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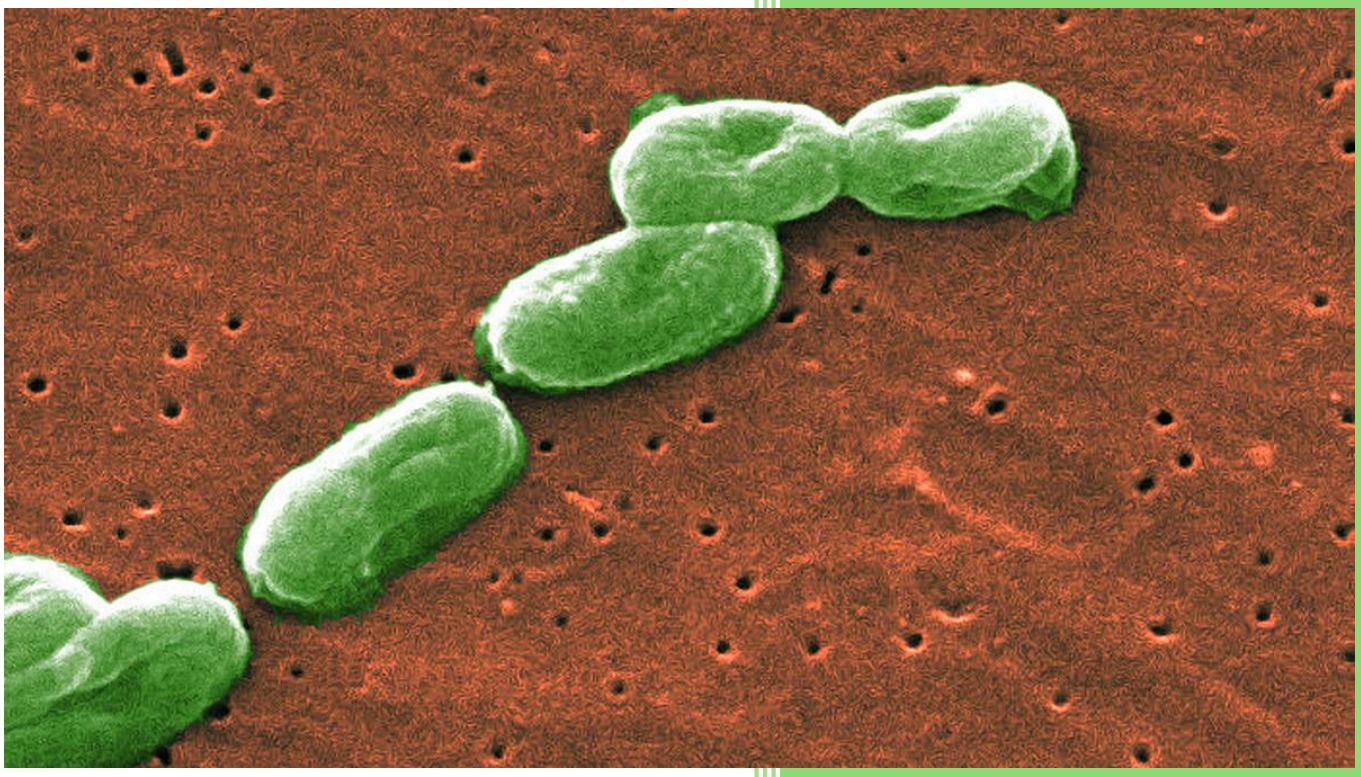
INDIAN ASSOCIATION OF MEDICAL MICROBIOLOGISTS – TELANGANA & ANDHRA PRADESH COMBINED CHAPTER (IAMM-TAPC CHAPTER)



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FROM THE PRESIDENT IAMM-TAPC CHAPTER

Dated:29.09.2025

Dr. B. Venkat Rao MD
Professor, President, IAMM TAPC Chapter

Dear Friends and Colleagues,

It gives me great pleasure to share that our E-bulletin is progressing excellently, keeping us updated with recent advancements in Microbiology and research-oriented articles. Our Association's Executive Committee has been working diligently, holding regular Zoom meetings to plan CMEs and upcoming conferences. I am happy to note that our association has successfully negotiated with both the Andhra Pradesh and Telangana State Medical Councils, for granting CME Credit hours

The Executive Committee of TAPC has also been successfully organizing webinars for the benefit of budding microbiologists. I extend my heartfelt gratitude to our Secretary - Dr. Vijendra Kawle, our Joint Secretary - Dr. M. Shabnum, our Dynamic Treasurer - Dr. A. Kishore, and Executive members – P. Sireesha, Dr. Dhanashree P. Inamdar, Dr. Mallika N., Dr. B. Sreekanth Reddy, Dr. B. Ankita for their outstanding efforts in organizing various academic activities under IAMM TAPC.

It is my privilege to warmly welcome all delegates and dignitaries to the **XXVIII IAMM TAPC Annual State Conference 2025**, being hosted by the Department of Microbiology, NIIMS, Hyderabad, on **11th and 12th October 2025**. The conference will be preceded by **13 pre-conference workshops** across diverse areas on **9th and 10th October 2025**, designed to benefit young microbiologists.

I am confident that this conference and its workshops will be power-packed with meaningful deliberations, inspiring our younger faculty and postgraduate students. The chosen theme, **"Modern Clinical Microbiology: Challenges, Opportunities, and Solutions,"** will shed light on many important yet less-explored aspects of our field.

I extend my best wishes to the dynamic organizing team, ably led by **Dr. P. Umabala, Organising Chairperson**, and **Dr. Neelima Sudharshan, Organising Secretary**. I wish all delegates a pleasant and memorable stay in Hyderabad, and I sincerely hope the conference will be a grand success.

Dr. B. Venkat Rao,
President IAMM-TAPC Chapter

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SECRETARY'S MESSAGE

Dr. K VIJENDRA
Secretary, IAMM-TAPC Chapter,
Consultant Microbiologist, Rainbow Children's Hospital,
Hyderabad, Telangana

It gives me immense pleasure to present this edition of the official e-bulletin of Indian Association Of Medical Microbiologists, Telangana and Andhra Pradesh Combined Chapter. It brings together an outstanding compilation of articles addressing current challenges and advances in microbiology and infectious diseases. The issue features an impressive line-up of experts covering updates on antimicrobial resistance, gut and vaginal microbiome, novel vaccine systems, challenges in Mycology and emerging/re-emerging infections and closing with the fascinating use of artificial intelligence in Microbiology. On behalf of the Executive council and all members of IAMM TAPC, I sincerely thank the distinguished contributors for their time, expertise and commitment. I am confident this e-bulletin will be an engaging and thought-provoking read for all our members.

It has been an immensely fulfilling year serving as the Secretary of IAMM TAPC. I am glad to share that the association continues to grow in strength and reach, with 226 new life and postgraduate members added since September 2024. This takes our total membership to over 1,000—a remarkable milestone that reflects the hard work and outreach of Executive council. The IAMM TAPC association is now registered with the Telangana and AP state medical councils for CME/CPD programs and all members can utilize the facility of availing credit points for their CME/conferences easily by applying for the same through the association. The EC has hosted the IAMM TAPC webinar series with online lectures by eminent senior faculty from the two states and also from national institutes. The online sessions were well received with attendance of over 100 participants for most lectures. In addition, the association's adoption of the Kahoot online quiz platform for use by members has added an interactive dimension to academic activities, especially among postgraduate students.

This year also marks a transition in the office of the Treasurer. The Executive council and all members of the IAMM TAPC association extend heartfelt gratitude to Dr. Kishore Sir, whose tenure witnessed not only a successful membership drive but also meticulous financial stewardship. Under his guidance, the association's accounts were maintained transparently,

with prudent investments ensuring steady financial growth. His contributions have left a lasting impact, and he will be deeply missed in the EC. We warmly welcome Dr. Sreekanth as the incoming Treasurer and look forward to continued excellence.

My sincere thanks to all senior faculty in the EC- President Venkata Rao sir, Vice president Uma Bala madam, Ex President Ranganathan Iyer sir, Ex Secretary Khaleel sir, Treasurer Kishore sir, Jt. secretary Dr. Shabnum and EC members Dr. Sireesha, Dr. Dhanashree, Dr. Ankitha, Dr Sreekanth and Dr Mallika for their support and valuable contribution throughout the year along with the conduct of PG pedagogue, journal critical review and the official News bulletin.

I congratulate and extend my gratitude to Uma Bala madam, Neelima madam and every member of organizing team from NIMS for hosting the XXVIII IAMM TAPC Annual Conference 2025 from October 10-12,2025. The theme of this conference, “Modern Clinical Microbiology: Challenges, Opportunities and Solutions,” is aptly reflected in the thoughtfully structured scientific program. The sessions are designed to highlight both core foundations and cutting-edge advancements, from evolving diagnostic techniques to antimicrobial stewardship, autoimmunity, invasive fungal infections, emerging viral threats and TB elimination strategies. The thoughtfully chosen guest lectures also explore the future of Microbiology, spanning career pathways, artificial intelligence in diagnostics, post-graduate training and GIS-based diagnostic networks. I am sure all delegates will find this meeting enriching and memorable. Looking forward to meet you all in Hyderabad. Thank you.

Dr Vijendra Kawle
Secretary IAMM TAPC,
Consultant Clinical Microbiology,
Rainbow Children's Hospitals, Hyderabad.

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XXVII IAMM-TAPC ANNUAL STATE CONFERENCE 2024


XXVII IAMM TAPC STATE CHAPTER
CONFERENCE - 2024

IAMM TAPC Chapter WEBINAR SERIES – II

(October 2024 to September 2025)

12th official webinar of the IAMM TAPC Chapter.

Date: **15th November 2024**

Time: 7pm-8pm

Topic: **What's New in TB! : Recent Advances in Mycobacteriology.**

Speaker: **Dr. V. Lakshmi**
Professor, Dept. of Microbiology,
Kamineni Academy of Medical Sciences & Research Center,
Hyderabad

13th official webinar of the IAMM TAPC Chapter.

Date: **10th December 2024**

Time: 6.30pm-7.30pm

Topic: **Ocular infections: Current perspectives and future directions.**

Speaker: **Dr. S. Lalitha Prajna,**
Director Laboratory Services,
Consultant Microbiology and Ophthalmology,
Aravind Eye Hospital, Madurai.

14th official webinar of the IAMM TAPC Chapter.

Date: **8th February 2025**

Time: 7pm-8pm

Topic: **Congenital Viral infections**

Speaker: Dr. Usha Kalawat
Principal & Professor & Head,
Department of Clinical Virology, SVIMS, Tirupati

15th official webinar of the IAMM TAPC Chapter.

Date: **1st April 2025**

Time: 7pm-8pm

Topic: **The Complement System and it's Clinical Relevance**

Speaker: Dr. Shiva Priya Eswaran
Senior Consultant and HOD Microbiology,
KIMS Secunderabad.

16th official webinar of the IAMM TAPC Chapter.

Date: **30th September 2025**

Time: 7pm-8pm

Topic: **From Sepsis to Survival: Getting Empirical Therapy Right In Intensive Care Units**

Speaker: **Dr. Mohammed Khaleel**
Vice Principal (Academics)
Professor & HOD, Microbiology
Mahavir Institute of Medical Sciences, Vikarabad, Telangana

ARTICLES

1. **2023 ICMR AMR Data: Wrong Directions from Armchair Analysis by Non-Medical Scientists. - Dr Sumit Rai,** Prof and Head; Dept of Clinical Microbiology, AIIMS Mangalagiri
2. **Role Of Vaginal Microbiome in Urinary Tract Infections – Dr. Jyothi Lakshmi,** Professor and Head, Department of Microbiology, Jangoan, Telangana
3. **The Changing Landscape of Emerging and Re-Emerging Infectious Diseases: A One Health Perspective - Dr. Lakshmi Jyothi T,** Additional professor, Department of Microbiology, AIIMS Bibinagar, Telangana
4. **Novel Vaccine Development and Delivery Systems - Dr. Animireddy Kishore,** Professor, Department of Microbiology, Apollo Institute of Medical Sciences and Research, Chittoor
5. **Infection Control Practices in ICU Settings - Dr Jaya Banerjee,** Sr consultant Microbiologist and IPCO, Yashoda Hospital, Secunderabad
6. **Gut Microbiome: In Health and Disease - Key Insights - Dr.D.S.Murty,** Professor of Microbiology, Sri Venkateswara Medical College, Tirupati, A.P.

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Article 1

2023 ICMR AMR Data: Wrong Directions from Armchair Analysis by Non-Medical Scientists.

Editorial: **Dr Sumit Rai,** Prof and Head; Dept of Clinical Microbiology, AIIMS Mangalagiri

The Indian Council of Medical Research (ICMR) has been presenting AMR data through the Antimicrobial Resistance Research & Surveillance Network (AMRSN) for over ten years now. The data is collected and collated to showcase drug resistance (unlike antibiogram data that is presented as susceptibility data) observed in six pathogenic groups on AMR. One must understand that this is point prevalence analysis of data, that's been labelled as surveillance. This should not be confused with the CDC NHSN based hospital acquired infection surveillance. Data collected from the network is used to track resistance trends and to observe any unusual resistance pattern. ICMR also presents this data with the disclaimer to not to extrapolate the data to community settings as it represents data from tertiary care hospitals. However, at the same time it gives a contradictory statement that the report "should guide the prevention and treatment interventions for AMR in the country" **[1]**

Unfortunately, the seventh detailed report from the ICMR AMR surveillance network that presents data from January 1st 2023 to December 2023 is quite peculiar and this is the report that is centric to this editorial. We shall be specifically referring to the text and tables mentioned in this report **[2]**. Some statements are encouraging, while some are controversial and should not be taken to the bench side in the clinical microbiology labs or bedside from the armchair analysis point of view of ICMR.

