3%) were pus, swabs 75.6% (56) and aspirates 25% (19). 16 (10.6%) were tracheal aspirates, and 13 (8.6%) blood. *Klebsiella pneumoniae* was commonest in pus (29, 39.1%), while *Pseudomonas aeruginosa* (7, 43%) in tracheal aspirates and *Acinetobacter* spp. (7, 53.8%) in blood. A fishbone analysis revealed that (20, 35%) of swab isolates were from surgical site infection with improper sample collection, minimal discharge, without fever, hence were colonisers. 25% (19) were drain aspirates collected directly from drain bag few days after insertion. For tracheal aspirates, 88% (14) were collected several days after intubation without clinical diagnosis of pneumonia. 6 % (1) was shifted to ward and 6 % (1) discharged.

Conclusion: AR does not always mean a resistance organism. It is important to exclude colonizers. An effective communication with the clinician is the key. A multi modal diagnostic stewardship approach can be used to tackle this problem.

13. Detection of Amp C β -Lactamase Production in Uropathogenic *Escherichia coli* Isolated from Urine Samples

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Introduction: Urinary tract infections (UTIs) are among the most common bacterial infections encountered in clinical practice, with *Escherichia coli* being the predominant uropathogen. The emergence of β -lactamase-mediated resistance, particularly Amp C β -lactamases, poses a significant therapeutic challenge due to resistance to penicillins, cephalosporins, and β -lactamase inhibitor combinations. Amp C enzymes often remain undetected in routine susceptibility testing, leading to treatment failure and inappropriate antibiotic use. Early and accurate detection of Amp C-producing uropathogenic *E. coli* is therefore essential for effective antimicrobial stewardship and infection control.

Materials & Methods: This cross-sectional study was conducted in the Department of Microbiology of Dr Ram Manohar Lohia Institute of Medical Science, Lucknow from January to December 2025. A total of 267 non-duplicate urine samples yielding *E. coli* isolates were included. Antimicrobial susceptibility testing was carried out by the Kirby-Bauer disc diffusion method in accordance with CLSI guidelines. Screening for Amp C β -lactamase production was done using cefoxitin disc diffusion. Phenotypic confirmation of Amp C production was performed using Disc approximation test and Himedia Ezy MIC strip. Data were analyzed using descriptive statistics.

Results: Out of 267 uropathogenic *E. coli* isolates, 158 was presumptive Amp C Producer via cefoxitin screening test. Out of which 27 were phenotypically confirmed Amp C producers via Disc approximation test and 26 via Himedia Ezy MIC strips. Amp C-producing isolate showed high levels of resistance to cephalosporins, fluoroquinolones and β -lactam/ β -lactamase inhibitor combinations, while comparatively better susceptibility was observed to carbapenems and aminoglycosides.

Conclusion: The study highlights a substantial prevalence of Amp C β -lactamase-producing uropathogenic *E. coli* among urinary isolates. Routine screening and confirmatory testing for Amp C production should be incorporated into diagnostic microbiology laboratories to ensure accurate detection and appropriate antimicrobial therapy. Early identification of Amp C producers is crucial to prevent therapeutic failure, limit the spread of multidrug-resistant organisms, and strengthen antimicrobial stewardship programs.

14. Clinical and Microbiological Profiling of Skin and Soft Tissue Infections in Diabetic Patients at A Tertiary Care Centre in Dehradun, Uttarakhand.

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Introduction: Skin and soft tissue infections (SSTIs) are frequent and potentially severe complications in patients with diabetes mellitus due to impaired immunity, hyperglycemia, and reduced tissue perfusion. Diabetic patients are predisposed to recurrent, severe, and polymicrobial infections, often caused by multidrug-resistant organisms. Early microbiological diagnosis and targeted antimicrobial therapy are essential to reduce morbidity, prolonged hospitalization, amputations, and mortality.

Materials and Methods: This cross-sectional study was conducted over 18 months (March 2023–September 2024) at a tertiary care centre in Dehradun, Uttarakhand. A total of 264 diabetic patients (>18 years) with clinically suspected skin and soft tissue infections were included. Pus aspirates, tissue samples, and wound swabs were processed by standard microbiological techniques. Isolates were identified by MALDI-TOF MS, and antimicrobial susceptibility testing was performed using the VITEK® 2 system. clinical details, glycemic status, and treatment outcomes were analyzed.

Results: A total of 171 bacterial isolates were recovered, including 93 Gram-positive cocci (54.4%) and 78 Gram-negative bacilli (45.6%). Clinically significant bacterial growth was observed in 125 cases (47.3%). *Staphylococcus aureus* was the predominant pathogen, with Methicillin-resistant *Staphylococcus aureus* (MRSA) constituting 61% of isolates. Common Gram-negative organisms included *Klebsiella pneumoniae*, *Escherichia coli*, *Pseudomonas* species and *Proteus* species showing high levels of antimicrobial resistance. Polymicrobial infections were identified in 16.8% of cases.

Conclusion: Skin and soft tissue infections in diabetic patients are frequently caused by multidrug-resistant organisms, with a high prevalence of MRSA and resistant Gram-negative bacilli. Early microbiological diagnosis, targeted antimicrobial therapy, and optimal glycemic control are crucial for improving treatment outcomes and limiting the emergence of antimicrobial resistance.

15. Comparative Evaluation of Colistin Susceptibility Testing Methods in Carbapenem-Resistant *Pseudomonas aeruginosa*: A Validation of Alternative Methodologies.

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Introduction: The global escalation of carbapenem-resistant *Pseudomonas aeruginosa* (CRPA) has revitalized the clinical use of colistin as a last-resort therapy. Accurate antimicrobial susceptibility testing (AST) is critical; however, the reference broth microdilution (BMD) method is technically demanding and resource-intensive. This study evaluates the diagnostic performance of two streamlined alternatives—Colistin Broth Disk Elution (CBDE) and Agar Dilution (AD)—within a high-burden clinical setting.

Materials & Methods: A total of 65 CRPA isolates from different clinical samples were collected between 1st April to 31st December 2025 were included in the study from diverse specimen types, including respiratory (28), pus (15), urine (14), body fluids (7), and blood (1). Isolates were tested for colistin MIC in triplicate using CBDE (1, 2, 4, 8 mcg/mL), AD (1, 2, 4, 8 mcg/mL) and BMD as reference standard. Performance was assessed via categorical agreement (CA), essential agreement (EA), error rates, sensitivity, and specificity.

Results: Both CBDE and AD demonstrated 100% CA with the reference BMD, successfully identifying all 3 resistant and 62 intermediate isolates. Consequently, both methods yielded a sensitivity of 100% and a specificity of 100% for the detection of colistin resistance. CBDE achieved an EA of 96.9% (63/65), while AD showed an EA of 92.3% (60/65). All observed discrepancies were within ± 1 doubling dilution of the reference MIC. No very major errors (VME) or major errors (ME) were detected across any specimen category.

Conclusion: CBDE and AD are highly reliable alternatives to BMD for colistin susceptibility testing in CRPA. Due to its superior essential agreement and simplified workflow, CBDE is particularly well-suited for routine clinical implementation to guide the management of life-threatening infections.

16. A study on Genotypic detection of nasal carriage of Methicillin-Resistant *Staphylococcus aureus* (MRSA) in Health Care Workers in a tertiary Care Hospital.

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Introduction: Methicillin-resistant *Staphylococcus aureus* (MRSA) is a major cause of both nosocomial and community-acquired infections. Methicillin resistance is mediated by the *mecA* gene. The anterior nares serve as the primary ecological niche for *S. aureus*, and healthcare workers (HCWs) colonized with MRSA play an important role in cross-transmission between hospitals and the community. Rapid and accurate detection of MRSA carriage among HCW, along with an understanding of its antibiotic susceptibility patterns, is essential.

Materials & Methods: The present study aimed to determine the prevalence of MRSA among HCW using both phenotypic and genotypic methods. Anterior nares swabs were collected and were processed for culture and susceptibility testing according to standard protocols. Cefoxitin (30µg) screening was done using disc diffusion method, and detection of the *mecA* gene was performed by polymerase chain reaction (PCR).

Results: A total of 407 healthcare workers were screened. *S. aureus* was isolated from 96 individuals (23.58%), of which 80 isolates were identified as MRSA. The overall prevalence of MRSA carriage among healthcare workers was 19.65%. The highest rate of MRSA carriage was observed among nurses 38 (40%), followed by doctors 15 (18.75%), laboratory technicians 14 (17.5%) and interns 13 (16.25%). Among the 80 MRSA isolates, 55 (68.75%) were found to be *mecA* gene-positive by PCR. All MRSA carriers were successfully decolonized using 2% mupirocin ointment.

Conclusion: This study highlights the importance of rapid and accurate identification of healthcare workers with nasal MRSA colonization to strengthen hospital infection control measures and decolonization protocols. Such interventions are crucial in preventing the transmission of MRSA within healthcare settings and limiting its spread into the community.

17. Detection of carbapenemase genes in wound isolates among road traffic accident (RTA) patients from a tertiary care Apex Trauma Centre, Northern India

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Introduction:

Carbapenems are considered last-line agents for the management of infections caused by multidrug-resistant gram negative bacilli (GNB). The present study aimed to evaluate carbapenem resistance and identify carbapenemase genes in wound isolates obtained from RTA patients using phenotypic assays with molecular confirmation.

Materials & Methods: This prospective study was conducted over a period of one and a half years at a tertiary care centre. Wound samples from RTA patients were processed using standard microbiological techniques. Species identification was performed using MALDI-TOF MS, followed by antibiotic susceptibility testing. Isolates showing carbapenem resistance on disk diffusion testing were further subjected to phenotypic carbapenemase detection tests and real-time PCR for gene detection.

Results: Among 227 patients, 89 GNB were isolated, of which 45 (50.56%) demonstrated resistance to carbapenems by disk diffusion testing. The Modified Hodge Test and combined disk test were positive in 5 (11.11%) and 15 (33.33%) isolates, respectively. PCR confirmed the presence of carbapenemase genes in 20 (44.44%) isolates. NDM was the predominant gene, detected in 16 isolates (80%), with *Klebsiella pneumoniae* being the most common carriers. Co-expression of NDM and OXA-48 was observed in 7 isolates (35%), while OXA-48 alone was detected in 4 isolates (20%).

Conclusion:

The substantial burden of NDM-producing GNB in trauma-associated wound infections highlights the importance of early molecular diagnosis, strict infection control measures, and robust antimicrobial stewardship to prevent further dissemination of carbapenem resistance.

18. Comparative Analysis of Procalcitonin and C-Reactive Protein in Bloodstream Infections among Febrile Neutropenic Pediatric Cancer Patients

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Introduction: Febrile neutropenia is a serious and potentially life-threatening complication in pediatric cancer patients receiving chemotherapy. Bloodstream infections (BSIs) are a major cause of morbidity and mortality, making early and accurate diagnosis essential. This study aimed to compare the diagnostic performance of procalcitonin (PCT) and C-reactive protein (CRP) in detecting BSIs in pediatric patients with chemotherapy-induced febrile neutropenia.

Materials & Methods: This prospective observational study was conducted at a tertiary care hospital in Northern India from August 2023 to July 2024. A total of 106 pediatric cancer patients with chemotherapy-induced febrile neutropenia were included. Blood cultures were performed to confirm BSIs, and serum PCT and CRP levels were measured at presentation. Diagnostic accuracy parameters and clinical outcomes were analyzed.

Results: Bloodstream infections were confirmed in 32 patients (30.2%), including 20 Gram-negative, 11 Gram-positive, and one fungal isolate. Mean PCT levels were significantly higher in Gram-negative infections compared to Gram-positive infections (19.27 ± 10.56 ng/mL vs. 2.57 ± 2.35 ng/mL, $p < 0.01$). CRP levels showed lower discriminatory ability (150.0 ± 35.2 mg/L vs. 45.0 ± 20.8 mg/L, $p < 0.05$). PCT demonstrated superior diagnostic accuracy (sensitivity 89.2%, specificity 83.5%, AUC 0.93) compared to CRP (sensitivity 76.3%, specificity 62.7%, AUC 0.76). Elevated PCT levels were significantly associated with increased intensive care admissions, prolonged hospital stays, and delayed antibiotic de-escalation ($p < 0.001$).

Conclusion: Procalcitonin is a more reliable biomarker than CRP for early detection of bloodstream infections in febrile neutropenic pediatric cancer patients, particularly for Gram-negative bacteremia, and may improve clinical decision-making and outcomes in pediatric oncology.

19. Nested PCR vs Real-time PCR for detection of *Orientia tsutsugamushi* among suspected cases of Scrub Typhus from Eastern Uttar Pradesh, India

Author: Prachi Paul

Co-Authors: Shabnam Kumari, Zinnu Rain, Sudhir Kumar, Pradyot Prakash

Institute: Institute of Medical Sciences, BHU

Introduction: Scrub typhus is a chigger-borne rickettsial disease caused by *Orientia tsutsugamushi* and represents a major public health concern in India. It is a common cause of acute undifferentiated febrile illness and is associated with significant morbidity and mortality if not diagnosed early. The present study aimed to detect *O. tsutsugamushi* in whole blood samples using nested PCR and real-time PCR, in addition to IgM ELISA, to improve diagnostic accuracy.

Materials & Methods: Clinically suspected scrub typhus cases, positive by IgM ELISA (n = 10), presenting with acute febrile illness, were enrolled. Blood samples were collected from these patients, while ELISA-negative healthy individuals (n = 2) served as controls. Nested PCR targeting the 620 bp region of the 56 kDa outer membrane protein gene and further real-time PCR targeting the 47 kDa outer membrane protein gene of *O. tsutsugamushi* were performed

Results: Of the 10 IgM-positive cases, 7 were positive by both nested PCR and real-time PCR. However, strain-level identification could not be achieved using either method with the primers employed. Nested PCR amplicons showed multiple non-specific bands on 2% agarose gel, complicating interpretation without sequencing. In contrast, real-time PCR yielded discrete, easily interpretable amplification signals with higher specificity.

Conclusion: Although nested PCR is highly sensitive for detecting *O. tsutsugamushi* in whole blood, this study demonstrates that real-time PCR is a more reliable diagnostic tool for *O. tsutsugamushi*. However, larger studies are required to validate these findings so that the real-time PCR protocol used in the present study may be used in the routine diagnosis of scrub typhus.

20. Epidemiology of multidrug resistant uropathogens over three years period at a tertiary care centre: a retrospective observational study

Author: Dr. Nidhi Bhatnagar

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Introduction: Urinary tract infections (UTIs) are among the most common bacterial infections encountered in clinical practice. Changing uropathogen profiles and rising antimicrobial resistance, including multidrug resistance, increasingly challenge empirical therapy. Continuous local surveillance of uropathogens and resistance trends is essential to guide appropriate treatment.

Materials & Methods: This retrospective observational study was conducted at a 600-bedded tertiary care centre from January 2023 to December 2025. Urine cultures with significant bacterial growth were included. Demographics, uropathogen distribution, and antimicrobial resistance patterns were analysed year-wise. Multidrug resistance (≥ 3 antibiotic classes), ESBL production, carbapenem, and vancomycin resistance were compared across the study period.

Results: A total of 345, 525, and 606 urine samples were culture-positive in 2023, 2024, and 2025, respectively. Females were more commonly affected than males across all three years, with the 21–40 years age group being the most frequently affected. *Escherichia coli* was the predominant uropathogen isolated throughout the study period, followed by *Enterococcus* species. Multidrug resistance was observed in 275 (79.7%), 430 (81.9%), and 471 (77.7%) isolates in 2023, 2024, and 2025, respectively. ESBL production was detected in 61.1%, 82.7%, and 74.5% of isolates during the corresponding years. Carbapenem resistance peaked in 2024 (50.9%), followed by 2025 (40.7%) and 2023 (23.8%). Vancomycin resistance among *Enterococcus* species was highest in 2024 (25.6%) and declined to 6.7% in 2025.

Conclusion: UTIs showed a high prevalence of multidrug-resistant uropathogens, with *E. coli* predominance and increasing ESBL and carbapenem resistance, underscoring the need for continuous local surveillance and antimicrobial stewardship.

21. Detection of Neisseria Gonorrhoeae and Chlamydia Trachomatis by Nucleic acid amplification test in genitourinary samples of Females in Reproduction Age Attending Obstetrics and Gynaecology OPD at a Tertiary Care Hospital.

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Co-Authors: Jyoti Srivastava, Anjali Agarwal, Sameena Jawaid, Sheetal Agarwal

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Introduction: Sexually transmitted infections (STIs) due to Chlamydia trachomatis (CT) and Neisseria gonorrhoeae (NG) are major causes of reproductive morbidity in women, often remaining asymptomatic. Accurate & easy diagnosis in resource-limited settings is essential for effective control & prevention.

Materials & Methods: A hospital-based cross-sectional analytical study was conducted in Microbiology Department, over a period of 1 year (1 January 2025 to 20 January 2026) in Hind Institute of Medical Sciences, Barabanki. A total of 100 women aged 18–49 years attending the outpatient department of Obstetrics & Gynaecology were enrolled using consecutive sampling after obtaining informed consent. Two Vaginal & One endocervical swabs were collected. Vaginal swabs were examined by wet mount and Gram stain & culture. Endocervical swab for detection of CT and NG using Truenat PCR. Bacterial vaginosis (BV) was diagnosed using Nugent's criteria.

Results: The prevalence of CT was 7% (5/65) and NG was 9% (6/65) with co-infection. Truenat detected all cases, whereas culture identified only one NG case and Gram stain detected two cases, confirming superior sensitivity of molecular testing. Bacterial vaginosis was detected in 12 of the participants. Infections were equally distributed among symptomatic and asymptomatic women ($p > 0.05$). Bacterial vaginosis co-existed in 60% (3/5) of CT-positive and of NG 50% (3/6) positive cases

Conclusion: This study highlights a significant burden of CT and NG, including asymptomatic infections, in reproductive-age women. Rapid point-of-care NAAT platforms like (Truenat) offer high sensitivity and are feasible in resource-limited settings. Routine molecular screening is strongly recommended to enable early detection and prevent long-term complications such as pelvic inflammatory disease and infertility.

22. Evaluating colistin Resistance in CRE: A Comparison of MIC Determination Methods

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Institute: Department of Microbiology, Dr. RMLIMS, Lucknow

Introduction: Antimicrobial resistance is a major global public health threat that undermines modern medical advances. Hospitals, especially ICUs, are key reservoirs for the emergence and spread of resistant bacteria due to selective pressure and horizontal transfer of resistance genes, leading to outbreaks caused by multidrug-resistant organisms such as *Enterobacterales*. Widespread use of carbapenems has driven the emergence of carbapenem-resistant *Enterobacterales*, primarily through carbapenemase production. The limited treatment options rely on colistin, whose increased use has led to resistance mediated by LPS modification and plasmid-borne *mcr-1* gene.

Materials & Methods: A prospective hospital-based study was conducted from July 2024 to July 2025, all the samples that were sent for bacterial culture and sensitivity were processed by routine procedures and confirmed by Automated methods. All confirmed isolates yielding phenotypical resistance to Imipenem/Meropenem or both were subjected to screening for Colistin resistance via E-Test. MIC of CRE yielding colistin resistance was compared using BMD and VITEK-2.

Results: Among 218 carbapenem-resistant *Enterobacterales* (CRE) isolates evaluated, 11 (5.05%) were found to be colistin resistant using MIC determination methods. *Klebsiella pneumoniae* predominated among the resistant isolates (10/11), with one isolate identified as *Escherichia coli*. All patients harboring colistin-resistant CRE (11/11) were admitted to the intensive care unit (ICU). Age-wise analysis showed that two patients were neonates, while five patients were aged ≥ 60 years, indicating a higher burden at the extremes of age.

Conclusion: Majority resistant isolates were identified as *Klebsiella pneumoniae* isolated from ICUs highlighting its significant role in the emergence of resistance to last-resort antimicrobials. Continuous surveillance and judicious use of carbapenems and colistin are essential to prevent further spread of colistin resistance among CRE.

23. Secondary Syphilis Mimicking Palmoplantar Psoriasis: A Clinically Misdiagnosed, Serologically Confirmed Case Report

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Institute: JNMCH, AMU

Introduction: Syphilis is a chronic sexually transmitted infection caused by *Treponema pallidum*, a fastidious spirochete that cannot be cultured in vitro and is primarily diagnosed by serological methods. Secondary syphilis represents the stage of systemic dissemination and is characterized by varied mucocutaneous manifestations, often leading to diagnostic dilemmas. Microbiological confirmation through standardized serological algorithms remains the cornerstone of diagnosis.

Materials & Methods: A 48-year-old male presented to the Integrated Counselling and Testing Centre (ICTC) for HIV screening. He had a two-month history of asymptomatic, hyperpigmented, scaly lesions over the palms and soles. The lesions had been previously misdiagnosed as palmoplantar psoriasis, and the patient was treated with topical corticosteroids without improvement. Detailed clinical history revealed high-risk sexual behavior and a past history of a painless genital ulcer. As per National AIDS Control Organization (NACO) guidelines, serological screening for syphilis was performed. The non-treponemal Venereal Disease Research Laboratory (VDRL) test was reactive with a high titer of 1:32. Confirmation by treponemal tests showed positive *Treponema pallidum* hemagglutination assay (TPHA) and fluorescent treponemal antibody absorption (FTA-Abs) tests. HIV serology was non-reactive. Based on serological profile and clinical correlation, a definitive diagnosis of secondary syphilis (palmoplantar syphilides) was established.

Results: The patient was treated with a single intramuscular dose of benzathine penicillin G (2.4 million units). Rapid clinical improvement with marked fading of lesions was observed within seven days. Partner evaluation and counselling were initiated, and serological follow-up using VDRL titres was advised.

Conclusion: This case highlights the diagnostic challenges associated with atypical presentations of secondary syphilis and underscores the pivotal role of serological test of Microbiology in establishing an accurate diagnosis. Timely and appropriate laboratory confirmation is essential to prevent clinical misdiagnosis, ensure prompt initiation of correct therapy, and improve overall patient outcomes.

24. Silent Invader in the ICU: Unravelling the Risk Factors for Burkholderiacepacia complex Bacteremia

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Co-Authors: Shiva Verma, Anupam Das, Manodeep Sen, Jyotsna Aggarwal

Institute: Dr. Ram Manohar Lohia Institute of Medical Sciences, Lucknow

Introduction: Burkholderiacepacia complex (Bcc) is a notorious Non-Fermenting Gram Negative Bacilli. It is most notably known as a serious respiratory pathogen in patients with Cystic Fibrosis and Chronic Granulomatous Disease but has also been the causative agent of respiratory tract infection and bacteremia in patients without CF.

Materials & Methods: Study Setting and Design: This was a retrospective, observational study conducted by the Department of Microbiology at Dr. RMLIMS, Lucknow. Controls were matched to case patients in a 3:1 ratio based on the ICU type and date of onset of *B. cepacia* bacteremia for the matched case. Study Duration: 1.01.2023 to 31.12.2025

Methodology: The electronic record system was accessed for the patient details including risk factors, comorbidities, duration of hospitalization, patient outcome.

Results: We reviewed records of 39 patients admitted in the ICU of our facility with 1 or more blood culture positive for BCC. The average age of patients was 51.2years, male: female ratio was 1.6. We compared the risk factors, comorbidities, and patient outcomes of these patients. 35.9% cases succumbed to sepsis, 46.1% cases had one or more underlying co-morbid condition. Risk factors of cases and controls were compared for association with Bcc infection in these patients.

Conclusion: Burkholderiacepacia complex (BCC) presents significant treatment challenges due to its extensive intrinsic resistance to many antibiotics. Accurate identification of the specific BCC isolate is crucial for optimizing patient outcomes. Individuals with underlying co-morbidities are particularly vulnerable to acquiring this infection. Additionally, prolonged hospital stays and multiple medical interventions further increase the risk of complications in these patients.

25. Microbiological Profile, Phenotypic and Genotypic Characterization of Antimicrobial Resistance Pattern in Clinical Isolates from Cancer Patients at Tertiary Care Hospital

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Co-Authors: Prof (Dr) Anjali Agarwal, Prof (Dr) Jyoti Srivastav, Dr Sheetal Agarwal

Institute: Hind Institute of Medical Sciences, Barabanki

Introduction: Globally 77% increase in cancer patients is predicted from 2022 to 2050. For successful management of cancer, effective antibiotic therapy is needed. This study aims to determine the bacterial pathogens, and anti-microbial resistance profile, phenotypic and genetic characterization in clinical isolates among cancer patients.

Materials & Methods: The study was conducted in Department of Microbiology, Hind Institute of Medical Sciences, Barabanki from 1 January 2025 to 31 December 2025. Urine, pus, sputum, blood and body fluid sample of cancer patients clinically suspected of bacterial infection were collected. Microorganism identification was done and antimicrobial susceptibility test done as per Clinical and Laboratory Standards Institute (CLSI) guidelines 2025. Drug resistance for gram positive bacteria for MRSA by cefoxitin disk (10µg) and for gram negative bacteria done by Modified carbapenem inactivation method (MCIM) and (DDST) for Extended Spectrum Beta Lactamase (ESBL). Further, Genotypic carbapenem resistance gene detection by multiplex RTPCR for NDM, KPC, OXA, VIM, IMP gene.

Results: Total 150 samples were processed including 96(64%) urine, 34(22.6%) pus, 18 (12%) sputum, 1(0.6%) blood and 1(0.6%) ascitic fluid. Among urine samples, 28(29.2%) were sterile and 34(35.4%) nonsignificant, while among 16(16.7%) *E. coli*, 8(8.3%) *Klebsiella*, 2(2.1%) *Pseudomonas*, 1(1.1%) *Coagulase negative staphylococcus aureus (CONS)*, 1(1.1%) *staphylococcus* and 6(6.3%) *Acinetobacter* was identified. Among pus, 10(29.4%) were NPG, while among 10(29.4%) *CONS*, 4(11.7%) *Klebsiella* spp., 3(8.8%) *Staphylococcus*, 3(8.8%) *E. coli* was found. Among sputum samples, 8(44.4%) was Non-pathogenic growth while in 1(5.5%) *Pseudomonas*, 2(11.1%) *E. coli*, 6(33.3%) *Klebsiella*, 1(5.5%) *Acinetobacter* were identified. In blood *Pseudomonas* was identified and Ascitic fluid was sterile. Carbapenem resistance isolates 19(67.8%) were MCIM positive for phenotypic and for ESBL 34(65.4%) were reported. In genotypic NDM gene was found in 27(93.1%) samples, OXA in 13(44.8%), KPC in 2(6.9%) and VIM in 2(6.9%).

Conclusion: The present study demonstrates the higher occurrence of UTI associated with antimicrobial resistance among common antibiotics groups. There is an urgent need to effectively address the antimicrobial resistance trend so the genotypic testing in cancer patients can reduce morbidity and mortality.

26. Comparative Evaluation of Phenotypic Methods Using mecA Genotyping as the Reference Standard for Detection of Methicillin-Resistant Staphylococcus aureus

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Institute: AIIMS Raebareli

Introduction: Accurate detection of Methicillin-Resistant Staphylococcus aureus (MRSA) is critical for effective infection control. Conventional phenotypic methods often struggle to differentiate true MRSA from Borderline Oxacillin-Resistant *S. aureus* (BORSA) or Modified *S. aureus* (MODSA). This study evaluated the diagnostic performance of various phenotypic screening methods against the genotypic gold standard (*mecA* gene PCR).

Materials & Methods: A cross-sectional study was conducted on 208 *S. aureus* isolates recovered from pyogenic infections. Identification was confirmed by coagulase and DNase tests. All isolates underwent phenotypic MRSA screening using Cefoxitin (30µg) disk diffusion as per CLSI guidelines, Oxacillin Agar Screening, and MRSA Chromogenic Agar. The results were compared with *mecA* gene detection by PCR to calculate sensitivity and concordance with *mecA* PCR.

Results: Of the 208 isolates, 195 (93.8%) were confirmed as *mecA*-positive MRSA. Cefoxitin disk diffusion detected all *mecA*-positive isolates but misclassified 13 *mecA*-negative isolates as resistant, indicating reduced specificity, likely attributable to BORSA/MODSA strains lacking the *mecA* gene. Among confirmatory media, MRSA Chromogenic Agar demonstrated the high performance, detecting 194/195 positives with a sensitivity of 99.4% and high concordance with *mecA* PCR ($p < 0.001$). In contrast, Oxacillin Agar Screening showed lower sensitivity (93.8%), missing 12 confirmed MRSA cases.

Conclusion: Cefoxitin disk diffusion remains the most reliable surrogate marker for *mecA*-mediated methicillin resistance. However, due to its reduced specificity, adjunctive use of MRSA chromogenic agar improves phenotypic confirmation, particularly in resource-limited settings where molecular methods are unavailable.

27. A study on bacteriological profile and its correlation with CRP in neonatal sepsis in tertiary teaching hospital.

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Introduction: Neonatal sepsis continues to be a significant cause of morbidity and mortality, particularly in resource-limited settings. Early diagnosis is challenging due to non-specific clinical manifestations. Although blood culture remains the diagnostic gold standard, delayed results limit early therapeutic decisions. C-reactive protein (CRP), an acute-phase reactant, is commonly used as an adjunct biomarker. This study aimed to evaluate the correlation between CRP levels and blood culture positivity and to analyze the microbial profile, including antimicrobial resistance patterns, in neonatal sepsis.

Materials & Methods: This retrospective observational study was conducted in the Department of Microbiology, Shri Ram Murti Smarak Institute of Medical Sciences, Bareilly, from May 2025 to October 2025. A total of 350 blood cultures from neonates with suspected sepsis were processed. CRP was considered positive at levels >6 mg/L. Blood cultures were processed using standard microbiological techniques. Antimicrobial susceptibility testing was performed by the Kirby–Bauer disk diffusion method in accordance with CLSI guidelines.

Results: Out of 350 blood cultures, 88 were positive, yielding a culture positivity rate of 25.1%. Gram-positive bacteria constituted 39.8% of isolates, predominantly coagulase-negative staphylococci (15.9%) and *Staphylococcus aureus* (12.5%). Gram-negative bacteria accounted for 38.6% of isolates, with *Klebsiella pneumoniae* (13.6%) and *Citrobacter freundii* (10.2%) being the most common; *Pseudomonas aeruginosa* was isolated in one case (1.1%). Fungal isolates constituted 21.6%, mainly *Candida tropicalis*. ESBL-producing organisms comprised 26.1% of bacterial isolates. CRP demonstrated a sensitivity of 76.1%, specificity of 45.0%, positive predictive value of 31.8%, and negative predictive value of 84.9%.

Conclusion: CRP exhibits good sensitivity and a high negative predictive value, supporting its role as an adjunct screening marker for neonatal sepsis. However, due to limited specificity, it should be interpreted in conjunction with blood culture results and clinical findings.

28. Natural Bioactive-Based Nanobioconjugates: A Computational Strategy against MDR Pathogens

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Introduction: The increasing prevalence of multidrug-resistant bacteria has become a critical challenge to global healthcare and limits the effectiveness of existing antibiotics. It is necessary to develop novel and effective alternative antimicrobial strategies. Bio fabrication of nanoparticles using natural secondary metabolites has gained significant attention as a green and sustainable antimicrobial strategy. These bio fabricated nanoparticles demonstrate enhanced antibacterial activity against MDR pathogens through multiple mechanisms such as membrane disruption, ROS generation, inhibition of biofilm formation and interference with essential cellular processes. This approach offers a promising platform for the development of next-generation nanotherapeutics to combat multidrug-resistant bacterial infections.

Materials & Methods: Based on documented antibacterial action, natural bioactive substances are chosen. To assess their binding interactions with selected bacterial proteins involved in resistance pathways, molecular docking is used.

Methodology

Screening and Selection of Therapeutic Compound

Synthesis of Inorganic Nanoparticles

Nanoparticle characterization techniques

Evaluation of Antimicrobial Activity against MDR Strains

Anti-bacterial activity

Zone of Inhibition

MIC

Biological TEM

Results: The molecular docking results revealed high-affinity interactions between the selected natural compounds and selected bacterial proteins, suggesting their promise as antibacterial agents. The suggested model suggests that such conjugation could improve the drugs' stability, bioavailability, and targeted distribution.

Conclusion: This study identifies promising natural antibacterial molecules through *in silico* screening and proposes their future bioconjugation with inorganic nanoparticles. The conceptual approach establishes a foundation for advanced experimental investigations aimed at developing nanotechnology-based therapeutics against multidrug-resistant bacterial infections.

29. Synergistic Potential of Curcumin–Vancomycin Therapy in Combating Methicillin- Resistant *Staphylococcus aureus* Infections: Exploring a Novel Approach to Address Antibiotic Resistance and Toxicity.

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Introduction: Methicillin-resistant *Staphylococcus aureus* (MRSA) infections remain a major clinical challenge due to increasing antibiotic resistance, biofilm formation, and toxicity associated with prolonged high-dose vancomycin therapy. Patients on peritoneal dialysis is especially vulnerable. Curcumin, a natural compound with antimicrobial, anti-inflammatory and antibiofilm activity, may enhance antibiotic effectiveness and reduce required doses.

Objective: To evaluate the antibacterial effect of curcumin alone in combination with vancomycin against MRSA strains and to assess curcumin-induced metabolic alterations in *S. aureus* using NMR-based metabolomics.

Materials & Methods: Antibacterial activity of curcumin was assessed using optical density– based growth inhibition assays on *S. aureus* MTCC-3160. Metabolic profiling of culture supernatants over 20 hours was performed using ¹H NMR spectroscopy to identify changes in key metabolites. Twenty clinical MRSA isolates were tested for the minimum inhibitory concentrations (MICs) of curcumin and vancomycin individually and in combination using the broth microdilution checkerboard method. Synergy was quantified using the fractional inhibitory concentration (FICI).

Results: Curcumin inhibited *S. aureus* growth and significantly suppressed key metabolic pathways, particularly acetate, isobutyrate, and choline production, indicating a bacteriostatic effect. Among 20 MRSA isolates, the curcumin–vancomycin combination markedly reduced MICs, with vancomycin’s MIC decreasing 0.5 µg/mL in all strains. Synergy (FICI 0.04–0.56) was observed in 17 strains, while 3 showed additive effects. The strongest synergy occurred in strain B-10866 (FICI 0.04).

Conclusion: Curcumin significantly enhances vancomycin efficacy against MRSA by reducing MICs and disrupting bacterial metabolic pathways. This combination offers a promising strategy to overcome antibiotic resistance while potentially lowering vancomycin-associated toxicity. Further in vivo validation warranted.

30. Beating the clock in blood stream infections: Direct antimicrobial susceptibility testing from positive blood culture broth- A comparative study.

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Introduction: Early administration of appropriate antimicrobial therapy plays a crucial role in reducing morbidity, mortality and overall health care costs. Rapid availability of preliminary antimicrobial susceptibility testing (AST) results. can assist clinicians in timely optimization of therapy. This study aimed to evaluate the concordance between AST performed from flagged blood culture bottles directly and AST obtained through an automated system by standard method.

Objective: To compare the performance of direct VITEK AST performed directly from positive blood culture bottles with standard VITEK AST performed from isolated colonies

Material and Methods: 80 aerobic blood culture bottles beeped positive by an automated blood culture system and seen as gram negative bacilli on direct microscopy were included in the study. The broth from each bottle underwent a two-step centrifugation process to pellet the organisms. The resulting sediment was used for preparing an inoculum comparable to 0.5 MacFarland to perform identification followed by antimicrobial susceptibility testing (AST) using the automated system and rates of various errors were calculated. Standard method (colony- based) of organism identification and AST were also conducted in parallel for comparison

Results: 80 gram-negative bacilli on direct gram staining from flagged blood culture bottle were included in study. Among these, 45(56.3%) were *Enterobacteriales* and 23 (28.8%) were non fermenters. Among *Enterobacteriales*, a categorical agreement of 98.3% was observed between direct antimicrobial susceptibility testing and standard automated AST, with a disagreement rate of 1.7% between two methods. Turnaround time was significantly reduced.

Conclusion: Direct automated VITEK 2 AST is a reliable and rapid alternative to conventional colony-based automated VITEK 2 testing and may facilitate early optimization of antimicrobial therapy.

31. Heterogeneous Vancomycin-Intermediate Staphylococcus aureus in MRSA: Prevalence, Detection methods, and Therapeutic Implications

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Introduction: Methicillin-resistant Staphylococcus aureus (MRSA) is a major cause of community-acquired and healthcare-associated infections. Vancomycin remains the cornerstone of MRSA therapy; however, the emergence of heterogeneous vancomycin-intermediate Staphylococcus aureus (hVISA) has been associated with vancomycin treatment failure due to difficulty in routine laboratory detection.

Materials & Methods: This prospective observational study was conducted at a tertiary care center in North India from May 2023 to April 2025. A total of 140 non-duplicate MRSA isolates from various clinical specimens were included. Identification was performed using MALDI-TOF MS and methicillin resistance was screened by cefoxitin disc diffusion and mecA PCR. Screening for hVISA was done using E-test MIC, broth microdilution, and vancomycin screening agar (BHIV4), with confirmation by PAP-AUC. Antimicrobial susceptibility testing and SCCmec typing were performed using standard methods.

Results: PAP-AUC confirmed hVISA in 23 (16.4%) isolates. Broth microdilution showed the highest sensitivity (91.3%) and negative predictive value (98.1%). Most hVISA isolates were community-acquired and predominantly recovered from pus samples. SCCmec type V was the most common genotype. All hVISA isolates were susceptible to linezolid, ceftaroline, and tigecycline (100%). Daptomycin and doxycycline showed susceptibility in 20/23 (87%) isolates, with resistance noted in 3/23 (13%).

Conclusion: hVISA shows a significant prevalence among MRSA isolates and necessitates reliable screening strategies. Alternative agents such as linezolid, ceftaroline, tigecycline.

32. Molecular Detection of Vancomycin and Methicillin Resistance in *Staphylococcus Aureus* Isolated from Various Clinical Samples among a Tertiary Care Hospital Moradabad

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Introduction: Vancomycin is the drug of choice for treatment of infections caused by methicillin resistance *Staphylococcus aureus* (MRSA). But in recent years incidence of vancomycin intermediate *S. aureus* (VISA) and vancomycin resistant *S. aureus* (VRSA) has been increasing in different areas of the world.

Material and methods: 314 MRSA strains were collected from different clinical samples and processed in the central laboratory of Teerthanker Mahaveer Medical College and Research Centre, Moradabad. Out of the 314 MRSA strains 4 VRSA, 14 VISA and 296 VSSA was found on the basis of minimum inhibitory concentration of vancomycin carried out by broth micro dilution (BMD) method. *S. aureus* DNA was extracted and PCR was performed for detection of *mecA*, *vanA* and *vanB* genes.

Result: Out of the 314 MRSA strains 296 (94.27%) were VSSA, 14 (4.46%) VISA and 4 (1.27%) VRSA was found through BMD method. The molecular characterization of the test strains detects the presence of *mecA*, *vanA* and *vanB* genes by PCR.

Conclusion: Detection of *vanA* and *vanB* genes among MRSA isolates from a tertiary care hospital Moradabad, India, alarms the spreading of the vancomycin resistant gene among clinical *S. aureus* isolates and other bacterial pathogens. Moreover, vancomycin is the drug of choice to treat the MRSA infections, development of vancomycin resistance poses a serious concern for healthcare system.

33. Occurrence of Inducible Clindamycin Resistance *Staphylococcus Aureus* Isolated from Clinical Samples in a Tertiary Care Hospital Moradabad, U.P.

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Introduction: Clindamycin is effective for treating *Staphylococcus aureus* infections in the skin and soft tissues. However, resistance caused by the inducible macrolide-lincosamide-streptogramin B (iMLSB) phenotype can lead to therapeutic failure in vivo, despite being susceptible in vitro in the Kirby-Bauer disk diffusion method. Resistance to macrolides can be caused via the *msrA* gene's efflux mechanism or the *erm* gene, which encodes enzymes that give inducible or constitutive resistance to MLSB antibiotics. Therefore, a simple D-test is recommended for regular detection.

Material and methods: This was a cross-sectional study conducted in the department of microbiology, Teerthanker Mahaveer Medical College and Research Centre, Moradabad, India. A total of 232 *S. aureus* strains were isolated from various clinical samples like pus, blood and respiratory samples. These isolates were subjected to routine identification followed by the Kirby-Bauer disk diffusion method and the D-test method.

Result: Out of 232 *Staphylococcus aureus* isolates, 158 were MRSA and 74 were MSSA. 49 inducible clindamycin resistance, 69 constitutive MLSB and 114 MS phenotypes were isolated from 232 *S. aureus* strains.

Conclusion: This study found a moderate incidence of the inducible clindamycin phenotype among the staphylococcal isolates examined. Clinical microbiology laboratories in locations with a high MRSA prevalence should consider performing the D-test on a routine basis. This prevents prescribing drugs with uncertain therapeutic effectiveness.

34. To study comparative evaluation of different diagnostic modalities (Blood culture, Widal test, Typhi dot and RT-PCR) for detection of *Salmonella typhi* infection in patients attending tertiary care hospital, Kanpur.

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Introduction: Typhoid fever continues to be a major public health concern in developing countries due to poor sanitation, unsafe drinking water, and overcrowding. Caused by *Salmonella enterica* serovar Typhi, the disease often presents as a non-specific febrile illness, making early and accurate laboratory diagnosis essential for effective management, prevention of complications, and rational use of antibiotics.

Materials & Methods: This study was a comparative study conducted in Department of Microbiology at Rama Medical College, Hospital & Research Centre, Kanpur from April 2024 to October 2025. A total of 70 samples were collected of the patients having complains of fever & weakness.

Results: Among the 70 patients, 49 were males and 21 females, spanning various age groups. In the present study the maximum age was observed in 16-30yrs of age with maximum samples received from department of medicine. Blood culture was positive in 28 (40%) cases, Widal test in 41 (58.6%), Typhi Dot in 44(62.9%), and rT-PCR in 51(72.9%) cases. rT-PCR demonstrated the highest sensitivity (96.4%), specificity (83.3%), positive predictive value(76.5%), and overall diagnostic accuracy (88.6%). Hepatomegaly was observed in 52 patients on LFT analysis.

Conclusion: rt-PCR has highest sensitivity and specificity among all the diagnostic modalities so we should start promoting it as 1st line of diagnostic parameter. But because typhi dot had good agreement with rt-PCR, typhi dot can also serve the purpose at tertiary care centre as it is cheaper and requires less manual expertise.

35. Combination of Modified Carbapenem Inactivation Method (Mcim) and EDTA-Modified Carbapenem Inactivation Method (Ecim) For Detecting Carbapenemase-Producing *Pseudomonas Aeruginosa*.

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Introduction: *Pseudomonas aeruginosa* can acquire carbapenem resistance through various mechanisms, including genomic mutations leading to the overexpression of efflux-pumps, intrinsic Amp C- β -lactamase, and/or reduced permeability, and/or through the acquisition of plasmid-mediated carbapenemases and/or extended-spectrum- β -lactamases (ESBLs). Identification of carbapenemase-harboring organisms is valuable in informing therapeutic and infection-control measures. This study aimed to characterize carbapenemase-producing *P. aeruginosa* isolates from clinical samples using phenotypic tests and evaluate their antimicrobial resistance patterns.

Material & Methods: A total of 112 non-duplicate *P. aeruginosa* were isolated from various clinical specimens over a period of 8 months. Carbapenem resistance was confirmed by disk diffusion method using CLSI guidelines (2025). Carbapenemase production was detected using modified Carbapenem Inactivation Method (mCIM) and EDTA- Carbapenem Inactivation Method (eCIM) tests. Antibiotics susceptibility testing was performed against pseudomonal infection using kirby-Bauer disc diffusion method.

Results: Among 112 suspected isolates, 25 were CRPA, of which 12 were carbapenemase producers. MBL producer 8 (66.6%), followed by serine carbapenemase 4 (33%).

Conclusions: These findings indicate that the mCIM combined with eCIM is useful for detecting and distinguishing different types of carbapenemase in *P. aeruginosa*.

36. A One Health Approach to Human Brucellosis: Integrated Diagnostics and Cytokine Profiling in Arthritic Complications

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Introduction: Brucellosis is a prevalent, but neglected zoonotic disease in India with nonspecific symptoms. This study assessed its prevalence, compared diagnostic methods, identified risk factors, and evaluated cytokine profiles in brucellosis-associated arthritis.

Materials & Methods: This prospective study included 320 patients suspected of human brucellosis. Test performed included RBPT, SAT, ELISA IgM/IgG, conventional PCR, RT-PCR, blood culture, and further cytokine analysis (IL-6, IL-10, IFN- γ , IL-2) was done.

Results: Out of 320 clinically suspected patients, 158 (49.3%) were positive for Brucella by either test. RBPT showed the highest sero positivity (32.5%), followed by ELISA IgG (30.0%), SAT (23.8%), ELISA IgM (23.4%), and combined ELISA IgG+IgM (7.5%). RT-PCR detected Brucella DNA in 40 (12.5%) cases, and 13 (4.0%) were positive by conventional PCR. Blood culture was positive in 6 (1.9%) cases. Phylogenetic analysis of the IS711 gene revealed that all study isolates clustered closely with the B. abortus reference strain, supported by high bootstrap values. Immunological analysis revealed elevated levels of IL-2 and IL-10 in Brucella-positive arthritis patients, indicating active immune stimulation concurrent with immune regulatory responses. Elevated ESR and CRP further support the presence of systemic inflammation. Cow contact and vaccination status showed positive trends towards association with brucellosis. In the one health paradigm, direct human-animal interactions were also prevalent.

Conclusion: ELISA emerged as the most sensitive serological assay, while molecular and phylogenetic analysis served as essential confirmatory methods, emphasising the need for an integrated diagnostic approach for effective brucellosis detection. Associations with raw dairy consumption and unvaccinated livestock emphasise the need for early diagnosis, effective animal immunization, and strengthened One Health-based public health interventions.

37. Prevalence of Carbapenem and Colistin Resistance among Gram-Negative Bloodstream Isolates in a Tertiary Care Hospital

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Introduction: The increasing prevalence of carbapenem-resistant Gram-negative bacilli (CR-GNB) poses a major therapeutic challenge worldwide. Colistin is often used as a last-resort agent for such infections; however, the emergence of colistin resistance further limits treatment options, particularly in bloodstream infections. The objective of the study is to determine the prevalence and organism-wise distribution of carbapenem resistance and colistin resistance among Gram-negative blood culture isolates in a tertiary care hospital.

Materials & Methods: This retrospective observational study was conducted in the microbiology laboratory of a tertiary care hospital over a four-month period. A total of 2492 blood culture samples were processed. Gram-negative isolates were identified using standard manual methods and automated processing with VITEK. Antimicrobial susceptibility testing was performed according to CLSI guidelines.

Carbapenem Resistance was detected by the Kirby–Bauer disk diffusion method on Mueller–Hinton agar using meropenem (10 µg) for Enterobacterales. Zone diameters ≥ 23 mm were considered susceptible, 20–22 mm intermediate, and ≤ 19 mm resistant. Colistin susceptibility was determined by the Colistin Broth Disk Elution (CBDE) method, and MIC interpretation was done using CLSI breakpoints, with 2 µg/mL considered intermediate and 4 µg/mL resistant.

Results: Out of 2492 samples, 52 Gram-negative bacilli were isolated. Carbapenem resistance was most frequent in *Klebsiella* spp. (59.6%), followed by *Acinetobacter baumannii* complex (32.7%), *Escherichia coli* (19.2%), *Pseudomonas* spp. (3.8%), and *Elizabeth kingia* spp. (1.9%). Colistin testing showed 3 isolates (4.9%) were resistant and 49 (78.7%) were intermediate. Resistant isolates included *Klebsiella* spp. (2) and *Acinetobacter baumannii* complex (1).

Conclusion: A high burden of carbapenem resistance was observed, with reduced colistin susceptibility indicating an alarming trend. Continuous surveillance, antimicrobial stewardship, and routine MIC-based testing are essential.

38. Correlation of Microbiological Profile and Multidrug-Resistant Organisms in Diabetic Foot Ulcers with HbA1c Levels and Amputation Outcomes.

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Institute: SGPGIMS, Lucknow

Introduction: Diabetes mellitus (DM) is a major global public health issue with rapidly rising prevalence. According to WHO, in India 77 million people above the age of 18 have diabetes, with 25 million pre-diabetic. Diabetic foot ulcers (DFU) is one of the most commonest and severe DM complication. The role of HbA1C in microbiological culture growth and its multi-drug resistant profile is still less research. So, the study was planned to analyze the HbA1c levels its correlations with microbiological profile, MDRO, amputation rate and peripheral neuropathy.

Materials & Methods: This prospective observational study was conducted in the Department of Microbiology, SGPGIMS, Lucknow, from June to December 2025. A total of 47 patients with DFU samples were received from which their culture and antimicrobial susceptibility was performed. Patient clinical profiling and HbA1c assessment were documented and its correlation was analyzed.

Results: Out of 47 DFU patients (male: female 2.3:1; mean age 52.51 ± 11.32 years), 27.5% patients showed growth of polymicrobial infections. The most common organism isolated was *Pseudomonas aeruginosa* (26.8%), followed by *Escherichia coli* and *Klebsiella pneumoniae* (17.1% each). *Candida* species and mycelial growth was also present in 02 patients. A total of 56.59% (p-value 0.05) organisms were multidrug-resistant, in which isolation of Non Lactose Fermenting organism with amputation was found to be significant (p-value = 0.039). The most susceptible drugs were Colistin (30), Imipenem (22), and Amikacin (30). Amputation rates were found to be 14.9% in HbA1c <6.5% vs. 40% in HbA1c >6.5% (P - value in patients with HbA1C >6.5% is 0.00059, shows highly significant) (Odd ratio = 35.7). Peripheral neuropathy (27.6%) occurred only in the uncontrolled group (p-value = 0.05)

Conclusion: In our tertiary care center, diabetic foot infections were mainly caused by Gram-negative bacilli, especially *Pseudomonas aeruginosa*. Poor glycemic control and neuropathy strongly correlated with severe infections, multidrug-resistant organisms, and limb loss. High resistance to third-generation cephalosporins and fluoroquinolones limits empirical therapy. Local antibiograms, early surgery, and glycemic control are vital to enhance outcomes and avert amputations.

