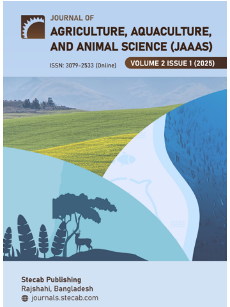

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Research Article

Prevalence Rate of Bacterial Infections in Urogenital Tract of Adult Goats, and Susceptibility to Antibiotics

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About Article

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ABSTRACT

This study conducted to identify the prevalence rate of pathogenic bacteria in urogenital tract of adult female goats including non-previously kidding and those kidding at least one time. Also, detection of bacterial species and their susceptibility to various antibiotics was aimed. Totally, 148 vaginal swab samples were collected from the adult female goats; 74 from non-kidding and 74 from kidding goats. In laboratory, various culture media and biochemical tests were used to cultivation and differentiation of bacterial isolates based on their colonies' morphology and reaction. Then, the Kirby-Bauer method was applied to test the susceptibility of the obtained bacterial species towards the applied antibiotics. Totally, the prevalence rate of bacterial infections among the study goats was 64.19%, in which, prevalence rate was significantly higher in non-kidding (78.38%) than kidding (50%) goats. The results of culture and biochemical tests showed the presence of *Escherichia coli* (30.53%), *Proteus mirabilis* (23.16%), *Klebsiella pneumoniae* (14.74%), *Pseudomonas aeruginosa* (10.53%), *Staphylococcus epidermidis* (11.58%), and *Staphylococcus aureus* (9.47%). Significantly, the findings of antibiotic susceptibility testing revealed that the study bacterial isolates were resistant to Amoxicillin, Amikacin, Ampicillin, Ceftazidime, Ceftriaxone, Cefotaxime and Cefepime; while intermediate resistance was identified with Gentamicin. However, significant sensitivity was recorded to Colisitin, Nitofurantion, Azithromycin, Ciprofloxacillin, Ofloxacine, Imipenem, Meropenem, Levofloxacine, and Nalidixic acid. In conclusion, the study indicates the high prevalence rate of bacterial infections in study animals, in particular non-kidding goats, with high incidence of resistance to different antibiotics. Therefore, furthermore studies using the advanced molecular diagnostic assays are of great importance to determine the epidemiology and presence of genes responsible on resistance of various bacteria.

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1. INTRODUCTION

Urogenital tract infection is one of the health problems that goats suffering from it in most countries and consider as the second most common disease after respiratory tract infection (Ahamed *et al.*, 2015; Sahay, 2020). Females are more susceptible to urogenital tract bacterial infections than males because the urethra is much closer to the anus in females, as well as the presence of prostate glands secreting bacteriostatic bacterial inhibitors in males (Al-Jubouri *et al.*, 2012). Generally, all female animals are susceptible to being affected by bacterial infections, especially older females, due to hormonal changes resulting from aging and general immunosuppression (Naber *et al.*, 2006; Mohammed *et al.*, 2018). Bacteria are considered the main cause of urinary tract infections at 95%, and most often bacteria that live in the digestive system, the vagina, and even around the urethra (urethra), where most of these bacteria are transmitted to the bladder and kidneys to cause the bacterial infections (Saleem *et al.*, 2021).

2. LITERATURE REVIEW

The main cause of urinary tract disease in the world is the bacterium pathogenic *Escherichia coli* that constitute 80-85% of urogenital tract infection, while staphylococci constitute 5-10% of uncomplicated urogenital tract infection (Ahamed *et al.*, 2015). There is a difference in the virulence of the types of bacteria that cause infection, as their gram-positive increases their pathogenicity directly or indirectly. These are called virulence factors, which combine the urease enzyme and work on hemolysin and produce bacteriocin and beta-lactamase to form biofilm and others (Hassan *et al.*, 2011). Resistance to antibiotics by the bacteria that cause bacterial infections has begun to increase recently due to the incorrect use of antibiotics (Madjeed *et al.*, 2022). Recently, studies in Iraq focused on bacterial isolation in bacterial infections by dvarious authors that showed the highest infection by different bacteria such as *Corynebacterium pyogenes*, and *Staphylococcus* spp. (Sawalha, 2019). Other studies investigated urinary bladder lesions among the slaughtered local calves demonstrating the high incidence of this infection suggesting the importance of additional research to reduce the economic damage resulting from the impact on the reproductive system of goats and reduce abortion (Iso, 2020; Lilo & AL-Jasim, 2020). Therefore, the current study was conducted to identify the pathogenic bacteria implicated in occurrence of bacterial infections in goats of Wasit province (Iraq).