1. The ICMR Annual Report [January 2-23 to December 2023] recommends "*Colistin or fosfomycin based combination strategy would be the best alternative for the treating MBL or DTR P. aeruginosa infection*". This seems to be quite an intuitive comment undermining the clinical implications of such statements, as Fosfomycin is not recommended against Pseudomonas aeruginosa as per the CLSI, EUCAST and Stanford guidelines **[3, 4, 5]**.

However, in the very same section, the report discourages the use of Linezolid for MRSA as it's an important anti TB drug in out country.

2. An encouraging statement is the use of oral drugs like Cotrimoxazole and Azithromycin for Enteric fever instead of opting in for 3rd generation cephalosporins and strongly discouraging the use of carbapenems for Enteric fever.
3. Among the key takeaways for Interpretations of common syndromic isolates and implications in clinical practice, ICMR recommends the use *"oral Fosfomycin and oral nitrofurantoin may be used to treat cystitis"*. Does this indicate combination oral therapy for treatment of cystitis? Similarly, a combination therapy of *"IV Amikacin and IV Ertapenem may be used to treat upper UTI or patient presenting with fever and urinary symptoms"*. Again, does it imply the same. One needs to tread carefully after encountering such a statement.
4. Non typhoidal Salmonella are like any other isolates of Enterobacterales in stool specimens; and to project Imipenem, Chloramphenicol and Azithromycin susceptibility implies treatment of diarrhoea caused by non-Typhoidal Salmonella with these drugs. To suggest *"oral azithromycin, trimethoprim / sulfamethoxazole and doxycycline are good options to treat bacterial diarrhoea for patients admitted in ward"* do not comply with the intended uses of these antibiotics. Even the off-label use of Azithromycin, cotrimoxazole and doxycycline, doesn't warrant its use as a treatment option for bacterial causes of diarrhoea, as suggested by this report.
5. Again, what classical textbooks, reference books on Clinical Microbiology and Infectious Diseases have always mentioned Pnemococcus, Streptococcus agalactiae, Neisseria meningitidis and E. coli as the commonest bacterial causes of meningitis, this report mentions *"Acinetobacter baumannii was the most common isolated organism followed by Klebsiella pneumoniae and Pseudomonas aeruginosa",* warranting first line use of colistin and minocycline. There have been no criteria to consider the clonality of the Acinetobacter isolates or to check their true pathogenicity. This is also tabulated in Table-2.5.
6. Presentation of Staphylococcus haemolyticus and Staphylococcus epidermidis data as pathogens again creates doubts on the authenticity of this data [Table-1.2, Table 2.2]. Without ruling out the true pathogenicity, data for Staphylococcus hominis has been presented as the most common organism isolated from blood cultures.

7. Table-1.26 enumerates isolation rates of diarrheagenic pathogens from non-faecal specimens. The clinical relevance of isolating Aeromonas from non-faecal specimens doesn't seem to have any clinical correlation whatsoever, or at least it's not been mentioned in the text.
8. Usually most common causes of diarrhoea are usually diarrheagenic E. coli, Shigella Vibrio or Campylobacter, but according to Table-1.25, *"The predominant species among diarrheal pathogens isolated from faeces sample identified was Non Typhoidal Salmonella (38.9%), followed by Aeromonas spp (28.0%), Escherichia coli Diarrheagenic (9.9%), Shigella (10.1%) and Vibrio cholerae (7.2%)"*. Non – Typhoidal Salmonella doesn't feature as the commonest cause of bacterial diarrhoeas in any of the standard textbooks, so this data may be moot.
9. Table-2.7 demonstrates susceptibility of E coli in blood to Fosfomycin, it needs to be highlighted that Fosfomycin has been strictly reserved only for the urinary isolates of E. coli and E. faecalis causing lower urinary tract infection **[3, 4, 5]**. While there are no breakpoints for non – urinary isolates of E. coli, EUCAST mentions that only for blood isolates of E. coli, with Fosfomycin MIC's of 8 ug/ml or below may be subjected to treatment with this drug. Without performing MIC based AST for Fosfomycin, its irrational to warrant its use in Non – Urinary isolates of E. coli. Similarly in Table-2.8, while majority centres have not performed or reported Fosfomycin susceptibility in Klebsiella pneumoniae in blood isolates, yet this ICMR report chose to publish this data, when the inherent presence of the FosA gene warrants this drug not to be tested or administered as treatment for K. pneumoniae.
10. In Table-2.10, the susceptibility of Ampicillin is more than that of 3rd generation cephalosporins (Cefotaxime and Ceftriaxone), which seems to be quite unpalatable. Seven and eight isolates from OPD and ward were non – susceptible to cefotaxime and twelve and seven isolates from OPD and ward were non – susceptible to ceftriaxone. While ESBL production has been reported from Typhoidal isolates of Salmonella, these 3GC resistant isolates do not find any mention about their ESBL status in the text.
11. In Table-2.12, again it's a universally proven fact that Nitrofurantoin doesn't act in alkaline urine which is produced by urease positive organisms like K. pneumoniae and that the

intrinsic presence of the FosA gene in K. pneumoniae doesn't warrant its use in urine, yet the data has been presented, which is misleading and deceptive.

12. In 2023, CLSI had removed the Gentamicin breakpoints from urinary isolates of Pseudomonas aeruginosa, yet the data is presented in Table-2.13. Since this report categorically states that it follows CLSI, this seems to counter the claim.
13. In Table-2.15, despite being clearly mentioned under CLSI M100 and EUCAST documents, Fosfomycin has been tested and reported in E. faecium. From the data it seems that most centres know this anomaly except maybe one centre but still, the data for only 7 isolates has been presented, which again violates the 30 isolates rule for cumulative antibiogram presentation by CLSI M39 **[6]**. Repeat anomalies for the use of Fosfomycin have been endorsed in this guideline even for the pus isolates of E. coli in Table-2.16, again this being known to most centres, yet data of 25 E. coli isolates has been presented. Similarly, Table-2.18 repeats the major error of Fosfomycin being used in K. pneumoniae and that too in pus and exudate isolates.
14. Regarding the data on Pseudomonas aeruginosa in Table 2.20, despite removal of Amikacin breakpoints from non – urinary isolates of P. aeruginosa and complete removal of all breakpoints of Gentamicin for all isolates of P. aeruginosa, in 2023 by CLSI, the ICMR still chose to present this despite admitting to adhere to CLSI guidelines as mentioned on page 75 as *"Susceptibility was tested following CLSI guidelines using disc diffusion or automated systems, except colistin, where a micro-broth dilution test was used"*. **[5]**.
15. CLSI clearly states that *"routine susceptibility testing is not indicated for nontyphoidal Salmonella spp isolated from intestinal sources"*. yet, Table-2.21 presents the susceptibility data of Salmonella spp faecal isolates from faecal samples. This is probably because as per the ICMR data, the most common bacterial cause of diarrhoea are nontyphoidal Salmonella spp as mentioned in Table-1.25 of this report.
16. Chapter three of this report fails to provide any susceptibility data for Cefepime, which is the drug of choice for the AmpC beta lactamase producing Enterobacterales especially for Enterobacter cloacae, Citrobacter, spp.
17. Data of resistance genes in K. pneumoniae, Figure-3.9 and 3.11 do not match as the former shows NDM prevalence at 9%, while the latter cites it at 35%. Same is the case with other genes and bacteria as well.

18. In the VAP data in Table-10.45, susceptibility data for Ampicillin and Cefazolin has been presented for Acinetobacter baumannii, and susceptibility data for Amoxi-Clav, Ampicillin, Cefazolin, Cefotaxime, Ceftriaxone and Gentamicin for Pseudomonas aeruginosa has been presented for which there are no breakpoints, so how were these included in the data. Same goes for Tigecycline susceptibility in A. baumannii for which there are no breakpoints (page 236).
19. The VAP Data was calculated *"using tailor-made definitions for Indian ICU's. The definitions are being validated against the currently used global criteria for ventilator-associated events"*. However, there are no references that cite the draft document for these "tailor made definitions", when the NHSN and CDC criteria already in place and being used by all hospitals with a formidable HICP program.
20. Other questionable data include reporting clindamycin in the urinary isolates of Staphylococcus aureus (Table 10.41), Fosfomycin for E. faecium (Table 10.40), Candida spp being the most common cause of UTI (~20% as per Tables 10.37 and 10.38).

While there are more points to discuss and deliberate, it's better to summarize, that just collecting and collating data from nodal and regional centres is not enough. Arm chair analysis by non – medical scientists in ICMR, who have no actual skills, knowledge and experience in working in a Clinical Microbiology laboratory will only churn out data that would cause more harm than benefit. To publish cumulative AMR data, one has to have sound medical knowledge as a Clinical Microbiologist, holding an MBBS and an MD / DNB degree with real world experience in a diagnostic clinical microbiology laboratory.

This report not only projects the AMR surveillance data as wrong information and guidance, but also creates doubts, if ICMR can be trusted as a statutory body which can be relied and banked upon to make national guidelines and policies and with names of senior Clinical Microbiologists in this report, there is serious doubt if this report went through the careful review by these contributors. The purpose of this editorial was to highlight the major flaws in the ICMR Annual Report [January 2023 to December 2023], so that Clinical Microbiologists and Clinicians, Physicians, Surgeons do not get carried away that because this is an ICMR report, it can be trusted and enacted upon.

In the end, one must trust their own local AMR data that must get reviewed by experts who have a formidable background experience in Clinical Microbiology Diagnostic Laboratories and who are well versed with all CLSI and EUCAST guidelines and documents.

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Article 2

Role Of Vaginal Microbiome in Urinary Tract Infections

Dr. Jyothi Lakshmi MD, Professor and Head, Department of Microbiology, Jangoan, Telangana

Urinary tract infections (UTIs) are a common clinical problem across the lifespan of women. Although UTIs are not systematically tracked, Survey data suggest that approximately 10 million outpatient visits for a diagnosis of UTI occur annually. Women are disproportionately affected, with an estimated lifetime risk of UTI of 60%.

In otherwise healthy, sexually active premenopausal women, these infections occur approximately every other year. As women age, UTIs become more common. A population-based study of community-onset UTI among women demonstrates an initial peak in the twenties ,30 per 1,000, decreases slightly during the later reproductive years, then steadily increases with every decade of life starting in late middle age, reaching a maximum of 125/1,000 at and above age 80.

In women, the vagina plays a key role in the pathogenesis of UTIs. The intestinal microbiota is the ultimate source of bacterial strains causing cystitis and pyelonephritis in the majority of cases. The initial step in the pathogenesis of UTI is colonization of the vaginal introitus and periurethra with the infecting uropathogens, followed by ascension of uropathogens via the urethra to the bladder and sometimes the kidneys to cause infection. Thus, understanding factors that affect the microbiota of the vagina is key to understanding the pathogenesis of UTI and to designing interventions to prevent UTIs.

<u>Protective</u> role of Lactobacilli in the vagina.

Vaginal microbiota (VMB) plays a key role in the pathogenesis of UTI: alterations in the VMB are associated with risks for UTI, and effects on the VMB associated with treatment of UTIs can affect the success of this therapy. Thus, a better understanding of the role of the VMB in UTI may lead to improved interventions to prevent and treat these infections.

In culture-based studies of vaginal samples from women without urogenital disease conditions, *Lactobacillus* species comprise 90% of the organisms present, and 80 to 90% of these lactobacilli produced H_2O_2, mostly attributable to *Lactobacillus crispatus* and *Lactobacillus jensenii* . Beginning with early studies utilizing DNA hybridization and quantitative real-time PCR (RT-PCR) of lactobacilli cultured from vaginal samples, numerous studies have identified *L. crispatus* as the predominant species present in healthy premenopausal women.

Several subsequent studies have characterized the VMB in states of health and disease using culture-independent methods, largely based on 16S ribosomal RNA bacterial gene sequencing. This study confirmed that most vaginal microbial communities (73%) were dominated by one or more species of *Lactobacillus* and that this genus constituted over half of all sequences obtained. Studies have definitively demonstrated that a *Lactobacillus*-dominated VMB is correlated with what was termed a "healthy vaginal micro-environment"

Conversely, the absence of vaginal lactobacilli has been associated with several disease states including bacterial vaginosis, HIV infection, and *Neisseria gonorrhoeae*, as well as vaginal colonization with *Escherichia coli*, the most common cause of UTI in women.

Proposed mechanisms through which lactobacilli may prevent vaginal colonization by uropathogens include competitive exclusion of uropathogens by adherence of *Lactobacillus* species to uroepithelial cells; lowering of vaginal pH by production of lactic acid; production of bacteriocins, surfactants, and other antimicrobial products; and finally, production of H_2O_2. *L. crispatus* is highly adherent to vaginal epithelial cells and produces high quantities of H_2O_2. Lactic acid concentrations are high in a lactobacillus-dominated VMB, and these conditions produce a potently antimicrobial environment *in vitro.* Lactobacilli also produce surfactants that inhibit growth of *E. coli* and other uropathogens.

Alteration in Microbiota Associated with UTI.

The VMB has been demonstrated to be altered at the time of UTI, in women with recurrent UTI, and following treatment of the infection, even in women without a history of recurrent UTI.

