Infect Epidemiol Med. 2016 Summer; Volume 2, Issue 3: 8-13 DOI:10.7508/iem.2016.03.003
Published online 2016 Summer **Original Article**

Prevalence and Antimicrobial Susceptibility Patterns of Bacteria Isolated from Different Clinical Infections in Hamadan, Iran

Farzad Khademi[1*], Arshid Yousefi-Avarvand[1], Pezhman Karami[1], Kiarash Ghazvini[1], Fahimeh Ghanbari[2]

[1]Antimicrobial Resistance Research Center, Department of Medical Bacteriology and Virology, Qaem University Hospital, School of Medicine, Mashhad University of Medical Sciences, Mashhad, IR Iran
[2] Department of Microbiology, Faculty of Bioscience, Islamic Azad University, Falavarjan Branch, Isfahan, IR Iran

*Corresponding author:*Farzad Khademi, Antimicrobial Resistance Research Center, Department of Medical Bacteriology and Virology, Qaem University Hospital, School of Medicine, Mashhad University of Medical Sciences, Mashhad, IR Iran. Tel: +98 9149679332, E-mail:k_farzad@yahoo.com

Submitted: June25, 2015; **Revised:** August 09, 2015; **Accepted:** August30, 2015

Background: The main objective of this study was to determine the prevalence and antimicrobial resistance profiles of the main bacteria which are responsible for urinary tract, blood stream, cerebrospinal fluid, lower respiratory tract, and wound infections in Hamadan province in the west of Iran.
Materials and Methods: In this study, a total of 773 urinary tract, 273 blood stream, 13 cerebrospinal fluid, 408 respiratory tract, and 147 wound positive samples were collected from patients who referred to Besat hospital from April 2013 to October 2014. Antibiotic susceptibility testing was performed by Modified Disk Diffusion Method (MDDM) against different classes of antibiotic.
Results: The most common pathogens isolated from urine tract, blood stream, cerebrospinal fluid, lower respiratory tract, and wound infections were *E. coli* 425 (54.9%), *S. aureus* 68 (24.9%), *Klebsiella* spp. 3 (23%), *P. aeruginosa* 110 (26.9%), and *S. aureus* 30 (20.4%) respectively. The overall prevalence of resistance to the antimicrobial agents tested in various clinical specimens is discussed in this study.
Conclusion: The high resistance rate was observed in our study to most used antibiotics. Therefore, setting up a comprehensive surveillance system is need to evaluate the distribution of organisms isolated and their drug resistance pattern over different period of time and place of Iran.

Keywords: Antimicrobial susceptibility, Clinical infections, Hamedan, Iran

1. Background

Bacterial infections are important causes of people mortality in the worldwide and disease-causing microbes that have become resistant to antibiotic therapy are a growing public health problem (1-3). Bacterial blood stream infections (BSIs) are one of the most common nosocomial infections and annually about 200,000 cases of bacteremia occurs with morbidity and mortality rate in the range of 20-50% in the worldwide (4). The timely and suitable use of antibiotics is the only way for treatment of bacteremia, however many of the bacterial pathogens are becoming resistant to the antimicrobial agents (4).

Urinary tract infections (UTIs) after respiratory tract infections are the most common infectious diseases and nearly 10% of the global population experience a UTI in their lifetime (5). Approximately 150 million UTIs occurs per year throughout the world (6). Some studies have shown that the urinary pathogens such as *E. coli*, *Klebsiella*, *Proteus*, and *Enterococcus* species are the main causes of UTI in the community (7). In most cases, empirical antimicrobial therapy is prescribed and for this purpose, it's extremely important to know the main bacteria which are involved in the UTIs and their antimicrobial resistance patterns (8, 9).

Bacterial meningitis is an acute infection (inflammation of the meninges, arachnoid, and subarachnoid space) in response to bacteria and bacterial products (10). This disease is a medical emergency that characterized with severe headache, fever, intolerance to light and sound, and stiffness of muscles especially neck muscles (10, 11). In patients suspected to bacterial meningitis, empirical antimicrobial therapy is started within 60 minutes and without delay (12). *S. pneumoniae*, *N. meningitidis*, *Streptococci group B*, *L. monocytogenes*, *H. influenza* (in community-acquired bacterial meningitis), *meningococcal*, *H influenzae type b* (Hib), and *pneumococcal* infections (in children) are the most common organisms responsible for bacterial meningitis (13). The rate of death in untreated bacterial meningitis is nearly 100% (10).