3. MATERIAL AND METHOD

3.1. Ethical approval

This study was licensed by the Scientific Committee of the College of Veterinary Medicine in the University of Wasit (Wasit, Iraq).

3.2. Samples

Totally, 148 vaginal swab samples were collected from adult female goats including 74 samples from those does not kidding previously and 74 samples from the goats that kidding at least one time. The swab samples were collected carefully, transferred to the laboratory, and cultured onto MacConkey agar (Hussein, 2019). For accurate diagnosis, colonies were recultured onto Hoyles Media and Mannitol salt agar. The isolates were then classified using biochemical tests and using the sugar fermentation test to characterize and classify bacteria (Sheet, 2018).

3.3. Statistical analysis

The One-Way ANOVA and t-test in the GrapPad Prism Software were applied to estimate significant differences between the obtained data at P<0.05 (Gharban *et al.*, 2022).

4. RESULTS AND DISCUSSION

4.1. Results

Totally, the prevalence rate of bacterial infections among the study goats was 64.19% (95/148), while 35.81% (53/148) were negatives (Figure 1). Among non-kidding goats, 78.38% (59/74) were positive to bacterial infection whereas 21.62% (16/74) were negatives (Figure 2). In kidding goats, the prevalence rate of bacterial infections was 50% (37/74) while 50% (37/74) were revealed a negative result (Figure 3). Significantly, the prevalence rate of bacterial infection was higher in non-kidding (78.38%) than kidding (50%) goats (Figure 4).

After isolating and diagnosing the bacteria in this study and after isolating separate Gram-positive and negative bacteria. The results showed there were 30.53% (29/95) of *E. coli* isolates, 23.16% (22/95) of *Proteus mirabilis* isolates 14.74% (14/95) of *Klebsiella pneumoniae* isolates, 10.53% (10/95) of Pseudomonas aeruginosa isolates, 11.58% (11/95) of *Staphylococcus epidermidis* isolates, and 9.47% (9/95) of *Staphylococcus aureus* isolates (Figure 5).

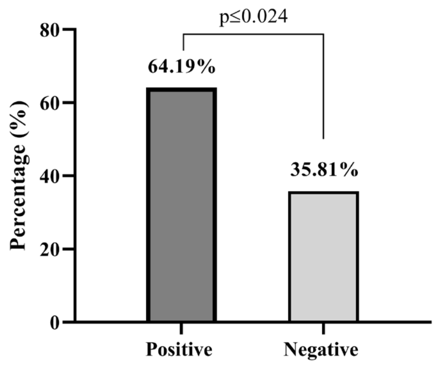

Figure 1. Total results for prevalence rate of bacterial infections among study goats

