



Antimicrobial Susceptibility Profile and Phylogenetic Analysis of Uropathogens in Jalalabad Afghanistan

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Absrtact

A cross-sectional study was conducted to investigate the prevalence and antimicrobial resistance patterns of uropathogenic bacteria in urine samples collected from patients at Kamawi Medical Laboratory, Jalalabad, Afghanistan. A total of 100 urine samples (61 females and 39 males) were collected. The study included confirmed UTI samples caused by bacteria, excluding samples with non-bacterial elements. The samples were cultured on various culture media and incubated at 37°C for 24 hours. Bacterial isolates were identified and antibiotic sensitivity testing was performed using the modified Kirby-Bauer disk diffusion method following Clinical Laboratory Standard Institute (CLSI) 2022 guidelines. The study identified a high prevalence (79%) of bacterial growth in urine samples. Among the isolates, *Escherichia coli* was the most prevalent (42%), followed by *Staphylococcus aureus* (22%), *Pseudomonas aeruginosa* (6%), *Klebsiella pneumoniae* (2%). Additional pathogens included Coagulase Negative Staphylococci (CONS) (4%), *Enterococcus faecalis* (2%), and *Candida* species (1%). Antibiotic resistance patterns revealed high resistance rates to commonly used antibiotics as ceftriaxone, ampicillin, and gentamicin, while fosfomycin and nitrofurantoin showed higher effectiveness. Molecular identification through 16S rRNA sequencing conducted at Macrogen, South Korea revealed discrepancies in species identification. While traditional methods identified some isolates as *E. coli* and *K. pneumoniae*, molecular analysis identified them as *Escherichia fergusonii* and *Klebsiella oxytoca*, respectively. Phylogenetic analysis using Molecular Evolutionary Genetics Analysis (MEGA) 11 software confirmed these findings and provided insights into the evolutionary relationships of the isolates. The study highlights the importance of accurate species identification and highlights the significant prevalence of uropathogenic bacteria in Jalalabad, Afghanistan, emphasizing the need for effective antibiotic management and infection control measures.

Keywords: Uropathogens, *E. coli*, *K. pneumoniae*, *K. oxytoca*, Phylogenetic analysis, 16S rRNA

Introduction

Urinary tract infections (UTIs) are one of the most prevalent infections affecting about 250 millions individuals each year, out of which 150 millions results in deaths globally, 40% to 50% victims are women while around 5% are men. The prevalence of women over men is due to the difference in anatomic structure of women, their size of urethra is shorter comparatively which results in rapid ascension of the microbes. These microbes are literally the normal gut flora as *Escherichia coli* into the lower UTI which further proceeds into upper UTI and pyelonephritis [1]. UTI is classified into two groups as simple infection and complex infection the



former characterized with more prevalence and unobstruction while the later is less prevalent with obstruction in it, the infection if not treated in time can result in kidney impairment [2]. Among the family Enterobacteriaceae the common most is *E. coli* [3]. UTI can result from mild sickness into acute sepsis, with the mortality rate of 20 -40%, both male and female can be infected, the ratio differs according to age, for age older than 70 years the female to male ratio 2:1 while for younger the ratio is quite different as 50:1 [4].

UTIs in the outpatients are the commonest bacterial infections among women. Unfortunately, these infections are from multi drug resistance (MDR) species isolates, the treatment of which is comparatively difficult, the cause of such extreme resistance can be misuse of chemotherapy with antibiotics for UTIs, age, male sex and recurrent UTIs [5]. ESBL production can be one of the resistance factors among Gram negative bacilli to third generation cephalosporins[6]. ESBL producing bacteria produce resistance genes types as Beta-lactamase TEM (*bla*TEM) and Beta-lactamase Supphidryl Variable (*bla*SHV) the type TEM-1 in *bla*TEM breaks down the beta lactam ring of penicillin and early cephalosporins while expanded-spectrum cephalosporins showed resistance due to CTX-M-1 [7]. These genes were found in beta lactamase producer uropathogens (*E.coli* and *K. pneumoniae*) [7]. *P.aeruginosa* infections are effectively treated with carbapenems [8]. Methicillin Resistant Staphylococcus aureus (MRSA) being a human uropathogen is associated with nosocomial infections, the resistance to methicillin is due to *mecA* gene UTIs account for 35 to 40% of hospital acquired infections, catheter associated urinary tract infection (CAUTI) is one of these infections resulting in over 1 million cases in hospitals and nursing home [9]. Hospitals witness a number of different pathogens causing UTI each year [10]. Hospital stay is also one of the factors [11]. The infection is generally self limiting but has the potential of recurrence due to having some self protecting properties as the production of various chemicals like toxins, and adhesions which enable these pathogens reside in the urinary tract. Their transmission among people is person to person via various contacts or possibly food or water [10].

E. coli has been the predominant pathogen causing UTIs in community acquired infections which is followed by Staphylococcus Saprophyticus, (10 to 15 %) a Coagulase Negative Staphylococci (CONS) from the genus Staphylococcus, accordingly Klebsiella, Enterobacter, Proteus and Enterococci followed respectively, infections with these all resulted into pyelonephritis and uncomplicated cystitis [12]. For community it was Group B Streptococcus (GBS) that was the most prevalent in pregnant individuals and newborns [13].

In newborns UTI can result into sepsis, with nonspecific features as vomiting, poor sucking of milk, lethargy, pallor, hypothermia, convulsions, anorexia and sometimes jaundice [14]. The analysis of 16s rRNA on urine sample is the evidence of presence of live bacteria in urine samples. Urine is not a sterile medium hence the chance to recover pathogenic bacteria are more [15].

Accurate diagnosis reduces the risk of antimicrobial resistance and antibiotics associated side effects. Molecular based analysis is costly but the results of which are extremely sensitive and specific individuals with UTI and negative for culture, 16S rRNA sequencing can be extremely beneficial for them, mostly for people with cardiovascular infections. All bacteria contain 16s rRNA genes that classifies them within genus and species level. Some complex cases for UTIs have been confirmed with molecular based analysis most commonly 16s rRNA gene sequencing. The specimen are directly processed for gene sequencing as they were previously processed for PCR followed by Sanger Sequencing. Comparison studies of culture with molecular



based analysis are available with low sensitivity and specificity [16, 17]. Circumcision may reduce the risk for UTI in children [18]. Children within the first two years of age often face febrile [17].

Significance of the study

The study signifies students gaining information about the literature, the teachers directing their students, and most importantly researchers which help them resume what has been done so far and will open doors to work ahead.