Lower respiratory tract infections (LRTIs) including pneumonia, acute bronchitis, and chronic obstructive pulmonary diseases (COPD) remains as the commonest illnesses in the elderly people in the worldwide (14, 15). As shown in many studies, *S. pneumoniae* is the most common bacterial etiologic agent of LRTIs followed by *H. influenza*, *Legionella* spp., and *C.pneumonia* respectively (16). Main risk factor for these diseases is age, and annually about 5 million people die from acute infections of the respiratory tract (16). So, in order to provide an appropriate guide in antimicrobial treatment of these deseases for physicians, identification of pathogens as well as their drug sensitivity patterns is very important (17).

When the microbial load exceeds from capacity of the clearance of immune system, bacterial wound infections occurs. The most prevalent bacteria isolated from wound infections are *S. aureus* and *P. aeruginosa*, which are resistant to many antibiotics. Therefore, the management of these diseases is need (18).

For decades, antimicrobial agents established as a useful way for effective treatment of bacterial infections, but the emergence of acquired resistance to antimicrobial drugs has become an important public health problem associated with serious consequences for the treatment of the bacterial infections (2).

2. Objectives

The main objective of this study was to determine the prevalence and antimicrobial resistance profiles of the main etiological agents which are responsible for urinary tract, blood stream, cerebrospinal fluid, lower respiratory tract, and wound infections in Hamadan province in the west of Iran.

3. Materials and Methods

3.1. Study design and sample collection

This study was conducted in the Hamadan's Besat hospital (Iran) between April 2013 and October 2014. In this period,

bacterial isolates of 2320 inpatients and outpatients suspected to clinical infections were collected from different clinical sources including, urine, blood, cerebrospinal fluid, tracheal aspirate, and wound specimens. The patient infection classified as community or hospital-acquired infections based on the clinical examination by physicians and recorded data of patients. Patients with bacterial colonization after more than 48 hours of hospitalization were defined as hospital-acquired infections.

3.2. Isolation and identification of bacteria

Pathogens identification was performed by culture, morphological, and biochemical properties. For urine culture, the midstream specimens of all urine samples were collected and then inoculated within one hour after sampling on different culture media such as blood agar and Mac Conkey agar. Plates were incubated at 37°C for 24-48 hours depending on the microorganism type.

Blood samples (3-5 mL) were cultured into 5 mL brain heart infusion broth and incubated at 37°C for 24 hours. Then in order to isolate pure bacteria, they were sub-cultured on blood agar, chocolate agar, and Mac Conkey agar plates and incubated for 24 hours at 37°C.

For cerebrospinal fluid (CSF), samples cultured on blood agar supplemented with 5% horse blood or chocolate agar. Then plates were incubated at 37°C for 24-48 hours.

Tracheal aspirates and wound specimens were obtained with aseptic methods. These specimens cultured on blood agar, chocolate agar, and Mac Conkey agar and then incubated at 37°C for 24 hours in order to isolate lower respiratory tract colonizers and contaminant organisms of wound.

Biochemical tests were done depending on the type of isolated bacteria (Gram-positive or Gram-negative) from various samples. In order to identify Gram positive bacteria; Catalase, Coagulase, Novobiocin, Optochin disk, CAMP test (for *S. agalactiae*), and Esculin agar (for *enterococci*), and for Gram negative bacteria; Triple Sugar Iron (TSI), Indole, Citrate, Urea, Lysine Decarboxylase (LDC), Oxidase (for *Pseudomonaceae*), and motility were performed.

