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A STUDY ON MICROBIOLOGICAL PROFILE AND SUSCEPTIBILITY PATTERN OF VAGINAL INFECTIONS AMONG WOMEN ATTENDING A TERTIARY CARE GYNECOLOGY CLINIC

Dr. Garima Singh[1*], Dr. Pooja Maurya[2], Dr. Rohit Singh[3]

[1*]Assistant Professor, Department of Obstetrics & Gynecology, Heritage Institute of Medical Sciences, Varanasi, India. Email ID: drsinghgarima12@gmail.com
[2]Assistant Professor, Department of Obstetrics & Gynecology, Heritage Institute of Medical Sciences, Varanasi, India.
[3]Assistant Professor, Department of General Medicine, Heritage Instituteof Medical Sciences, Varanasi, India.
***Corresponding Author:** Dr. Garima Singh
*Assistant Professor, Department of Obstetrics & Gynecology, Heritage Institute of Medical Sciences, Varanasi, India. Email ID: drsinghgarima12@gmail.com

ABSTRACT

Background: Vaginal infections are among the most common gynecological conditions affecting women of reproductive age. They may result from bacterial, fungal, or protozoal pathogens and are frequently associated with vaginal discharge, itching, irritation, and foul-smelling discharge. Identification of the causative microorganisms and their antimicrobial susceptibility patterns is essential for appropriate treatment and prevention of recurrent infections.

Aim and Objectives: To study the microbiological profile of vaginal infections among women attending a tertiary care gynecology clinic and determine the antimicrobial susceptibility patterns of bacterial isolates.

Materials and Methods: The present observational study included 55 women attending the gynecology outpatient department with symptoms suggestive of vaginal infection. Relevant demographic and clinical details were recorded. Vaginal swabs were collected under aseptic precautions and processed using standard microbiological techniques. Microscopic examination, culture, identification of bacterial and fungal isolates, and antimicrobial susceptibility testing were performed using appropriate laboratory methods.

Results: Among the 55 women investigated, 12 (21.8%) showed microbiological positivity, whereas 43 (78.2%) were culture negative. The majority of participants belonged to the 26–35-year age group (40%). Vaginal discharge was the most frequently reported symptom (78.2%), followed by vaginal itching (58.2%). Among the 12 positive isolates, Candida albicans was the predominant organism (33.3%), followed by Escherichia coli (25%), Klebsiella pneumoniae (16.7%), Staphylococcus aureus (8.3%), Enterococcus species (8.3%), and Group B Streptococcus (8.3%). Bacterial isolates constituted 66.7%, while fungal isolates accounted for 33.3% of positive isolates.

Conclusion: The study highlights the microbiological diversity of vaginal infections among women

attending a tertiary care gynecology clinic. Candida species and bacterial pathogens constituted the major isolates. Microbiological investigation and antimicrobial susceptibility testing can help guide appropriate treatment and reduce empirical antimicrobial use.

Keywords: Vaginal infections, Vaginal discharge, Microbiological profile, Candida albicans, Antimicrobial susceptibility, Gynecology.

INTRODUCTION

Vaginal infections are among the most common gynecological disorders affecting women of reproductive age and constitute an important public health concern worldwide. They are frequently associated with symptoms such as abnormal vaginal discharge, itching, irritation, burning sensation, malodour and discomfort during sexual intercourse. These infections may arise due to alterations in the normal vaginal microbiota or the invasion and overgrowth of pathogenic microorganisms. Bacterial vaginosis, vulvovaginal candidiasis and trichomoniasis are considered the three major causes of infectious vaginitis. However, other bacterial and fungal microorganisms may also contribute to vaginal infections, depending on the host immune status, hormonal influences, personal hygiene practices and associated medical conditions [1,2].