Multiple culture-based studies showed that women with recurrent UTI often have increased rates of colonization with *E. coli* and depletion of the normally predominant H_2O_2-producing lactobacilli, suggesting that vaginal colonization with H_2O_2-producing lactobacilli may prevent *E. coli* vaginal introital colonization and UTI.

Alteration of the VMB associated with loss of estrogen

Among the manifold effects of the loss of estrogen at the time of menopause are changes in the vaginal microbiome of most women, decreasing the relative amounts of *Lactobacillus* present.

Recurrent UTIs are considered among the features of the genitourinary syndrome of menopause, which is characterized by thinning of the vaginal epithelium, various symptoms associated with vulvovaginal atrophy, and relative loss of lactobacilli in the VMB.

treatment of menopause-associated estrogen deficiency with topical estrogen preparations such as estrogen cream or an estradiol-releasing vaginal ring (Estring) has been demonstrated to reduce the rate of recurrent UTI and restore vaginal lactobacilli in most women.

Effect of Contraceptive method on VMB and risk of UTI.

Numerous studies have demonstrated that spermicidal products containing compounds such as nonoxynol-9 disrupt the VMB by depleting lactobacilli and increasing *E. coli* colonization and increasing the risk of UTI.

This adverse effect appears to be mediated by a direct toxic effect on vaginal *Lactobacillus* spp.

Oral contraceptives appear to reduce the rate of bacterial vaginosis but are neutral with respect to risk of UTI.

Clinical implications.

The interactions between the VMB and the risks of UTI, treatment choices, and possible means of UTI prevention lead to several fairly evident clinical implications.

First, lifestyle considerations may be discussed with patients.

Postmenopausal women without contraindications to the use of topical hormone therapies may be offered such medications for primary or secondary prevention of UTI.

Though spermicidal contraceptives are less commonly used at present, these may be substituted with methods having a neutral effect on UTI, such as hormonal contraceptives

Finally, the use of oral or intravaginal probiotics to attempt to restore protective vaginal lactobacilli is an attractive option that would, in theory, likely help reduce the use of antimicrobials in preventive strategies

Summary

The vagina is a key anatomical site in the pathogenesis of UTI, serving as a potential reservoir for infecting uropathogenic bacteria ascending from the intestinal source.

The vagina is also an important site at which interventions that positively affect the VMB can be instituted to attempt to decrease risk of UTI.

The VMB is a dynamic and often critical factor in this pathogenic interplay, because changes in the characteristics of the VMB resulting in the loss of normally protective *Lactobacillus* spp. increase the risk of UTI.

Interventions designed to maintain homeostasis of the VMB and/or to ameliorate adverse effects of exposures such as antimicrobials or menopause hold promise for future preventive or therapeutic options, potentially avoiding additional use of antibiotics.

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Article 3

The Changing Landscape of Emerging and Re-Emerging Infectious Diseases: A One Health Perspective

Dr. Lakshmi Jyothi T, Additional Professor, Department of Microbiology, AIIMS Bibinagar, Telangana

1. Introduction

Emerging and re-emerging infections constitute one of the most significant threats to global health in the twenty-first century. *Emerging infections* refer to diseases caused by newly identified pathogens or by known pathogens appearing in new populations or geographic regions. Classic examples include HIV in the late twentieth century, Nipah virus in South Asia, SARS and COVID-19 in the last two decades, and Zika virus in the Americas (Levitt et al., 2012; Morens et al., 2008). *Re-emerging infections* are those that were previously controlled but have resurged because of ecological, social, or biological changes; tuberculosis, cholera, dengue, and scrub typhus are notable examples, many of which show increasing drug resistance or expanded transmission cycles (Sarma, 2017; Dikid et al., 2013).

A complex web of drivers—environmental, demographic, technological, and behavioral—underpins these trends. Together they underscore the importance of integrated surveillance, rapid diagnostics, antimicrobial stewardship, and a One Health approach that bridges human, animal, and environmental health to detect, prevent, and respond to threats early and effectively.

2. Global Drivers

The rising frequency and geographic reach of emerging and re-emerging infections reflect dynamic interactions among ecological, social, and biological forces:

Globalization and travel. Rapid movement of people, animals, and goods facilitates swift transcontinental dissemination of pathogens. Outbreaks such as SARS (2003), H1N1 influenza (2009), and COVID-19 (2019) demonstrate how localized events can become global crises within weeks (Levitt et al., 2012; Morens et al., 2008).

Climate change. Warming temperatures, altered precipitation patterns, and shifting humidity regimes modify vector ecology and pathogen survival. Vectors such as *Aedes* spp. are extending their range into subtropical and temperate zones, increasing the risk of dengue, chikungunya, and Zika transmission; changing water and sanitation conditions also amplify risks of leptospirosis and cholera (Wang et al., 2021).

Deforestation and urbanization. Encroachment into natural habitats and rapid, often unplanned, urban growth increase human–wildlife and peri-domestic animal contacts, raising the probability of zoonotic spillovers. Nipah virus and Ebola are salient examples where habitat disruption preceded human outbreaks (Sarma, 2017; Cupertino et al., 2020).

Antimicrobial resistance (AMR). The widespread and often inappropriate use of antibiotics in human medicine, veterinary practice, and agriculture accelerates resistance. Once-treatable infections — including tuberculosis and typhoid — are increasingly complicated by multi-drug resistance; hospital-associated pathogens such as carbapenem-resistant Enterobacterales and MRSA pose continuing threats to health systems (Gupta & Garg, 2023; Mourya et al., 2019).

Socioeconomic and political factors. Poverty, conflict, mass displacement, and fragile health systems undermine routine prevention and control measures. Interrupted immunization programs in conflict zones precipitate outbreaks of vaccine-preventable diseases such as measles and polio (Heymann & Rodier, 2001).

3. Indian Scenario

India’s heterogeneous geography, high population density, and tropical to subtropical climate create a milieu that is particularly conducive to both emergence and re-emergence of infectious diseases.

Recurrent re-emerging infections—scrub typhus, leptospirosis, and cholera—are frequently associated with monsoon-linked flooding, population displacement, and inadequate sanitation (Dikid et al., 2013). Vector-borne viral diseases, especially dengue and chikungunya, place regular strain on urban health services, while Japanese encephalitis persists in certain regions and seasonal influenza and H1N1 cause periodic waves in metropolitan centers (Patel et al., 2021; Sarma, 2017).

Post-COVID circulation patterns have also shifted: unusual timing and intensity of respiratory syncytial virus (RSV) and influenza outbreaks in children illustrate how population-level immunity and pathogen ecology can change rapidly (Patel et al., 2021).

National institutions have strengthened India's capacity to detect and respond to these threats. The National Centre for Disease Control (NCDC) leads outbreak investigation and epidemic intelligence; the Integrated Disease Surveillance Program (IDSP) enables decentralized reporting and rapid response; and the Indian Council of Medical Research (ICMR), through its Virus Research and Diagnostic Laboratory (VRDL) network, provides laboratory confirmation and technical support. Together these bodies have enhanced preparedness, although implementation varies across states and more cohesive data-sharing and state-level ownership are still needed (Heymann & Rodier, 2001; Bankar et al., 2022; Mourya et al., 2019).

4. Key Challenges

Despite measurable progress, several persistent gaps limit India’s ability to prevent and contain emerging and re-emerging infections:

1. **Inadequate public health infrastructure.** Many rural and peri-urban areas lack laboratory facilities, cold-chain capacity, and trained personnel. Clinical case detection often precedes laboratory confirmation, delaying targeted responses (Dikid et al., 2013).

2. **Diagnostic bottlenecks.** Advanced molecular platforms (RT-PCR, multiplex assays) remain concentrated in tertiary centers. District laboratories frequently lack appropriate biosafety infrastructure for handling high-risk pathogens, impeding rapid confirmation and containment (Sarma, 2017; Patel et al., 2021).

3. **Antimicrobial resistance.** India faces a high AMR burden across community and hospital settings. Although ICMR has established AMR surveillance networks, coverage and representativeness remain uneven, limiting the capacity to inform stewardship and policy at scale (Gupta & Garg, 2023; Mourya et al., 2019).

4. **Behavioral, cultural and communication barriers.** Vaccine hesitancy, delays in care-seeking, and stigma hamper early detection and uptake of preventive measures. Effective risk communication tailored to local contexts is often lacking (Rajaji et al., 2018).

5. **Fragmented multisectoral integration.** Although the One Health concept is recognized in policy circles, operational integration of human, animal, and environmental surveillance is inconsistent. Veterinary and ecological data are rarely synthesized with human health intelligence to generate timely early-warning signals (Cupertino et al., 2020).

6. **Sustainability and financing.** Many surveillance and laboratory initiatives rely on central funds and time-limited grants. Variable state-level investment and gaps in long-term financing threaten continuity of training, infrastructure maintenance, and rapid response capacity (Bankar et al., 2022).

5. Addressing the Challenge

A resilient response to emerging and re-emerging infections requires a combination of technical, operational, and policy measures:

- **Strengthen and decentralize laboratory systems.** Expand molecular and point-of-care diagnostics to district levels, while ensuring appropriate biosafety and quality assurance through accreditation and continuous training.
- **Operationalize One Health.** Institutionalize mechanisms for routine data-sharing and joint risk-assessment across human, animal, and environmental health sectors. Shared surveillance platforms and multidisciplinary rapid response teams can facilitate early recognition of spillover events.
- **Enhance diagnostic and antimicrobial stewardship.** Promote syndromic testing algorithms, multiplex platforms where appropriate, and robust stewardship programs that span hospitals, community clinics, and veterinary practice.
- **Invest in vaccine research and equitable distribution.** Support translational research and manufacturing capacity, and ensure vaccines are allocated equitably during emergencies and routine immunization drive ups.
- **Community engagement and risk communication.** Build sustained community partnerships, tailor messages to local contexts, and address barriers to care-seeking and vaccination through culturally sensitive interventions.
- **Sustainable financing and governance.** Encourage state ownership of surveillance programs, diversify funding sources, and incorporate monitoring and evaluation to demonstrate impact and secure long-term support (Gupta & Garg, 2023; Trovato et al., 2020).

6. The Way Forward

Category	Examples	Drivers/Reasons	Impact
Emerging Viral	COVID-19, Nipah, Zika, Ebola, H5N1	Zoonotic spillover, globalization	Pandemics, high mortality
Re-emerging Viral	Dengue, Chikungunya, Measles	Vector spread, vaccine gaps	Recurring outbreaks
Emerging Bacterial	MDR-TB, CRE, MRSA	Antimicrobial resistance, hospital spread	Hard-to-treat infections
Re-emerging Bacterial	Cholera, Scrub Typhus, Leptospirosis	Sanitation lapses, floods	Seasonal epidemics
Parasitic	Drug-resistant Malaria, Leishmaniasis	Drug resistance, climate change	Persistent endemicity
Fungal	Candida auris, Azole-resistant Aspergillus	Antifungal misuse, ICU outbreaks	Severe mortality in immunocompromised
Healthcare-Associated Infections (HAIs)	Klebsiella, Pseudomonas, Acinetobacter	Hospital environment, AMR	Prolonged hospitalization, high cost

Emerging infectious threats are fundamentally ecological and societal problems as much as they are biomedical. Effective preparedness demands early warning systems, interoperable data architecture, rapid and equitable access to diagnostics and therapeutics, and meaningful community participation. Academic bodies and professional networks—such as IAMM TAPC—play an important role in capacity building through continuing education, workshops, technical bulletins, and collaborative research, all of which strengthen resilience and readiness at national and regional levels (Spernovasilis et al., 2022).

7. National Response: ICMR/VRDL Network, NCDC, IDSP, and NVBDCP

India's surveillance and response ecosystem includes:

- **ICMR / Virus Research and Diagnostic Laboratory (VRDL) Network.** With >120 labs, the VRDL system provides laboratory confirmation and outbreak support. It was central during COVID-19, Nipah outbreaks, and Zika detection (Mourya et al., 2019).
- **National Centre for Disease Control (NCDC).** Leads outbreak investigations, epidemic intelligence, training, and technical guidance for states.
- **Integrated Disease Surveillance Programme (IDSP).** A decentralized, electronic reporting platform that compiles weekly data, deploys rapid response teams, and enables near real-time detection (Bankar et al., 2022).
- **National Vector Borne Disease Control Programme (NVBDCP) and IHIP portal.** NVBDCP leads prevention and elimination of malaria, dengue, chikungunya, kala-azar, filariasis, and Japanese encephalitis. Its Integrated Health Information Platform (IHIP) enables real-time case reporting down to the sub-district level, enhancing disease intelligence and early warning capacity.

Together, these initiatives form the backbone of India's preparedness and response architecture. Strengthening interoperability across these platforms and embedding One Health data streams are critical next steps.

8. Conclusion

Emerging and re-emerging infections are an enduring feature of the modern era, driven by globalization, climate change, antimicrobial resistance, ecological disruption, and sociopolitical forces (Levitt et al., 2012; Morens et al., 2008; Sarma, 2017). India's experience—with annual dengue surges, recurrent influenza waves, and sporadic Nipah outbreaks—demonstrates both vulnerability and capacity for response (Dikid et al., 2013; Patel et al., 2021).

To mitigate future threats we must:

- Strengthen integrated surveillance that bridges human, animal, and environmental data streams;

- Ensure rapid and equitable access to diagnostics, vaccines, and therapeutics;
- Implement antimicrobial stewardship at scale;
- Engage communities to foster trust and improve health-seeking behaviors; and
- Secure sustained political and financial commitment.