Materials and Methods

Sample Collection

A cross sectional study was conducted by collecting a total of 100 urine samples from patients (both male and female) who visited Kamawi Medical Laboratory, Jalalabad Afghanistan using standard procedure, as the collection container being sterile, wider and seal packed before the use. Clean catch midstream urine (20 mL) was preferred from each patient, the specimen were labeled properly [19]

Inclusion and Exclusion Criteria

Confirmed UTI samples due to bacteria from both male and female were all included while samples with fungal elements, parasite and other elements causing UTI like symptoms were excluded from the study.

Sample Processing and Culturing

The samples were appropriately transported to the Kamawi Medical Laboratory, Nangarhar, Jalalabad in sterile condition, and cultured using various culture media i.e. 5% sheep Blood Agar, Cystin Lactose Electrolyte Deficient (CLED), macConkey Agar and were incubated for 24 hours at 37°C [20]. The media used were from Oxoid UK.

Identification of Bacterial Isolates

The pathogens were identified using Macroscopic, microscopic and Biochemical testing of the isolates as given below:

Macroscopic Identification

Macroscopic examination of the colonies after the growth included color, texture, pigmentation, swarming and string formation, as the swarming is inhibited by the medium Cysteine Lactose Electrolyte Deficient (CLED) and shall not be observed in it, MacConkey Agar which is considered a selective and differential for gram negative bacteria is almost always productive in uropathogens giving distinct characteristics to lactose fermenting colonies and non-lactose fermenting colonies. The former appearing pink red on the medium while the latter appearing pale yellow, such phenomenon is due to the presence of neutral red on the medium which results in the drop and rise of the pH causing the colonies to change the color [21].

Microscopic Identification

For the microscopic examination of the isolates, the bacteria were stained using Gram's staining, which showed the Gram negativity and positivity alongside the morphology of the bacteria. The distinct color of the bacteria is a result of the chemical and structural makeup of the cell wall of the bacteria i.e. Gram positive and Gram negative cell wall [22].



Biochemical Identification

Various biochemical tests were performed as oxidase, Indole, Urease, Citrate, Catalase, Triple Sugar Iron (TSI), Mannitol Fermentation [23].

Antibiotic Sensitivity Testing

Antibiotic sensitivity testing was carried out using the standard Clinical Laboratory Standard Institute (CLSI) 2022 by carrying out the modified Kirby-bauer disk diffusion method. The antibiotics used are given below along with their concentration.

Antibiotics used in the current study

The antibiotics used were Gentamicin (CN) with the concentration 10ug, Ceftriaxone (CRO) 30 ug, Amoxicillin/Clavulanate (AMC) 30ug, Ofloxacin (O) 5ug, Linezolid (LZD) 30ug, Ampicillin (AMP) 30ug, Ciprofloxacin (CIP) 5ug, Cefuroxime (CFM) 30ug, Ceftazidime (CAZ) 30ug, Nitrofurantoin (N) 300ug, Erythromycin (E) 5ug.

Molecular Identification and Phylogenetic Analysis

Samples post isolation and identification were sent to Macrogen (South Korea) for 16SrRNA sequencing. The sequence obtained was submitted to National Center for Biotechnology Information (NCBI) database and was compared with other sequences by using Basic Local Alignment Search Tool (BLAST) [24]. Further using BLAST results phylogenetic analysis was performed by constructing phylogenetic tree using Molecular Evolutionary Genetics Analysis (MEGA) 11 Software [25].

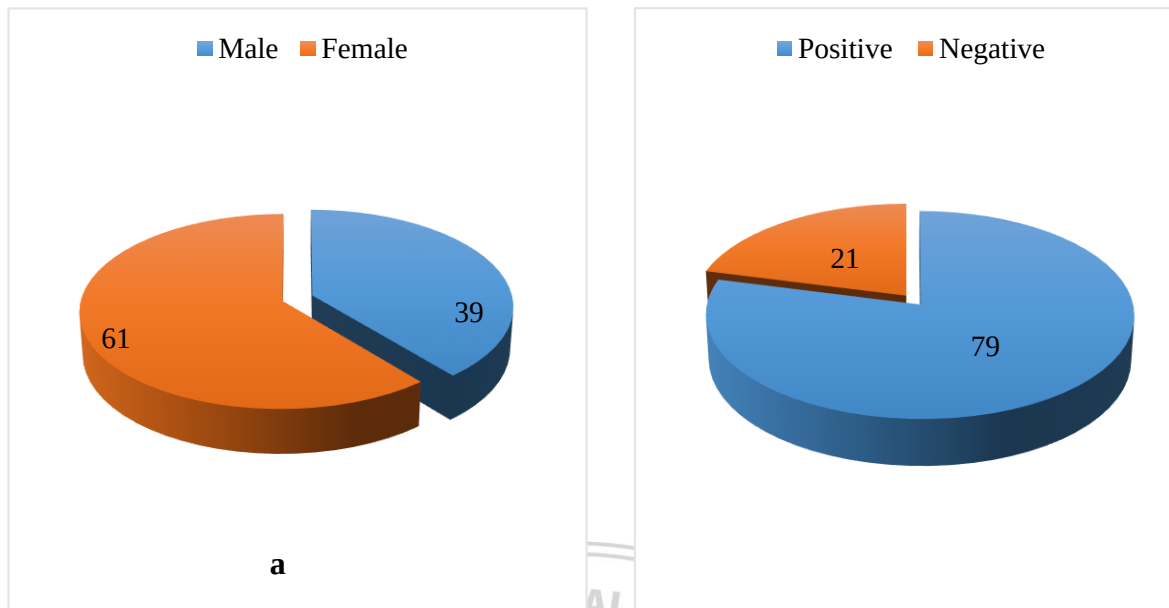
Statistical Analysis

The data was interpreted using Microsoft Excel spreadsheet and after that, it was analyzed through the SPSS v. 26.0 [26].

Results

Samples Distribution

During this cross sectional study, a total of 100 urine samples were collected, out of which 61 (61%) were from female while 39 (39%) were from male (Figure 4.1a). All the samples were cultured on media like Blood Agar, macConkey, and CLED. Among the total samples 79% samples were positive for bacterial growth while the remaining 21% showed no bacterial growth.



Identification

Post primary culture on media like Blood Agar, macConkey, and CLED, their colony characteristics were noted. Further, they were also observed for lactose and non-lactose fermentation and identified with Gram's staining and different biochemical tests as catalase, coagulase, indole, urease, TSI and oxidase.