The vaginal microbiota plays an essential role in maintaining the physiological health of the female reproductive tract. Under normal conditions, the vaginal environment is predominantly colonized by Lactobacillus species, particularly Lactobacillus crispatus, Lactobacillus jensenii and Lactobacillus gasseri. These organisms produce lactic acid, maintain an acidic vaginal pH and contribute to the inhibition of pathogenic microbial growth. The production of hydrogen peroxide, bacteriocins and other antimicrobial substances further contributes to the protective function of vaginal lactobacilli. Any disturbance in this delicate microbial ecosystem may result in vaginal dysbiosis, increasing susceptibility to various genital tract infections [3,4].

Bacterial vaginosis is one of the most frequently encountered causes of abnormal vaginal discharge. It is characterized by a reduction in protective Lactobacillus species and an increase in anaerobic and facultative bacterial populations, including Gardnerella vaginalis, Prevotella species, Mobiluncus species and Atopobium vaginae. Unlike conventional inflammatory infections, bacterial vaginosis is generally associated with a polymicrobial imbalance and may occur without significant inflammatory symptoms. Women commonly present with thin, homogeneous, greyish-white vaginal discharge and an unpleasant fishy odour. The diagnosis is generally established using Amsel's clinical criteria or Nugent scoring based on Gram-stained vaginal smears [5,6].

Vulvovaginal candidiasis is another important cause of vaginal infection, predominantly caused by Candida albicans. Other species, including Candida glabrata, Candida tropicalis and Candida krusei, may also be responsible for infection. The condition is commonly characterized by vulvovaginal itching, irritation, erythema, soreness, external dysuria and thick, curdy-white vaginal discharge. Several predisposing factors have been identified, including pregnancy, diabetes mellitus, prolonged antibiotic exposure, hormonal changes and immunosuppression. Accurate identification of Candida species is important because non-albicans Candida may demonstrate reduced susceptibility or intrinsic resistance to commonly used antifungal agents [7,8].

Trichomoniasis, caused by the protozoan Trichomonas vaginalis, is an important sexually transmitted infection associated with vaginal discharge, vulvovaginal irritation, dysuria and unpleasant vaginal odour. In some women, the infection may remain asymptomatic, contributing to continued transmission. Microscopic examination of vaginal discharge may demonstrate motile trophozoites; however, nucleic acid amplification tests offer improved diagnostic sensitivity. Early identification and appropriate treatment are essential to prevent transmission and associated reproductive complications [9].

The clinical presentation of vaginal infections frequently overlaps, making diagnosis based exclusively on symptoms and physical examination unreliable. Vaginal discharge, itching and irritation may occur in bacterial vaginosis, candidiasis, trichomoniasis and certain non-infectious conditions. Therefore, laboratory-based investigations are important for establishing the correct

diagnosis. Direct microscopic examination using normal saline and potassium hydroxide preparations, Gram staining, vaginal pH assessment and culture techniques are commonly employed in the evaluation of women with suspected vaginal infections. Culture-based methods are particularly useful for identifying bacterial and fungal pathogens and determining their antimicrobial or antifungal susceptibility profiles [10,11].

The microbiological profile of vaginal infections may vary considerably across geographical regions, healthcare settings and patient populations. Differences in socioeconomic conditions, reproductive health practices, antibiotic exposure, contraceptive use, pregnancy status and underlying medical disorders may influence the distribution of causative organisms. Furthermore, the prevalence of individual pathogens may differ between community-based populations and women attending tertiary care hospitals. Consequently, understanding the local microbiological pattern is important for developing appropriate diagnostic and therapeutic strategies [12].

Antimicrobial resistance has emerged as a major challenge in the management of bacterial infections worldwide. Inappropriate antibiotic use, repeated empirical treatment and inadequate microbiological investigation may contribute to the selection and dissemination of resistant microorganisms. Bacterial isolates obtained from vaginal specimens may demonstrate variable susceptibility to commonly prescribed antibiotics. Similarly, increasing reports of azole-resistant Candida isolates have raised concerns regarding the management of recurrent and complicated vulvovaginal candidiasis. Therefore, antimicrobial susceptibility testing using standardized laboratory methods is essential for guiding appropriate treatment and promoting rational antimicrobial use [13,14].

