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Original Research Article

SILENT RESISTANCE: EMERGING ANTIMICROBIAL PATTERNS IN VAGINAL INFECTIONS AT A RURAL MEDICAL COLLEGE HOSPITAL

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ABSTRACT

Background: Abnormal vaginal discharge is a common clinical presentation among women of reproductive age, with bacterial vaginosis, vulvovaginal candidiasis, and trichomoniasis being the predominant causes. Increasing antimicrobial resistance, biofilm formation, and shifts in vaginal microbiota have reduced the effectiveness of syndromic management, particularly in resource-limited settings. Local microbiological surveillance is essential to guide empirical therapy and antimicrobial stewardship. The objective is to determine the spectrum of pathogens associated with vaginal discharge and to assess their antimicrobial susceptibility patterns in a rural medical college hospital.

Materials and Methods: A prospective, hospital-based cross-sectional observational study was conducted over one year in the Departments of Obstetrics & Gynaecology and Microbiology at a rural tertiary care hospital. A total of 449 women aged 18–45 years presenting with abnormal vaginal discharge were included using convenience sampling. Vaginal swabs were collected under aseptic conditions and processed using standard microbiological techniques. Antimicrobial susceptibility testing was performed using the Kirby–Bauer disc diffusion method following CLSI guidelines. p-value< 0.05 considered statistically significant.

Results: A total of 472 isolates were obtained from 449 participants. Normal vaginal flora constituted 47.7% of isolates followed by Gram-negative bacteria (21.0%), Gram-positive bacteria (14.8%), and fungal growth (16.1%). The most common pathogens were methicillin-resistant coagulase-negative staphylococci (10.8%), Enterococcus (10.4%), and Candida species (16.1%). Gram-negative organisms more prevalent in older age groups with p -value <0.001. Enterobacteriaceae showed high resistance to beta-lactam antibiotics and Gram-positive organisms exhibited high resistance to penicillin but showed relatively better susceptibility to linezolid and vancomycin. Multidrug-resistant organisms including vancomycin-resistant enterococci and a pan-drug-resistant Klebsiella isolate were also identified.

Conclusion: The study reveals a high burden of pathogenic vaginal isolates with emerging antimicrobial resistance in a rural tertiary care setting. The presence of multidrug-resistant organisms highlight the limitations of syndromic management. These findings underscore the need for microbiology-guided therapy, routine local antibiogram surveillance and strengthen the antimicrobial stewardship to ensure effective management of vaginal infections.

Keywords: Vaginal discharge, Antimicrobial resistance, Rural health, Antibiogram.

INTRODUCTION

Abnormal vaginal discharge is among the commonest reasons women of reproductive age groupseeking gynaecological care worldwide.It reflects a heterogeneous set of disorders that substantially impair quality of life. The majority of symptomatic cases are due to three causes bacterial vaginosis (BV), vulvovaginal candidiasis (VVC), and trichomoniasis — each of which carries distinct microbiological features with overlapping clinical consequences including pelvic inflammatory disease, adverse pregnancy outcomes, and increased susceptibility to sexually transmitted infections.[1]

Recent molecular and epidemiological work has shown that Bacterial Vaginosis not as a single-pathogen illness but as a polybacterial dysbiosis characterized by loss of Lactobacillus dominance and expansion of anaerobicbacterias. The composition and stability of the vaginal microbiota determine susceptibility to both recurrent dysbiosis and acquisition of sexually transmitted pathogens.[2] This ecological view helps explain why Bacterial Vaginosis frequently recurs after standard.[3]

Therapeutic management of Bacterial vaginosis is challenged by two related problems. First, commonly used agents — nitroimidazoles for BV and trichomoniasis, and azoles for candidiasis — remain broadly effective in many settings, but treatment failure and recurrence are increasingly reported and have multifactorial causes (microbial persistence, biofilm formation, and organism-level resistance).[4,5] Second, biofilm-associated colonies and a growing prevalence of non-albicans Candida and other resistant organisms reduce antifungal and antibacterial susceptibility. Hence limiting the effectiveness of syndromic, empirical treatment that remain common in resource-limited settings.[6]

In India where recent regional studies shown that there is a wide heterogeneity in pathogen distribution and antimicrobial susceptibility. There is a raising concerns about the continued reliance on syndromic management without local antibiograms. A 2025 scoping review of studies from the region found variable prevalence of Gardnerella, Mobiluncus, Staphylococcus spp., and others, and reported moderate to high resistance to several commonly used antibiotic classes, underscoring the need for microbiological surveillance to guide empiric therapy.[7] At the same time, antimicrobial resistance in sexually transmitted pathogens remains a global public-health problem that can spread via travel and population mobility, reinforcing the urgency of local surveillance and stewardship.[8]

Due to the high clinical burden, microbiome-mediated susceptibility, biofilm-associated persistence, and shifting susceptibility patterns, a prospective, culture-based studies that describe local aetiology and antibiograms are essential to optimise patient care and antimicrobial stewardship, particularly in rural and semi-urban hospitals where laboratory resources are constrained. Hence the present study was conducted at a rural medical college hospital to find the prevalence of pathogens in vaginal discharge and their antimicrobial susceptibility to inform local empirical treatment guidelines.

