

Vajinal Akıntı Kültürlerinden İzole Edilen Vajinit Etkeni Mikroorganizmaların Tanımlanması ve Antimikrobiyal Duyarlılık Profillerinin Değerlendirilmesi

Identification of Vaginitis-Causing Microorganisms Isolated From Vaginal Discharge Cultures and Evaluation of Their Antimicrobial Susceptibility Profiles

 Erkan Sanmak¹,  Zeynep Ayaydin²,  Ömer Tammo³

¹Mardin Eğitim ve Araştırma Hastanesi, Tıbbi Mikrobiyoloji Laboratuvarı, Mardin, Türkiye.

²Mardin Artuklu Üniversitesi, Tıp Fakültesi, Tıbbi Mikrobiyoloji Ana Bilim Dalı, Mardin, Türkiye.

³Harran Üniversitesi, Tıp Fakültesi, Kadın Hastalıkları ve Doğum Bölümü, Şanlıurfa, Türkiye.

ÖZ

Giriş: Vajinal enfeksiyonlar, vajinal mikrobiyal dengenin bozulmasıyla ilişkilidir ve sıklıkla bakteriyel etkenler rol oynamaktadır. Bu çalışmada, vajinal akıntı şikayetiyle başvuran hastalardan alınan vajinal sürüntü örneklerinde izole edilen mikroorganizmaların belirlenmesi ve bunların antimikrobiyal duyarlılık profillerinin değerlendirilmesi amaçlanmıştır.

Yöntem: Retrospektif olarak planlanan çalışmaya, Mardin Eğitim ve Araştırma Hastanesi, Kadın Hastalıkları ve Doğum birimlerine vajinal akıntı yakınmasıyla başvuran ve kültürlerinde mikroorganizma üremesi saptanan 266 hasta dahil edilmiştir. Tanımlayıcı analizlerde Gram boyama, konvansiyonel biyokimyasal yöntemler ve VITEK-2 sistemi kullanılmış; antibiyotik duyarlılığı ise standart protokollerle değerlendirilmiştir.

Bulgular: İzole edilen mikroorganizmaların %49,3'ü Gram pozitif, %48,1'i Gram negatif bakterilerden, %2,6'sı ise Candida türlerinden oluşmuştur. En sık tespit edilen etkenler Escherichia coli (E. coli) (%35,7), koagülaz negatif stafilokoklar (%19,9), Streptococcus agalactiae (%14,6), Staphylococcus aureus (%9,3) ve Klebsiella spp. (%9,3) olmuştur. E. coli colistin, meropenem ve imipenem; Gram pozitif bakteriler ise linezolid, tigecycline ve vankomisine yüksek duyarlılık göstermiştir.

Sonuç: Vajinal akıntıya en sık neden olan etkenin E. coli olduğu saptanmıştır. İzolatların antimikrobiyal duyarlılık profillerinin bilinmesi, etkili tedavi planlaması ve komplikasyonların önlenmesi açısından klinik önem taşımaktadır.

Anahtar Kelimeler: escherichia coli, antimikrobiyal duyarlılık, mikrobiyal tanımlama, vajinal akıntı, vajinit

ABSTRACT

Objective: Vaginal infections are often associated with disruption of the normal vaginal microbiota, with bacterial pathogens being the most common causative agents. This study aimed to identify the microorganisms isolated from vaginal discharge samples of patients presenting with vaginal complaints and to evaluate their antimicrobial susceptibility profiles.

Method: This retrospective study included 266 patients who presented to the Obstetrics and Gynecology outpatient clinics or inpatient services of Mardin Training and Research Hospital with complaints of vaginal discharge and had positive vaginal culture results. Microorganism identification was performed using Gram staining, conventional biochemical methods, and the VITEK-2 system. Antimicrobial susceptibility testing was conducted according to standard laboratory protocols.

Results: Among the isolated microorganisms, 49.3% were Gram-positive bacteria, 48.1% were Gram-negative bacteria, and 2.6% were identified as Candida species. The most frequently isolated pathogens were Escherichia coli (E. coli) (35.7%), coagulase-negative staphylococci (19.9%), Streptococcus agalactiae (14.6%), Staphylococcus aureus (9.3%), and Klebsiella spp. (9.3%). E. coli showed the highest susceptibility to colistin, meropenem, and imipenem, while Gram-positive isolates exhibited the greatest sensitivity to linezolid, tigecycline, and vancomycin.

Conclusion: E. coli was identified as the most common pathogen associated with vaginal discharge. Understanding the antimicrobial susceptibility profiles of these isolates is essential for guiding appropriate treatment strategies and preventing recurrent infections and potential complications.

Keywords: escherichia coli, antimicrobial susceptibility, microbial identification, vaginal discharge, vaginitis

Sending Date: 15.06.2025 **Acceptance Date:** 28.08.2025

Correspondence: Zeynep Ayaydin, Mardin Artuklu University, Faculty of Medicine, Department of Medical Microbiology, Mardin, Türkiye.