3.3. Antibiotic susceptibility test

The antimicrobial susceptibility test of isolates was performed on Muller Hinton agar by modified disk diffusion method (MDDM) according to the Clinical and Laboratory Standards Institute (CLSI) guideline (19). For this purpose, suspensions of pure bacteria equivalent to standard 0.5 McFarland (1.5×10^8 CFU.mL^{-1}) were prepared in sterile saline, and susceptibility test of bacterial isolates to different groups of antibiotics including Aminoglycosides (amikacin and gentamicin), Carbapenems (imipenem), Cephalosporins 1st (cefazolin), Cephalosporins 2st (cefotaxime), Cephalosporins 3st (ceftazidime, ceftizoxime, cefexime, ceftriaxone), Nitrofurans (nitrofurantoin), Penicillins (piperacillin), Quinolones (ciprofloxacin and nalidixic acid), Sulfonamides (trimethoprim-sulfamethoxazole), Glycopeptides (vancomycin), Macrolides (azithromycin) were performed. After plate incubation at 37°C for 24 hours, diameter of the zone of growth inhibition was evaluated based on CLSI guideline. We used *E. coli* (ATCC 25922) as control strain for antibiotic susceptibility testing.

3.4. Statistical analysis

The frequency of drug resistance was expressed as percentage. All statistical analyses were done by SPSS v.15 software. The proportions were considered statistically significant if *P*-value was less than 0.05.

4. Results

In this study, 1614 bacterial isolates from different clinical specimens (773, 273, 13, 408, and 147 isolates from urine, blood, cerebrospinal fluid, tracheal aspirate, and wound samples respectively) from inpatients and outpatients were collected. From 1614 bacterial isolates, 885 (54.8%) were obtained from female patients and 729 (45.2%) from male patients, with an age range of 15 to 73 years ($P > 0.05$). Also 22.1% (357 isolates) of all bacterial isolates were Gram-positive and 77.9% (1257 isolates) were Gram-negative. The most prevalent organisms in different samples are shown in Fig. 1 and 2. *E. coli* 425 (62.5%), *Klebsiella* spp. 32 (22.6%), *P. aeruginosa* 32 (22.6%), *Klebsiella* spp. 3 (37.5%), *P. aeruginosa* 110 (31.4%), and *P. aeruginosa* 22 (27.8%), were the main Gram negative bacteria isolated from UTI, BSI, CSF, tracheal aspirate, and wound specimens respectively (Fig. 1). Also, CoNS 40 (42.5%), *S. aureus* 68 (51.5%), *S. aureus* 2 (40%), *S. aureus* 23 (39.6%), *S. aureus* 30 (44.1%), were the main Gram positive bacteria isolated from UTI, BSI, CSF, tracheal aspirate, and wound specimens respectively (Fig. 2).

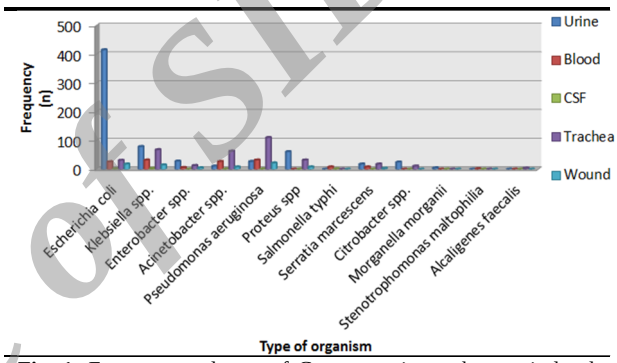

Fig. 1. Frequency and type of Gram negative pathogens isolated from different clinical samples.

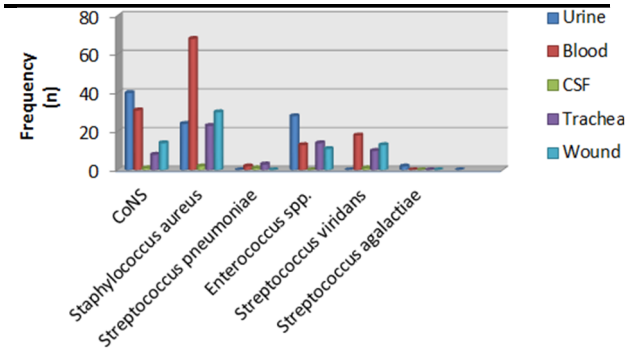

Fig. 2. Frequency and type of Gram positive pathogens isolated from different clinical samples. CoNS*: Coagulase-Negative *Staphylococci.*

In our study, antibiotic susceptibility test was performed by modified disk diffusion method. Tables 1-5 showed the overall prevalence of resistance to the antimicrobial agents tested in Gram positive and Gram negative bacteria which isolated from various clinical specimens.