39. Antiadhesive Activity of Biosurfactants against biofilm producing organisms found in Medical Devices.

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Introduction: Biofilm formation on indwelling medical devices is a major threat in healthcare-associated infections (HAIs), particularly catheter-related infections, as biofilms confer resistance to antimicrobials and contribute significantly to morbidity and mortality. Earlier Medical devices coated with chemical agents often fail to eliminate biofilms completely, necessitating the development of biocompatible anti-adhesive agents. Microbial biosurfactants, especially those produced by microorganisms inhabiting hydrophobic, thus these organic compounds can be used as an alternative

Materials & Methods: Microorganisms were isolated from petroleum-rich/contaminated sites and screened for biosurfactant production using microbiological and biochemical methods. Identification and characterization of biosurfactants were performed using analytical techniques, including LC–MS. Concurrently, biofilm-producing pathogens—*Escherichia coli*, *Pseudomonas aeruginosa*, *Klebsiella* spp., *Acinetobacter* spp., *Staphylococcus aureus*, coagulase-negative staphylococci (CONS), and *Candida* species—were isolated from medical devices (catheter tips, suction tips, and endotracheal tube tips). Anti-adhesive activity of biosurfactants extracted from culture broths was assessed by a microtiter plate assay.

Results: *Aspergillus fumigatus* and *Aspergillus oryzae* were isolated as potent biosurfactant producers. LC–MS analysis revealed production of sphingolipids by *A. fumigatus*, glycolipids by *A. oryzae*, and a combination of both in selected isolates. The biosurfactants demonstrated significant anti-adhesive activity against all tested biofilm producers, with inhibition ranging from 60% to 90%. The strong anti-adhesive effects observed highlights the potential of fungal biosurfactants as effective agents against device-associated biofilms. Their biocompatibility and broad-spectrum activity make them attractive alternatives to conventional chemical agents.

Conclusion: Bio surfactants derived from *Aspergillus* species show promising anti-biofilm activity against major HAI-associated pathogens, warranting further in vivo evaluation and potential clinical application in preventing catheter-related infections.

Serology Abstracts

40. Utility of hs- CRP, Serum Ferritin and Lipoprotein (a) in Early Risk Assessment of Type 2 Diabetes Mellitus

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Introduction: Type 2 Diabetes Mellitus (T2DM) is a chronic metabolic disorder characterized by insulin resistance and persistent hyperglycaemia. Growing evidence suggests that low grade systemic inflammation plays a pivotal role in the development of insulin resistance and cardiovascular complications associated with T2DM. Biomarkers such as high sensitivity C-reactive protein (hs-CRP), Serum ferritin and Lipoprotein (a) are increasingly recognized as important indicators of inflammatory and cardiovascular risk.

Objective: To evaluate and compare the levels of hs-CRP, Serum Ferritin and Lipoprotein (a) in newly diagnosed T2DM patients and healthy control subjects.

Materials & Methods: This case control study included 180 participants aged 30-65 years, comprising 90 newly diagnosed T2DM patients and 90 age matched healthy controls. Serum hs-CRP was measured using a turbidimetric immunoassay, serum ferritin by semi-auto analyzer and Lipoprotein (a) by immunoassay. Statistical analysis was performed using SPSS and independent t-tests were applied to assess differences between groups.

Results: Levels of hs-CRP, Serum Ferritin and Lipoprotein (a) were significantly higher in patients with T2DM compared with healthy control subjects. The differences between the two groups were highly statistically significant for all three biomarkers ($p < 0.001$)

Conclusion: Newly diagnosed T2DM patients exhibit significantly elevated inflammatory and cardio metabolic biomarkers, reflecting the role of chronic inflammation and oxidative stress in disease pathogenesis. Estimation of hs-CRP, Serum Ferritin and Lipoprotein (a) may be useful for early stratification, monitoring disease progression and

41. A comparative study of Rheumatoid Factor and Anti-Citrullinated Protein Antibody Profiles in Rheumatoid Arthritis.

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Institute: Integral Institute of Medical Sciences & Research, IU.

Introduction: Rheumatoid arthritis is a chronic systemic disorder characterized by persistent synovial inflammation, progressive joint destruction and significant functional disabilities with a global prevalence of 0.5-1 % and 0.28-0.7 % in India. RF is widely used in the diagnosis of rheumatoid arthritis, but its usefulness is limited due to low specificity and frequent positivity in other autoimmune diseases, chronic infections, and even healthy individuals. In contrast, Anti-CCP antibodies provide much higher specificity and are strongly associated with early disease onset.

Materials & Methods: This comparative case control study included 172 participants categorized into 2 groups - 86 with (RA) and 86 with clinically suspected cases of RA with joint pain (disease control). The study adhered to EULAR/ACR criteria for inclusion patients clinically suspected of having RA. Peripheral blood samples were collected, and serum was tested for RF and Anti-CCP antibodies using ELISA. The diagnostic performance of both markers is being assessed and compared.

Results: This study outlines biomarker patterns in 86 RA cases, showing predominance of dual RF + Anti-CCP positivity (58.9%). Single-marker positivity for RF (12.9%) & Anti-CCP (16.1%) occurred less frequently. A small subset (12.1%) was seronegative for both markers. Overall, dual positivity represents the dominant serological profile in this study. Across both groups, Group C and Group DC, female participants dominate, which is consistent with the known higher prevalence of rheumatoid arthritis among females. The peak age for RA is 41-50 years and second peak age is 31-40 years. These two age groups together account for approx. 68% of all RA cases.

Conclusion: As we know Anti-CCP antibodies are a more specific and reliable biomarker for the diagnosis of RA than RF. However, using both RF & Anti-CCP together provides better diagnostic confidence. Early inclusion of Anti-CCP testing can help in timely diagnosis and improved management of patients with RA.

42. Seasonal Trends and Etiological Profile of Acute Febrile Illness: A Laboratory- Based Surveillance Study from a Tertiary Care Centre in Eastern Uttar Pradesh

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Co-Authors: Dr Pranshu Pandey

Institute: Maharshi Devraha Baba Autonomus State Medical College, Deoria

Introduction: Acute febrile illness (AFI) is a major cause of healthcare utilization in low- and middle-income countries, including India, and poses significant diagnostic challenges in tropical regions due to overlapping clinical presentations of vector-borne and zoonotic infections. Laboratory-based sentinel surveillance plays a crucial role in identifying etiological agents and understanding seasonal patterns of AFI.

Materials & Methods: A retrospective, laboratory-based observational study was conducted from January to December 2025. Surveillance data from the Sentinel Surveillance Hospital (SSH) laboratory were analyzed for total samples tested and laboratory-confirmed positivity for dengue, chikungunya, scrub typhus, leptospirosis, Japanese encephalitis, and malaria. Seasonal trends and co-positivity were assessed.

Results: A total of 1,434 samples were tested during the study period. Scrub typhus emerged as the most common etiology (n = 124), followed by leptospirosis (n = 16) and dengue (n = 15). Co-positivity for scrub typhus and leptospirosis was observed in two cases. Peak positivity for AFI pathogens was noted during the post-monsoon months (August–October), with a marked increase in scrub typhus cases in October (n = 51). Dengue cases were sporadic with mild seasonal clustering. No malaria positivity was detected during the study period.

Conclusion: Scrub typhus was the predominant cause of acute febrile illness in this region, demonstrating a strong post-monsoon seasonal trend. Continuous laboratory-based surveillance is essential for early etiological identification and for guiding timely public health interventions in endemic settings.

43. A Comparative study of diagnostic performance of weil felix, enzyme linked immunosorbent assay and real time polymerase chain reaction targeting 47kda gene for detection of acute scrub typhus infection.

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Co-Authors: R. Sujatha

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Scrub typhus (mite-borne typhus) Tsutsugamushi temporary camps are a disease) is an acute, febrile, infectious illness that is caused by *Orientia (Rickettsia) tsutsugamushi* which belongs to Rickettsiaceae family. Scrub typhus remains difficult to diagnose and standard lab tests are often unreliable, more than a century after its initial description.

Materials & Methods: This was a Comparative Observational study conducted in the Department of Microbiology, Rama Medical College from April 2024 to September 2025. A total no. of 60 samples from patients of PUO was collected and was comparatively analysed by Weil-Felix, IgM ELISA and RT-PCR.

Results: Out of 60 clinical samples 36 (60%) were Males and 24 (40%) were Females mainly 0-15years of age. Most of the patients belong to rural areas reflecting exposure to mite- infested rural environments. Month-wise distribution revealed a higher number of cases during the monsoon month i.e July to September. Fever was the predominant symptom present followed by headache in 48 (80%) and myalgia in 46 (76.6%). The prevalence of Weil-Felix was 6.6%, 7 patients tested positive for IgM ELISA i.e prevalence of 11.6%, 10 patients were positive by RT-PCR i.e prevalence of 16.7%.

Conclusion: RT-PCR targeting the 47 k Da gene demonstrated the highest diagnostic accuracy, particularly in early infection and therefore serves as gold standard. However, its routine use is limited by cost and technical requirements, ELISA can be performed as it is cost effective.

44. To Study The Seroprevalence of Hepatitis B Virus Infection Markers and its Associated Risk Factors in Patients Attending in Rama Medical College, Kanpur

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Co-Authors: Dr R. Sujatha

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Introduction: Hepatitis B virus (HBV) infection remains a major global and national health concern and is leading cause of chronic liver disease, cirrhosis, and hepatocellular carcinoma. The infection often remains asymptomatic for prolonged period, making early diagnosis through serological and molecular markers essential for prevention and control.

Materials & Methods: This Observational study was conducted in the department of microbiology of Rama Medical College from 2024 April to 2025 September. Blood samples were screened for Hepatitis B serological markers by ICT, ELISA & rT PCR. Demographic details, blood investigation, risk factors were Analyzed using SPSS version 22.0 software program.

Results: Out of 70 HBsAg-positive individuals 41(58.6%) were males and 29(41.4%) were females. The age-wise distribution showed maximum positivity in the 31–40 years group (31%). Among the positive samples, 24(34.2%) were positive for HBeAg, confirming active viral replication, while 12(17.1%) had anti-HBc (IgM) positivity, suggesting recent infection. The mean viral load was 3.8×10^4 IU/ml. The most significant risk factors identified were blood transfusion (25.7%), dialysis (21.4%), and tattooing (17.1%). Healthcare workers had the highest infection rate (17.14%)

Conclusion: Serological profiling revealed that substantial proportion of infected individuals was in phases associated with active viral replication and high infectivity. The low overall vaccination coverage observed in the study population emphasizes the urgent need to strengthen adult immunization programs.

Mycology Abstracts

45. Unveiling the Burden of Chronic Pulmonary Aspergillosis among Post-Tuberculosis Patients: A Cross-Sectional Hospital Based Study

Author: Dr. Shobhana R Dubey

Co-Authors: Dr. Shweta Suman, Dr. Atul R Rukadikar, Dr. Aroop Mohanty

Institute: AIIMS Gorakhpur

Introduction: Clinical studies about detailed spectrum of aspergillosis in treated tuberculosis (TB) patients are lacking. Hence, a study was undertaken at the All-India Institute of Medical Sciences, Gorakhpur India. Treated patients of pulmonary TB having any symptom such as haemoptysis, cough with expectoration, weight loss, and whose chest X-ray showed residual cavitation was enrolled for the study.

Objectives-

To determine the burden of chronic pulmonary aspergillosis in post- pulmonary tuberculosis patients visiting AIIMS Gorakhpur.

To assess presenting symptoms, comorbidities and risk factors associated with CPA.

To determine the positivity rates of mycological tests (KOH, fungal culture, Aspergillus IgG ELISA, and PCR)

To compare Aspergillus PCR results with fungal culture for CPA diagnosis.

Materials & Methods: A hospital-based cross-sectional study was conducted in a tertiary care hospital of Eastern Uttar Pradesh. Sputum and blood samples coming to pulmonary medicine OPD with clinical and radiological features and who fulfil the inclusion criteria were included in the study. Demographic details, predisposing factors, and clinical findings were noted. Samples were processed as per standard guidelines. ELISA and PCR were performed as per manufacturers instruction.

Results: Aspergillus IgG antibody was positive in 41.8% of the study population, making serology the most sensitive diagnostic modality for detecting CPA among post-tuberculosis patients. The overall diagnostic yield of conventional methods for culture positivity was 13.64%, PCR positivity was 18.18%, KOH positivity was 7.3% respectively.

Conclusion: The findings support the adoption of a standardized diagnostic algorithm for post-TB patients, prioritizing Aspergillus IgG testing, CT thorax imaging, and adjunct PCR, especially in symptomatic individuals with residual lung lesions.

46. Phenotypic characterization of *Candida* causing blood stream infections at a tertiary care hospital in western Uttar Pradesh: Changing Trends

Author: Dr. Sanjeet Singh

Co-Authors: Vandana Sardana, Premlata Yadav

Institute: SRMS IMS, Bareilly

Introduction: Candidemia is one of the common causes of blood stream infection worldwide, leading to significant mortality & morbidity. A paradigm shift of *C.albicans* to Non-albicans *Candida* (NAC) has led to the escalation in resistance to empirically used antifungals.

Objectives:

To determine the prevalence of Candidemia

To speciate the *Candida* isolates obtained from blood samples

To determine antifungal susceptibility of *Candida* isolates causing blood stream infections

Materials & Methods: Prospective study (January 2025-December 2025). Blood samples, were processed by the automated BACTEC system. Bottles beeped positive for growth were subcultured onto blood agar and MacConkey's agar. Culture smears showing budding yeast cells were further identified by VITEK-2 system using YST card and antifungal susceptibility testing was determined by VITEK-2 AST-YS08 card.

Results: Prevalence of candidemia was 2.9% (out of total blood cultures received-3419), out of which 62% of cases accounted to NAC. Among NAC, commonest isolate was *C.tropicalis* (23%), followed by *C.glabrata* (12%) & *C.parapsilosis* (8%). Among antifungals tested, NAC isolates were significantly sensitive to Echinocandins (80%), of which *C.tropicalis* showed highest sensitivity to Echinocandins. *C.glabrata* showed sensitivity to MICAFUNGIN (100%) & AMPHOTERICIN B (100%) but resistant to CASPOFUNGIN (41%). *C.glabrata* showed resistance to FLUCONAZOLE (100%), VORICONAZOLE (80%), FLUCYTOSINE (80%), *C.albicans* showed lower rate of resistance to Azoles [VORICONAZOLE (26%), FLUCONAZOLE (36%)]

Conclusion: Emergence of multidrug resistant Non albicans *Candida* causing blood steam infections has become a therapeutic threat. Speciation of *Candida* isolates becomes essential owing to their innate resistance to Antifungals, especially *C.glabrata* and *C.krusei* being inherently resistance to azoles.

47. Proteomic analysis of *Aspergillus fumigatus* secretome over different days reveals a persistent 71 kDa immunogenic protein

Author: Aishwarya Nikhil

Co-Authors: Raj Kishor, Ragini Tilak, Dr. Munesh Kumar Gupta

Institute: Department of Microbiology, Institute of Medical Science, B.H.U, Varanasi-221005

Introduction: *Aspergillus fumigatus* is an airborne fungal pathogen causing allergic reactions to invasive pulmonary infections. Traditional diagnostics are time-consuming, necessitating efficient detection methods, with secreted proteins key to virulence via nutrient absorption and tissue invasion. Secretome analysis identifies allergens and immunoreactive molecules, offering insights into virulence factors, drug targets, and immunodiagnostics.

Materials & Methods: *A. fumigatus* inoculum (0.08-0.1 OD, 1 mL) was cultured in SDB media across six flasks, with secretory proteins isolated from days 4, 8, 12, 16, 20, and 24. Protein concentrations were quantified using the BCA and Nano Drop (UV 280 nm) methods, followed by SDS-PAGE, Western blot analysis with a primary antibody from mouse serum, along with an HRP-secondary antibody, and 2D-electrophoresis.

Results: Protein concentration increased over time: BCA (D4: 106 µg/ml, D8: 195, D12: 301, D16: 406, D20: 503, D24: 597 µg/ml); Nano Drop (D4: 135, D8: 235, D12: 362, D16: 432, D20: 542, D24: 623 µg/ml). SDS-PAGE showed degradation after day 16, with stable 91 and 54 kDa proteins; Western blot detected a persistent 71 kDa immunogenic protein across days 8-24; 2D-electrophoresis localized 71 kDa protein at pI 4-5.

Conclusion: Secretory protein levels rise continuously, with a stable 71 kDa immunogenic protein persisting, providing new insights into *A. fumigatus* secretome for further virulence and diagnostic exploration.

48. A Study of *Candida tropicalis* and their Antifungal Susceptibility Pattern

Author: Dhananjay Kumar

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Institute: National Institute of Medical Sciences & Research, Jaipur

Introduction: *Candida tropicalis* is among the most frequently isolated *Candida species* from clinical specimens of patients admitted to intensive care units, particularly those with hematologic malignancies or those requiring prolonged catheterization or receiving broad-spectrum antibiotics. The species appears to have greater propensity to cause invasive disease in neutropenic patients and may be responsible for higher mortality than *Candida albicans*. With this background this study was done on clinical specimens from outpatients and inpatients at NIMS hospital, Jaipur, Rajasthan.

Materials & Methods: This study was done from September 2024 to August 2025 on clinical specimens of all ages and both sexes received in Microbiology laboratory were processed as per the standard microbiological procedures. *Candida tropicalis* were identified by conventional microbiological techniques and confirmed by Vitek-2 Compact system (BioMerieux) and Anti-Fungal Susceptibility of *Candida* isolates was also done by Vitek-2.

Results: A total of 59 *Candida tropicalis* isolates were recovered from various clinical samples. Voriconazole showed highest susceptibility 58/59 (98.3%) followed by Micafungin 57/59 (96.6%), Caspofungin 56/59 (94.9%), and Amphotericin B 56/59 (94.9%). Lower susceptibility was observed with Flucytosine, where 53/59 (89.8%) followed by Fluconazole 52/59 (88.1%).

Conclusion: *Candida tropicalis* emerged as a significant *Candida species* isolated from both outpatient and inpatient clinical specimens at a tertiary care center in Rajasthan. *Candida tropicalis* showed high susceptibility to Voriconazole, echinocandins, and Amphotericin B, while reduced susceptibility was observed with Fluconazole and Flucytosine. Routine antifungal susceptibility testing is essential to guide effective therapy and monitor emerging resistance patterns optimize antifungal stewardship.

49. Species Distribution and Antifungal Susceptibility Pattern of Candida Isolates from Clinical Samples in a Tertiary Care Hospital”

Author: Dr. Rahul Ranjan

Co-Authors: Divakar Srivastava², Rakesh Mukhia³, Razia Khatoon⁴

Institute: Hind Institute of Medical Sciences, Mau, Ataria, Sitapur

Introduction: Candida species are important opportunistic fungal pathogens causing a wide spectrum of infections. The increasing prevalence of non-albicans Candida species and antifungal resistance necessitates routine species identification and antifungal susceptibility testing for effective patient management.

Objectives: To determine the demographic profile, species distribution, and antifungal susceptibility pattern of Candida isolates from various clinical samples.

Materials & Methods: This cross-sectional study included 85 non-duplicate Candida isolates obtained from OPD and IPD patients. Samples included urine, blood, sputum, vaginal swab, and pus. Identification was done using standard mycological methods including KOH mount, germ tube test, and species-level identification. Antifungal susceptibility testing was performed against fluconazole, voriconazole, itraconazole, ketoconazole, miconazole, nystatin, amphotericin B, and caspofungin.

Results: The mean age of patients was 44.7 ± 17.6 years, with a slight female predominance (50.6%). Most isolates were obtained from OPD patients (67%), and urine was the most common sample (28.2%). Candida albicans (52.9%) was the predominant species, followed by Candida tropicalis (31.8%), Candida krusei (9.4%), Candida glabrata (4.7%), and Candida dubliniensis (1.2%). All isolates were 100% sensitive to amphotericin B. Sensitivity to azole antifungals was variable, with fluconazole showing 56.5% sensitivity. High resistance was observed to nystatin (54.1%).

Conclusion: Candida albicans remains the most common isolate; however, non-albicans Candida species constitute a significant proportion. The observed azole resistance underscores the need for routine antifungal susceptibility testing to guide appropriate therapy.

Keywords: Candida species, Antifungal susceptibility, Non-albicans Candida, Azole resistance.

50. Rare Cases of Disseminated Cryptococcosis from Soft Tissue and Lung Tissue in Young Immunocompromised Patients

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Institute: Sanjay Gandhi Post Graduate Institute of Medical Sciences. Lucknow

Introduction: Cryptococcosis is the infection caused by *Cryptococcus neoformans* or other species, usually affects the CNS. The majority of disseminated cryptococcal infections occur in patients with acquired immunodeficiency syndrome (AIDS) or other immunocompromised states.

OBJECTIVE: Here we present two cases of *Cryptococcus neoformans* infection in young immunocompromised patients.

1st case- A 28year male, presented to the OPD with chief complaints of fever, headache, cough x 1 week.

Past history: The patient is k/c/o Alports syndrome, Hypertension with Chronic kidney disease. Patient is a ABO compatible renal transplant recipient (Date of transplant-23.1 2024). Patient is on triple immunosuppression. Chest X ray, HRCT Chest revealed cavitary lesions with ground glass opacity. On KOH of lung biopsy tissue: Few round budding cells seen. CSF was positive by calas test (titre 1:4). On culture of Lung bx and CSF *Cryptococcus neoformans* grew, confirmed by MALDI-TOF. Tab Flucytosine was given. Patient is on lifelong Fluconazole prophylaxis.

2nd Case: A 33year male, presented to the OPD with **Chief complaints** of Non healing anterior left midhigh ulcer x 6 months. Ulcer initially started 6 months back with rash, associated with redness, fever. Then slowly started increasing in size.

Past history: Hepatitis C virus positive. Live related ABO compatible kidney transplant recipient, date of transplant: 22/6/23, is on dual immunosuppression.

Ulcer was examined.1st Swab for microscopy showed few round budding yeast like cells and culture was s/o- *Cryptococcus neoformans* further confirmed by MALDI TOF for which patient was started on IV Amphotericin B. The patient improved and was discharged with advice to continue wound dressing.

Results: These two case reports are rare cases of disseminated *Cryptococcosis* in immunocompromised patients with no history of bird droppings nearby.

Conclusion: We summarize the biological aspects of *Cryptococcus* the diagnosis and management of pulmonary and soft tissue cryptococcosis.

51. Bench to Bedside Evaluation of Newer Topical Antifungals in Dermatophytosis: Correlating In Vitro Susceptibility with Clinical Outcomes Using Combination Oral Therapy

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Co-Authors: Prashant Gupta, Gopa Banerjee, Swastika Suvirya, Parul Verma

Institute: Autonomous State Medical College, Amethi, Uttar Pradesh

Introduction: Dermatophytosis is a common superficial fungal infection in tropical regions such as India and is increasingly associated with chronicity, relapse, and treatment failure. While resistance to systemic antifungals has been reported, limited data correlate in vitro antifungal susceptibility with in vivo clinical outcomes, particularly for newer topical agents used in combination therapy.

Objectives: To correlate the in vitro antifungal susceptibility profiles of systemic and newer topical antifungal agents with clinical outcomes in patients with dermatophytosis treated with combination oral and topical therapy.

Materials & Methods: This study included in vitro and in vivo components. Antifungal susceptibility testing was performed on 204 dermatophyte isolates (*Trichophyton rubrum*, *T. mentagrophytes/interdigitale*, *T. tonsurans*, and *Epidermophyton floccosum*) using the CLSI broth microdilution method (M38-A3). Minimum inhibitory concentrations (MICs) were determined for fluconazole, itraconazole, griseofulvin, luliconazole, and sertaconazole. Clinically, 204 culture-confirmed dermatophytosis patients received combination therapy with oral fluconazole or itraconazole plus topical luliconazole or sertaconazole. Treatment outcomes were assessed as complete cure, treatment failure, or relapse.

Results: Fluconazole demonstrated consistently higher MIC values than itraconazole across all dermatophyte species (MIC₉₀: 32–64 µg/ml vs 0.25–0.5 µg/ml), indicating lower in vitro potency. This was reflected clinically, with itraconazole-based regimens achieving higher cure rates (66.1%) compared to fluconazole (62.2%). Among topical agents, luliconazole showed uniformly low MICs (MIC₅₀/MIC₉₀: 0.004 µg/ml), whereas sertaconazole exhibited higher MIC ranges (MIC₉₀ up to 2 µg/ml). Correspondingly, luliconazole combined with itraconazole resulted in a 100% cure rate, compared to 80% with sertaconazole.

Conclusion: A strong concordance was observed between in vitro antifungal susceptibility and clinical response. Lower MICs of itraconazole and luliconazole translated into superior therapeutic outcomes, supporting their rational use in combination therapy for dermatophytosis.

52. Evaluation of graphene oxide and zinc oxide antifungal activity against fungal pathogen *Candida auris*.

Author: Megha Singh

Co-Authors: Dr. Shalini Malhotra, Dr. S.P. Singh, Dr. Sunil Chauhan and Dr. Ankit Chauhan.

Institute: Department of Microbiology, ABVIMS and Dr. RML Hospital, New Delhi.

Introduction: *Candida* species is the third most common cause of bloodstream infections in hospital care units. Globally *Candido* referred to as *Candida auris* has emerged as a multidrug-resistant health care associated fungal pathogen with increasing reported cases in the last two decades. There are limited antifungal agents that are effective against *C. auris*, hence there is a requirement of novel agents to combat its resistance. Nanomedicine based therapy including various nanoparticles such as silver, titanium oxide, carbon based and zinc oxide can offer a promising technology to fight the fatal spread.

Materials & Methods: Twelve *Candida auris* strains were isolated from the various clinical samples received in Department of Microbiology, ABVIMS and Dr RML Hospital, New Delhi. Zinc oxide nanoparticles were formulated by Spanhel sol gel method and graphene oxide were performed by modified hummer's method and characterized by various techniques.

Antifungal activity of zinc oxide and graphene oxide was performed according to CLSI document based microbroth dilution method and MIC was recorded at various concentrations.

Results: Individual MIC (Minimum Inhibitory Concentration) values of zinc oxide and graphene oxide 40 and 20 µg/ml. making resistant pathogen fall in susceptible range.

Conclusion: We evaluated zinc oxide and graphene oxide against *Candida auris* and the study shows that both the nanoparticles possess antifungal activity and can enhance efficacy of present therapeutics.

53. Beyond Dermatophytes: Emerging Role of Non-Dermatophyte Fungi in Onychomycosis— Clinical Spectrum, Risk Factors, and Treatment Outcomes

Author: Pragya Pandey

Co-Authors: Sonakshi Srivastava, Anupam Das, Jyotsna Agarwal

Institute: RMLIMS, LUCKNOW

Introduction: Onychomycosis is a common fungal infection of the nails characterized by discoloration, thickening, brittleness, and functional impairment, significantly affecting quality of life. Although dermatophytes, particularly Trichophyton species, have traditionally been considered the primary causative agents, recent studies demonstrate an increasing role of non-dermatophytic moulds and yeasts as true pathogens. Organisms such as *Candida*, *Aspergillus*, *Fusarium*, *Acremonium*, and phaeoid moulds are being reported with greater frequency, especially in tropical and subtropical regions.¹

Materials & Methods: A retrospective study was carried out in the Department of Microbiology from January to December 2025. A total of 256 nail samples obtained from clinically suspected cases of onychomycosis were included. Samples were collected in the microbiology laboratory and subjected to direct microscopic examination using potassium hydroxide (KOH) mount, followed by culture on Sabouraud Dextrose Agar. Fungal isolates were identified and confirmed using Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF MS).

Results: Out of the 256 samples analyzed, 27 cases (10.5%) were confirmed as non-dermatophyte onychomycosis. The most commonly affected age group was 21–30 years, with a male predominance (71.4%). *Candida* species were the predominant isolates (52%), mainly *Candida krusei*, followed by *Aspergillus* species (33%), *Fusarium* species (7.5%), and phaeoid molds (7.5%). Fingernails were more frequently involved (70%) than toenails (48%). Nail bed involvement was most common (37%), followed by distal lateral involvement (26%). Associated risk factors were identified in 33% of cases, with diabetes mellitus being the most frequent (44%). Clinical resolution with itraconazole therapy was observed in 52% of patients.

Conclusion: Non-dermatophyte fungi represent an emerging and significant cause of onychomycosis, underscoring the importance of accurate species identification using advanced diagnostic modalities for optimal management.

54. Clinical and Molecular Epidemiology of *Candida utilis* Candidemia in a Neonatal Intensive Care Unit: Risk Factors, Antifungal Susceptibility, and Phylogenetic Analysis

Author: Kalpana Kuntal

Co-Authors: Prashant Gupta, Vijay Sonkar, Vivek Kumar, Vimala Venkatesh

Institute: King George's Medical University,

Introduction: Neonatal candidemia remains an important cause of morbidity and mortality in neonatal intensive care units (NICUs). Recent shifts in epidemiology toward non-*albicans* *Candida* species have highlighted the need for species-level identification and antifungal susceptibility testing, particularly for emerging uncommon yeasts such as *Candida utilis*.

Materials & Methods: We conducted an observational study in a tertiary care NICU in India including neonates with blood culture-confirmed *C. utilis* candidemia (January 2022–December 2025). Clinical and outcome data were extracted from records. Blood culture isolates were identified by MALDI-TOF MS. Antifungal susceptibility testing was performed by CLSI broth microdilution against fluconazole, voriconazole, amphotericin B, and caspofungin. Molecular confirmation and phylogenetic relatedness were assessed by sequencing the ITS (ITS1–5.8S–ITS2) region, followed by alignment and phylogenetic tree construction with bootstrap analysis. Logistic regression evaluated predictors of mortality.

Results: Forty-five neonates were included; 30/45 (66.7%) survived and 15/45 (33.3%) died. Non-survivors had significantly lower birth weight ($p=0.012$) and gestational age ($p=0.023$) with higher prematurity ($p=0.003$). Central line exposure ($p<0.001$) and mechanical ventilation within 72 h of onset ($p<0.001$) were strongly associated with mortality. Fluconazole showed a broader MIC distribution (MIC₅₀/MIC₉₀: 1/16 $\mu\text{g/mL}$) compared with amphotericin B, voriconazole, and caspofungin. On multivariable analysis, mechanical ventilation within 72 h remained dependently associated with mortality ($p=0.001$). Monthly distribution showed sporadic occurrence with intermittent clustering.

Conclusion: *Candida utilis* is an emerging cause of neonatal candidemia with substantial mortality. Species confirmation, MIC surveillance, and phylogenetic analysis may support early detection of clustering and strengthen infection prevention strategies in NICU settings.

55. Candidemia in Paediatric population: An Emerging Threat!

Author: Krishnendu R

Co Author: Asfia Sultan, Nandini, Parvez Anwar Khan

Institute: Jawaharlal Nehru Medical College, Aligarh Muslim University

Introduction: Candidemia is a major cause of bloodstream infection in neonatal and pediatric intensive care units (ICUs) and is associated with high morbidity and mortality. The increasing predominance of non-albicans *Candida* species and emerging resistance to commonly used antifungal agents, particularly fluconazole, have made management challenging. Early identification of species and prompt initiation of appropriate antifungal therapy are key factors influencing patient outcomes.

Objectives: To evaluate the species distribution of *Candida* isolates, antifungal resistance patterns, and risk factors associated with candidemia in neonatal and pediatric ICU patients.

Materials & Methods: A prospective observational study was conducted in the Department of Microbiology, JNMC, AMU, Aligarh. A total of 4,177 blood cultures were processed, of which 732 (17.52%) were positive. 85 (11.6%) *Candida* isolates were identified. Species identification, antifungal susceptibility testing, and risk factors associated were analyzed.

Results: Non-albicans *Candida* species accounted for 80 (94.1%) of the isolates. *Candida parapsilosis* was the most common isolate identified in 32 (40.0%), followed by *Candida tropicalis* in 12 (15%). Fluconazole resistance was observed in 12 (15%) isolates, including resistance among the commonly isolated non-albicans species. The major risk factors associated with candidemia were central venous catheters in 62(73%), thrombocytopenia in 58(68%), mechanical ventilation in 45(53%), low birth weight (LBW/VLBW/ELBW) in 39 (45%), neutropenia in 16 (19%), and steroid therapy in 14(16%). 64(75%) patients had sepsis, 22(26%) had septic shock, 19(22%) had acute kidney injury and 9(11%) had hepatitis.

Conclusion: This study highlights a clear shift towards non-albicans *Candida* species with notable fluconazole resistance. Identifying risk factors, promoting early diagnosis, and implementing antifungal stewardship programs can aid in timely initiation of appropriate therapy, which can improve patient outcomes.

56. Therapeutic Drug Monitoring of Voriconazole in Adult Hemato-Oncological Patients with Invasive Aspergillosis

Author: Dr Saurabh Kumar Nande

Co-Authors: Prof. Prashant Gupta, Prof. Gopa Banerjee, Dr. Shailendra Prasad Verma

Institute: Department Of Microbiology, King George's Medical University, Lucknow, UP

Introduction: Invasive aspergillosis is a life-threatening fungal infection affecting immunocompromised adult hemato-oncological patients. Voriconazole is the drug of choice; however, marked Inter-patient pharmacokinetic variability may result in subtherapeutic or suprathereapeutic levels and drug-related toxicity. Therapeutic drug monitoring is therefore recommended to optimize outcomes and minimize adverse effects.

Materials & Methods: This prospective study included 51 adult hemato-oncological patients with suspected invasive aspergillosis. Therapeutic drug monitoring of voriconazole was performed on the 5th, 7th, 10th and when feasible, 14th day after initiation. Serum trough levels were measured using ultra-high-performance liquid chromatography and microbiological bioassay methods. Patients were categorized as subtherapeutic, therapeutic or suprathereapeutic, Clinical response, adverse drug reactions and dose modification were analyzed. The study was approved by the Institutional Ethics Committee (Reference No. XXIII-PGTSC-IIA/P32; dated 13 May 2024).

Results: Marked inter-patient variability in voriconazole serum concentrations was observed. Therapeutic drug monitoring enabled identification of subtherapeutic and suprathereapeutic levels, allowing timely dose adjustments. Patients attaining therapeutic trough levels showed better clinical response, while suprathereapeutic levels were associated with hepatic, ocular and neurological adverse effects. Brand-based analysis demonstrated variability in achieving therapeutic drug levels.

Conclusion: Therapeutic drug monitoring of voriconazole is crucial for optimizing antifungal therapy in adult hemato-oncological patients with invasive aspergillosis. Routine monitoring enables individualized dose adjustment, improve outcomes and reduces toxicity. Variability between formulations further supports the need for monitoring to ensure adequate drug exposure.

57. Author: (Presenting Author name should be bold and underlined)

Authors: Dr. Surbhi

Co-Authors: Dr. Rungmei S.K. Marak, Mr. Puspak Ghosh, Dr. Subhash Yadav, Dr. Zafar Neyaz, Dr. Manoj Jain

Institute: Sanjay Gandhi Post Graduate Institute of Medical Sciences, Lucknow

Introduction: *Histoplasma capsulatum var capsulatum* is the causative agent of histoplasmosis, a severe fungal infection. Acute primary, chronic cavitory, and progressive disseminated histoplasmosis are the three forms. In this study we aimed to study the prevalence, demographic pattern, presenting symptoms, risk factors and clinical outcomes in patients with *Histoplasma capsulatum* infection.

Materials & Methods: This ambispective study was conducted in the Microbiology laboratory of a Tertiary Care Centre, from 2015 to 2025. In collaboration with Endocrinology, Pathology and Radiology departments. The adrenal biopsy samples from suspected patients of histoplasmosis were collected and sent to the Mycology laboratory. Direct microscopy i.e. 10% KOH wet mount, Giemsa and Gram staining were performed for the detection of histoplasmosis. Culture was done on Sabouraud's dextrose agar and incubated at 37°C & 25°C for 8 weeks. The patient's demographic details and clinical features were filled in a proforma and analysed and incubated at 37°C & 25°C for 8 weeks. The patient's demographic details and clinical features were filled in a proforma and analyzed.

Results: During the study period (2015-2025), 198 adrenal biopsy samples were received from patients with suspected Histoplasmosis. Of which 33 (16.67%) samples were positive for *Histoplasma capsulatum*. These samples included adrenal biopsies (31); pus (1) and skin biopsy (1). Maximum number of samples were positive in the year 2024 (29.4%). Microscopy was positive for *Histoplasma capsulatum* in all the 33 samples; however, culture was positive in only 20 (60%). Majority of the patients belonged to the age group of 61-80 years. Median age of affected patients were 57 years. A male predominance of 94% was seen. All the patients were on immunosuppressants and 80% had Type II Diabetes Mellitus. Most of the patients presented with weight loss (72%), fever (44%) and decreased appetite (36%). All the patients were treated with liposomal amphotericin B. No mortality was seen amongst the patients

Conclusion: Awareness of clinical presentation, risk factors and underlying comorbidities are needed to provide timely diagnosis and appropriate treatment for patients with *Histoplasma capsulatum* infection.

Virology Abstracts

58. Screening of Blood Donors for Parvovirus B19 in a Tertiary Care Centre of Lucknow

Author: Dr Poonam Tiwari

Co-Authors: Prof. Vineeta Mittal

Institute: Dr Ram Manohar Lohia Institute of Medical Sciences Lucknow

Introduction: Parvovirus B19 is a clinically significant transfusion-transmissible virus associated with adverse outcomes in pregnant women, patients with hemolytic disorders, and immunocompromised individuals. Despite this risk, routine donor screening for Parvovirus B19 is not universally practiced in India

Materials & Methods: A cross-sectional study was conducted among 250 voluntary blood donors at a tertiary care centre in Lucknow. Donors were selected according to standard eligibility criteria. Serum samples were tested for Parvovirus B19 IgM and IgG antibodies using enzyme-linked immunosorbent assay (ELISA). Blood group distribution and serological results were analysed

Results: Out of 250 blood donors, 34 (13.6%) IgM positive, indicating recent infection, while 216 (86.4%) were IgM negative. IgG antibodies detected in 167 donors (66.8%), suggesting past exposure, whereas 83 donors (33.2%) IgG negative. Blood group distribution showed predominance of Rh-positive donors, with B+ve (85) being the most common, followed by O+ ve (70), A+ ve (65), and AB+ ve (21). Rh-negative groups included B-ve (5), A- ve (2), and O- ve (1).

Conclusion: This study demonstrates a high seroprevalence of Parvovirus B19 IgG antibodies and a considerable proportion of IgM positivity among blood donors, indicating active circulation of the virus in the community. These findings emphasise the potential risk of transfusion-transmitted Parvovirus B19 and support consideration of selective donor screening, particularly for blood components intended for high-risk recipients.

59. Viral profile of Acute Respiratory Infections in children less than 2 years

Author: Marak DAK

Co-Authors: Gupta V, Jain S

Institute: Government Medical College & Hospital (GMCH), Chandigarh

Introduction: Acute respiratory infections (ARI) are a leading cause of mortality and morbidity among children in India, particularly below two years. As of 2025, Influenza remains the most prevalent virus, followed by RSV, Rhinovirus and Coronavirus. Due to limited data on viral respiratory infections in children under two years in Chandigarh, this study aims to identify the causative respiratory viruses

Materials & Methods: This prospective cross-sectional study included nasopharyngeal samples from children under 2 years with ARI admitted between May 2024 and September 2025. Samples were subjected to Multiplex PCR testing for 14 viral respiratory viruses.

Results: In this study, RSV was the most frequently detected virus (40%) followed by H3N2 (15%), Adenovirus (11%), Rhinovirus (11%), Influenza B (6 %), Coronavirus, Bocavirus and Pandemic H1N1 (3%). The overall viral positivity rate was 75%, with single-virus infections in 48%, dual infections in 18%, and triple infections in 3% of cases. Males constituted 70% of patients, while females were 30%, and 16% were less than 1 month. Cough (79%) and fever (49%) were the most common symptoms. Viral detection peaked in December, with slight rise in February and September. Children aged 0–1 month showed severe symptoms, require oxygen support and experience longer hospital stay.

Conclusion: Respiratory viral infections are highly prevalent among children under two years with ARI, with RSV emerging as the predominant pathogen in our setting. This highlights the importance of multiplex PCR for early diagnosis, seasonal surveillance, and targeted management to reduce disease burden.

60. Detection and Correlation of HBV-DNA With HbeAg and Anti- HbeAg Serological Status in HbsAg Positive Patients in a Tertiary Care Hospital

Author: Dr. Monalisa Baidya

Co-Authors: Dr. Neelima Kulshetha, Dr. Divakar Srivastava, Dr. Rakesh Kumar Mukhia, Dr. Razia Khatoon, Dr. Riddhi Singh

Institute: Hind Institute of Medical Sciences, Mau, Ataria, Sitapur

Introduction: Serological detection of HBV is considered to be the cornerstone for diagnostic and therapeutic purposes but their values in different stages of infection are doubtful. In the recent years genetic and molecular techniques have proven to be more accurate. Still the serological titres seem to be informative and useful in prediction of HBV-DNA status. Hence, the present study was planned to detect and correlate the HBV-DNA level with the HBsAg and Anti-HBe serological status in HBsAg-positive patients.

Materials & Methods: A total of 80 HBsAg positive patients (age range 16-80 years; mean age 42.43 ± 17.63 years; 65% males) were enrolled in the study. Quantitative HBsAg, HBeAg and AntiHBeAg assessments were performed using chemiluminescent immunoassay and enzyme-linked Immunosorbent assay (ELISA). HBV-DNA assessment was done using TRUENAT based PCR method. Data was statistically analyzed using Mann-Whitney U and chi-square test. ROC analysis was also performed.

Results: HBV DNA was detected in 73/80 (91.3%) cases. HBeAg and Anti HBeAg were detected in 27.5% and 42.5% cases respectively. HBV-DNA showed a significant association with HBsAg and HBeAg but not with anti HBeAg. There was a strong positive significant correlation of HBsAg levels and HBV-DNA levels ($r > 0.7$; $p < 0.001$). HBeAg levels also showed a mild significant positive correlation with HBV-DNA levels ($r = 0.414$; $p < 0.001$). On ROC analysis, HBsAg and HBeAg had area under the curve values of 0.965 and 0.743. HBsAg was 79.5% sensitive and 100% specific in detection of HBV-DNA while HBeAg was 80.8% sensitive and 85.7% specific in detection of HBV-DNA.

Conclusion: The findings of study depicted high prevalence of HBV-DNA positivity in HBsAg positive hospitalized patients. Quantitative HBsAg and HBeAg levels emerged as useful predictors of HBV-DNA positivity.

61. Molecular Surveillance of Acute Respiratory Viral Infections in Central India: Etiology, Co-infection Patterns, and Clinical Correlates”

Author: Harjeet Singh Maan

**Co-Authors: Deepti Chaurasia, Lokendra Dave, Shweta Sharma, Praveen Dandekar,
Garima Kapoor**

**Institute: State Virology Laboratory, Department of Microbiology, Gandhi Medical College,
Bhopal, Madhya Pradesh**

Introduction: Acute respiratory infections (ARI) are a major cause of morbidity and hospitalization in India, especially among children and older adults. Concurrent circulation of multiple respiratory viruses with overlapping symptoms complicates clinical diagnosis. This study aimed to characterize the viral etiology of ARI in a sentinel population from Bhopal using multiplex PCR, assessing virus distribution, co-infections, and demographic–clinical correlates.

Materials & Methods: A short-term molecular surveillance study was carried out at the State Virology Laboratory, Gandhi Medical College, Bhopal, from July to October 2025. Nasopharyngeal and/or oropharyngeal swabs from patients with influenza-like illness (ILI) and severe acute respiratory infection (SARI) were tested using a multiplex real-time RT-PCR panel for Influenza A (H1N1pdm09, H3N2), Influenza B, Respiratory Syncytial Virus (RSV A/B), Adenovirus, Rhinovirus, and SARS-CoV-2. Demographic, clinical, and laboratory data were analyzed descriptively, including the evaluation of mono- and co-infections across different age groups and clinical categories.

Results: Of the 121 respiratory samples examined, a considerable proportion tested positive for one or more respiratory viruses. RSV A/B and Adenovirus emerged as the most prevalent pathogens, particularly among children aged ≤ 5 years. Influenza viruses and SARS-CoV-2 were more frequently detected in adult populations. Co-infections, including dual and triple viral detections, were commonly observed, particularly among SARI cases and pediatric patients. A significant correlation was identified between viral type and age group ($p < 0.05$). Symptoms such as breathlessness and hypoxia demonstrated a strong association with severe disease.

Conclusion: This study illustrates the varied circulation of respiratory viruses and a significant burden of co-infections in central India. Multiplex molecular diagnostics are instrumental for acute respiratory infection (ARI) surveillance and can facilitate prompt clinical and public health decision-making.

62. Spectrum of Viral Pathogens in Pneumonia Leading to Hospitalization among Children Under Five Years: A Multiplex RT-PCR Analysis

Author: Ashish Singh

Co-Authors: Ankur Goyal, Vikas Kumar, Vinay, Ramshitij, Neeraj Yadav

Institute: Sarojini Naidu Medical College, Agra

Introduction: Community-acquired acute viral respiratory tract infections are among the most common and significant health challenges affecting children under five. These infections are a leading cause of pediatric hospital admissions and contribute substantially to global childhood Morbidity and healthcare burden. CAV-RTIs encompass a wide clinical spectrum, ranging from mild upper respiratory tract illnesses to more severe lower respiratory tract conditions.

Materials & Methods: The study was conducted in Department of Microbiology, SN Medical College, Agra, a tertiary care hospital. Children under 5 years of age with symptoms of acute respiratory tract infections are included in the study.

Nasopharyngeal swabs are taken and Multiplex RT-PCR using commercial respiratory panels are performed. The panel included Human Parechovirus, Human coronavirus, Human parainfluenza virus 1-4, Influenza A virus, H1 influenza virus, Influenza A, B, C viruses, Enterovirus, Human metapneumovirus (A/B), Human adenovirus, RSV (A/B) and Human rhinovirus.

Results: Total 100 children are included in the study, 50 from OPD and 50 from IPD out of which 21 samples were found to be positive for any virus by multiplex RT-PCR. Prevalence of CAV- RTI was found to be 21%.

Hospitalization was required in patients infected with Adenovirus and RSV with Enterovirus/Rhinovirus co-infection. Patients infected with Enterovirus and Human Influenza virus were treated in OPD. RSV infection was appreciated in both hospitalized and non-hospitalized patients.

Conclusion: The present study provides valuable insights into the etiologies of CAV-RTIs in children under 5 years. Knowing the etiologies will help in targeted treatment. Unnecessary use of antibiotic may be prevented.

63. Myxovirus resistance gene as a novel biomarker in acute respiratory viral infection.

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Co-Authors: Ishan, Vikas Patel, Dharamveer Singh, Sangram S Patel, Rungmei S K Marak, Atul Garg

Institute: Sanjay Gandhi Post graduate institute of medical science

Introduction: The human myxovirus resistance protein 1 (MxA) is a key effector of the interferon-induced antiviral response and exhibits broad activity against diverse viral pathogens. Its expression is tightly regulated by type I and type III interferons (Haller et al.). Nearly 80% of all antibiotics are prescribed in primary healthcare settings, the majority for respiratory tract infections, highlighting the need for reliable biomarkers to differentiate viral from bacterial aetiologies (Greece).

Materials & Methods: This prospective study was conducted from April 2024 to the present. Clinically suspected respiratory infections were evaluated using classical culture techniques for bacterial identification and RT-PCR for viral detection. Following confirmation of infection, blood samples were collected, peripheral blood mononuclear cells were isolated, and RNA was extracted and quantified at 200 ng for cDNA synthesis. MxA gene expression was assessed using the $2^{\Delta\Delta Ct}$ method.

Results: Of 150 screened patients, 116 met the inclusion criteria for acute respiratory infection. Most cases presented as influenza-like illness (ILI), with a subset classified as severe acute respiratory infection (SARI). The cohort included 60 males and 41 females (median age: 40 years). Among the enrolled subjects, 44 had viral infections, 30 had bacterial infections including some with sepsis and 34 were healthy controls. Influenza accounted for 32 viral cases, predominantly Influenza A (pdm-09 and H3N2), followed by Influenza B (n=9), rhinovirus (n=2), and hMPV (n=1). Expression analysis was done using the $2^{\Delta\Delta Ct}$ analysis.

MxA expression demonstrated strong discriminatory capacity as a biomarker for acute respiratory infections, with median relative fold changes of 2.82 in SARS-CoV-2 and 3.44 in influenza A/B, resulting in an overall viral median of 3.22. In contrast, bacterial infections exhibited markedly lower expression (0.12), comparable to healthy controls. MxB demonstrates significantly lower discriminatory potential than its homolog MxA, failing to provide high-sensitivity detection of respiratory viruses. Research shows MxB has modest median relative fold changes of 0.57 for SARS-CoV-2, 0.85 for Influenza A, and 0.168 for Influenza B, yielding a combined viral median of 0.822.

Conclusion: With declining morbidity from SARS-CoV-2, most acute respiratory infections continue to be of viral origin. Early identification of viral aetiologies supporting appropriate antiviral therapy can minimize unnecessary antibiotic use and strengthen antibiotic stewardship efforts. A point-of-care MxA-based assay could provide rapid differentiation between viral and bacterial infections and guide optimal clinical decision-making.

64. To Determine Correlation of HBV DNA and HBeAg Status in HBsAg Positive Asymptomatic Patients in a Tertiary Care Hospital, Barabanki, Uttar Pradesh, India.