E-mail: zeynepayaydin@gmail.com

Cite as: Sanmak E, Ayaydin Z, Tammo O. Identification of Vaginitis-Causing Microorganisms Isolated From Vaginal Discharge Cultures and Evaluation of Their Antimicrobial Susceptibility Profiles. Kocaeli Med J 2025; 14(2): 135-141 doi: 10.5505/ktd.2025.47897

Copyright © Published by Kocaeli Derince Training and Research Hospital, Kocaeli, Türkiye.

INTRODUCTION

Vaginal infections are among the most common gynecological conditions, affecting a substantial proportion of women at least once in their lifetime. They typically arise from disruptions in the normal vaginal microbiota and present with a variety of clinical manifestations, including abnormal vaginal discharge, pruritus, irritation, malodor, burning sensation, dyspareunia, dysuria, and mucosal erythema or edema (1).

It is estimated that more than 30% of vaginitis cases are attributable to bacterial pathogens (2). The most prevalent etiological agents include bacterial vaginosis (40-45%), vulvovaginal candidiasis (20-25%), and trichomoniasis (15-20%), whereas non-infectious forms such as atrophic, irritant, or allergic vaginitis account for approximately 5-10% of all cases (3).

If left untreated, vaginal infections may lead to serious reproductive health complications, including pelvic inflammatory disease (PID), infertility, and preterm birth during pregnancy. Therefore, accurate identification of the causative microorganisms and the implementation of effective antimicrobial therapy are of critical importance. However, the growing global threat of antimicrobial resistance poses a significant challenge, potentially restricting treatment options, prolonging infection duration, contributing to therapeutic failures, and increasing morbidity and mortality rates (4,5).

In this context, regional monitoring of antimicrobial susceptibility patterns plays a vital role in guiding empirical treatment decisions and minimizing the risk of treatment failure. The present study aims to identify the most frequently isolated bacterial pathogens and their antimicrobial susceptibility profiles in vaginal swab cultures obtained from patients presenting with vaginal discharge who admitted to gynecology outpatient clinics in our region.

MATERIALS AND METHODS

This retrospective study included 266 female patients who presented with complaints of vaginal discharge to the gynecology outpatient clinics or were hospitalized in the gynecology wards of Mardin Training and Research Hospital, and whose vaginal cultures demonstrated positive microbial growth. The inclusion criterion for this study was the presence of vaginal discharge in female patients presenting to gynecology outpatient clinics, whereas those without vaginal discharge were excluded from the analysis. Demographic and clinical characteristics, including age, pregnancy status, history of sexual activity, and presence of systemic diseases, were recorded for all participants. As the data used in this retrospective study were obtained from the hospital record system and no patient-specific identifiable information was utilized, informed consent was not required.

Vaginal swab specimens were obtained using sterile cotton-tipped applicators and immediately transported to the microbiology laboratory under appropriate transport conditions. Gram-stained smears were prepared from each sample and examined microscopically to assess the presence of epithelial cells, leukocytes, and predominant bacterial morphotypes.

Each specimen was inoculated onto 5% sheep blood agar (RTA,

Turkey), eosin-methylene blue (EMB) agar (RTA, Turkey), and chocolate agar (RTA, Turkey), followed by incubation under appropriate atmospheric conditions. Bacterial growth was evaluated based on colony morphology and growth density, and colonies exhibiting significant growth were subjected to further analysis.

Isolated microorganisms were identified through Gram staining, conventional biochemical testing, and the VITEK-2 automated identification system (BioMérieux, France), in accordance with the manufacturer's protocols. Antimicrobial susceptibility testing was conducted in compliance with the standards of the European Committee on Antimicrobial Susceptibility Testing (EUCAST version 15.0).

RESULTS

A total of 266 patients with pathogenic microorganisms isolated from vaginal swab cultures were included in the study. The demographic and clinical characteristics of the participants are summarized below.

Of all patients, 79 (30%) were pregnant and 187 (70%) were non-pregnant. Regarding sexual activity, 212 (80%) reported being sexually active, whereas 54 (20%) were not. Systemic diseases were identified in 53 patients (20%), while 213 (80%) had no known chronic medical conditions. Among those with systemic diseases, the distribution was as follows: diabetes mellitus in 16 patients (30.2%), hypertension in 13 (24.5%), cardiovascular disease in 11 (20.8%), chronic obstructive pulmonary disease (COPD) in 8 (15.1%), and thyroid disorders in 5 (9.4%).