Finally, the main bacteria isolated from hospital-acquired infections (HAI) and community-acquired infections (CAI) were *Acinetobacter* spp. and *E. coli* respectively.

5. Discussion

The global spread of resistance to antibiotics among bacterial infections is a growing problem and results in a lot of attention following reports of international expansion of multi-resistant *S.*

pneumoniae, meticillin-resistant *S. aureus*.and *Enterobacteriaceae* resistant to cephalosporins (20). This phenomenon is one of the main challenges facing mankind public health in the worldwide and require global cooperation (21).

In agreement with similar studies, our data showed that the prevalence of Gram negative bacteria, 1257 (77.9%), in different clinical infections was higher than Gram positive 357 (22.1%) pathogens (22). Among bacterial infections investigated, urinary tract infection was more frequent (47.8%). Our study on UTI samples revealed that *E. coli* 425 (54.9%) and *Klebsiella* spp.79 (10.2%) were the most common organisms isolated and followed by *Proteus* spp. 61 (7.8%), CoNS 40 (5.1%), *Enterobacter* spp. 28 (3.6%), and *Enterococcus* spp. 28 (3.6%). Similar results have been reported by Farajnia *et al.* (5). In the present study, the most of the urine specimens were obtained from outpatients (community-acquired infections). To assess drug resistance in all samples no differentiate were performed between bacteria isolated from community and hospital-acquired infections. The highest resistance rate of the *E. coli* isolates were against trimethoprim-sulfamethoxazole 278 (65.4%) and nalidixic acid 235 (55.2%). The lowest resistance rates were against nitrofurantoin 24 (5.6%) and amikacin 42 (9.9%) (Table 1). These results are comparable with susceptibility profiles observed from other studies (5). The highest and lowest resistance levels to nitrofurantoin were observed in *Acinetobacer* spp. (100%) and *S. agalactiae.* From 773 bacteria isolated of UTI, 485 (62.7%) were obtained from female patients and 288 (37.3%) from male patients. This result is comparable with Farajnia*et al*. report (5). This suggests that UTI is an important problem in women.

Table 1. Antibiotic susceptibility profile of organisms isolated from UTIs.

Organism	Resistance Rate (%)												
	AN	**GEN**	**TMP-SXT**	**CIP**	**CAZ**	**CT**	**CFM**	**NA**	**NIT**	**V**	**CRO**	**CTX**	**CZ**
E. coli (N=425)	42 (9.9)	83 (19.5)	278 (65.4)	71 (16.7)	83 (19.5)	93 (21.9)	151 (35.5)	235 (55.2)	24 (5.6)	NA	127 (29.9)	121 (28.4)	NA
***Klebsiella*spp.** (N=79)	21 (26.6)	29 (36.7)	48 (60.7)	30 (38)	33 (41.8)	34 (43)	43 (54.4)	39 (49.3)	33 (41.8)	NA	42 (53.1)	31 (39.2)	NA
P. aeroginosa (N=27)	10 (37)	15 (55.5)	22 (81.5)	13 (48.1)	15 (55.5)	15 (55.5)	27 (100)	18 (66.6)	21 (77.8)	NA	23 (85.1)	19 (70.3)	NA
***Enterobacter* spp.** (N=28)	4 (14.2)	6 (21.4)	16 (57.1)	7 (25)	3 (10.7)	3 (10.7)	8 (28.6)	13 (46.4)	2 (7.1)	NA	4 (14.2)	4 (14.2)	NA
***Proteus* spp.** (N=61)	9 (14.7)	15 (24.6)	35 (57.3)	9 (14.7)	13 (21.3)	13 (21.3)	23 (37.7)	19 (31.1)	20 (32.8)	NA	18 (29.5)	18 (29.5)	NA
M. morganii (N=5)	1 (20)	2 (40)	3 (60)	2 (40)	1 (20)	1 (20)	2 (40)	3 (60)	1 (20)	NA	1 (20)	2 (40)	NA
***Acinetobacer*spp.** (N=11)	10 (90.9)	11 (100)	11 (100)	11 (100)	10 (90.9)	11 (100)	11 (100)	11 (100)	11 (100)	NA	11 (100)	11 (100)	NA
***Citrobacter*spp.** (N=25)	1 (4)	3 (12)	16 (64)	10 (40)	4 (16)	6 (24)	8 (32)	15 (60)	4 (16)	NA	11 (44)	6 (24)	NA
S. marcescens (N=18)	8 (44.4)	12 (66.6)	16 (88.9)	8 (44.4)	8 (44.4)	10 (55.5)	15 (83.3)	15 (83.3)	14 (77.8)	NA	10 (55.5)	12 (66.6)	NA
CoNS* (N=40)	1 (2.5)	NA	10 (25)	8 (20)	NA	5 (12.5)	16 (40)	NA	2 (5)	0 (0)	6 (15)	7 (17.5)	8 (20)
S. aureus (N=24)	4 (16.6)	NA	8 (33.3)	5 (20.8)	NA	6 (25)	15 (62.5)	NA	4 (16.6)	0 (0)	4 (16.6)	7 (29.1)	5 (20.8)
***Enterococcus* spp.** (N=28)	11 (39.3)	NA	22 (78.6)	13 (46.4)	NA	10 (35.7)	20 (71.4)	NA	4 (14.3)	1 (3.5)	11 (39.3)	13 (46.4)	12 (42.8)
***S. agalactiae* (N=2)**	0 (0)	NA	0 (0)	1 (50)	NA	0 (0)	1 (50)	NA	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)