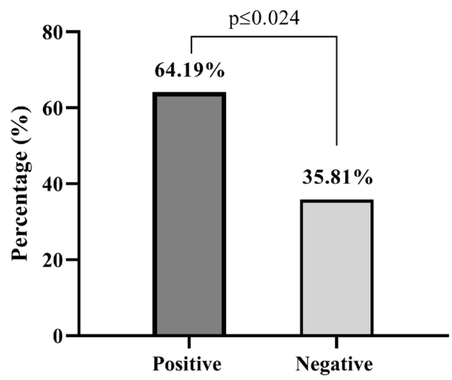

Figure 2. Prevalence rate of bacterial infections among the non-kidding goats

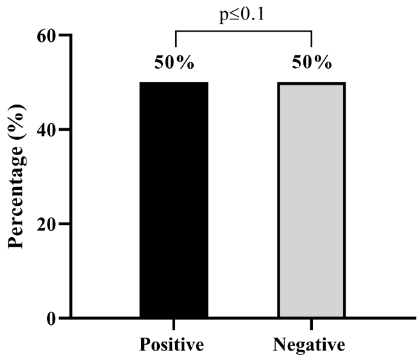

Figure 3. Prevalence rate of bacterial infections among the kidding goats

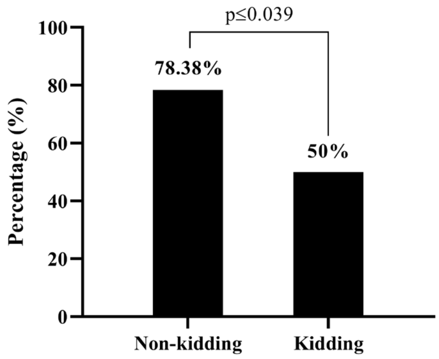

Figure 4. Prevalence rate of bacterial infections among non-kidding and kidding goats

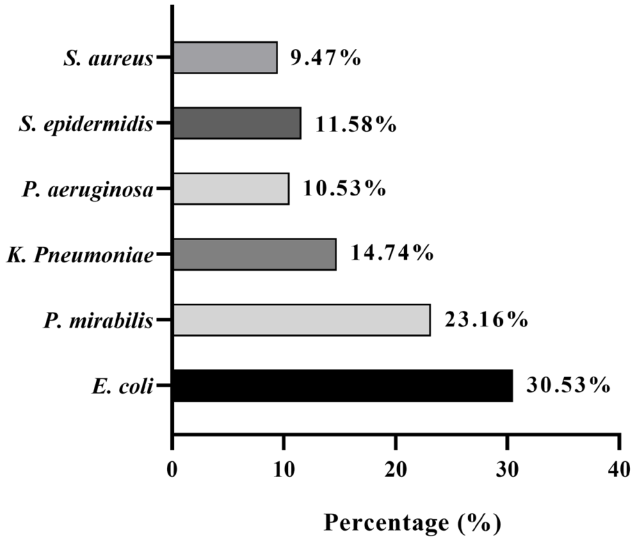

Figure 5. Results of isolated bacteria from positively infected goats

The present study examined the susceptibility of study bacterial isolates to antibiotics using disc diffusion method. Significantly, the findings revealed that the isolates were resistant to Amoxicillin, Amikacin, Ampicillin, Ceftazidime, Ceftriaxone, Cefotaxime and Cefepime; while intermediate resistance was identified with Gentamicin. However, significant sensitivity was recorded to Colisitin, Nitofurantion, Azithromycin, Ciprofloxacillin, Ofloxacine, Imipenem, Meropenem, Levofloxacine, and Nalidixic acid (Table 1).

Table 1. Results of susceptibility of study bacterial isolates (total number = 95) to various antibiotics (total number = 17)

Types of antibiotic	Susceptibility pattern			p-value
	Resistant	Intermediate	Sensitive	
Amoxicillin	67 (70.53%) *	14 (14.74%)	14 (14.74%)	0.011 S
Ampicillin	59 (62.11%) *	26 (27.37%)	10 (10.53%)	0.019 S
Ceftazidime	72 (75.79%) *	18 (18.95%)	5 (5.26%)	0.032 S
Ceftriaxone	44 (46.32%) *	34 (35.79%)	17 (17.89%)	0.044 S
Cefotaxime	59 (62.11%) *	24 (25.26%)	12 (12.63%)	0.039 S
Cefepime	41 (43.16%) *	33 (34.74%)	21 (22.11%)	0.041 S
Amikacin	60 (63.16%) *	19 (20%)	16 (16.84%)	0.038 S
Gentamicin	23 (24.21%)	51 (53.68%) *	21 (22.11%)	0.046 S
Azithromycin	2 (2.11%)	11 (11.58%)	82 (86.32%) *	0.024 S
Colistin	11 (11.58%)	6 (6.32%)	78 (82.11%) **	0.025 S
Nitrofurantoin	14 (14.74%)	8 (8.42%)	73 (76.84%) *	0.031 S
Nalidixic acid	16 (16.84%)	17 (17.89%)	62 (65.26%) *	0.037 S
Ciprofloxacillin	20 (21.05%)	24 (25.26%)	51 (53.68%) *	0.04 S
Ofloxacine	4 (4.21%)	7 (7.37%)	84 (88.42%) *	0.019 S
Levofloxacine	9 (9.47%)	11 (11.58%)	75 (78.95%) *	0.011 S
Meropenem	17 (17.89%)	29 (30.53%)	49 (51.58%) **	0.029 S