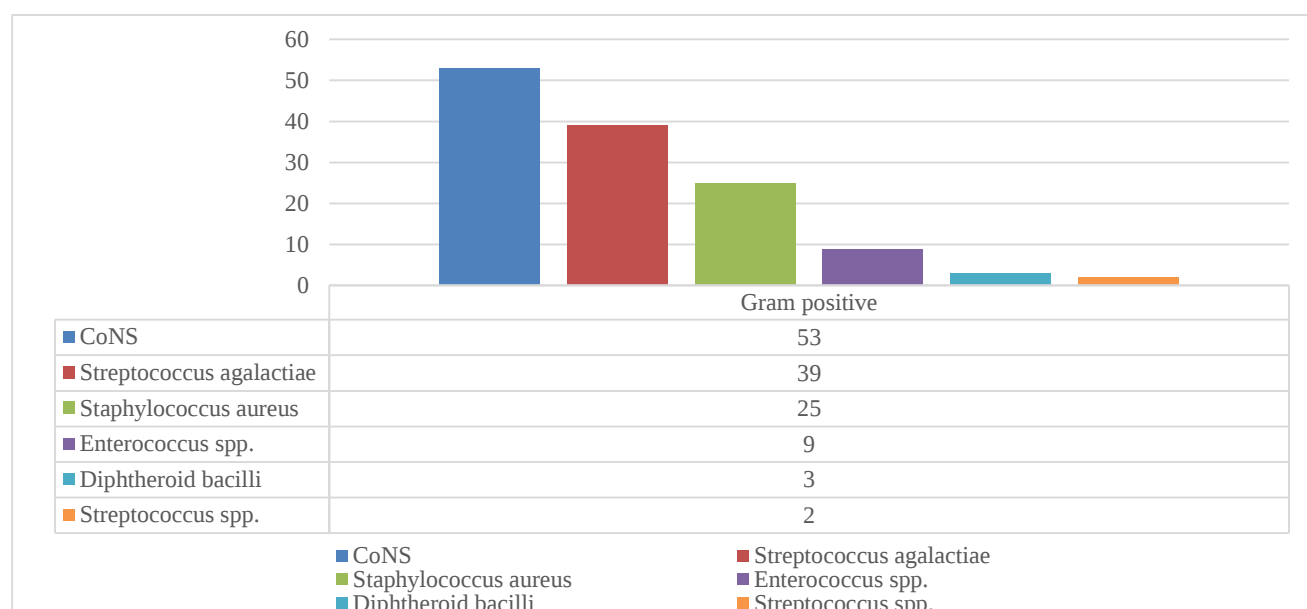
Age distribution revealed that 72 patients (27%) were between 18–25 years, 114 (43%) between 26–35 years, 53 (20%) between 36–45 years, and 27 (10%) were aged 45 years or older. The mean age of the study population was 30 years. These findings demonstrate that vaginal discharge affects women across all age groups and may be influenced by factors such as sexual activity and the presence of systemic comorbidities.

Among the 266 microorganisms isolated, 131 (49.3%) were Gram-positive bacteria, 128 (48.1%) were Gram-negative bacteria, and 7 (2.6%) were *Candida* species. The distribution of Gram-positive and Gram-negative bacterial isolates is detailed in Tables 1 and 2, respectively. The most frequently identified pathogens were *Escherichia coli* ($n = 95$, 35.7%), coagulase-negative staphylococci (CoNS) ($n = 53$, 19.9%), *Streptococcus agalactiae* ($n = 39$, 14.6%), *Staphylococcus aureus* ($n = 25$, 9.3%), and *Klebsiella* species ($n = 25$, 9.3%).

Antimicrobial susceptibility profiles of the predominant bacterial isolates are presented in Tables 3, 4, and 5. *E. coli* demonstrated the highest susceptibility to colistin (100%), meropenem (100%), imipenem (97.1%), tigecycline (96.1%), gentamicin (95.3%), nitrofurantoin (95.1%), amikacin (94.5%), and cefepime (93.1%), while the lowest susceptibility rates were observed for cefuroxime (21.1%), ampicillin (41%), and cefazolin (44.8%) (Table 3).

Klebsiella spp. exhibited complete susceptibility to colistin (100%), meropenem (100%), and gentamicin (100%), with high susceptibility rates also noted for imipenem (94.1%), cefepime (92.8%), nitrofurantoin (90.9%), and piperacillin/tazobactam (90.4%). The lowest susceptibility was recorded for ampicillin (6.2%), cefuroxime (6.6%), levofloxacin (8.8%), and cefazolin (33.3%) (Table 3).

Table 1. Gram Positive Bacteria (n)



CoNS: Coagulase-Negative Staphylococci

Table 2. Gram Negative Bacteria (n)