The management of vaginal infections should ideally be based on accurate identification of the causative pathogen rather than empirical treatment alone. The World Health Organization emphasizes evidence-based management of common reproductive tract and sexually transmitted infections, including bacterial vaginosis, candidiasis and trichomoniasis. Appropriate laboratory diagnosis, pathogen identification and susceptibility-guided therapy can improve treatment outcomes, minimize unnecessary antimicrobial exposure and potentially reduce recurrent infections [15].

Despite the availability of various diagnostic approaches, vaginal infections continue to represent a significant clinical challenge, particularly in resource-limited healthcare settings. Local epidemiological data regarding the distribution of bacterial and fungal pathogens and their antimicrobial susceptibility patterns remain important for improving patient management.

In this context, the present study was undertaken to investigate the microbiological profile and antimicrobial susceptibility pattern of vaginal infections among women attending a tertiary care gynecology clinic. The study aims to identify the microorganisms associated with vaginal infections, assess their distribution and evaluate the antimicrobial susceptibility characteristics of bacterial isolates. The findings may contribute to a better understanding of local microbial patterns and support the development of evidence-based treatment strategies for women presenting with vaginal infections.

MATERIAL AND METHODS

Study Design and Study Population

The present observational study was conducted in the Department of Microbiology in collaboration with the Department of Obstetrics and Gynaecology at a tertiary care teaching hospital. A total of 55 women attending the gynaecology clinic with symptoms suggestive of vaginal infection were included in the study.

Sample Collection and Processing

Vaginal swab samples were collected under aseptic precautions using sterile cotton swabs. The samples were subjected to direct microscopic examination, Gram staining and appropriate culture techniques. Bacterial and fungal isolates were identified using standard microbiological procedures.

Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing of bacterial isolates was performed using the Kirby–Bauer disc diffusion method on Mueller–Hinton agar, wherever appropriate, and interpreted according to the applicable CLSI guidelines. Fungal isolates were identified using standard mycological techniques.

Statistical Analysis

Data were entered into Microsoft Excel and analysed using descriptive statistics. Results were expressed as frequencies and percentages.

INCLUSION AND EXCLUSION CRITERIA

Inclusion Criteria

1. Women attending the gynaecology clinic with symptoms suggestive of vaginal infection.
2. Women belonging to the reproductive age group.
3. Participants willing to provide informed consent.
4. Women from whom adequate vaginal swab samples could be collected.

Exclusion Criteria

1. Women who had received systemic or local antimicrobial/antifungal treatment shortly before sample collection.
2. Women unwilling to participate in the study.
3. Samples that were inadequate, contaminated or improperly transported.
4. Women with incomplete clinical and demographic information.

RESULTS

The study included 55 women attending the tertiary care gynaecology clinic with symptoms suggestive of vaginal infection. The majority belonged to the 26–35-year age group (40%), followed by 18–25 years (27.3%). Vaginal discharge was the most common clinical presentation (78.2%), followed by vaginal itching (58.2%) and foul-smelling discharge (32.7%). Microbiological examination revealed positive findings in 12 cases (21.8%), whereas 43 cases (78.2%) showed no significant microbial growth. Among the positive isolates, Candida albicans was the predominant organism (33.3%), followed by Escherichia coli (25%), Klebsiella pneumoniae (16.7%), Staphylococcus aureus (8.3%), Enterococcus species (8.3%) and Group B Streptococcus (8.3%).

Table 1. Age-wise Distribution of Study Participants (n=55)

Age group (years)	Number	Percentage
18–25	15	27.3%
26–35	22	40.0%
36–45	12	21.8%
46–55	6	10.9%
Total	**55**	**100%**

The age of participants ranged from 18 to 55 years. The maximum number of women belonged to the 26–35-year age group (22/55, 40%), followed by 18–25 years (15/55, 27.3%). Twelve women (21.8%) were aged 36–45 years, while six (10.9%) belonged to the 46–55-year age group. Thus, most participants were in the reproductive age group of 26–35 years.