Imipenem	10 (10.53%)	14 (14.74%)	71 (74.74%) *	0.013 S
p-value	0.0086 **	0.011 *	0.0052 **	-

Significance (p<0.05) *

4.2. Discussion

Our findings detected that the prevalence rate of bacterial infections among study goats was 64.19%; in which, bacterial infection was significantly higher in non-kidding (78.38%) than kidding (50%) goats. These results were in agreement with that observed by Ibrahim *et al.* (2020) and Alwan *et al.* (2023) but differed from those found by Kubaisy (2013) and Ondari (2020),. The reason may be due to differences in the size, environment, and nature of the sample because the animals were given antibiotics before taking the samples, which may have led to the absence of bacterial growth in the sample (Al-Abdali, 2010). This may be the result of a non-bacterial infection that may be viruses, parasites, fungi, or anaerobic bacteria (Brooks *et al.*, 2007). Abedin *et al.* (2022) detect the infection rate at 66% in goats of multiple births, and this is due to the reason for high rate of hormonal and differences in anatomical (Raka *et al.*, 2010).

The results of current study detected that the bacteria species obtained were included *E. coli* (30.53%), *P. mirabilis* (23.16%), *K. pneumoniae* (14.74%), *P. aeruginosa* (10.53%), *S. epidermidis* (11.58%), and *S. aureus* (9.47%). This result of *E. coli* was agreed with Ondari (2020) who found 37.87%, as well as Nabbugodi (2013) who reported 40%, while this percentage disagreed with Ahmed *et al.* (2019), who reported 70.49%. The high rate of *E. coli* bacteria may be isolated The cause of urinary tract infection compared to the rest of the intestinal bacteria is due to the presence of these normal flora bacteria in huge numbers in the human gastrointestinal tract as a natural flora, in addition to the possession of multiple harmful factors such as the production of the hemolysin enzyme, as well as the ability to form a biofilm, helps to cause and sustain the infection (Alsamarai and Abdulaziz, 2016). The *P. mirabilis* bacteria is in second with bacterial infections at 18.2%, and these results agree with other researchers (Abedin *et al.*, 2022; Salami et al 2022; Shati *et al.*, 2022), who detected different infection rates; while disagree with the results of Khorshid (2005) in Kirkuk, as well as Tabasi *et al.* (2015). This reason is due to the presence of *E. coli* bacteria in the first place, followed by *P. mirabilis* bacteria due to kidney problems and the formation of kidney stones (Saeed & Mansoor, 2015). However, bacteria were identified on blood culture media and MacConkey culture and based on some of the differentiating characteristics of each type of bacteria, the different types of bacteria that cause bacterial infections (Cowan & Steels, 2009; Al-Saffar, 2019). The percentage of infection by *K. pneumoniae* bacteria was agreed with Abdullah *et al.* (2010) who detected 17.6%, as well as Ondari (2020) who reported 13.6%, and the current results showed disagreement with Ali *et al.* (2018) and Haider *et al.* (2010). The difference in the rates of results is because the strains of *K. pneumoniae* bacteria depend on their ability to adhere to mucous surfaces, and this is the first step for infection to occur, without adherence, the bacteria lose a large part of its virulence (Huang *et al.*, 2012). Regarding the *P. aeruginosa* bacteria, the results agree with Abedin *et al.* (2022) found 9.8% and disagree with Lilo and AL-Jasim (2020) who identified 41.3%. These conditions may be due to the number of samples, the difference in health conditions of animals during talk sampling, and some development of resistance in some strains of bacteria that cause bacterial infections (Sabir *et al.*, 2014). The isolation of *Staphylococcus* spp. are agreed with Smita (2020) who found that the results of S. epidermidis, *S. aureus* by 13.44% and 5.38%, respectively. Razgar and Raoof (2018) recorded a rate of 19.35% for *S. aureus* and with Kazemier (2014) who recorded a rate of infection at 19.35%. These results disagree with the results in current research, and this difference in results is attributed to both *S. aureus* and S. epidermis caused by contaminated skin found on the female urinary tract when samples were taken (Wistrom *et al.*, 2014).