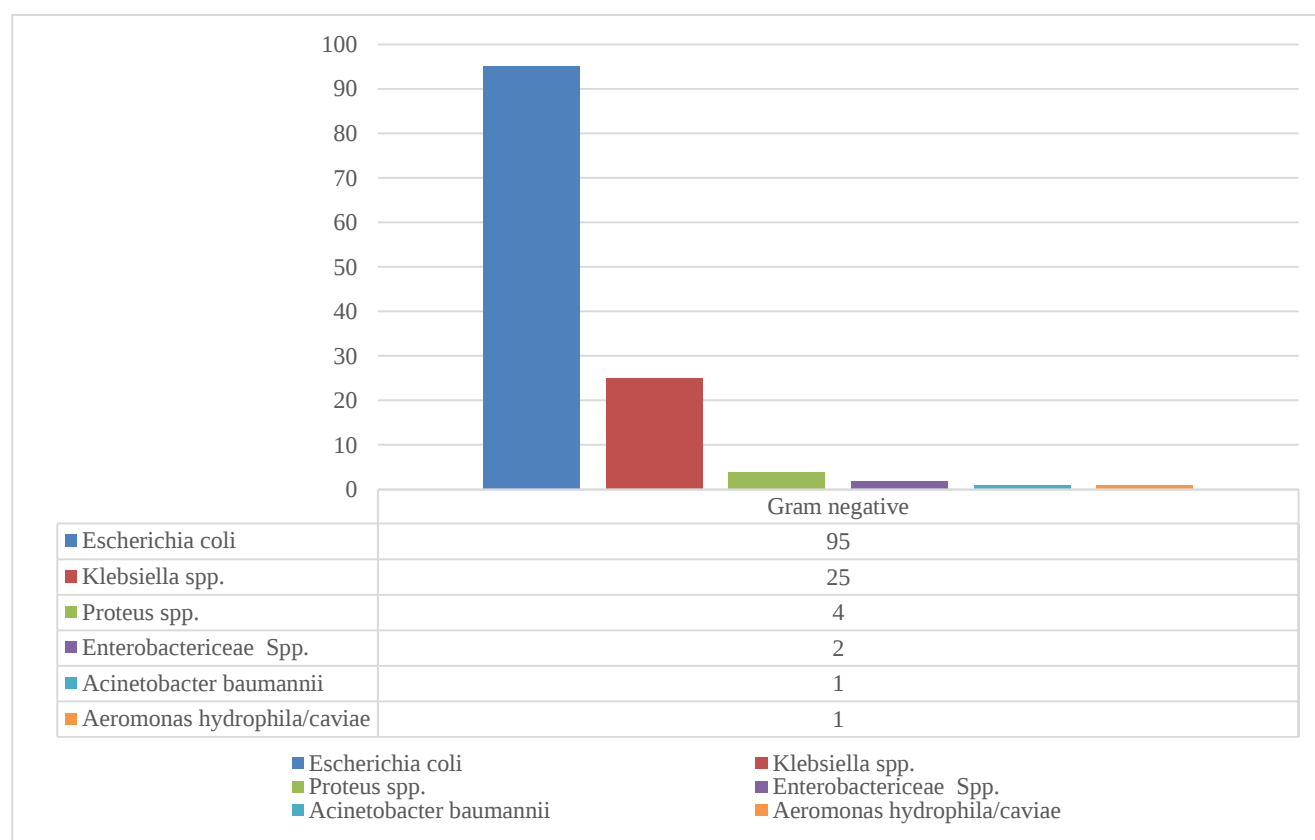
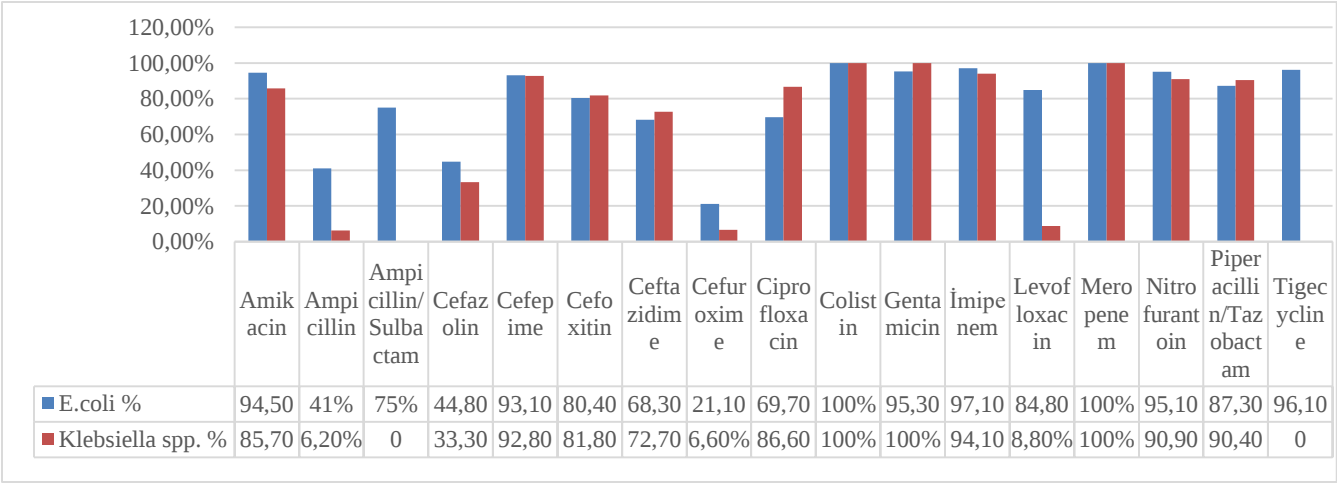