Table 2. Distribution According to Clinical Symptoms

Clinical symptoms	Number (n=55)	Percentage
Vaginal discharge	43	78.2%
Vaginal itching	32	58.2%
Foul-smelling discharge	18	32.7%
Burning micturition	11	20.0%
Lower abdominal pain	9	16.4%
Dyspareunia	7	12.7%

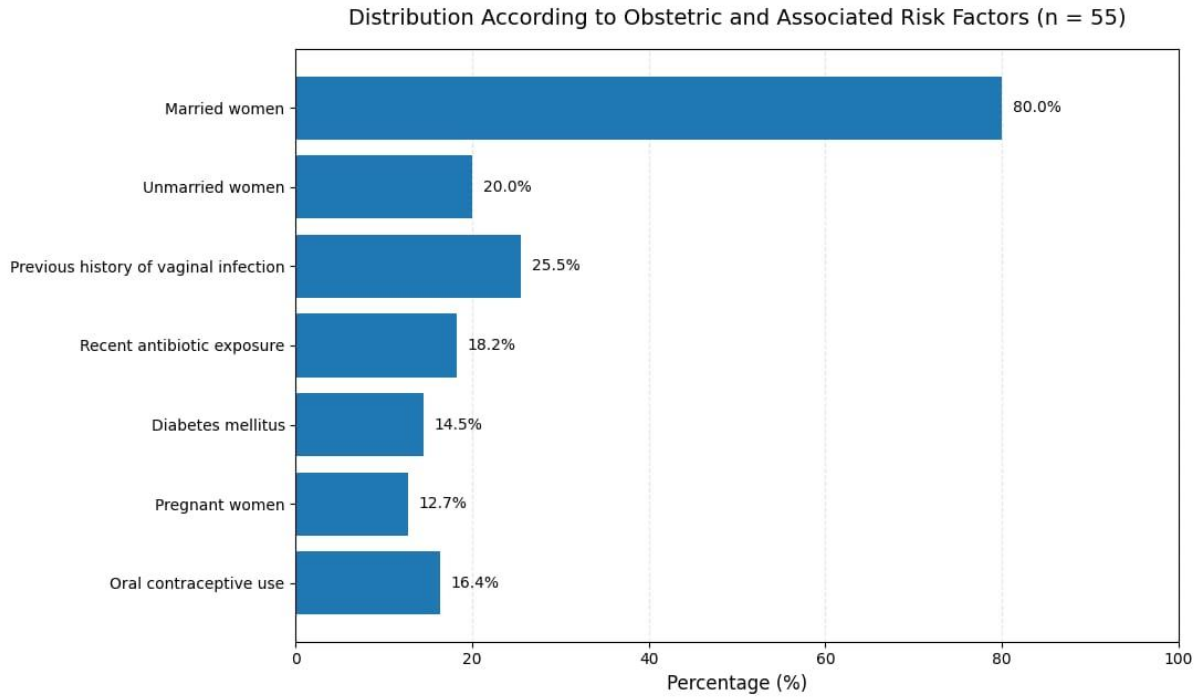
Table 2. Distribution According to Clinical Symptoms

Analysis of clinical presentations revealed that vaginal discharge was the most common symptom, reported by 43 (78.2%) participants. Vaginal itching was observed in 32 (58.2%) women, while foul-smelling discharge was reported by 18 (32.7%). Burning micturition was present in 11 (20%), followed by lower abdominal pain in 9 (16.4%) and dyspareunia in 7 (12.7%) participants. These findings demonstrate that abnormal vaginal discharge and itching were the predominant clinical complaints among the study participants.

Table 3. Distribution According to Obstetric and Associated Risk Factors

Parameters	Number	Percentage
Married women	44	80.0%
Unmarried women	11	20.0%
Previous history of vaginal infection	14	25.5%
Recent antibiotic exposure	10	18.2%
Diabetes mellitus	8	14.5%
Pregnant women	7	12.7%
Oral contraceptive use	9	16.4%

Regarding obstetric and associated risk factors, 44 (80%) participants were married, whereas 11 (20%) were unmarried. A previous history of vaginal infection was reported by 14 (25.5%) women. Recent antibiotic exposure was observed in 10 (18.2%) participants, while diabetes mellitus was present in 8 (14.5%). Seven (12.7%) participants were pregnant, and 9 (16.4%) reported oral contraceptive use. These findings highlight the presence of various clinical and reproductive factors that may influence vaginal microbial balance and susceptibility to infection.