Table 1: Antibiotic susceptibility profile of organisms isolated from UTIs.
AN, amikacin; GEN, gentamicin; TMP-SXT, trimethoprim-sulfamethoxazole; CIP, ciprofloxacin; CAZ, ceftazidime; CT, ceftizoxime; CFM, cefixime; NA, nalidixic acid; NIT, nitrofurantoin; V, vancomycin; CRO-ceftriaxone; CTX, cefotaxime; CZ, cefazolin. *CoNS, Coagulase-Negative *Staphylococci*; NA, not applicable.

Isolation rate of bacteria in the blood specimens of suspected patients to BSI was 16.9% (P> 0.05). From 273 bacteria isolated of BSI, 108 (39.5%) were obtained from female patients and 165 (60.5%) from male patients. Similar to urinary tract infections, in blood stream infections the prevalence of Gram negative was higher than Gram positive bacteria (51.6% *vs.* 48.4%). As shown in Fig. 1 and 2, *S. aureus* 68 (24.9%), *Klebsiella* spp. 32 (11.7%), *P. aeroginosa* 32 (11.7%), CoNS 31 (11.3%), *Acinetobacter* spp. 27 (9.8%), *E. coli* 26 (9.5%), *S. viridans* 18 (6.5%), *Enterococcus* spp. 13 (4.7%), *S. typhi* 8 (2.9%), *S. marcescens* 8 (2.9%), *Enterobacter* spp. 6 (2.1%), *S. pneumonia* 2 (0.7%) and *S. maltophilia* 2 (0.7%) were the most prevalent organisms causing BSI. Similar results have been reported in studies of Iranian, American, and European researchers (23). Among Gram negative and positive bacteria isolated from blood infections the highest resistance rate found in *S. maltophilia, Acinetobacer* spp., and *P. aeroginosa*, which were resistant to most commonly tested antibiotics (Table 2).

Table 2. Antibiotic susceptibility profile of organisms isolated from BSIs.