Table 1: Colony characteristics on MacConkey agar and CLED Media

Bacteria	Colony characteristics
<i>E.coli</i>	MacConkey: Pink pin point flat dry colonies CLED: Raised Yellow colonies with deeper yellow color in the center
<i>K. pneumoniae</i>	MacConkey and CLED: Larger moister and mucoid colonies forming string pink in color
<i>S. aureus</i>	MacConkey: No growth CLED: Shiny golden Dry colonies
<i>P. aeruginosa</i>	MacConkey and CLED: Brown to green color colonies based on the pigment produced by the strain

Bacterial Isolates	No of Isolates	Gram Staining	macConkey Agar	Oxidase test	Indole test	Urease Test	Citrate Test	Catalase Test	TSI	Mannitol Fermentation
<i>E. coli</i>	42	-ive	LF	-	+	-	-	NA	A/A	NA
<i>S. aureus</i>	22	+ive	NA	NA	NA	NA	NA	+	NA	+

<i>K. pneumoniae</i>	06	-ive	LF	-	-	+	-	NA	A/K	NA
<i>P. aeruginosa</i>	02	-ive	NLF	+	-	-	-	NA	K/K	NA

Table 2: Results of Biochemical Tests

+: Positive, -: Negative, **LF**: Lactose fermenter, **NLF**: Non-lactose fermenter, **A/A**: Acid/Acid (fermentation of glucose, lactose, and/or sucrose), **A/K**: Acid/Alkaline (glucose fermentation only), **K/K**: Alkaline/Alkaline (no fermentation), **NA**: Not Applicable

Prevalence of Uropathogens

The prevalence of uropathogens in the positive samples were as *E. coli* (14%) for male while (28%) for female, so the total prevalence for *E. coli* was 42% in all the samples. For *S. aureus* 7 % for male while 15% for female, *P. aeruginosa* was recorded 5 % for male while 1 % for female, *K. pneumoniae* was 2 % for female while no positive for male, Coagulase Negative Staphylococci (CONS) was found to be 01% in male and 3 % in female, *Enterococcus faecalis* 1% each in male and female, *Candida* species also yielded in one sample. The results are depicted in Table 4.3 and Figure 4.2.

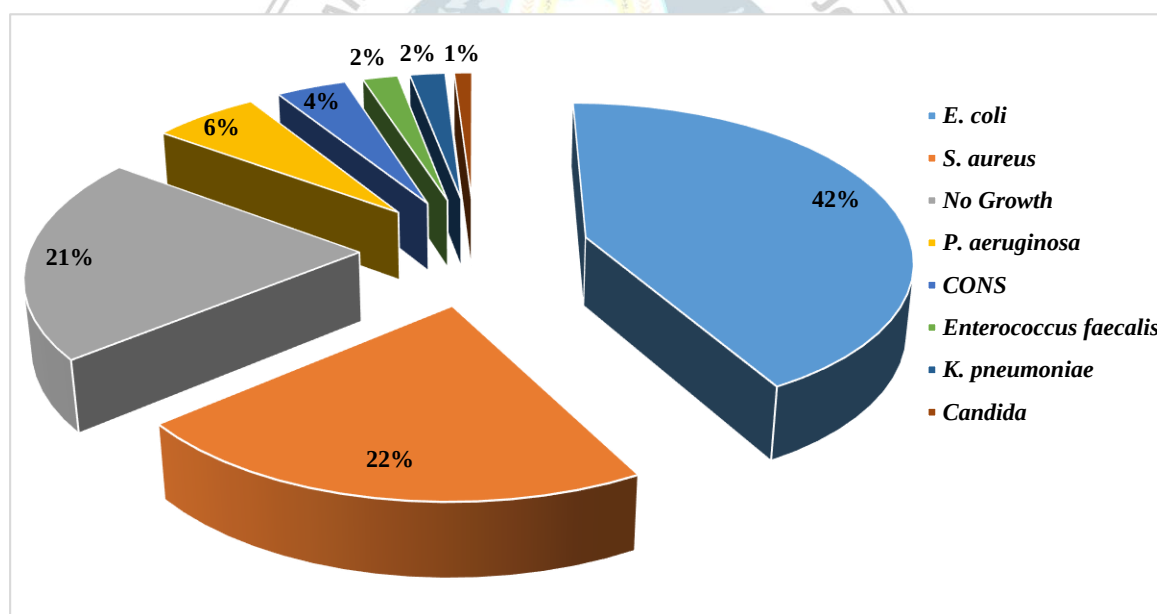


Figure 2: Demographic Analysis: Species wise Distribution

Antimicrobial Resistance Pattern of the Isolates

All the positive isolates were subjected to antibiotic sensitivity testing (AST) using 11 different antibiotics listed above, their detail is give below.

Escherichia coli

All the *E. coli* isolates (42) were subjected to AST, the results showed that that fosfomycin (90.90%) and nitrofurantoin (72.72%) are the most effective antibiotics against the tested isolates, while ceftriaxone (93.94%), ampicillin (93.94%), Ofloxacin (87.88%) and gentamicin (81.20%) show high resistance rates.

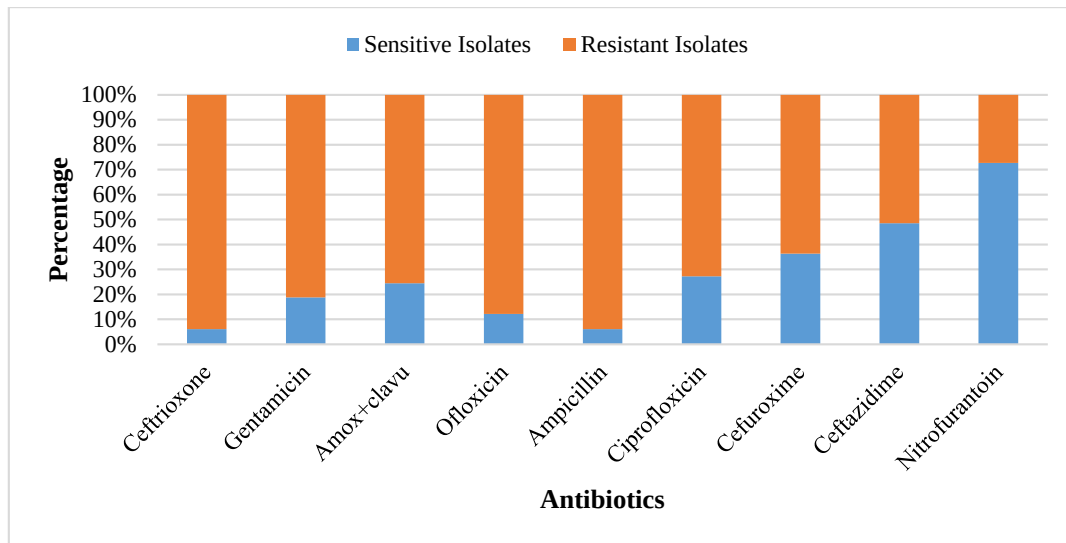


Figure 3: AST results of *E. coli*

Pseudomonas aeruginosa

All the *P. aeruginosa* isolates (06) were subjected to AST, the results showed that that fosfomycin (50.50%) and ceftazidime (50.50%) are the most effective antibiotics against the tested isolates, while ceftriaxone, Amox+Clavu, ampicillin and nitrofurantoin show high resistance rates i.e. 100%.