Antibiotics are very useful in fighting pathogens and their use has reduced mortality from bacterial infections worldwide. However, antibiotic resistance continues to increase due to the overuse of description of antibiotics, as well as genetic and environmental factors (Larsson and Flach, 2022). Antibiotic treatment of bacterial infections is not recommended systematically. However, it is important to understand the sensitivity of these pathogens to antibiotics, because resistant strains of bacterial infections may due to presence of antibiotic resistance genes (Jian *et al.*, 2021). In addition, children with diarrhea caused by bacterial infections or diarrhea that persists after bacterial infections diagnosis may require antimicrobial treatment. Bacterial infections are twice as likely to be resistant to various antibiotics, since most bacterial isolates are commonly used to treat diarrhea and other diseases (Mancuso *et al.*, 2021). This is consistent with observations from other studies that there is some flexibility, and the high level of resistance observed is explained by the bacterial infections, so the prevalence of this species is the result of diverse distribution and evolution Antibiotic treatment promotes the selection of stress-resistant isolates (Fair and Tor, 2014; Banin *et al.*, 2017). Nkang *et al.* (2009) also presented the results of drug susceptibility testing of different groups of bacterial isolates, which showed high resistance to ampicillin, erythromycin and nalidixic acid. Bacterial isolates were least resistant to mecillin, ceftriaxone and gentamicin. Antimicrobial susceptibility patterns in samples containing multiple pathogenic strains. In addition, the authors demonstrated antibiotic susceptibility profiles in samples containing combinations of pathogenic strains. Afum *et al.* (2022) found that many bacterial isolates are highly resistant to antibiotics commonly used to treat diarrhea. As this study shows, resistance has recently become problem. The emergence and diversity of multidrug-resistant strains has increased in India in recent years (Gandra *et al.*, 2019). Tuvei (2017) showed that a number of bacterial isolates are resistance as follows: amoxicillin-clavulanic acid (12.8%), co-trimoxazole (59%), Tetracycline (51.3%), ciprofloxacin (23%), Cotrimoxazole (44.2%), tetracycline and azithromycin (44.2%); however, all clinical isolates were sensitive to imipenem. Du *et al.* (2018)

found that resistance rates of 1% and 28 %, respectively. However, due to the small population; no statistical analysis was performed to stratify strains based on pathotype and geographic origin. Colistin is an ancient antibacterial agent, but its use in human medicine is primarily for the treatment of drug-resistant Pseudomonas and Klebsiella species (Freitas *et al.*, 2023). Colistin is widely used to prevent and treat bacterial infections due to intrinsic activity against various bacteria, as well as low acquired resistance and poor absorption after oral administration reduces the infection in newborns. Resistance to colistin was acquired in animal strains of bacterial infections was rare in the past, but has become more common in recent years (Gogry *et al.*, 2021).

5. CONCLUSION

The current study indicates the high prevalence rate of bacterial infections in study animals, in particular non-kidding goats, with high incidence of resistance to different antibiotics. Therefore, furthermore studies using the advanced molecular diagnostic assays are of great importance to determine the epidemiology and presence of genes responsible on resistance of various bacteria.

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