MATERIALS AND METHODS

Study Design and Setting: This research was executed as a prospective, hospital-based, cross-sectional observational study spanning 12 months, from January 2025 to December 2025. The research was conducted in the Department of Obstetrics and Gynaecology, in partnership with the Department of Microbiology at a rural medical college hospital.

Study Populations: The study population comprised women of reproductive age who attended the gynaecology outpatient department with complaints of abnormal vaginal discharge during the study period.

Inclusion and Exclusion Criteria:

Women between the ages of 18 and 45 who given informed consent were included in the study. Participants who had not received systemic or topical antibiotics in the prior seven days were included in the study. Pregnant women, immunocompromised individuals, those who had used vaginal medications or douches in the preceding 72 hours were excluded from the study.

Sample Size and Method of Sampling:

Convenience sampling was used to enrol all eligible patients who came to the gynaecology outpatient department during the study period. Total of 449 participants were recruited for the study.

Data Collection: After getting informed consent from the study participants a structured study questionnaire was used to get a detailed clinical history.

Trained clinicians used sterile cotton swabs to collect vaginal swabs. Samples were collected from the posterior fornix or lateral vaginal wall with no contamination from the vulva or cervix and the swabs that were collected were quickly sent to the microbiology lab for more work.

Standard microbiological culture methods to isolate and identify bacterial and fungal pathogens from vaginal swab specimens. Standard methods like colony morphology, Gram staining, and the appropriate biochemical tests to identify the isolates, following standard lab procedures. The Kirby–Bauer disc diffusion method was used to test for antimicrobial susceptibility based on the Clinical and Laboratory Standards Institute (CLSI). Antibiotics were chosen based on what doctors usually prescribe for vaginal infections.The CLSI criteria were used to measure the zone diameters and classify them as sensitive, intermediate or resistant.

Data Analysis and Statistics: The collected data were entered into a MS Excel and analysed using Jamovi.Categorical variables were expressed as proprotions. Fischer exact test were used to find the

associations. p-value less than 0.05 were considered statistically significant.

RESULTS

Table 1: Distribution of Study Participants by Age, Isolate Characteristics, and Pathogen Profile

Variable	Category	n	Percentage (%)
Age Distribution (Persons) (n = 449)	18–30	155	34.5
	30–45	196	43.7
	45–60	79	17.6
	60–75	15	3.3
	75–85	4	0.9
	Total	449	100
Age Distribution (Isolates) (n = 472)	18–30	161	34.1
	30–45	207	43.9
	45–60	82	17.4
	60–75	15	3.2
	75–85	7	1.5
	Total	472	100
Pathogen Profile (n = 472)	Gram Negative	99	21
	Gram Positive	70	14.8
	Mixed vaginal flora	2	0.4
	Fungal Growth	76	16.1
	Normal Growth	225	47.7
	Total	472	100

Table 2: Association between age group and isolated pathogen

Age Group (Years)	Fungal Growth	Gram Negative	Gram Positive	Mixed Vaginal Flora	Normal Growth	p-value
18–30	30 (18.6%)	23 (14.3%)	24 (14.9%)	0 (0.0%)	84 (52.2%)	<0.001*
30–45	29 (14.0%)	42 (20.3%)	28 (13.5%)	0 (0.0%)	108 (52.2%)	
45–60	14 (17.1%)	20 (24.4%)	18 (22.0%)	2 (2.4%)	28 (34.1%)	
60–75	3 (20.0%)	7 (46.7%)	0 (0.0%)	0 (0.0%)	5 (33.3%)	
75–85	0 (0.0%)	7 (100.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	
Total	76 (16.1%)	99 (21.0%)	70 (14.8%)	2 (0.4%)	225 (47.7%)	