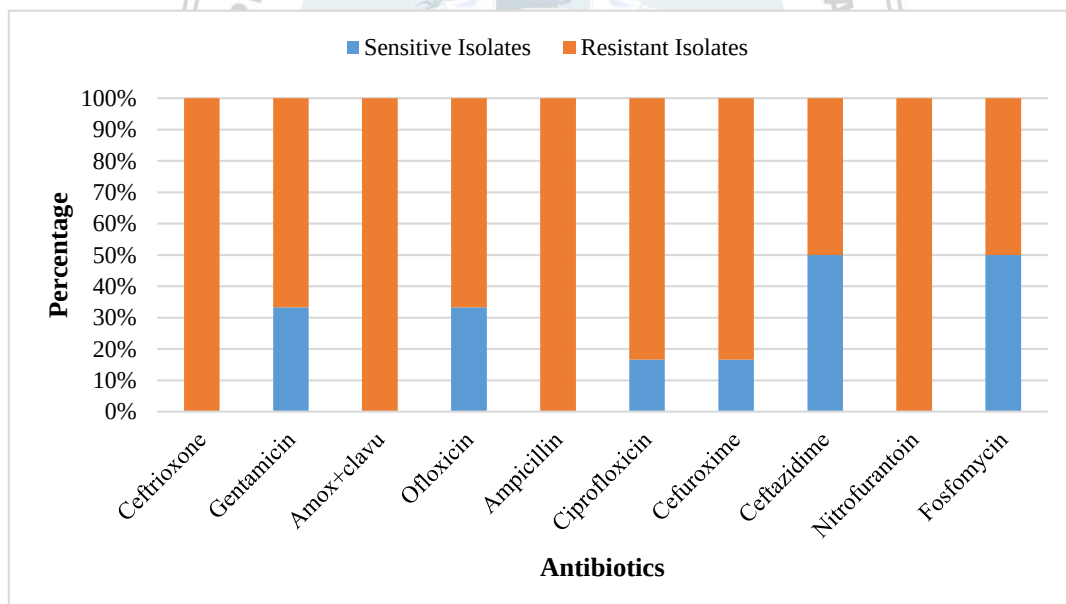


Figure 4: AST results of *P. aeruginosa*

Staphylococcus aureus

All the *S. aureus* isolates (22) were subjected to AST, the results showed that that fosfomycin (72.27%) and amox+clavu (63.6%) are the most effective antibiotics against the tested isolates, while ampicillin (95.5%), erythromycin (89.6%), and Ofloxacin (85.4%) show high resistance rates.

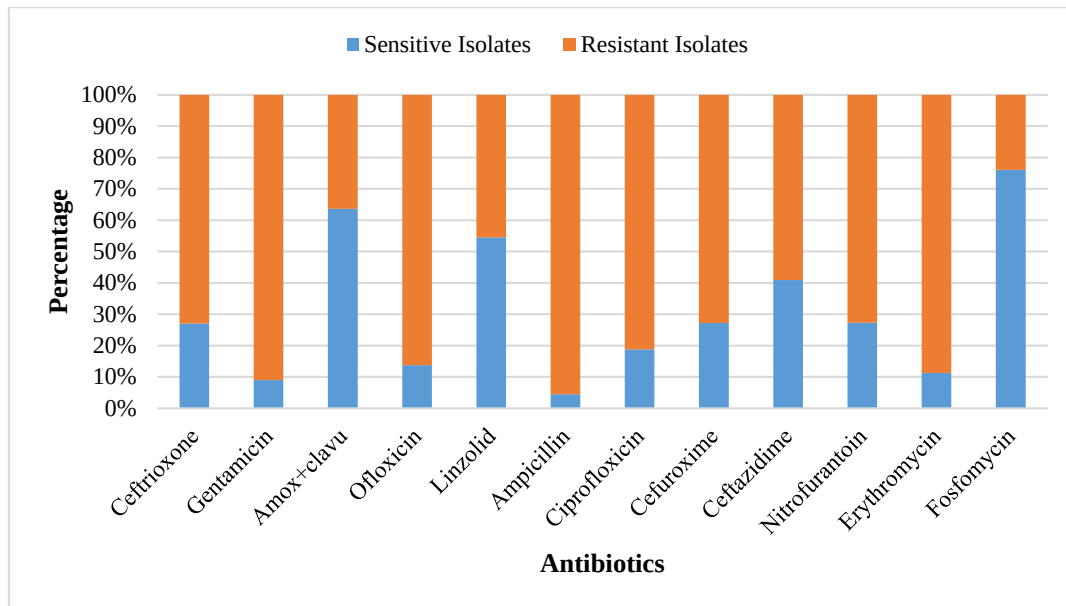


Figure 5: AST results of *S. aureus*

Klebsiella pneumoniae

All the *K. pneumoniae* isolates (02) were subjected to AST, the results showed that that ceftazidime (100%) followed by Ciprofloxacin, Cefuroxime, Amox+Clavu and ceftriaxone (50%) each are the most effective antibiotics against the tested isolates, while Ampicillin, fosfomycin, Nitrofurantoin and gentamicin show high resistance rates i.e. 100%.