A genuine One Health approach—rooted in multidisciplinary collaboration and operationalized through coordinated governance—offers the best path to reduce the disruptive impact of future outbreaks and to build resilient, adaptive health systems.

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Article 4

Novel Vaccine Development and Delivery Systems

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Introduction

Vaccines have transformed global health by preventing infectious diseases and reducing morbidity and mortality. However, the emergence of novel pathogens, increasing antimicrobial resistance, and the need for rapid and scalable solutions highlight the importance of advancing vaccine technology. Recent developments focus not only on creating novel vaccines but also on improving their delivery systems for better immunogenicity, safety, and accessibility. This article explores novel approaches in vaccine development and the cutting-edge delivery systems shaping the future of immunization.

Historical Perspective

The journey of vaccines began with Edward Jenner's smallpox vaccine in 1796. Since then, traditional vaccines such as live-attenuated and inactivated vaccines have played a pivotal role. While effective, these vaccines face challenges such as cold chain dependency, limited shelf life, and reduced efficacy against emerging variants. Advances in biotechnology and nanotechnology have fueled a new era of vaccine development.

Modern Vaccine Development Approaches

Modern vaccines move beyond classical methods by leveraging molecular biology, immunoinformatics, and genetic engineering. Some key innovations include:

1. DNA Vaccines

- Plasmid DNA encoding antigenic proteins is delivered into host cells.
- Host cells produce the protein, eliciting an immune response.
- Advantages: Stability, rapid design, and scalability.
- Example: ZyCoV-D for COVID-19.

2. mRNA Vaccines

- Messenger RNA encoding viral proteins is delivered to host cells.
- Host machinery synthesizes the proteins, stimulating immune responses.
- Advantages: Rapid development, high efficacy, no risk of genome integration.
- Examples: Pfizer-BioNTech and Moderna COVID-19 vaccines.

3. Vector-Based Vaccines

- Use harmless viral vectors to deliver genetic material of pathogens.
- Trigger strong cellular and humoral immunity.
- Examples: Oxford-AstraZeneca COVID-19 vaccine.

4. Subunit and Recombinant Protein Vaccines

- Use purified antigenic fragments of pathogens.
- Safe, but may require adjuvants to enhance immunogenicity.
- Examples: Hepatitis B and HPV vaccines.

5. Reverse Vaccinology

- Bioinformatics-based approach to identify antigens from genomic data.
- Enables rapid discovery of vaccine candidates.

Novel Delivery Systems

Delivery systems are crucial for ensuring that vaccines reach target sites effectively while maintaining stability. Some emerging systems include:

1. Nanoparticle-Based Delivery

- Lipid nanoparticles (LNPs) encapsulate mRNA or DNA.
- Improve stability, cellular uptake, and controlled release.
- Widely used in mRNA vaccines for COVID-19.

2. Microneedle Patches

- Contain vaccine formulations in microneedles that dissolve upon skin penetration.
- Advantages: Painless administration, no need for trained personnel, self-administration possible.

3. Virus-Like Particles (VLPs)

- Non-infectious, mimic viral structure.
- Highly immunogenic.
- Example: HPV vaccine.

4. Oral and Nasal Delivery Systems

- Oral: Polio vaccine (Sabin).
- Nasal: Influenza vaccines.

- Advantages: Easy administration, induction of mucosal immunity.

5. Biodegradable Polymers

- Deliver antigens in a sustained manner.
- Reduce the need for multiple doses.

Challenges in Novel Vaccine Development

- **Cold Chain Requirements**: mRNA vaccines require ultra-cold storage.
- **Equity in Distribution**: Developing countries face challenges in access.
- **Safety and Long-Term Monitoring**: Novel technologies require rigorous evaluation.
- **Variants and Mutations**: Emerging strains can reduce efficacy.

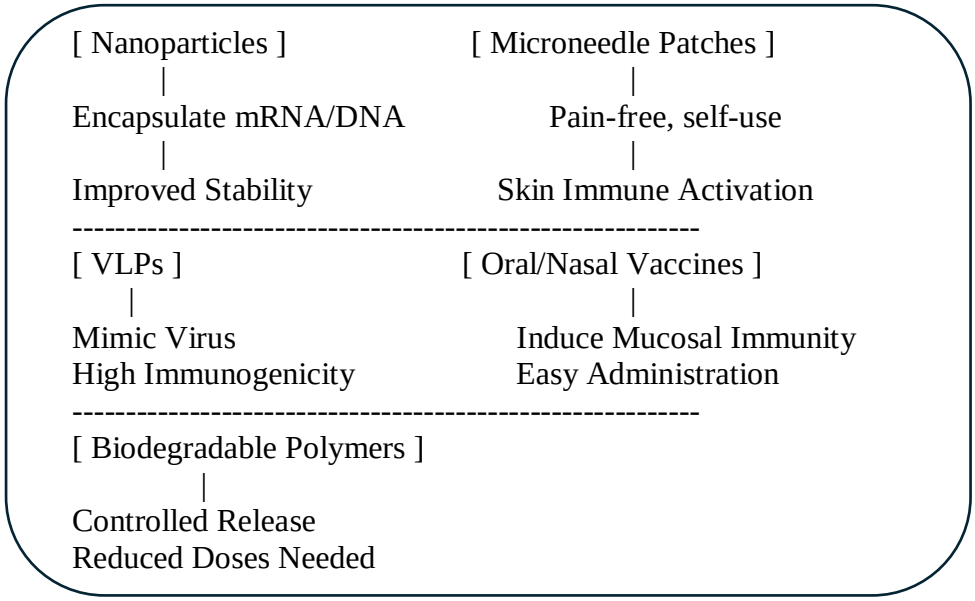
Future Directions

The future of vaccines lies in **personalized vaccines**, **pan-pathogen vaccines**, and **AI-driven antigen discovery**. Combination of vaccines with **immune modulators** and the use of **wearable biosensors** for immune monitoring are promising directions. Development of thermostable vaccines will further improve global accessibility.

Flowchart: Novel Vaccine Development Process

Pathogen Identification
↓
Genomic & Proteomic Analysis
↓
Antigen Selection (Reverse Vaccinology)
↓
Vaccine Design (DNA, mRNA, VLPs)
↓
Preclinical Testing (Animal Models)
↓
Clinical Trials (Phase I-III)
↓
Regulatory Approval & Manufacturing
↓
Distribution & Delivery Systems

Diagram: Novel Vaccine Delivery Systems



Conclusion

Novel vaccine development and delivery systems are revolutionizing preventive medicine. From genetic platforms like mRNA and DNA vaccines to advanced delivery systems such as microneedle patches and nanoparticles, these innovations promise faster, safer, and more effective immunization strategies. Addressing challenges like cold chain requirements, equitable access, and emerging variants will ensure vaccines reach their full potential in safeguarding global health.

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Article 5

Infection Control Practices in ICU Settings

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Protecting Our Frontlines: Best Infection Prevention and Control Practices in ICU

Why Infection prevention and Control Practices Matters in the ICU? It really matters, as ICUs are epicentre for infection in the hospital. ICU is a place which is specially staffed, specially equipped, dedicated to the observation, care and treatment of patients with the threatening illness. ICUs are high-risk environments where patients are especially vulnerable to infections due to:

- medical condition of the patients (Sick and elderly patients),
- patients with comorbid condition,
- weakened immune systems,
- invasive devices & its frequent handling and
- prolonged hospital stays.

ICU patients with infections can be community acquired infections or healthcare-associated infections (HAIs). The most significant risk factor for ICU- acquired infections is the use of invasive devices, including mechanical ventilation, central venous catheter, and urinary catheters, leading to infections such as ventilator-associated pneumonia (VAP), catheter-associated urinary tract infections (CAUTI), central line-associated bloodstream infections (CLABSI), peripheral line associated bloodstream infections (PLABSI). Apart from these, other common sites of infections include GI tract infections (Clostridiodes difficile), Cellulitis, thrombophlebitis due to extravasation of IV Canula etc These infections not only increase morbidity and mortality but also prolong hospital stays and raise healthcare costs. Hence, IPC in Intensive Care Unit (ICUs) is a vital component of patient safety.

India faces unique challenges in ICU infection control, including high patient loads, limited staff-patient ratios, inconsistent compliance with protocols, and variable infrastructure. Despite these challenges, strict adherence to evidence-based IPC practices can significantly reduce infection rates, improve outcomes and also save lives.

Three (3) indispensable elements of IPC in Intensive Care Units (ICUs):

- ✓ Standard Precautions,
- ✓ Transmission based precautions and
- ✓ Bundle care (Insertion and maintenance) to prevent Device Associated Infections

1. **Standard Precautions:** Set of work, practices used to minimize transmission of health care associated infections (HAIs). It applies to all Healthcare Providers (HCPs), regardless of infectious status of patients and to ensure a basic level of infection prevention and control. Vital components include-

- ✓ Hand Hygiene
- ✓ Use of appropriate PPE
- ✓ Environmental cleaning & disinfection and
- ✓ Disinfection & Sterilisation of equipment

a. **Hand hygiene:**

Hand hygiene is the cornerstone of infection prevention. **According to WHO,** improving hand Hygiene practices may reduce pathogen transmission in health care facility by **50% as** hands are the most common vehicle to transmit healthcare associated pathogens**.**

All healthcare providers (HCPs) must follow the **WHO's "5 Moments for Hand Hygiene"**:

I Before touching a patient
II Before performing aseptic procedures
III After exposure to body fluids
IV After touching a patient
V After touching patient surroundings

Appropriate steps and techniques of hand hygiene (6 steps for hand rub for 20-40 seconds and 7 steps for hand wash for 40- 60 seconds) must be followed. Use of **alcohol-based hand rubs** is encouraged when hands are not visibly soiled, while soap and water should be used after contact with organic matter, visibly dirty hands and after contact with the patients infected with Clostridiodes difficile.

b. Use of Personal Protective Equipment (PPE):

The basic objective of the use of PPE is to protect the skin and mucous membrane of the HCPs as well as the patient from contracting the infection. Use of PPE is essential, particularly when managing patients with communicable diseases or during high-risk procedures. Appropriate use of PPE (gloves, gowns, cap, masks, face shields, aprons and shoe cover) must be decided according to the anticipated exposure and the type of isolation precautions required. PPE must be worn and removed (donning and doffing) in correct sequence to avoid contamination. A **buddy system** to observe donning and doffing of PPE is recommended. When onsite "buddies" are not available to monitor; remote buddies are also acceptable. The remote buddies can view the procedures via video conferencing on their computers. Reuse of disposable PPE must be avoided, unless specifically designated as "reusable". Used PPE should be disposed of following BMW (Bio-Medical Waste) Management Rules.

Key points regarding use of GLOVES:

- Gloves are not a substitute for hand hygiene.
- Routine use of glove is not recommended. Universal gloving can lead to significant increase in HAIs
- Common Indications:
  - ✓ Before a sterile procedure
  - ✓ Anticipation of contact with blood and body fluids
  - ✓ Contact with a patient during contact precautions

- Hand hygiene should be performed before gloves use to prevent possible cross contamination of gloves with HCPs flora in case of glove damage or improper use.
- Hands must be washed immediately after removal of gloves to prevent cross contamination as it creates a moist, warm and occlusive environment between the skin and the glove; which is **"safe haven"** for microorganisms.
- Double gloving should always be practiced while giving care to Viral hemorrhagic fever patients.

c. Environmental cleaning & disinfection:

Environmental surfaces in ICUs can harbour pathogens if not cleaned and disinfected properly. Environmental cleaning must focus on frequent cleaning of high-touch surfaces (bed rails, IV pumps, monitors) along with use of appropriate disinfectants as per the standard guidelines and institution's protocol. Strict cleaning and disinfection protocols must be followed between patient shifts or discharges (terminal cleaning). Housekeeping staff must be trained and supervised to ensure cleaning protocols are followed consistently.

For floor cleaning, it is best practice to use a two- or three-bucket system for mopping. This can be facilitated on the cleaning cart or on a separate trolley, if a full cleaning cart is not available. Two-bucket system (routine cleaning): one bucket contains a detergent or cleaning solution and the other contains rinse water. Three-bucket system (for disinfection): one bucket contains the detergent or cleaning solution; one contains rinse water and one the disinfectant solution.

Routine air sampling in ICU is not recommended as HAI rates are not related with levels of general microbial contamination of air and there are no standard guideline mentioning the permissible level of microbial contamination of air. CDC recommends targeted air surveillance with specific indications:

I. Investigation of outbreak. II. For research purpose
II. After reconstruction or newly constructed buildings
III. For short term evaluation of a change in infection control practices

CDC and HICPAC have recommendations in both **2003 Guidelines for Environmental Infection Control in Health-Care Facilities** and **the 2008 Guideline for Disinfection and Sterilization in Healthcare Facilities** that state that the CDC does not support disinfectant fogging. These recommendations refer to the spraying or fogging of chemicals (e.g., formaldehyde, phenol-based agents, or quaternary ammonium compounds) as a way to decontaminate environmental surfaces or disinfect the air in patient rooms. These recommendations do not apply to newer technologies involving fogging for room decontamination (e.g., ozone mists, vaporized hydrogen peroxide), however CDC does not yet make a recommendation regarding these newer technologies.

CDC guideline- Best Practices for Environmental Cleaning in Healthcare Facilities: in Resource-Limited Settings and Indian guideline- G**uidelines for Implementation of Kayakalp initiative** can be taken as reference for establishing the institution's policy.