Table 3. E. coli and Klebsiella spp. Susceptibility Rates (%)



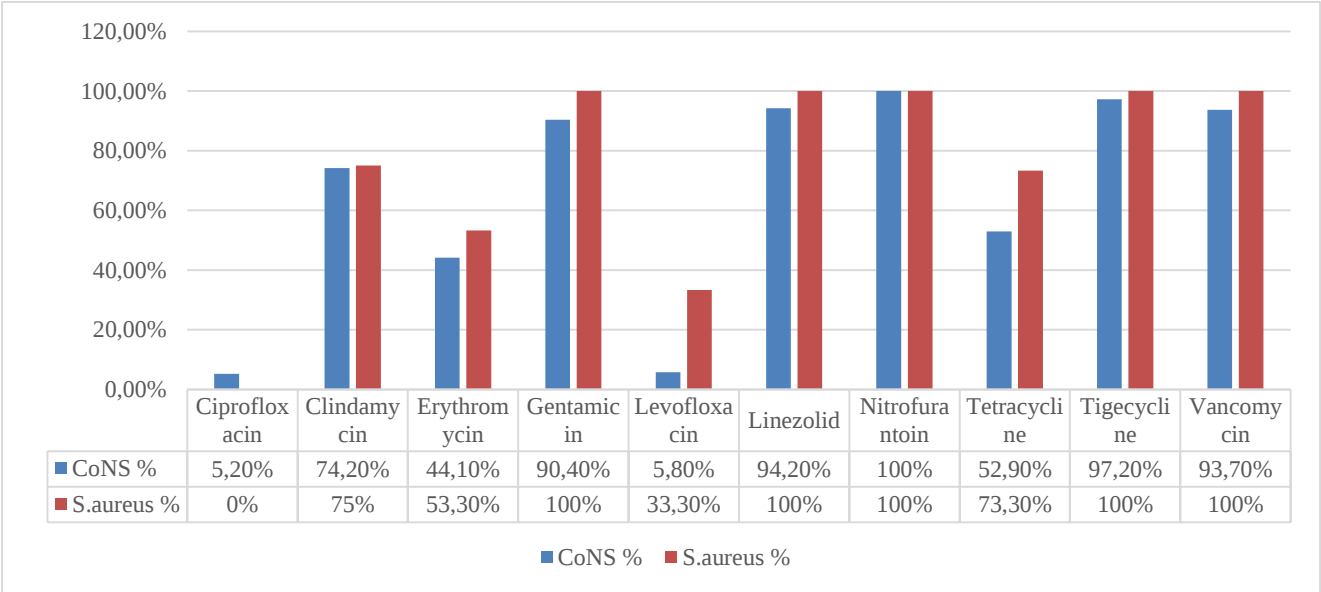
For CoNS, the highest susceptibility was observed with nitrofurantoin (100%), tigecycline (97.2%), linezolid (94.2%), vancomycin (93.7%), and gentamicin (90.4%). The lowest rates were recorded for ciprofloxacin (5.8%) and levofloxacin (5.2%) (Table 4).

S. aureus isolates demonstrated complete susceptibility (100%) to nitrofurantoin, tigecycline, linezolid, vancomycin, and gentamicin, whereas susceptibility to ciprofloxacin was absent (0%) and low for levofloxacin (33.3%) (Table 4).

The antimicrobial profile of S. agalactiae revealed 100% susceptibility to linezolid, penicillin G, tigecycline, and vancomycin. Nitrofurantoin showed a susceptibility rate of 87.5%, followed by erythromycin (68.1%), clindamycin (50%), and tetracycline (13.6%). No susceptibility was detected for levofloxacin (0%) (Table 5).