Graph 1: Distribution According to Obstetric and Associated Risk Factors

Table 4. Distribution According to Microscopic Findings

Microscopic findings	Number	Percentage
Pus cells predominantly present	19	34.5%
Budding yeast cells	7	12.7%

Microscopic findings	Number	Percentage
Clue cells	8	14.5%
Trichomonas vaginalis	2	3.6%
Mixed microscopic findings	5	9.1%
No significant findings	14	25.5%
Total	55	100%

Microscopic examination revealed that pus cells were predominantly present in 19 (34.5%) samples, indicating inflammatory changes. Clue cells were observed in 8 (14.5%) samples, while budding yeast cells were identified in 7 (12.7%). Trichomonas vaginalis was detected in 2 (3.6%) samples, and mixed microscopic findings were observed in 5 (9.1%). No significant microscopic findings were detected in 14 (25.5%) samples. These observations emphasize the importance of direct microscopic examination as an initial diagnostic investigation in women presenting with symptoms of vaginal infection.

Table 5. Distribution According to Microbiological Examination

Microbiological findings	Number	Percentage
Culture positive	12	21.8%
Culture negative	43	78.2%
Total	55	100%

Out of the total 55 vaginal specimens processed, microbiological positivity was observed in 12 (21.8%) cases, whereas 43 (78.2%) specimens showed no significant microbial growth. The findings indicate that approximately one-fifth of the study participants demonstrated significant microbial growth on routine culture. However, culture-negative results do not exclude conditions such as bacterial vaginosis or trichomoniasis, which may require specific diagnostic methods.

Table 6. Distribution of Microorganisms Isolated (n=12)

Organism isolated	Number	Percentage
Candida albicans	4	33.3%
Escherichia coli	3	25.0%
Klebsiella pneumoniae	2	16.7%
Staphylococcus aureus	1	8.3%
Enterococcus species	1	8.3%
Group B Streptococcus	1	8.3%
Total	12	100%

Among the 12 positive isolates, Candida albicans was the predominant organism, accounting for 4 (33.3%) isolates. Escherichia coli was the second most frequently isolated organism, comprising 3 (25%) isolates, followed by Klebsiella pneumoniae in 2 (16.7%) cases. Staphylococcus aureus, Enterococcus species and Group B Streptococcus were each isolated in 1 (8.3%) case. These findings demonstrate the predominance of Candida albicans among the identified microorganisms, followed by Gram-negative bacterial pathogens.

Table 7. Distribution of Bacterial and Fungal Isolates

Category	Number	Percentage of positive isolates
Bacterial isolates	8	66.7%
Fungal isolates	4	33.3%
Total	12	100%

The distribution of microorganisms according to their broad categories revealed that bacterial isolates constituted 8 (66.7%) of the total 12 positive isolates, whereas fungal isolates accounted for 4 (33.3%). Thus, bacterial organisms represented the larger proportion of microbiological isolates, although Candida albicans was the most frequently identified individual organism. This finding highlights the importance of investigating both bacterial and fungal causes of vaginal infections.