Author: Dr. Ramendra Pratap Singh

Co-Authors: Anjali Agarwal, Jyoti Srivastava, Rajesh Kumar

Institute: HIMS Barabanki

Introduction: Every year over 1,15,000 Indians die of hepatitis B related complications. Hepatitis B surface antigen (HBsAg) positivity in the general population ranges from 1.1% to 12.2%, with an average prevalence of 3-4%.

Materials & Methods: This cross-sectional analytical study conducted in Microbiology Department included 100 patient sample, aged 18 to 80 years, both sexes, who attended out and in patient Department of Hind Institute of Medical Sciences, Barabanki, UP, from the 1st March 2025 to 31st December 2025 and tested positive for HBsAg by CLIA (Chemiluminescence Immunoassay) after detailed history and written consent were taken. HBeAg levels by ELISA (Enzyme Linked Immunosorbent Assay) and was quantitative Hepatitis B viral load DNA using Real Time PCR was evaluated.

Results: Among 100 CLIA HBsAg positive sample, the mean age of the studied patients was 35 years, 63(63%) were male, and 37 (37%) were female. Majority of patients (32%) belonged to age group 31-40 years. Family history was the most common risk factor. Of the 100 HBsAg reactive patient, the 'e' antigen (HBeAg) was positive in 35 patients (35%) and HBV DNA levels ranged in between 139 IU/ML and 748.08 X 10⁸ IU/ML. According to the Spearman test, HBV DNA levels differed significantly between HBeAg positive and negative patients P= 0.031

Conclusion: HBV-DNA levels were significantly higher in HBeAg positive patients. In case of non-availability of facility for HBV PCR, detectable HBeAg should be taken as surrogate marker for HBV DNA in hepatitis B patients.

65. A Comprehensive Study of HPV Genotypes and Their Association with Bacterial Vaginosis in Women above 18 Years of Age Attending OPD of Hind Institute of Medical Sciences, Barabanki

Author: Dr. Pratibha Pandey

Co-Authors: Jyoti Srivastava, Sameena Jawaid, Anjali Agarwal

Institute: HIMS, Barabanki

Introduction: Cervical cancer is a major malignancy among women worldwide, with persistent infection by high-risk Human Papillomavirus as the principal etiological factor. Indian studies report HPV positivity in up to 98% of invasive cervical carcinoma cases, predominantly HPV16 and HPV31. Bacterial vaginosis is a common vaginal infection that may influence HPV acquisition and persistence. This study evaluates high-risk HPV genotypes and their association with bacterial vaginosis.

Materials & Methods: This hospital-based cross-sectional analytical study was conducted in the Department of Microbiology, HIMS, Barabanki, after ethical approval and informed consent. The study duration was from 1st January 2025 to 1st January 2026. 55 sexually active women aged 18–45 years with gynecological complaints were enrolled by consecutive sampling. Two vaginal swabs and one cervical swab were collected aseptically. Vaginal swabs were examined by wet mount and Gram staining. Bacterial vaginosis was diagnosed using Nugent's scoring system and Amsel's criteria. Cervical swabs were tested for high-risk HPV genotypes using chip-based real-time duplex PCR.

Results: Out of the 55 samples processed, 9/11 (16%) were positive for high-risk HPV genotypes 16 and 31, while 2/11 (3.6%) were positive for high-risk HPV genotypes 18 and 45. Co-infection with HPV and bacterial vaginosis was observed in 05/11 cases (45%), while 6/11 cases (55%) showed HPV infection with intermediate Nugent scores. A notable correlation was observed with intermediate Nugent scores (4–6), suggesting a possible association between altered vaginal flora and HPV infection. Coexistence of BYLC in four cases and *Trichomonas vaginalis* in one case was also observed among HPV-positive women.

Conclusion: The study suggests bacterial vaginosis may influence the persistence of high-risk HPV infection.

66. Molecular Identification of Hepatitis C Virus Infection and Its Association with Viral Load in Chronic Liver Disease Patients.

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Co-Authors: Geeta Gupta, Varun Goel, Ashutosh Rawat

**Institute: Department of Microbiology, Santosh medical College & Hospital, Ghaziabad UP.
Government Institute of Medical Sciences, Greater Noida, Uttar Pradesh**

Introduction: Hepatitis C virus (HCV) infection is a major etiological factor contributing to chronic liver disease (CLD) and its complications, including cirrhosis and hepatocellular carcinoma. Molecular detection and quantification of HCV RNA are essential for accurate diagnosis, assessment of disease progression, and clinical management. The objectives of the study were to determine the proportion of HCV infection in newly diagnosed CLD patients from western Uttar Pradesh, India,

Materials & Methods: A cross-sectional study was conducted on 200 clinically diagnosed CLD patients attending a tertiary care center. Serum samples were screened for anti-HCV antibodies using (CMIA). Molecular confirmation was performed by real-time reverse transcriptase polymerase chain reaction (RT-PCR) for detection of HCV RNA. Quantitative viral load estimation was carried out for all HCV RNA-positive samples.

Results: Among 200 clinically diagnosed CLD patients, 127 (63.5%) were reactive for anti-HCV antibodies by CLIA, indicating a high prevalence of HCV exposure. HCV RNA was detected in 44 cases, accounting for 22% of total CLD patients and 34.6% of seropositive individuals, confirming active viral replication in approximately one-third of anti-HCV-positive cases. The observed decline from serological to molecular positivity highlights the importance of HCV RNA testing for accurate diagnosis, staging, and therapeutic decision-making.

Conclusion: This study reveals a high burden of Hepatitis C virus exposure among CLD patients in Western Uttar Pradesh. The presence of HCV RNA in a significant subset confirms its etiological role, while the discrepancy between serological and molecular findings highlights the need for confirmatory HCV RNA testing for accurate diagnosis and management.

67. Distribution of Hepatitis C Virus Genotypes in Western Uttar Pradesh and Its Clinical Association.

Author: Shivangi Gupta

Co-author: Dr. Sudhir Singh

Institute: Teerthanker Mahaveer Medical College & Research Centre, Moradabad (U.P.), India,

Introduction: The Hepatitis C virus (HCV) infection is still a significant public health challenge in India with genotype distribution affecting treatment efficacy and disease advancement. Regional data about HCV genotypes and their corresponding clinical features are scarce in Western Uttar Pradesh. To determine the distribution of HCV genotypes among patients in Western Uttar Pradesh and examine their correlation with clinical history.

Material and methods: This cross-sectional research was performed on HCV reactive patients in a Teerthanker Mahaveer Hospital in Moradabad. HCV viral load was carried out with the help of RT-PCR test, viral load positive patients' samples were further subjected to determine the genotype. Demographic information and clinical history, including symptoms, risk factors and comorbidities were documented. Data were examined using descriptive statistics with outcomes articulated as frequencies and percentages.

Result: Out of 345 anti-HCV reactive samples, 163 (47.2%) patients were positive for HCV RNA. Out of 163 HCV RNA positive samples, the most predominant genotype was found genotype 3 (65%), followed by genotype 1 (23.3%) but other genotypes were rarely found in this study. The majority of individuals presented asymptotically with tiredness being the most often reported symptom. A history of blood transfusion, injectable medication usage or prior surgical interventions was often noted. Genotype 3 was more often linked to clinical manifestation than other genotypes

Conclusion: Genotype 3 continues to be the prevalent HCV genotype in Western Uttar Pradesh and has a significant correlation with clinical manifestations. Comprehending regional genotype distribution and clinical associations is crucial for enhancing patient care and informing public health policies.

68. Evaluation of the Therapeutic Potential of a Bacteriophage Targeting Multidrug – Resistant *Pseudomonas Aeruginosa*.

Author: Pragati Awasthi

Co-Authors: Dr. Nisha Rathor, Dr. Siva Prasad Reddy B., Dr. Rama Chaudhry

Institute: National Institute of Medical Science & Research, Nims University Jaipur, Rajasthan.

Introduction: The global rise in antibiotic resistance poses a significant threat, diminishing the efficacy of common antibiotics against widespread bacterial infections. WHO considered Carbapenem Resistant *Pseudomonas aeruginosa* (CRPA) as a high-priority pathogen. In India its prevalence is a significant concern. Bacteriophages are promising antibacterial agents with the ability to lyse specific bacteria without affecting the normal human microbial flora.

Materials & Methods: Twenty-one Multidrug-resistant (MDR) *P. aeruginosa* were isolated from clinical samples like blood, endotracheal aspirate, bronchoalveolar lavage, pus, pleural fluid, and sputum. The Identification and antimicrobial susceptibility of *P. aeruginosa* were performed by Vitek-2. The bacteriophage was isolated from sewage water using standard procedure. The presence of phage was confirmed by spot assay and plaque assay and visualized by Transmission Electron Microscopy. The host range of isolated bacteriophage was analysed on twenty MDR *P. aeruginosa* isolates.

Results: A bacteriophage isolated against MDR *P. aeruginosa* from sewage sample, showed clear lytic zone on spot assay and produced plaques of 1.5 mm diameter. The TEM showed bacteriophage with an icosahedral head and a long, flexible, non-contractile tail, features of the class *Caudoviricetes*. The *Pseudomonas* phage lysate exhibited a broad host range, effectively lysing 14 (70%) out of 20 MDR *P. aeruginosa* isolates.

Conclusion: The isolated bacteriophage showed a broad host range antibacterial activity, by lysing 70 % of tested MDR *P. aeruginosa* isolates, demonstrating its high lytic ability and suitability to be developed as a potential therapeutic agent with further characterization.

Mycobacteriology Abstracts

69. Leprosy in Elimination Era: Microbiological Spectrum & Epidemiological Trends

Author: Dr. Neelam Singh

Co-Authors: Mitra Kar, Ashima Jamwal, Neeti Mishra

Institute: T.S. Mishra Medical College & Hospital, Lucknow.

Introduction: Leprosy is significant public health issue in developing nations, including India. It is a concern of endemic area. Early detection and accurate classification are essential to prevent disability and guide effective management.

Material Method: A retrospective observational study was conducted over one year at a tertiary care Hospital. Patients presenting with clinically suspected lesions were included in the study. A detailed clinical assessment and SSS (slit- skin smear) evaluation was performed in all suspected cases and positive cases were defined. Demographic and clinical data was retrieved from medical records. Cases were classified as Paucibacillary (PB), Multibacillary (MB) according to standard guidelines.

Result: Total suspected Leprosy cases were 58, 7 were confirmed (12%). Out of 7 patients; 5 were PB, 2 MB cases based on clinical and microbiological criteria. Bacteriological index (BI) in PB cases ranged from +1 to +3, while both MB cases had +4 BI index. PB cases presented with hypopigmented patches, numbness over hands and feet while mild fever, erythematous nodules, numbness, nasal stuffiness were observed in MB cases.

Conclusion: Microbiologically and epidemiologically monitoring remain crucial to sustain elimination. The study highlights the importance of active surveillance even in elimination era, particularly in low prevalence and border population.

Keywords: leprosy, paucibacillary, Multibacillary, Bacteriological index, Hypopigmented patches, Nodules.

70. Erythema Nodosum Leprosum Necroticans in a young girl as an initial presentation of Lepromatous Leprosy: An unusual manifestation

Author: Dr Shreya Poddar

Co-Authors: Dr Moin Ahmad Siddiqui, Dr Savita Chaudhary

Institute: Era's Medical College and Hospital

Introduction: Childhood leprosy is an important epidemiological marker of active community transmission. Pediatric cases constitute a significant proportion of leprosy cases in endemic areas, ranging from 4.7% to 9.5% of total cases in India. Multibacillary forms such as Lepromatous Leprosy and Borderline Lepromatous leprosy are rarely seen in children, due to their effective cell mediated immune response, and short incubation period.

Case: An 11-year-old girl presented to our Dermatology OPD with reddish, raised, painful nodules and target lesions over face and limbs. These were associated with high grade fever on and off. Few nodules had ulcerated, discharging seropurulent material, and some were covered with brown-black adherent crust. Bilateral ulnar nerves were symmetrically thickened and non-tender. Ear infiltration was present and madarosis was absent. There was no history of contact with a case of leprosy.

A four-site slit skin smear was performed, which showed acid-fast bacilli, with a bacillary index of 5+, suggesting multibacillary leprosy. Histopathological examination was consistent with Erythema Nodosum Leprosum. A diagnosis of Lepromatous Leprosy with Erythema Nodosum Leprosum Necroticans was made. The patient was started on oral prednisolone 30mg daily, oral diclofenac sodium 25mg twice daily and multibacillary multidrug treatment (MB MDT) comprising 50 mg of Dapsone daily, 50 mg of Clofazimine daily, with 450 mg of rifampicin and 150mg Clofazimine, once a month, given together as a supervised dose.

Conclusion: Erythema nodosum leprosum with necrotic lesions as a primary presentation in a child is uncommon and is seldom reported.

71. A Case Report of Isolated Bilateral Testicular Tuberculosis

Author: Dr. Rajat Mishra

Co-Authors: Laxman Yadav, Jitendra Devrari, Vinita Rawat

Institute: VCSG GIMS&R Srikot, Garhwal (UK)

Introduction: Testicular tuberculosis is a rare form of extrapulmonary tuberculosis and poses a significant diagnostic challenge due to its nonspecific clinical presentation, often mimicking other infective or neoplastic scrotal conditions. Early microbiological diagnosis is crucial to prevent complications and ensure appropriate management. We report a rare case of bilateral testicular tuberculosis presenting as scrotal abscess.

Case Profile: A 34-year-old male, chef by occupation, presented with progressively increasing bilateral scrotal swelling associated with dull aching pain for one month, more pronounced on the right side, along with low-grade fever. There was no history of trauma, urinary symptoms, constitutional complaints, or prior tuberculosis. General and systemic examinations were unremarkable. Local examination revealed bilateral tender scrotal swelling without skin involvement or inguinal lymphadenopathy. Routine hematological and biochemical investigations were within normal limits, and serological tests for HIV, hepatitis B, and hepatitis C were non-reactive.

Ultrasonography-guided drainage of the scrotal abscess was performed. The aspirated pus was subjected to microbiological analysis, which demonstrated acid-fast bacilli on Ziehl–Neelsen staining. Mycobacterial culture confirmed *Mycobacterium tuberculosis*, and drug susceptibility testing showed sensitivity to first-line anti-tubercular drugs including isoniazid, rifampicin, ethambutol, and streptomycin. The patient was initiated on anti-tubercular therapy as per national guidelines and followed up for six months, showing complete clinical recovery with resolution of pain and swelling and no recurrence.

Conclusion: This case emphasizes the importance of considering genitourinary tuberculosis in chronic scrotal infections and highlights the role of timely microbiological diagnosis and drug susceptibility testing for optimal patient outcomes.

72. Laboratory-Based Surveillance of Tuberculosis Using Conventional and Molecular Diagnostics at a Tertiary Care Centre in North India

Author: Dr Sana Islahi

Co-Authors: Sweta Singh, Pramod Kumar, Shefali Gupta

Institute: All India Institute of Medical Sciences Hospital, Raebareli, Uttar Pradesh,

Introduction: Tuberculosis (TB) remains a major public health challenge in India. Strengthening laboratory-based diagnosis using rapid molecular assays alongside conventional methods is pivotal for early detection and drug resistance surveillance. This study evaluates the diagnostic yield of various microbiological investigations for TB and assesses rifampicin resistance patterns at a tertiary care centre in North India.

Materials & Methods: A retrospective, laboratory-based observational study was conducted in the Mycobacteriology Laboratory, Department of Microbiology, AIIMS Raebareli. Data from January to December 2025 were analyzed. Samples from suspected pulmonary and extrapulmonary TB cases were subjected to AFB smear microscopy, Truenat MTB RT-PCR with rifampicin resistance detection, mycobacterial culture on solid media, and Line Probe Assay (LPA) wherever indicated. Descriptive statistical analysis was performed.

Results: Out of 5,976 samples processed for AFB microscopy, 237 (3.9%) were smear positive. Truenat MTB RT-PCR detected MTB in 435 of 4,838 samples (9.0%). Rifampicin resistance was observed in 11.3% of MTB-positive cases, while 19.4% showed indeterminate resistance results, out of which 92.8% samples had low/very low DNA quantity. Molecular diagnostics demonstrated higher sensitivity compared to smear microscopy and facilitated early drug resistance detection.

Conclusion: The combined use of molecular and conventional diagnostic modalities significantly improves TB detection and rifampicin resistance surveillance. Strengthening laboratory services is essential for effective implementation of NTEP and TB control efforts.

73. Multi-district Analysis of a Disease beyond the Lung: An Epidemiological Dynamic of EPTB in Foothills and Plains

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Co-Authors: Dr Aarti Kotwal

Institute: Himalayan Institute of Medical Sciences, Swami Rama Himalayan University

Introduction: Tuberculosis (TB), continues to be a public health crisis with the incidence of extrapulmonary-TB (EPTB) are on rising globally. Delayed clinical presentation, diagnostic-delays due to paucibacillary nature & drug-resistance (DR) leads to increase EPTB related morbidity and mortality which fundamentally undermined the END-TB strategy. We assessed the epidemiological characteristics of EPTB suspects without prior ATT & pulmonary-TB history, attending our rural DOTS catering health-center of Uttarakhand.

Materials & Methods: Study population comprised 604 subjects from July' 2020 - February' 2022 from Uttarakhand (n=455) and neighboring districts of Uttar-Pradesh (n=149) reflecting regional mobility. A multi-model diagnostic approach like smear-microscopy, culture, real-time PCR, CBNAAT & LPA was employed.

Results: Out of 604 suspects, 139 (23.0%) were microbiologically-confirmed EPTB. Dehradun (EPTB-confirmed=26.0%, DR-TB=21%), Haridwar (EPTB-confirmed=20.1%, DR-TB=28.0%) districts of Uttarakhand exhibited as pronounced EPTB hotspot with highest DR-TB cases. Among neighboring districts of Uttar Pradesh, Bijnor & Saharanpur led with 22.1% & 21.0% EPTB cases respectively with highest DR-TB cases. Both states reported significant and nearly equal (Uttarakhand=23.0%, Uttar Pradesh=24.0%) EPTB case load with the highest burden in 21-40 years age-group. Highest positivity rates were recorded among females (55.0%) in Uttarakhand while males (62%) in Uttar-Pradesh. 5.9% cases showed INH-mono-resistance on LPA.

Conclusion: This study highlights a substantial EPTB burden in Uttarakhand and Uttar-Pradesh especially in Dehradun and Haridwar districts of Uttarakhand and Bijnor district of Uttar-Pradesh and need high surveillance. Also highlights the crucial role of LPA in EPTB management and ensuring that treatment regimens are tailored accordingly beyond rifampicin status and helping to prevent the elevation of drug-resistance in primary EPTB cases.

74. Prevalence of MDR-TB In Pulmonary Tuberculosis Patients Attending A Tertiary Care Hospital.

Author: Dr. Sriyans Singh

Co-Authors: Prof. (Dr.) Razia Khatoon, Dr. Shahid Khan.

Institute: Hind Institute of Medical Sciences, Ataria, Sitapur, UP.

Introduction: Multidrug-resistant tuberculosis (MDR-TB) remains a major public health concern and threatens effective tuberculosis control, particularly in high-burden settings. Early detection of drug resistance among newly diagnosed pulmonary TB cases is essential to ensure appropriate treatment and prevent transmission.

Objectives:

To assess the prevalence of MDR-TB among newly diagnosed pulmonary tuberculosis patients in a tertiary care center and to compare the diagnostic yield of Ziehl–Neelsen (ZN) microscopy, fluorescent microscopy, and MTB RT-PCR (Truenat).

Materials & Methods: A cross-sectional study was conducted on 210 newly diagnosed, microbiologically confirmed pulmonary TB patients. Sputum samples were examined using ZN staining, fluorescent microscopy, and MTB RT-PCR (Truenat).

Molecular drug susceptibility testing was performed to detect rifampicin and isoniazid resistance. Demographic and socio-economic data were analyzed using the Modified B. G. Prasad classification.

Results: ZN microscopy detected *Mycobacterium tuberculosis* in 189 cases (90.0%), while fluorescent microscopy detected 192 cases (91.4%). MTB RT-PCR (Truenat) detected MTB in all 210 cases (100%), including smear-negative patients. The highest number of cases was observed in the 51–60 years age group (20.0%). Most patients belonged to Class II (44.8%) and Class III (26.2%) socio-economic groups. Rifampicin resistance was detected in 7 patients (3.3%), isoniazid resistance in 1 patient (0.5%), and MDR-TB in 1 patient (0.5%). Overall, 96.7% of patients were drug-sensitive.

Conclusion: The prevalence of MDR-TB among newly diagnosed pulmonary TB patients was low (0.5%). However, the presence of rifampicin resistance highlights the need for routine molecular drug susceptibility testing to enable early detection and appropriate management of drug-resistant TB.

75. Enhanced Anti-Tubercular Efficacy of Phytochemical–Drug Hybrid Compounds over Existing Regimen Drugs: A Computational Study

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Introduction: *Mycobacterium tuberculosis*, remains a major worldwide health problem due to the increasing frequency of multidrug-resistant strains, the length of therapy, and the considerable drug-induced toxicity. Integrating phytochemicals with computational drug discovery offers safer, effective anti-tubercular candidates and therapies.

Materials & Methods: Anti-tubercular phytochemicals and traditional TB drugs were found using public databases such as PubChem, ChEMBL, and IMPPAT. From the RCSB Protein Data Bank, important M. tuberculosis protein targets related to redox metabolism, DNA replication, lipid biosynthesis, and cell wall transport were chosen. To assess ligand-target interactions, molecular docking was carried out using Auto Dock Vina and Swiss Dock. Toxicity profiles, pharmacokinetic behavior, and drug-likeness were predicted using Swiss ADME and related in-silico methods. Hybrid drug candidates were designed using medicinal chemistry concepts and then computationally assessed.

Results: A number of phytochemical-drug hybrid compounds showed acceptable drug-likeness, decreased hepatotoxicity risk, enhanced projected gastrointestinal absorption, and positive binding affinities for important mycobacterial targets. When compared to current TB treatments, mathematical modelling revealed optimal elimination patterns

Conclusion: This study demonstrates that integrating medicinal plant phytochemicals with computational drug design can accelerate the identification of promising anti-TB candidates. The findings support further experimental validation of these hybrid molecules as safer and more effective therapeutic options for tuberculosis.

76. Clinico-microbiological profile and outcomes in hospitalized patients of Tuberculous Meningitis at a tertiary care center in Northern India.

Author: Sreya Deb

Co-Authors: Akshay Kumar Arya, Vikramjeet Singh, Siddharth Singh, Karan Singh, VK Paliwal, Richa Misra

Institute: Sanjay Gandhi Postgraduate Institute of Medical Sciences, Lucknow

Introduction: Tuberculous meningitis (TBM) is a severe manifestation of extra pulmonary tuberculosis with high morbidity and mortality. This study aimed to assess the clinico-microbiological profile and outcomes in hospitalized patients of TBM at a tertiary care center in northern India.

Materials & Methods: This three-year observational, single-centre cohort study was carried out between January 2023 to December 2025. A total of 1296 clinically suspected patients of meningitis admitted in Neurology ward at our centre were included. CSF samples underwent cytology, Ziehl-Neelsen stain, Lowenstein-Jensen culture, and Xpert MTB/RIF Ultra assay. Electronic medical records were reviewed for clinical details and patient outcomes.

Results: Xpert MTB/RIF Ultra assay detected *Mycobacterium tuberculosis* in 142 samples, all clinically and radiologically diagnosed as TBM. Mean age was 29 years with female preponderance (n=83, 58.4%). Elevated CSF proteins (46 to 500 mg/dL) were seen in 66.9% (n=95) and 58.4% (n=83) samples demonstrated lymphocyte predominance. AFB microscopy showed low sensitivity of 5.6% (8/142). Culture was positive in 26.7% (38/142). The median time to culture positivity was 35 days. Among the 142 Xpert-positive samples, 41.5% (n=59) were trace detected. Rifampicin resistance was identified in 13.3% (n=19), indeterminate in 48.5% (n=69), and absent in 38% (n=54). Overall mortality was 21.1% (n=30).

Conclusion: Xpert MTB/RIF Ultra assay not only enabled rapid TBM diagnosis, but helped detect **104 cases** of TBM more than routine diagnostics (microscopy and culture alone) which would otherwise go undiagnosed. However, the high frequency of Rifampicin-indeterminate results and low culture yield lead to suboptimal management and significant mortality.

77. Everything is Tuberculosis!!

Author: Dr. Sonakshi Dwivedi

Co-Authors: Dr. Akshay Kumar Arya, Dr. Vikramjeet Singh, Dr. Richa Mishra

Institute: SGPGIMS Lucknow

Introduction: Tuberculosis (TB) predominantly affects the lungs but it can also involve any organ. Diagnosing Extrapulmonary Tuberculosis (EPTB) can be challenging because of its wide range of clinical presentations. This case series discusses five complex cases of EPTB that highlights the importance of considering TB as a possible differential diagnosis regardless of atypical symptoms and radiological features.

Materials & Methods: All five patients presented between January to December 2025 at SGPGIMS Lucknow, a tertiary care center in North India. Samples for investigations were as follows: adrenal biopsy, joint pus, omental biopsy, endobronchial ultrasound-guided transbronchial needle aspiration and cerebrospinal fluid. Clinical features, laboratory investigations, diagnostic evaluation, treatment, and outcomes were analyzed of each patient. All samples were subjected to microscopy, histopathology, Cartridge-Based Nucleic Acid Amplification Testing (CBNAAT) and culture.

Results: Three males and two females with a mean age of 46.8 years presented to the SGPGIMS OPD with fever and fatigue (median time - 35 days). Three patients were immunocompetent. Whereas, one was found to be diabetic with renal transplant and the other one had metastatic thyroid carcinoma. Mycobacterium tuberculosis complex (MTBC) was detected in all cases. The CBNAAT was positive in four cases while culture yielded colonies in one case after eight weeks of incubation. Biopsy specimen of three patients revealed granulomatous inflammation.

Conclusion: The wide range of clinical presentations of EPTB can result in diagnostic and treatment dilemmas. A high index of clinical suspicion is important in an endemic setting like India.

78. Cytotoxicity and permeability profiles of novel nanoconjugates in *M. tuberculosis* H37Rv-infected THP-1 cell

Author: Dr Niharika Pandey

Co-Authors: Dr Vineeta Mittal, Dr Rolee Sharma

Institute: Integral University, Lucknow, Uttar Pradesh

Introduction: Drug-resistant tuberculosis remains a critical global health challenge, necessitating advanced therapeutic strategies to overcome traditional antibiotic limitations. Graphene based nanomaterials have raised expectations in the last few decades in the field of biomedicines and reduced graphene oxide is among one of the potent nanoparticles used widely as antimicrobial agent because of its good dispersibility and as well as its efficient functionalization. The bacterial cell membranes serve as a promising target for developing new antibacterial drugs since some important biomolecules, such as the membrane-based efflux pump systems, play an important role in bacterial pathogenicity and antimicrobial resistance, hence keeping in view about the recent advancements to combat multi drug resistance in bacteria like the combination of nanomaterials with antibiotics has been evaluated to lower the occurrence of antimicrobial resistance development, reduced graphene oxide with first line anti tuberculosis drugs were taken into consideration to inhibit mycobacterial growth while assessing the successful penetration of the novel conjugates into the bacterial cell wall.

Materials & Methods: Propidium iodide (PI) was used as a probe for the detection of cells with compromised cell membranes. Mid log phase grown mycobacteria H37Rv were collected by centrifugation and seeded on the 96 well plate followed by THP-1 cell lines in triplicate manner exposed with reduced graphene oxide and the conjugates at their respective minimum inhibitory concentration values. Subsequently 30 μ M PI was added to wells and plates were incubated for 30-40min, followed by washing and were visualized under fluorescence microscope.

Results: We found that high dosage of nanoconjugates treatment significantly disrupted the membrane integrity of H37Rv through the membrane potential staining. These results demonstrated that nanoconjugates, inhibited mycobacterial growth which was closely associated with their ability to disrupt the bacterial membrane structures and functions. The relative Propidium Iodide incorporation indicated that prepared formulation of the nanoconjugates have sufficient antimycobacterial potential at different time points.

Conclusion: *In vitro* evaluations using the THP-1 human monocytic cell line demonstrated significantly reduced cytotoxicity compared to free drug counterparts, highlighting the biocompatibility of the rGO particles.

Hospital Infection Abstracts

79. Viral Hepatitis in a Healthcare Facility: Status, Awareness, and Preventive Gaps

Author: Dr Loveleena

Co-Authors: Dr Richa Pandey

Institute: DSLPASC, Pratapgarh

Introduction: Healthcare workers are at increased risk of acquiring hepatitis B virus (HBV) and hepatitis C virus (HCV) due to frequent occupational exposure. Implementing effective preventive measures is therefore essential. This study aimed to evaluate the prevalence of HBV and HCV infections among healthcare workers at DSLPASC, Pratapgarh, to identify gaps in protection and guide strategies for safeguarding this high-risk group. Given that viral hepatitis is preventable and treatable, such evidence is vital for sustaining the health of healthcare personnel.

Materials & Methods: This cross-sectional study included 276 healthcare workers, comprising nurses, midwives, physiotherapists, laboratory technicians, radiographers, and blood bank staff. Demographic and vaccination-related information was collected using a structured questionnaire. Blood samples were subsequently obtained and analyzed for hepatitis B surface antigen (HBsAg) and anti-HCV antibodies

Results: Of the 276 participants, two were positive for HBsAg, while none tested positive for anti-HCV antibodies, resulting in an HBsAg prevalence of 0.72%. Only 17 healthcare workers (6.15%) reported having received any dose of the HBV vaccine, and merely three (1.08%) had completed the recommended three-dose schedule. Awareness regarding the availability of the HBV vaccine was notably low, with only 42 participants (15.2%) reporting prior knowledge.

Conclusion: Despite substantial occupational exposure, the prevalence of HBV and HCV infections among healthcare workers was low. However, the markedly inadequate vaccination coverage and poor awareness of preventive measures reveal significant gaps in hepatitis prevention practices. Strengthening awareness initiatives, improving access to vaccination, and prioritizing institutional policies that promote HBV immunization are crucial to reducing occupational risk in primary healthcare settings.

Parasitology Abstracts

80. Epidemiological, demographical, clinic-microbiological characteristics of patients with visceral leishmaniasis – A 10-year retrospective analysis

Author: Dr. Surbhi

Co-Authors: Dr. Awadhesh Kumar, Dr. Sangram Singh Patel, Dr. Nidhi Tejan, Dr. Chinmoy Sahu

Institute: Sanjay Gandhi Post Graduate Institute of Medical Sciences, Lucknow

Introduction: Visceral leishmaniasis is considered to be the second most common cause of death amongst tropical diseases. Of these, more than 90% of cases are reported from 13 highly endemic countries including India. This study was done to have a better understanding of the prevalence of visceral leishmaniasis in Uttar Pradesh. Also, clinical presentations, laboratory parameters, outcomes were also evaluated.

Materials & Methods: A 10-year (January 2014 to December 2023) retrospective study was conducted at a tertiary care center in North India. Clinically suspected individuals were diagnosed with VL using a fresh peripheral whole blood sample that was tested by the immunochromatographic assay detecting anti-rK39 IgG. Demographic details, clinical features, laboratory parameters of the patients who were tested positive were extracted from the Hospital Information System (HIS)

Results: Of the 1104 patients with suspected visceral leishmaniasis, 30 (2.7%) patients were tested positive for visceral leishmaniasis using the immunochromatographic assay detecting anti-rK39 IgG. Most of them belonged to the age group of 14-60 years (66.67%). Maximum cases in this study were reported in the months of October followed by February. In this study, the cases were reported from 5 districts of Uttar Pradesh (Gorakhpur, Sultanpur, Ballia, Deoria, Jaunpur) and 5 districts of Bihar (Siwan, West Champaran, East Champaran, Gopalganj, Saran). The most common clinical symptom amongst patients with visceral leishmaniasis are fever (93.3%) followed by pancytopenia (86.7%), fatigue (83.3%), weight loss (76.6%) and hepatosplenomegaly (66.7%). 19 (63.3%) patients presented with this classic triad of hepatosplenomegaly, fever, and pancytopenia. Bone marrow aspirate smear showed the presence of leishmania amastigotes only in 9 (30%) patients. Of the 30 patients, 3 (10%) died. Most of the patients in our study received monotherapy of Liposomal amphotericin B.

Conclusion: Visceral Leishmaniasis is a complex, systemic fatal clinical syndrome caused by a *Leishmania donovani*. The disease is difficult to diagnose and treat, due to its non-specific clinical presentation. A timely diagnosis, appropriate management can help in decreasing the mortality and morbidity due to this disease.

81. Faecal Calprotectin as a Non-Invasive Biomarker of Mucosal Healing in Ulcerative Colitis: A Prospective Observational Study

Author: Dr. Dipika Tyagi

Co-Authors: Dr. Awadhesh Kumar

Institute: SGPGIMS, Lucknow

Introduction: Ulcerative colitis (UC) is a chronic inflammatory bowel disease in which therapeutic goals have evolved from symptomatic control to the achievement of endoscopic mucosal healing. Faecal calprotectin (FCP) correlates more closely with endoscopic disease activity than conventional inflammatory markers such as C-reactive protein and erythrocyte sedimentation rate. Serial faecal calprotectin measurement during follow-up may represent a reliable, non-invasive tool for monitoring treatment response, potentially reducing reliance on repeated endoscopic assessment.

Objectives: To evaluate whether two consecutive faecal calprotectin values <250 mg/kg after treatment can predict endoscopic mucosal healing in patients with active ulcerative colitis.

Methods: This prospective observational study enrolled 200 patients with ulcerative colitis, either newly diagnosed or presenting with disease flare. Baseline evaluation included colonoscopy with assessment using the Mayo endoscopic score, Montreal classification, and faecal calprotectin estimation performed three days post-colonoscopy. After exclusions, 84 patients were followed monthly with serial faecal calprotectin measurements until either two consecutive values <250 mg/kg were achieved or a maximum follow-up period of one year was completed. All patients subsequently underwent follow-up sigmoidoscopy. Clinical disease activity was assessed using the Simple Clinical Colitis Activity Index (SCCAI), and endoscopic severity was graded using the Mayo endoscopic score.

Results: Sixty-seven patients achieved two consecutive faecal calprotectin values <250 mg/kg within 12 months of follow-up. All of these patients demonstrated endoscopic mucosal healing, defined as a Mayo endoscopic sub score ≤ 1 . The positive predictive value of serial faecal calprotectin <250 mg/kg for mucosal healing was 100%, with a sensitivity of 84.2% and specificity of 100%.

Conclusion: Two consecutive faecal calprotectin values below 250 mg/kg reliably predict endoscopic mucosal healing in ulcerative colitis. Serial faecal calprotectin measurement may serve as a practical, non-invasive biomarker for disease monitoring and treatment follow-up in patients with UC.

**Others (HIV, Medical Education,
AI) Abstracts**

82. Serum Vitamin D Status and disease severity in pediatric Vitiligo: A Case-Control analysis

Author: Dr Gopal Prasad Poddar

Co-Authors: Dr. Kshitij Saxena & Dr Moin Ahmad Siddiqui, Dr. Neha Khan

Institute: ERA'S Lucknow Medical College and Hospital, Lucknow

Introduction: Vitiligo is a depigmenting skin condition characterized by specific melanocyte depletion, Resulting in melanin attenuation inside the skin's damaged regions. Vitamin D₃, an essential vitamin, plays a role in immunological response and may help regulate Melanocyte activity. Reduced sun exposure and altered vitamin D metabolism have been proposed as contributory factors in vitiligo, particularly in children.

Materials & Methods: This cross-sectional case-control study was conducted over six months in the dermatology Outpatient department of a tertiary care centre. Thirty pediatric patients diagnosed with vitiligo were enrolled as cases, along with thirty age- and sex-matched healthy controls. Disease severity in cases was assessed using the Vitiligo Area Severity Index (VASI). A Detailed history of daily sun exposure was obtained and categorized into predefined duration. Serum vitamin D levels were measured in both cases and controls using the chemiluminescence method after obtaining informed consent.

Results: Children with vitiligo showed significantly lower mean serum vitamin D levels compared to healthy controls (24.7 ± 6.8 vs 30.6 ± 6.3 ng/mL; $p < 0.001$). Vitamin D deficiency and insufficiency were more prevalent among cases (30% and 56.7%) than controls (13.3% and 43.3%) ($p = 0.027$). No significant correlation was observed between serum vitamin D levels and VASI scores ($p > 0.05$).

Conclusion: Pediatric patients with vitiligo have significantly lower serum vitamin D levels compared to healthy controls, irrespective of sun exposure. Although vitamin D deficiency is common, it does not correlate with disease severity, suggesting a possible role of vitamin D in the etiopathogenesis of vitiligo.

83. Development and evaluation of Objective Structured Practical Examination (OSPE) as a formative assessment tool for Clinical Microbiology residents

Author: Parul Jain

Co-Authors: Vimala Venkatesh, Amita Jain, Shalini Bhalla, Sandeep Bhattacharya, Suyog Sindhu, Rakesh Kumar Dixit

Institute: King George's Medical University, Lucknow

Introduction: Objective Structured Practical Examination has been tried as a successful formative assessment tool in several branches of Medicine but not yet for Microbiology residency program. The educational milestones also do not exist in this branch. This study was done to develop educational milestones and OSPE stations for Microbiology residency program of India and evaluate them for feasibility and learner acceptability.

Materials & Methods: Delphi analysis was done to formulate the milestones in Mycobacteriology. OSPE stations were then developed to assess the milestones decided. All were observed stations manned by examiners who were not faculty members. Finally, after the assessment, by taking feedback from the learners, an evaluation of the method was done.

Results: Total 31 Microbiology residents underwent the evaluation. Their scores were higher at stations assessing knowledge and skills and comparatively lower in those assessing communication and teaching. Students found it a very useful method of evaluation particularly because it gave them insight towards the application of their learning in real life scenarios, helped them identify the gaps in knowledge and motivated them

Conclusion: OSPE is feasible even in settings with less number of trained faculty members provided checklists and scoring lists are made comprehensively. The milestones described here may be used for further development of the same in other branches of Microbiology.

84. Implication of Sexually Transmitted Infections with regard to Their Influence on Infertility, In a Tertiary Care Hospital of North India.

Author: Dr. Palak Arora

Co-Authors: Dr. Sulekha Nautiyal, Dr. Anjali Choudhary, Dr. Aakriti Gupta, Dr. Kxitiba Pandey,

**Institute: Shri Guru Ram Rai Institute of Medical and Health Sciences. SGRRU,
Dehradun (Uttarakhand).**

Introduction: According to National AIDS Control Organization (NACO), STIs rank among the top five conditions for which sexually active adults seek health care in the developing countries. This study was designed to detect *Chlamydia trachomatis*, *Neisseria gonorrhoeae*, *Mycoplasma genitalium*, *Herpes simplex virus (HSV) 1&2*, *Ureaplasma urealyticum*, *Gardnerella vaginalis* and *Trichomonas vaginalis* using Multiplex RT-PCR in females attending infertility clinic.

Materials & Methods: This prospective cross sectional study was conducted in Department of Microbiology in collaboration with Department of Obstetrics and Gynaecology of SGRRIM&HS and SMIH, Dehradun over a period of 18 months. 100 female participants attending infertility clinic were included. 75 and 25 study participants were included in primary and secondary infertility groups respectively. HVS was collected and Multiplex RT-PCR for Detection of STI pathogens (TRUPCR STD Panel Kit, 3B Blackbio Biotech India ltd) was used.

Results: A positivity of 0%, 0%, 24% and 30.7% in primary infertility group and 12%, 12%, 4% and 8% in secondary infertility group were observed for *Chlamydia trachomatis*, *Neisseria gonorrhoeae*, *Mycoplasma genitalium* and *Ureaplasma urealyticum* respectively. Using the Chi-square test (defined threshold of 0.05), statistically significant association between the above infections and type of infertility was observed. *HSV 1*, *Gardnerella vaginalis* and *Trichomonas vaginalis* were detected but not statistically significant while *HSV 2* was not detected in any sample.

Conclusion: The significant associations between certain STIs and infertility reinforce the importance of comprehensive STI screening in infertile women, thus aiding in management of such cases.

85. Role of Mini-CEX as a Tool for Evaluating and Improving Medical Education among Post Graduates in the Department of Microbiology: A cross-sectional study from a Government Medical College.

Author: Dr. Manish Kumar

Co-Authors: Dr. Shalabh Jauhari

Institute: Govt. Doon Medical College, Dehradun, Uttarakhand

Introduction: Clinical competence is vital in postgraduate (PG) training, yet assessments primarily focus on theoretical knowledge rather than practical skills. This study aimed to introduce and assess the effectiveness of Mini-Clinical Evaluation Exercise (Mini-CEX) in improving clinical and diagnostic skills among microbiology PG students while gathering faculty and student perceptions regarding its utility.

Materials & Methods: A cross-sectional study was conducted over 12 months in the Department of Microbiology at a Government Medical College in Northern India. Five microbiology PGs underwent five Mini-CEX sessions, each in a different laboratory setting: Bacteriology, Virology, Mycology, Parasitology, and Serology & Immunology. Five trained faculty members assessed students on five core competencies: Sample Collection & Processing, Microscopy & Identification, Clinical Judgement, Professionalism & Laboratory Safety, and Interpretation & Communication of Reports, using a 9-point rating scale.

Results: A statistically significant improvement was observed across all Mini-CEX domains from first to final assessment. Microscopy and Laboratory Identification Skills showed the highest improvement (5.2 ± 0.97 to 8.5 ± 0.5 , $p = 0.0004$), followed by Clinical Judgement (5.9 ± 0.92 to 8.6 ± 0.4 , $p = 0.002$). Sample Collection and Processing Techniques had the highest final score (8.8 ± 0.35). By the final assessment, 100% of students achieved Superior ratings. Faculty and residents endorsed Mini-CEX as an effective assessment tool, despite minor concerns over session duration and effort required.

Conclusion: Mini-CEX significantly improves microbiology PGs' clinical competency, diagnostic skills, and confidence, making it a valuable formative assessment tool for laboratory-based medical education.

86. Socio-Cultural Factors Influencing Antimicrobial Resistance and its Mitigation: A Survey of Healthcare Professionals

Author: Shalini Trivedi

Co-Authors: R Harsvardhan, Ankita Sengar, Jai Kishun

Institute: Sanjay Gandhi Postgraduate Institute of Medical Sciences, Lucknow

Introduction: AMR is a rising global threat that requires urgent attention. Appropriate usage of antibiotics should be promoted along with a focus on barriers that lead to their irrational use. This paper aims to assess the knowledge, attitudes, and decision-making behaviour of healthcare professionals regarding antimicrobial resistance with a focus on socio-cultural determinants and potential strategies for strengthening AMR mitigation.

Materials & Methods: This was a questionnaire-based survey of healthcare professionals. Data was collected using a digital dissemination method (Google form) sent to the participants via email and WhatsApp. The Google Forms-coded questionnaire was analyzed with SPSS version 23, and the proportions of each group were defined. Pearson Chi-square test was used for categorical data, with a significance level set at $p < 0.05$.

Results: A total of 117 HCPs responded. Socio-cultural determinants like Over-the-counter drug availability, using antibiotics for viral infection, patient-driven prescribing, peer and senior influence in prescribing practices were found to be statistically significant. Providing clear written and verbal instructions to patients, explaining the importance of completing the full course of antimicrobials, was identified as the preferred method to encourage patients to adhere to antimicrobial regimens. Conducting regular training and workshops on AMR and participating in AMSP were the preferred mitigation strategy.

Conclusion: An effective AMS program should not only address the knowledge domain, but also focus on hierarchical influences, strengthen prescribing policies, regulate OTC, and reduce diagnostic delays. Therefore, while designing interventions, these socio-cultural dynamics should also be considered to yield sustainable

87. Enhancing Surgical Site Infection Prevention through Antimicrobial Stewardship: Role of Interdisciplinary Collaboration

Author: Fatima Khan

Co-Authors: Tamkin Khan, Enas Mushtaq, Manzoor Ahmad

Institute: JNMCH, AMU

Introduction: Surgical site infections (SSIs) remain a major contributor to postoperative morbidity, prolonged hospitalization, and increased antimicrobial consumption. Inappropriate surgical antimicrobial prophylaxis (SAP), particularly the excessive use of broad-spectrum antibiotics, accelerates antimicrobial resistance. Integrating Antimicrobial Stewardship Programs with infection prevention and control strategies through interdisciplinary collaboration is essential for improving SSI outcomes. This study describes an AMSP driven quality improvement initiative aimed at strengthening SSI prevention by optimizing SAP practices.

Materials & Methods: A multidisciplinary quality improvement project was conducted in a tertiary care teaching hospital using a Point-of-Care Quality Improvement framework. The team comprised surgeons, microbiologists, infection control professionals, nursing staff, and hospital administrators. Baseline SSI rates and SAP practices were reviewed, followed by root cause analysis. Surgical prophylaxis protocols were modified in accordance with international guidelines and local clinical context. Interventions were implemented through sequential Plan–Do–Study–Act cycles focusing on appropriate antibiotic selection, timing, and duration, operating theatre discipline, and regular staff training. SSI surveillance was carried out until stitch removal.

Results: Post-intervention analysis demonstrated improved adherence to standardized SAP protocols with a reduction in unnecessary broad-spectrum antibiotic use. Enhanced interdisciplinary coordination led to better compliance with IPC practices. A decline in SSI rates was observed compared to baseline, along with increased awareness of rational antimicrobial use.

Conclusion: An AMSP-led interdisciplinary approach effectively bridges the gap between protocol and practice in SSI prevention. Continuous training, teamwork, and systematic monitoring are crucial for sustaining improvements. Integrating antimicrobial stewardship with IPC initiatives can significantly reduce SSI burden in resource-constrained

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Bacteriology Abstracts

1. A rare case of lung abscess caused by *Parvimonas micra* identified through biofire joint panel: A breakthrough in diagnostic conundrum

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Introduction: *Parvimonas micra*, an emerging **pathogen** generally found as commensal in the oral cavity and gastrointestinal tract.

Materials & Methods: We present a case report of 55 Y/M, referred from another hospital on oxygen support (2-3 liters), presented in emergency department with right sided subcostal chest pain which exacerbates on lying down position, tachypnic with history of fever with chills since 15 days and dry cough since 4 days. On examination patient was afebrile, with deranged vitals. No h/o Tuberculosis, T2DM, hypertension. Chest X-ray showed presence of large abscess in right lung. Intercostal drain pus was sent for microbiological investigation.

Results: Gram staining revealed presence of plenty of gram- positive cocci in pairs& short chains with two different morphologies. Pus culture showed growth of only *Streptococcus spp.* which was sensitive to all first line antibiotics. Multiplex real time PCR using joint panel of BioFire's Film Array was also done using drain pus which detected *Parvimonas micra* & *Streptococcus spp.* Vancomycin (1gm i.v TDS) and Metronidazole (500 mg TDS) was given for 6 days and patient was discharged in good condition. Patient had a history of chewing tobacco and maintaining poor oral hygiene which might have led gingival crevices to lodge *Parvimonas micra* and possible source for development of lung abscess.

Conclusion: Advanced diagnostic modalities like BioFire's Film Array system using joint panel can be an excellent modality for rapid and accurate detection and identification of anaerobic bacterial pathogens in pus samples in settings where appropriate anaerobic culture facility is not available.

2. Antibiotic Susceptibility Pattern among Uropathogens in a Tertiary Care Hospital: A Retrospective Analysis

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Introduction: Urinary tract infections (UTIs) are among the most common bacterial infections encountered in both outpatient and inpatient settings. The growing prevalence of antimicrobial resistance among uropathogens poses a major challenge to effective empirical therapy. Knowledge of the local distribution of uropathogens and their antibiotic susceptibility patterns is essential for guiding appropriate treatment and strengthening antimicrobial stewardship. This study aimed to analyse the antibiotic susceptibility patterns of uropathogens isolated in a tertiary care hospital.

Materials & Methods: A retrospective laboratory-based analysis of urinary isolates received in the Department of Microbiology, IIMSR, Lucknow, India, was performed between January 2023 and December 2025.

Results: A total of 7,551 urine samples were processed during the study period. Of these, 63.6% were sterile, 10.5% showed insignificant growth, and 8.4% were contaminated. Significant bacteriuria was observed in 17.5% of samples, yielding 1,321 uropathogens. Gram-negative organisms predominated, with *Escherichia coli* (43.4%) being the most common isolate, followed by *Klebsiella* spp. (7.2%). Among Gram-positive isolates, *Enterococcus* spp. (24.9%) and *Staphylococcus* spp. (13.1%) were frequently identified. Antibiotic susceptibility patterns varied across isolates. Sensitivity to cotrimoxazole, nitrofurantoin, and fosfomycin was 40%, 78.8%, and 89% respectively among IPD isolates, while higher susceptibility (68.6%, 87.9%, and 96%) was observed in OPD isolates.

Conclusion: The study demonstrates variable antibiotic susceptibility patterns among uropathogens, with higher resistance rates observed in hospital-acquired isolates. Continuous surveillance and regular updating of institutional antibiograms are essential to support evidence-based empirical therapy and combat antimicrobial resistance.

3. Evaluation of Serological Assays Versus Multiplex Real-Time PCR in the Diagnosis of Brucellosis Among PUO Patients: A Hospital-Based Study

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Introduction: Brucellosis is a neglected zoonotic disease caused by facultative intracellular Gram-negative bacteria of the genus *Brucella*

Objectives: The present study aimed to compare and evaluate the diagnostic efficacy of commonly employed serological assays and multiplex Real-Time Polymerase Chain Reaction (m-RT PCR) for the detection of brucellosis in patients presenting with PUO.