Patient and Staff Safety can be enhanced by **Horizontal approach to infection prevention.**

Horizontal approach = Successful Hand Hygiene + Effective Environmental

d. Disinfection & Sterilisation of equipment:

Disinfection and sterilization are essential for ensuring that medical and surgical instruments do not transmit infectious pathogens to patients. Spaulding classification is generally used as strategy for reprocessing contaminated medical devices. The system classifies a medical device as critical, semicritical or noncritical on the basis of risk to patient safety from contamination on a device. The system also established three levels of germicidal activity (sterilization, high-level disinfection, and low-level disinfection) for strategies with these three classes of medical devices. Few important recommendations as per guideline for Disinfection and Sterilization in Healthcare Facilities (2008) are –

Healthcare workers must wear appropriate PPE to preclude exposure to infectious agents or chemicals. In hospitals, cleaning, disinfection, and sterilization of patient-care devices should be in a central processing department- **Central sterile services department** (CSSD), in order to more easily control quality. Patient-care items must be cleaned meticulously with water and detergent/enzymatic cleaners, to remove visible organic residue (e.g., residue of blood and tissue) and inorganic salts before high-level disinfection or sterilization procedures. Medical devices must be cleaned immediately after use (at the point of use) because soiled materials become dried onto the instruments. Dried or baked materials on the instrument make the removal process more difficult and the disinfection or sterilization process less effective or ineffective. Guidelines for Central Sterile Supply Department (CSSD) & Mechanized Laundry, ministry of health & family welfare government of India can be referred for establishing CSSD department in the organizations

2. Transmission based precautions: These are set of infection control practices which should be followed for the patients, who are infected or likely to be infected with infectious agents having specific modes of transmission - Contact (Direct and Indirect), Airborne and Droplet. These additional (second-tier) precautions should be practiced over and above standard precautions. These precautions mainly focus on patient placement (type of isolation room), type of precautions to be followed during transfer of patient, type of PPE to be used, single use patient dedicated equipment and disinfection of the rooms apart from most important component- hand hygiene practice. There are three types of T**ransmission based precautions**:

I. Contact precautions (eg: MDRO, MRSA, VRE, *Clostridioides difficile)*
II. Airborne precautions (eg: *Mycobacterium tuberculosis* Measles, Varicella)
III. Droplet precautions (eg: Influenza, pneumonia. diphtheria)

Contact precautions: Patient must be isolated preferably in standard isolation room. HCPs must wear gown and surgical mask when close contact (< 3 feet) with patient is anticipated and also upon room entry. HCPs must adhere to hand hygiene practices.
While handling with diarrhoea patients *with* ***C. difficile***, only **Hand wash** is recommended.

Airborne precautions: Negative pressure isolation room and appropriate PPE (N95 mask) for HCPs is recommended, whenever aerosol (Small particles < 5 microns) transmissible disease or aerosol generating procedure is anticipated.

Droplet precautions: Droplet precautions are intended to prevent the spread of infectious agents that transmitted through respiratory droplets (size: >5 µm). HCPs must wear surgical mask when close contact (<3 feet) and upon the room entry. During transport, patient should wear surgical mask. Along with droplet mode, there is also possibility of transmission of infections by contact.

,

3. Maintenance of bundle care to prevent Device Associated Infections (DAI):

A care bundle is collection of intervention that are evidenced based, it means to ensure that the application of all these interventions is consistent for all patients at all times thereby improving outcomes.

Urinary Catheter Care Bundle for Preventing Catheter-Associated Urinary Tract

Insertion Bundle criteria
Appropriate Indication
Only sterile items should be used
Catheter should be inserted by non-touch technique with strict asepsis
Continuous closed drainage system must be used
Catheter must be properly secured after placement.

Maintenance Bundle criteria	
Closed drainage system	
Urinary Cather secured	
Drainage bag above floor &below bladder level	
Catheter care (aseptic)	Hand hygiene
	Meatal care
Single use glove while handling/ emptying	
No contact b/w bag and jug	
Separate jug for collection	
Assessment of readiness to remove – documented?	

Central Line Care Bundle for Preventing Central Line Associated Blood Stream Infections (CLABSI)

Insertion Care Bundle
Hand Hygiene and glove
Selection of insertion site
Skin antiseptic- ▪ Chlorhexidine is preferred. ▪ Povidone Iodine for age< 2months and allergic to chlorhexidine
Use of semipermeable dressing
Catheter must be properly secured after placement

Maintenance Care Bundle	
Daily aseptic CL care during handling	Hand hygiene
	Rub the hub with alcohol swab
	Dressing with 2% CHG
Any local signs of infection?	
Dressing changed?	
Assessment of readiness to remove – documented?	

Care Bundle for Preventing Ventilator Associated Events/ Pneumonia (VAE/VAP)

Mechanical Ventilator Bundle Care
Head end elevation at 30^0- 45^0
Adherence to Hand Hygiene
Daily Oral Care
DVT prophylaxis
Daily sedation vacations and assessment of readiness to extubate-documented?
Need of PUD prophylaxis assessed?
Cuff Pressure (25-30)
Subglottic suctioning

Components of Care bundle are subject to change, being revised time to time and updated in different guidelines. Eg: One of the components of care bundle for mechanical ventilator is 'daily oral care with 2% Chlorhexidine solution'. It was being followed since long however, recent update added a recommendation for daily toothbrushing with Normal saline for oral care. Oral care with chlorhexidine is not recommended as per new update. (Infect Control Hosp Epidemiol: Strategies to prevent ventilator-associated pneumonia, ventilator-associated events, and no ventilator hospital acquired pneumonia in acute-care hospitals: 2022 Update)

Compliance to the care bundle=

Number of patients on device where all components of care bundle are followed X 100

Total number of patients on device

MULTIMODAL STRATEGIES OF WHO

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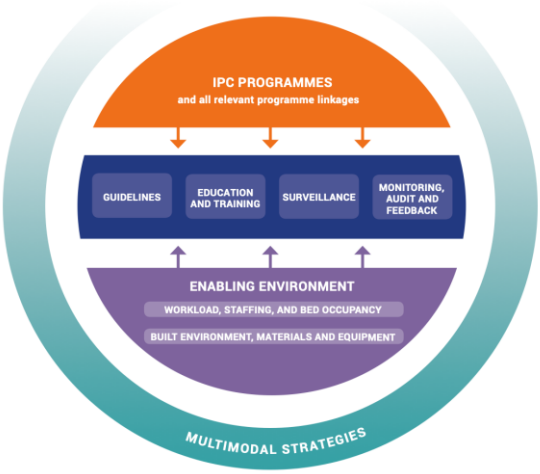

Multimodal implementation strategies are a core component of effective infection prevention and control (IPC) programmes according to the WHO Guidelines on Core Components of IPC programmes at the National and Acute Health Care Facility Level.

For effective IPC control, emphasis has been given on guidelines, education and training, surveillance and monitoring & audit.

The base of these strategies, it is essential to enable the environment, where most of the time we face challenges.

1. **Guidelines:** Plenty of guidelines for infection prevention-to tell us what to do? Implementing these strategies on the ground is important.
2. **Education and training:** Continuous training of ICU staff on IPC guidelines is non-negotiable. Hospitals should:
    a. Conduct induction training for all new staff
    b. Offer refresher courses every 6–12 months
    c. Use visual reminders, posters, and videos to reinforce practices
    d. Engage doctors, nurses, and housekeeping in infection control education.
3. **Surveillance:** Surveillance has been described as systematic observation, data collection, analysis and interpretation of data on specific events/ infections and disease, followed by dissemination of that information with evaluation for changes in IPC within the facility. Outcome surveillance includes- Hospital Acquired Infection (HAI) Surveillance, Mortality/ morbidity rate, antimicrobial resistance (AMR) surveillance and Needle stick/ sharp/ splash injury (NSSSI) surveillance.

HAI Surveillance: It can be of many types. Laboratory based ward liaison surveillance is most commonly used and best method. These specifically aims at high-risk areas such as ICUs, where IPCN prospectively monitor cases in ICUs and check lab reports.

4. **Monitoring, audit and feedback:** Monitoring and feedback are essential to assess the problem, drive appropriate change and document practice improvement. Audit tools (approved checklist) are important considerations to assess the compliance rate of the IPC practices, which are being followed in ICUs such as Hand hygiene audit, PPE usage audit, Bundle care (insertion and maintenance) audit, BMW segregation audit and De-escalation audit.

   Audit tool for active surveillance of HAI includes Care Bundle audit form for devices + HAI Surveillance Form. These two is being used to analyse and to fill the HAI Surveillance reporting form.

   Routine **surveillance** is critical to understanding trends and identifying outbreaks. Infection control teams should:

   - Track infection rates (VAP, CLABSI, CAUTI) and surgical site infections in post-surgery patients.
   - Analyse causes and implement corrective actions
   - Share data with ICU staff to create awareness
   - Conduct audits and feedback sessions regularly

     This promotes a culture of safety and continuous improvement.

WORKFLOW OF SURVEILLANCE IN ICU:

Perform Surveillance (Bundle Care check for the devices + HAI Surveillance for the patient)
Onsite Correction (whenever required)

⬇

Laboratory based surveillance (data collection).
Analysis of the data available and incorporate into reporting form HAI

⬇

Root cause analysis

⬇

Corrective Action and Preventive Action

Challenges in Indian ICUs:

Some common issues faced include:

- ✓ Lack of Infrastructure
- ✓ Staff shortages and burnout (Inadequate patient nurse ratio)
- ✓ Non-compliance with protocols due to Lack of "culture of safety culture" is very much evident in our HCFs- need to change the attitude
- ✓ Inadequate PPE supply during high-demand periods

- ✓ Limited isolation facilities for infected patients

Addressing these requires administrative commitment, adequate resource allocation, and teamwork across departments.

Conclusion:

ICU take the major chunk of HAIs and that is the reason, we feel, ICU is the area, where Infection control practices must be more focussed

Infection control in ICU settings is a shared responsibility. In the Indian context, where resources may be limited and patient load is high, simple & cost-effective practices like hand hygiene, daily device checks, care bundle audit and basic aseptic techniques can make a significant difference.

Investing in infection prevention is not just a safety measure—it is an essential part of delivering quality healthcare. Infrastructure plays a **critical role** in strengthening **Infection Prevention and Control (IPC)** practices in healthcare facilities. Well-planned infrastructure **removes barriers** to IPC, makes compliance **easier for staff**, and creates a safer environment for patients and healthcare providers. By fostering a strong culture of infection control and its consistent practices can save lives and improve patient outcomes in ICUs across India.

Indian hospitals can reduce HAIs, save lives, and improve trust in the healthcare system.

ICU is a fragile ecosystem and infection control is the key to maintaining balance.
Vigilance is the price of safety in the ICU

Reference:

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3. CDC- Guideline for Disinfection and Sterilization in Healthcare Facilities (2008), updated June 2024
4. Guidelines for Central Sterile Supply Department (CSSD) & Mechanized Laundry, Ministry of Health & Family Welfare Government of India
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6. CDC- NHSN guidelines for surveillance of device associated Infections 2025
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Article 6

Gut Microbiome: In Health and Disease Key Insights

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INTRODUCTION

The human gut microbiome, a complex and dynamic ecosystem composed of trillions of microorganisms, including bacteria, viruses, fungi, and archaea, plays a pivotal role in maintaining health and influencing disease. Residing primarily in the large intestine, this microbial community has co-evolved with humans over millennia, forming a symbiotic relationship that profoundly impacts physiological processes ranging from digestion and immunity to brain function and metabolism. Advances in sequencing technologies and microbiome research over the past two decades have revolutionized understanding of the gut microbiota, revealing its critical role in both health maintenance and the pathogenesis of numerous diseases.

Composition and Development of the Gut Microbiome

The gut is estimated to contain 100 trillion microbes with over 3 million genes—far exceeding human genetic material.