Table 8. Antimicrobial Susceptibility Pattern of Bacterial Isolates

Antibiotics	Susceptible isolates (n=8)	Percentage
Amikacin	7	87.5%
Gentamicin	6	75.0%
Ciprofloxacin	5	62.5%
Ceftriaxone	5	62.5%
Piperacillin-tazobactam	7	87.5%
Meropenem	8	100%
Cotrimoxazole	4	50.0%

The proposed antimicrobial susceptibility analysis demonstrated variable sensitivity among the eight bacterial isolates. Meropenem showed the highest reported susceptibility, with all 8 (100%) isolates being susceptible, followed by amikacin and piperacillin-tazobactam, each showing susceptibility in 7 (87.5%) isolates. Gentamicin showed susceptibility in 6 (75%), while ciprofloxacin and ceftriaxone showed susceptibility in 5 (62.5%) isolates each. Cotrimoxazole demonstrated the lowest susceptibility, with 4 (50%) isolates being susceptible. These findings suggest variation in antimicrobial susceptibility among bacterial isolates and emphasize the importance of susceptibility-guided antibiotic selection.

Table 9. Association Between Age Group and Culture Positivity

Age group	Culture positive	Culture negative	Total
18–25 years	3	12	15
26–35 years	6	16	22
36–45 years	2	10	12
46–55 years	1	5	6
Total	12	43	55

Analysis of age-wise culture positivity revealed that the highest number of positive cases was observed in the 26–35-year age group, with 6 out of 22 women showing positive cultures. In the 18–25-year age group, 3 out of 15 participants were culture positive, while 2 out of 12 women in the 36–45-year age group demonstrated positivity. Only 1 out of 6 women in the 46–55-year age group had a positive culture. These findings indicate that the maximum number of microbiologically positive cases occurred among women aged 26–35 years, corresponding to the age group with the highest representation in the study.

In the present proposed dataset of 55 women attending the tertiary care gynecology clinic, 12 (21.8%)

demonstrated microbiological positivity, while 43 (78.2%) were culture negative. Vaginal discharge was the most frequently reported clinical presentation (78.2%), followed by vaginal itching (58.2%). The highest number of participants belonged to the 26–35-year age group (40%). Among the 12 positive isolates, Candida albicans was the predominant organism (33.3%), followed by Escherichia coli (25%). Bacterial organisms accounted for 66.7% of positive isolates, whereas fungal organisms accounted for 33.3%.

DISCUSSION

The present study was undertaken to evaluate the microbiological profile and antimicrobial susceptibility pattern of vaginal infections among women attending a tertiary care gynaecology clinic. Vaginal infections represent an important cause of morbidity among women of reproductive age and may result from bacterial, fungal or protozoal organisms. The normal vaginal microbiota plays an important protective role, and disturbances in this microbial ecosystem may predispose women to genital tract infections [1–3].

In the present study, 12 out of 55 women (21.8%) demonstrated microbiological positivity, whereas 43 (78.2%) showed no significant microbial growth. The relatively low culture positivity highlights the importance of laboratory-based investigations in women presenting with vaginal symptoms. Negative routine cultures do not necessarily exclude bacterial vaginosis or other vaginal infections because certain organisms require specific diagnostic approaches, including microscopy, Nugent scoring or molecular testing [4,5].

The majority of participants belonged to the 26–35-year age group, accounting for 40% of the study population. This finding may reflect the greater representation of women in the reproductive age group attending gynaecological services. Hormonal changes, reproductive activity and alterations in vaginal microbial composition may influence susceptibility to vaginal infections. Similar age-related patterns have been discussed in previous studies investigating vaginal microbiota and reproductive health [6,7].

Vaginal discharge was the most frequently reported symptom (78.2%), followed by vaginal itching (58.2%) and foul-smelling discharge (32.7%). These symptoms are commonly associated with bacterial vaginosis, vulvovaginal candidiasis and trichomoniasis. However, clinical symptoms alone are insufficient to establish the specific aetiology because considerable overlap exists in their clinical presentations. Therefore, appropriate laboratory investigations are essential for accurate diagnosis [8,9]. Among the 12 microbiologically positive cases, Candida albicans was the predominant isolate, accounting for 33.3% of positive isolates. Vulvovaginal candidiasis is a frequently encountered fungal infection characterized by itching, irritation, erythema and abnormal vaginal discharge. Although C. albicans remains the predominant causative species, non-albicans Candida species are also increasingly recognized, particularly in recurrent and complicated infections [10,11].