*Fischer Exact test used

Table 3: Spectrum of Pathogens Isolated from High Vaginal Swab

Pathogen Isolated	n	proportions
Normal vaginal flora	227	48.10%
Enterococcus	49	10.40%
Candida Albicans	41	8.70%
Candida non albicans	35	7.40%
Ecoli	26	5.50%
MRCONS	51	10.80%
Streptococci	13	2.80%
Klebsiella pneumoniae	12	2.50%
Vancomycin resistant enterococcus	7	1.50%
Vancomycin Intermediate enterococcus-VIE	3	0.60%
Methicillin sensitive coagulase negative staphylococcus- MSCONS	3	0.60%
Methicillin sensitive staphylococcus aureus	3	0.60%
Acinetobacter	1	0.20%
PAN DR Klebsiella Pneumoniae	1	0.20%

Table 4: Antibiotic susceptibility pattern of Enterobacteriaceae

Antibiotic	Klebsiella(13)				E. coli (26)			
	I	S	R	Not Tested	I	S	R	Not Tested
Ampicillin	0 (0%)	0 (0%)	5 (38.5%)	8 (61.5%)	3 (11.5)	2 (7.7)	14 (53.8)	7 (26.9)
Ciprofloxacin	3 (23.1%)	5 (38.5%)	4 (30.8%)	1 (7.7%)	2 (7.7)	8 (30.8)	9 (34.6)	7 (26.9)
Cefazolin	3 (23.1%)	3 (23.1%)	6 (46.2%)	1 (7.7%)	4 (15.4)	8 (30.8)	11 (42.3)	3 (11.5)
Ceftriaxone	0 (0%)	5 (38.5%)	6 (46.2%)	2 (15.4%)	1 (3.8)	15 (57.7)	7 (26.9)	3 (11.5)
Tetracycline	0 (0%)	6 (46.2%)	3 (23.1%)	4 (30.8%)	0 (0)	15 (57.7)	5 (19.2)	6 (23.1)
Amoxyclav	4 (30.8%)	5 (38.5%)	2 (15.4%)	2 (15.4%)	5 (19.2)	11 (42.3)	5 (19.2)	5 (19.2)
Meropenem	0 (0%)	9 (69.2%)	2 (15.4%)	2 (15.4%)	0 (0)	21 (80.8)	2 (7.7)	3 (11.5)
Ceftazidime	1 (7.7%)	6 (46.2%)	6 (46.2%)	0 (0%)	2 (7.7)	12 (46.2)	10 (38.5)	2 (7.7)
Piperacillin–Tazobactam	3 (23.1%)	7 (53.8%)	2 (15.4%)	1 (7.7%)	4 (15.4)	18 (69.2)	1 (3.8)	3 (11.5)
Levofloxacin	1 (7.7%)	6 (46.2%)	3 (23.1%)	3 (23.1%)	1 (3.8)	10 (38.5)	8 (30.8)	7 (26.9)
Cotrimoxazole	0 (0%)	9 (69.2%)	4 (30.8%)	0 (0%)	1 (3.8)	17 (65.4)	5 (19.2)	3 (11.5)
Cefepime	0 (0%)	6 (46.2%)	6 (46.2%)	1 (7.7%)	4 (15.4)	14 (53.8)	5 (19.2)	3 (11.5)

Table 5: Antibiotic susceptibility pattern of Streptococcoi (n=13)

Antibiotic	I	S	R	Not Tested
Tetracycline	2 (15.38%)	4 (30.77%)	5 (38.46%)	2 (15.38%)
Levofloxacin	2 (15.38%)	8 (61.54%)	2 (15.38%)	1 (7.69%)
High-Level Gentamicin	0 (0%)	6 (46.15%)	0 (0%)	7 (53.85%)
Linezolid	2 (15.38%)	10 (76.92%)	1 (7.69%)	0 (0%)
Penicillin	0 (0%)	3 (23.08%)	10 (76.92%)	0 (0%)
Vancomycin	1 (7.69%)	10 (76.92%)	1 (7.69%)	1 (7.69%)
Chloramphenicol	2 (15.38%)	8 (61.54%)	2 (15.38%)	1 (7.69%)

Table 6: Antibiotic susceptibility pattern of Enterococcus(n=59)

Antibiotics	I	S	R	Not Tested
Tetracycline	3 (5.08%)	19 (32.20%)	28 (47.46%)	9 (15.25%)
Levofloxacin	5 (8.47%)	34 (57.63%)	19 (32.20%)	1 (1.69%)
High-Level Gentamicin	0 (0%)	53 (89.83%)	2 (3.39%)	4 (6.78%)
Linezolid	6 (10.17%)	27 (45.76%)	18 (30.51%)	8 (13.56%)
Penicillin	0 (0%)	3 (5.08%)	52 (88.14%)	4 (6.78%)
Vancomycin	13 (22.03%)	31 (52.54%)	8 (13.56%)	7 (11.86%)
Chloramphenicol	2 (3.39%)	32 (54.24%)	8 (13.56%)	17 (28.81%)