Materials & Methods: A total of 200 blood samples were collected from patients with fever of unknown origin. Each sample was analyzed using the Rose Bengal Plate Test (RBPT), Serum Agglutination Test (SAT), enzyme-linked immunosorbent assays (ELISA) for detection of anti-*Brucella* IgM and IgG antibodies, and multiplex real-time PCR. Molecular typing was performed on PCR positive samples to identify *Brucella* species

Result: Among the 200 PUO cases, SAT showed positivity in 35 (17.5%) cases, followed by ELISA IgM in 20 (10.0%), m-RT PCR in 19 (9.5%), RBPT in 12 (6.0%), ELISA IgG in 3 (1.5%), and combined SAT and RBPT positivity in 7 (3.5%) cases. Molecular analysis of m-RT PCR-positive samples identified *Brucella abortus* DNA in 16 (8.0%) cases and *Brucella melitensis* DNA in 3 (1.5%) cases.

Conclusion: Brucellosis remains an important yet under diagnosed cause of PUO. While serological assays, particularly SAT and ELISA IgM, are useful for initial screening, their variability limits stand-alone use. Multiplex real-time PCR provides definitive diagnosis and species-level identification. An integrated diagnostic approach combining serological and molecular methods enhances diagnostic accuracy and supports timely and effective patient management.

4. Prevalence and Antimicrobial Susceptibility Patterns of *Enterococcus* Species Isolated from Various Clinical Specimens: A Retrospective Observational Study

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Introduction: Enterococcus species have emerged as significant nosocomial pathogens, causing a wide range of infections including urinary tract infections, bloodstream infections, wound infections, and intra-abdominal infections.

Their intrinsic resistance and increasing acquisition of high-level aminoglycoside resistance and vancomycin resistance pose major therapeutic challenges. Continuous local surveillance of prevalence and antimicrobial susceptibility patterns is essential to guide empirical therapy and support antimicrobial stewardship. This study aims to determine the prevalence of *Enterococcus* spp. isolated from various clinical specimens and to analyse their antimicrobial susceptibility patterns in a tertiary care hospital.

Materials & Methods: This retrospective observational study included 273 patients with *Enterococcus* isolates collected from January 2023 to December 2025. Demographic details, department-wise distribution, species identification, and antimicrobial susceptibility patterns were analysed.

Results: Of the 273 patients, 189 (69%) were females and 84 (31%) were males. The majority were inpatients (72%). The most affected age group was 21–30 years (33%). *Enterococcus faecium* was the predominant species (41%), followed by *E. faecalis* (30%) and *Enterococcus* spp. 29%. Among IPD isolates, Linezolid (98%), Teicoplanin (97%), and Vancomycin (90%) showed the highest susceptibility, while marked resistance was observed to fluoroquinolones. OPD isolates showed excellent susceptibility to Linezolid and Vancomycin (100%). High-level aminoglycoside resistance (HLAR) was detected in 62% of isolates, and vancomycin-resistant *Enterococcus* (VRE) was identified in 10%.

Conclusion: The study highlights a substantial burden of *Enterococcus* infections with high levels of antimicrobial resistance. The presence of HLAR and VRE under scores the need for routine surveillance, strict infection control measures, and judicious antibiotic use to optimize patient management.

5. Microbiological Profile and Antimicrobial Resistance Pattern of Bloodstream Infections in Patients at a Tertiary Care Hospital, Indore

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Introduction: Bloodstream infections (BSIs) are a leading cause of morbidity and mortality among hospitalized patients, especially in intensive care units. Rapid progression to sepsis and septic shock, combined with rising antimicrobial resistance, creates significant treatment challenges. The range of causative organisms and their resistance patterns varies across regions and over time, emphasizing the need for continuous local surveillance.

Materials & Methods: This observational cross-sectional study was conducted from January 2025 to December 2025 at a tertiary care hospital in Indore. Blood samples from patients suspected of bloodstream infection were collected aseptically and processed using the BacT/Alert automated blood culture system. Positive cultures were subcultured on blood agar and MacConkey agar. Identification and antimicrobial susceptibility testing were performed using the Vitek 2 Compact system. Antibiotic susceptibility results were interpreted according to Clinical and Laboratory Standards Institute guidelines. Multidrug-resistant, extensively drug-resistant, and pandrug-resistant isolates were defined as per European Centre for Disease Prevention and Control and Centers for Disease Control and Prevention criteria.

Results: Out of 792 blood culture samples processed, 143 (18%) were culture positive. Gram-positive bacteria predominated, accounting for 58% of isolates, followed by Gram-negative bacteria at 39% and non-albicans *Candida* species at 2%. *Staphylococcus aureus* was the most common isolate, followed by coagulase-negative *Staphylococcus* and *Enterococcus* species. Among Gram-negative organisms, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Escherichia coli*, and *Acinetobacter baumannii* complex were frequently isolated. Gram-negative isolates showed high resistance to third-generation cephalosporins and fluoroquinolones, with carbapenem resistance mainly among *Klebsiella* and *Acinetobacter* species.

Conclusion: Gram-positive organisms predominated, while resistant Gram-negative pathogens highlight the urgent need for surveillance, stewardship, and infection control to reduce mortality.

6. Evaluation of in Vitro Synergy of Ceftazidime–Avibactam and Aztreonam against Carbapenem-Resistant *Enterobacteriales* (CRE) Isolates from ICU Patients in a Tertiary care hospital: A cross sectional study

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Introduction: Carbapenem-resistant Enterobacteriales (CRE) represent a major global health concern due to limited therapeutic options. The combination of ceftazidime–avibactam (CZA) and aztreonam (ATM) has shown promising activity against CRE; however, simple, and standardized laboratory methods for detecting in vitro synergy are limited. Aim: To evaluate in vitro synergy of Ceftazidime–Avibactam and Aztreonam against CRE isolates from various clinical samples

Materials & Methods: This cross-sectional study was conducted in Department of Microbiology, SGPGI, Lucknow, from June to December 2024. A total of 121 non-duplicate CRE isolates from ICU patients were included. Identification was performed using conventional Methods and MALDI-TOF MS. Carbapenemase production was assessed using modified carbapenem inactivation method (mCIM) and EDTA-modified CIM (eCIM). Synergy between CZA and ATM was tested using double disc diffusion method (DDDM) and broth disc elution method (BDEM).

Results: *Klebsiella pneumoniae* was the predominant isolate (62%), followed by *Escherichia coli* (26%) and *Enterobacter cloacae* (10%). Carbapenemase production was detected in 92 isolates by mCIM/eCIM. Synergy was observed in 89 isolates by DDDM and 92 isolates by BDEM, showing excellent concordance.

Conclusion: A high prevalence of CRE, predominantly *Klebsiella pneumoniae*, was observed among ICU patients. Both phenotypic methods demonstrated a high rate of in vitro synergy between ceftazidime–avibactam and aztreonam, supporting their routine use in clinical laboratories to guide effective therapy against CRE.

7. A Retrospective one Year Study of Antibiogram and Antimicrobial Susceptibility Trends of Blood Culture Isolates among Patients in a Tertiary Care Hospital in North India

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Introduction: Bloodstream infections range from bacteremia to fulminant septic shock. Empirical antimicrobial therapy is often initiated before susceptibility results, emphasizing the importance of antibiogram in initial treatment. This study was conducted to study the antibiogram and antimicrobial susceptibility trends of blood culture isolates among the patients of suspected blood stream infections in a tertiary care hospital.

Materials & Methods: The present retrospective study was conducted over a period of one year from 1 January 2025 to December 2025. A total of 1132 blood culture samples were collected in BACTEC 9050 automated system. The positive flagged bottles were cultured on Blood, Mac Conkey and Chocolate agar. Organisms were identified by standard microbiological techniques. Antibiotic susceptibility testing was done by Kirby Bauer disc diffusion method and results were interpreted according to CLSI guidelines, 2025. Antibiogram was prepared to find the resistance pattern of each species.

Results: A total of 1132 suspected blood stream infections were obtained during the study period and 356 (31.4%) BACTEC bottles flagged positive. Gram positive bacilli accounted for 256(71.9%) and Gram negative organisms were 100 (28%). Staphylococcus aureus 139 (39%), Staphylococci other than Staphylococcus aureus 104(29%) and Acinetobacter baumannii 39(10.8%) were the most common isolated organisms. The most sensitive antibiotics were Teicoplanin, Vancomycin and Linezolid. High resistance was observed for Penicillin, Erythromycin and Ceftriaxone.

Conclusion: The study highlights the increasing antimicrobial resistance trends among bacterial isolates and emphasizes the need for continuous surveillance, knowledge of local antibiogram and rational antibiotic usage.

8. Unmasking Nocardia in a Silico tuberculosis Patient – A Case Report

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Introduction: Pulmonary nocardiosis is an uncommon opportunistic infection caused by *Nocardia* species, often affecting individuals with impaired immunity or underlying lung disease. It commonly mimics pulmonary tuberculosis both clinically and radiologically, leading to diagnostic delays, especially in tuberculosis-endemic regions. Occupational exposure to silica and uncontrolled diabetes mellitus further increase susceptibility due to impaired host defenses. We report a case of pulmonary nocardiosis in a stone crusher with prior pulmonary tuberculosis, initially suspected to have silico tuberculosis.

Materials & Methods: A 45-year-old male stone crusher presented with chronic progressive dyspnea, dry cough for 6–8 months, and acute onset high-grade fever for 8 days. Clinical examination, laboratory investigations, radiological imaging, and microbiological evaluation of sputum samples were performed. Sputum was subjected to Gram staining, Ziehl–Neelsen staining, modified Ziehl–Neelsen staining using 1% sulphuric acid, and CBNAAT to rule out tuberculosis.

Results: The patient had uncontrolled diabetes mellitus (HbA1c 9.2%), leukocytosis, elevated ESR and CRP. CT chest revealed thin-walled cavitory lesions with surrounding consolidation, bilateral centrilobular nodules, and pleural effusion, raising suspicion of silico tuberculosis. However, sputum AFB smear and CBNAAT were negative. Gram stain demonstrated gram-positive thin branching filamentous bacilli. Modified Ziehl–Neelsen staining showed weakly acid-fast branching filaments, confirming *Nocardia* species. Further growth on blood agar confirmed the diagnosis of pulmonary nocardiosis.

Conclusion: Pulmonary nocardiosis should be considered in patients with chronic lung disease, occupational silica exposure, and diabetes mellitus who presented with tuberculosis-like features but have negative mycobacterial tests. Early microbiological identification using modified acid-fast staining is crucial for accurate diagnosis and appropriate management, thereby preventing morbidity and misdiagnosis.

9. Study of Vancomycin-Resistant Enterococci in Catheter-Associated Urinary Tract Infections with Special Reference to Biofilm Formation.

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Introduction: Enterococci have been recognized as a significant cause of hospital associated infections. In hospital associated urinary tract infections, they are the second most common organisms recovered. The development of vancomycin resistance is a threat in hospital settings. Biofilm formation is also an important virulence factor contributing to drug resistance. The aim of the study is to know the prevalence of vancomycin resistant enterococci in catheter associated urinary tract infection and role of biofilm formation in the association of catheter associated urinary tract infection.

Materials & Methods: Total 100 catheter associated urinary tract infection cases were included. The control consisted of 100 cases of non-catheterized urinary tract infection. Bacteriological identification and susceptibility testing were done as per standard protocol. Biofilm formation was investigated using simple tube method.

Results: Overall culture positivity in catheter associated urinary tract infection was 28%. Enterococci (39.28%) were the predominant pathogens followed by Escherichia coli (35.71%). In the current study the prevalence of vancomycin resistant enterococci was 17.86%. Strong biofilm was mainly produced by resistant isolates (36.36%). Biofilm formation by vancomycin resistant enterococci was statistically significant (p-value=0.02). Vancomycin resistant enterococcus infection was also more common in catheter associated urinary tract infection (p-value = 0.000003).

Conclusion: An aggressive approach is necessary for vancomycin resistant enterococcus detection and control.

Observational studies, strict adherence to standard infection control practices and continuous monitoring of hospital associated urinary tract infection are recommended measures to reduce the incidence of infections by biofilm forming organism and optimize their management.

10. Colistin as a Last Resort Drug in VAP: Susceptibility Testing Using Colistin Broth Disc Elution

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Institute: Sarojini Naidu Medical College

Introduction: Ventilator-associated pneumonia (VAP) is a serious infection in mechanically ventilated patients, frequently caused by multidrug-resistant Gram-negative bacteria. The growing burden of carbapenem resistance has markedly reduced therapeutic choices, positioning colistin as a vital last-line antibiotic. Accurate determination of colistin susceptibility is crucial for optimal clinical management. Although broth microdilution (BMD) is the reference standard, its routine use is limited due to technical and logistical constraints. The colistin broth disc elution (CBDE) method provides a simpler and more feasible alternative for routine laboratory practice.

Materials & Methods: The study was conducted in the Department of Microbiology, SNMC, from June 2025 to December 2025. Endotracheal aspirate samples collected aseptically from patients with suspected ventilator-associated pneumonia (VAP) admitted to intensive care units, selected based on the Clinical Pulmonary Infection Score (CPIS) criteria were received in the bacteriology laboratory. Quantitative cultures were performed on blood agar and MacConkey agar, followed by incubation at 37°C for 18–24 hours. Gram-negative isolates were identified using conventional biochemical methods. Routine antimicrobial susceptibility testing was performed using the Kirby-Bauer disc diffusion method. Colistin susceptibility testing was performed using the colistin broth disc elution (CBDE) method with cation-adjusted Mueller–Hinton broth. A standardized 0.5 McFarland inoculum was used and minimum inhibitory concentrations (MICs) were interpreted as per CLSI recommendations for above.

Results: A total of 84 Gram-negative isolates were included in the study. The predominant organisms isolated were *Klebsiella pneumoniae* (56.7%), followed by *Acinetobacter baumannii* complex (26.7%) and *Pseudomonas aeruginosa* (10%), with other non-fermenting Gram-negative bacilli recovered in smaller proportions. Colistin MICs determined by the CBDE method is currently under process.

Conclusion: The CBDE method appears to be a practical and reliable tool for assessing colistin susceptibility in VAP-associated Gram-negative infections. Its use can support appropriate antimicrobial therapy and enhance stewardship efforts, particularly in resource-limited settings.

11. Antimicrobial Susceptibility Pattern of Bacteria Isolated from Patients with Otitis Media

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Co-Authors: Dr. Vineeta Khare, Dr. Priyanka Shukla, Dr. Syed Mohd Faiz

Institute: Era University Lucknow (Uttar Pradesh)

Introduction: Otitis media is one of the most prevalent pediatric diseases worldwide and a leading cause of healthcare visits and antibiotic prescriptions in children. It is frequently associated with Eustachian tube dysfunction following upper respiratory tract infections and may present in acute otitis media or chronic otitis media forms. Bacterial pathogens play a significant role in disease development and persistence, leading to recurrent infections and complications such as hearing loss. The aim of this study was to determine the risk factors, bacterial profile and the antimicrobial susceptibility pattern of the isolates from patients with Otitis media.

Materials & Methods: This cross-sectional study involved 96 ear swab specimens obtained from patients clinically diagnosed with Otitis media. swabs were cultured for microbial identification according to standard protocol. The performed antimicrobial susceptibility testing using Kirby-Bauer disc diffusion method and also automated system (vitek2compact).

Results: Total number of bacterial isolates was 96. The most common bacterial isolates were *Pseudomonas aeruginosa* (59.3%) followed by *Proteus mirabilis* (21.8%), *Staphylococcus aureus* (10.4%), *Acinetobacter baumannii* (3.1%), *Klebsiella pneumoniae* (2%), *Escherichia coli* (2%), *Enterococcus faecalis* (1%). Among the *Pseudomonas aeruginosa* isolates maximum sensitivity was found to Piperacillin/Tazobactam (98%) followed by Meropenam (96%) and Levofloxacin (91%).

Conclusion: *Pseudomonas aeruginosa* was the predominant bacterial isolate, accounting for more than half of the cases, followed by *Proteus mirabilis*, while other organisms were detected at much lower frequencies.

12. Rising Antimicrobial Resistance in Uropathogenic *E. coli*: Exploring Fosfomycin Role in Current UTI Management

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Institute: Department of Microbiology, Santosh Medical College, and Hospital

Introduction: *Escherichia coli* is a common cause of Urinary tract infection worldwide. There has been an exponential rise in the emergence of multidrug resistant *E. coli*, mediated by beta-lactamase enzymes such as extended-spectrum beta-lactamases (ESBL), Amp C beta-lactamases, and carbapenemases, which poses a major therapeutic challenge. Fosfomycin has re-emerged as a potential alternative for treating UTIs caused by resistant strains. Aim: To determine the prevalence of ESBL, Amp C, and carbapenemase production among uropathogenic *E. coli* isolates and to assess their susceptibility to fosfomycin.

Materials & Methods: This prospective study was conducted in the Department of Microbiology, Santosh Medical College & Hospital, Santosh Deemed to be University, Ghaziabad from September 2024 to February 2025. A total of 2160 non-duplicate midstream urine samples received in the Microbiology laboratory were processed. A total of 243 *E. coli* isolates were obtained. Antimicrobial susceptibility testing was performed using the Kirby–Bauer disc diffusion method as per CLSI 2024 guidelines. ESBL, Amp C, and carbapenemase production were detected using standard phenotypic screening and confirmatory tests. Fosfomycin susceptibility was assessed by the disc diffusion method. The agar dilution method was planned to detect MIC in case any resistance to Fosfomycin is observed.

Results: Among the 243 *E. coli* isolates, ESBL, Amp C, and carbapenemase production alone was observed in 16.88%, 2.1%, and 2.1% of isolates, respectively. Co-production of beta-lactamases was detected in 35.8% of isolates, with ESBL and Amp C co-production being the most common. Carbapenemase-producing *E. coli* constituted 9.9% of isolates. All isolates, including beta-lactamase producers, demonstrated 100% susceptibility to fosfomycin. High resistance was noted against third- and fourth-generation cephalosporins, while relatively lower resistance was observed to nitrofurantoin and amikacin.

Conclusion:

The current study highlights a significant magnitude of beta-lactamase-mediated resistance among uropathogenic *E. coli*. Fosfomycin demonstrated uniformly high in-vitro effectiveness against all isolates, indicating its potential usefulness as a treatment option for urinary tract infections caused by multidrug-resistant *E. coli*. Judicious use of fosfomycin is essential to preserve its efficacy.

13. Bacteriological Profile and Antibiotic Susceptibility Patterns in Bronchoalveolar Lavage Samples: A Retrospective Study (2022–2025)

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Co-Authors: Akanksha Gupta, Anupam Das, Jyotsna Agarwal

Institute: Dr. Ram Manohar Lohia Institute of Medical Sciences, Lucknow

Introduction: Lower respiratory tract infections (LRTIs) remain a leading cause of morbidity, particularly in critical care settings. Bronchoalveolar lavage (BAL) serves as a vital diagnostic tool for identifying causative pathogens in severe cases, yet the rising prevalence of multidrug-resistant (MDR) organisms significantly complicates treatment protocols.

Materials & Methods: A retrospective observational study was conducted on 3,313 BAL samples collected between 2022 and 2025. Samples underwent culture and sensitivity testing to analyze bacterial identification and antibiograms. The study specifically focused on tracking resistance trends, including Carbapenem Resistance (CR), Extended-Spectrum Beta-Lactamase (ESBL) production, and evolving resistance patterns in Gram-positive cocci.

Results: Positivity rates ranged from 62.2% to 72.9%, with Gram-negative bacilli dominating throughout the study. While *Acinetobacter baumannii* was the leading pathogen (25–31%) from 2022 to 2024, a significant shift occurred in 2025, with *Klebsiella pneumoniae* emerging as the most frequent isolate (27.1%), surpassing *A. baumannii* (22.29%). Overall CR rates peaked at 76.7% in 2023 but declined to 62.1% in 2025; however, *A. baumannii* consistently retained >90% resistance. Significant shifts occurred in *Staphylococcus aureus* in 2025: Methicillin Resistance (MRSA) dropped to 52.6% from a previous range of 75–100%, but Vancomycin resistance (VRSA) was detected in one out of 20 samples, whereas it was 0% in prior years. Linezolid remained 100% effective.

Conclusion: The microbial landscape has shifted towards *K. pneumoniae* dominance. While the decline in carbapenem resistance is promising, the emergence of VRSA warrants urgent attention and continuous surveillance to preserve reserve antibiotics like Linezolid.

14. Prevalence of uropathogens and their susceptibility pattern at tertiary care hospital, Barabanki, UP

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Co-Authors: Dr. Nidhi Bhatnagar, Dr. Sameena Jawaid, Dr. Sheetal Agarwal, Dr. Jyoti Srivastava, Dr. Anjali Agarwal

Institute: Hind Institute of Medical Sciences, Barabanki, Lucknow

Introduction: Urinary tract infections are the most common bacterial infections affecting individuals of all age group. The widespread and inappropriate use of antibiotics has led to the emergence of multidrug-resistant uropathogens. Knowledge of microbial spectrum and antimicrobial susceptibility pattern is essential for selection of appropriate therapy.

Materials & Methods: A retrospective observational study was conducted at Hind Institute of Medical Sciences, Barabanki, from Jan to Dec 2024 (12 months). All urine samples received in bacteriology laboratory were cultured on CLED agar, incubated at 37° C for 24 hrs and antimicrobial susceptibility was performed as per CLSI guidelines 2024. Cultures showing significant bacteriuria were included in and their antimicrobial susceptibility pattern was assessed. Statistical analysis was performed using MS excel.

Results: Total 1362 urine samples were received, of which 525 samples showed significant bacteriuria. Most common age group affected was 21-40 years. Male: female ratio was 1:1.5. There was 428 Gram negative and 97 Gram positive bacteria isolated. Among Gram negative uropathogens, most common were 295(69%) E. coli, followed by 33(8%) Pseudomonas species and 29(7%) Citrobacter species. Enterococcus (83%) was the most common Gram-positive bacteria isolated. Gram negative isolates were most susceptible to colistin (100%) followed by fosfomycin (90%) and meropenem (70%). Most sensitive drug for Gram positive isolate was linezolid (91%), followed by vancomycin (85%).

Conclusion: E. coli remains the most common uropathogen, with an alarming rise in antimicrobial resistance. Regular monitoring of prevalence and susceptibility pattern is crucial to formulate effective antibiotic policies and to reduce the burden of resistant infections.

15. Title: Prevalence of Multi – Drug – Resistant Organisms in Pyogenic Liver Abscess

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Institute: Sanjay Gandhi Postgraduate Institute of Medical Sciences

Introduction: The emergence of multidrug –resistant (MDR) organisms has increasingly affected treatment outcomes in pyrogenic liver abscess. This study was undertaken to assess the prevalence of MDR organisms among patients diagnosed with pyrogenic liver abscess.

Materials & Methods: This observational study included 30 patients with clinically and radiologically confirmed pyogenic liver abscess admitted over duration of one year. Pus aspirate was collected under aseptic precautions. Bacterial identification was carried out using MALDI-TOF. Antimicrobial susceptibility testing was performed by Kirby-Bauer disc diffusion method following CLSI guidelines. Multidrug resistance was defined as resistance to at least one antimicrobial agent in three or more classes.

Result: The study included a total of 30 patients with pyogenic liver abscess. Among the 30 samples 10 were sterile, and 20 showed bacterial growth. Of the culture positive samples 8 were Gram positive and 12 were Gram negative isolates. Overall, Gram negative bacilli predominated among the isolates.

Antimicrobial susceptibility testing revealed a high level of resistance to commonly used antibiotics. Resistance to multiple antimicrobial classes was frequently observed, indicating a high prevalence of multidrug resistant (MDR) organisms.

Non-fermenters, especially *Acinetobacter* spp. showed the highest resistance rates across most antimicrobial groups.

Conclusion: The present study highlights a high burden of multidrug resistant organisms among the isolates analysed, with Gram-negative bacteria being the predominant pathogens. These findings emphasize the urgent need for judicious antibiotic use.

16. Microbial Spectrum and Antibiotic Susceptibility Pattern of Pus Culture in A Tertiary Care Hospital: Emphasizing Multi-Drug Resistance Prevalence

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Co-Authors: Nishtha Singh, Nidhi Bhatnagar, Anjali Agarwal, Jyoti Srivastava

Institute: Hind Institute of Medical Sciences, Barabanki

Introduction: Pyogenic infections can be caused by various microorganisms and mixed infections are common which require antibiotic therapy. The inappropriate use of antibiotics has resulted in development of multi drug resistance. Hence microbial spectrum and susceptibility profile is necessary to implement proper treatment and prevent resistance.

Materials & Methods: A retrospective study was carried out from 1January 2024 -31December 2024, 409 pus samples were collected during study period. The samples were cultured on Blood agar and MacConkey agar. After aerobic incubation at 37°C overnight, microorganisms were identified by standard methods and antibiotic susceptibility done by Kirby Bauer disc diffusion method and interpreted as per CLSI guidelines 2024.

Results: The present study showed 381 (93.15%) growth. Among 250 Gram negative (65 %), Escherichia coli (92) was most common followed by Pseudomonas spp.63, Acinetobacter spp 35, Citrobacter spp 41, Proteus spp 16 with two Serratia and one of Morganella. Among 131Gram-positive (34.4%), 105 isolates were Staphylococcus aureus and 26 were Enterococcus spp. More isolates were from indoor admission (303) as compared to outdoor (78). Male (250) were more infected as compared to female (131). 107 (28.08%) isolates were multi-drug resistant and their association with indoor admitted male patient was significantly associated ($p<0.05$). MRSA isolates were 84 (22%).

Conclusion: Multi drug resistance has become major public health problem. Our study shows increased resistance to antibiotics among indoor admitted patients which is a serious problem. Regular surveillance with antimicrobial stewardship program should be implemented to ensure better therapeutic strategy to reduce morbidity and mortality.

17. Bacteriological profile and antimicrobial sensitivity patterns of Lower Respiratory Tract infection in patients attending a tertiary care hospital of western Uttar Pradesh

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Introduction: Lower respiratory tract infections (LRTIs) are a major cause of morbidity and mortality, particularly in developing countries, and are increasingly complicated by antimicrobial resistance. This study aimed to analyze the bacterial etiology of LRTIs and their susceptibility testing (AST) patterns in a tertiary-care hospital of Western Uttar Pradesh.

Materials & Methods: This study was conducted from January 2025 to December 2025 and included 1831 patients with clinical suspicion of LRTI. Respiratory samples: sputum, endotracheal aspirates, and bronchoalveolar lavage fluid, were collected and cultured on appropriate media. Bacterial identification was performed using conventional methods. AST was performed using Kirby–Bauer disc diffusion method as per CLSI M100, 35th edition

Results: Out of 1,831 samples, 692 (37.8%) showed significant bacterial growth. *Klebsiella pneumoniae* (38.3%) was most frequently isolated organism followed by *Pseudomonas spp.* (22.4%), *Escherichia coli* (16.5%) and *Acinetobacter baumannii* (10.7%), *Klebsiella pneumoniae* showed susceptibility to colistin (99.5%), tigecycline (90.2%), imipenem (31.7%), meropenem (35.7%), amikacin (34.1%), tobramycin (31.7%), gentamicin (27.7%), piperacillin–tazobactam (15.9%), ceftazidime (12.8%), ceftriaxone (7.3%), minocycline (3.7%). Male predominance was observed, with most isolates obtained from patients aged above 60 years.

Conclusion: The study demonstrates a high burden of multidrug-resistant Gram-negative pathogens in LRTIs. This highlights the importance of culture and AST, which enables clinicians to shift from broad empirical therapy to targeted, definitive treatment. This not only improves clinical outcomes and reduces treatment failure but also minimizes unnecessary exposure to higher antibiotics, thereby helping to curb the emergence of antimicrobial resistance.

18. Prevalence And Clinico-Microbiological Profile of Vancomycin-Resistant Enterococci (VRE) In Various Clinical Samples: A 2024–2025 Study From A Tertiary Care Hospital In Prayagraj, Uttar Pradesh

Author: Dr. Akanksha Pandey

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Institute: Motilal Nehru Medical College, Prayagraj

Introduction: Enterococci have emerged as significant nosocomial pathogens due to their intrinsic and acquired resistance to multiple antimicrobials. Vancomycin-resistant Enterococci (VRE) pose a serious therapeutic challenge and are associated with increased morbidity, mortality, and healthcare costs.

Objectives: To determine the prevalence of VRE and analyse their clinico-microbiological profile among various clinical samples received at a tertiary care hospital (Motilal Nehru medical college) in Prayagraj, Uttar Pradesh.

Materials & Methods: Study design: Prospective observational study

Duration: 2 years

Samples: urine, blood, pus, wound swabs, and other clinical specimens were identified using standard microbiological techniques.

Sample size: 500

Antimicrobial susceptibility testing - Kirby–Bauer disk diffusion method as per CLSI guidelines.

Vancomycin resistance confirmation -vancomycin screen agar and/or MIC determination by E-test.

Clinical and demographic data of patients were analysed.

Results: Out of 175 Enterococcus isolates, 17 (9.7%) were identified as vancomycin-resistant Enterococci (VRE). The majority of VRE isolates were recovered from urine, followed by blood and pus samples. VRE infections were predominantly observed in ICU-admitted patients, those with prolonged hospital stay, prior antibiotic exposure, and invasive procedures. The isolates showed high resistance to ampicillin and high-level gentamicin, while linezolid and daptomycin remained highly effective.

Conclusion: The increasing prevalence of VRE highlights the need for continuous surveillance, strict infection control practices, and judicious use of antibiotics. Early detection and appropriate antimicrobial stewardship are essential to prevent further spread of VRE in healthcare settings.

19. Impact of Diagnostic Stewardship Interventions on Blood Culture Positivity and Contamination Rates: A Pre- and Post-Intervention Analysis

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Co-Authors: Shiva Verma, Akanksha Gupta, Rimjhim, Anupam Das, Jyotsna Agarwal

Institute: Dr. Ram Manohar Lohia Institute of Medical Science, Lucknow

Introduction: Blood culture positivity and contamination rates are critical quality indicators for diagnostic yield. This study evaluated the impact of diagnostic stewardship interventions on these rates in pediatric patients.

Materials & Methods: A retrospective analysis at a tertiary care hospital compared two periods: Pre-intervention (June 1–Sept 12, 2025) and Post-intervention (Sept 13, 2025–Jan 12, 2026). Interventions included staff sensitization, periodic feedback, and reinforcement of aseptic collection techniques

Results: Out of 414 pre-intervention cultures, 257 (62.1%) were positive and 20 (4.83%) were contaminated. Post-intervention (n=417), positivity rose to 300 (71.9%) while contamination increased marginally to 22 (5.28%). Sterile cultures decreased significantly from 137 to 95.

Conclusion: Stewardship interventions successfully improved diagnostic yield (positivity). Although contamination rose slightly, it remained near acceptable benchmarks, underscoring the need for sustained training and monitoring✓.

20. Antimicrobial Resistance Patterns of *Pseudomonas aeruginosa* Isolated from Clinical Specimens: A Prospective Study from a Tertiary Care Hospital in North India

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Co-Authors: Abhineet mehrotra, Umar Rashid Khan

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Introduction: *Pseudomonas aeruginosa* is a major opportunistic pathogen and an important cause of healthcare-associated infections, particularly among immunocompromised patients. Its intrinsic resistance and remarkable ability to acquire multidrug resistance severely limit therapeutic options. Continuous local surveillance of prevalence and antimicrobial susceptibility patterns is therefore essential to guide empirical therapy and strengthen antimicrobial stewardship. This study aimed to determine the prevalence, specimen-wise distribution, and antimicrobial resistance profile of *P. aeruginosa* isolated from clinical specimens in a tertiary care hospital in North India.

Materials & Methods: A prospective study was conducted in the Department of Microbiology, Integral Institute of Medical Sciences and Research, Lucknow, from July to December 2025. A total of 700 non-duplicate clinical specimens, including pus, urine, sputum, wound swabs, and blood, were processed using standard microbiological techniques. Identification was performed by conventional biochemical methods, and antimicrobial susceptibility testing was carried out by the Kirby–Bauer disc diffusion method following CLSI guidelines. Isolates were classified as multidrug-resistant (MDR), extensively drug-resistant (XDR), or pan-drug-resistant (PDR).

Results: *P. aeruginosa* was isolated from 16.4% (115/700) of specimens, with the highest recovery from pus samples (46%), followed by sputum (15%) and urine (13%). Most isolates were obtained from inpatients (54.3%). The highest departmental distribution was observed in Surgery (17.8%), followed by Medicine (15.7%) and TB & Chest (13.5%). High resistance rates were noted against ceftazidime (66.4%) and imipenem (52.3%), whereas lower resistance was observed to piperacillin–tazobactam (18%) and piperacillin (30%). MDR, XDR, and PDR phenotypes were detected in 27.8%, 9%, and 1.7% of isolates, respectively.

Conclusion: The high prevalence of resistant *P. aeruginosa* highlights the urgent need for continuous surveillance, rational antibiotic use, and strengthened infection control strategies.

21. Colistin-Sparing Therapeutic Options Against Genotypically Characterized Carbapenemase-Producing *Klebsiella* Species (bla_{NDM}, bla_{OXA-48}, and bla_{KPC}) in a Tertiary Care Centre in North India

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Co-Authors: Dr. Arti Agrawal, Dr. Pragya Shakya, Dr. Parul Garg, Dr. Barsha Das

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Introduction: Carbapenem-resistant Enterobacterales (CRE) have emerged as an urgent public health threat in the world including India. Carbapenem resistance is mostly mediated by the production of carbapenemase enzymes that are present on the mobile genetic elements. The majority of CRE infections worldwide are caused by: *Klebsiella pneumoniae*. Other causative organisms may include *Escherichia coli*, *Klebsiella oxytoca* and *Enterobacter cloacae*. Colistin is considered as last resort, since colistin monotherapy presents with many difficulties, colistin is administered in combination with an additional drug. Colistin sparing options include eg-Tigecycline, Ceftazidime-Avibactam Aztreonam, Imipenem-Relebactam, Meropenem- Vaborbactam, Fosfomycin .

Materials & Methods: Clinical isolates of *Klebsiella* species recovered from patient specimens (urine, blood, sputum, pus, & other body fluids) Over a period of 1 year (2025- 2026) SAMPLE SIZE: $n = Z^2(pq)/d^2 = 120$ Isolates showing reduced susceptibility or resistance to carbapenem are included. Genotypic detection of gene (KPC, NDM, OXA-48) is done by Multiplex PCR Kit. The MIC (Minimum Inhibitory Concentration) broth discelution test is a method used to determine the susceptibility of Colistin. Colistin sparing drugs interpretive criteria is based on CLSI guidelines.

Result: Prevalence of various gene in *Klebsiella* species by genotypic method is NDM 41%, OXA-48: 25%, KPC: 7%, NDM, KPC, OXA -48: 6%, NDM & OXA -48: 54% Colistin is sensitive for 96% *Klebsiella* isolates. Ceftazidime avibactam+Azetronam is sensitive for NDM gene, Imipenem relebactam, Meropenem vaborbactam works best for KPC, Tigecycline & Fosfomycin are also good options for carbapenem resistant enterobacterales

Conclusion: Effective colistin-sparing therapeutic options are available for carbapenemase-producing *Klebsiella* species when guided by genotypic profiling. Integration of molecular resistance mechanisms into routine diagnostics can optimize antimicrobial selection, improve patient outcomes, and support antimicrobial stewardship by preserving colistin as a last-resort agent.

22. Bacteriological Profile and Characterisation of MDR/XDR Patterns in Pyogenic Infections at a Tertiary Care Hospital in Indore

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Introduction: Pyogenic infections are common in India and can affect different parts of the body such as the skin and soft tissues, respiratory tract, and internal organs. These infections are primarily caused by bacteria such as *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Escherichia coli*, and *Pseudomonas aeruginosa*. Treatment of pyogenic infections has become increasingly challenging due to the growing prevalence of multidrug-resistant (MDR) and extensively drug-resistant (XDR) bacteria. Understanding the causes of disease, associated risk factors, and appropriate treatment options is important for effective management and better patient outcomes.

Materials & Methods: This hospital-based descriptive retrospective study was conducted in the Microbiology Laboratory of Index Medical College and Hospital, Indore, from December 2024 to November 2025. A total of 362 pus samples from patients of all age groups and both genders were processed using standard microbiological methods. Bacterial identification was performed by conventional biochemical tests. Antimicrobial susceptibility testing was carried out according to CLSI guidelines. Isolates were categorized as MDR and XDR using standard international definitions.

Results: Of the 362 pus samples, 174 (46%) yielded significant bacterial growth. Gram-negative bacilli (56.3%) predominated over Gram-positive cocci (43.7%). Among Gram-negative isolates, *Escherichia coli* (25.8%) and *Klebsiella pneumoniae* (21.8%) were most common, while *Staphylococcus aureus* (26.4%) was the predominant Gram-positive isolate. MDR was detected in 71 isolates, and 31 isolates were classified as XDR. Among Gram-negative bacilli, 40.2% were MDR and 33.6% were XDR, with highest XDR rates observed in *Acinetobacter* spp. and *Proteus mirabilis*. Among Gram-positive cocci, 47.2% isolates were MDR, while no XDR strains were detected.

Conclusion: The study highlights a high prevalence of MDR and XDR pathogens in pyogenic infections, emphasizing the need for routine antimicrobial susceptibility testing and strengthened antimicrobial stewardship programs.

23. Bacteriological Profile and Antimicrobial Susceptibility Trends of Wound Infections in a Tertiary Care Hospital of Eastern Uttar Pradesh

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Introduction: Wound infections remain a leading cause of morbidity and prolonged hospitalization in resource-limited regions. In Eastern Uttar Pradesh, the challenge is exacerbated by a high volume of trauma cases and emerging multidrug-resistant (MDR) strains. This study aims to delineate the current bacteriological landscape and resistance patterns to guide empirical therapy in this geographic belt.

Materials & Methods: A prospective study was conducted over 12 months (2025) at a tertiary care hospital in Eastern UP. Pus swabs and aspirates from 350 patients with clinical wound infections (post-operative and trauma cases) were processed. Identification was performed using standard biochemical techniques, and Antimicrobial Susceptibility Testing (AST) following CLSI M100 35th Edition guidelines using Kirby-Bauer disc diffusion method.

Results: Out of 350 samples processed, 285 (81.4%) yielded significant aerobic bacterial growth. Gram-negative bacilli (58.2%) predominated over Gram-positive cocci (41.8%). The most common Gram-negative isolates were *Escherichia coli* (24.6%), *Pseudomonas aeruginosa* (18.2%), *Klebsiella pneumoniae* (10.5%), and *Acinetobacter baumannii* (4.9%). Among Gram-positive cocci, *Staphylococcus aureus* was the predominant isolate (32.3%), followed by coagulase-negative staphylococci (9.5%). Methicillin-resistant *Staphylococcus aureus* (MRSA) constituted 55.1% of *S. aureus* isolates. High resistance was observed to penicillin, erythromycin, ciprofloxacin, third-generation cephalosporins, and fluoroquinolones. ESBL production was noted in approximately 42% of Enterobacterales. Good susceptibility was observed to vancomycin, linezolid, carbapenems, piperacillin-tazobactam, and amikacin.

Conclusion: The study highlights a shift toward MDR Gram-negative infections in Eastern Uttar Pradesh. The high prevalence of MRSA and ESBL-producing GNB necessitates a shift from broad-spectrum empirical use to culture-directed therapy. Continuous regional surveillance and a robust Hospital Antibiotic Policy are critical to curb the escalating resistance in tertiary care settings.

24. Fosfomycin resistance in carbapenem-resistant *Escherichia coli* causing urinary tract infections

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Introduction: Urinary tract infections (UTIs) are among the most common infectious diseases, with *Escherichia coli* recognized as the leading causative pathogen. However, the emergence of multidrug-resistant strains has significantly limited the available therapeutic options for treating uropathogenic *E. coli*. Fosfomycin is increasingly being used as a last-line oral agent for UTIs, but its clinical effectiveness is now under threat due to the rising incidence of fosfomycin resistance.

Materials & Methods: This cross-sectional study was conducted over a period of eight months and included a total of 1,849 urine samples collected from hospitalized patients at a tertiary care hospital. The samples were cultured on cysteine lactose electrolyte-deficient (CLED) agar. Lactose-fermenting colonies showing significant colony counts were subjected to preliminary identification, followed by species-level identification and antimicrobial susceptibility testing using the VITEK 2 Compact automated system with GN-ID and AST-N405 cards.

Results: Of the 1,849 urine samples analyzed, 600 (32.45%) demonstrated significant growth of Gram-negative bacteria. Among these, *Escherichia coli* accounted for 500 isolates (83.33%). Of the *E. coli* isolates, 50 (10%) were carbapenem-resistant, and among these resistant strains, 10 (2%) exhibited resistance to fosfomycin. Overall, 450 *E. coli* isolates were recovered from female patients.

Conclusion: *Escherichia coli* is the leading cause of urinary tract infections. Multidrug-resistant uropathogenic *E. coli* strains continue to show high in vitro susceptibility to fosfomycin. However, the emergence of fosfomycin resistance associated with its increased use in clinical practice highlights the need for appropriate monitoring and stewardship measures.

25. Antimicrobial Resistance Trends in Enteric Fever Pathogens: A Review of Typhoidal Salmonella at a tertiary care teaching hospital

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Introduction: Enteric fever is a serious systemic disease caused by *Salmonella enterica* serovars Typhi and Para typhi (A, B, and C). The illness is widespread in low- and middle-income countries, yet comprehensive incidence data from these regions remain limited. In India, the estimated rate of culture-confirmed typhoid is about 377 cases per 100,000 people, with a case fatality close to 1%. Although antibiotics are generally effective in treatment, the growing challenge lies in managing infections due to the shifting antimicrobial resistance patterns observed in typhoidal *Salmonella* strains. This study review year-wise resistance and susceptibility trends in *Salmonella* Typhi and *Salmonella* Para typhi A/B, highlighting the evolving burden of antimicrobial resistance across commonly used therapeutic agents

Materials & Methods: A total of 172 clinical *Salmonella* isolates collected between January 2023 and October 2025 from diverse patient populations. A retrospective analysis of isolates, patient age/gender and resistance profile was done to estimate the changing trend of antimicrobial resistance over 3 years.

Results: Demographic analysis revealed higher resistance in adult isolates compared to pediatric cases, with male predominance across *Salmonella* Typhi and *Salmonella* Para typhi isolates. Out of the three Typhoidal *Salmonella*, *S. Typhi* was found to be most common. A high percentage of resistance of Fluoroquinolone's was found in all 3 years. *Salmonella Typhi* demonstrated fluctuating resistance to ciprofloxacin (23.7% in 2023, rising to 45.9% in 2024, then declining to 13.9% in 2025), while ceftriaxone resistance was high in 2023 (57.9%) but nearly absent thereafter. *S. Para typhi a* exhibited notable ciprofloxacin resistance (38.9% in 2023, dropping to 13.3% in 2024, then rising again to 36.8% in 2025), with sporadic carbapenem resistance. *S. Para typhi B* isolates were limited to 2025 but showed 100% resistance to ciprofloxacin. Carbapenem resistance (ertapenem, imipenem) was sporadic and low, while trimethoprim/sulfamethoxazole resistance was absent across all years.

Conclusion: Our findings highlight dynamic shifts in resistance, with fluoroquinolone resistance persisting as a major concern and cephalosporin resistance declining over time. The emergence of *S. Para typhi B* with multidrug resistance in 2025 is alarming. Continuous surveillance, rational antibiotic use, and stewardship programs are critical to mitigate the evolving AMR threat in enteric fever pathogens.

26. Pulmonary Nocardiosis: A Case Report From tertiary care hospital.

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Institute: Hind Institute of Medical Sciences, Barabanki

Introduction: Nocardia species are opportunistic pathogens, primarily affect immunocompromised individuals. With the rising prevalence of conditions such as HIV infection, malignancy, and long term corticosteroid use, the incidence of Nocardial infections has increased. Although uncommon, Nocardia can also cause serious disease in immunocompetent hosts, often mimicking other pulmonary infections and leading to delayed diagnosis.

Materials & Methods: We present the case of a 50-year-old male with chronic obstructive pulmonary disease (COPD), initially diagnosed with pulmonary tuberculosis following detection of acid-fast bacilli (AFB) on Ziehl–Neelsen staining. He underwent 6 months of anti-tubercular therapy but experienced progressive worsening of symptoms, including persistent productive cough. Further evaluation was performed using bronchoscopy, and bronchial lavage fluid was submitted for microbiological analysis. Direct microscopy with potassium hydroxide (KOH) preparation revealed delicate, narrow (0.5–1 μm) bacterial filaments branching at right angles. Acid-fast staining demonstrated pink/red, branching, beaded filaments consistent with *Nocardia* species. Culture confirmed *Nocardia* infection. Antimicrobial susceptibility testing revealed resistance to multiple agents, including amoxicillin–clavulanic acid, minocycline, gentamicin, tobramycin, ciprofloxacin, and trimethoprim–sulfamethoxazole. Despite supportive care, the patient succumbed to cardiopulmonary arrest secondary to pneumonia and COPD 4 days after diagnosis.

Conclusion: Pulmonary nocardiosis remains a rare but highly consequential infection, associated with significant morbidity and mortality. Its clinical similarity to tuberculosis often results in misdiagnosis and inappropriate therapy. Rapid, reliable diagnostic methods are essential to ensure timely identification of the pathogen and initiation of effective antimicrobial treatment, thereby reducing mortality and improving patient outcomes.

27. Comparative Evaluation of Standard versus Direct Antimicrobial Susceptibility Testing From Positive Blood Cultures in a Tertiary Care Hospital

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Introduction: Sepsis is the one of the leading causes of morbidity and mortality. Direct antimicrobial susceptibility testing (DST) significantly lowers the reporting time by 24 hours as compared to standard antimicrobial susceptibility testing (AST). This study was conducted to compare the DST method with the standard method.

Materials & Methods: This is a prospective study conducted over a period of three months (November, 2025 to January, 2026) in a tertiary care hospital in North India. A total of 196 blood culture samples were collected and processed in BACTEC 9050 automated system. From positive flagged bottles, Direct Gram stain was performed. DST was done after interpretation of Gram stain. Cultures were done for AST. Organisms were identified by standard microbiological techniques. Categorical agreement between AST and DST was calculated using AST as the reference method. Results were interpreted according to CLSI guidelines 2025.

Results: A total of 196 suspected blood stream infections were obtained during the study period and 89 (45%) BACTEC bottles flagged positive. Gram positive bacilli accounted for 71.7% and Gram negative organisms were 28%. Staphylococcus aureus (36%), Staphylococci Other than Staphylococcus aureus (31.7%) and Acinetobacter baumannii (9%) were the most common isolated organisms. The categorical agreement between the two methods was found to be 91%.

Conclusion: DST can reduce the turnaround time by 24 hours thus enabling earlier initiation of antibiotic therapy in septic anemic patients. It is an accurate and rapid method which can significantly improve patient outcome and reduce development of antimicrobial resistance.

28. Carbapenemase Production by Phenotypic Method in Carbapenem Resistant Enterobacteriaceae & Its Effect on Antimicrobial Susceptibility Pattern in Tertiary Care Hospital

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Introduction: Enterobacteriales are among the most frequent causes of hospital-acquired infections. These organisms can cause serious illnesses such as bloodstream infections, pneumonia, and urinary tract infections. Carbapenems are considered last-resort antibiotics for treating severe infections caused by resistant bacteria. However, the emergence of carbapenem-resistant Enterobacteriaceae (CRE) has become a major public health concern. These bacteria produce enzymes called carbapenemases, which break down carbapenem antibiotics and make treatment options extremely limited.

Materials & Methods: Bacterial isolates were collected from clinical samples obtained from hospitalized patients. Initial screening for carbapenem resistance was performed using the disk diffusion method. Isolates showing reduced susceptibility were further tested using the Modified Carbapenem Inactivation Method (mCIM) to confirm carbapenemase production. Antimicrobial susceptibility testing against commonly used antibiotics was also carried out to determine remaining treatment options.

Results: Among 355 Enterobacteriaceae isolates, most patients were aged 21–40 years, with male predominance. Urine was the commonest sample. *E. coli* was the predominant organism. Extremely high carbapenem resistance was observed, with 100% resistance to meropenem. Overall, 71.3% isolates were carbapenemase producers by mCIM.

Conclusion: Carbapenem-resistant Enterobacteriaceae represent a serious challenge in hospital settings. In resource-limited laboratories where molecular tests are not readily available, the mCIM offers a simple, low-cost, and effective method for early detection. Early identification supports appropriate antibiotic selection and helps prevent the spread of these dangerous pathogens

29. Recurrent Invasive Salmonella Infection in a Child with Colitis and Multisystem Inflammation: A Diagnostic Challenge Suggesting Underlying Immune Dysregulation

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Introduction: Salmonella infections are common causes of acute gastroenteritis in endemic regions; however, recurrent invasive Salmonella infections, particularly with systemic inflammatory manifestations, are unusual and may indicate underlying immune dysregulation. Early-onset inflammatory bowel disease (IBD) with extra-intestinal features represents a heterogeneous group that includes monogenic immune disorders.

Case Description: We report a young male child with recurrent admissions over 2023–2024 for bloody diarrhoea, abdominal pain, arthritis involving small joints of the lower limbs, palpable purpura, and suppurative lymphadenopathy. Initial valuation favoured ulcerative colitis with reactive arthritis. Microbiological evaluation revealed culture-proven invasive Salmonella infection on two occasions—Salmonella Para typhi B during one admission and Salmonella Typhi during a subsequent episode. Both episodes required inpatient management. Given the multisystem involvement and recurrent invasive infections, the diagnostic consideration broadened to early-onset IBD with primary immune dysregulation, and the patient is currently under evaluation for autoimmune lymphoproliferative syndrome (ALPS) or ALPS-like disorders.