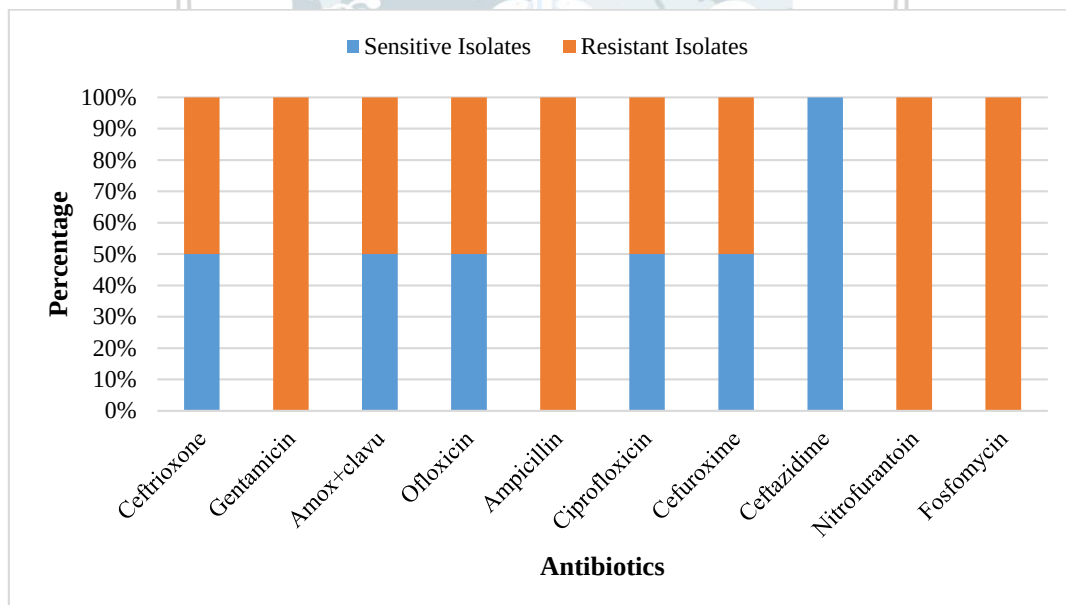


Figure 6: AST results of *K. pneumoniae*

Molecular Identification of the Isolates

Among the positive isolates 4 different isolates one from each *E. coli*, *P. aeruginosa*, *S. aureus* and *K. pneumoniae* were further evaluated at molecular level by sequencing its 16s rRNA by sending it to Macrogen,



Korea. For this purpose, pure colonies were isolated and transported at 4°C in nutrient agar plates. The sequence results obtained were cleaned with FinchTV (<https://digitalworldbiology.com/FinchTV>), nucleotides with no or overlapping signals were deleted. After cleaning the sequences, it was subjected to NCBI nucleotide BLAST to get matched results. Top 15 highly matched sequences were downloaded in FASTA format and their multiple sequence alignment was performed in MEGA 11 software (<https://www.megasoftware.net/>) and phylogenetic tree was constructed. Two of the species were identified as *E. coli* and *K. pneumoniae* using conventional methods but molecular level identification proved them to be quite different species of the same genus i.e. *E. fergusonii* and *K. oxytoca*. Further, the sequences were also submitted to NCBI database for the allotment of Accession numbers. The accession numbers are mentioned below.

Table 3: NCBI Accession numbers of the isolates in NCBI

S. No.	Isolate	NCBI Accession Number
1	<i>S. aureus</i>	PQ013753
2	<i>P. aeruginosa</i>	PQ013754
3	<i>E. fergusonii</i>	PQ013755
4	<i>K. oxytoca</i>	PQ013750

Phylogenetic Analysis

Subsequently, phylogenetic trees were made using similar sequences by neighbor joining method for each isolated bacterial strain. The phylogenetic tree showed that our identified *S. aureus* isolate showed similarity to MZ462055 *S. aureus* strain as shown in Figure below. Isolated *P. aeruginosa* showed similarity to OR756454 *P. aeruginosa* strain QS107 as shown in Figure below. Similarly, the isolated *E. coli* (conventionally identified) showed similarity to OM250486 *E. fergusonii* strain PW1 as shown in Figure below. while the isolated *K. pneumoniae* (conventionally identified) showed similarity to MF144435 *K. oxytoca* strain as shown in Figure below.

Neighbor-Joining method is one of the latest methods in creating a phylogenetic tree [27]. The conclusion from 1000 replicates resulted in the bootstrap tree that represents the evolutionary history of all the taxa analyzed. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [28]. Maximum Composite Likelihood method was used to compute the evolutionary distance. 16 nucleotide sequences were analyzed; the included codon positions were 1st+2nd+3rd+Noncoding. Sequences that were not clear or ambiguous were removed using (pairwise deletion option). The final dataset showed 1371 positions for *S. aureus*, 1393 positions for *P. aeruginosa*, 687 positions for *E. fergusonii* and 742 positions for *K. oxytoca*. MEGA11 conducted all the Evolutionary analyses [25].