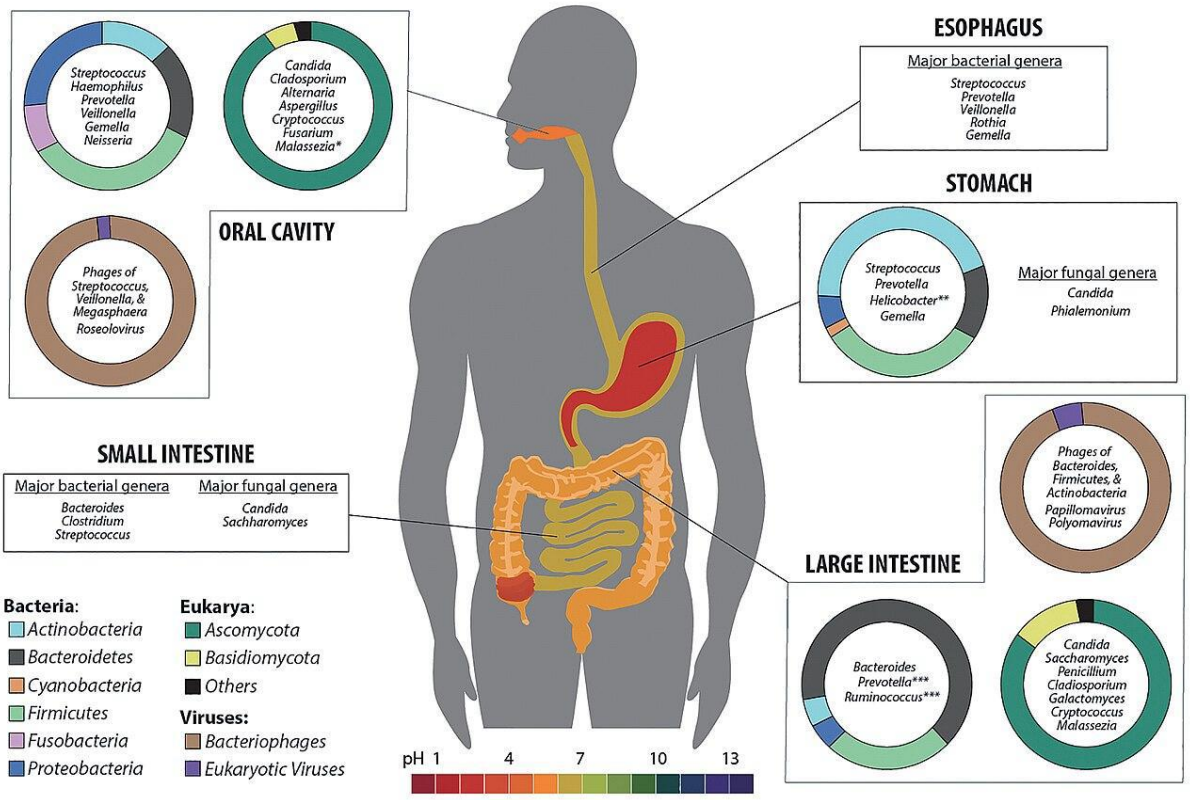
Each individual's microbiome is unique, shaped by:

- Genetic factors
- Environment
- Diet & Lifestyle

The predominant phyla are **Bacteroidetes and Firmicutes.**

Key genera include:

- **Beneficial:** *Lactobacillus, Bifidobacterium, Akkermansia*
- **Potentially Harmful in Excess:** *Clostridium, Enterobacteriaceae*
- **Others:** Actinobacteria, Proteobacteria, Verrucomicrobia



(By Ethan Hillman et al - https://doi.org/10.1264/jsme2.ME17017, CC BY 4.0, https://commons.wikimedia.org/w/index.php?curid=163282038)

DEVELOPMENT OF GUT MICROBIOME

Gut microbiome development begins at birth and influenced by the mode of delivery and breastfeeding.

- **Vaginal Delivery:** Colonization by maternal vaginal/fecal microbes (*Lactobacillus*, *Bifidobacterium*).
- **Cesarean Section:** Colonization by skin/environmental microbes (*Staphylococcus*, *Streptococcus*).
- **Breastfeeding:** Promotes *Bifidobacterium* via human milk oligosaccharides (HMOs)—natural prebiotics.

Diet, especially transitioning from milk to solids, dramatically increases diversity. By age three, the microbiome assumes an adult-like configuration but remains flexible throughout life in response to diet, antibiotics, stress, and illness.

The Gut Microbiome's Role in Maintaining Health

A balanced and diverse gut microbiome is essential for numerous physiological functions. One of its primary roles is in digestion and nutrient metabolism. Gut microbes break down complex carbohydrates, fibres, and resistant starches that human enzymes cannot digest, producing short-chain fatty acids (SCFAs) such as acetate, propionate, and butyrate. These SCFAs serve as energy sources for colonocytes, regulate gut motility, and exhibit anti-inflammatory properties. Butyrate, in particular, is crucial for maintaining the integrity of the intestinal epithelial barrier and has been linked to reduced risk of colorectal cancer.

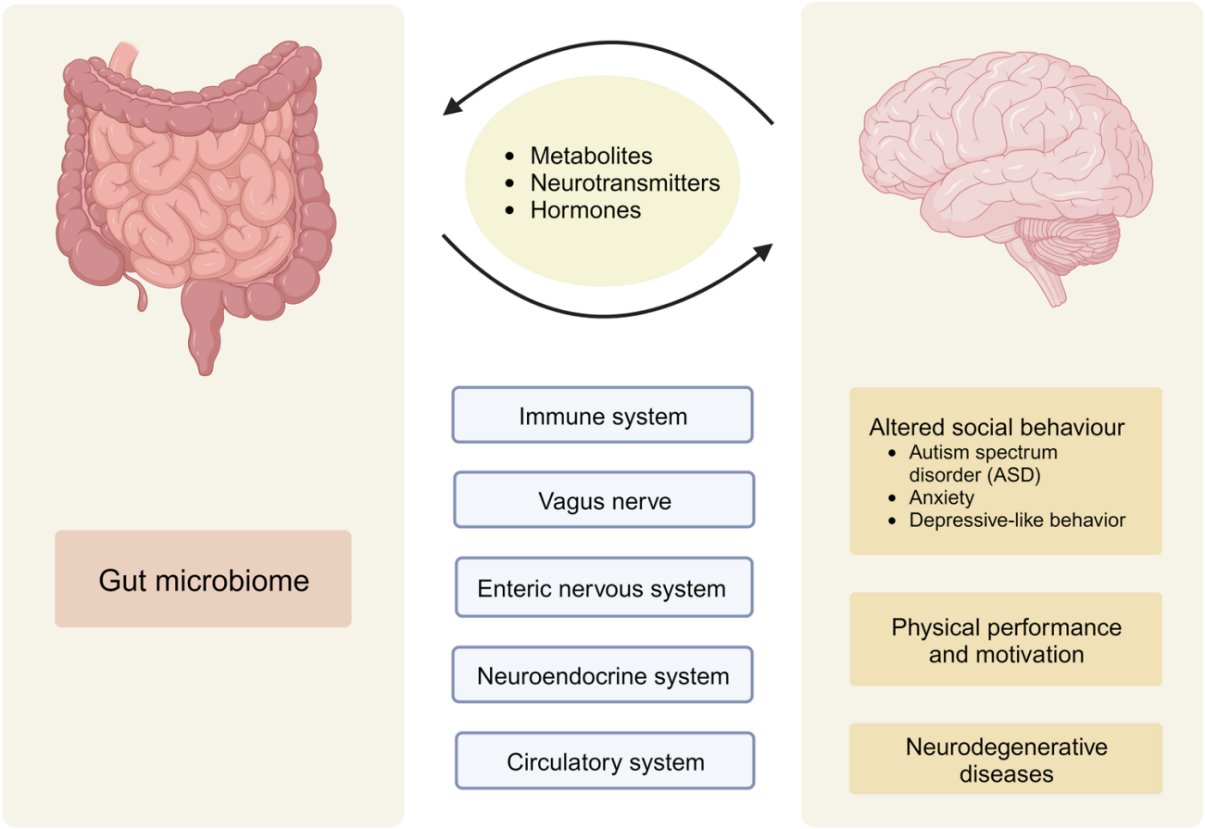
Key Functions of the Gut Microbiome Include:

1. **Digestion and nutrient absorption:** The gut microbiome helps break down complex carbohydrates, proteins, and fats, and absorbs essential nutrients.
2. **Immune system modulation:** The gut microbiome plays a crucial role in shaping the immune system, promoting tolerance, and preventing excessive inflammation.
3. **Production of vitamins and hormones:** Certain gut microbes produce vitamins (e.g., vitamin K and biotin) and hormones (e.g., serotonin and dopamine) that are essential for maintaining health.
4. **Maintenance of the gut barrier:** The gut microbiome helps maintain the integrity of the gut epithelial barrier, preventing the translocation of toxins and undigested food particles into the bloodstream.
5. **Prevention of diseases:** A balanced gut microbiome is associated with a reduced risk of various diseases, including inflammatory bowel disease, obesity, diabetes, and certain types of cancer.
6. **Regulation of the immune system:** The gut microbiome helps regulate the immune system, preventing excessive inflammation and autoimmune diseases.
7. **Modulation of the brain-gut axis:** The gut microbiome influences the brain-gut axis, which is linked to mental health, cognitive function, and mood regulation.

GUT BRAIN AXIS:

Emerging research has highlighted the gut-brain axis—a bidirectional communication network linking the gut and the central nervous system. Gut microbes produce neurotransmitters such as serotonin, dopamine, and gamma-aminobutyric acid (GABA), and they influence the hypothalamic-pituitary-adrenal (HPA) axis, which regulates stress responses. This connection suggests that the microbiome may impact mood, cognition, and behavior, with implications for conditions such as anxiety, depression, and autism spectrum disorders.

Microbiota gut-brain axis



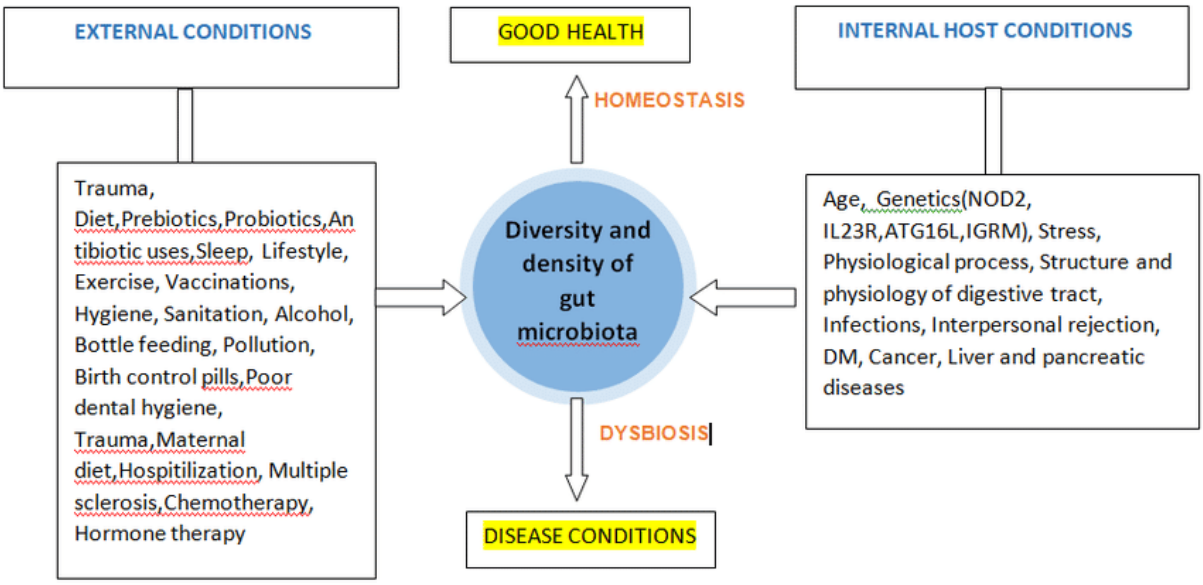
Source: (https://biorender.com/)

How Gut Microbiome Affects Mental Health

- Neurotransmitter Production: *Lactobacillus* & *Bifidobacterium* produce serotonin, dopamine, and GABA, regulating mood.
- **Short-Chain Fatty Acids (SCFAs):** Butyrate, acetate, propionate help reduce brain inflammation & support memory.
- **Immune System & Inflammation:** Dysbiosis (imbalance) can trigger neuroinflammation, increasing depression & anxiety risk.
- **Vagus Nerve Communication:** Gut microbes can send signals to the brain via the vagus nerve, influencing emotions.

Dysbiosis and Disease

When the balance of the gut microbiome is disrupted—a state known as dysbiosis—it can contribute to the development of various diseases. Dysbiosis is characterized by reduced microbial diversity, loss of beneficial microbes, and/or overgrowth of pathogenic species.



Source: (https://www.researchgate.net/profile/Kallem-Sharat-Venkat-Reddy2/publication/343361936/figure/fig2/AS:919614145974277@1596264506557/Causes-of-gut-microbial-dysbiosis.ppm)

Factors that Disrupt the Gut Microbiome

1. **Antibiotics and antimicrobials:** Exposure to antibiotics and antimicrobials can disrupt the balance of the gut microbiome.
2. **Diet:** A diet high in processed foods, sugar, and saturated fats can alter the gut microbiome.
3. **Stress:** Chronic stress can disrupt the gut microbiome and compromise gut health.
4. **Lifestyle factors:** Lack of sleep, physical inactivity, and exposure to environmental toxins can also impact the gut microbiome.

Dysbiosis can be triggered by factors such as prolonged antibiotic use, poor diet (high in fat and sugar, low in fibre), chronic stress, infections, and certain medical conditions.

Mechanisms of Illness:

1. **Increased gut permeability:** Dysbiosis can lead to increased gut permeability, allowing toxins and undigested food particles to pass through the gut barrier and into the bloodstream, triggering inflammation and oxidative stress.

- Example: Individuals with celiac disease have been shown to have increased gut permeability, leading to the passage of gluten into the bloodstream and triggering an immune response.

2. **Impaired neurotransmitter production:** Dysbiosis can disrupt the production of neurotransmitters, leading to changes in mood, cognitive function, and behavior.

- Example: Individuals with Parkinson's disease have been shown to have reduced levels of the beneficial bacteria Bifidobacterium and increased levels of the pathogenic bacteria Enterobacteriaceae.

3. **Exacerbation of inflammation:** Dysbiosis can exacerbate inflammation in the gut and throughout the body, contributing to the development and progression of various diseases.

- Example: Individuals with rheumatoid arthritis have been shown to have increased levels of the pro-inflammatory cytokine TNF-alpha, which is produced by the gut microbiome.