Results: Discussion: While previous studies have reported an association between Salmonella exposure and ulcerative colitis in endemic regions, these were largely based on serology or molecular detection and did not address invasive disease or immune dysfunction. In contrast, recurrent culture-confirmed typhoidal Salmonella bacteraemia, combined with colitis, arthritis, vasculitic rash, and suppurative lymphadenopathy, strongly raises suspicion of an underlying defect in immune regulation or host defence mechanisms rather than isolated inflammatory bowel disease.

Conclusion: This case highlights the importance of considering primary immune dysregulation in children presenting with IBD-like colitis and recurrent invasive Salmonella infections, and underscores the need for close collaboration between Microbiology, Gastroenterology, and Immunology in such complex presentations.

30. Antimicrobial resistance patterns among gram negative bloodstream and respiratory isolates in a tertiary care hospital: Special emphasis on cefepime/enmetazobactam susceptibility

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Introduction: According to WHO antimicrobial resistance reports, multidrug-resistant gram-negative bacilli increasingly complicate bloodstream and respiratory infections in tertiary care hospitals. Rising resistance to β -lactams and fluoroquinolones has increased carbapenem use, highlighting the need for carbapenem-sparing alternatives. This study aimed to evaluate the antimicrobial resistance patterns among gram-negative bloodstream and respiratory isolates, with special emphasis on the in-vitro susceptibility of cefepime–enmetazobactam.

Materials & Methods: A retrospective observational study was conducted on 100 non-duplicate gram-negative isolates recovered from blood and sputum samples in a tertiary care hospital. Bacterial identification was performed using standard microbiological techniques. Antimicrobial susceptibility testing was carried out by the Kirby–Bauer disc diffusion method in accordance with CLSI guidelines. Susceptibility to multiple antibiotic classes, including β -lactam/ β -lactamase inhibitor combinations, cephalosporins, carbapenems, aminoglycosides, and fluoroquinolones, was analyzed.

Results: *Pseudomonas* spp. were the predominant isolates ($\approx 70\%$), followed by *Klebsiella pneumoniae* ($\approx 18\%$), *Klebsiella oxytoca* ($\approx 7\%$), and *Escherichia coli* ($\approx 5\%$). Bloodstream isolates demonstrated higher resistance to ampicillin ($>95\%$), early-generation cephalosporins ($\approx 85\%$), and fluoroquinolones ($\approx 65\%$) compared to respiratory isolates. Carbapenems retained good activity in both groups ($>85\%$). Cefepime–enmetazobactam showed better susceptibility in respiratory isolates ($\approx 80\text{--}85\%$) than bloodstream isolates ($\approx 70\text{--}75\%$), with variable activity against *Pseudomonas* spp.

Conclusion:

The study highlights a high burden of antimicrobial resistance among gram-negative bloodstream and respiratory isolates. Cefepime–enmetazobactam shows promising in-vitro activity and may serve as a potential carbapenem-sparing option when guided by susceptibility testing.

31. Genomic Insights into colistin resistance among CRGNB isolates; evolutionary dynamics and in-vitro evaluation of combination antibiotic approaches to combat antimicrobial resistance

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Introduction: Colistin is a last-resort antibiotic for infections caused by carbapenem-resistant Gram-negative bacteria (CR-GNB). India bears a high antimicrobial resistance (AMR) burden, with nearly 83% of hospitalized patients colonized or infected with multidrug-resistant organisms. The rising emergence of colistin resistance further threatens available therapeutic options and represents a major global public health concern.

Objective: This study aimed to elucidate the genomic determinants and evolutionary dynamics of colistin resistance among CR-GNB isolates and to assess the in-vitro efficacy of combination antibiotic therapies as alternative treatment strategies.

Materials & Methods: A total of 400 clinical CR-GNB isolates were subjected to antimicrobial susceptibility testing, including colistin MIC determination. Whole-genome sequencing was performed for resistome profiling, detection of chromosomal mutations, and identification of mobile genetic elements associated with colistin resistance. Clonal relatedness was assessed using PFGE. Checkerboard assays were conducted for multiple antibiotic combinations to determine fractional inhibitory concentration indices (FICI), and synergistic combinations were further evaluated by time-kill assays, with bactericidal activity defined as a ≥ 2 -log₁₀ CFU/mL reduction.

Results: Carbapenem resistance was primarily mediated by *bla*NDM (57.7%), followed by *bla*oxa-48-like (29.5%) and *bla*VIM (10.5%), with 7.5% of isolates resistant to colistin in *bla*NDM-1, *bla*NDM-4, & *bla*NDM-5 along with *bla*OXA-48 namely *bla*OXA-181 & *bla*OXA-232 were identified. Phylogenomic analysis revealed substantial genetic diversity, including the rare ST1076 in *Pseudomonas aeruginosa*. *bla*NDM, *bla*oxa-48 positive *Escherichia coli* and *Klebsiella pneumoniae* harbored IncFIIA, IncA/C, and IncFIB plasmids. Synergistic activity (FICI ≤ 0.5) was observed for colistin-meropenem, imipenem-meropenem, and colistin-minocycline combinations, with no antagonism detected.

Conclusion: Epidemic IncFIIA, IncA/C, and IncFIB plasmids play a central role in disseminating carbapenem resistance. Synergistic antibiotic combinations, particularly colistin-based regimens, may offer effective therapeutic options against CR-GNB infections.

32. Emerging Nosocomial Threat: *S. maltophilia* Pneumonia in Mechanically Ventilated Patients

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Institute: AIIMS Rishikesh

Introduction: *Stenotrophomonas maltophilia* stands as the only clinically relevant species in its genus, manifesting as an obligate aerobic, non-fermentative, Gram-negative bacillus thriving in diverse aquatic and humid niches. Globally, it poses a rising nosocomial threat, particularly in lower respiratory tract infections (LRTIs) like pneumonia, fueled by intrinsic multidrug resistance to carbapenems, β -lactams, and aminoglycosides. This retrospective analysis at a tertiary care centre in North India delineates patient demographics, microbiological profiles, and clinical traits of *S. maltophilia* LRTIs from January to June 2025.

Materials & Methods: Respiratory specimens—sputum, endotracheal aspirates, bronchoalveolar lavage—from clinically diagnosed LRTI cases were processed via Gram staining, culture on blood, MacConkey, and chocolate agars (37°C, 18–24 hours, 5–10% CO₂), and confirmed by VITEK-2 for identification and antimicrobial susceptibility testing (AST). Demographic, clinical, and radiological data were extracted from records.

Results: Twenty-three isolates emerged, predominantly linked to mechanical ventilation (15/23, 65.2%) and ICU stays (7/23, 30.4%). Pneumonia signs affected 9/23 (39.1%), with COPD in 3/23 (13.0%) and carcinoma in 2/23 (8.7%). AST revealed strong susceptibility: minocycline (20/23, 87.0%), levofloxacin (17/23, 73.9%), trimethoprim-sulfamethoxazole (16/23, 69.6%), underscoring viable alternatives amid broad resistances.

Conclusion: *S. maltophilia* emerges as a formidable respiratory pathogen in ventilated, ICU patients. High minocycline susceptibility guides therapy, yet β -lactam/aminoglycoside resistance curtails options. Prompt VITEK-2-based identification and targeted antibiotics are imperative to curb mortality.

33. *Aeromonas* Species as Emerging Uropathogens: Institutional Case Series and Systematic Review

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Introduction: *Aeromonas* spp. is Gram-negative bacilli found in various aquatic environments and sea foods. Although it has been recognized as an emerging pathogen in humans leading to gastrointestinal infections and septic anemia, its association with urinary tract infection (UTI) is poorly characterized.

Objective: We aimed to characterize the epidemiology, risk factors and microbiological spectrum of UTIs caused by *Aeromonas* spp.

Materials & Methods: We conducted a retrospective analysis of culture-confirmed *Aeromonas* UTIs diagnosed at a tertiary-care centre in Lucknow, India, (January 2023-December 2025). This was complemented by a systematic review of MEDLINE, CINAHL, and Embase databases, including all eligible reports published up to January 2026. Demographic characteristics, underlying risk factors, species distribution, antimicrobial susceptibility patterns, and clinical outcomes were analysed.

Results: Fifty-six cases were identified (47 from literature, 9 institutional cases). The predominant species were *A. caviae* (46.4%), *A. hydrophila* (35.7%), and *A. veronii* biovar *sobria* (5.4%). Major risk factors included urological structural abnormalities (23.2%), malignancy/immunosuppression (23.2%), catheterization (19.6%), chronic liver disease (16.1%), and diabetes mellitus (14.3%). Combined urological factors (catheterization and structural abnormalities) accounted for 42.9% of cases. Geographic distribution showed predominance in Asia, particularly India. The majority of isolates remained susceptible to commonly used antimicrobials; however, sporadic resistance to carbapenems and fluoroquinolones was observed.

Conclusion: *Aeromonas* species should be recognised as emerging uropathogens, particularly in patients with urological interventions or immunocompromising conditions. Early microbiological identification and susceptibility-guided therapy are essential for optimal clinical outcomes.

34. Molecular Characterization of *Vibrio cholerae* O195 strain isolated from Sputum sample of a patient of bronchiectasis in Delhi, India

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Abstract: Non-O1/non-O139 serogroup vibrios have been associated with sporadic cases of gastrointestinal infections as well as extra intestinal infection including septicemia, wound infection, peritonitis, skin infection, cellulitis, urinary tract infection, etc. We report an unusual case of non-O1, non-O139 *V. cholera* isolated from sputum sample in a 55-year-old female diagnosed as acute exacerbation of COAD with type II respiratory failure. Blood culture was sterile and from stool samples, no pathogenic organisms were isolated. Two consecutive isolates of *V. cholerae* were confirmed by serotyping and PCR based detection of virulence genes at the National Referral Institute as *V. cholera* O195.

35. Occurrence of Carbapenem Resistant Gram Negative Bacteria by Using Modified Carbapenem Inactivation Method

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Co-Authors: Dr. Pinaki Patel

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Introduction: Carbapenem-resistant Gram-negative bacteria (CR-GNB) have emerged as a major global public health concern due to limited treatment options and highly associated with morbidity and mortality. Resistance is primarily mediated by the production of carbapenemase enzymes, including metallo- β -lactamases (MBLs) and serine carbapenemases, which hydrolyze carbapenem antibiotics and render them ineffective. Gram-negative pathogens such as Enterobacterias, *Escherichia coli* and *Pseudomonas aeruginosa*, *Klebsiella pneumoniae* common causes of healthcare-associated infections, including bloodstream infections, pneumonia, urinary tract infections, and surgical site infections.

Materials & Methods: This observational study was conducted for one year in the Bacteriology section of Microbiology lab, Teerthanker Mahaveer Hospital. The samples were inoculated on appropriate culture media. Then AST of isolated organisms was performed as per Clinical and Laboratory Standards Institute (CLSI) guidelines 2025.

Results: Out of 150 Gram-negative bacterial isolates, in which 50 isolates (33.3%) were metallo- β -lactamase (MBL) producers and 49 isolates (32.7%) were serine carbapenemase producers. Overall, 99 isolates (66%) showed carbapenemase production, while 51 isolates (34%) were non-carbapenemase producers.

Conclusion: The Modified Carbapenem Inactivation Method (mCIM) proved to be a reliable, simple, and cost-effective phenotypic assay for detecting carbapenem-resistant Gram-negative bacteria. These findings indicate that the mCIM combined with eCIM is useful for detecting and distinguishing different types of carbapenemase in Enterobacteriaceae.

36. Evaluation of direct microbial identification by MALDI-TOF MS and antimicrobial susceptibility testing for early diagnosis of blood stream infections.

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Co-Authors: Nidhi Tejan, Nida Fatima, Nidhi Yaduvanshi, Romya Singh, Irfan Hasan, Sangram Singh Patel and Chinmoy Sahu

Institute: Sanjay Gandhi Post Graduate Institute of Medical Science, Lucknow

Introduction: Bloodstream infections (BSI) related mortality rates are increasing worldwide making it a medical emergency. This study has evaluated a new method for direct detection of pathogens and to perform direct antimicrobial susceptibility testing from the positive flagged blood culture. Early diagnosis and prompt treatment with appropriate antibiotics is the utmost need.

Materials & Methods: A 30-minute protocol for pellet formation was developed using the positive blood culture bottle broth by triton X, SDS and saponin method for direct identification of pathogens. Clinical blood culture samples from patients, positive for Gram-negative bacteria were included in the study (160 for direct identification and 250 for direct antimicrobial susceptibility testing). We compared results with routine method.

Results: The agreement of Triton X, SDS and saponin direct identification method compared to the conventional method was 96.2%, 91.8% and 90% respectively. A total of 960 pathogen and antimicrobial agent combinations were tested, 99.8% antimicrobial sensitivity testing results by direct method showed categorical agreement with the standard routine disc diffusion method.

Conclusion: Overall, the newer method of direct microbial identification and antibiotic sensitivity testing is both time and cost effective.

37. Antimicrobial Susceptibility Pattern of Pathogens Causing Catheter Associated Urinary Tract Infection: A Cross-Sectional Study at Tertiary Care Centre Indore

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Introduction: Catheter-associated urinary tract infection (CAUTI) is one of the most common healthcare-associated infections, accounting for a substantial proportion of hospital-acquired infections. Prolonged use of indwelling urinary catheters significantly increases the risk of infection, emphasizing the need for continuous surveillance of causative pathogens and their antimicrobial susceptibility patterns.

Materials & Methods: A cross-sectional study was conducted from July 2023 to June 2024 among catheterized patients who developed clinical features of urinary tract infection after 48 hours of catheter insertion. Urine samples were processed using standard microbiological techniques, including microscopic examination and culture. Identification of isolates was performed based on colony morphology and biochemical reactions. Antimicrobial susceptibility testing was carried out using the modified Kirby–Bauer disc diffusion method, and results were interpreted according to CLSI 2023 guidelines.

Results: Out of 992 catheterized patients, 78 developed symptoms of UTI, of which 38 showed significant bacterial growth. *Escherichia coli* was the most common isolate (44.7%), followed by *Klebsiella* spp. (18.4%), *Pseudomonas* spp. (13.1%), *Enterococcus* spp. (21.0%), and *Staphylococcus* spp. (5.2%). Gram-negative isolates exhibited high susceptibility to amikacin, carbapenems, nitrofurantoin, and fosfomycin, while *Enterococcus* spp. was highly susceptible to ampicillin, vancomycin, linezolid, and nitrofurantoin. A total of 5601 catheter-days were recorded, yielding a CAUTI rate of 6.4 per 1000 catheter-days.

Conclusion: CAUTI remains a significant patient safety concern. Strict adherence to aseptic catheter insertion, catheter care bundles, and antimicrobial stewardship is crucial to reduce infection rates and improve patient outcomes.

38. Pre-operative Urine Microbiology in elective percutaneous Nephrolithotomy: Implication for antibiotic stewardship

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Institute: HIMS, Dehradun

Introduction: Background: Infective complications remain an important concern in patients undergoing elective percutaneous nephrolithotomy (PCNL). Renal stones may harbour bacteria despite absence of overt infection. Pre-operative urine culture and antimicrobial susceptibility testing (AST) in antibiotic-naïve patients provide useful information for peri-operative antibiotic planning and antimicrobial stewardship. Objectives: To describe the pre-operative urine culture yield, microbiological spectrum, and antimicrobial susceptibility profile of urinary isolates in antibiotic-naïve patients undergoing elective PCNL.

Materials & Methods: This prospective descriptive study was conducted for a year at a tertiary care centre and included patients scheduled for elective PCNL who had not received antimicrobial therapy prior to surgery. Midstream clean-catch urine samples received from patients were subjected to aerobic bacterial culture using standard microbiological techniques. Organism identification and AST were performed using an automated system, and susceptibility results were interpreted according to Clinical and Laboratory Standards Institute guidelines. Data were analysed descriptively focusing on culture positivity, organism groups, and antibiotic class-wise susceptibility.

Results: Fifty patients were included with a mean age of 43.9 years; 33 (66%) were male. Pre-operative urine cultures were positive in 12 patients (24%). All culture-positive isolates were Gram-negative bacilli. Antimicrobial susceptibility demonstrated higher susceptibility to carbapenems (75%) and aminoglycosides (75%), moderate susceptibility to nitrofurans (58%), and lower susceptibility to fluoroquinolones (25%) and cephalosporins (33%).

Conclusion: Nearly one-fourth of antibiotic-naïve patients undergoing elective PCNL had positive pre-operative urine cultures, predominantly due to Gram-negative organisms. Reduced susceptibility to commonly used oral agents and preserved activity of higher-end antibiotics highlight the importance of pre-operative microbiological screening for peri-operative antibiotic selection and stewardship.

39. A Study on Carbapenemase Genes in Frequently Isolated Non-Fermenters from Respiratory Samples of Ventilated Patients

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Co-Authors: Prof. Vimala Venkatesh, Dr. Sheetal Verma, Prof. Prashant Gupta, Prof. Zia Arshad

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Introduction: Non-fermenting Gram-negative bacilli (NFGNB) are important causes of ventilator-associated respiratory infections and are frequently associated with multidrug resistance, particularly carbapenem resistance mediated by carbapenemase enzymes. The emergence of such resistance poses a major therapeutic and infection-control challenge in intensive care units.

Materials & Methods: This hospital-based observational study was conducted in a tertiary care center. Respiratory samples (endotracheal aspirates and bronchoalveolar lavage) from mechanically ventilated patients were processed using standard microbiological methods. Non-fermenters were identified by conventional methods. Antimicrobial susceptibility testing was performed according to CLSI guidelines. Detection of carbapenemase genes was carried out using polymerase chain reaction (PCR) techniques.

Results: A high level of carbapenem resistance was observed among non-fermenting isolates. A significant proportion of carbapenem-resistant isolates harboured carbapenemase correlating with limited susceptibility to commonly used antimicrobials.

Conclusion: The high prevalence of carbapenemase-producing non-fermenters highlights the need for routine molecular surveillance, strict infection control practices, and rational antibiotic use in critical care settings.

40. Antimicrobial Susceptibility Profile of Bacterial Isolates from Cases of Respiratory Tract Infection at Tertiary Care Center Firozabad, U.P.

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Co-Authors: Dr Hariom Sharan, Dr Lekha Tuli, Dr Nisha Chaudhary

Institute: ASMC Firozabad

Introduction: Respiratory tract infection (RTI) is an infectious disease that affects the upper or lower respiratory tract. RTIs are a major cause of death globally and common reason for irrational antibiotics use. They can be caused by a variety of viruses and bacteria. Types of RTIs affect the nose, sinuses, pharynx and larynx.

AIM AND OBJECTIVES: To isolate, identify and do culture and antibiotic sensitivity of bacterial isolates from sputum samples of patients presenting with respiratory tract infections.

Materials & Methods: This retrospective study was conducted in the Microbiology department of Autonomous State Medical College, Firozabad, U.P. Wherein 110 sputum samples were collected from Outpatients Department of all age groups and genders from January 2025 to December 2025. The samples were cultured on Blood agar and MacConkey agar and the isolates were identified biochemically. These were subjected to antibiotic susceptibility testing by Kirby-Bauer disk diffusion method as per the latest CLSI guidelines.

Results: Out of 220 sputum samples, 76(34.54%) showed bacterial growth out of which 32(42.1%) were *Pseudomonas aeruginosa*, 16(21.05%) were *Staphylococcus aureus*, 12(15.78%) were *Enterococcus* spp. 08(10.52%) were *Acinetobacter* spp. 04(5.26%) were *Escherichia coli* and 04(5.26%) were *Candida albicans*. The most common pathogen isolated was *Pseudomonas aeruginosa* (42.1%) which was found sensitive to Piperacillin Tazobactam followed by Ceftazidime, Tobramycin and Ofloxacin. *Staphylococcus aureus* showed maximum sensitivity to Vancomycin and Linezolid followed by Clindamycin and Cotrimoxazole.

LEARNING MESSAGE: The antibiogram of bacterial isolates from cases of respiratory tract infection in an area aids the physicians to choose the most appropriate and effective treatment regimen and helps in preventing the spread of Drug Resistance and treatment failure in the community.

41. Prevalence, Microbiological Profile, and Antibiotic Susceptibility of Anaerobic Bacteria in Pus Samples: A Retrospective Study from a Tertiary Care Hospital

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Co-Authors: Dr. Diksha Shukla, Dr. Akshay Kumar Arya, Dr. Sangram Singh Patel ,Dr. Nidhi Tejan, Dr. Chinmoy Sahu, Dr. Rungmei S. K. Marak

Institute: Sanjay Gandhi Postgraduate Institute of Medical Sciences, Lucknow

Introduction: Anaerobic bacterial infections are frequently under recognized in clinical practice despite their substantial contribution to deep-seated infections, particularly in the context of abscesses, necrotic tissue, and post-surgical applications. The ability of these organisms to thrive in low-oxygen environments presents unique diagnostic challenges, especially in Health care settings lacking specialized laboratory infrastructure for anaerobic culture.

Materials & Methods: This retrospective study analyzed 5400 pus specimens processed for anaerobic bacterial growth. Specimens were cultured using anaerobic media and incubated in oxygen-free environments. Bacterial identification was done by MALDI-TOF MS. Antibiotic susceptibility was assessed using EUCAST guidelines.

Results: Out of 5400 pus specimens, 30 (0.55%) were positive for anaerobic bacterial growth. The most commonly isolated species included *Bacteroides fragilis* (26.66%) and *Bacteroides* spp. (20%). Along with other anaerobes, single cases of *Peptostreptococcus anaerobius*, *Peptostreptococcus* species, *Leuconostoc citreum*, *Prevotella bivia*, *Propionibacterium acnes* & *Lactobacillus* species were identified. Polymicrobial infections accounted for 53% of the total positive cases.

Conclusion: This study underscores the necessity for heightened diagnostic vigilance and resource allocation for anaerobic culture in tertiary care settings. Antimicrobial susceptibility testing revealed considerable resistance to metronidazole in some isolates, emphasizing the need for routine susceptibility screening and evidence-based therapeutic strategies.

42. Missed Diagnoses: The Limitations of Culture and Microscopy in Bacterial Detection from Cerebrospinal Fluid

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Introduction: Meningitis caused by bacteria is a clinical emergency that leads to high mortality and morbidity. To date, hundreds of pathogenic microorganisms have been proven to cause meningitis. However, in most cases (40-60%), the etiology remains unknown, which could be due to a wide range of factors such as suboptimal time of sample collection, inability to identify the causative agent due to large number of causative microorganisms, or the detected pathogen being unknown. This study was planned to analyse the bacterial etiology of meningitis in patients with strong clinical suspicion of bacterial meningitis.

Materials & Methods: This was a retrospective study done in the department of Microbiology, at a single tertiary care centre of North India. We retrospectively reviewed the CSF reports of all adult clinically suspected patients of meningitis sent for culture from January 2025 to December 2025. The study population was divided into two groups as Culture positive and Culture negative bacterial meningitis. All the laboratory reports of study participants, including ADA, CBC, TLC, DLC, Viral markers were retrospectively studied.

Results: A total of 884 CS samples were received from January 2025 to December 2025. Out of which, 169 CSF samples showed bacterial growth (19%), while in remaining 81%, CSF were sterile. The various bacterial species isolated included, *Acinetobacter baumannii*, *Staphylococcus aureus*, *Enterococcus spp.*, *Klebsiella pneumoniae*. Out of all the patients whose CSF cultures were sterile, nearly 15% showed CSF picture suggestive of bacterial meningitis, indicating that cultures can miss on some 10-20% cases of bacterial meningitis.

Conclusion: CSF culture and microscopy alone are not sufficient in diagnosing etiology in bacterial meningitis. Molecular techniques like, PCR and sequencing are needed to diagnose such missed cases.

43. Performance of Direct MALDI-TOF MS Using Sepsityper in Positive Blood Cultures from Haemato-Oncology Patients.

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Introduction: Rapid and precise identification of pathogens is critical for improving outcomes in immunocompromised haemato-oncology patients with bloodstream infections. Early identification of the causative agent plays a crucial role in guiding targeted antibiotic therapy; timely interventions significantly improve patient outcomes and decreasing duration of hospitalizations, acting as a cost-effective approach in sepsis management.

Objective: To evaluate the impact of direct MALDI-TOF MS identification from positive blood cultures in haemato-oncology patients

Materials & Methods: We conducted a 11-month retrospective study of 735 positive blood cultures from hemato-oncology patients. Positive blood culture broth was used for rapid organism identification using a Sepsityper kit over MALDI-TOF. Organism identification was confirmed subsequently from colonies grown on solid media.

Results: Out of 735 samples, Gram-negative bacilli were the predominant isolated (65%), followed by Gram-positive cocci (20.6%). The total pathogens identified were predominantly Enterobacterales, followed by Non-fermenters, Gram-positive cocci (*Staphylococcus aureus*, *Enterococcus* species), atypical organisms and Yeast. The rapid identification workflow identified 67 contaminants, including *Staphylococcus* other than *Staphylococcus aureus* (57.9%), Gram-positive bacilli (25%) and *Micrococcus* species (17.1%) assisting physicians to differentiate them from true pathogens.

Conclusion: Direct processing of positive blood cultures using MALDI-TOF significantly reduces the time for organism identification from an average of 24 hours (conventional method) to 30 minutes - 1 hour to administer effective and targeted antimicrobials in haemato-oncology patients. This clinical practice not only accelerates appropriate treatment but also helps to minimize unnecessary hospitalization and antibiotic treatment. This approach of diagnostic stewardship supports fulfillment of goals of antimicrobial stewardship.

44. Microbiological Spectrum And Antimicrobial Susceptibility Patterns In Clinically Suspected osteomyelitis: A Prospective Observational Study

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Institute: KGMU, Lucknow, India.

Introduction: Osteomyelitis is a serious bone infection associated with significant morbidity and therapeutic challenges due to varied microbial etiology and evolving antimicrobial resistance. Early identification of causative pathogens and their susceptibility profiles is essential for effective clinical management.

Aims and Objectives: To determine the microbiological profile of clinically suspected osteomyelitis cases and analyze the AST pattern of isolated pathogens.

Materials & Methods: A prospective observational study was conducted over three years in the Departments of Microbiology and Orthopaedics at King George's Medical University, Lucknow. A total of 100 patients aged above 18 years with clinically suspected bone and joint infections were included. Blood, pus, and bone biopsy samples were collected under aseptic conditions. Patients with tumors, cysts, non-union fractures, and old trauma were excluded. Samples were processed using standard microbiological techniques, and antimicrobial susceptibility testing was performed as per CLSI 2022 guidelines.

Results: Microbial growth was obtained in 78% of cases, while 24.8% were culture-negative. *Staphylococcus aureus* was the most common isolate (28.6%), followed by *Pseudomonas aeruginosa* (\approx 11–12%) and *Escherichia coli* (\approx 8–9%). Other Gram-negative organisms included *Klebsiella pneumoniae*, *Proteus mirabilis*, and *Acinetobacter* spp. Gram-positive bacteria constituted 53.8% of culture-positive isolates, while Gram-negative organisms accounted for 46.2%. No fungal isolates were detected. Gram-positive isolates were most sensitive to vancomycin, linezolid, and teicoplanin, with high resistance to penicillin and fluoroquinolones. Gram-negative isolates showed better sensitivity to piperacillin–tazobactam, amikacin, and carbapenems, while resistance to cephalosporins and fluoroquinolones was common.

Conclusion: *Staphylococcus aureus* remains the predominant pathogen in osteomyelitis, with a significant contribution from Gram-negative bacteria. Continuous surveillance of microbial patterns and resistance profiles is vital for optimizing empirical therapy and improving patient outcomes.

Keywords: Osteomyelitis, Microbiological profile, *Staphylococcus aureus*, Antimicrobial susceptibility, Bone infection.

45. Molecular characterization of Biofilm Formation and Antibiotic Susceptibility in *Stenotrophomonas Maltophilia* in Hospitalized Patients.

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Co-Authors: Dr. Sheetal Verma, Prof. Vimala Venkatesh, Prof. R.K. Kalyan, Dr. Saurabh Kashyap

Institute: KGMU, LUCKNOW

Introduction: *Stenotrophomonas maltophilia* is an emerging opportunistic, multidrug-resistant Gram-negative bacillus increasingly associated with hospital-required infections. Its ability to form biofilms on medical devices enhances persistence, antibiotic resistance and disease severity, posing significant therapeutic challenges in hospitalized patients.

Materials & Methods: A hospital-based observational study was conducted in the Department of Microbiology, KGMU, Lucknow, over a period of one year. Clinical samples including blood, urine, pus, respiratory specimens, cerebrospinal fluid and other body fluids were collected from hospitalized patients. A total of 180 isolates from hospitalized patients were included. Identification was confirmed by MALDI-TOF MS. Antibiotic susceptibility testing was performed using standard methods.

Results: A total of 180 non-duplicate clinical isolates of *Stenotrophomonas maltophilia* were analyzed. The majority of isolates were recovered from respiratory samples (37%), followed by blood (32%), with remaining isolates obtained from Body fluids, Pus, Urine, CSF, and BAL specimens. Most isolates were obtained from ICU patients, highlighting the organism's strong association with critical care settings. Antimicrobial susceptibility testing revealed high susceptibility to minocycline and levofloxacin. Minocycline showed 88.33% sensitivity, with 9.44% resistance and 2.22% intermediate susceptibility. Levofloxacin demonstrated 88.33% sensitivity, 10.55% resistance, and 1.11% intermediate susceptibility. In contrast, trimethoprim-sulfamethoxazole exhibited a lower sensitivity rate (76.66%), with 23.33% resistance.

Conclusion: *Stenotrophomonas maltophilia* predominantly causes ICU-associated respiratory and bloodstream infections. Minocycline and levofloxacin remain the most effective agents, highlighting the need for ongoing antimicrobial resistance surveillance

Limitation- Biofilm formation and Molecular test was not performed (Result awaited)

46. Septic Shock caused by XDR *Klebsiella pneumoniae* in ICU: The Challenge of Last-Resort Therapy

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Co-Authors: Dr. Neeti Mishra, Dr. Aditya Mishra

Institute: T.S. Misra Medical College & Hospital, Lucknow

Introduction: The rise of Extensively Drug-Resistant (XDR) *Klebsiella pneumoniae* represents a formidable challenge in critical care, particularly when these opportunistic pathogens harbor carbapenemase genes that render standard antibiotics ineffective. In ICU, central venous catheters frequently act as reservoirs for these biofilm-forming organisms, causing life-threatening infections, like septic shock, and Multi-Organ Dysfunction Syndrome (MODS). As these strains most of the time remain sensitive only to "last-resort" polymyxins like Colistin, the treatment is severely restricted. This is especially precarious for patients with comorbidities such as Diabetes Mellitus, who are more susceptible to such aggressive isolates. This report details specifically a strain sensitive only to Colistin, guided a complex clinical course.

Materials & Methods: A 62-year-old female with history of Type 2 Diabetes presented with fever for 4 days, abdominal pain, and vomiting. She arrived at hospital with decompensated septic shock, non-recordable vitals and altered sensorium. Following ICU admission and central line insertion, CVP tip was sent for culture & sensitivity. Identification was performed by gram staining, motility, standard biochemical tests, and Antimicrobial Susceptibility Testing (AST) was done, which showed the isolate sensitive to Colistin (*Klebsiella pneumoniae*).

Results: The CVP tip culture showed significant growth of mucoid colonies on media. On gram staining & biochemical tests the isolate was *Klebsiella pneumoniae*. The AST profile revealed resistance to all tested cephalosporins, carbapenems, aminoglycosides, and fluoroquinolones, sensitive only to Colistin. The patient's condition was further complicated by Acute Kidney Injury (AKI) requiring multiple sessions of dialysis, Purpura fulminans, and septic encephalopathy. Due to poor prognosis the patient expired after few days.

Conclusion: This case showed the grim prognosis associated with XDR *K. pneumoniae* in healthcare settings. The isolation of a colistin-only sensitive strain from CVP line highlights the catastrophic potential of catheter-related infections. It emphasizes the need for rapid diagnosis and the implementation of aggressive antibiotic stewardship and infection control policies to manage cases where therapeutic options are nearly exhausted.

47. Burden and Microbiological Profile of Catheter-Related Bloodstream Infections in Critically Ill ICU Patients Using Standardized Diagnostic Techniques

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Co-Authors: Dr. Vimala Venkatesh, Dr. Sheetal Verma, Dr. D Himanshu

Institute: King George Medical College

Introduction: Catheter-related bloodstream infection (CRBSI) is a major cause of preventable morbidity and mortality in intensive care units. Accurate diagnosis requires integration of clinical findings with robust microbiological techniques. This study aimed to assess the burden, clinical impact, and microbiological spectrum of CRBSI in critically ill patients using standardized diagnostic methods.

Materials & Methods: This prospective observational study included 135 ICU patients with indwelling central venous catheters at a tertiary care hospital. Demographic data, comorbidities, ICU severity scores, catheter dwell duration, microbiological findings, and outcomes were recorded. Paired blood cultures were collected simultaneously from peripheral veins and catheter lumens. Removed catheter tips underwent semi quantitative culture (Maki's method) and BHI broth enrichment. CRBSI was classified as definitive, probable, or possible based on CDC/IDSA criteria. Descriptive statistical analysis was performed.

Results: Among 135 ICU patients, 79 (58.5%) had definitive/probable CRBSI. Bacterial isolates predominated (83.5%), mainly Gram-negative bacilli, while 16.5% were fungal (*Candida* spp.). while 56 (41.5%) had no evidence of CRBSI. Definitive CRBSI was associated with prolonged catheter dwell time, higher severity scores, adverse outcomes, and multidrug resistance

Conclusion: CRBSI imposes a substantial burden in critically ill patients. The use of paired blood cultures combined with semi quantitative and enrichment techniques improves diagnostic accuracy. Strengthening catheter care bundles and microbiological surveillance is essential to reduce CRBSI-associated morbidity and mortality.

48. Deciphering the Molecular Landscape of *mexA* and *mexC* Genes in *Burkholderia cepacia* complex from clinical samples.

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Introduction: *Burkholderia cepacia* complex (BCC) comprises genetically related opportunistic pathogens with large, versatile genomes and intrinsic resistance to multiple antimicrobials. Among key resistance mechanisms, *mexA*- and *mexC*- mediated efflux pumps play a pivotal role in multidrug resistance. Understanding their distribution in clinical isolates is essential for effective therapy and infection control.

Objectives: To study *mexA/mexC* efflux genes and their association with antimicrobial resistance and clinical outcomes in *Burkholderia cepacia* complex.

Materials & Methods: This ongoing hospital-based prospective observational study was conducted in the department of Microbiology, King George's Medical University, Lucknow, over one year. A total of 170 clinical samples, *Burkholderia cepacia* complex isolates identified by MALDI-TOF MS were subjected to antimicrobial susceptibility testing and PCR detection of *mexA* and *mexC* genes, followed by statistical analysis.

Results: Interim analysis included 170 isolates, *Burkholderia cenocepacia* was the predominant species (58.8%), followed by *B.cepacia* (40.0%), while *B.multivorans* and *B. gladioli* were rarely isolated (0.6% each). High resistance rates were observed to ciprofloxacin (56.5%) and levofloxacin (52.9%). Moderate resistance was noted to minocycline (48.2%), cefoperazone (48.2%), and cotrimoxazole (31.8%). In contrast, resistance to meropenem (4.1%) and ceftazidime (5.9%) remained low. At interim assessment, 137 (80.6%) patients were discharged and 33(19.4%) expired during hospital stay. Molecular analysis of *mexA* and *mexC* genes is ongoing.

Conclusion: The study demonstrates a high burden of antimicrobial resistance among *Burkholderia* species, particularly to fluoroquinolones, with frequent isolation from critically ill patients. The retained susceptibility to meropenem and ceftazidime highlights their potential therapeutic role.

49. Characterization of coagulase negative staphylococcus isolated from neonatal blood cultures at a tertiary care center: A descriptive study

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Introduction: Neonatal sepsis is a major cause of morbidity and mortality, especially in preterm and low birth weight infants requiring intensive care. Coagulase negative staphylococcus is an important cause of neonatal bloodstream infections, posing diagnostic challenges in distinguishing true infection from contamination.

Objectives: To characterize coagulase negative staphylococcus isolated from neonatal blood cultures for species distribution, antimicrobial susceptibility patterns, and presence of virulence genes.

Materials & Methods: Neonates admitted to the neonatal intensive care unit with blood cultures yielding coagulase negative staphylococcus are included, and 185 isolates obtained so far. Species identification by MALDI-TOF MS, antimicrobial susceptibility testing are performed by standardized laboratory techniques. Detection of selected virulence genes is carried out using molecular methods.

Results: Interim analysis included 185 neonates, with 104 males and 81 females, with a mean age of 7.10 days with a standard deviation 6.63 days and mean birth weight of 1.92 kilogram with a standard deviation of 0.65 kilograms. Most were preterm. *Staphylococcus haemolyticus* was the most frequently isolated organism, followed by *Staphylococcus epidermidis* and *Staphylococcus hominis*. Antimicrobial susceptibility testing showed high resistance to penicillin at 84.9 % and erythromycin at 91.4 %. Cefoxitin resistance in 75.7 % of isolates. Gentamicin demonstrated 72.4 % susceptibility, while vancomycin showed 99.5 % susceptibility. At interim assessment, 164 (88.65%) neonates were discharged and 21(11.35%) had expired. Molecular analysis of virulence genes is ongoing.

Conclusion: This ongoing study is expected to provide clinically relevant data to differentiate true infection from contamination, guide rational antimicrobial therapy, and strengthen infection control practices in neonatal intensive care units.

50. Isolation and Characterisation of Carbapenem-Resistant *Escherichia coli* from Clinical Samples

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Introduction: The emergence of carbapenem-resistant *Escherichia coli* (CREC) represents a serious challenge to global healthcare due to limited treatment options and increased rates of morbidity and mortality. Carbapenems are considered last-resort antibiotics for severe infections caused by multidrug-resistant Gram-negative bacteria. The increasing occurrence of carbapenem-resistant *E. coli* from clinical settings highlights the need for continuous surveillance and detailed characterisation to understand resistance patterns and guide effective infection control strategies. Hon'ble Prime Minister of India, Mr. Narendra Modi also highlighted antimicrobial resistance (AMR) in his "Man ki Baat" in the end of the year 2025.

Materials & Methods: This cross-sectional study was conducted over a period of eight months and included a total of 600 clinical samples, including Blood, Urine, Pus, collected from hospitalised patients at Subharti Medical College, Meerut. Isolation and Identification of *Escherichia coli* were carried out using standard microbiological techniques and identification was made based on culture characteristics, Gram's staining, and biochemical tests. Antimicrobial susceptibility was evaluated using the Kirby-Bauer disk diffusion method in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines.

Results: Of 600 clinical samples from blood (250), urine (200) and pus (150), Gram's negative *Escherichia coli* was isolated from 300 samples. Of these 300 (50%) samples including Blood (100) 33.3%, Urine (150) 50%, Pus (50)16.6% exhibited significant growth of Gram-negative bacteria. *E. coli* isolates were further evaluated for carbapenem-resistance and the results revealed that 80 isolates from Blood, 100 from Urine and 20 from Pus were carbapenem-resistant. It suggests that *E. coli* isolated from blood showed highest (80%) carbapenem-resistance followed by urine (66.6%) while *E. coli* isolates from pus showed lowest (20%) carbapenem-resistance.

Conclusion: The study highlights the increasing occurrence of carbapenem-resistant *Escherichia coli* in clinical samples and underscored the importance of routine screening for carbapenem resistance in healthcare settings. Early detection, regular surveillance, and strict implementation of antimicrobial stewardship and infection control measures are essential to prevent the further spread of carbapenem-resistant *E. coli*.

51. Pathogens and the Bladder: Decoding the Infective Footprints in Carcinoma

Author: Ankana Ganguly

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Introduction: Chronic urinary infection and repeated catheterisation promote urothelial dysplasia and malignant transformation. Recurrent inflammation, biofilm formation, and bacterial toxins alter the bladder microenvironment, generating mutagenic oxidative stress. This study examined the association of infective and clinical correlates of UBCA with urinary pathogens, multidrug resistance (MDR), and tumour invasiveness.

Materials & Methods: A 12-month retrospective study was done on patients with histologically confirmed UBCA (n=114) undergoing TURBT. Age- and sex-matched UTI non-CA patients served as controls. Pre-TURBT urine cultures were processed using CLSI protocols. Recurrent catheterisation (≥ 3 /year), comorbidities, & lifestyle factors—were correlated with tumour grade. Statistical analysis done using GraphPad prism (v.10).

Results: Mean age was 66 ± 15 years; 68% were male. Gram-negative uropathogens were isolated in 67% cases—*Klebsiella pneumoniae* (29.4%), *E. coli* (20.6%), & *Proteus mirabilis* (17.6%). *Proteus* & *Pseudomonas* showed strong association with recurrent catheterisation ($p < 0.01$). Gram-negative infection correlated with muscle-invasive condition (81%, $p < 0.001$, Cramer's $V > 0.6$), increased odds of invasiveness (OR 3.1, $p = 0.002$) and catheterisation (OR 2.8, $p = 0.01$), tumours associated were larger (5.4 cm vs 2.8 cm; $p < 0.0001$). *Klebsiella* & *Pseudomonas* were exclusive to high-grade UBCA. MDR pathogens were detected in 58% isolates (OR 1.99, RR 1.73). Meropenem (28.4%), fosfomycin (25%) & nitrofurantoin (25.4%) retained highest sensitivity, while cefuroxime, amikacin & amoxiclav showed least.

Conclusion: Chronic infection & MDR gram-negative pathogens show a strong association with invasive bladder carcinoma. Repeated catheterisation results in infection-inflammation cycles, promoting squamous metaplasia & high-grade transformation. Routine pre-operative urine culture, targeted therapy & infection control are essential to uro-oncologic management. Microbial profiling can identify high-risk patients.

52. Colistin Heteroresistance Surveillance in ICU Patients with Multi-Drug Resistant Infections

Author: Pratima Kumari

Co-Authors: Saumya Singh, Vidushi Sharma

Institute: Department of Microbiology, United Institute of Medical Sciences, Prayagraj

Introduction: Colistin remains a critical last-resort antibiotic for multidrug-resistant (MDR) Gram-negative infections in intensive care units (ICUs). However, colistin heteroresistance—resistant subpopulations within apparently susceptible isolates—poses significant treatment challenges and often escapes detection by standard susceptibility testing. This study aimed to determine the prevalence of colistin heteroresistance among MDR *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and Enterobacterales isolates from ICU patients using population analysis profiling (PAP).

Materials & Methods: MDRO isolates were collected from ICU patients between May 2025 and December 2025. Carbapenemase production was confirmed using modified carbapenem inactivation method (mCIM), EDTA-carbapenem inactivation method (eCIM), carbapenem disc test (CDT), and Modified Hodge test per CLSI 2024 guidelines. Colistin susceptibility was determined by broth microdilution (BMD) according to CLSI 2024 and NCDC guidelines. All colistin-intermediate isolates underwent PAP to detect heteroresistance, defined as resistant subpopulations growing above the susceptibility breakpoint.

Results: Of 122 MDRO isolates, 18 (14.75%) showed colistin resistance by BMD, while 104 (85.25%) were intermediate. PAP analysis revealed 6/104 (5.77%) exhibited heteroresistance, with resistant subpopulations at frequencies of 8.5×10^{-7} to 3.2×10^{-6} . Heteroresistance was observed in *K. pneumoniae* (2/25, 8%), *A. baumannii* (2/34, 5.88%), *P. aeruginosa* (1/26, 3.85%), and *E. coli* (1/19, 5.26%). All heteroresistant isolates were from ICU patients, with 66.7% having prior colistin exposure and 83.3% being carbapenem-resistant.

Conclusion: Colistin heteroresistance exists in phenotypically intermediate MDR isolates. PAP-based surveillance in ICUs may improve detection and inform treatment decisions in critically ill patients.

Keywords: Colistin, heteroresistance, surveillance, ICU, multidrug resistance, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, Enterobacterales

53. Genetic characterization and transmission pattern of tetracycline resistance gene in tigecycline and carbapenem resistant *Klebsiella pneumoniae* isolates

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Institute: Sanjay Gandhi Post Graduate Institute of Medical Sciences, Lucknow

Abstract:

Background: The increasing prevalence of tigecycline and carbapenem-resistant *K. pneumoniae* (CRKP) poses a serious challenge, especially in resource-limited settings

Objective: The study aimed to determine the phenotypic and genotypic prevalence of carbapenem and tetracycline resistance *K. pneumoniae* isolates along with the transferability pattern of carbapenem and tetracycline resistance gene in these isolates.

Methodology: Clinical isolates from pus and respiratory samples were identified using biochemical tests and MALDI-TOF MS. AST was performed by the Kirby-Bauer disc diffusion method, and MICs were determined by BMD method. PCR was performed to detect carbapenemase (*bla*_{NDM}, *bla*_{OXA-48}, *bla*_{KPC}) and tetracycline resistance genes [*tet*(A), *tet*(B), *tet*(K), *tet*(M), *tet*(S)], followed by Sanger sequencing for validation. Conjugation assays assessed gene transferability.

Results: Out of 152 carbapenem resistance *K. pneumoniae* isolates, a total of 20.39% (n=31/152) were tigecycline resistant by BMD assay. Screening of antibiotic resistance genes revealed presence of *tet*(A) in 12.90% (n=4/31), *tet*(B) in 3.20% (n=1/31) isolates, while *tet*(K), *tet*(M), *tet*(S) were absent in all isolates. Conjugation assay revealed that these genes are present on plasmid as well as chromosome but not transferring from one isolate to other isolates. Complete genome assembly, plasmid assembly and gene annotation showed the exact position and reason of gene transfer.

Conclusion: Our result indicated that due to presence of resistance gene on plasmid is the basic cause of transmission. So, there are no way to control it without prohibiting wrong prescription antibiotics and performing infection control measures.

Serology Abstracts

54. Dengue Surveillance at ASMC Lalitpur: A Microbiological Study from the Bundelkhand Region.

Author: Dr. Riya Singh

Co-Authors: Madhurendra Singh Rajput, Pooja Gupta, Keshaw Nishad, Deshni Singh

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Introduction: Dengue remains a significant mosquito-borne disease in India. Rapid urbanization and climate change contribute to recurrent outbreaks. NS1 antigen-based laboratory surveillance is crucial for early detection and effective outbreak control.

Materials & Methods: Patients presenting with clinically suspected dengue infection were enrolled in a hospital-based surveillance study. A total of 395 blood samples were collected from these suspected cases. Venous blood was drawn under strict aseptic conditions, following which serum was separated for laboratory analysis. The separated serum samples were subjected to laboratory testing for dengue NS1 antigen, using both enzyme-linked immunosorbent assay (ELISA) and rapid diagnostic test (RDT) methods.

Results: Among 394 clinically suspected dengue cases, 49 (12.4%) were laboratory confirmed by NS1 antigen detection using both rapid diagnostic test and ELISA. The affected age group ranged from 5 to 65 years, with maximum positivity observed among individuals aged 20–45 years. Geographical analysis revealed a wide distribution of dengue cases across Lalitpur district, including Lalitpur city, Jakhaura, Mandawara, Bar, Masora, Bastrawan, Amerkheda, Chanderi, Radhapur, and Basatguva. The predominant clinical presentations were acute febrile illness, myalgia, arthralgia, retro-orbital pain, nausea, vomiting, and cutaneous rash.

Conclusion: Dengue remains a significant public health concern in the Lalitpur region, predominantly affecting young adults, and underscores the need for continuous laboratory-based surveillance at ASMC Lalitpur to enable early diagnosis, prompt management, and effective region-specific vector control.

55. Leptospirosis: An emerging neglected tropical disease-Serological trends from a Tertiary care centre

Author: Dr. Soham Bhattasali

Co-Authors: Prof. R. K. Kalyan, Prof. Vimala Venkatesh, Prof. Prashant Gupta, Dr. K.K. Gupta, Dr. Sanjeev Kumar Verma

Institute: King George's Medical University

Introduction: Leptospirosis is an emerging zoonotic infection and a neglected tropical disease with diverse clinical manifestations, often resulting in under diagnosis. Serological tests such as Anti Leptospira IgM ELISA play a crucial role in early laboratory confirmation

Materials & Methods: A retrospective observational study was conducted in the Department of Microbiology at King George Medical University, Lucknow from 1st January, 2025 to 31st December, 2025. Serum samples received from clinically suspected cases of leptospirosis over one year were tested for Anti Leptospira IgM antibodies using ELISA as per the manufacturer's instructions. Results were interpreted as positive, negative, or equivocal, and month-wise distribution was analyzed

Results: Out of 4,663 serum samples tested, 404 samples (8.7%) were positive for Anti Leptospira IgM antibodies. A distinct seasonal pattern was observed, with increased positivity during the monsoon and post-monsoon months (July–October). The highest number of positive cases was recorded in October, followed by July. Lower positivity rates were observed during the winter months

Conclusion: Leptospirosis remains an important emerging neglected tropical disease with a clear seasonal predominance. IgM ELISA is a useful diagnostic tool for early detection. Knowledge of seasonal trends can assist clinicians in early suspicion, timely diagnosis, and appropriate management, thereby reducing disease burden.

56. Comparative Evaluation of Scrub Typhus by Using Weil-Felix and Rapid Card Test with ELISA as confirmatory test

Author: Dr. Rashmi Singh

Co-Authors: Dr. Shadma Yaqoob , Dr. Sarah Hassan, Dr. Sana Siddique, Dr. Vaibhav Shukla, Dr. Vineeta khare, Dr. Priyanka Shukla

Institute: Era University Lucknow, Uttar Pradesh

Introduction: Scrub typhus, caused by *Orientia tsutsugamushi*, is an underdiagnosed acute febrile illness prevalent in many parts of India. Early diagnosis is crucial to prevent severe complications and reduce mortality. Conventional Weil-Felix test has long been used due to its affordability, but its sensitivity and specificity are relatively low. Rapid card tests have recently emerged as promising diagnostic alternatives with quicker turnaround times and improved accuracy.

