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Isolation and Identification of pathogens from High Vaginal Swab of Women visiting Duhok Maternity Hospital

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ABSTRACT

The distribution of normal, aberrant, and *Candida*-associated microorganisms as well as the isolation of pathogenic bacteria are the main topics of this study, which reports the microbiological profile of high vaginal swabs taken from 100 women. Normal microorganisms accounted for 51.0% (51/100), aberrant microorganisms for 27.0% (27/100), and *Candida* spp. for 22.0% (22/100), indicating a significant amount of non-commensal or opportunistic flora. *Enterococcus faecalis* was the most common bacterial isolate (19/27, 70.3%) among the 27 culture-positive cases, followed by *Escherichia coli* (4/27, 14.0%), Staphylococcus spp. (3/27, 11.0%), and *Klebsiella* sp. (1/27, 3.7%). These results demonstrate the significant contribution of *Candida* species and *E. faecalis* to the vaginal microbiota, indicating a high prevalence of pathogenic and opportunistic organisms that may have consequences for antibiotic stewardship and clinical care**.** This study was conducted to evaluate high vaginal abnormalities, and the most common bacteria was *E. faecalis* it shows high sensitivity to (linezolid) antibiotic.

Keywords: Vaginal swabs, Pathogens, Maternity hospital, Antibiotic

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Introduction

The vaginal flora, which is home to a wide variety of microorganisms, makes up the vagina's dynamic ecology. Additionally, it protects against a variety of infections and keeps the vaginal pH acidic [1]. Because changes in the vaginal microbiome can have a substantial impact on both mother and fetal outcomes, vaginal health is especially important during pregnancy. During pregnancy, the vaginal environment experiences a number of physiological changes that impact the equilibrium of microbial communities due to hormonal shifts [2]. *Lactobacillus* species predominate in the healthy vaginal microbiome and are essential for sustaining an acidic environment by producing lactic acid [3]. Understanding vaginal microbiology is crucial because imbalances in these microbes can result in a number of health problems [4]. Microorganisms from high vaginal swabs (HVS) of pregnant women are identified and isolated to identify diseases that may cause difficulties such as low birth weight, miscarriage, premature labor, and neonatal infections [1, 3].

According to studies, BV and aerobic vaginitis may overlap and result in a mixed disease; however, it is yet unknown if one condition can develop into the other [5]. It is impossible to overestimate the significance of preserving a healthy vaginal microbiome, particularly during pregnancy. The intricate relationships within the vaginal microbiome and their effects during pregnancy are still being studied. This article aimed to isolate and identify the pathogens from high vaginal swabs from pregnant/unpregnant women who attended the Duhok Maternity Hospital.

Materials and Methods

This study was based on laboratory descriptive data, evaluation of high vaginal swab samples, and identification of abnormal bacterial pathogens. The study was conducted in Duhok Maternity Hospital, where patients attended for routine high vaginal examinations for various purposes. The study included women who presented with symptoms such as abnormal discharge, itching, burning, and discomfort during urination, all of which are indicators of vaginal infection. The high vaginal swab samples were taken from the upper vaginal area using sterile cotton and sent to the laboratory for analysis to ensure accuracy and prevent contamination. After that, the sample was examined under a microscope to look for any abnormal bacteria, yeast, or other microorganisms that might be present. This was done using the Gram staining technique, which is used to distinguish between Gram-positive and Gram-negative bacteria and observe their morphology. The sample was then inoculated onto suitable culture media, such as blood agar and MacConkey agar, and incubated under conditions that were suitable for the growth of bacteria. Once the bacteria had grown and were identified using colony characteristics and standard biochemical tests, and the antibiotic sensitivity test was used with standard procedures to test the isolated bacteria against various antibiotics, the results were recorded as sensitive (S), resistant (R), and intermediate (M); the treatment was determined based on the antibiotic sensitivity test results; the collected dates were analyzed as a percentage, and the normal and abnormal conditions were computed.