Diseases Associated with a Disrupted Gut Microbiome

Gastrointestinal Diseases

1. Inflammatory bowel disease (IBD): Conditions such as Crohn's disease and ulcerative colitis are linked to an imbalance in the gut microbiome.
2. Irritable bowel syndrome (IBS): IBS symptoms may be triggered or exacerbated by an imbalance in the gut microbiome.
3. Gastroesophageal reflux disease (GERD)

Metabolic Disorders

The gut microbiome is also implicated in metabolic disorders. Obesity and type 2 diabetes are associated with altered microbiota composition, including a higher Firmicutes-to-Bacteroidetes ratio and reduced microbial diversity.

1. Obesity and weight gain.
2. Type 2 diabetes and Insulin resistance
3. Metabolic syndrome

Mental Health and Neurological Disorders :: Alterations in Gut Microbiome and influence on Gut brain axis:

- **Depression:** People with depression have lower *Lactobacillus* and *Bifidobacterium*.
- **Anxiety:** Mice given gut bacteria from anxious humans show anxious behavior.
- **Autism Spectrum Disorder (ASD):** Children with ASD have more *Clostridium* bacteria, which may worsen symptoms.
- **Parkinson's Disease:** Patients have overgrowth of *Enterobacteriaceae*, worsening motor symptoms.

Other Diseases

1. **Autoimmune diseases:** Conditions such as rheumatoid arthritis and lupus may be linked to an imbalance in the gut microbiome. In humans, early-life antibiotic exposure and reduced microbial diversity are associated with increased risk of autoimmune disorders.
2. **Cancer:** Some research suggests that the gut microbiome may play a role in the development and progression of certain types of cancer.
3. **Cardiovascular disease:** Alterations in the gut microbiome may contribute to the development of cardiovascular disease. Certain gut microbes metabolize dietary nutrients like choline and L-carnitine (found in red meat) into trimethylamine (TMA), which is then converted by the liver into trimethylamine N-oxide (TMAO). Elevated TMAO levels are associated with increased atherosclerosis and risk of heart attack and stroke.

Therapeutic Interventions Targeting the Gut Microbiome

Given the microbiome's central role in health and disease, there is growing interest in therapeutic strategies to modulate its composition and function. Dietary interventions are among the most accessible and effective approaches.

The Important Interventions are:

1. Probiotics

Probiotics are live microorganisms that confer health benefits when administered in adequate amounts.

Types of Probiotics

1. Lactobacillus: Commonly found in fermented foods like yogurt and sauerkraut.
2. Bifidobacterium: Often used to support gut health and immune function.
3. Streptococcus: Some strains are used as probiotics, particularly in fermented foods.

Probiotics are used to prevent or treat various conditions, including diarrhea, IBS, and IBD.

2. Prebiotics

Prebiotics are non-digestible fibers that serve as food for beneficial microorganisms in the gut.

Types of Prebiotics

1. Inulin: A fructan found in chicory root, garlic, and onions.
2. Fructooligosaccharides (FOS): Found in foods such as bananas, onions, and garlic.
3. Galactooligosaccharides (GOS): Found in human milk and some legumes.
4. Arabinogalactan: Found in larch wood and some plant-based foods.

Food Sources

1. Fruits: Bananas, apples, and berries are good sources of prebiotic fibers.
2. Vegetables: Onions, garlic, and asparagus are rich in prebiotic fibers.
3. Legumes: Legumes such as beans and peas are good sources of prebiotic fibers.
4. Whole grains: Whole grains such as oats, barley, and wheat contain prebiotic fibers.

Prebiotics are used to promote gut health, improve digestion, and enhance immune function.

3. **Synbiotics:**

Prebiotics can be combined with probiotics to create synbiotics, which can have enhanced benefits.

4. **Fecal Microbiota Transplantation (FMT):**

Fecal microbiota transplantation (FMT) is a more direct intervention, involving the transfer of processed stool from a healthy donor into the gastrointestinal tract of a recipient.
FMT has been used to treat recurrent *Clostridium difficile* infections with high success rates.
Potential applications: FMT is being explored as a potential treatment for other conditions, including IBD and metabolic disorders.

5. **Dietary Interventions:**

1. **Fiber-rich diets:** Diets high in fibre can promote the growth of beneficial microorganisms.
2. **Polyphenol-rich foods:** Foods rich in polyphenols, such as fruits and vegetables, can have prebiotic effects.
3. **Avoiding processed foods:** Avoiding processed foods and added sugars can help maintain a balanced gut microbiome.

6. **Lifestyle modifications:** Engaging in regular physical activity, managing stress, and getting adequate sleep can also support gut health.

Future Directions

Microbiome-Modulating Medications: Microbiome-modulating medications are pharmaceuticals designed to target the gut microbiome, either by modifying its composition or function, to prevent or treat various diseases.

Targeting specific microorganisms: Medications can be designed to target specific microorganisms or microbial pathways.

Modulating the gut-brain axis: Medications can also target the gut-brain axis to modulate the gut microbiome's influence on brain function and behavior.

Precision medicine: Precision medicine approaches can be used to tailor therapeutic interventions to an individual's unique gut microbiome profile.

Microbiome-based biomarkers: Microbiome-based biomarkers can be used to diagnose and monitor diseases.

Research to identify Novel therapeutic targets: to develop effective treatments for various diseases.

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Journal Critical Review

Bacteriology:

Lau CL, Ramli R, Periyasamy P, Tan TL, Neoh H, Mohamad Yusof A, et al. Performance of direct-from-blood-culture disk diffusion antibiotic susceptibility testing and its impact on antibiotic adjustment in bloodstream infections at a Malaysian tertiary center. Microbiol Spectr. 2025 Jun 18;0(0):e02863-24. doi:10.1128/spectrum.02863-24

Dr. Yogaraj N, 1st Year, Govt Medical College, Ongole

Title Of The Article : Performance Of Direct-From-Blood-Culture Disk Diffusion Antibiotic Susceptibility Testing And Its Impact On Antibiotic Adjustment In Bloodstream Infections At A Malaysian Tertiary Center

Journal Name : Microbiology Spectrum - ASM (American Society For Microbiology)

Year : 18 June 2025 **Volume : 0** (Not Assigned) **Pages : 0** (Not Assigned)

Author(S) : Chee Lan Lau, Ramliza Ramli, Petrick Periyasamy, Toh Leong Tan, Hui-Min Neoh, Aliza Mohamad Yusof, Zainina Zainal Abidin, Noranati Zulkiflichia, Mohd Syazwan Mohd Saaid, Munirah Abdul Aziz, Isa Naina-Mohamed

1.Background & Rationale

What is the clinical or research problem addressed? This study addressed that increased development of resistance to broadsprectrum antibiotic in bloodstream infections in low resource settings due to 1.Unneccessory prolonged exposure to broadspectrum antibiotics till the AST results were ready to adjust the active class of antibiotics. 2.Increased prescribtion and usage of WATCH drugs in bloodstream infection till the exact AST results obtained to adjust the antibiotic course.3.To check the reliability of dAST (done directly from positive blood culture bottles) which is the low cost, in-house alternative method to give early AST results to modify the drug course early than conventional method.

Why is this study important in the current context? This study is important because increased antimicrobial resistance in bloodstream infections cause high mortality in low resource setting. Rapid susceptibility results are critical for timely treatment with ACTIVE

antibiotics and to shorten the exposure of inactive broadspectrum antibiotics. To reduce the routine use of WATCH drugs,where ACCESS drugs showed sensitivity . To prove that dAST provides a low-cost, practical alternative to expensive diagnostics, especially valuable in LMICs with high antimicrobial resistance.

Briefly describe prior knowledge and the knowledge gap this study attempts to fill.

Previous studies, mainly from Western settings have shown that direct disk diffusion (dAST) from positive blood cultures can shorten the time to susceptibility results and improve antibiotic use, though concerns remain about standardization and reliability. However, evidence from low and middle-income countries (LMICs) particularly in Southeast Asia, is very limited despite the high burden of antimicrobial resistance. Advanced rapid diagnostics are often too costly and inaccessible in these regions.This study therefore addresses the gap by evaluating the in-house performance of dAST and its influence on antibiotic adjustment in a Malaysian tertiary care hospital.

2.Study Design & Methods

What was the primary aim or hypothesis? Is it clearly stated and relevant?

The primary aim of the study was to evaluate the performance of direct-from-blood-culture disk diffusion antibiotic susceptibility testing (dAST) compared with conventional AST (cAST) and to assess its impact on antibiotic adjustment in bloodstream infections.Yes, the aim is clearly stated and highly relevant**,** as it addresses the urgent clinical need for rapid, low-cost susceptibility testing in regions with high antimicrobial resistance and limited access to advanced diagnostics.

Was the methodology appropriate, comprehensive, and up to date?

Yes, the methodology was appropriate and aligned with current standards up to date.

As here prospective single-center design was used, with dAST performed by Kirby–Bauer disk diffusion and validated against cAST using VITEK 2 and standard methods. Organisms were identified with MALDI-TOF MS, and interpretation followed updated CLSI guidelines. Statistical analyses were comprehensive, ensuring reliability and comparability of results.

Were the inclusion/exclusion criteria, sample size, and controls appropriate?

Yes, the criteria and controls were generally appropriate. The study included adults (≥18 years) with positive blood cultures from medical, surgical, and ICU wards ensuring clinical relevance. Common contaminants such as CoNS and Corynebacterium spp. were excluded to avoid bias

which was appropriate. The sample size of 318 positive blood cultures over one year was reasonable, though a formal sample size calculation was not reported. Conventional AST served as the control reference, which is the accepted gold standard.

3.Key Findings

Summarize the main findings : The study analyzed 318 positive blood cultures and found that dAST results were available ~35 hours earlier than conventional AST. Overall, dAST achieved a 91.5% categorical agreement with cAST across 3,561 organism–antibiotic combinations with acceptable error rates (VME 3.6%, ME 3.3%, mE 5.2%).High agreement was seen for most common pathogens such as Staphylococcus aureus, Pseudomonas aeruginosa and Acinetobacter baumannii. Importantly, dAST-guided reporting significantly improved the prescribing of active antibiotics though it had limited impact on optimizing use of WHO "ACCESS" antibiotics.

Were the results statistically and clinically significant? Yes. The results were statistically significant as shown by the marked improvement in prescribing ACTIVE antibiotics after dAST (73.0% vs 89.3%,

$p < 0.001$). They were also clinically significant since dAST reduced turnaround time by ~35 hours and achieved high categorical agreement (>90%) for most key pathogen–antibiotic combinations enabling earlier and more accurate treatment decisions in bloodstream infections.

4.Critical Appraisal

Are the conclusions supported by the results? Yes. The conclusions were well supported by the results. The study demonstrated that dAST significantly shortened turnaround time, showed high categorical agreement with cAST and improved the timely use of ACTIVE antibiotics gave the answer for authors' research. Although the impact on WHO "ACCESS" antibiotic prescribing was limited, this was transparently reported making the conclusions balanced and consistent with the findings.

Are alternative explanations considered? Yes, the study considered alternative explanations for its findings. It highlighted that variations in dAST performance may due to unstandardized inoculum and manual handling. The authors also acknowledged that most prior studies are from Western settings, where resources differ. However, factors like clinician prescribing habits and stewardship policies were not deeply explored.

Have the authors discussed strengths and limitations? Yes, the authors discussed both strengths and limitations. **Strengts :** prospective study using clinical samples with updated CLSI guidelines and recent identification methods (MALDI-TOF, VITEK 2). They also highlighted the low-cost applicability of dAST in resource-limited settings.

Limitations : This Study conducted in the laboratory which works from 9am to 4pm only,also a single center based study.it showed potential variability due to unstandardized inoculum and manual methods and the sample size calculation was not performed. They also acknowledged that the impact on antibiotic prescribing may have been influenced by local clinical practices and stewardship gaps.

How does the study compare with previous similar studies? This study results about categorical agreement comparable to previous studies from India and China and similar to results from the US, Canada, and Australia. While error rates were slightly higher than those reported in China, they were consistent with Australian data. As observed in earlier studies, "piperacillin-tazobactam showed weaker agreement, whereas *Pseudomonas aeruginosa* and *Acinetobacter spp.* demonstrated excellent reliability".

How would you improvise on this if it was you? 1)I will conduct this study in multicenter with larger to get generalized results.I Will calculate sample sizes formally with known p,q values. 2)I will use Standardize inoculum preparation to improve reproducibility. 3)later I will Integrate dAST reports with Antimicrobial stewardship programs.

5.Relevance to Practice or Research

How does this study impact clinical practice, policy, or future research?

Impact of this study in clinical practice : This study shows that dAST enables faster, reliable results improving timely use of active antibiotics in bloodstream infections. Reduce the use of WATCH drugs not uncommonly to prevent development of resistance against them.

This Study helps to create a new clinical policy with dAST in bloodstream infection and integration into stewardship programs. as a low-cost diagnostic tool in resource-limited settings.

Future research should focus on multicenter validation, standardization and cost-effectiveness to guide broader implementation.

Does it raise new questions or open avenues for further work?

Yes, the study raises new questions and avenues for further work. It highlights the need to evaluate dAST in multicenter and diverse healthcare settings.

6.Conclusion : This study results gave valuable contribution in proving that dAST is best,low-cost,rapid and reliable method in LMICs to adjusting antibiotics in bloodstream infection. It will helps to safeguard those watch,reserve group antibiotics for future generation by reduce the unneccessory usage of those drugs critical healthcare setup.