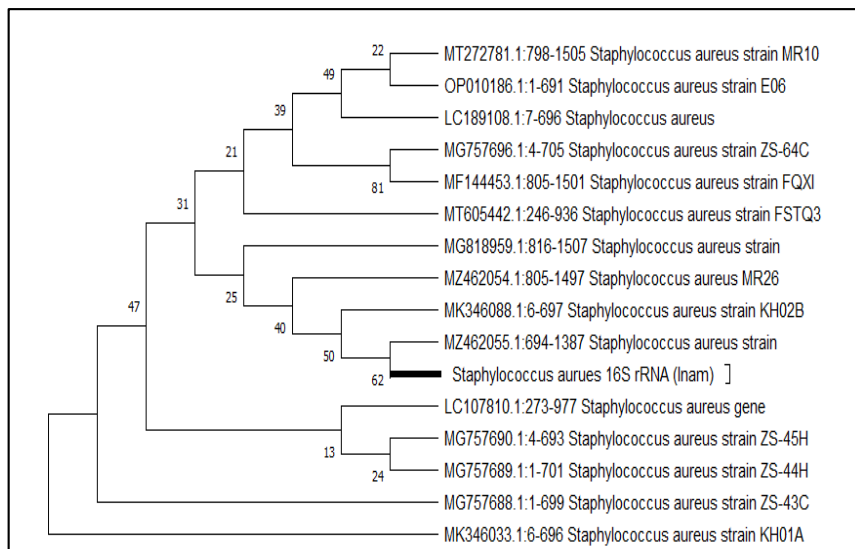


Figure 7: Phylogenetic Tree of 16S rRNA sequence of *S. aureus*

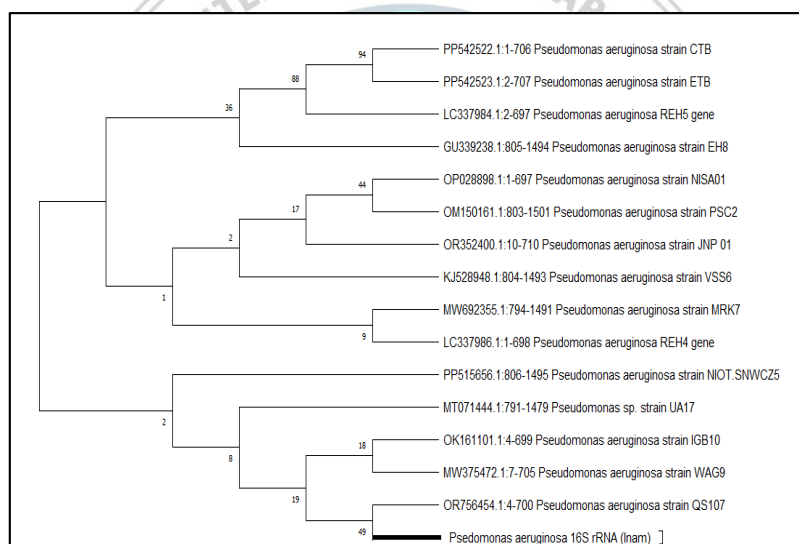


Figure 8: Phylogenetic Tree of 16S rRNA sequence of *P. aeruginosa*

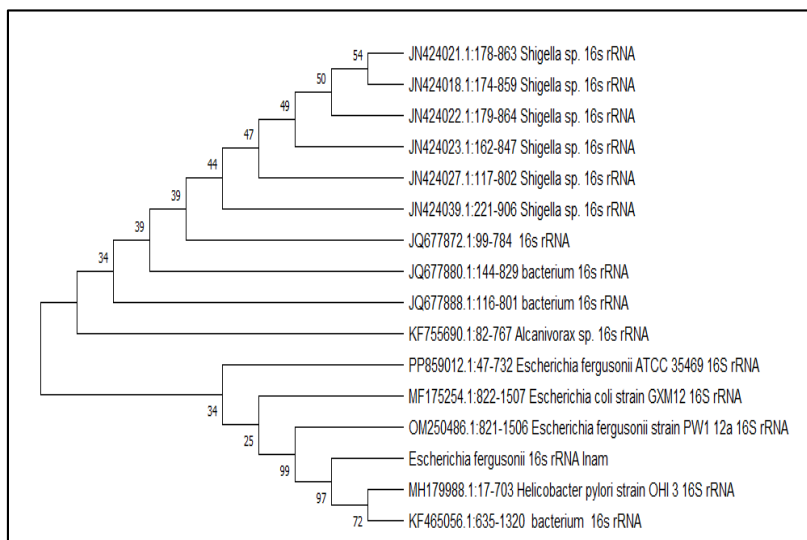


Figure 9: Phylogenetic Tree of 16s rRNA sequence of *E. fergusonii*

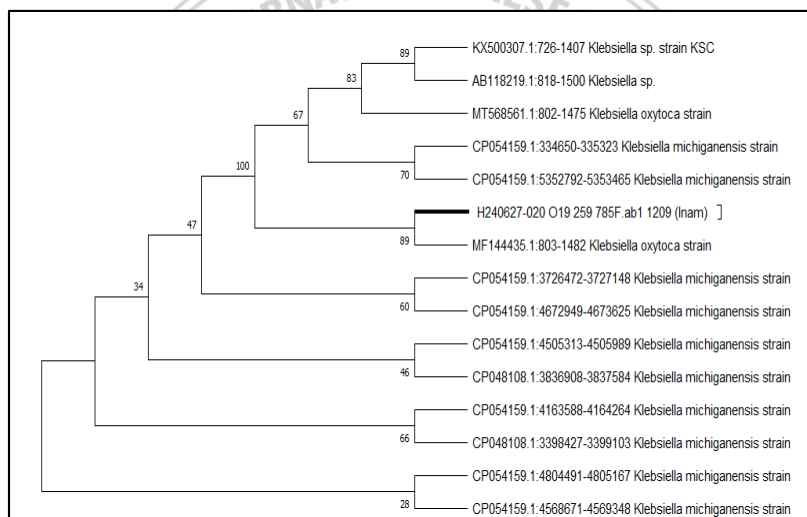


Figure 10: Phylogenetic Tree of 16s rRNA sequence of *K. oxytoca*

DISCUSION

The findings of the current study align with previous research on the prevalence and distribution of uropathogens. A significant proportion of the urine samples (79%) showed bacterial growth, indicating a high prevalence of urinary tract infections (UTIs) among the studied population. This prevalence is consistent with the study by [29], which reported a 65.9% positivity rate for urine cultures. The higher prevalence in females (61%) compared to males (39%) also corresponds with the gender distribution in UTI studies, such as those by [30].

The antimicrobial resistance patterns observed in this study highlight significant concerns regarding the efficacy of commonly used antibiotics as the most common antibiotics have grown resistance percentage that aligns the study with the previous studies. The resistance patterns of *E. coli* were particularly alarming, with high resistance rates to ceftriaxone (93.94%), ampicillin (93.94%), ofloxacin (87.88%), and gentamicin (81.20%). These findings are consistent with those reported by [29] and [30], who also noted substantial



resistance to these antibiotics. The effectiveness of fosfomycin (90.90%) and nitrofurantoin (72.72%) against *E. coli* is encouraging and suggests these antibiotics as potential first-line treatments for UTIs caused by *E. coli*.

P. aeruginosa exhibited high resistance rates to ceftriaxone, amoxicillin-clavulanate, ampicillin, and nitrofurantoin (all 100%). This resistance pattern aligns with [31], who reported similar resistance trends. The moderate effectiveness of ceftazidime (50%) and fosfomycin (50%) indicates that these antibiotics could still be considered for treatment, though with caution. *Staphylococcus aureus* isolates showed significant resistance to ampicillin (95.5%), erythromycin (89.6%), and ofloxacin (85.4%). These findings are comparable to those of [30] and [32], who reported high resistance rates for these antibiotics. However, the effectiveness of fosfomycin (72.27%) and amoxicillin-clavulanate (63.6%) offers some therapeutic options for infections caused by *S. aureus*. *Klebsiella pneumoniae* isolates were highly resistant to gentamicin, ampicillin, fosfomycin, and nitrofurantoin (all 100%). This resistance pattern is consistent with findings by [33] and [34]. The moderate sensitivity to ceftazidime (100%) and ciprofloxacin, linezolid, cefuroxime, and amoxicillin-clavulanate (50% each) provides some options for targeted therapy.

The identification of bacterial isolates using 16s rRNA sequencing in this study provides significant insights into the limitations of conventional phenotypic and biochemical methods. The discrepancies observed between conventional and molecular identification underscore the critical need for advanced genetic techniques in clinical microbiology. Our findings align with the observations made by [35], who highlighted that phenotypic systems often fall short in accurately identifying bacteria at the species level due to the variability in biochemical characteristics among closely related species. In our study, isolates initially identified as *E. coli* and *K. pneumoniae* through conventional methods were later found to be *E. fergusonii* and *K. oxytoca*, respectively, following 16s rRNA sequencing. This misidentification illustrates the inherent limitations of phenotypic methods, which are also corroborated by the work of [36], where phenotypic misidentifications were corrected through molecular techniques.