Materials & Methods: This study involved clinically suspected scrub typhus patients who were subjected to both the Weil-Felix test (OX-K agglutination) and rapid immune chromatographic card test. Sensitivity, specificity, positive predictive value (PPV), and negative predictive value (NPV) of the both methods were calculated using clinical diagnosis and serological confirmation by ELISA test.

Results: Total number of samples was 100 in which, 3 samples positive by RDT, 6 samples positive by Weil-Felix, 6 samples positive by ELISA.

Conclusion: In diagnosis of Scrub typhus RDT showed high sensitivity and low specificity and Weil-Felix showed good specificity and low sensitivity as compared to IgM ELISA, it demonstrates high sensitivity, specificity, and overall diagnostic accuracy, making it a reliable and effective alternative for the routine laboratory diagnosis of scrub typhus. Its ease of performance, reproducibility, and ability to detect infection early further support its use as a standard diagnostic tool. Incorporation of rapid testing in routine clinical settings, especially in endemic areas, can significantly enhance early diagnosis and improve patient management outcomes. Results of Weil-Felix test need to be interpreted with caution.

Conclusion: In diagnosis of Scrub typhus RDT showed high sensitivity and low specificity and Weil-Felix showed good specificity and low sensitivity as compared to IgM ELISA, it demonstrates high sensitivity, specificity, and overall diagnostic accuracy, making it a reliable and effective alternative for the routine laboratory diagnosis of scrub typhus. Its ease of performance, reproducibility, and ability to detect infection early further support its use as a standard diagnostic tool. Incorporation of rapid testing in routine clinical settings, especially in endemic areas, can significantly enhance early diagnosis and improve patient management outcomes. Results of Weil-Felix test need to be interpreted with caution.

57. A case of vitiligo co existing with lichen planus affecting nails.

Author: Dr. Saniya Afzal

Co-Authors: Dr. Savita Chaudhary, Dr. Ankita Kumari, Dr. Kajal Bansal

Institute: Era's Lucknow Medical College and Hospital

Introduction: Vitiligo is an acquired depigmentation skin disease caused by the immune-mediated death of melanocytes. Lichen Planus is a chronic immune-mediated disease affecting skin, appendages and mucous membranes. Nail lichen planus is an inflammatory disorder of the nails with potential for cosmetic disfigurement and functional impairment.

Case: The patient was a 37-year old male came to our Dermatology outpatient department with complaints of white lesions over dorsal aspect of both arms and feet from 4-years. Lesions initially occurred over right arm and gradually progressed to involve the left arm, left leg and right leg within a time period of 1 year. On examination multiple well defined depigmented macule were present over dorsal aspect of both hand and feet size measuring from 0.5x0.5 being the smallest to 2x10 being the largest. Nail examination showed longitudinal ridging, onycholysis and pup tenting over nails of both great toes and all finger of both hands. Dermoscopy of skin lesion showed ill-defined margins, white structureless area with white glow, perifollicular depigmentation with satellite lesions. Dermoscopy of nails showed longitudinal ridging, mottled redness on lunula. Punch biopsy of 3.5 mm from hand macule on histopathology showed decrease in number of melanocytes with lympho-histiocytic infiltrates and spongiosis suggestive of vitiligo. Histopathology of the nail showed hypergranulosis of nail matrix and nail bed epithelium, saw-tooth acanthosis, and lichenoid band.

Conclusion: After thorough research, we could not find any literature on vitiligo co existing with lichen planus affecting nails. Hence, we report this case for unusual presentation.

58. Co-Infection of Hepatitis B And Hepatitis C Virus Among HIV Infected Patients. A Retrospective Cross-Sectional Study in a Tertiary Care Hospital, Kanpur

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Co-Authors: R. Sujatha

Institute: Rama Medical College Hospital and Research Centre, Kanpur

Introduction: Human Immunodeficiency Virus (HIV) shares common routes of transmission with Hepatitis B virus (HBV) and Hepatitis C virus (HCV). Co-infection with HBV or HCV among HIV-infected individuals is associated with increased morbidity, reduced survival, faster progression to severe liver disease, and complications related to antiretroviral therapy. The prevalence of HBV and HCV co-infection among HIV patients varies widely across different regions of India. Therefore, understanding the regional burden of these co-infections is essential for early diagnosis, appropriate management, and improvement in the quality of life of people living with HIV/AIDS.

Materials & Methods: This retrospective cross-sectional study was conducted at Rama Medical College Hospital and Research Centre, Kanpur, over a nine-month period from January 2025 to September 2025. A total of 800 serum samples from patients admitted to critical care units were analyzed. Laboratory investigations were performed in the Department of Microbiology. HIV-positive samples were further screened for Hepatitis B surface antigen (HBsAg) and anti-HCV antibodies using standard rapid test and Tridot kits. Demographic details and associated risk factors were assessed.

Results: Out of 800 samples tested, 27 were reactive for HIV infection. HBV infection was detected in 0.625% (5/800) patients, while HCV infection was detected in 0.125% (1/800) patients. Co-infection was observed in both genders but was more common among males. Intravenous drug abuse was identified as the most significant risk factor, followed by blood transfusion, needle stick injury, and diabetes mellitus.

Conclusion: HIV-infected patients are at increased risk of HBV and HCV co-infections, particularly those with high-risk behaviors such as intravenous drug use. Routine screening for Hepatitis B and Hepatitis C should be an integral part of the follow-up of all HIV-positive patients to reduce morbidity and delay disease progression.

59. Scrub Typhus with Cardiac Manifestations: A Retrospective Clinical and Microbiological Correlation Study

Author: Ankita Rai

Co-Authors: Tushar Gautam, Jaya Garg, Jyotsna Agarwal

Institute: Dr. RMLIMS Lucknow

Introduction: Scrub typhus caused by *Orientia tsutsugamushi*, transmitted by bite of larval trombiculid mites (“chiggers”). Laboratory parameters play crucial role in early diagnosis, predicting severity and organ dysfunction. Cardiac injury in Scrub is uncommonly reported. This study emphasizes on clinical outcomes and correlates them with significant laboratory abnormalities.

Materials & Methods: This retrospective observational study was conducted at Dr. RMLIMS hospital over a period of 6 months. A total of N = 121 patients with acute febrile illness and laboratory-confirmed scrub typhus IgM positivity were included. Demographic details, clinical features and laboratory parameters were recorded, correlated with clinical severity, outcomes. Incidence and clinical significance of cardiac involvement using cardiac biomarkers including Hs-CRP, NT- Pro BNP and cardiac troponin I levels was seen. Data were analyzed using appropriate statistical methods, and correlations between cardiac marker elevation and clinical parameters were assessed. A p-value <0.05 was considered statistically significant.

Results: The mean age of patients was 38.6 ± 17.4 years (range: 3–80 years). There were 54 (56.3%) males and 42 (43.7%) females. Elevated Troponin I was observed in 17/22 patients (77.3%), elevated CK-MB was observed in 9/14 patients (64.29%), and elevated LDH was observed in 49/61 patients, elevated Hs CRP in 55/70 (78.57%) patients.

Conclusion: Cardiac involvement was present in approximately one-third of scrub typhus patients. Patients with clinical cardiac involvement had significantly higher cardiac biomarker levels compared to those without involvement. Troponin I levels, CK-MB levels, LDH levels were significantly higher in patients with cardiac involvement compared to those without involvement whereas Hs CRP levels were comparatively high in both the group of patients. Cardiac involvement was associated with significantly increased mortality.

60. An Observational Study on Rickettsioses in Paediatrics Patients at a Tertiary Care Centre

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Co-Authors: Prof. R. K. Kalyan, Prof. S. N Singh, Dr. Sanjeev kumar verma.

Institute: King George 'S Medical University, Lucknow

Introduction: Rickettsial infections are an important cause of acute febrile illness in children, particularly in tropical and subtropical region. Hence, reliable laboratory methods are essential for early detection and management.

Materials & Methods: This prospective observational study was conducted in a tertiary care hospital (KGMU, LUCKNOW) and included pediatric patients (1 month to 14 years) presenting with acute febrile illness. Serum samples were tested using Antiscrub typhus IgM ELISA and Weil–Felix tests.

Results: A total of 185 pediatric patients presenting with acute febrile illness were evaluated. Anti-scrub typhus IgM ELISA was positive in 31 (16.8%) patients. The Weil–Felix test was positive in 30 (16.2%) patients. Concordant positivity between IgM ELISA and Weil–Felix was noted in 11 cases, whereas the remaining samples demonstrated discordant serological results. Weil- felix showed predominant agglutination with OX-2 and OX-19 antigens, suggestive of spotted fever group and typhus group reactivity, while OX-K positivity was observed in few cases.

Conclusion: The study demonstrates that Anti scrub IgM ELISA is a more specific and reliable diagnostic modality than the Weil–Felix test, which shows variable antigen reactivity and cross-reactivity.

Limitation- Molecular test was not performed to confirm the diagnosis.

61. Meta-Analysis of Opportunistic Infections- Tuberculosis, Cryptosporidiosis and Cryptococcosis in HIV Patients at a Tertiary Care Hospital in Kanpur

Author: Deep Preeti Lall

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Introduction: Opportunistic infections occur in individuals with compromised immunity and are caused by bacterial, viral, fungal, or parasitic pathogens. Tuberculosis is the most common opportunistic infection and a leading cause of mortality among HIV patients. *Cryptococcus neoformans* is a common opportunistic infection of the central nervous system in HIV patients, while *Cryptosporidium parvum* is an enteric pathogen responsible for life-threatening illness in immunocompromised individuals.

Materials & Methods: This retrospective cross-sectional study was conducted over a period of five years (September 2020–October 2025) in the Department of Microbiology at Rama Medical College Hospital and Research Centre, Kanpur. Twenty sputum samples from HIV-positive patients were tested for *Mycobacterium tuberculosis*. Ten CSF samples from HIV patients with clinical features of meningitis were evaluated for *Cryptococcus neoformans*. Twenty stool samples from HIV patients were examined for *Cryptosporidium parvum* using standard diagnostic methods.

Results: Out of 20 sputum samples, 12 were positive for *Mycobacterium tuberculosis* (1 by ZN stain, 3 by LJ culture, and 8 by TrueNat). Among 10 CSF samples, 2 were positive for *Cryptococcus neoformans* in the 30–40-year age group; both were ICT positive, with one positive each by India ink and Gram stain. Of 20 stool samples, 4 were positive for *Cryptosporidium parvum* in the 20–30-year age group; all were ICT positive and two were modified ZN stain positive.

Conclusion: Tuberculosis, cryptococcosis, and cryptosporidiosis remain major opportunistic infections with significant morbidity in immunocompromised population. Integrated screening programmes, improved diagnostic access, and evidence-based management are essential to mitigate complications and mortality.

62. Seroprevalence of Leptospirosis in a Tertiary Care Centre in Lucknow, Uttar Pradesh in Year 2025

Author: Kshetrimayum Luxmipyari Devi

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Introduction: Leptospirosis is a globally prevalent zoonotic disease in India since 1931. If not diagnosed and treated early, it can result in potentially fatal outcomes. While most infections present as mild, flu-like illness, a smaller proportion progress to severe multi-organ involvement. Due to significant underreporting, especially from Uttar Pradesh, this study was undertaken to assess the sero prevalence and burden of leptospirosis in this region.

Materials & Methods: This cross-sectional study was conducted over one year from January to December 2025 at a tertiary care centre in Uttar Pradesh. A total of 1707 serum samples were collected from patients presenting with acute febrile illness, from outpatient and inpatient cases. All samples were tested for *Leptospira*-specific IgM antibodies using IgM ELISA following standard laboratory protocols.

Results: Out of 1707 samples tested, 141 (8.3%) were positive for *Leptospira* IgM antibodies. A clear seasonal trend was observed, with the majority of positive cases occurring during the post-monsoon period. The highest number of positive cases, 64 out of 141 cases was recorded in September and October, with a peak in September.

Conclusion: Routine screening for leptospirosis should be included in the diagnostic workup of febrile patients. Early laboratory diagnosis can facilitate prompt treatment, thereby reducing morbidity and mortality.

63. To Study the Sero-Prevalence of Hiv Infection at a Tertiary Care Hospital, Kanpur

Author: Meenakshi Trivedi

Co-Authors: R. Sujatha

Institute: Rama Medical College Hospital and Research Centre, Kanpur

Introduction: Human Immunodeficiency Virus (HIV) is the causative agent of Acquired Immunodeficiency Syndrome (AIDS) and belongs to the Lentivirus subgroup of the Retroviridae family. HIV/AIDS continues to be a major global public health concern, with India having the third largest population of people living with HIV. Transmission occurs mainly through heterosexual contact, blood transfusion, percutaneous and mucosal exposure, and perinatal routes. Studying the sero prevalence of HIV in healthcare settings helps assess disease burden and identify high-risk populations for effective prevention and control strategies.

Materials & Methods: This retrospective cross-sectional study was conducted in the Department of Microbiology, Rama Medical College Hospital and Research Centre, Kanpur, over a six-month period from January 2025 to June 2025. A total of 600 serum samples collected from patients attending the hospital were screened for HIV infection. Laboratory testing was performed using standard HIV screening methods, including rapid card test, Tridot test, and ELISA, following recommended guidelines. Demographic details and risk factors were analyzed among reactive cases.

Results: Out of 600 samples tested, 27 were reactive for HIV, resulting in a sero prevalence of 4.5%. Higher sero prevalence was observed among males (63%) compared to females. The most affected age group was 40–60 years (41%). A majority of HIV-positive patients were from rural areas (56%) and were married (81%). High-risk behaviors such as intravenous drug use (37%), needle sharing (44.4%), and multiple sexual partners (26%) were commonly observed.

Conclusion: Although the sero prevalence of HIV was relatively low in this study, HIV continues to contribute significantly to the disease burden. Regular screening, early diagnosis, and focused awareness programs targeting high-risk groups are essential to control the spread of HIV infection.

64. A Clinical and Mycological Study of Superficial Mycoses in a Tertiary Health Care Hospital.

Author : Sara Khan Abid

Co-authors: Priyanka Shukla, Vineeta Khare, Sarah Hassan, Savita Chaudhary, Moin Ahmad Siddiqui

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Introduction:

Superficial mycoses are common fungal infections affecting humans globally, with dermatophytes being the most frequent cause. This study aims to analyse the clinico-mycological profile of superficial mycoses and identify the most common species in North India. We hypothesize that *Trichophyton rubrum* is the predominant species in India. Objective of our study is to identify the causative species of superficial mycoses.

Material and method:

This cross-sectional study was conducted from May 2024 to September 2025 at a tertiary care hospital in Era's Lucknow Medical College and Hospital, Department of Dermatology. The study included 140 isolates from skin, nail and hair samples. Direct microscopy using KOH wet mount, culture on SDA, and slide culture methods were used. Identification of isolates was done with LPCB. Frequency and percentage distributions summarized the types of dermatophyte species and patient demographics, and associations between patient characteristics (age, gender) and dermatophyte infections were determined.

Results:

Among 140 isolates, infections were more common in males, with the highest prevalence in individuals aged 31-50 years. Tinea corporis was the most common clinical type. Dermatophytes were the most frequent pathogens, with *Trichophyton mentagrophytes* being the predominant species followed by *Trichophyton rubrum*. Non-dermatophytes such as *Acremonium*, *Candida albicans*, *Penicillium sp.* and *Fusarium sp* were also isolated.

Conclusion:

Superficial mycoses are more prevalent in older, low-income groups. Dermatophytosis, especially Tinea corporis, is the most common clinical presentation. Understanding the fungal infection burden in a region is important for planning infrastructure, epidemiological studies, and treatment interventions.

Keywords: Sabouraud dextrose agar, Lactophenol cotton blue, Potassium hydroxide, Slide culture.

Mycology Abstracts

65. Evaluation of Antifungal Susceptibility Pattern of Candida Species Isolated From Blood Sample By Using Vitek®2 Platform In Neonates And Children At Tertiary Care Hospital

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Introduction: Candidemia is one of the major causes of morbidity and mortality in health care settings worldwide, especially in the paediatric population. Despite an increase in awareness about fungal bloodstream infections (BSIs) in recent years, few studies have been conducted on candidemia in India.

Materials & Methods: The Retrospective study was conducted at Microbiology department of UPUMS, Saifai, Etawah from Jun 2025 to Nov 2025 to evaluate antifungal susceptibility pattern of *Candida* isolated in the laboratory from blood samples accurately by using automated VITEK® 2 systems.

Results: Overall, 67 isolates of *Candida* species were recovered, including *C. albicans* and non-albicans *Candida* species. Among those echinocandins (caspofungin and micafungin) demonstrated excellent activity against most *Candida* species. Amphotericin B resistance was low but present in selected species like *Candida albicans*, *Candida lipolytica*, and *Candida krusei*. Resistance to fluconazole was more prominent in non-albicans *Candida* species, especially *Candida tropicalis* and *Candida lipolytica*, indicating the growing concern of azole resistance among these isolates.

Conclusion: This study emphasizes the importance of early identification and species-specific antifungal susceptibility testing in paediatric candidemia cases. Ongoing surveillance of resistance patterns is essential to inform empirical treatment strategies and mitigate the impact of emerging drug resistance among *Candida* species in neonates and children.

66. Iron Modulation Drives Biofilm Formation and Virulence Enzyme Production in Emerging Clinical Candida Species: Implications for Diagnostics and Therapeutics

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Introduction: The changing epidemiology of candidemia indicates a rise in non-albicans Candida species, especially resistant Candida auris and emerging Candida utilis. Although iron impacts fungal virulence, its role in these species remains poorly understood.

Objective: This study investigates how manipulating iron levels influences biofilm formation, virulence enzymes, and antifungal susceptibility in clinical isolates.

Materials & Methods: 216 isolates of Candida utilis, Candida albicans, and Candida auris from bloodstream infections over two years were identified via phenotypic methods, MALDI-TOF MS, VITEK 2, and 18S rRNA PCR. Susceptibility was tested using disc diffusion and broth microdilution with ferrous sulphate. Virulence enzyme activities and biofilm formation were assessed under iron-rich and control conditions.

Results: Candida auris showed multidrug resistance, especially to fluconazole and caspofungin, with iron increasing caspofungin MICs up to 16-fold. Candida utilis exhibited strong biofilm formation and increased phospholipase and proteinase activities in the presence of FeSO₄, and also showed 4- to 32-fold increases in fluconazole resistance. Biofilm biomass was unaffected by iron, but enzyme activities varied by species and enzyme. Candida albicans had high proteinase and hemolysin activity but responded minimally to iron.

Conclusion: Iron differentially influences virulence-associated traits and antifungal resistance across these Candida species. C. utilis exhibits iron-responsive increases in phospholipase and proteinase activities together with amplified azole resistance, while C. auris shows iron-linked enhancement of echinocandin resistance and sustained expression of key virulence-associated enzymes. These results underscore the importance of accounting for host iron levels and species-specific responses when managing candidemia and indicate the potential for therapies targeting iron.

67. Galactomannan Antigen Positivity by ELISA in Serum and BAL Samples at a Tertiary-care Centre in North India

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Institute: KGMU Lucknow

Introduction: Galactomannan (GM) antigen detection in serum and bronchoalveolar lavage (BAL) samples is widely used as a non-invasive adjunct laboratory test in the evaluation of suspected invasive aspergillosis, particularly in tertiary-care settings. However, GM testing is frequently performed across diverse clinical specialties, and test positivity does not necessarily equate to proven or probable disease. Understanding institutional patterns of GM positivity may help contextualize test utilisation and interpretation. This study analysed the pattern and distribution of GM ELISA positivity among clinical samples received at a tertiary-care centre in North India.

Materials & Methods: A retrospective analysis of 1233 clinical samples received over one year for GM ELISA testing was performed. Of these, 1059 were serum samples and 174 were BAL fluid samples. Clinical subgroup assessment included patient demographics, clinical specialty, age-group distribution, and monthly trends.

Results: Overall, 287 of 1233 samples (23.3%) were GM-positive. Positivity was markedly higher in BAL samples (104/174; 59.8%) compared with serum samples (183/1059; 17.3%). Clinical haematology patients contributed a higher proportion of positive results. Monthly positivity ranged between 16–30%, with increased positivity observed during the monsoon and early winter months. Male patients demonstrated higher GM positivity than females, and most positive samples were from patients aged 18–60 years.

Conclusion: GM ELISA demonstrated higher positivity in BAL samples compared to serum, with variation across clinical groups and seasonal trends. These findings reflect institutional patterns of GM test positivity and underscore the importance of interpreting results in conjunction with clinical and radiological findings.

68. Disseminated Talaromyces Mimicking Tuberculosis And Histoplasmosis In Advanced HIV: A Diagnostic Pitfall From North India

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Introduction: Talaromyces caused by the thermally dimorphic fungus *Talaromyces marneffeii* is a life-threatening fungal infection which primarily affects individuals with advanced HIV disease with a CD4 count <100 cells/ μ L. It presents as localised or disseminated disease causing cutaneous lesions on the face and extremities but clinical presentation is frequently non-specific and mimics histoplasmosis and tuberculosis. Here we report a case of a 40-year-old PLHIV male with disseminated tuberculosis admitted with new onset nodulo-ulcerative lesions suspected as histoplasmosis on histopathology, subsequently diagnosed as Talaromyces.

Materials & Methods: Skin biopsy specimens were subjected to histopathological examination and fungal culture. Microscopy and CBNAAT for TB was negative. Histopathology suggested a diagnosis of histoplasmosis. Fungal culture on Sabouraud's dextrose agar incubated at 25° C demonstrated mold-phase growth with yellow-green colonies, radial sulcation, and a characteristic diffusible red pigment. Lactophenol cotton blue mount revealed septate hyphae with penicillium-like branching. Thermal dimorphism was demonstrated by conversion to the yeast phase at 37 °C, showing fission with transverse septation, confirming the diagnosis of *Talaromyces marneffeii*.

Results: Based on culture and dimorphism, diagnosis was revised to talaromyces. The patient was treated with intravenous amphotericin B induction therapy followed by oral itraconazole, resulting in marked clinical improvement.

Conclusion: Disseminated talaromyces can closely mimic tuberculosis and histoplasmosis in people living with advanced HIV, particularly in tuberculosis-endemic regions. Reliance on histopathology alone may lead to misdiagnosis. This case highlights a critical diagnostic pitfall and emphasizes the need for definitive microbiological confirmation, including fungal culture and demonstration of thermal dimorphism, to ensure accurate diagnosis and appropriate antifungal therapy.

69. Fungal Infection in Burn Patients: A Prospective Study in A University Hospital

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Co-Author: Prof. Gopa Banerjee, Prof. Prashant Gupta, Prof. Vijay Kumar, Prof. Madhu Kumar

Institute: King George's Medical University, Lucknow

Introduction: Burn patients are highly susceptible to fungal infections due to disruption of skin barriers, prolonged hospitalization, extensive use of broad-spectrum antibiotics, and immunosuppression. Fungal burn wound infections are associated with increased morbidity, mortality, and prolonged hospital stay, making early diagnosis and appropriate antifungal therapy crucial.

Aim: To assess the frequency of fungal infections in burn wounds with respect to the degree of burn and percentage of total body surface area (TBSA) involved.

Objectives: To characterize fungal isolates from burn wounds, study their antifungal susceptibility patterns, and correlate mycological culture findings with histopathology.

Materials & Methods: This prospective observational study was conducted in the burn unit and department of microbiology of King George's Medical University, Lucknow. Burn wound samples were collected from patients with clinical suspicion of fungal infection. Samples were subjected to direct microscopy using KOH mount, fungal culture, and histopathological examination where indicated. Fungal isolates were identified by standard mycological methods, and antifungal susceptibility testing was performed as per CLSI guidelines. Clinical parameters including degree of burn, TBSA, risk factors, and outcomes were analysed.

Results: Out of the total samples studied, fungal infection was detected in 22 cases. *Candida* species and filamentous fungi, including *Aspergillus* and *Mucorales*, were the predominant isolates. Higher incidence of fungal infection was observed in patients with deep burns and TBSA involvement greater than 40%. Histopathology aided in diagnosis in cases where culture was negative, particularly for *Mucorales*. All *Candida* isolates were susceptible to fluconazole.

Conclusion: Fungal infections in burn patients are significantly associated with higher TBSA and deeper burns. A combination of mycological culture and histopathology improves diagnostic accuracy. Early detection and antifungal susceptibility-guided therapy are essential to improve patient outcomes.

70. Diagnostic Utility of Galactomannan Assay in Invasive Aspergillosis: A One-Year Retrospective Study from a Tertiary Care Centre

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Co-Authors: Prof. Gopa Banerjee, Prof. Vimala Venkatesh, Prof. Prashant Gupta

Institute: King George Medical University, Lucknow

Introduction: Invasive aspergillosis (IA) is a life-threatening fungal infection, particularly in immunocompromised patients. Early diagnosis is challenging due to non-specific clinical manifestations and limitations of conventional diagnostic methods. Galactomannan (GM) antigen detection has emerged as a useful adjunct for early diagnosis of IA. This study evaluates the role of galactomannan assay in diagnosing invasive aspergillosis at a tertiary care center over a one-year period.

Materials & Methods: This retrospective observational study was conducted at King George's Medical University, Lucknow, over a period of one year. Laboratory records of serum and bronchoalveolar lavage (BAL) samples received for galactomannan testing from clinically suspected cases of invasive aspergillosis were reviewed. Galactomannan assay was performed using enzyme immunoassay and interpreted using standard cut-off values. Data were analyzed descriptively and correlated with available clinical and radiological findings

Results: During the study period, 825 serum samples and 143 BAL samples were tested for galactomannan. Serum galactomannan was positive in 138 samples, yielding a positivity rate of 16.7%. BAL galactomannan showed positivity in 83 samples, with a markedly higher positivity rate of 58.0%. BAL samples demonstrated a significantly better diagnostic yield compared to serum samples in clinically suspected cases of invasive aspergillosis.

Conclusion: Galactomannan assay is a valuable adjunctive diagnostic tool in invasive aspergillosis. BAL galactomannan demonstrates superior diagnostic yield compared to serum testing and plays an important role in early diagnosis, facilitating timely initiation of antifungal therapy.

71. Phenotypic characterization and biofilm production of *Candida* Bloodstream Isolates from Intensive Care Units in Tertiary Care Hospital

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Co-Authors: Dr Sweta Singh, Dr Sana Islahi, Dr Kali Charan Das, Dr Manu Sharma

Institute: AIIMS Raebareli U.P.

Introduction: Candidemia is a major cause of sepsis in intensive care units (ICUs) and is associated with high morbidity and mortality. A global shift from *Candida albicans* to non-*albicans* *Candida* (NAC) species has complicated management due to variable antifungal susceptibility and virulence factors such as biofilm formation. Local data on species distribution and resistance patterns remain limited.

Materials & Methods: A prospective observational study was conducted from January–December 2025 in the Department of Microbiology, AIIMS Raebareli. Adult and neonatal ICU patients with culture-confirmed bloodstream infections were included. *Candida* isolates identified using standard phenotypic methods including Gram stain, colony morphology, *Candida* CHROM agar, germ tube test, and slide culture microscopy. Biofilm formation was assessed by the tube crystal violet method. Antifungal susceptibility testing was performed according to CLSI M44 guidelines.

Results: Forty *Candida* bloodstream isolates were analysed. Non-*albicans* *Candida* predominated (97.2%), with *C. parapsilosis* (38.9%), *C. tropicalis* (30.6%), *C. krusei* (19.4%), and *C. glabrata* (8.3%) being the most frequent; *C. albicans* accounted for 2.8%. Germ tube test was negative in 97.2% of isolates. Biofilm production was observed in 40%, including 12.5% strong producers. Most isolates were susceptible to fluconazole, while amphotericin B and echinocandins showed excellent activity.

Conclusion: ICU-associated candidemia is predominantly caused by non-*albicans* *Candida* species with significant biofilm-forming ability and variable antifungal susceptibility. These factors contribute to therapeutic complexity and adverse outcomes. Routine species-level identification, biofilm assessment, and susceptibility testing may facilitate early targeted therapy and improve clinical outcomes.

72. A Case Report on a Respiratory Co-Infection in an Elderly Patient: Pulmonary Tuberculosis Complicated by *Strongyloides stercoralis* hyper infection

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Introduction: *Strongyloides stercoralis* is an intestinal nematode that can cause chronic infection and may remain undetected for years. In elderly patients, it can progress to hyper infection syndrome with pulmonary involvement and sepsis, resulting in high mortality if not promptly recognised.

Case Description / Materials & Methods: A 60-year-old female presented with a productive cough, persistent low-grade fever, and hemoptysis for around 1 year. She was diagnosed with pulmonary tuberculosis based on radiological evidence and a positive sputum AFB smear, and anti-tubercular therapy (ATT) was initiated. One month later, she re-presented with worsening respiratory symptoms, progressive breathlessness, abdominal discomfort, and bloating, and was admitted to the ICU with acute respiratory distress syndrome (ARDS) and sepsis-like symptoms. To evaluate for an additional infection, Blood, Urine, and BAL samples were sent to the microbiology department for Gram stain, bacterial culture, and fungal culture.

Results: Blood culture yielded growth of *E. coli*, while the Urine culture was sterile and direct microscopy of the BAL sample revealed motile filariform larvae of *Strongyloides stercoralis* raises suspicion of hyper infection syndrome. Stool microscopy and Giemsa staining subsequently confirmed the presence of *Strongyloides stercoralis* larvae. Ivermectin was initiated in conjunction with the continuation of ATT, resulting in rapid and significant clinical improvement.

Conclusion: This case emphasises the importance of considering strong lyoidiasis in patients with confirmed pulmonary tuberculosis who show unexplained clinical deterioration. Early microbiological diagnosis and timely initiation of ivermectin therapy can be life-saving.

73. CrAg LFA Based Early Diagnosis of Cryptococcal Meningitis cases in People living with HIV (PLHIV).

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Co-Authors: Aishwarya Nikhil, Ragini Tilak, Munesh K. Gupta.

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Introduction: Cryptococcal meningitis (CM) remain a primary cause of mortality in retro-positive patients. CM is diagnosed by detection of capsulated budding yeast cells in India ink wet mount, culture, detection of polysachharide capsular antigen or molecular test. As a life- threatening condition, prompt and accurate diagnosis is crucial.

Materials & Methods: We conducted a prospective study on PLHIV presenting with headaches at the ART clinic, suspecting cryptococcal meningitis. CSF samples were immediately sent to the mycology lab, centrifuged at 2,000 rpm for 10 minutes. India ink wet mounts and cultures were prepared from the sediment, while CrAg antigen testing used the supernatant. Cryptococcus isolates from SDA and BA growth were identified via standard mycological procedures

Results: In this study, we enrolled 150 PLHIV presenting with headaches. CrAg testing was positive in 12 cases, culture in 8, and India ink wet mount showed capsulated budding yeast in 7. Using a composite reference standard (any test positive), sensitivities were 100% for CrAg, 66.7% for culture, and 58.3% for India ink.

Conclusion: CrAg offers rapid, highly sensitive, and specific diagnosis of cryptococcal meningitis but remains costly. In resource-limited settings, India ink wet mounts and culture provide viable, affordable alternatives.

74. Mycological Profile of Invasive Fungal Rhino-Sinusitis in Tertiary Care Centre in Dehradun, Uttarakhand

Author: Dr. Kuldeep Arya

**Co-Authors: Dr. Arti Negi, Dr. Nidhi Negi, Dr. Hitendra Singh, Dr. Yogita Rawat,
Dr. Shalabh Jauhari**

Institute: Government Doon Medical College, Dehradun

Introduction: Invasive fungal Rhino-sinusitis (IFRS) is a potential life-threatening infection predominantly affecting immunocompromised individuals, with increasing incidence in tertiary care settings. Early identification of the causative fungal pathogens is crucial for timely diagnosis, targeted therapy, and improved patient outcomes.

Materials & Methods: This prospective observational study was conducted in the Department of Microbiology, Govt. Doon Hospital, Dehradun, from 1 January 2024 to 31 December 2025. A total of 55 clinically suspected rhino-sinusitis patients aged above 18 years were included. Clinical samples were collected in the Central Laboratory under aseptic conditions. Direct microscopic examination was performed using KOH mount along with fungal culture on Sabouraud Dextrose Agar with chloramphenicol (SDA + C) incubated at 25°C and 37°C. Fungal isolates were identified based on colony morphology and lactophenol cotton blue (LPCB) mount findings.

Results: Out of the total 55 samples received, maximum numbers of samples i.e. 30 (54.5%) were received from age group 31–40 years, and maximum fungal culture positivity was seen in age group 41–50 years 22 (40 %) patients. 17 (30.9%) showed fungal growth. *Aspergillus flavus* was the most common isolate, identified in 11 (20%) patients.

Conclusion: Fungal Rhino-sinusitis constituted a significant proportion of cases in the studied population, with *Aspergillus flavus* being the predominant pathogen. Direct microscopy using KOH mount proved to be a useful rapid screening tool, though culture remains the gold standard for definitive diagnosis. Early mycological diagnosis is crucial to prevent disease progression and complications.

75. Spectrum of Fungal Pathogens in Mycotic Keratitis: A Culture-Based Analysis in a Tertiary Care Setting

Author: Dr. Neha Arya

Co-Authors: Dr. Nidhi Negi, Dr. Arti Negi, Dr. Yogita Rawat, Dr. Shalabh Jauhari

Institute: Government Doon Medical College, Dehradun

Introduction: Mycotic keratitis is a severe, sight-threatening corneal infection, particularly common in developing countries like India. It constitutes a significant portion of microbial keratitis cases and is challenging to diagnose and treat due to its subtle clinical signs and limited antifungal options. The condition often follows corneal trauma with vegetative matter and is associated with risk factors like contact lens use, corticosteroid therapy, ocular surgery, and pre-existing corneal disease. Its prevalence is higher in warm, humid climates typical of tropical and subtropical regions.

Materials & Methods: The prospective study was conducted in the Central Laboratory, Department of Microbiology, over a period of 20 months (November 2023 to June 2025). A total of 33 patients with clinically suspected fungal keratitis were included. Corneal scrapings were collected by ophthalmologists after obtaining informed consent and submitted for mycological evaluation. Specimens were processed using standard mycological techniques, including direct microscopy and culture on multiple fungal media for identification of pathogenic fungi.

Results: Maximum numbers of samples (%) were received from age group 31–40 years, and maximum fungal culture positivity was seen in age group 41–50 years (40 %). Most common fungus was *Fusarium* species (15.2%).

Conclusion: The study underscores the importance of prompt and accurate microbiological diagnosis in the management of fungal keratitis. The combination of KOH mount and fungal culture provides a reliable approach for early detection.

76. Exploring the Clinical Presentation and Mycological Investigation of *Sarocladium kiliense* in an Immuno compromised 75-Year-Old Female: A Case Report

Author: Dr. Sakshi Gautam

Co-Authors: Dr. Vineeta Rawat

Institute: VCSGGMSR, Srinagar, Uttarakhand

Introduction: *Sarocladium kiliense* is a rare, emerging opportunistic fungal pathogen that predominantly affects immunocompromised individuals. Accurate identification is difficult due to its morphological resemblance to other filamentous fungi, frequently resulting in misdiagnosis with conventional methods.

Materials & Methods: A 75-year-old immunocompromised female with poor hygiene, malnutrition, and cognitive impairment presented with boggy scalp swelling and patchy alopecia. Initial potassium hydroxide microscopy revealed septate hyphae, and empirical antifungal therapy was initiated. However, the patient showed no clinical improvement and returned after two months with persistent lesions.

Results: Repeat mycological evaluation was performed. Although conventional culture suggested *Trichophyton violaceum*, definitive identification using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) identified the pathogen as *Sarocladium kiliense* with 99.9% confidence.

Conclusion: This case emphasizes the diagnostic challenges associated with rare fungal pathogens such as *Sarocladium kiliense* and highlights the essential role of advanced diagnostic techniques like MALDI-TOF MS in guiding appropriate therapy and improving outcomes in immunocompromised patients.

77. Emerging Role of *Aspergillus terreus* in Invasive Aspergillosis: A case series highlighting diagnostic and therapeutic challenges

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Co-Authors: Sonakshi Srivastava, Anupam Das, Jyotsna Agarwal

Institute: Dr RMLIMS Lucknow

Introduction: *Aspergillus terreus* is an increasingly recognized cause of invasive aspergillosis, particularly in immunocompromised and critically ill patients. Its intrinsic resistance to amphotericin B poses therapeutic challenges, making early diagnosis and species-level identification essential for effective management.

Materials & Methods: We describe a series of four cases of *Aspergillus terreus* infection diagnosed from respiratory and other relevant clinical specimens, including bronchoalveolar lavage and biopsy. Detailed analysis of clinical presentation, underlying risk factors, radiological findings, microbiological characteristics, therapeutic interventions, and clinical outcomes was performed. Fungal identification was based on direct microscopy, culture characteristics on Sabouraud dextrose agar, and morphological confirmation using lactophenol cotton blue staining and confirmed by MALDI-TOF.

Results: All patients presented with persistent respiratory symptoms, including fever, cough, and dyspnea, with poor response to empirical antibacterial therapy. Radiological imaging revealed features suggestive of invasive fungal infection such as nodular opacities, consolidations, and cavitary lesions. Common predisposing factors included immunosuppression, prolonged intensive care unit stay, corticosteroid use, and underlying pulmonary disease. Direct microscopic examination demonstrated septate hyphae. Fungal cultures yielded characteristic cinnamon-brown, powdery colonies within 3–5 days, and microscopic morphology showed biserial phialides covering the upper portion of the vesicle, confirming *A. terreus*. Despite initiation of targeted antifungal therapy, three patients succumbed to the infection, highlighting the aggressive nature of invasive *A. terreus* infection, while the remaining one patient showed varying degrees of clinical and radiological improvement.

Conclusion: These case reports emphasize the emerging clinical importance of *Aspergillus terreus* in invasive aspergillosis. Prompt laboratory diagnosis, accurate species identification, and early initiation of appropriate antifungal therapy are crucial for improving patient outcomes, especially in high-risk populations.

78. Molecular Analysis of Pneumocystis jirovecii and DHPS Gene Mutations in Immunocompromised Patients from North India

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Background: Pneumocystis jirovecii pneumonia (PCP) is a major opportunistic infection in immunocompromised patients. Mutations in the dihydropteroate synthase (DHPS) gene associated with sulfonamide exposure necessitate molecular surveillance.

Objectives: To detect Pneumocystis jirovecii, assess DHPS gene mutations, describe clinical profiles, and evaluate atypical respiratory pathogens.

Methods: This ongoing cross-sectional study is being conducted over three years at a tertiary care centre in North India. Immunocompromised patients aged over five years with progressive dyspnea, non-productive or minimally productive cough, low-grade fever, malaise, and supportive chest imaging are being enrolled. Patients receiving PCP therapy for more than 48 hours and pregnant or breastfeeding women are excluded. Diagnosis is performed using microscopy, serum β -D-glucan (where available), and real-time PCR. DHPS gene analysis and molecular screening for Chlamydia pneumoniae, Mycoplasma pneumoniae, and Legionella pneumophila are being undertaken.

Results: Interim analysis of 17 patients shows male predominance (82.4%) with a mean age of 30.9 years. HIV/AIDS is the most common underlying condition (76.5%). Mean CD4 count among HIV patients with available data is 68.3 cells/ μ L. Atypical respiratory pathogens were detected infrequently, with Chlamydia pneumoniae and Mycoplasma pneumoniae identified in one patient each (5.9%); no confirmed co-infection with Pneumocystis jirovecii was observed. Legionella pneumophila was not detected.

Conclusion: Interim findings indicate that PCP affects young immunocompromised males, particularly those with HIV infection. Ongoing DHPS gene mutation analysis will clarify potential sulfonamide resistance. Limitations include small sample size, incomplete diagnostic data, restricted pathogen screening, and single-centre design.

Virology Abstracts

79. Seroprevalence of Viral Hepatitis among the major tribal population located in Lakhimpur Khiri district of Uttar Pradesh

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Introduction: Tharu tribes are the major tribal communities of Uttar Pradesh and are endemic to the Indo-Nepal border regions. Due to their remote location, they are vulnerable to various infectious diseases, including viral hepatitis. Viral hepatitis predominantly causes Hepatitis A, B, C, E which are mainly caused by exposure to contaminated water, poor hygiene practices (Hepatitis A, E) and exposure to infected blood and body fluid (Hepatitis B, C). Therefore, the proposed study was conducted to assess the seroprevalence of viral hepatitis of Tharu tribes residing in Lakhimpur Khiri, (U.P.).

Materials & Methods: Blood samples were collected from the Subjects of the village Nijhota of district Lakhimpur Khiri. Seroprevalence of anti-HAV-Ab, anti-HEV-IgG, anti-HBcAb, anti-HCV Ab and HBsAg was assessed through ELISA. A questionnaire-based demographic details and risk factors was captured and analysed.

Results: A total of 106 individuals were subjects in this study, out of which 55 were males, and 51 were females. The ELISA tests showed the positivity of 90/106 for HAV-Ab, 13/106 for HEV-IgG and 20/106 for HBcAb. No positive case for HCV Ab and the only one case are found the positive for HBsAg a viral load of 2368 copies/ml. The risk factor like groundwater consumption (80/106), open defecation (13/106), and body tattooing/shaving outside (41/106) was found common among the studied population.

Conclusion: The seroprevalence of HAV-Ab HEV-IgG and HBcAb was 84.91%, 12.26% and 18.87%, respectively. The seroprevalence among the male was comparatively higher than females. The above results indicated the previous exposure to hepatitis virus infections and possible association of studied risk factors. The above study strongly emphasises the periodic advocacy and awareness for prevention of viral hepatitis and implementation of routine Hepatitis vaccination in the UIP.

80. Molecular epidemiology of high risk HPV genotypes: Age specific prevalence and poly genotypic patterns among females visiting a tertiary care hospital of Uttarakhand.

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Introduction: Human papilloma virus (HPV) is the most common sexually transmitted infection worldwide affecting approximately 50% of sexually active adolescents. Cervical cancer ranks 2nd most common cancer among Indian women, with mortality of more than 70,000 cases, annually in India. Prevalence varies by lifestyle and socioeconomic factors. High risk HPV genotypes 16 and 18 cause approximately 70% of cases.

Materials & Methods: A cross-sectional study was conducted over a period of 06 months in the Department of Microbiology. 986 cervical swab samples were collected from symptomatic and asymptomatic female patients visiting Gynaecology OPD. All samples were processed for HPV DNA isolation using multiplex real time PCR (TRUPCR HPV high risk genotyping kit).

Results: Out of 986 samples, 93 (9.43%) were positive for HPV DNA. Mono genotypic infections predominated (69.8%) as compared to the poly genotypic cases (30.1%). Among the most common HR HPV genotypes, 15 cases (23.07%) of mono HPV-16 and only 02 cases (3.07%) of mono HPV-18 were seen. Among the poly genotypic infections, HPV 16 was seen as the most common genotype in combination with genotypes 18, 31 and 33. Comparison between various age groups and their genotypic pattern was done with 25-34 years of age group showing maximum HPV positivity, with 57.9% mono positivity and 39.5% poly genotypic positivity.

Conclusion: This study reveals 9.43% HR HPV prevalence which is consistent with the other studies from Northern India (0.4 – 16.6 %). Distribution of infections among young age group and predominance of HPV 16 necessitates targeted vaccination and routine screening.

81. Etiologic Involvement of Enterovirus and Human Bocavirus in Acute Flaccid Paralysis Cases in India

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Introduction: Acute flaccid paralysis (AFP), characterized by the rapid onset of asymmetric paralysis, can be caused by a variety of viral infections or coinfections. The clinical manifestations range from conjunctivitis, respiratory tract infection, myocarditis, meningitis, encephalitis, and neonatal sepsis, like illness. Human Bocavirus (HBoV), a newly classified member of the Parvoviridae family, has possible etiological involvement.

Materials & Methods: Total 586 stool specimens were collected and VP1 capsid region, used for detection of human enteroviruses (HEV), human boca viruses (HBoV) and Saffold viruses in direct clinical specimen.

Results: HEV RNA was detected in 103 (17.6%) by targeting 5' UTR region. Out of them, 71 (12.11%) were NPEV, partially sequenced by VP1 which revealed the prevalence of echovirus (ECV) 19 (n = 6), ECV 11 (n = 7), ECV 18 (n = 4), ECV 33 (n = 5), ECV 29 (n = 1), ECV 25 (n = 2), ECV 24 (n = 3), ECV 3 (n = 3), ECV 14 (n = 2), ECV 13 (n = 1), ECV 2 (n = 1), ECV 20 (n = 2), ECV 27 (n = 4), ECV 6 (n = 2), CV A10 (n= 2), CV A9 (n = 1), CV A6 (n = 2), CV B4 (n = 1), CV B5 (n = 3), CV B6 (n = 3), EV 80 (n = 1), EV 83 (n = 1), EV 97 (n = 2).

Total 63 (10.75%) HBoVs were detected, consists of HBoV-1 (n = 8), HBoV-2 (n = 15), HBoV-3 (n = 9) and HBoV- 4 (n = 5). Out of them 9 (1.5%) were in co-infection with NPEVs and showed 0.9 - 5.6% divergence at nucleotide level. Total 9 (1.5%) Saffold viruses was detected and characterized by VP1 sequencing.

Conclusion: Molecular typing of these viruses is useful for characterizing emerging serotypes and their epidemiological investigation.

82. Association of Cytokine Profiles with Clinical Manifestations of Dengue in a Tertiary Care Centre

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Introduction: Dengue remains a major cause of morbidity in Uttar Pradesh, with recurrent seasonal outbreaks. Although NS1 antigen and IgM antibody assays are routinely used for diagnosis, they provide limited insight into disease severity. Emerging evidence indicates that host immune responses, particularly cytokine alterations, play a crucial role in determining the clinical spectrum of dengue. However, region-specific data correlating cytokine profiles with clinical categories of dengue are limited.

Materials & Methods: A hospital-based observational study was conducted from April 2024 to March 2025 at the Department of Microbiology, AIIMS Raebareli. Patients attending Medicine and Paediatrics OPD/IPD with clinical suspicion of dengue were enrolled. Diagnosis was confirmed using NS1 antigen and/or IgM ELISA. Demographic data, clinical features, and laboratory parameters were recorded. Serum levels of IL-6, TNF- α , IL-10, and IFN- γ were measured using ELISA kits to assess immune response patterns across different dengue categories and healthy controls.

Results: Cytokine profiling revealed heterogeneous immune responses. Mean levels of IFN- γ , TNF- α , and IL-10 were higher in dengue patients than in healthy controls, but these differences were not statistically significant, reflecting substantial inter-individual variability. In contrast, post hoc analysis revealed significantly elevated IL-6 levels (19.2pg/ml) in severe dengue compared with other clinical categories ($p = 0.042$).

Conclusion: IL-6 emerges as the most informative cytokine associated with dengue severity and may serve as a useful adjunct to clinical assessment for identifying patients at risk of severe disease.

83. Distribution of Dengue virus Serotypes in Western Uttar Pradesh Population.

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Institute: CCS University, Meerut and LLRM Medical College Meerut.

Introduction: Dengue is an endemic arbovirus illness in the tropical world. It is a viral disease caused by serotypes (DEN1-4) of the virus and transmitted through an infected Aedes mosquito bite. After malaria, it is the second most frequent mosquito-borne disease that affects humans. According to WHO, in 2024, there is 77,18,585 laboratory confirmed cases worldwide, and 11,201 deaths from dengue. In India, 2,00,334 people reported while 233 deaths.

Materials & Methods: The study was conducted in department of Microbiology LLRM Meerut. total number of 1921 blood samples were tested for dengue, in the period of July - December 2025. NS1-Ag & IgM-Ab ELISA was done by NIV Pune Kits and MARILISA. Further proceeded for serotyping; total 96 samples were subjected to testing for DEN,1-4 by HiMedia MBPCR kit. RNA Extraction of samples was done with Invitrogen.

Results: Total 1921 Blood Samples were tested for Dengue IgM and NS1 Ag. 121 NS1 and 26 IgM were found positive. Serotyping was done for 96 positive NS1; in which Positive serotypes were found in the cases. there was 1 positive case in DEN-1, however good numbers (34) in DEN2; simultaneously we found 13 positive cases in DEN-3; although no positivity was found in DEN-4 serotypes.

Conclusion: In our analysis, the data has shown significance in NS1 Antigen positive cases and in the serotyping as well. During the sample collection period (July- December 2025), the majority of positivity in NS1 cases were increased in the month of October, November, there were 58 cases in November and 34 NS1 positive in October. Additionally, we have significant serotyping data with DEN-2(34) and DEN-3(13) serotypes in our western UP Population, moreover DEN-1 was relatively less associated with only 6 positives, furthermore we could not find any positive DEN-4 in our all 96 cases. in this study we conclude there is DEN-2 and DEN-3 serotypes are Considerably associated with the western UP population.

84. Genotypic Characterization of Human Papillomavirus in Carcinoma Cervix: A Regional Comparative Study

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Institute: S.N. Medical College Agra

Introduction: Cervical carcinoma remains a major public health challenge in low- and middle-income countries, including India, where regional variations in human papillomavirus (HPV) genotype distribution and limited molecular surveillance affect prevention strategies. While HPV-16 and HPV-18 are globally dominant, emerging data from India indicate an increasing contribution of non-16/18 high-risk genotypes, underscoring the need for region-specific molecular characterization integrated with screening modalities.