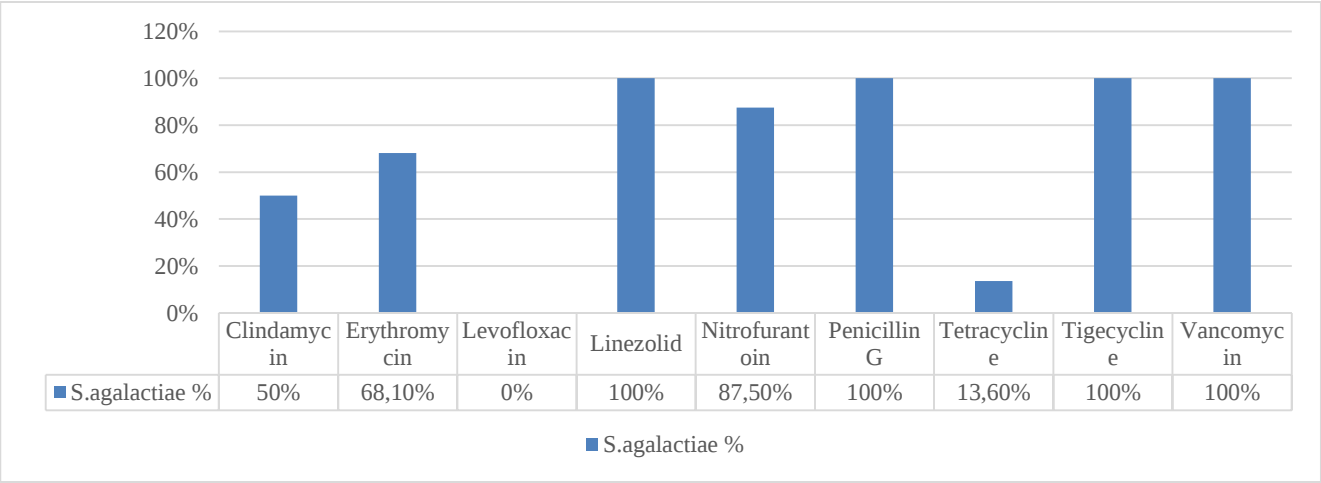
In summary, the most common bacterial isolates in this study were E. coli, CoNS, S. agalactiae, and S. aureus. E. coli is a major pathogen implicated in urinary tract infections (UTIs), septicemia, pneumonia, and meningitis. Klebsiella species can cause pneumonia, UTIs, septicemia, and meningitis. CoNS are recognized opportunistic pathogens that may lead to pneumonia, UTIs, septicemia, and meningitis, particularly in immunocompromised individuals. S. aureus is associated with skin and soft tissue infections (e.g., abscesses, cellulitis) as well as more severe diseases such as septicemia and endocarditis. S. agalactiae is an important cause of neonatal infections, including septicemia, pneumonia, and meningitis, and is also associated with postpartum maternal infections such as endometritis.

Table 4. CoNS and S.aureus Susceptibility Rates (%)



CoNS: Coagulase-Negative Staphylococci

Table 5. *S.agalactiae* Susceptibility Rates (%)



DISCUSSION

The etiological spectrum of vaginal infections includes *Candida* species, *Trichomonas vaginalis*, *Gardnerella vaginalis*, enterobacteria, staphylococci, enterococci, and group B streptococci (6). Previous studies have reported the prevalence of bacterial vaginosis (BV) in approximately 22–50% of women, *Candida* species in 17–39%, and *T. vaginalis* in 4–35% of cases (7).

In Türkiye, Albayrak et al. (8) analyzed vaginal discharge samples from 300 women and found that bacterial vaginosis, *T. vaginalis*, and *Candida* species were the most frequently detected pathogens. Consistent with these findings, the present study also identified bacterial agents as the predominant isolates, whereas *Candida* species were less commonly detected (Table 1, Table 2). Similarly, Vural Yılmaz et al. (9), in a study of 189 prepubertal girls with vulvovaginitis, reported that group A beta-hemolytic streptococci and *Haemophilus influenzae* were the most frequent pathogens, highlighting that the etiological profile in this age group differs from that seen in women of reproductive age.

In a 2022 study, Chaabaawi et al. investigated 250 pregnant women and reported a 43.2% prevalence of *Candida* vaginitis, with *Candida albicans* accounting for 49.6% of isolates. In contrast, our study reported a markedly lower prevalence of *Candida* spp. (2.6%), suggesting that pregnancy may be a significant risk factor for *Candida* vaginitis (10). In line with this, Altan et al. (11) found a prevalence of *Candida* spp. of 24.5% among 1,000 women, while Malak et al. (12) reported *Candida* spp. in 18.4% of women with vaginal discharge, rising to 60% among pregnant participants.

Börekeçi et al. (13) analyzed vaginal swabs from 86 women with gynecological complaints and found coagulase-negative staphylococci (CoNS) to be the most common isolate (46.5%), followed by *Staphylococcus aureus* (25.6%), *Streptococcus agalactiae* (7%), *Escherichia coli* (5.8%), and *Candida* spp. (2.3%). Despite variations in distribution rates, these results are consistent with our findings, particularly regarding the predominance of bacterial pathogens and the relatively low frequency of *Candida* spp. (Table 1, Table 2).

Cengiz et al. (14) examined vaginal swab cultures from 310 women aged 18–40 years and reported *Candida* spp. (39.8%) as the most prevalent pathogen, followed by alpha-hemolytic streptococci (21.2%), *S. aureus* (16.8%), and *E. coli* (12.4%). This contrasts with our results, in which *E. coli* was the leading pathogen and *Candida* spp. had the lowest prevalence (Table 2). Similarly, Marnach et al. (15) identified *Candida* spp. as the most frequent cause of vaginitis, with prevalence rates ranging from 17% to 39%. Again, this differs from our findings, where *E. coli* accounted for the highest proportion of isolates (35.7%) (Table 2).

In a study from India, Shanmugam et al. (16) investigated 175 women with vaginitis and reported bacterial vaginosis in 42.3% and vulvovaginal candidiasis in 19.4% of cases, a distribution pattern similar to that observed in our study. In a large multicenter investigation, Wójkowska-Mach et al. (17) analyzed samples from 4,994 women and found *Enterococcus faecalis* (29.2%), *E. coli* (26.3%), *S. agalactiae* (13.1%), and *Candida* spp. (24.3%) to be the most common isolates.