The use of 16s rRNA sequencing provided accurate species-level identification and phylogenetic analysis, demonstrating its superiority over traditional methods. This is consistent with the findings of [37], who advocate for the use of genetic testing when conventional methods are inconclusive. The high confidence in

identification through molecular methods in our study, evidenced by the accurate placement of our isolates within established phylogenetic trees, supports the reliability of 16s rRNA sequencing in clinical diagnostics.

The submission of sequences to the NCBI database and the assignment of accession numbers enhance the reproducibility and accessibility of our findings. This practice, also highlighted in the studies by [38], facilitates future research and surveillance by providing a reference for comparison. Our sequences, now publicly available, contribute to the broader scientific effort to map bacterial genomes and understand their diversity.

Accurate identification of bacterial species is paramount for effective clinical management. Misidentification can lead to inappropriate treatment strategies, impacting patient outcomes. Our study underscores the necessity of incorporating molecular techniques in routine diagnostics, particularly when conventional methods yield ambiguous results. This perspective is shared by previous research, such as the work of [37].

Limitations of the Study

Lack of previous data available on the current work in the elected territory was challenging as the litterateur helps to identify the scope of work. Current study was the only study carried out in the area.

Conclusion

In this study, a total of 100 urine samples were analyzed, with a majority of 61% from females and 39% from males. Bacterial growth was observed in 79% of the samples. Molecular analysis identified two isolates as different species within the same genus, demonstrating the importance of molecular techniques in precise bacterial identification. Phylogenetic analysis further elucidated the evolutionary relationships among the isolates, underscoring the complexity and diversity of uropathogenic bacteria.

Recommendations

For accurate bacterial identification molecular based analysis is the standard Gold traditional method results in false species identification leading to false data collection Commonly used antibiotics have acquired resistance and better antibiotics be prescribed post urine culture and sensitivity.

Annexures

Standard ID



16S rRNA service report

Order Number : HC01039403
Sample name : 719_contig_1

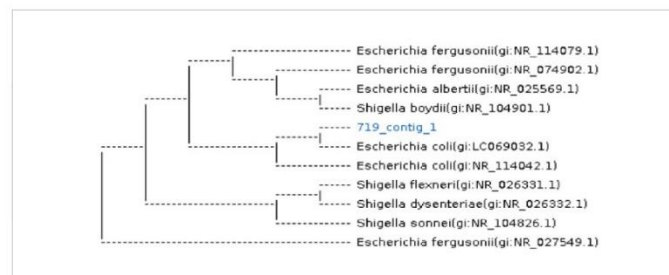
Information

Primer Information

Sequencing Primer Name	Primer Sequences	PCR Primer Name	Primer Sequences
785F 5'	(GGA TTA GAT ACC CTG GTA) 3'	27F 5'	(AGA GTT TGA TCM TGG CTC AG) 3'
907R 5'	(CCG TCA ATT CMT TTR AGT TT) 3'	1492R 5'	(TAC GGY TAC CTT GTT ACG ACT T) 3'

Subject						Score		Identities	
Accession	Description	Length	Start	End	Coverage	Bit	E-Value	Match/Total	Pct.(%)
CU928158.2	Escherichia fergusonii	458871	48184	48334	0	2730	0.0	1494/1501	99.53

Kingdom	Family	Genus	Species
Bacteria	Enterobacteriaceae	Escherichia	Escherichia fergusonii



Characterization

Escherichia is a genus of Gram-negative, nonspore-forming, facultatively anaerobic, rod-shaped bacteria from the family Enterobacteriaceae. In those species which are inhabitants of the gastrointestinal tracts of warm-blooded animals, Escherichia species provide a portion of the microbially derived stroma K for their host. A number of the species of Escherichia are pathogens. The genus is named after Theodor Escherich, the discoverer of Escherichia coli.

Some strains of E. fergusonii are pathogenic. It is known to infect open wounds, in humans and may also cause bacteremia or urinary tract infections. Strains causing these infections have been found to be highly resistant to the antibiotic ampicillin, though some are also resistant to gentamicin and chloramphenicol. An antibiotic-resistant strain of the species was found to be associated with an incidence of cystitis in a 52-year-old woman in 2008.



Standard ID

16S
rRNA Full
Sequencing



16S rRNA service report

Order Number : HC01039403

Sample name : 259_contig_1

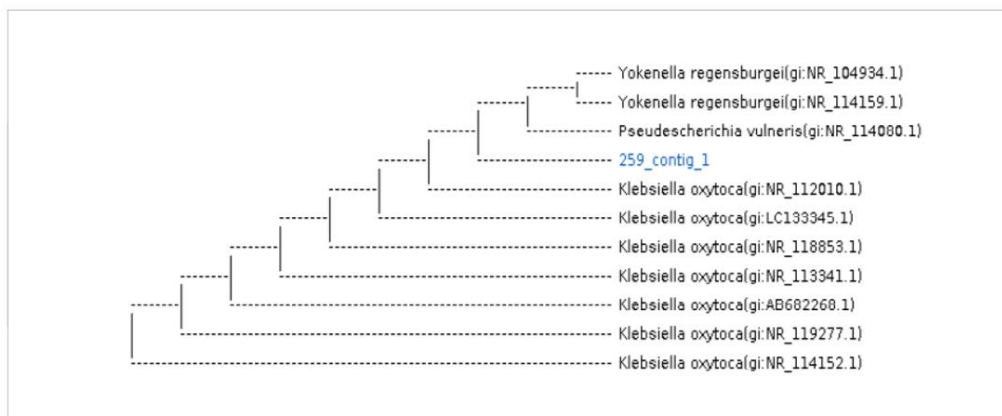
Information

Primer Information

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785F	5' (GGA TTA GAT ACC CTG GTA) 3'	27F	5' (AGA GTT TGA TCM TGG CTC AG) 3'
907R	5' (CCG TCA ATT CMT TTR AGT TT) 3'	1492R	5' (TAC GGY TAC CTT GTT ACG ACT T) 3'

Subject						Score		Identities	
Accession	Description	Length	Start	End	Coverage	Bit	E-Value	Match/Total	Pct.(%)
NR_118853.1	Klebsiella oxytoca	1502	18	1488	97	2654	0.0	1461/1472	99.25

Kingdom	Family	Genus	Species
Bacteria	Enterobacteriaceae	Klebsiella	Klebsiella oxytoca



Characterization

Klebsiella is a genus of nonmotile, Gram-negative, oxidase-negative, rod-shaped bacteria with a prominent polysaccharide-based capsule. Klebsiella species are routinely found in the human nose, mouth, and gastrointestinal tract as normal flora; however, they can also behave as opportunistic human pathogens. Klebsiella species are known to also infect a variety of other animals, both as normal flora and opportunistic pathogens.