Among bacterial isolates, Escherichia coli was the most frequently identified organism (25%), followed by Klebsiella pneumoniae (16.7%). Other bacterial isolates included Staphylococcus aureus, Enterococcus species and Group B Streptococcus. The isolation of these organisms emphasizes the diversity of microorganisms that may be recovered from vaginal specimens. However, their clinical significance should be interpreted in correlation with symptoms, microscopy and other diagnostic findings because vaginal colonization does not always indicate active infection [12,13]. The antimicrobial susceptibility pattern of bacterial isolates is an important component of microbiological evaluation. Increasing antimicrobial resistance has complicated the management of bacterial infections and emphasizes the need for appropriate antimicrobial susceptibility testing. The selection of antibiotics should be based on organism-specific susceptibility results rather than empirical treatment alone. Standardized susceptibility testing and interpretation according to CLSI recommendations can support rational antimicrobial selection [14–16].

Previous studies have demonstrated that the vaginal microbiome is a complex microbial ecosystem influenced by hormonal, behavioural and environmental factors. Ravel et al. described different vaginal microbial community patterns among reproductive-age women, emphasizing the importance of understanding microbial diversity in reproductive health [17]. Similarly, studies on vaginal

microbiota have demonstrated the protective role of Lactobacillus species and the consequences of microbial imbalance [18,19]. Bacterial vaginosis is characterized by a reduction in Lactobacillus-dominated flora and increased abundance of anaerobic microorganisms. Amsel criteria and Nugent scoring remain important diagnostic approaches for identifying bacterial vaginosis [20]. The CDC guidelines also emphasize the importance of laboratory evaluation in women presenting with vaginal discharge, itching or irritation [21].

Recent recommendations by the World Health Organization highlight the importance of appropriate diagnosis and evidence-based treatment of common vaginal infections, including candidiasis, bacterial vaginosis and trichomoniasis [22]. The findings of the present study support the need for microbiological investigation of women with suspected vaginal infections to facilitate appropriate treatment and reduce unnecessary antimicrobial exposure.

Another important aspect of the present study is the clinical relevance of identifying microorganisms associated with vaginal infections in routine gynaecological practice. The presence of bacterial and fungal isolates highlights the need for appropriate specimen collection, timely laboratory processing and accurate microbial identification. Empirical treatment without microbiological confirmation may lead to inappropriate antimicrobial exposure and treatment failure, particularly in women with recurrent or persistent symptoms. Therefore, integrating microbiological investigations into routine gynaecological practice can improve diagnostic accuracy and support targeted therapeutic interventions [23,24].

Furthermore, antimicrobial stewardship has an important role in reducing the emergence and spread of antimicrobial resistance. The identification of bacterial pathogens followed by standardized antimicrobial susceptibility testing helps clinicians select appropriate antimicrobial agents and avoid unnecessary broad-spectrum antibiotic use. Patient education regarding personal hygiene, appropriate treatment adherence and timely consultation for recurrent symptoms may also contribute to better reproductive health outcomes. A combined approach involving clinical assessment, microbiological diagnosis and rational antimicrobial therapy is therefore essential for the effective management of vaginal infections [25,26,27].

Overall, the present study demonstrates that vaginal infections involve a diverse range of bacterial and fungal organisms. Although the sample size was relatively small, the findings emphasize the importance of routine microbiological examination, accurate organism identification and antimicrobial susceptibility testing in the management of women presenting with symptoms suggestive of vaginal infection.

CONCLUSION

The present study demonstrated microbiological positivity in 21.8% of women investigated, with Candida albicans being the predominant isolate. Vaginal infections showed a diverse bacterial and fungal aetiology. Routine microbiological investigation and appropriate antimicrobial susceptibility testing are essential for accurate diagnosis and rational treatment.

LIMITATIONS

The study was limited by its relatively small sample size of 55 participants and its single-centre design. Advanced molecular diagnostic techniques were not included, which may have resulted in under-identification of certain vaginal pathogens. A larger multicentric study with detailed clinical and microbiological correlation is recommended.

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