Result & Discussion

The current data, the sample size is 100, categorized into three mutually exclusive groups: normal microorganisms, aberrant microorganisms, and *Candida* spp. The predominance of normal microorganisms (51%) suggests that, in this sample, the majority of the microbiological findings correspond to expected or commensal flora, consistent with the concept that many body sites harbor a "normal" microbiome rather than overt pathogens. Meanwhile, the combined proportion of aberrant plus Candida spp. microorganisms is 49%, implying that almost half of the isolates deviate from typical patterns, which may reflect colonization by opportunistic organisms or early dysbiosis [6, 7].

The 22% prevalence of *Candida* spp. is quantitatively higher than the Candida positivity rates reported in some hospital-based microbiology surveys (around 1–2% of culture requests), but this is likely explained by the clinical setting and specimen type, as *Candida* tends to be enriched in specific samples such as vaginal, oral, or superficial swabs. Several epidemiological studies report overall Candida prevalence in vaginal or superficial samples around 15–27%, which is broadly comparable to your 22%, suggesting that your sample falls within the expected range for such population [8, 9].

The current study results show, 27 pathogenic bacterial isolates were recovered from high vaginal swabs, giving a total of n = 27 with percentages summing to 100%, as follow: *Enterococcus faecalis* 19/27 (70.3%), *Escherichia coli* 4/27 (14.0%), *Staphylococcus* spp. 3/27(11.0%), and *Klebsiella* sp.1/27 (3.7%).

Since the vaginal area contains a variety of microorganisms, our study sought to determine whether abnormal bacteria were present in high vaginal swab samples from 100 patients at Duhok Maternity Hospital. All of the patients had either severe or mild symptoms of vaginal infections. Because E. faecalis is a common resident of the gastrointestinal tract and the vaginal opening is anatomically close to the anus, intestinal bacteria are frequently transferred to the vaginal area, this is near to a study done by Hassan et al. [10], in Kurdistan Region, which mentioned that enteric bacteria can easily colonize the vaginal are due to anatomical proximity, and also similar to a study done by Chávez de Paz et al. [11], which reported the same finding.

The dominance of *Enterococcus faecalis* (70.3%) indicates that this organism is the most frequently isolated pathogenic bacterium in your high vaginal swab samples. Enterococci are known as opportunistic pathogens associated with urinary tract and genital infections, and their high prevalence here may reflect local colonization patterns, possible antibiotic exposure (e.g., prior cephalosporins or broad-spectrum antibiotics), or underlying host factors such as diabetes or impaired immunity [12].

The second-most frequent isolate is *Escherichia coli* (14.0%), which is a classic cause of urinary tract and genital-tract infections and is often linked to ascending fecal–perineal contamination. The presence of *Staphylococcus* spp. (11.0%) and a single *Klebsiella* sp. isolate (3.7%) further supports the polymicrobial nature of some vaginal infections, with potential for mixed or recurrent infections if host defenses are compromised [13].

Additionally, *E. faecalis* responded differently to antibiotics, The current investigation shows that isolates of *E. faecalis* demonstrated complete resistance to(gentamicin) due to (HLAR) and high sensitivity to (linezolid) due to modes of action by blocking protein synthesis early in the translation process, this is near to a study done by Al-Khafaji & Althahab [14], in Iraq, which showed high resistance to aminoglycosides and high sensitivity to linezolid, and also similar to a study done

The distribution of the normal vaginal microbiota, especially the decrease in protective lactobacillus species, and patient antibiotic misuse are the main causes of the elevated rate of antibiotic resistance. This is near to a study done by Abdul-Aziz *et al.* [15], in Iraq, which mentioned that reduction of *Lactobacillus* and misuse of antibiotics increase infection risk, and also similar to a study done by [16,17,18,19] which confirmed the same concept found in the abnormal bacteria in high vaginal swabs.

Conclusion

This study was conducted to evaluate high vaginal abnormalities, and the most common bacteria was *E. faecalis* it shows high sensitivity to (linezolid) antibiotic.

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