Table 7: Antibiotic susceptibility pattern of MRCONS (n=51):

Antibiotics	Methicillin Resistant Coagulase Negative Staphylococcus			
	I	S	R	Not Tested
Ciprofloxacin	2 (3.92%)	22 (43.14%)	16 (31.37%)	11 (21.57%)
Gentamicin	0 (0%)	38 (74.51%)	3 (5.88%)	10 (19.61%)
Erythromycin	7 (13.73%)	8 (15.69%)	36 (70.59%)	0 (0%)
Linezolid	10 (19.61%)	33 (64.71%)	7 (13.73%)	1 (1.96%)
Cotrimoxazole	2 (3.92%)	33 (64.71%)	16 (31.37%)	0 (0%)
Clindamycin	3 (5.88%)	33 (64.71%)	13 (25.49%)	2 (3.92%)
Chloramphenicol	0 (0%)	38 (74.51%)	6 (11.76%)	7 (13.73%)
Cefoxitin	0 (0%)	3 (5.88%)	48 (94.12%)	0 (0%)
Tetracyclin	1(1.9%)	33 (64.7%)	8 (15.68%)	9 (17.64%)

Table 8: Antibiotic susceptibility pattern of MSSA (n=3)and MSCONS(n=3)

Antibiotic	Methicillin -Sensitive Staphylococcus aureus				Methicillin-Sensitive Coagulase Negative Staphylococcus			
	I	S	R	Not Tested	I	S	R	Not Tested
Cefoxitin	0 (0%)	3 (100%)	0 (0%)	0 (0%)	0 (0%)	3 (100%)	0 (0%)	0 (0%)
Ciprofloxacin	0 (0%)	1 (33.3%)	1 (33.3%)	1 (33.3%)	0 (0%)	2 (66.7%)	0 (0%)	1 (33.3%)
Cotrimoxazole	0 (0%)	3 (100%)	0 (0%)	0 (0%)	0 (0%)	3 (100%)	0 (0%)	0 (0%)
Gentamicin	0 (0%)	2 (66.7%)	0 (0%)	1 (33.3%)	0 (0%)	2 (66.7%)	0 (0%)	1 (33.3%)
Linezolid	0 (0%)	2 (66.7%)	1 (33.3%)	0 (0%)	2 (66.7%)	1 (33.3%)	0 (0%)	0 (0%)
Tetracycline	0 (0%)	2 (66.7%)	1 (33.3%)	0 (0%)	0 (0%)	2 (66.7%)	0 (0%)	1 (33.3%)
Erythromycin	1 (33.3%)	1 (33.3%)	1 (33.3%)	0 (0%)	2 (66.7%)	1 (33.3%)	0 (0%)	0 (0%)
Clindamycin	0 (0%)	2 (66.7%)	1 (33.3%)	0 (0%)	2 (66.7%)	1 (33.3%)	0 (0%)	0 (0%)
Chloramphenicol	1 (33.3%)	1 (33.3%)	0 (0%)	1 (33.3%)	0 (0%)	2 (66.7%)	0 (0%)	1 (33.3%)

Among 449 participants 472 vaginal isolates were obtained, predominantly from women aged 30–45 years. Normal vaginal flora accounted for nearly half of isolates (47.7%), followed by Gram-negative (21.0%), Gram-positive (14.8%), and fungal growth (16.1%). Age was significantly associated with isolate type with p value <0.001 with Gram-negative organisms more common in older women and normal flora and fungi in younger groups. Microbiological profiling showed predominance of normal flora, methicillin-resistant coagulase-negative staphylococci, Enterococcus, and Candida species. Enterobacteriaceae demonstrated high resistance to beta-lactams but retained sensitivity to carbapenems. Gram-positive organisms showed resistance to penicillin, with senstivity to linezolid and vancomycin at the same time methicillin-resistant isolates exhibited multidrug resistance.

DISCUSSION

The present study highlights a clinically important but often under-recognized pattern of vaginal infections in a rural medical college hospital: although normal vaginal flora remained the single most common culture outcome. Women aged 30–45 years contributed the largest share of participants and isolates, but the distribution of pathogens varied significantly by age, with Gram-negative organisms becoming more frequent in older women. This age-wise shift suggests that vaginal infection ecology may change across the reproductive and peri-menopausal spectrum, possibly owing to hormonal changes, altered vaginal pH, comorbidities, and repeated antibiotic exposure, though these factors were not directly measured in the present study.