Materials & Methods: This hospital-based cross-sectional study was carried out over an 18-month period from April 2023 to January 2025 at a tertiary care hospital in Agra. A total of 500 symptomatic women between 25 and 65 years of age were recruited. Cervical specimens were obtained from all participants for Pap smear examination and HPV DNA testing. Visual Inspection with Acetic Acid was performed using 5 % Acetic acid

Results: HPV DNA was detected in 13% (65/500) of participants. No significant association was observed between HPV positivity and sociodemographic or behavioral variables. Abnormal cytology showed strong association with HPV positivity (74.7%; $p < 0.001$). Pap smear demonstrated sensitivity of 86.2% and specificity of 95.6%, while VIA showed higher sensitivity (100%) but lower specificity (62.8%). HPV-16 was the predominant genotype (44.6%), followed by HPV-39 (18.5%) and HPV-51 (13.8%); 29.2% of HPV-positive women harbored multiple genotypes.

Conclusion: The study underscores substantial regional variation in the distribution of high-risk HPV genotypes beyond the traditionally dominant HPV-16 and HPV-18 types, reflecting the evolving epidemiological landscape of HPV infection. It also demonstrates a strong and consistent association between HPV positivity and the presence of cytological abnormalities, reinforcing the etiological role of HPV in cervical carcinogenesis.

85. Seroprevalence of hepatitis D virus infection among hepatitis B virus-infected patients attending UPUMS, Saifai: A cross-sectional study

Author: Dr. Radhika

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Institute: UPUMS Saifai

Introduction: HDV (Hepatitis D virus) is a defective RNA virus that requires HBV (Hepatitis B virus) for the replication; therefore, HDV can only get transmitted to the people who also have HBV infection and lead severe liver disease. Globally, the geographical distribution of HDV infection among HBV-positive people is very heterogeneous. In India, limited data are available on prevalence of HDV among hepatitis B surface antigen (HBsAg)-positive patients. The aim of our study was to determine the seroprevalence of HDV infection among HBsAg-positive cases.

Materials & Methods: This hospital-based cross-sectional study was carried out in the Department of Microbiology. 87 HBsAg-positive samples were included in the study. HBsAg-positive samples were subjected to anti HDV IgM and IgG ELISA Kit by Elabscience®. Demographic profiles and clinical parameters were taken from all the patients.

Results: The mean age of HBsAg-positive patients was 36.6 years (SD: 14.6), with a male: female ratio of 2:1. Out of 87 HBsAg-positive patients, serological evidence of delta virus infection was observed in 6 patients (6.8%); 4 (4.6%) patients were positive for anti HDV IgG antibodies, and 2 (2.3%) were positive for anti HDV IgM antibodies.

Conclusion: This study provides evidence that seroprevalence of HDV coinfection in the case of Hepatitis B is low (6.8%) in the western part of Uttar Pradesh; understanding the seroprevalence of Hepatitis D helps public health authorities to allocate resources effectively and design target interventions.

86. Establishment of a Multiplex Nested Polymerase chain reaction for the identification of Herpes group of Viruses from various clinical specimens.

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Co-Authors: Sthita Pragnya Behera, Ritesh Kumar, Nirbhay Singh, Imbisat Fatma, Ashutosh Tiwari, Gaurav Raj Dwivedi.

Institute: ICMR-Regional Medical Research Centre Gorakhpur Uttar Pradesh.

Introduction: The family *Orthoherpesviridae* includes major human pathogens: Herpes simplex viruses (HSV-1 & HSV-2), varicella-zoster virus (VZV), cytomegalovirus (CMV), and Epstein- Barr virus (EBV). These viruses establish lifelong latent infections, causing mild muco cutaneous lesions to severe encephalitis and meningitis, especially in newborns and immunocompromised patients. Multiplex PCR offers major advantage in quick detection, sensitivity, specificity, and cost-effectiveness simultaneous detection of multiple herpesviruses compared to single-target PCR.

Materials & Methods: A multiplex nested PCR assay for HSV, VZV, CMV & EBV was carried targeting the short gene fragments (gD: HSV, ORF29: VZV, Immediate early: HCMV and GP220: EBV) of gene from different clinical specimens (n=2289) like serum, urine, eye swab, crusts, throat swab (TS), CSF.

Results: Of 2289 specimens tested, 248 (10.83%) were positive for herpes viruses. HSV positivity was highest in urine (8.33%) followed by serum (4.27%), and CSF (1.90%). VZV predominated in crusts (89.47%) followed by throat swabs (28.00%), serum (2.86%), urine (1.64%), and CSF (1.20%). CMV was mainly detected in urine (27.87%). EBV was higher positive in serum (2.18%). Among positives, 140 were males and 108 females. In this study, co-infections were also detected: HSV-VZV in 2 cases, HSV-CMV in 2, VZV-CMV in 2, HSV-EBV in 3, and VZV-EBV in 1 case.

Conclusion: The study detected overall 10.83% positive for herpes group of viruses in multiplex assay followed by sanger sequencing. VZV and CMV was detected highest in crusts (89.47%) and urine (27.87%) specimens respectively. Herpes virus was significantly associated with Acute encephalitis and Acute febrile illness patients.

87. Prevalence of Respiratory Syncytial Virus in cases of Acute Respiratory Infection in children.

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Introduction: Pediatric acute respiratory infections are a global health burden, predominantly caused by viruses. Respiratory syncytial virus (RSV) accounts for approximately 24.8 million cases and 76,600 deaths annually in children under five. Due to overlapping clinical features of all viral acute respiratory infections (ARI), molecular diagnosis by RT-PCR remains the gold standard method.

Materials & Methods: The study was conducted from January 2025 to December 2025 among children aged less than 14 years presenting with ARI. Total of 136 respiratory specimens, comprising nasopharyngeal and/or oropharyngeal swabs, were collected. Viral RNA extraction was performed, followed by reverse transcription polymerase chain reaction (RT-PCR). Samples were analyzed for presence RSV subtypes A and B.

Results: Out of 136 respiratory samples, 16 (11.8%) were positive for RSV, with RSV B predominating (11/16 cases; 69%) over RSV A (5/16 cases; 31%); RSV cases were more predominant among infants and commonly presented with fever, cough, chills, and breathlessness.

Conclusion: RSV contributes significantly to pediatric ARI, with RSV-B emerging as the dominant circulating subtype. RT-PCR proved to be a sensitive and reliable method for RSV detection and subtype differentiation, enabling definitive etiological diagnosis for prompt treatment and thus reducing mortality and morbidity in infants. Continuous molecular surveillance of circulating RSV subtypes supports rational clinical management by reducing empirical antibiotic use and unnecessary investigations.

88. Laboratory diagnosis of measles infection using molecular and serological test in a tertiary care center in India

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Institute: Sanjay Gandhi Postgraduate Institute of Medical Sciences, Lucknow

Introduction: Measles is an acute, highly contagious human disease caused by a Measles virus (MeV) belonging to the family Paramyxovirus. It is an enveloped, single-stranded, negative-sense RNA virus which is highly contagious and causes acute viral infection characterized by a prodromal illness of fever, coryza, cough, and conjunctivitis followed by the appearance of a generalized maculopapular rash.

Materials & Methods: Children of Uttar Pradesh (with age < 15 years) suffering from fever with rash were included in this study. Throat swabs, urine, and nasal swabs (clinical samples) were collected for Conventional PCR and serum samples were collected for serological testing (IgM ELISA) from January 2025 to December 2025. Measles IgM ELISA was performed using Anti-measles virus NP ELISA IgM kit (EUROIMMUNE) as per the kit protocol. For Conventional PCR RNA extraction from clinical samples was performed using the Qiagen Viral RNA Mini Kit, followed by One-step RT- PCR as per WHO protocol. Molecular identification was done by sequencing followed by sequence analysis which was done by sequencer & Phylogenetic Analysis by Mega 5.5.

Results: A total 4782 specimens (urine/throat swab) were subjected to conventional reverse transcription PCR, of which 135 (2.8%) were positive for measles virus. A total of 7512 serum samples were tested for IgM of measles and Rubella. Out them 925 (12.3%) samples were found to be positive for measles. PCR positive products were sent to NIV Mumbai for sequencing and the resultant positive sequence was analyzed & all the positive sequence was genotyped and was found to be D8.

Conclusion: Result infers that combined serological and molecular testing should be done in pediatric patients with history of fever along with rash for the diagnosis of measles infection. Further, molecular typing of such virus is useful for characterizing emerging serotypes or unidentified/new strains which will ultimately help in their epidemiological investigation.

89. Association of Human Oncogenic Viruses with Clinico pathological Features of Differentiated Thyroid Cancer

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Introduction: Differentiated thyroid cancer (DTC) is the most common endocrine malignancy. Oncogenic DNA viruses have been implicated in the pathogenesis, tumorigenesis, and prognosis of several human cancers. Among them, Parvovirus B19, cytomegalovirus (CMV), human papillomavirus (HPV), and Epstein–Barr virus (EBV) have been suggested to play a role in DTC. This study aimed to investigate the prevalence of these oncogenic viruses in patients with DTC and to correlate viral detection with clinic pathological features.

Materials & Methods: In this prospective case-control study, thyroid tissue samples (2 mg) were collected from patients undergoing surgery for clinically diagnosed DTC. Samples were preserved in Triazole reagent and stored at -80°C . Viral DNA was extracted, assessed for integrity by agarose gel electrophoresis, and quantified using Nano Drop spectrophotometry. PCR amplification was performed on adequate DNA-positive samples. Viral detection was then correlated with the clinical characteristics of the patients.

Results: Among 75 DTC cases, the prevalence of viral DNA was: Parvovirus B19 in 47 cases (62.7%), HPV in 32 cases (42.7%), EBV in 7 cases (9.3%), and CMV in 5 cases (6.7%). In contrast, the control group (n=75) showed lower detection rates: Parvovirus B19 in 10 (13.3%), HPV in 15 (20%), EBV in 7 (9.3%), and CMV in 0 (0%). The mean age of the patients was 39.05 years, with a male-to-female ratio of 1:3 in the cases and 1:8 in the controls. Mean tumour size was 5.63 cm in cases versus 10.12 cm in controls. Statistical analysis demonstrated a strong association between DTC and the presence of Parvovirus B19 and HPV. EBV prevalence was similar in both groups, while CMV was detected only in DTC patients.

Conclusion: Parvovirus B19 infection was more frequently observed in DTC patients. It was associated with smaller tumor size, lower TSH levels, shorter duration of symptoms, and a higher incidence of lymph node metastasis. These findings suggest a potential contributory role of viral infection, particularly Parvovirus B19 and HPV, in the pathogenesis and clinical behavior of DTC.

90. Clinical and Molecular Profile of UL97 Mutations in Gancyclovir-Resistant CMV Infection at a Tertiary Care Center

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Introduction: Human cytomegalovirus (HCMV) is a ubiquitous pathogen that can cause severe disease in transplant recipients.

First-line therapy consists of Gancyclovir and Valgancyclovir, the use of these agent has markedly reduced the morbidity and mortality among the patients but prolonged use of these Drugs has led to the emergence of drug resistant CMV. About 90% of gancyclovir resistance Results from mutations in the HCMV Phosphotransferase UL 97 gene that impairs. Phosphorylation of Gancyclovir. Most of these mutations occur within the putative ATP-binding (codons 460 to 520) and substrate recognition (codons 590 to 607) sites of UL97. Gancyclovir resistance may be of prognostic value and could allow the timely choice of Alternative antivirals.

Materials & Methods: The Present study was conducted in Virology Department of SGPGIMS. A total 302 post –transplant patients were included in present study (n=302). The study period was from April 2023 to March 2025 (277 renal transplant patient & 25 bone marrow Transplant patient). Out of 302 samples, CMV RT-PCR was Positive for 59 Samples (19.54 %). From that 59 positive sample, we have sent 10 samples for Sanger – Sequencing in which we have found UL97 mutation in only 2 samples.

Result: CMV Positivity: Overall it is 20%, in which 38% (n=47) is in bone marrow transplant patients and 18% (n=12) in Renal transplant patients. All patients with CMV infections were associated with Thrombocytopenia and liver dysfunction (Elevated SGOT and SGPT) Out of the 59 CMV RTPCR Positive patients, 28 (47.5%) patients clinically Responded to gancyclovir treatment and turned CMV negative by second week.

Conclusion: UL 97 mediated Gancyclovir resistance is an emerging threat that will worsens the outcome in Transplants/ immunocompromised patients. Early detection and modified management are crucial to improve the survival rates among the immunocompromised patients.

91. Atypical Herpes Zoster Ophthalmicus with Extra-Dermatoma Lesions in an Immunocompetent Young Female

Author: Dr. Neha Shaikh

Institute: Era Medical College and Hospital

Introduction: Herpes zoster ophthalmicus (HZO) results from reactivation of latent varicella-zoster virus in the ophthalmic division of the trigeminal nerve. In immunocompetent individuals, herpes zoster typically presents with painful vesicular eruptions confined to a single dermatome. The occurrence of additional non-contiguous or extra-dermatoma lesions is uncommon and may lead to diagnostic confusion with primary varicella or disseminated zoster. Such atypical presentations are rarely reported, particularly in young and otherwise healthy patients

Materials & Methods: We describe the case of a 23-year-old immunocompetent female who presented with a 5-day history of painful vesicular lesions over the left forehead, upper eyelid, and periorbital region, corresponding to the ophthalmic branch of the trigeminal nerve. Two days after the onset of facial lesions, she developed multiple scattered vesicular eruptions over the trunk, clinically separate from the primary dermatome. There was no history suggestive of immunosuppression, systemic illness, recent drug intake, or previous similar episodes. Ophthalmologic evaluation revealed conjunctival congestion with keratitis. Routine hematological investigations were within normal limits, and HIV serology was non-reactive. Tzanck smear demonstrated multinucleated giant cells, supporting herpesvirus infection. VZV serology revealed positive IgG and negative IgM, supporting viral reactivation. PCR testing for VZV could not be performed due to non-availability. Based on clinical correlation, a diagnosis of atypical herpes zoster ophthalmicus with extra-dermatoma spread in an immunocompetent host was established. The patient was treated with oral acyclovir, analgesics, and topical ocular therapy, resulting in complete resolution without sequelae.

Conclusion: This case highlights that herpes zoster ophthalmicus may rarely present with extra-dermatoma lesions even in immunocompetent individuals. Awareness of such atypical manifestations is essential to prevent misdiagnosis and ensure timely antiviral therapy, thereby reducing the risk of ocular and systemic complications.

92. Spectrum of Respiratory Viruses in Children with Acute Respiratory Illness at Tertiary Care Center in Western Uttar Pradesh

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Co-Authors: Dr. Amit Garg, Dr. Prem Prakash Mishra, Dr. Karvi Agarwal, Dr. Priyanka Mahour, Janish Malik

Institute: LLRM Medical College, Meerut

Introduction: Respiratory virus infections are a major cause of severe acute respiratory illness worldwide, especially in children. According to the National Family Health Survey (NFHS-5), carried out between 2019 and 2021, Acute Respiratory Illness (ARI) was responsible for almost 14.3% of fatalities, contributes significantly to the yearly national burden.

Materials & Methods: This study was conducted in Microbiology department of LLRM Medical College and associated SVBP Hospital, Meerut in the year 2025. Nasopharyngeal and oropharyngeal swabs were collected from patients presented with symptoms of acute respiratory tract infection in hospital. Nucleic acid extraction was done and then they were subjected to RT-PCR to detect 8 respiratory viruses.

Results: Among the 70 evaluated samples, 57 (81.4%) were found positive with at least one pathogen. Human rhinoviruses were most frequently detected (35.71%) followed by respiratory syncytial virus (RSV) (34.28%). Coinfection of two or more viruses was present in 16 (28%) children. Infants were the most susceptible group, with a clear male predominance.

Conclusion: Respiratory viruses play a major role in causing respiratory infections in children. Rhinovirus and RSV were found to be the most common pathogens causing peak during winter season, especially among infants younger than one year. The clinical presentation can vary from mild cough and cold to severe disease such as acute respiratory distress syndrome and other life-threatening conditions. The use of RT-PCR allows for rapid and accurate identification of viral infections, helping clinicians avoid unnecessary antibiotic use and improve patient care, infection control, and epidemiological surveillance.

93. Evaluation of viral load by Truenat in laboratory confirmed cases of Hepatitis B under 12 years of age.

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Introduction: The history of HBV in children is variable. Understanding viral load patterns, a key determinant of disease activity and transmission risk, across pediatric age groups can inform monitoring and management strategies in rural population.

Objective: To evaluate the Hepatitis B virus (HBV) viral load distribution across different age groups in a pediatric cohort (<12 years) attending a tertiary care center with laboratory-confirmed infection.

Materials & Methods: A total of 2270 children under 12 years from rural part of Western Uttar Pradesh were screened from January 1, 2025 to December 31, 2025 using Chemiluminescent Microparticle Immunoassay (CLIA) ARCHITECT HBsAg Qualitative II (Abbott Diagnostics). All CLIA-positive cases were confirmed for HBV DNA along with viral load estimation using Truenat™ HBV Quantitative Real-Time PCR (Molbio Diagnostics Pvt. Ltd). PCR-confirmed cases were stratified into three age groups: 1-4, 5-8, and 9-12 years for detailed analysis.

Results: A total of 92 cases were flagged positive using CLIA. Among CLIA confirmed cases, 89 were confirmed positive by PCR. The overall PCR-confirmed positivity rate was 3.92% (89/2270). Among the positive cases, male to female ratio was 1.17:1. Most cases of HBV infection was among age group of 9-12 years and least was in age group of 1-4 years. Viral load greater than 20000 IU/ml was highest among 9-12 age group followed by 1-4-year age group.

Conclusion: This study establishes a substantial burden of active HBV infection (3.92%) in pediatric population along with a significantly high viral load among children between age group of 9-12 years as well as 1-4 years in rural area. Instead of strict implementations of screening and immunization programs there is still a need to find the missing link in order to grab this epidemic by its neck.

94. Comparison of Conventional Virus Isolation Technique with RT-PCR for Enterovirus Detection in Stool Specimens from Patients of Acute Flaccid Paralysis

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Co-Authors: Jasmeet Singh, Dr. Nikky Nyari Srivastava, Dr. Dharamveer Singh, Dr. Atul Garg

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Introduction: Every year Enteroviruses (EVs) causes different diseases and infect millions of people. Cell culture is conventional method of choice for the detection of enteroviruses in Acute Flaccid Paralysis (AFP) cases. In this study, we compared cell culture and polymerase chain reaction (PCR) methods for the detection of EVs in AFP suspected children below 15 years of age. A total of 789 stool samples were cultured in Rhabdomyosarcoma (RD) cell line. The specimens were tested for 5' UTR by Pan EV Real-time PCR and VP1 PCR. The clinical manifestations of EVs range from conjunctivitis, respiratory tract infection, myocarditis, meningitis, encephalitis, and neonatal sepsis, like illness. The important neurological presentations were recorded in AFP cases, where EV is identified as a foremost etiological agent.

Materials & Methods: A total 789 patients involving 432 males and 357 females from different district of Uttar Pradesh, India from May 2015 to April 2016. The two stool samples ≥ 24 hour apart collected from children (≤ 15 years), clinically suspected for AFP syndrome. Stool supernatant was inoculated on Human rhabdomyosarcoma (RD) cell and other was used for direct RNA extraction. The inoculated cells show a characteristic cytopathic effect (CPE) for EV. RNA extraction was done and then followed by rRT-PCR for the detection of Pan EV and VP1 PCR.

Results: A total of 109 out of 789 specimens (13.81%) were found to be positive for enterovirus from cell culture, 163 (20.65%) were found positive from Pan Enterovirus Real time PCR, and 152 (19.26%) were found positive from VP1 PCR. The present data indicated that PCR represents a significant improvement over cell culture technique.

Conclusion: Molecular methods were found to be useful for rapid and specific detection of EVs with higher sensitivity compared with the conventional cell culture method, which was recognized as the "gold standard" for laboratory diagnosis of enteroviruses diagnosis of enteroviruses, will make more confident for the detection of EVs. In this study we also found that RT-PCR is the most suitable method for detection of enteroviruses and should be used as a method of choice for laboratory diagnosis.

95. Evaluating pooling strategy for detection of SARS-CoV-2 on Automated RT-PCR platform

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Institute: ASMC Hardoi

Introduction: COVID-19, an international health emergency has caused significant mortality across the world. Diagnosis of SARS-CoV-2, a causative agent of COVID-19 is the mainstay in planning public health measure to control the spread of pandemic. RT-PCR is the gold standard approach for diagnosis of SARS-COV-2. Automated RT-PCR platforms have been approved by US FDA and have high sensitivity and resource saving. Pooling strategies have been evoked to increase the throughput of RT-PCR. The present study is planned to establish the role of pooling on Automated Abbott m2000 Real Time Systems.

Materials & Methods: We planned a parallel pooling strategy for detection of SARS-CoV-2, on Automated Abbott m2000 Real Time System. Here we tested 480 test samples individually and in pool of 10 consecutive samples (1 log dilution) to determine the effect of pooling.

Results: In the present study, on parallel testing of 480 samples individually and in pool of 10, we found all the negative samples were accurately detected in pool of 10 (specificity 100%). 31 positive SARS-CoV-2 samples were also accurately flagged in pool of 10 (sensitivity 73.8%).

Conclusion: Pooling of SARS-CoV-2 test samples on Automated Abbott m2000 Real Time System allows increase in throughput, requires less expertise and above all chances of manual errors decrease, leading to increase in sensitivity of results. We report pool of 10 to be accurate for surveillance of SARS-CoV-2 in large populations where if low viral load is missed is of less significance.

Mycobacteriology Abstracts

96. Clinical Profile and Treatment Outcomes of Drug-Resistant Tuberculosis in Programmatic Settings: A Study from Referral Centre

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Institute: Baba Raghav Das Medical College Gorakhpur Uttar Pradesh

Introduction: Drug resistant tuberculosis (DR-TB) remains a major global health concern due to prolonged treatment duration, drug toxicity, and challenges in patient adherence. Evaluation of clinical characteristics and treatment outcomes is crucial for improving patient management strategies. This study aimed to assess the clinical profile and treatment outcomes of DR-TB patients diagnosed using molecular methods.

Materials & Methods: This was an observational study conducted at IRL lab, Baba Raghav das Medical College, Gorakhpur. A total of 172 DR-TB patients diagnosed by line probe assay were followed under the national tuberculosis elimination program. All the treated patients were categorized as cured, ongoing treatment, loss to follow-up, and death. Demographic variables, clinical parameters, co-morbidities, behavioural factors, and source of infection were analysed in relation to treatment outcomes using descriptive statistics.

Results: Among 172 DR-TB patients, 119 (69.18%) were cured, 27 (15.70%) were lost to follow-up, 19 (11.04%) were on ongoing treatment, and 7 (4.06%) died during treatment. Male patients predominated across all outcome groups. The highest mean age was observed in the death group (40.29 ± 1.88 years), while the ongoing treatment group had the lowest (27.05 ± 14.24 years). The lowest mean BMI was recorded among deceased patients (17.30 ± 1.70), indicating an association between undernutrition and mortality. Behavioural risk factors were more frequent among patients lost to follow-up.

Conclusion: Although favourable outcomes were achieved in most DR-TB patients, loss to follow-up and mortality remain significant challenges. Advanced age, poor nutritional status, prior treatment history, and behavioural factors were associated with unfavourable outcomes. Strengthening patient-centred follow-up, nutritional support and behavioural counselling is essential for treatment success.

97. Frequency of Microbiologically Confirmed Genitourinary Tuberculosis among Clinical Suspects: A Retrospective Analysis from 2022 to 2025

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Introduction: Genitourinary tuberculosis (GUTB) is a significant cause of morbidity in endemic regions but often remains underdiagnosed due to its insidious onset and paucibacillary nature. Laboratory confirmation is essential to prevent irreversible renal damage and infertility. This study evaluates the diagnostic yield of standard mycobacteriological tests in cases of GUTB.

Materials & Methods: A retrospective study was conducted over a period of 3 years (2022 to 2025). Urine samples referred to the Intermediate Reference laboratory for TB at the department of Microbiology, KGMU were processed according to NTEP guidelines by centrifuging them at $3,000\text{--}4,000 \times g$ for 15–20 minutes. The resulting sediment was processed for acid-fast bacilli (AFB) smear microscopy and cartridge-based nucleic acid amplification test (CBNAAT) according to standard protocols.

Results: Of the 527 samples tested, 21 (3.9%) were positive for *M. tuberculosis* by microscopy and/ or CBNAAT, with one case of rifampicin resistance. The positive cases were primarily aged 15–60 years with equal gender distribution; none of the patient was HIV positive.

Conclusion: Though *M. tuberculosis* was detected in about 4% of the study population, the frequency of detection can be increased by spreading awareness among clinicians regarding appropriate urine sample collection and processing. Detection of rifampicin resistance in one case also highlights the importance of drug resistance detection and patient-tailored treatment in GUTB patients.

98. Diagnostic Performance of GeneXpert MTB/RIF versus Line Probe Assay for Identification of Mycobacterium tuberculosis and Rifampicin Mono-resistance.

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Institute: Uttar Pradesh University of Medical Sciences, Saifai

Introduction: Emergence of drug-resistant tuberculosis (TB) poses a major global challenge to TB elimination efforts. Conventional diagnostic methods are limited by the low sensitivity of microscopy, technical complexity and long turnaround time of culture. Rapid molecular assays such as the Line Probe Assay (LPA) and Xpert MTB/RIF have therefore become essential tools for early detection of Mycobacterium tuberculosis and rifampicin-resistant TB in both AFB smear-positive and smear-negative sputum samples.

Objectives: To determine and compare the sensitivity, specificity and predictive value of GeneXpert MTB/RIF and LPA for Detection of Mycobacterium tuberculosis.

Materials & Methods: A total of 475 sputum samples from patients at Uttar Pradesh University of Medical Sciences suspected of having drug-resistant tuberculosis were initially collected and tested using CBNAAT (GeneXpert® Dx system version 4.4a, LPA (Geno Type MTBDR plus VER 2.0), and MGIT culture. Of these, 33 samples were contaminated and 24 were identified as non-tuberculous mycobacteria (NTM); thus excluding 57 samples. The remaining 418 samples were included for analysis, and sensitivity, specificity and predictive values were calculated to evaluate the diagnostic accuracy.

Results: Against culture MGIT as the gold standard for TB diagnosis, GeneXpert had a sensitivity, specificity, positive predictive value, and negative predictive value of 82.1, 98%, 96.5% and 89.1% respectively, while LPA had 94%, 98%, 96.9% and 96.1% respectively. For diagnosis of rifampicin mono-resistance GeneXpert had sensitivity 90.09%, specificity 98.50% while LPA that had sensitivity 93.9% and specificity 99.3%.

Conclusion: GeneXpert demonstrated better diagnostic performance than AFB microscopy but lower performance compared to LPA. Furthermore, for the detection of rifampicin mono resistance, LPA outperformed GeneXpert MTB/RIF, making it a superior alternative to culture for rifampicin resistance detection.

99. Comparative Evaluation of Phenotypic (BACTEC MGIT 960) and Genotypic (Line Probe Assay) Methods for Detecting Drug-Resistant Tuberculosis in eastern Uttar Pradesh

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Introduction: Quick and accurate detection of drug resistance, especially rifampicin (RMP) and isoniazid (INH), is crucial for managing multidrug-resistant TB (MDR-TB). We assessed the performance of genotypic Line Probe Assay (LPA) against phenotypic BACTEC MGIT 960 liquid culture (gold standard).

Materials & Methods: From January to December 2024, 70 MDR-TB isolates were selected from 3,125 laboratory-confirmed TB specimens. We calculated sensitivity, specificity, positive predictive value (PPV), negative predictive value (NPV), accuracy, and prevalence for RMP and INH resistance.

Results: MGIT 960 and LPA found 60 RMP resistant cases as true positive and 8 true negative. However, LPA definitely gave false results for 2 susceptible isolates. Despite this discordance, statistical analysis showed a sensitivity of 96.77% (95%CI:88.83–99.61%) and a specificity of 100% (95%CI:63.06–100%). RMP resistance was found in 88.57% cases with 100% PPV, 80% NPV, and 97.14% overall accuracy. When testing for INH resistance, MGIT 960 surely identified 63 isolates as resistant. Moreover, 7 isolates were classified as susceptible. LPA correctly found INH resistance in 62 isolates, with one false-negative and one false-positive result. The sensitivity and specificity were 98.41% (95%CI:91.47–99.96%) and 85.71% (95%CI:42.13–99.64%), respectively. INH resistance was found in 90% cases with 98.41% PPV, 85.71% NPV, and 97.14% accuracy regarding the test performance.

Conclusion: LPA showed high sensitivity and accuracy for RMP and INH resistance detection, though specificity was slightly lower for INH. These results affirm phenotypic methods as a reference standard and support integrating genotypic and phenotypic approaches to enhance MDR-TB diagnosis.

100. Discordance Between Genotypic and Phenotypic Fluoroquinolone Resistance Testing in *Mycobacterium tuberculosis*: an overlooked problem

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Co-Authors: Dr. Parul Jain, Prof. Raj Kumar Kalyan, Prof. Vimala Venkatesh, Dr. Shruti Radera

Institute: King George's Medical University, Lucknow

Introduction: Fluoroquinolones (FQs) are pivotal in treating multidrug-resistant *Mycobacterium tuberculosis* (MDR-TB), yet discrepancies between genotypic and phenotypic assays for FQ resistance complicate clinical decision-making.

Objective: To evaluate concordance between the Second-Line Line Probe Assay (SL-LPA) and Liquid Culture Drug Susceptibility Testing (LCDST) in detecting FQ resistance among *M. tuberculosis* isolates.

Materials & Methods: A total of 1,402 clinical isolates were tested using both SL-LPA and LCDST. Genotypic resistance was determined by detecting mutations in the *gyrA* and *gyrB* genes using the GenoType MTBDRsl assay, whereas phenotypic resistance was assessed by measuring bacterial growth inhibition at critical FQ concentrations with the BACTEC MGIT 960 system. Isolates were classified into six categories based on their resistance profiles. For binary analysis, results were categorized simply as "Resistant" or "Sensitive." Agreement statistics, including sensitivity, specificity, positive predictive value (PPV), negative predictive value (NPV), Cohen's kappa, and McNemar's test, were calculated.

Results: Concordance between SL-LPA and LCDST was observed in 1,234 isolates (88.0%). Binary analysis demonstrated an observed agreement of 88.0% with a sensitivity of 84.5% and an NPV of 88.2%, but a specificity of 90.7% and a PPV of 87.6%. Cohen's κ was 0.841, indicating strong agreement, while McNemar's test revealed significant discordance ($\chi^2 = 52.46$; $p < 0.0001$).

Conclusion: Although SL-LPA exhibits high sensitivity for ruling out FQ resistance, its lower specificity necessitates cautious interpretation of genotypic resistance. These findings support the complementary use of both genotypic and phenotypic testing to improve diagnostic accuracy in MDR-TB management.

101. Utility of MALDI-TOF MS in identification of non-tuberculous mycobacteria: A comparative study with Line Probe Assay

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Institute: King George's Medical University, Lucknow

Introduction: Non-tuberculous mycobacteria (NTM) are increasingly recognized as clinically significant pathogens. Accurate species-level identification is essential due to differences in pathogenicity and antimicrobial susceptibility. While line probe assay (LPA) is widely used for NTM identification, it is resource-intensive. MALDI-TOF MS offers a rapid alternative; however, its performance for NTM identification requires further evaluation.

Objective: To assess the utility of MALDI-TOF MS for identification of non-tuberculous mycobacteria and compare its performance with line probe assay in a tertiary care diagnostic laboratory.

Materials & Methods: This is a descriptive study where culture-positive isolates from MGIT-960 liquid culture system were screened by immunochromatographic testing using the MPT64 antigen test; MPT64-positive isolates were excluded as *Mycobacterium tuberculosis*, while MPT64-negative isolates were identified by MALDI-TOF MS and compared with line probe assay.

Results: Eighteen NTM isolates were analyzed by both MALDI-TOF MS and LPA. Good concordance was observed for rapid-growing species such as *Mycobacterium fortuitum*. Isolates identified as *Mycobacteroides abscessus/chelonae* complex by LPA were identified as *Mycobacteroides abscessus* by MALDI-TOF MS. However, discordant results were observed in some isolates, including misidentification of LPA-confirmed *Mycobacterium fortuitum* as non-mycobacterial organisms such as *Nocardia* and *Bacillus*.

Conclusion: MALDI-TOF MS shows promise as a rapid adjunctive tool for identification of non-tuberculous mycobacteria, especially for selected rapid-growing species. However, variable performance and occasional misidentification highlight the need for Data base expansion and further optimization.

102. Evaluation of GeneXpert Ultra for diagnosis of Osteoarticular Tuberculosis in a tertiary care centre in Lucknow.

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Co-Authors: Vineeta Mittal, Richa Sinha, Vineet Kumar

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Introduction: Osteoarticular tuberculosis (OATB) is a form of EPTB affecting bones and joints. OATB remains a significant diagnostic challenge due to its paucibacillary nature. Conventional smear microscopy lacks sensitivity, and culture has long turn-around time. The Xpert MTB/RIF Ultra assay is rapid, automated cartridge-based NAAT. This study evaluates the diagnostic utility of Xpert MTB/RIF Ultra in detecting *Mycobacterium tuberculosis* in suspected OATB cases.

Materials & Methods: A cross-sectional study was conducted on 102 clinical samples from January - December 2025 from patients suspected of OATB. Various specimens including synovial fluid, bone biopsy, pus aspirates and para spinal collections were processed. Xpert MTB/RIF Ultra assay was done on all samples.

Results: Out of 102 samples, 27.45% were positive for MTB complex. Among positive samples, 7.14% were high detected, 46.42% were low detected, 17.8% were very low detected, 28.57% were trace detected and 64.28% and 7.14% were rifampicin sensitive and rifampicin resistant respectively. All trace detected samples were rifampicin indeterminate. Most common sample was bone biopsy (60.71%) followed by pus aspirate (25%), synovial fluid (10.71%) and paraspinal collections (3.57%) among positive samples. Male and female ratio in positive samples was 1:1 and most common age group was 20-30 years.

Conclusion: Xpert MTB/RIF Ultra is a rapid and highly effective tool for the diagnosis of Osteoarticular TB. Its ability to detect low bacterial loads and provide simultaneous rifampicin susceptibility results significantly reduces the time to treatment initiation compared to traditional culture, which is crucial for preventing permanent joint destruction and neurological deficits.

103. Multifocal lupus vulgaris involving atypical cutaneous sites: a rare case report

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Co-Authors: Dr. Savita Chaudhary, Dr. Reyan Abdul Jamil, Dr. Ankita Kumari, Dr. Kajal Bansal

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Introduction: Lupus vulgaris is the most common manifestation of cutaneous tuberculosis accounting for nearly 75% of adult cases and 1-2% of extra pulmonary tuberculosis. It is a chronic progressive paucibacillary disease occurring in individuals with moderate to high immunity and usually presents as a solitary plaque on the face or buttocks. Multi focal involvement at uncommon cutaneous sites is rare.

Case: A 51 year old woman came to our dermatology outpatient department with asymptomatic red raised lesions over the left upper lip and right forearm for 3 years. The lesions had an insidious onset with progressive involvement of the forearm within 3-4 months, gradually increasing in size and associated with mild pruritus and no discharging sinus. Cutaneous examination revealed a single well defined shiny erythematous plaque measuring 2x2 cm over the left perioral area and a well-defined erythematous plaque with central adherent necrotic crust and peripheral scaling measuring 1.5-2cm over the right forearm. No regional lymphadenopathy was noted, and systemic examination including chest radiography was normal. Ziehl Neelsen staining for acid fast bacilli was negative. Dermoscopy revealed white structure less areas, follicular plugging, linear vessels over an erythematous background and abundant white yellow scales. Diascopy demonstrated apple jelly nodules at the periphery of the lesion.

A 3.5 mm punch biopsy from the forearm showed epithelioid cell granulomas with Langhans giant cells and lymphocytic infiltration involving the upper and deep dermis, consistent with granulomatous dermatitis suggestive of lupus vulgaris.

Conclusion: Multifocal lupus vulgaris involving uncommon cutaneous sites is rare. Hence, we report this case.

104. Comparative analysis of Mutation Detected on GeneXpert and LPA of rpoB gene in Rifampicin resistance TB isolates

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Co-Authors: Charul Singh, Priyanka Yadav, Dr. Amit Garg, Jitender Singh

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Introduction: GeneXpert MTB/RIF detects rifampicin resistance by targeting the 81-bp rifampicin resistance-determining region (RRDR) of the rpoB gene using five overlapping molecular beacon probes (A–E). Specific probe patterns suggest particular mutations, which can be further characterized by Line Probe Assay (LPA). Correlating GeneXpert probe patterns with LPA wild-type (WT) and mutation (MUT) bands is important for accurate interpretation of rifampicin resistance.

Materials & Methods: This retrospective study was conducted at the Intermediate Reference Laboratory (IRL), LLRM Medical College, Meerut, from January 2025 to December 2025. A total of 94 presumptive Mycobacterium tuberculosis drug-resistant clinical samples were tested using both GeneXpert MTB/RIF and first-line LPA. GeneXpert probe patterns (A–E) were analysed and correlated with corresponding rpoB WT and MUT band patterns on LPA to identify associated mutation within the RRDR.

Results: Among the 94 samples analysed, 88(93.6%) showed complete concordance between GeneXpert probe absence and LPA mutation profiles, with loss of specific WT bands and Corresponding MUT band patterns indicating the same rpoB mutation regions. In 6 samples, although the final rifampicin resistance results of GeneXpert and LPA were same, but the mutation in GeneXpert probe absence did not match the mutation identified by LPA WT and MUT band patterns. These discrepancies are attributable to differences in assay design: GeneXpert uses overlapping molecular beacon probes and kinetic PCR analysis, whereas LPA uses discrete WT probes and mutation-specific probes with endpoint detection.

Conclusion: Both GeneXpert and LPA detect rifampicin resistance by targeting the 81-bp RRDR of the rpoB gene, but their principles differ. GeneXpert identifies resistance based on delayed probe binding during real-time PCR, which may indicate resistance even when all probes are present, including silent or rare mutations. In contrast, LPA detects only known mutations covered by its probes; mutations outside probe coverage may appear as WT. Therefore, GeneXpert probe patterns do not directly correspond to LPA codon-specific probes, highlighting the importance of understanding methodological differences for accurate interpretation of rifampicin resistance.

105. Tubercular meningitis in 3.5 year old child with hydrocephalus in western Uttar Pradesh – A case report .

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Co-Authors: Dr. Ankur Goyal

Institute: Sarojini Naidu medical college, Agra

Introduction : Tubercular meningitis (TBM) is a serious form of extra pulmonary tuberculosis in children, often complicated by hydrocephalus and associated with high morbidity. Microbiological diagnosis is challenging due to the paucibacillary nature of cerebrospinal fluid (CSF). Molecular techniques such as Xpert MTB/RIF have improved early detection. This poster presents a microbiologically confirmed case of Tubercular meningitis with hydrocephalus in a 3.5-year-old child.

Materials & Methods: A 3.5-year-old male child presented with fever and headache for one week, cough and cold for two weeks, and altered sensorium for one day. There was a history of tuberculosis contact (mother). Clinical examination revealed neck rigidity and sluggishly reactive pupils. CSF samples were subjected to cyto chemical analysis and microbiological testing, including Xpert MTB/RIF assay. Neuroimaging was performed to evaluate intracranial complications.

Results: CSF analysis showed a total cell count of 200 cells/cu mm with lymphocytic predominance (65%), elevated protein (211.12 mg/dL), and reduced glucose (25.41 mg/dL). Xpert MTB/RIF detected Mycobacterium tuberculosis (very low load) with no rifampicin resistance. NCCT head revealed hydrocephalus. Hematological findings showed anemia (Hb 8.7 g/dL). Based on clinical, radiological, and microbiological findings, a diagnosis of TBM with hydrocephalus was made. The child was started on HRZE anti-tubercular therapy with pyridoxine, along with corticosteroids and supportive management.

Discussion: Smear microscopy is often negative in pediatric TBM due to low bacillary load. In this case, Xpert MTB/RIF played a crucial role in rapid microbiological confirmation and detection of rifampicin susceptibility, enabling timely initiation of appropriate therapy. Quantitation of csf is important factor in xpert Tb test, atleast 1 ml of CSF should be processed. Larger volume of csf, when centrifuged and concentrated, increase the likelihood of detecting mycobacterium tuberculosis, especially in paucibacillary pediatric cases.

Conclusion: Early microbiological diagnosis using molecular methods such as Xpert MTB/RIF is essential in pediatric TBM to ensure prompt treatment, guide drug therapy, and prevent severe neurological complications.

106. Pulmonary Tuberculosis with Concomitant Aspergillus Co-infection in a Cirrhotic Adolescent Presenting with Fatal Respiratory Failure: A rare case report

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Co-Authors: Dr. Romya Singh, Dr. Riti Srivastava, Dr. N.P. Singh, Dr. Rekha Bhandari

Institute: Noida international institute of medical sciences, Greater Noida

Introduction: Pulmonary tuberculosis (TB) remains endemic in developing countries, while pulmonary aspergillosis is an opportunistic infection seen primarily in immunocompromised hosts.

Co infection with *Mycobacterium tuberculosis* and *Aspergillus* species is rare in pediatric patients and is associated with high morbidity and mortality. Chronic liver disease with cirrhosis causes immune dysfunction, predisposing affected individuals to severe and atypical infections.

Materials & Methods: We report a 16 year old boy with chronic liver disease, decompensated portal hypertension, and splenomegaly who presented with fever, cough, progressive breathlessness, and abdominal distension. Examination revealed gross ascites and acute hypoxemic respiratory failure requiring intensive care. Chest imaging showed bilateral pulmonary infiltrates. Bronchoscopy was performed and bronchoalveolar lavage samples were processed using Ziehl Neelsen staining, chip based nucleic acid amplification test for tuberculosis potassium hydroxide mount and fungal culture.

Results: Bronchoalveolar lavage demonstrated acid fast bacilli and molecular testing confirmed *Mycobacterium tuberculosis*. Concurrently, potassium hydroxide mount revealed septate hyaline hyphae and fungal culture yielded *Aspergillus* species. A diagnosis of pulmonary tuberculosis with concomitant pulmonary aspergillosis was established. The patient was initiated on weight adjusted anti tubercular therapy and antifungal treatment with close liver function monitoring. Despite aggressive antimicrobial therapy and intensive supportive care, the patient deteriorated rapidly and succumbed to refractory respiratory failure.

Conclusion: This case highlights a rare and fatal dual pulmonary infection in a cirrhotic adolescent. It emphasizes the importance of early suspicion, comprehensive microbiological evaluation of bronchoalveolar lavage, and prompt multidisciplinary management in immunocompromised pediatric patients presenting with severe respiratory illness and high mortality.

107. Stool-based Truenat as a non-invasive frontline diagnostic tool for pediatric pulmonary tuberculosis: A Cross-sectional study from a tertiary-care pediatric center.

Author: Dr. Anushka Soni

Co-Authors: S. Nandwani, S.B. Mathur, B. Kumar.

Institute: PGICH, Noida

Background: Pediatric pulmonary tuberculosis (TB) is frequently underdiagnosed due to difficulties in obtaining respiratory samples and the paucibacillary nature of disease. Stool-based molecular testing offers a non-invasive alternative, particularly in young children who swallow sputum. Although WHO recommends stool testing with Xpert MTB/RIF, evidence for stool-based Truenat remains limited. We evaluated the diagnostic accuracy of stool Truenat for pediatric pulmonary TB using a composite reference standard (CRS).

Materials & Methods: In a prospective cross-sectional study (August–December 2025) at a tertiary pediatric hospital in northern India, children (<18 years) with presumptive pulmonary TB provided paired respiratory and stool samples within 24 hours. Stool samples were processed by homogenization–dilution–centrifugation and tested using Truenat MTB/MTB-RIF. Respiratory samples underwent smear microscopy, Truenat testing, and culture (LJ and MGIT). TB diagnosis was classified by CRS. A second stool sample was collected from CRS-positive children initially stool-negative. Diagnostic accuracy was calculated against CRS, and discordant rifampicin results were resolved by line probe assay.

Results: Of 112 children, 15 (13.4%) were CRS-positive (12 microbiologically confirmed; 3 clinico-radiological). Stool Truenat detected MTB in 10/12 confirmed cases (sensitivity 83.3%, 95% CI 51.6–97.9), with two additional detections on repeat stool testing (incremental yield 18.2%). All 97 CRS-negative children were stool-negative (specificity 100%, 95% CI 96.3–100). PPV was 100%, NPV 98.0%, and overall accuracy 96.4%, with strong agreement with CRS ($\kappa = 0.82$). Rifampicin susceptibility concordance between stool and respiratory samples was 80%.

Conclusion: Stool-based Truenat shows high accuracy, excellent specificity, and strong agreement with CRS, supporting its integration into NTEP diagnostic algorithms for decentralized, child-friendly detection of pediatric pulmonary TB.

Hospital Infection Abstracts

108. Surveillance of Ventilator associated events in a tertiary care hospital in India: A Six month observational study

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Co-Authors: Dr. Sulekha Nautiyal, Dr. Iva Chandola, Dr. Saranya Datta

Institute: SGRRIM&HS, Patel Nagar, Dehradun

Introduction: Ventilator-associated pneumonia (VAP) is one of the most common and severe complications in patients receiving invasive mechanical ventilation, contributing significantly to morbidity and mortality in intensive care units (ICUs). It affects approximately 5–40% of patients ventilated for more than 48 hours, with the risk varying across different ICU settings. To improve objectivity and standardization in surveillance, the Centers for Disease Control and Prevention (CDC), through the National Healthcare Safety Network (NHSN), introduced the ventilator-associated events (VAE) framework in 2013.

Materials & Methods: This observational surveillance study was conducted in a tertiary care teaching hospital in India over a period of six months (June to November 2025). VAE surveillance was carried out across multiple ICUs & HDUs using standardized NHSN definitions. Monthly denominator data on ventilator days were collected from all participating units. VAE events were identified through routine infection control surveillance and compiled centrally. VAE rates were calculated per 1000 ventilator days

Results: During the study period, a total of 8062 ventilator days were recorded. 39 ventilator-associated events were identified, resulting in an overall VAE rate of 5/1000 ventilator days. Inter-unit variability in VAE occurrence was observed, with certain ICUs contributing a higher proportion of events, while several units reported no VAE during the surveillance period

Conclusion: VAE surveillance using standardized definitions is a necessity in modern day infection control practices, particularly in a tertiary care hospital setting and provides valuable insights into ventilator-associated complications. Continuous monitoring and implementation of targeted preventive strategies may help reduce ventilator-related morbidity and improve patient outcomes in ICUs.

109. Antimicrobial consumption pattern in patients admitted in ICU at a tertiary care institute

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Introduction: Antibiotics are the most often administered drugs in patients admitted to the ICU as these patients are critically ill and exhibiting a substantial consumption of these antimicrobial substances. Higher antibiotic consumption in ICU settings leads to antibiotic resistance among these critically ill patients, which may increase mortality, morbidity, hospital cost, and length of hospital stay

Materials & Methods: The current study was conducted on 196 patients over 3 months, admitted to I.C.U of a tertiary-care institute in Lucknow, India. Patient details were recorded through a daily visit to the medical records department and details were collected directly from the patient's case record file consisting of all the necessary information regarding antibiotic therapy.

Results: A total of 30 common antibiotics were utilized in the treatment of the patients, and the WHO DDD approach was employed to analyze the antimicrobial use pattern. Ceftriaxone had the largest usage [in DDD/100 bed days] of these drugs, followed by Metronidazole [43.8%], Piperacillin-Tazobactam [39.2%], Amikacin [25%], and Clindamycin [20.9%].

Conclusion: It is concluded that very high utilization rates of antibiotics prescribed in the ICU in our institution are a matter of concern and need to be improved by the use of local antibiogram guidelines, regular audits, continuous surveillance and antimicrobial stewardship programs using antibiotic restriction and antibiotic cycling policies.

110. Assessment of Antibiotic Use and Antimicrobial Resistance Awareness in Adults Visiting a Tertiary-Care Hospital: Findings from a WHO Tool-Adapted Cross-Sectional Study.

Author: Ranjana Rohilla

Co-Authors: Sulekha Nautiyal, Malvika Singh

Institute: AIIMS Rishikesh

Understanding public knowledge, attitudes and practices (KAP) is essential to design effective antimicrobial stewardship and behavioural interventions, particularly in low- and middle-income settings such as India.

Materials & Methods: A cross-sectional survey was conducted over 15 days at a tertiary-care teaching hospital in Dehradun, Uttarakhand, using probability sampling (sampling interval=2). A structured questionnaire adapted from the WHO multi-country public awareness survey was administered electronically. Knowledge (0–10), attitude (8–40) and practice (0–7) scores were computed. Inappropriate antibiotic use was defined as non-prescription use, self-medication and/or premature discontinuation among respondents reporting antibiotic use in the preceding year. Multivariable logistic regression identified independent predictors.

Results: Among 3,906 participants, 15.7% reported antibiotic use within the preceding year; 32.3% used antibiotics without prescription and 41.4% discontinued treatment early. Mean knowledge, attitude and practice scores were 6.8 ± 2.1 , 28.6 ± 5.4 and 4.1 ± 1.9 , indicating a knowledge–practice gap. Older age, female gender, higher education and urban residence were associated with lower odds of inappropriate use. Each unit increase in knowledge score reduced odds of inappropriate use by 18% (aOR 0.82, 95% CI 0.79–0.85), while each five-point rise in attitude score reduced odds by 12% (aOR 0.88, 95% CI 0.81–0.95).

Conclusion: Inappropriate antibiotic use remains common despite moderate awareness of AMR. Multifaceted interventions integrating education, regulatory enforcement and antimicrobial stewardship are required to address behavioural drivers of misuse.