Data from China further underscore population-specific differences in pathogen distribution. Zhang et al. (18) studied 3,099 girls with vaginitis and reported bacterial growth in 399 cases, with *H. influenzae* (30.31%), *S. aureus* (15.75%), and *S. agalactiae* (7.64%) as the most frequent pathogens—findings that differ notably from our results, particularly with the high rate of *H. influenzae* in this pediatric population (Table 1).

Yasin et al. (19) reported bacterial vaginosis in 35.5%, candidiasis in 23.8%, and trichomoniasis in 3.3% of 214 vaginal swab cultures, with *E. faecalis* and *E. coli* as the predominant isolates. Gram-positive organisms were generally susceptible to vancomycin, ceftiofur, ciprofloxacin, clindamycin, and gentamicin, while Gram-negative isolates were sensitive to ciprofloxacin, gentamicin, and meropenem—patterns largely consistent with our antimicrobial susceptibility results (Table 3, Table 4).

Similarly, Bitew et al. (20) found an overall bacterial vaginosis prevalence of 48.6% in 210 women, with 69.5% of bacterial isolates being Gram-negative and 30.5% Gram-positive. High resistance rates to penicillin, tetracycline, and erythromycin were noted among Gram-positive bacteria, whereas ceftiofur and tobramycin demonstrated good

activity. In Gram-negative bacteria, resistance was high to tetracycline, ampicillin, and amoxicillin, while amikacin and tobramycin remained effective. These susceptibility profiles closely parallel those observed in our study (Table 3, Table 4).

Limitations of the Study

This study has certain limitations that should be considered when interpreting the results. First, as it was conducted in a single center, the findings may not be fully generalizable to broader or more diverse populations. Second, the cross-sectional design captures only a single time point, providing a snapshot of the microbial distribution and antimicrobial susceptibility patterns without accounting for potential seasonal or temporal variations. Third, although valuable culture-based data were obtained, molecular diagnostic techniques—which could have allowed for more precise pathogen identification and detection of resistance genes—were not utilized. Furthermore, the absence of detailed clinical parameters, such as symptom severity, underlying comorbidities, and treatment outcomes, limited the ability to establish direct correlations between microbiological results and clinical presentations. Future multi-center studies with larger, more heterogeneous populations, coupled with the integration of advanced molecular methods, are warranted to provide a more comprehensive understanding of the etiology and antimicrobial susceptibility profiles of vaginitis.

CONCLUSION

In this study, the most frequently isolated bacterial pathogens from vaginal discharge samples were *Escherichia coli* (n = 95, 35.7%), coagulase-negative staphylococci (CoNS) (n = 53, 19.9%), *Streptococcus agalactiae* (n = 39, 14.6%), *Staphylococcus aureus* (n = 25, 9.3%), and *Klebsiella* spp. (n = 25, 9.3%). *Candida* spp. were detected at a markedly lower prevalence (2.6%), underscoring the predominance of bacterial etiologies in this cohort. These results align with findings from several national and international studies, although notable differences emerged based on regional and demographic factors, particularly in pediatric and pregnant populations.

The identification of the principal causative organisms and their antimicrobial susceptibility patterns provides important guidance for clinicians in selecting appropriate empirical treatment. In the context of rising antimicrobial resistance, the availability of local microbiological data is crucial for enabling timely, targeted therapy—thereby enhancing treatment effectiveness, reducing recurrence rates, and mitigating the risk of severe complications such as ascending genital tract infections, infertility, and adverse pregnancy outcomes.

Overall, this study contributes valuable regional epidemiological evidence that can inform future research and support the development of clinical guidelines for the effective diagnosis and management of vaginitis.

Ethics Committee Approval: This study was approved by the Non-Interventional Clinical Research Ethics Committee of Mardin Artuklu University, Faculty of Medicine, with decision number 2025/4-45, dated April 22, 2025.

Authors' contributions: Conceptualization: ES, ZA, OT; Study Design: ES, ZA, OT; Supervision: ES, ZA; Resources and Materials: ES,

OT; Data Collection: ES,OT; Data Analysis and Interpretation: ES,ZA,OT; Literature Search: ES, ZA; Manuscript Writing: ES, ZA, OT; Critical Review and Editing: ZA

Conflict of Interest: The authors declare that there is no conflict of interest regarding the publication of this article.

Funding: This study received no financial support from any funding agency, commercial entity, or organization.

Acknowledgments: The authors declare that there are no acknowledgments to be made for this study.

Informed Consent: Informed consent was not obtained as the study was retrospective.