Klebsiella oxytoca is a Gram-negative, rod-shaped bacterium that is closely related to *K. pneumoniae*, from which it is distinguished by being indole-positive; it also has slightly different growth characteristics in that it is able to grow on melzitose, but not 3-hydroxybutyrate. Species from the genus *Klebsiella* are frequently accountable for nosocomial infections in humans. They have the ability to colonize many different areas of the human body such as the skin, GI tract, sterile wounds, urine, and skin. While *Klebsiella oxytoca* does not cause as many of these infections as the more commonly known *Klebsiella pneumoniae*, the genus *Klebsiella* was deemed responsible for 8% of all nosocomial bacterial infections in the United States and Europe. Due to this incidence rate, *Klebsiella* spp. are considered one of the most significant infectious pathogens in the United States.

Standard ID



16S rRNA service report

Order Number : HC01012671
Sample name : 389_contig_1

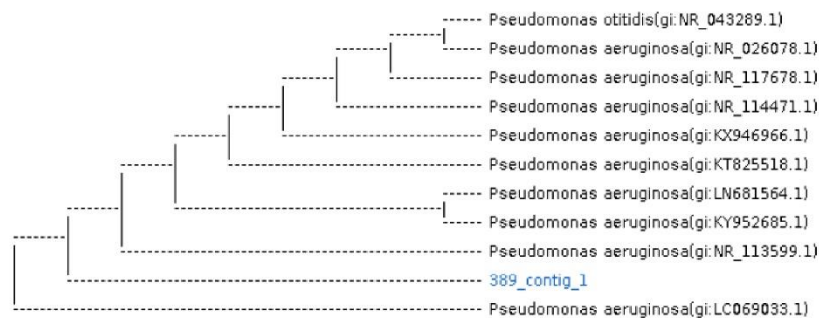
Information

Primer Information

Sequencing Primer Name	Primer Sequences	PCR Primer Name	Primer Sequences
785F	5' (GGA TTA GAT ACC CTG GTA) 3'	27F	5' (AGA GTT TGA TCM TGG CTC AG) 3'
907R	5' (CCG TCA ATT CMT TTR AGT TT) 3'	1492R	5' (TAC GGY TAC CTT GTT ACG ACT T) 3'

Subject						Score		Identities	
Accession	Description	Length	Start	End	Coverage	Bit	E-Value	Match/Total	Pct.(%)
CP012001.1	Pseudomonas aeruginosa	6317050	696957	698432	0	2713	0.0	1474/1476	99.86

Kingdom	Family	Genus	Species
Bacteria	Pseudomonadaceae	Pseudomonas	Pseudomonas aeruginosa



Characterization

Pseudomonas is a genus of Gram-negative, aerobic gammaproteobacteria, belonging to the family Pseudomonadaceae containing 191 validly described species. The members of the genus demonstrate a great deal of metabolic diversity, and consequently are able to colonize a wide range of niches.

P. aeruginosa rarely causes disease in healthy humans. It is usually linked with patients whose immune system is compromised by diseases or trauma. It gains access to these patients' tissues through the burns, for the burn victims, or through an underlying disease, like cystic fibrosis.

Standard ID



16S rRNA service report

Order Number : HC01012671
Sample name : 359_contig_1

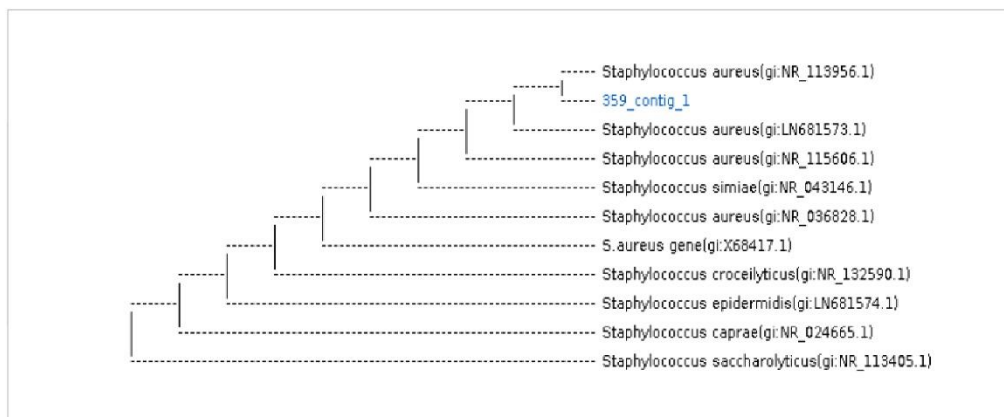
Information

Primer Information

Sequencing Primer Name	Primer Sequences	PCR Primer Name	Primer Sequences
785F	5' (GGA TTA GAT ACC CTG GTA) 3'	27F	5' (AGA GTT TGA TCM TGG CTC AG) 3'
907R	5' (CCG TCA ATT CMT TTR AGT TT) 3'	1492R	5' (TAC GGY TAC CTT GTT ACG ACT T) 3'

Subject						Score		Identities	
Accession	Description	Length	Start	End	Coverage	Bit	E-Value	Match/Total	Pct.(%)
CP011526.1	Staphylococcus aureus	2755072	503061	504551	0	2728	0.0	1487/1491	99.73

Kingdom	Family	Genus	Species
Bacteria	Staphylococcaceae	Staphylococcus	Staphylococcus aureus



Characterization

Staphylococcus is a genus of Gram-positive bacteria. Under the microscope, they appear round (cocci), and form in grape-like clusters. The Staphylococcus genus includes at least 40 species. Most are harmless and reside normally on the skin and mucous membranes of humans and other organisms.

Staphylococcus aureus is the most common cause of staph infections and is responsible for various diseases including: mild skin infections (impetigo, folliculitis, etc.), invasive diseases (wound infections, osteomyelitis, bacteremia with metastatic complications, etc.), and toxin-mediated diseases (food poisoning, toxic shock syndrome or TSS, scaled-skin syndrome, etc.). Infections are preceded by colonization. Common superficial infections include carbuncles, impetigo, cellulitis, folliculitis. Community-acquired infections include bacteremia, endocarditis, osteomyelitis, pneumonia and wound infections are less common. S. aureus also causes economically important mastitis in cows, sheep and goats.



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