111. Hospital Environmental Surface and Air Microbiological Surveillance: One-Year Audit and Impact of Targeted Interventions

Author: Dr. Romya Singh

Co-Authors: Dr. Radha Chauhan, Dr. Riti Srivastava, Dr. N.P. Singh

Institute: Noida International Institute of Medical Sciences, Greater Noida

Introduction: Hospital environmental surfaces and indoor air serve as important reservoirs for microorganisms implicated in healthcare-associated infections (HAIs). Regular surveillance of both surface contamination and air quality is essential, particularly in critical care areas, to guide infection prevention strategies.

Materials & Methods: A prospective surveillance audit was conducted from January to December 2025. Environmental surface swabs were collected from intensive care units (ICUs), operation theatres (OTs) and labour rooms using sterile swabs and processed by standard culture methods. Air sampling was performed using the passive settle plate. Isolates were identified by conventional microbiological techniques. Baseline surveillance was carried out during the first six months, followed by implementation of targeted infection control interventions. Post-intervention surveillance was conducted during the subsequent six months.

Results: A total of 37 isolates were recovered during the pre-intervention phase which was reduced to 13 isolates post intervention, showing an overall reduction of 64.9%. Environmental surface isolates decreased from 28 to 10 indicating a 63.4% reduction. Coagulase-negative staphylococci (CONS) were the most frequent surface isolates, followed by aerobic spore bearers (ASB) and *Staphylococcus aureus* while air sample isolates reduced from 9 to 3, showing a 66.7% reduction. ASB predominated in air samples followed by CONS. ICUs showed the highest baseline contamination.

Conclusion: Implementation of targeted infection control interventions resulted in a consistent >60% reduction in both surface and airborne isolates. Regular environmental and air monitoring, combined with timely corrective measures, is an effective strategy for strengthening infection prevention practices and enhancing patient safety.

112. Study of Risk Factors, Prevalence, Bacteriological Profile of Catheter Associated Urinary Tract Infections & Its Antimicrobial Susceptibility Pattern in Critical Care Unit in a Tertiary Care Hospital, Rajasthan

Author: Dr. Ritika Kumari

Co-Authors: Dr. Preeti Srivastava

Institute: Jaipur National University Institute for Medical Sciences and Research Centre Jaipur.

Introduction: CAUTI is the most common device associated infections acquired from hospital settings. Among 25% of patients hospitalized & 70% critically ill ICU patients undergo urinary catheterization which in poses a risk for developing CAUTI. Each additional day indwelling catheter remains in-situ is associated with 3-7% increased risk of acquiring CAUTI.

Materials & Methods: Catheter specimens of urine were obtained by clamping off above port, allowing collection of freshly voided urine & aspirated via sterile syringe & was subjected to direct microscopy & culture. Urine samples were cultured by semi-quantitative technique onto MacConkey agar, Blood agar & Hi Crome UTI Agar. If no growth was detected, reported as sterile, if present, total number of colonies per ml was counted. Colony count of 10³- 10⁵ CFU/ml was taken significant for processing. Presence of 3 or more types of colonies was reported as mixed growth. Identification of bacterial isolates was done by determining colony characteristics, biochemical reactions & antimicrobial susceptibility testing.

Results: Among 207 samples, 30 patients developed CAUTI. CAUTI rate was 2.26 per 1000 catheter days. Out of 30 patients, 20 male patients (66.6%) & 10 female patients (33.33%) developed CAUTI showing male predominance. Most common isolate was Enterococcus species. Largest proportion of patients belonged to the 50–59 age group (30%) followed by 70–79 years 16.%).

Conclusion: CAUTI is significantly associated with increased morbidity & mortality rate. Inappropriate & recurrent use of antibiotics for treating CAUTI promotes antimicrobials resistance so evidence based diagnosis of CAUTI & use of appropriate antimicrobial therapy based on microbiological testing is crucial in ICU settings.

113. Microbiological Profile, Antimicrobial Resistance Patterns, and Clinical Outcomes of Gram-Negative Bacteria Causing Ventilator-Associated Pneumonia in a Tertiary Care Hospital.

Author: Dr. Shivani Saini

Co-Authors: Dr. Sheetal Verma, Dr. Vimala Venkatesh, Dr. Zia Arshad

Institute: King George's Medical College

Introduction: Ventilator-associated pneumonia (VAP) is a major healthcare-associated infection in intensive care units, contributing to increased morbidity, mortality, prolonged hospital stay, and excessive antimicrobial consumption. The emergence and rapid spread of multidrug-resistant (MDR) Gram-negative bacteria have further complicated management. Generation of local epidemiological data on microbiological profiles, antimicrobial resistance patterns, and patient outcomes is crucial for guiding empirical therapy and strengthening antimicrobial stewardship and infection control practices.

Materials & Methods: This prospective observational study was conducted in a tertiary care university hospital. Endotracheal aspirate samples from 100 clinically suspected VAP patients were processed using standard microbiological methods. Bacterial isolates were identified; antimicrobial susceptibility testing was performed using Kirby–Bauer disc diffusion, VITEK MIC determination where applicable, interpreted according to CLSI guidelines. Resistance patterns to commonly used antibiotics, including carbapenems and colistin, were analyzed. Clinical outcomes (survival/mortality), comorbidities, ICU severity scores (APACHEII, SOFA), relevant laboratory parameters were analyzed.

Results: Gram-negative bacteria predominated among VAP isolates. *Acinetobacter baumannii* (39.6%) was most common pathogen, followed by *Pseudomonas aeruginosa* (27.7%), *Klebsiella pneumoniae* (14.9%), other non-fermenters and Enterobacterales. High burden of antimicrobial resistance was observed, with 66.4% isolates exhibiting carbapenem resistance. Resistance to third-generation cephalosporins and fluoroquinolones was widespread, while colistin showed highest in-vitro susceptibility. Mortality was higher among patients with carbapenem-resistant Gram-negative bacteria.

Conclusion: The study demonstrates predominance of carbapenem-resistant Gram-negative bacteria, particularly *Acinetobacter baumannii*, in VAP. Continuous surveillance of resistance patterns is imperative to optimize empirical therapy, reduce adverse outcomes, and strengthen antimicrobial stewardship in critical care settings.

Parasitology Abstracts

114. Concurrent Infection of Plasmodium falciparum and Plasmodium vivax in a Paediatric Patient

Author: Dr. Tripti Mishra

Co-Authors: Dr. Dayawanti Kumari, Dr. Ashima Jamwal, Dr. Gerlin Varghese

Institute: T.S. Misra Medical College and Hospital, Lucknow, Uttar Pradesh, India

Introduction: India contributes significantly to the global burden of malaria. Mixed infections constitute a distinct clinical entity that is often underdiagnosed due to the dominance of one species over the other in peripheral smears. While Plasmodium vivax was historically termed benign, recent trends suggest severe complications when co-existing with Plasmodium falciparum.

Objective: To report a case of dual infection in a paediatric patient and emphasize the critical role of careful microscopic examination in preventing treatment failure and relapse.

Materials & Methods: A 12-year-old male presented to the paediatric outpatient department with high-grade fever, chills, and rigor for three days, accompanied by nausea and abdominal pain. There was no history of travel. The patient underwent haematological profiling, microscopic examination of peripheral blood smears, and rapid antigen detection testing.

Result: Haematology revealed a haemoglobin level of 10 g/dl and a platelet count of 42000/mm³, indicating significant thrombocytopenia. Microscopy showed multiple ring forms and crescent-shaped gametocytes of Plasmodium falciparum. Rapid diagnostic tests were positive only for Plasmodium vivax-specific lactate dehydrogenase. The patient was treated with artemisinin-based combination therapy and primaquine, resulting in rapid clinical improvement and discharge on day 5.

Conclusion: Mixed infections pose a diagnostic challenge, as Plasmodium vivax forms can mimic those of Plasmodium falciparum. A diagnosis of mono-infection could lead to inadequate treatment; specifically, omitting primaquine would leave the patient vulnerable to relapse. This case reinforces the importance of maintaining a high index of suspicion for co-infections in endemic zones.

115. Observational Cross-Sectional Study on Selected Intestinal Protozoal Parasites in Patients with Inflammatory Bowel Disease (IBD)

Author: Dr. Mohd Kismat Khan

Co-Authors: Prof. Prashant Gupta, Prof. Gopa Banerjee, Dr. Suruchi Shukla,

Institute: King George's Medical University, Lucknow

Introduction: Inflammatory bowel disease (IBD) is a chronic, relapsing inflammatory disorder of gastrointestinal tract, comprising ulcerative colitis and Crohn's disease. With increasing prevalence in developing countries, IBD poses a significant healthcare burden. Intestinal protozoal infections may mimic or exacerbate disease activity, making parasitological evaluation clinically relevant in endemic settings.

Objectives: To evaluate stool samples from patients with IBD for detection of *Entamoeba histolytica* and *Giardia lamblia*.

Materials & Methods: This ongoing observational cross-sectional study includes stool samples (≥ 5 g) collected from 80 diagnosed IBD patients attending a tertiary care hospital. Samples were examined using standard parasitological techniques, including direct wet mount microscopy and microscopy following concentration methods. Antigen detection was performed using rapid immune chromatographic assays. Molecular detection using real-time PCR for both organisms is planned, and results are awaited. Study was approved by Institutional Ethics Committee of King George's Medical University, Lucknow, and written informed consent was obtained from all participants.

Results: Among the 80 IBD patients studied, *Giardia lamblia* was detected in one patient (1.25%), confirmed by stool microscopy and antigen detection targeting $\alpha 1$ -giardin and CWP1 antigens. *Entamoeba histolytica* was not detected in any sample by microscopy or antigen detection. Real-time PCR results are pending.

Conclusion: Preliminary findings indicate a low detection rate of intestinal protozoal parasites among patients with IBD in this cohort from North India. Completion of molecular analysis may further clarify the true burden and diagnostic yield of protozoal infections in IBD patients.

116. Intrathoracic Extension of Amoebic Liver Abscess in a Migrant Patient

Author: Dr. Richa Pandey

Co-Authors: Dr. Loveleena

Institute: Dr. Sonelal Patel Autonomous State Medical College, Pratapgarh

Introduction: Amoebic liver abscess (ALA) is the most common extraintestinal manifestation of *Entamoeba histolytica* infection and is frequently encountered in individuals from endemic regions. Although most cases respond to medical therapy, intrathoracic extension is a rare but potentially fatal complication requiring early diagnosis and intervention.

Materials & Methods: Diagnosis was established based on clinical features, laboratory parameters, imaging studies, and microbiological and serological investigations.

Results: Laboratory evaluation revealed neutrophilic leukocytosis with basophilia, elevated alkaline phosphatase, mild transaminitis, and hyperbilirubinemia. Blood cultures were sterile.

Abdominal ultrasonography demonstrated a solitary hypoechoic lesion measuring 7.8 × 8.2 cm in the right hepatic lobe, consistent with a liver abscess without internal septations. Chest X-ray (PA view) showed right-sided pleural effusion with elevation of the right hemidiaphragm, suggestive of intrathoracic extension.

Stool examination detected ova of *Ascaris lumbricoides* and cysts of *Entamoeba histolytica*. Serum *Entamoeba histolytica* IgG antibodies were positive, confirming the diagnosis of amoebic liver abscess.

Conclusion: Intrathoracic extension of amoebic liver abscess is an uncommon but serious complication. Prompt recognition using imaging and serology, along with timely medical management, is crucial to reduce morbidity and mortality and achieve favorable outcomes.

117. Assessment of Performance of Rapid Diagnostic Test as compared to Peripheral Blood Smear Microscopy for the Diagnosis of Malarial parasites among febrile patients at a Tertiary Care Centre in North India.

Author: Shalini Shah

Co-Authors: Manodeep Sen Mohd Saquib. Nikhil Gupta. Jyotsna Agarwal

Institute: Dr RMLIMS Lucknow

Introduction: Malaria is the leading cause of death in developing countries, particularly in tropical and Sub tropical regions. Limitations in Malaria diagnostics are that RDTs may give false negatives at low parasitemia or due to *pfhrp2/3* gene deletions and false positives from cases with recent malaria treatment with parasite clearance and cross-reactivity with other infections. Microscopy accuracy depends on expertise and parasite density; low-level infections may be missed, requiring repeat smears over 12–24 hours.

Materials & Methods: A Cross-sectional hospital-based study was conducted in the microbiology department, Dr RMLIMS Lucknow. Peripheral Blood Smear Microscopy & Rapid Diagnostic Test (PARAMAX Tulip Diagnostics (P) Ltd) were performed and their results were compared.

Results: Overall incidence of malaria over 1 year (Jan-Dec 2025) was 3.36% (98/2920). Majority of patients were female (53.1%) and major age group affected was from 21–40 years (44.9%). *Plasmodium vivax* was the predominant species (96.9%). Most common parasitic index value observed was 0.2 (38.8%) indicating most patients had low parasitemia at time of diagnosis. Maximum cases reported from Sitapur (42.9%), followed by Lucknow 28.6%. Most cases were reported during monsoon. Maximum cases were reported in July (25.5%), followed by June (24.5%). Diagnostic evaluation of rapid card in comparison with peripheral blood smear microscopy as gold standard, showed a high sensitivity (98.99%) and specificity (99.75%). Its positive predictive value was 93.33%, while negative predictive value was 99.96%, indicating excellent diagnostic reliability.

Conclusion: Overall, the findings emphasize need for strengthened vector control measures, early diagnosis and timely treatment, especially during the monsoon to reduce the burden of malaria in endemic areas.

118. Radiological Spectrum of Ring-Enhancing Brain Lesions: A Retrospective Study from North India

Author: Zeba malik

Co-Authors: Dr. Suruchi Shukla, Prof. Anit Parihar

Institute: King George's Medical University, Lucknow, UP.

Introduction: Ring enhancing lesions (RELs) on neuroimaging represent a diagnostic challenge due to their diverse etiologies ranging from infections to neoplasms. In developing countries like India, infectious causes are highly prevalent, yet comprehensive radiological analyses remain limited. Integrating radiology with molecular and serological approaches may enhance diagnostic accuracy.

Materials & Methods: To evaluate the prevalence, demographic distribution, anatomical location, and radiological features of RELs in a tertiary care center using one-year radiological data.

A retrospective study of 513 patients with RELs was conducted between January–December 2023. Demographic data, radiological findings (CT/MRI), lesion location, and diagnosis were extracted. Statistical summaries, cross-tabulations, and visualizations were prepared.

Results: The mean age was 27.6 years, with nearly equal male (50.7%) and female (49.3%) distribution. The most common etiologies were tuberculoma (43.1%), neurocysticercosis (27.9%), meningitis (10.1%), and metastasis (3.7%). Lesions predominantly involved the parietal and frontal lobes, with tuberculomas and neurocysticercosis showing strong predilection for these sites. Advanced MRI features such as restricted diffusion in abscesses and lipid–lactate peaks in tuberculomas were crucial differentiators.

Conclusion: Infectious causes continue to dominate the spectrum of RELs in India, unlike Western countries where neoplasms predominate. Radiological features, particularly advanced MRI, play a pivotal role in differential diagnosis and guiding therapy. Public health measures targeting tuberculosis and neurocysticercosis remain essential, supported by serological and molecular tools is vital for accurate differentiation, guiding therapy, and reducing unnecessary invasive procedures.

119. A Rare Case of co-infection in lung: Echinococcus species and Aspergillus species in a Diabetic female.

Author: Vidushi Singh

Co-Authors: Rungmei S K Marak, Tasneem Siddique, Aparna, Alok Nath

Institute: Sanjay Gandhi Post-Graduate Institute of Medical Sciences (SGPGIMS) Lucknow UP India.

Introduction: Echinococcosis is a parasitic disease caused by the larval stage of tapeworm of the genus *Echinococcus* which is mainly seen in animals. Humans are the accidental hosts where the ingestion of eggs of *E. granulosus* develops into the larval stages of the disease called Hydatid disease. It is globally prevalent but is endemic in most underdeveloped regions including India. *Aspergillus*, saprophytic mold is widespread in the environment; its spores are easily inhaled. Pulmonary *Aspergillosis* is a presentation in mostly immunocompromised patients. Here I will present a rare case of coexistence of pulmonary aspergillosis with *echinococcosis*.

Case presentation: A 57-year-old female patient presented to the pulmonary OPD with chief complaints of breathlessness, cough with expectoration, hemoptysis, fatigue for 6 months. The patient was diabetic and is on oral-glycemic drugs, non-hypertensive. Patient had pulmonary tuberculosis 2 years back and took treatment for 6 months. Patient gave history of contact with cattles. Family history not significant CT (Chest) revealed consolidation (ground glass appearance), collapse with low density areas showing air foci within left upper lobe. Ultrasonography of the whole abdomen revealed few cysts with thin enhancing walls in liver.

10% KOH of Broncho-Alveolar Lavage revealed plenty septate fungal hyphae with acute angle branching with multiple hooklets of *Echinococcus species*. Gram stain also showed plenty pus cells, with multiple hooklets of *Echinococcus*. The fungal cultures were negative although Fungal PCR detected *Aspergillus flavus* species in BAL sample. Culture for bacteria and mycobacteria were sterile. Galactomanan levels, IgM ELISA for *Echinococcus* were raised. Tab Voriconazole and Albendazole were started and patient improved within 10 days of treatment.

Conclusion: Pulmonary Co-infections of parasites with fungal etiology are rarer findings but a high clinical suspicion is necessary to make a timely and correct diagnosis.

120. Beyond Bacteria and Viruses!! Decoding Diarrhea in Liver Transplant Recipient: A Case Study on Cryptosporidium

Author: Dr. Vikramjeet Singh

Co-Authors: Dr. Ashima Jamwal, Dr Awadhesh Kumar, Prof. Rungmei SK Marak

Institute: SGPGIMS, Lucknow

Introduction: Cryptosporidium species are coccidian protozoan parasites known to cause self-limiting diarrhea in immunocompetent individuals and chronic, potentially life-threatening diarrhea in immunocompromised hosts, such as organ transplant recipients. Early diagnosis and appropriate therapy are critical to mitigate morbidity in these patients.

Materials & Methods: We present a case of a post-living donor liver transplant recipient (modified right lobe graft, December 2024) who developed acute watery diarrhea with abdominal cramps on postoperative day 9. Stool microscopy, modified acid-fast staining (Kinyoun), and trichrome staining were negative for ova, cysts, and microsporidia. Clostridioides difficile toxin A & B testing and culture were also negative. However, BioFire® GI multiplex PCR panel detected Cryptosporidium spp. on December 31, 2024.

Results: Based on the molecular diagnosis, the patient was started on oral nitazoxanide 200 mg once daily for 14 days. He showed clinical improvement and was discharged on January 24, 2025 with stable vitals, tolerating full oral diet, and maintained on immunosuppressive therapy (wysolone, tacrolimus, cellcept), along with antihypertensive and insulin.

Conclusion: This case highlights the utility of multiplex molecular diagnostic tools in detecting fastidious enteric pathogens like Cryptosporidium in immunocompromised hosts, especially when conventional microscopy fails. Timely diagnosis and targeted therapy ensured a favorable outcome. Clinicians should maintain a high index of suspicion for Cryptosporidium in post-transplant patients presenting with diarrhoea, even in the absence of classic microscopic findings.

**Others (HIV, Medical Education,
AI) Abstracts**

121. Role of Environmental Surveillance in Infection Control in Integral Medical College in Lucknow

Author: Dr. Abhinav Gautam

Co-Authors: Dr. Noor Jahan, Dr Shweta Kumari

Institute: Integral Institute of Medical Sciences, Lucknow

Introduction: The hospital environment can serve as a significant source of microorganisms implicated in healthcare-associated infections (HAIs), especially in critical care settings. Environmental surveillance plays an important role in identifying contamination at an early stage and guiding focused infection control measures.

Materials & Methods: A six-month prospective observational study was carried out in intensive care units, operation theatres, and neonatal care areas. A total 180 environmental samples were obtained from frequently touched surfaces, medical equipment, air, and water sources following standard microbiological procedures. Isolates were identified using conventional methods, and antimicrobial susceptibility testing was performed according to standard guidelines. Corrective infection control interventions were implemented, followed by repeat environmental sampling.

Results: Microbial growth was detected in 46 of 180 samples (25.5%). Gram-negative bacilli accounted for the majority of isolates (52%), followed by coagulase-negative staphylococci (30%) and *Staphylococcus aureus* (18%). *Acinetobacter* species and *Pseudomonas aeruginosa* were commonly recovered from ICU surfaces and sink areas. After strengthening cleaning protocols, improving equipment disinfection, and reinforcing staff training, repeat sampling demonstrated a reduction in contamination from 25.5% to 11.2%.

Conclusion: Environmental surveillance serves as an effective supportive tool for infection control programs in tertiary care hospitals. A risk-based approach targeting high-risk areas facilitates early detection of potential environmental sources of infection and helps minimize contamination. Regular, focused surveillance can play a key role in reducing HAIs and improving patient safety.

122. Impact of Proper Hygiene on Antibiotic Duration in General Medicine Wards in Integral Institute of Medical Science & Research

Author: Dr. Patel Kirmi Shailesh Kumar

Co-Authors: Dr. R K Khare

Institute: Integral Institute of Medical Sciences, Lucknow

Introduction: Antimicrobial resistance is an increasing global concern, largely driven by inappropriate and prolonged use of antibiotics. While antibiotics remain the cornerstone of infection management, supportive measures such as proper hygiene and infection-control practices significantly influence patient outcomes. Effective hygiene reduces environmental contamination and transmission of pathogens, thereby improving treatment response and potentially shortening the required duration of antibiotic therapy.

Materials & Methods: This observational assessment was carried out in a general medicine ward where enhanced hygiene measures were consistently practiced. These included strict hand hygiene, regular disinfection of patient surroundings, aseptic management of intravenous lines and urinary catheters, proper wound care, and adherence to respiratory hygiene. Patients admitted with uncomplicated infections such as community-acquired pneumonia, urinary tract infections, and skin and soft tissue infections were evaluated. Clinical status, including temperature trends, symptom resolution, and vital parameters, was monitored daily. Antibiotic therapy was reassessed after 72 hours based on clinical response.

Results: A majority of patients demonstrated noticeable clinical improvement within 48 to 72 hours. Early resolution of fever, improvement in presenting symptoms, and hemodynamic stability were commonly observed. Due to reduced chances of cross-infection and secondary hospital-acquired infections, antibiotics could be discontinued after a shorter duration of three days in several cases, without evidence of clinical deterioration or relapse during hospitalization.

Conclusion: Maintaining proper hygiene serves as a crucial non-pharmacological intervention in infection management. By lowering infection burden and supporting faster recovery, it enables judicious use of antibiotics, reduces unnecessary prolongation of therapy, and contributes to effective antimicrobial stewardship.

123. The Emergence of Agentic AI as a Diagnostic Partner in Clinical Microbiology

Author: Dr. Meenakshi Singh

Co-Authors: LT. (Dr.) Reena Sachan, Dr. Garima Gaur, Dr. Anjali

Institute: Moti Lal Nehru Medical College Prayagraj, U.P

Introduction: As of 2026, clinical microbiology laboratories face unprecedented pressures from rising sample volumes and a global shortage of specialized personnel. Traditional diagnostic workflows, while reliable, are often hindered by lengthy turnaround times (24–72 hours) and manual interpretation risks. This study explores the transformative role of Artificial Intelligence (AI) — transitioning from simple decision-support tools to "Agentic AI" diagnostic partners — in accelerating pathogen identification and precision treatment.

Materials & Methods: We evaluated the integration of deep learning (DL) and machine learning (ML) models across three core diagnostic pillars:

Automated Image Analysis: Using Convolutional Neural Networks (CNNs) for real-time Gram stain interpretation and colony morphology recognition.

Rapid Molecular Interpretation: Applying ML to analyze complex Next-Generation Sequencing (NGS) and MALDI-TOF MS datasets.

Predictive Antimicrobial Susceptibility Testing (AST): Utilizing genomic-based models to forecast phenotypic resistance before traditional growth-based results are available.

Results: Current AI-driven platforms demonstrate identification accuracies exceeding 95% in under 5 minutes for common pathogens such as *E. coli* and *S. aureus*. In 2026, agentic AI solutions have shown the capacity to autonomously trigger reflex testing and flag high-risk multi-drug resistant (MDR) cases for immediate clinical review, reducing time-to-effective-therapy by an average of 12–18 hours. Furthermore, integrated systems like APAS Independence and Pheno MATRIX have achieved over 99% agreement with human experts in excluding negative cultures, significantly reducing the manual workload.

Conclusion: AI has evolved into an essential diagnostic collaborator in the modern microbiology laboratory. By providing "super-speed" identification and "super-prediction" of resistance, AI enables a shift from reactive to proactive infectious disease management. Future implementation must prioritize robust data governance and "explainable AI" to ensure these tools remain safe, transparent, and ethically integrated into patient care.

124. AI as the New Study Partner: Evaluating Generative AI for Self-Directed Learning in Medical Microbiology

Author: Dr. Roshni Agarwal

Co-Authors: Dr. Amit Kumar, Dr. Shweta Sharma, Dr. Vaibhav Agarwal

Institute: Autonomous State Medical College Kanpur Dehat

Introduction: Self-Directed Learning (SDL) is vital for medical students, especially with the shift toward Competency-Based Medical Education (CBME). Generative AI (GenAI) offers new avenues to enhance SDL, yet its impact on content quality and efficiency remains under-explored.

Materials & Methods: This pre-post interventional study involved 83 second-year MBBS students (N=83). Participants first completed a traditional SDL assignment (Assignment 1) using textbooks. Following a training session on a structured "Stepwise Prompting Workflow," they completed a second assignment (Assignment 2) using AI tools like ChatGPT. Outcomes were measured using a validated 10-item rubric (scored 0–20), time logs, and feedback surveys.

Results: AI integration led to a transformative improvement in academic performance. Mean rubric scores rose from 57.1% (Traditional) to 86.2% (AI-assisted) ($p < 0.001$), with a huge effect size (Cohen's $d = 2.8$). Efficiency also improved significantly, with the average completion time dropping by 43% (from 44.5 to 25.4 minutes). Inter-rater reliability was excellent (ICC = 0.92). While 92% of students praised the speed of synthesis, 85% verified AI outputs with standard textbooks, reflecting a healthy skepticism regarding accuracy.

Conclusion: AI-integrated SDL significantly boosts the quality and efficiency of medical student learning. The results advocate for a "Human-in-the-Loop" approach, where AI acts as a sophisticated co-pilot. Formal training in "AI literacy" and verification skills is essential to maximize benefits while mitigating risks like hallucinations.

125. From Training to the Trenches: Evaluating the professional readiness of postgraduate residents in Microbiology

Author: Dr. Pranshu Pandey

Co-Authors: Dr. Rajesh Kumar Verma

Institute: Uttar Pradesh University of Medical Sciences, Saifai, Etawah, UP

Introduction: Professional readiness constitutes the fusion of requisite skills and psychological preparedness necessary to execute industry-specific responsibilities effectively. The National Medical Commission (NMC) has introduced a refined competency-based postgraduate curriculum across all specialties, incorporating 360-degree training for future professionals. However, during residency training, the primary focus remains on academic proficiency, often leaving the nuances of "micromanagement" and administrative leadership unaddressed. Consequently, early-career professionals may struggle to navigate the diverse administrative and logistical responsibilities encountered in the field.

Materials & Methods: A questionnaire-based cross-sectional study was conducted. Data were collected via Google Forms from young microbiologists currently serving as Senior Residents or Junior Faculty at various medical colleges. The primary comparative analysis focused on the experiences of professionals working in rural versus urban settings. Responses were compiled in Microsoft Excel and analysed for various outcomes.

Results: Around 35 valid responses were recorded with male to female ratio of 1.9:1. Among the responders, 22 are currently posted as Assistant Professor while 13 as senior resident. About 34% (n=12) responders are currently working in rural areas while rest (n=23) in urban area. Majority of responders were from State Autonomous colleges 58% (n=7) among rural workplace. The completeness of faculty was partial in majority of rural workplace while it was mostly complete in urban workplaces (50% and 61% respectively). Almost similar responses towards somewhat trained to not at all trained in micromanaging laboratory were recorded from Microbiology professionals in urban and rural workplaces (70% and 75% respectively). Around 67% of Microbiologists have been given extra administrative responsibilities other than their departments in rural colleges.

Conclusion: Young microbiologist being posted to places with no to partial faculty have a big responsibility on their shoulders where they have to multitask between setting up laboratory, teaching MBBS graduates and also deliver to extra administrative responsibilities and with little to no exposure to these logistical obligations during the residency program, the professional hardships just increase exponentially.

Glimpse of Microbiology Department of SGPGIMS

Established on: **1st May 1988**

Founding faculty: **Prof. A. Ayyagari and Late Prof. (Dr) TN Dhole**

Current Faculty: **Eleven in number**

Vision

- **Patient care** - through diagnosis of infectious diseases. To enhance our reputation as a world class diagnostic, teaching and research institution and make our Department a Centre of Excellence.
- **Teaching and Training** - conducting routine classes with new updates in field of infectious diseases. We aspire to maintain highest academic standards offered to our students and quality of support as well as professional ethics.
- **Research** - Initiating and conducting innovative research works in the department. We aim to continuously enhance our clinical capabilities and contribute to scientific breakthroughs. More than 20 Crore projects has been completed in department.

Courses Offered

- MD Microbiology: 6 seats per year
- PDCC (Infectious Diseases): 2 seats per year
- MSc Medical Virology: 6 per year
- PhD: 5 per year
- Apart from this, observership and internship of students from different universities
- Student: Mentor ratio = 14:11 = 1:1

Important Landmarks

- The department was first to start **PDCC (Infectious Diseases)** course in India and one of few centers running **MSc (Medical Virology)**.
- Department is recognized as **WHO National Surveillance for Polio, Measles & Rubella** in the States of UP & Bihar and takes important steps for maintenance of mild and vaccine strains of polio isolated from the states. The laboratory has contributed the most for the elimination of polio in Northern India.
- First center in UP to start automated **MIC testing for bacteria and MALDI-TOF MS for microbial pathogen identification**.
- The department offers facility for diagnosis of **opportunistic and invasive fungal pathogens**.
- The department offers for the detection of **opportunistic coccidian & other parasitic infections in automated panels**.
- Established **BSL-3 for TB** advanced diagnosis and anti-tubercular drug susceptibility testing in 2024.
- One of pioneer center to start **viral culture** techniques.
- The Virology laboratory is well equipped for the viral diagnostic services including tissue culture PCR/Real time PCR for **endemic arboviruses**.
- In 2023, Department Health Research (DHR) & ICMR, New Delhi selected Department of Microbiology, SGPGIMS, Lucknow for establishing new **“Viral Research and Diagnostic Laboratory (VRDL Lab)”**
- Recent CSR grant from IOCL for **establishing Illumina NGS platform** with Deeplex Myc TB kit for Centre of Excellence in Tuberculosis.

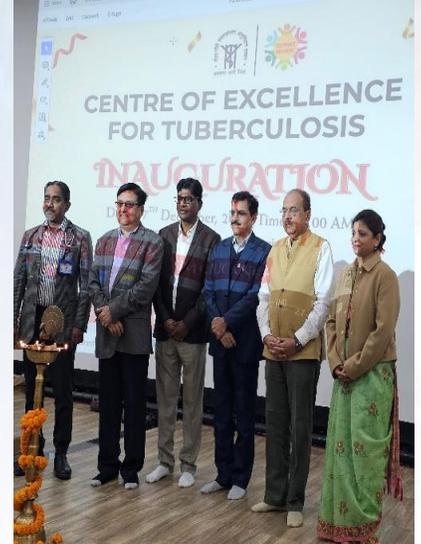
Glimpse of Microbiology Department of



New Mycology Laboratory



First Ever National PG Assembly for MD Students in Uttar Pradesh in Microbiology in



Inauguration of BSL-3 Lab for TB



Diagnostic Stewardship Lab for AST



Walkathon on World HIV Day 2023



Diagnostic Stewardship Lab for Bacterial and Fungal Identification



Department of Virology conducted Two National training Workshop for faculty and residents in 2025



37th Foundation Day, 5th May 2025



DHR ICMR Team, VRDL Laboratory



Our Education Partners



For use of registered medical practitioners, hospitals & laboratories only
CORE DIAGNOSTICS

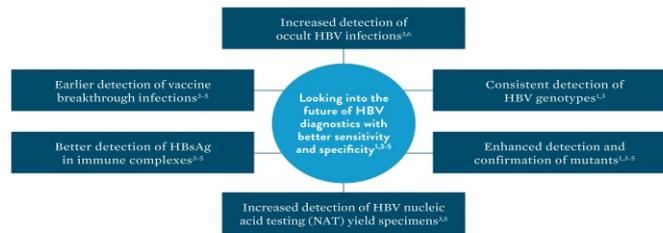
HBsAg NEXT SOLUTION

Delivering Enhanced Detection of HBV to Help Improve Healthcare Outcomes

HEPATITIS B VIRUS (HBV) DIAGNOSTIC CHALLENGES

- Substitution and insertion mutants are constantly evolving within hepatitis B surface antigen (HBsAg) and continue to challenge laboratory tests.¹
- High-risk groups (e.g., immunocompromised patients with occult HBV infection) require the highest level of HBsAg assay performance because HBV reactivation can be fatal.²

WHAT IF YOU COULD PUSH THE LIMITS OF HBV DIAGNOSTICS IN YOUR HEALTHCARE SYSTEM?



INTRODUCING THE NEXT GENERATION OF HBV DIAGNOSTICS

Abbott's HBsAg Next Qualitative solution offers enhanced detection of HBV infection to help improve patient outcomes and maintain safe blood supplies.



CORELABORATORY.ABBOTT

INTENDED USE^{3,7,8,9}

The HBsAg Next Qualitative assay is a chemiluminescent microparticle immunoassay (CMIA) for the qualitative detection of HBsAg in human serum and plasma, including specimens collected post-mortem (non-heart-beating), on the Alinity i and ARCHITECT Systems.

The HBsAg Next Qualitative assay is intended to be used as an aid in the diagnosis of HBV infection and as a screening test to prevent transmission of HBV to recipients of blood, blood components, cells, tissue and organs.

For the confirmation of samples found to be repeatedly reactive by HBsAg Next Qualitative, use HBsAg Next Confirmatory.

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 Modular product design with individual components for specific detection of viral and bacterial targets

AltoStar® real-time PCR solutions
 Modular product design with individual components for specific detection of viral and bacterial targets

RealStar® real-time PCR solutions
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Free combination of any FlexStar® RT-PCR Detection Mix 1.5 with the FlexStar® RT-PCR Amplification Mix 1.5

Multiplex Rapid Open Kits Compatible Across All Thermal Cyclers

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AUTOMATED TESTING FOR HEPATITIS A, B, C, D AND E VIRUS

Hepatitis Portfolio:
Viral load monitoring on high performance level:

	AltoStar® HAV RT-PCR kit 1.0	AltoStar® HBV PCR kit 1.5	AltoStar® HCV RT-PCR kit 1.5	RealStar® HDV RT-PCR kit 1.0	RealStar® HEV RT-PCR kit 2.0
Sample Volume	1000µl	1000µl	1000µl	1000µl	1000µl
Genotypes detected	All	HBV genotypes A to H	HCV genotypes 1 to 6	HDV RNA of all eight clades	HEV genotypes 1 to 3
Analytical Specificity	≥99%	≥99%	≥99%	≥99%	≥99%
Limit of detection	8.31 IU/mL (95% confidence interval: 4.17 - 11.99 IU/mL)	10.2 IU/mL (95% confidence interval: 7.8 - 15.8 IU/mL)	11.1 IU/mL (95% confidence interval: 7.8 - 18.5 IU/mL)	9.48 x10 ³ IU/L	0.20 IU/mL (95% confidence interval: 0.12 - 0.45 IU/mL)
Linear range	20 - 10,000,000 IU/mL	25 - 10,000,000 IU/mL	4x10 ³ to 4x10 ⁷ IU/L	1 to 10,000,000 IU/L	
Order no.	AS0211543	AS0211513	AS0211513	401003	272013
Box	96 RDN	96 RDN	96 RDN	96 RDN	96 RDN
Type of kit	Qualitative	Qualitative + Quantitative	Qualitative + Quantitative	Qualitative + Quantitative	Qualitative + Quantitative
NBSC Traceability	2nd and 3rd WHO standard, NBSC 05062 and 15276	4th WHO standard, NBSC 10266	5th WHO standard, NBSC 14150	1st WHO standard, NBSC	1st WHO standard, PEI K23910

RealStar®/ AltoStar® real-time PCR kits

Real-time PCR kits for the detection of :

Human adenovirus, herpesviruses and polyomaviruses

- Human adenovirus (quantitative)
- Cytomegalovirus (quantitative)
- Epstein-Barr virus (quantitative)
- Human herpesvirus 6A and 6B (quantitative)
- Herpes simplex virus 1 and 2 (quantitative)
- Varicella-zoster virus (quantitative)
- HSV-1 and HSV-2 and VZV
- BK virus (quantitative)
- JC virus (quantitative)

Enteric viruses and bacteria

- Human adenovirus
- Norovirus genotype I and II
- Rotavirus
- Clostridium difficile toxin A and B
- EHEC (Shiga toxin 1 and Shiga toxin 2 and ipaH)

Tropical and other viruses, bacteria and parasites

- Crimson-Congo haemorrhagic fever virus
- Trypanosoma cruzi
- Chikungunya virus
- Dengue virus
- Filovirus and Ebola virus
- Lassa virus
- Rift Valley fever virus
- West Nile virus
- Yellow fever virus
- Zika virus
- Malaria (Plasmodium species)
- Dengue serotyping (1-4)
- Malaria serotyping (P. malariae, P. ovale, P. knowlesi, P. vivax, and P. falciparum)
- Chagas
- Hantavirus
- Orthoreovirus
- Zoonotic Orthoreovirus

Respiratory viruses, bacteria and fungi

- Human adenovirus
- Enterovirus and rhinovirus
- Human influenza A and B and swine flu (H1N1)
- Human influenza A and B
- Middle East respiratory syndrome coronavirus (MERS-CoV)
- Severe acute respiratory syndrome coronavirus (SARS-CoV-2)
- Human metapneumovirus A and B
- Human parainfluenza virus 1 - 4
- Respiratory syncytial virus A and B
- Bordetella pertussis and Bordetella parapertussis
- Pneumocystis jirovecii

Blood borne viruses

- Hepatitis A virus (quantitative)
- Hepatitis B virus (quantitative)
- Hepatitis C virus (quantitative)
- Hepatitis D virus (quantitative)
- HIV 1 (quantitative)
- HIV 2 (quantitative)
- Hepatitis E virus (quantitative)
- Parvovirus B19 (quantitative)

AltoStar® Automation

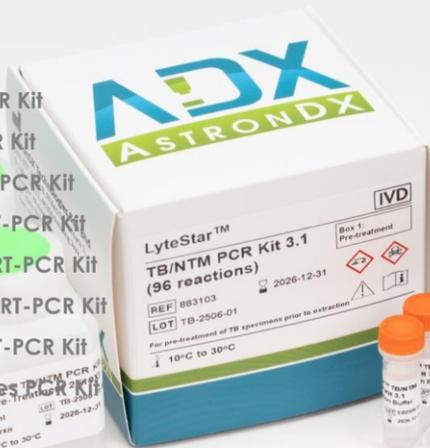
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DermaGenius® 3.0 Complete

Multiplex real-time PCR kit

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DermaGenius® 2.0 Complete

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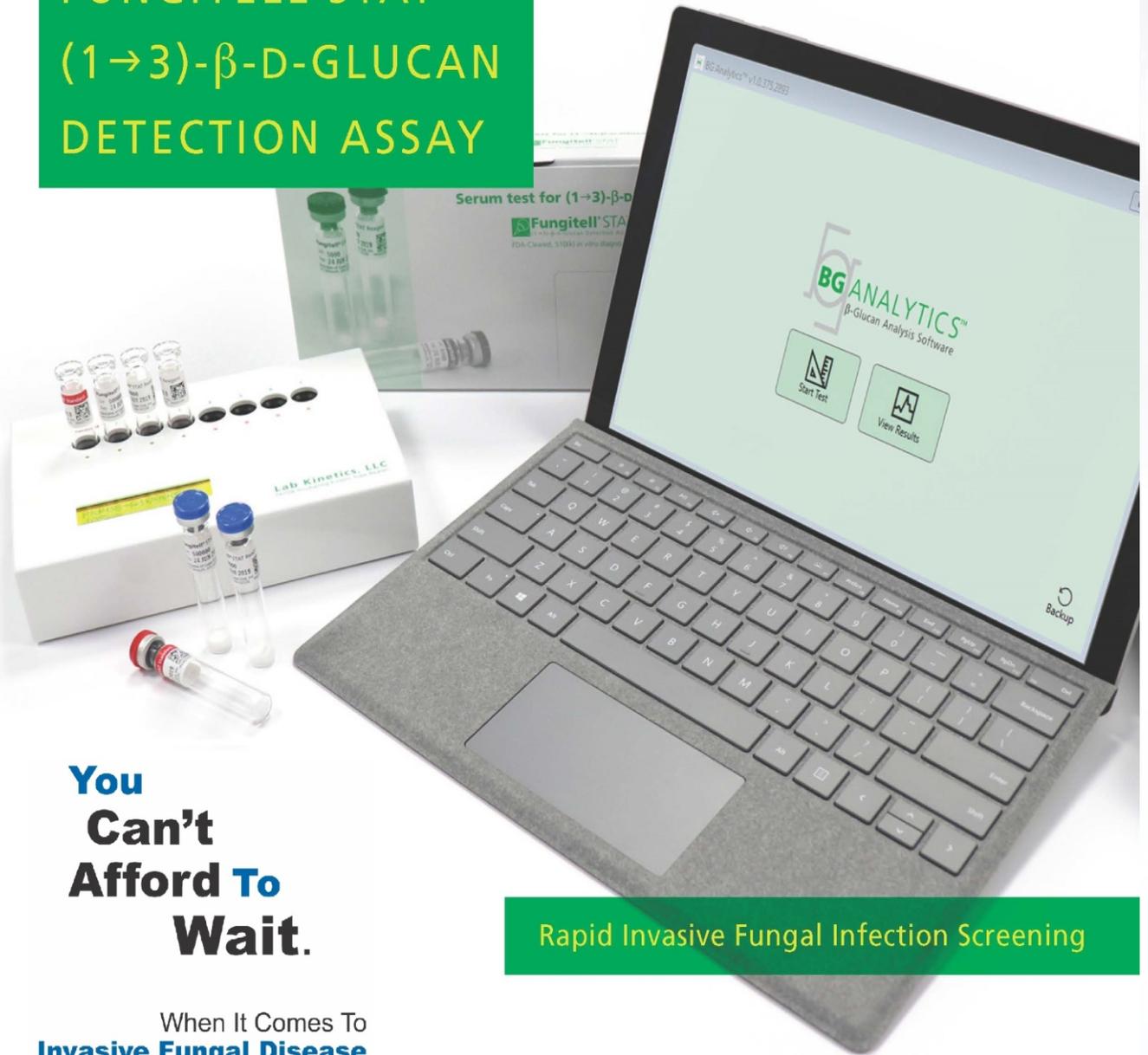
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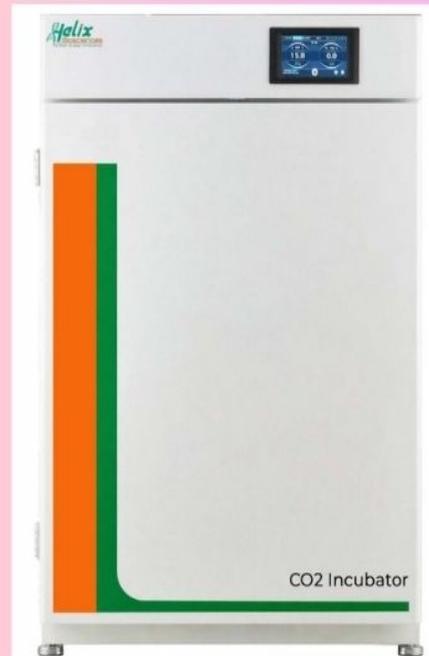
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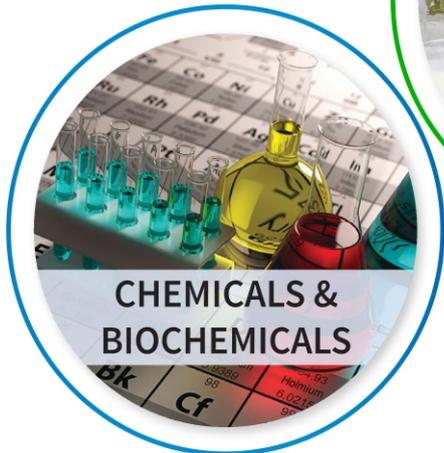
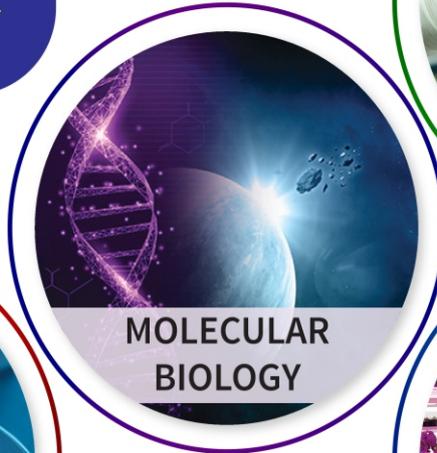
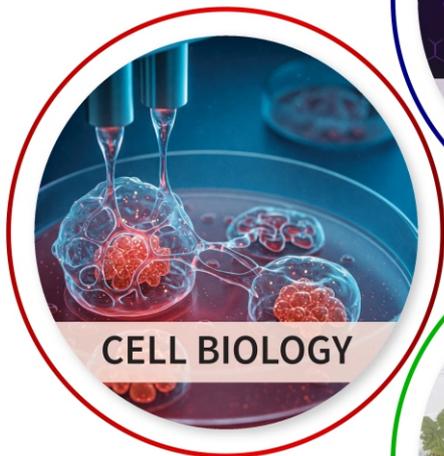
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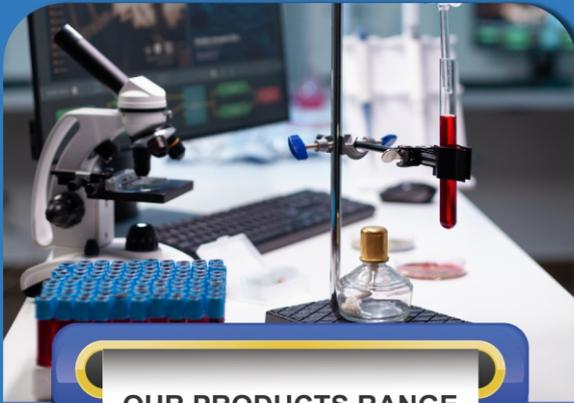
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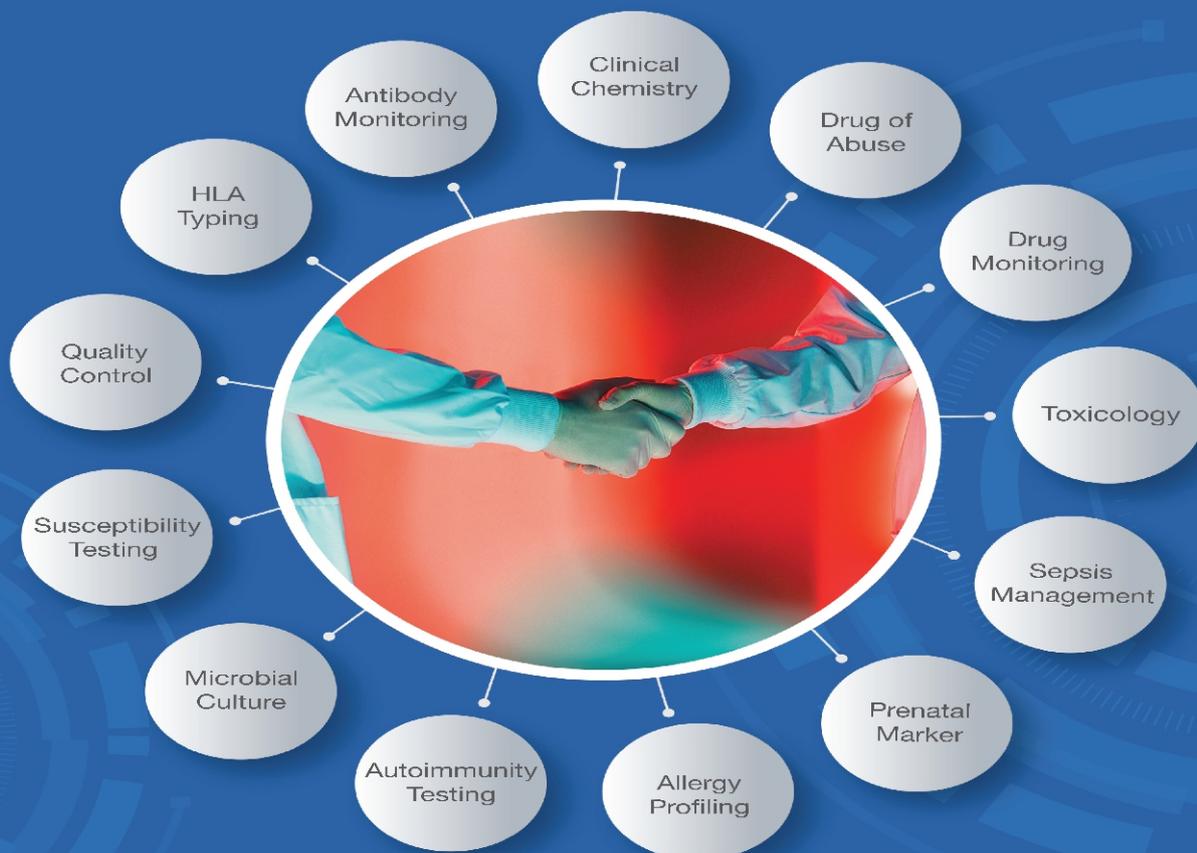
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HLA: Human leukocyte antigen.

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