REFERENCES

- Holloway D. Nursing considerations in patients with vaginitis. *Br J Nurs.* 2010;19:1040–1046.
- Kalkancı A, Çiftçi B, Aydan B, Kuştımur S, Güner H. Vajinitis ötanısı almış olgularda vajinal kültür sonuçlarının etkenlerine göre dağılımı. *Türkiye Klin J Gynecol Obst.* 2005;15(3):137–139.
- Liu C, Zhang Y, Kong S, Tsui I, Yu Y, Han F. Applications and therapeutic actions of complementary and alternative medicine for women with genital infection. *Evid Based Complement Alternat Med.* 2014;2014:658624.
- Pamukçuoğlu S, Pamukçuoğlu MH, Tünay H, Arslan F, Uzel Taş H. Gram negatif bakterilerin dağılımı ve direnç profillerinin incelenmesi. *J Clin Anal Med.* 2015;6(6):742–745.
- Aysert-Yıldız P, Yıldız Y, Habibi H, Eser S, Özgen-Top Ö, Özger HS, et al. *Stenotrophomonas maltophilia* bacteremia: from diagnosis to treatment. *J Infect Dis Clin Microbiol.* 2022;4(4):258.
- Lowe NK, Neal JL, Ryan-Wenger NA. Accuracy of the clinical diagnosis of vaginitis compared to a DNA probe laboratory standard. *Obstet Gynecol.* 2009;113(1):89–95.
- Anderson MR, Klink K, Cohnsen A. Evaluation of vaginal complaints. *JAMA.* 2004;291(11):1368–1379.
- Albayrak HT, Albayrak AM, Bakır A, Şahin İ. Vulvovajinal enfeksiyon tanı yöntemlerinin karşılaştırılması ve predispozan faktörlerin etkilerinin incelenmesi. *Düzce Üniv Sağlık Bil Enst Derg.* 2020;10(1):52–57.
- Vural Yılmaz Z, Yılmaz E, Gültekin İB, Kara OF, Küçüközkan T. Vulvovajinal enfeksiyonu olan kız çocuklarında vajinal kültür sonuçları. *J Gynecol Obstet Neonatol.* 2016;13(2):58–60.
- Chaabaawi A, Sucu M, Karakoyun AS, Ünal N, Kara E, İlkit M. Gebelerde *Candida* vajinitinin epidemiyolojisi. *Türk Mikrobiyol Cem Derg.* 2022;52(2):109–118.
- Altan G, Hazırolan G, Mumcuoğlu İ, Atalay CR, Aksoy A, Aksu Koca N. Vulvovajinal kandidoz ve vajinal kolonizasyondan izole edilen *Candida* izolatlarında bazı virülans faktörlerinin ve antifungal duyarlılığın araştırılması. *Türk Mikrobiyol Cem Derg.* 2023;53(3):163–173.

12. Malak A, Aydın Kurç M, Gülen D, Kaya AD, Taşdemir N, Varol G. Vulvovajinal kandidiyazis: risk faktörleri ve infeksiyon etkenlerinin dağılımı. *Sağlık Bil Değer.* 2024;14(1):66–70.
13. Börekçi B, İngeç M, Aktaş O. Jinekolojik şikayetleri olan hastalarda vajinal mikroflora üzerine bir araştırma. *Ankara Üniv Tıp Fak Derg.* 2003;35: 57–60.
14. Cengiz SA, Cengiz L, Us E. Gebe kadınların vajinal akıntılarından üretilen mikroorganizmaların dağılımı ve antibakteriyellere duyarlılıkları. *OMÜ Tıp Derg.* 2004;21(2):84–89.
15. Marnach ML, Wygant JN, Casey PM. Evaluation and management of vaginitis. *Mayo Clin Proc.* 2022;97(2):347–358.
16. Shanmugam SR, Balasundharam A, Thomas IN, Bir R, James JJ. A cross-sectional clinical investigation of organisms causing vaginal discharge in patients in rural Tamil Nadu, India. *Cureus.* 2023;15(1):e33979.
17. Wójkowska-Mach J, Pomorska-Wesołowska M, Romanik M, Romaniszyn D. Prevalence and antimicrobial susceptibility profiles of microorganisms associated with lower reproductive tract infections in women from southern Poland–retrospective laboratory-based study. *Int J Environ Res Public Health.* 2021;18(1):335.
18. Zhang M, Liu J, Pan YC, Liu HL, Shu J, Wu XM, et al. Analysis of pathogenic bacteria and drug resistance among girls with bacterial vaginitis. *Infect Drug Resist.* 2023;16:1849–1863.
19. Yasin J, Ayalew G, Dagnaw M, Shiferaw G, Mekonnen F. Vulvovaginitis prevalence among women in Gondar, Northwest Ethiopia: special emphasis on aerobic vaginitis causing bacterial profile, antimicrobial susceptibility pattern, and associated factors. *Infect Drug Resist.* 2021;14:4567–4580.
20. Bitew A, Abebaw Y, Bekele D, Mihret A. Prevalence of bacterial vaginosis and associated risk factors among women complaining of genital tract infection. *Int J Microbiol.* 2017;2017:4919404.