

To investigate the prevalence of leukorrhea among women attending Gauhati Medical College & Hospital and to accurately identify associated pathogenic microorganisms through conventional and molecular (16S rRNA sequencing) analyses.: Reg No: 698

Syeda Tamanna
Assam Don Bosco University

CORRESPONDING AUTHOR

Dr Syeda Tamanna, Assam Don Bosco University

Email: syedatamanna40@gmail.com

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ABSTRACT

Introduction:Leukorrhea, a non-bloody vaginal discharge, can be physiological or pathological. Pathological leukorrhea is commonly caused by microbial infections and presents symptoms like itching, burning, and pain. Early and accurate microbial identification is essential for effective treatment and management. **Methods:**A total of 50 vaginal swab samples were collected from women experiencing leukorrhea at a tertiary care hospital in Guwahati. The samples were subjected to morphological (colony characteristics), biochemical (Gram staining, catalase, citrate, indole), and molecular (16S rRNA gene sequencing) analyses. Fungal identification was done using LPCB staining and chromogenic media. **Results:**Biochemical and morphological methods identified common pathogens such as *E. coli*, *Klebsiella* spp., *Staphylococcus* spp., and *Candida albicans*. However, molecular analysis revealed the presence of *Staphylococcus cohnii* and *Stutzerimonas stutzeri*, highlighting discrepancies in traditional identification techniques. This underscores that species-level confirmation is only achievable through molecular sequencing methods, especially for atypical or non-culturable organisms. **Discussion:**The highest prevalence of leukorrhea was observed among women aged 30–35. Traditional methods were insufficient for definitive species-level identification, proving the critical need for sequencing technologies in microbial diagnostics. **Conclusion:**Accurate detection of pathogenic microbes causing leukorrhea requires integrating molecular sequencing techniques with classical methods. Sole reliance on morphological and biochemical tests can lead to misidentification and suboptimal treatment. This study emphasizes the need for molecular diagnostics to inform precise clinical interventions.

KEYWORDS

Leukorrhea, Pathogenic microbes, 16S rRNA sequencing, Molecular identification, Reproductive tract infections (RTIs)