A major finding in this series was the predominance of Enterococcus, methicillin-resistant coagulase-negative staphylococci (MRCONS), and Candida

species among abnormal isolates. This differs from several Indian and international studies in which Escherichia coli was the leading aerobic bacterial isolate in symptomatic vaginal discharge or aerobic vaginitis. For example, studies from Puducherry, Bangalore, and Visakhapatnam reported E. coli as a common or predominant bacterial isolate, while a retrospective study from Italy also found a high burden of enteric Gram-negative organisms in vaginitis.[9-12] In contrast, in the current study Enterococcus and MRCONS were more prominent. Because coagulase-negative staphylococci can sometimes represent colonizers rather than true pathogens, their high frequency should also be interpreted in light of clinical symptoms and inflammatory findings, which were not correlated here.

Candida albicans remained slightly more common than non-albicans Candida. This is important because multiple recent studies, including Indian data, have reported an increasing contribution of non-albicans Candida in vulvovaginal infection, especially in recurrent or treatment-exposed cases.[9,13] Present study findings therefore align with the broader concern that empirical syndromic treatment, especially when it assumes only C. albicans, may miss the changing epidemiology of vaginal candidiasis.

Younger women more often showed normal flora or fungal growth, whereas Gram-negative isolates were relatively more frequent in older age groups. A similar age-related drift toward aerobic and enteric organisms has been noted in aerobic vaginitis literature, especially among peri-menopausal and post-menopausal women, where reduced estrogen and lactobacillary depletion may favor colonization by intestinal bacteria and inflammatory flora.[12,14]

The resistance pattern among Enterobacteriaceae in this study is particularly concerning. Both E. coli and Klebsiella showed substantial resistance to ampicillin and cephalosporins, but sensitive to meropenem and piperacillin–tazobactam. This broadly agrees with Indian and non-Indian studies showing that vaginal Gram-negative isolates increasingly display poor susceptibility to commonly used first-line drugs, while carbapenems remain more sensitive.[12,15–17] At the same time identification of a pan-drug-resistant Klebsiella pneumoniae isolate, even if only one case, is a serious warning signal.

Among Gram-positive cocci, the high burden of penicillin resistance in Enterococcus and Streptococci is another notable result. Enterococcus showed poor susceptibility to penicillin and only moderate susceptibility to vancomycin and linezolid, with vancomycin-resistant and vancomycin-intermediate enterococcal isolates also present. This is more alarming than many earlier reports, where vancomycin and linezolid retained near-universal activity against Gram-positive vaginal isolates.[12,15,18] In that sense, current results may reflect a local escalation of resistance among vaginal Gram-positive isolates, especially enterococci, and underscore the need for close microbiological surveillance in rural referral centers.

In the present study, MRCONS showed marked resistance to cefoxitin and erythromycin, with only moderate-to-good susceptibility to linezolid, cotrimoxazole, clindamycin, gentamicin, and chloramphenicol.Previous studies have also shown that staphylococcal vaginal isolates may carry substantial macrolide and methicillin resistance, while linezolid generally remains active.[15,19] This pattern again argues against blind empirical prescribing, particularly of macrolides or beta-lactams, for persistent vaginal discharge.

Similar to studies from Chennai, Puducherry, Jaipur, and Bangalore, it confirms that vaginal infections in Indian hospital settings are microbiologically heterogeneous and often include Candida, E. coli, Klebsiella, Enterococcus, and staphylococci.[9,10,15,20] However, compared with many of those studies, current study shows a stronger signal of resistant Enterococcus, methicillin-resistant CONS, and even vancomycin non-susceptibility. That makes this study valuable because it reflects a rural setting where resistance surveillance is often sparse, yet empirical antibiotic use may be common.

The findings also have practical therapeutic implications that preserved activity of carbapenems against many Gram-negative isolates and the retained susceptibility of some Gram-positive isolates to linezolid and vancomycin indicate that higher-end agents are still effective in many cases; however, these drugs are not ideal for routine empiric use in uncomplicated vaginitis because of cost stewardship concerns, and the risk of accelerating resistance.

CONCLUSION

This study demonstrates a substantial burden of pathogenic vaginal isolates with emerging antimicrobial resistance in a rural tertiary care setting with a predominance of normal flora. The presence of multidrug-resistant organisms, including vancomycin non-susceptible enterococci and resistant Klebsiella shows the growing threat of “silent resistance” in routine gynaecological infections.

The high resistance to commonly used antibiotics shows the limitations of syndromic management. These findings emphasize the need for microbiology guided treatment with regular antibiogram surveillance and strengthened antimicrobial stewardship to ensure management of vaginal infections.

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