Parasitology:

Di Pietra G, Gargiulo R, Ortalli M, Petrullo L, Oliva E, Raglio A, et al. Comparative analysis of commercial and "in-house" molecular tests for the detection of intestinal protozoa in stool samples. Parasites Vectors. 2025;18:320

Dr. Mohammed Abdul Basith, 2nd Year, Govt Medical College, Nizamabad

Title of the Article: Comparative analysis of commercial and "in-house" molecular tests for the detection of intestinal protozoa in stool samples.

Journal Name: BMC (Bio Med Central)

Journal Year: 2025, 4th June (Accepted)

2025**,** 1st August (Published)

Volume: 18

Pages: 1-11

Authors: Guiseppe Di Pietra[1,2], Raffaele Gargiulo[3], Margherita Ortalli[4], Luciana Petrullo[5], Ester Oliva[6], Annibale Raglio[7], Annachiara Frigo[8], Ignazio Castagliuolo[2,9], Valeria Besutti[9]

Background & Rationale:

Q1) What is the clinical or research problem addressed?

A)Technical difficulties encountered in the diagnosis of parasitic diseases through molecular technique (RT-PCR) in stool samples.

Q2) Why is this study important in the current context?

A)-Routine testing for stool samples is performed mostly for bacterial pathogens.

-Parasites are not commonly tested and often neglected.

-Failure to promptly diagnose parasitic diseases in stool samples can result in significant complications.

Q3) Briefly describe prior knowledge and the knowledge gap this study attempts to fill?

A)Prior Knowledge:

-The diagnosis of parasitic infections in stool has traditionally depended on microscopic techniques such as wet mount, concentration methods, and staining, which are cost-effective but require specialized expertise.

-The accurate detection of parasites by RT-PCR, even in low concentrations, yields valuable information regarding regional prevalence and supports clinical suspicion.

Knowledge Gap:

-Emerging parasites such as Blastocystis, Dientamoebafragilis which are often neglected as they are more prevalent in areas with poverty and poor sanitation were also detected in this study by PCR, thereby addressing a significant knowledge gap.

-The molecular assays assessed in this study helped in the detection of multiple parasites in a single stool sample.

-More over RT-PCR provides results within hours which enables faster clinical diagnosis and outbreak control.

-With the help of RT-PCR we can detect the parasites without relying on culture.

Study Design & Methods:

Q1) What was the primary aim or hypothesis? Is it clearly stated and relevant?

A) To assess the performance of the commercial RT-PCR (Aus Diagnostics Company) in combination with the in-house RT-PCR against the conventional microscopic reference method.

Q2)Was the methodology appropriate, comprehensive and up to date?

A)Yes

-Preservatives were used as the stool samples were not immediately processed.

-A validated DNA extraction method was employed (MagNA technology).

-Positive and negative controls were used in both “In-house” and “commercial”assays.

Q3) Were the inclusion/exclusion criteria, sample size and controls appropriate?

A)-Inclusion/exclusion criteria were not mentioned in the methodology.

-Sample size and controls were appropriate.

Key findings:

Q1) Summarize the main findings?

A)-Out of the 355 stool samples, 230 stool samples were deemed fresh, whereas 125 were preserved in para-pak media.

-Microscopic examination revealed that 285 samples were positive for parasitic stool infections:

a) Giardia duodenalisin 78 stool samplesb) Cryptosporidium spp. in 18 stool samples

c) Dientamoebafragilis in 67 stool samplesd) Entamoeba histolytica/dispar in 21 stool samples

e) Blastocystis hominis in 62 stool samplesf) Co-infections (≥ 2 parasites) in 39 stool samples

Giardia duodenalisdetection	Conventional	Commercial RT-PCR	In-House RT-PCR
230 fresh stool samples	66 were positive	61 were positive	65 were positive
125 preserved stoolsamples	23 were positive	23 were positive	26 were positive
Out of total 355 samples	89 were positive	84 were positive	91 were positive

Commercial RT-PCR: 8 FN, 3 FP results; In-House RT-PCR: 6 FN, 8 FPresults

Cryptosporidium spp.detection	Conventional	Commercial RT-PCR	In-House RT-PCR
230 fresh stool samples	16 were positive	15 were positive	12 were positive
125 preserved stool samples	3 were positive	3 were positive	3 were positive
Out of total 355 samples	19 were positive	18 were positive	15 were positive

Commercial RT-PCR: 4 FN, 3 FP results; In-House RT-PCR: 4 FN results

Dientamoebafragilisdetection	Conventional	Commercial RT-PCR	In-House RT-PCR
230 fresh stool samples	64 were positive	55 were positive	54 were positive
125 preserved stool samples	31 were positive	31 were positive	31 were positive
Out of total 355 samples	95 were positive	86 were positive	85 were positive

Commercial RT-PCR: 30 FN, 21 FP results; In-House RT-PCR: 30 FN, 20 FP results

Q2)Were the results statistically and clinically significant?

A) -Statistically significant as the cohen's kappa score (k-score) was > 0.8 which shows an excellent level of agreement between the two molecular assays.

-Clinically not significant (as no clinical history was available to support the positive results)

Critical Appraisal:

Q1) Are the conclusions supported by the results?

A) Yes(as both the molecular assays showed remarkable results in terms of sensitivity and specificity for the detection of most of the parasites. However, the results were not consistent for the detection of D. fragilis).

Q2) Are alternates explanations considered?

A) Yes (Had mechanical preprocessing been performed on the stool samples, the detection rate would have been better, as high-quality DNA could be extracted).

Q3) Have the authors discussed strengths and limitations?

A) Yes

Q4) How does the study compare with previous similar studies?

A) This study was partially consistent with prior studies that revealed variable sensitivity and specificity in detecting parasites, necessitating a detailed discussion for improved understanding.

Q5) How would you improvise on this if it was you?

A)-Adequate amount of stool should have been collected (0.5-2g)

-By employing mechanical disruptionto the stool sample using bead-beating(e.g. silica)

-Institute's should regularly participate in external QA programs to ensure accuracy and reliability of results.

-Regularly validate performance of RT-PCR: specificity.

Q6) Strengths of this study.

A)-Commercial RT-PCR and In-House RT-PCR exhibited remarkable efficacy when used in combination utilising fixed faecal specimens for the detection of G. duodenalis and Cryptosporidium spp.

-Neglected parasites like Blastocystis and Dientamoebafragiliswere also detected in this study.

-Results obtained by RT-PCR are objective and less dependent on human error.

-RT-PCR helps in parasitic load estimation, thereby increasing the sensitivity and also fastens turnaround time and helps in accurate quantification.

Q7) Major limitations or biases.

A)-No access to the patient's clinical records which includes critical demographic information such as age, sex and comorbidities.

-Another confounding variable arises from the study's dependence on traditional microscopic analysis as the benchmark for diagnosing parasitic infections, even though there is substantial evidence of variability in sensitivity that relies on the expertise of the microscopist.

-Mechanical preprocessing was not employed for the fresh and fixed samples to improve the efficacy of DNA extraction.

-Unavailability of the means to sequence the amplicons to reexamine the samples which were negative on microscopic examination but tested positive by molecular assays.

Q8) Your suggestions for improvements.

A)-Homogenization of stool before processing to ensure even distribution.

-Incorporation of mechanical disruption (e.g. Silica Gel) to improve the quality of extracted genomic DNA.

-By employing stools-specific extraction kit to remove PCR inhibitors.

-By Correlating positive results with clinical historywe can distinguish between the active infection and the colonization.

Q) How does this study impact clinical practice, policy or future research?

A)-Detects even low levels of parasitic nucleic acids thus helping in detection of asymptomatic cases.

-Reduces false negative results compared to microscopy.

-Helps in epidemiological surveillance by providing rapid, sensitive and specific detection of pathogen's genetic material.

-RT-PCR helps differentiate between pathogenic and non-pathogenic strains, guiding the correct therapy and avoiding unnecessary medication.

-RT-PCR can be used in clinical trials to quantify parasite load before and after treatment, enabling precise assessment of treatment effectiveness.

Q) Does it raise new questions or open avenues for further work?

A) Yes

-What is the correlation between parasite load and clinical severity?

-How do we interpret RT-PCR results in the absence of clinical symptoms?

-Can point-of-care RT-PCR systems be developed for endemic regions?

-What are the best internal controls and reference standards for stool-based RT-PCR?

Conclusion:

-Although the two molecular assays assessed in this study showed excellent results in identifying parasitic stool infections, especially in the fixed stool samples which provided high-quality DNA for PCR analysis,but they also presented false positive and false negative outcomes which could have been prevented had the mechanical preprocessing been conducted prior to subjecting the samples toMagNA technology.

-Moreover, the identification of D. fragilis remains inconsistent as it is evident that the trophozoites of D. fragilis are very fragile and susceptible to harsh environmental conditions making it difficult to survive for long duration.

-The biggest drawback of this study was lack of clinical records to support thepositive results.

-It is clear that PCR techniques yield remarkable and promising outcomes concerning accurate parasite detection.

-Nonetheless, it is crucial to further standardize the procedures for sample collection, preservation, and nucleic acid extraction in order to obtain consistent results.

Virology:

Patil VD, Chowdhary R, Malhotra AG, Singh J, Biswas D, Joshi R, et al. Uncovering SARS-CoV-2 molecular epidemiology across the pandemic transition: insights into transmission in clinical and environmental samples. Viruses. 2025;17(5):726

Dr. Mythili T, 1st Year, Govt Medical College, Kadapa

Title of the article:

Uncovering SARS-COV-2 Molecular Epidemiology Across the Pandemic Transition: Insights into Transmission in Clinical and Environmental Samples.

Journal, Year, Volume, Pages:

Viruses, 2025, Vol.17, Article 726.

Authors:

Vrushali D.Patil, Rashmi Chowdhary, Anvita Gupta Malhotra, Jitendra Singh, Debasis Biswas, Rajnish, Jagat Rakesk Kanwar

Background and Rationale:

This study explores the transmission of SARS-CoV-2 using both clinical and environmental samples. While respiratory droplets remain the main route of spread, evidence points toward possible fecal-oral transmission, particularly in low-sanitation regions. Wastewater surveillance has proven useful as a cost-effective early warning tool, yet correlations between clinical and sewage data in India are limited. This study addresses that gap by longitudinally assessing nasopharyngeal, saliva, stool and sewage samples from Central India to investigate viral persistence, variant trends and silent circulation.

Study Design and Methods:

- Aim: This study clearly aims to analyze SARS-CoV-2 transmission through clinical (nasopharyngeal, saliva, stool) and sewage samples and to track variant epidemiology from 2021-2024.
- Design: Observational study
- Sample size: 60 COVID-19 positive patients; 156 sewage samples from a hospital.
- Techniques: qRT-PCR, Next Generation Sequencing (NTS), virus isolation using Vero E6 cell lines.
- Strengths:

  Use of advanced molecular methods,

  Inclusion of wide range of sample types (Clinical and Environmental).
- Limitations: No COVID negative group, Small clinical cohort (n=60).

Key Findings:

- Viral RNA detected in all nasal swabs, 90% of saliva and 30% of stool samples.
- Infectious virus recovered from 70% of nasal and 65% of saliva samples, but only 2 stool samples from immunocompromised individuals.
- Sewage samples had viral RNA, though no live virus.
- Waste water surveillance picked up viral RNA 1-2 months before new clinical cases emerged, demonstrating its predictive power.
- Variants tracked aligned with known pandemic waves: Delta (2021), BA.2.75(2022), XBB(2023) and JN.1(2024).
- Some patients continued shedding virus in stool after respiratory samples tested negative, suggesting possible faeco-oral spread.
- Statistical and clinical significance: The findings are clinically valuable for outbreak forecasting, though the absence of statistical analysis limits confidence in comparisons.

Critical Appraisal:

Strength of the study:

- Multi-sample approach (nasopharyngeal, saliva, stool, sewage) provides a broad view of transmission.

- Extended observation over three years.
- Identification of hidden viral circulation in sewage..
- Advanced molecular methods (qRT-PCR, Next Generation Sequencing, Virus isolation) ensures reliability of findings.
- Saliva testing validation supports a non-invasive alternative to NP swabs.
- Early warning potential of wastewater surveillance detects viral RNA weeks before clinical cases.

Major Limitations or Biases:

- Small clinical cohort (n=60) limits generalizability of results.
- Single center study introduces regional bias, not representatives of wider populations.
- No control group (COVID-negative patients or community sewage sites) weakens comparative analysis.
- Inconsistent stool sampling (only 37 patients consented, no serial samples) reduces robustness of faeco-oral transmission findings.
- No statistical modeling or quantitative viral load analysis weakens claims of correlation between sample types and epidemic trends.
- Challenges of scaling wastewater surveillance (cost, infrastructure) remain unexplored.

Suggestions for improvement:

- Increase Sample size and diversity.
- Add COVID negative patients as a control groups.
- Enhance stool sampling strategy, ensure serial collections from all patients.
- Correlate viral loads in NP, saliva, stool and sewage. Relate viral loads to clinical severity and shedding duration.
- Clearly document ethical approval, informed consent and data protection methods
- Provide statistical summaries, graphs and timelines of variant emergence.

Relevance to Practice or Research:

- Practice: It validates saliva testing and wastewater monitoring as practical diagnostic and surveillance strategies.
- Research: It opens pathways for larger multicentric studies, advanced sequencing and modeling of SARS-CoV-2 transmission.

Conclusion:

This study highlights saliva as a reliable alternative to nasopharyngeal swabs and wastewater surveillance as an effective early-warning tool for SARS-CoV-2. While limited by small sample size, single-center design and lack of controls, it provides important groundwork for larger multicentric studies that can strengthen pandemic preparedness and public health policy.

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