Organism	Resistance Rate (%)													
	AN	**GEN**	**TMP-SXT**	**CIP**	**CAZ**	**CT**	**CFM**	**PIP**	**IPM**	**AZM**	**V**	**CRO**	**CTX**	**CZ**
E. coli (N=26)	12 (46.1)	13 (50)	18 (69.2)	13 (50)	16 (61.5)	19 (73.1)	19 (73.1)	8 (30.7)	3 (11.5)	9 (34.6)	NA	17 (65.4)	13 (50)	NA
***Klebsiella*spp.** (N=32)	13 (40.6)	20 (62.5)	25 (78.1)	17 (53.1)	22 (68.7)	23 (71.8)	27 (84.3)	12 (37.5)	9 (28.1)	14 (43.7)	NA	21 (65.6)	21 (65.6)	NA
P. aeroginosa (N=32)	21 (65.6)	24 (75)	23 (71.8)	19 (59.3)	25 (78.1)	27 (84.3)	29 (90.6)	20 (62.5)	4 (12.5)	22 (68.7)	NA	28 (87.5)	27 (84.3)	NA
***Enterobacter* spp.** (N=6)	1 (16.6)	2 (33.3)	4 (66.6)	1 (16.6)	0 (0)	2 (33.3)	3 (50)	2 (33.3)	0 (0)	1 (16.6)	NA	3 (50)	3 (50)	NA
S. typhi (N=8)	0 (0)	1 (12.5)	4 (50)	2 (25)	1 (12.5)	1 (12.5)	3 (37.5)	0 (0)	0 (0)	0 (0)	NA	2 (25)	2 (25)	NA
S. maltophilia (N=2)	2 (100)	1 (50)	2 (100)	1 (50)	1 (50)	1 (50)	2 (100)	2 (100)	0 (0)	1 (50)	NA	2 (100)	1 (50)	NA
***Acinetobacter*spp.** (N=27)	22 (81.5)	26 (96.3)	26 (96.3)	25 (92.6)	27 (100)	27 (100)	27 (100)	25 (92.6)	19 (70.4)	26 (96.3)	NA	27 (100)	27 (100)	NA
S. marcescens (N=8)	1 (12.5)	4 (50)	5 (62.5)	3 (37.5)	2 (25)	3 (37.5)	5 (62.5)	1 (12.5)	0 (0)	1 (12.5)	NA	3 (37.5)	3 (37.5)	NA
CoNS* (N=31)	6 (19.3)	17 (54.8)	16 (51.6)	10 (32.2)	18 (58)	15 (48.4)	20 (64.5)	NA	NA	NA	0 (0)	9 (29)	12 (38.7)	17 (54.8)
S. aureus (N=68)	20 (29.4)	34 (50)	30 (44.1)	25 (36.7)	41 (60.3)	40 (58.8)	48 (70.1)	NA	NA	NA	2 (2.9)	38 (55.9)	28 (41.2)	35 (51.5)
***Enterococcus* spp.** (N=13)	3 (23.1)	11 (84.6)	12 (92.3)	5 (38.4)	8 (61.5)	7 (53.8)	10 (76.9)	NA	NA	NA	1 (7.7)	8 (61.5)	7 (53.8)	10 (76.9)
S. viridans (N=18)	6 (33.3)	7 (38.9)	9 (50)	7 (38.9)	8 (44.4)	9 (50)	16 (88.9)	NA	NA	NA	0 (0)	5 (27.8)	5 (27.8)	7 (38.9)
S. pneumonia (N=2)	0 (0)	0 (0)	1 (50)	1 (50)	1 (50)	0 (0)	2 (100)	NA	NA	NA	0 (0)	0 (0)	0 (0)	1 (50)

Table 2: Antibiotic susceptibility profile of organisms isolated from BSIs.
AN, amikacin; GEN, gentamicin; TMP-SXT, trimethoprim-sulfamethoxazole; CIP, ciprofloxacin; CAZ, ceftazidime; CT, ceftizoxime; CFM, cefixime; PIP,piperacillin; IPM,imipenem; AZM, azithromycin; V, vancomycin; CRO-ceftriaxone; CTX, cefotaxime; CZ, cefazolin. *CoNS, Coagulase-Negative *Staphylococci*; NA, not applicable.

We investigated 13 outpatients, from cerebrospinal fluid isolates of which 5 (38.4%) were Gram positive (*S. aureus* 40%, CoNS 20%, *S. viridans* 20%, and *S. pneumonia* 20%) and 8 (61.6%) were Gram negative (*Klebsiella* spp. 37.5%, *E. coli* 25%, *P. aeroginosa* 12.5%, *Acinetobacter* spp. 12.5%, and *S. typhi* 12.5%). The resistance rate to trimethoprim-sulfamethoxazole and cefixime antibiotics in all bacterial pathogens isolated from CSF specimens was 100%, and also no resistance to vancomycin, ceftriaxone, and cefotaxime in Gram positive bacteria was observed (0%), which may act as good choices for the antimicrobial treatment (Table 3).

Table 3. Antibiotic susceptibility profile of organisms isolated from CSF infections.

Organism	Resistance Rate (%)													
	AN	**GEN**	**TMP-SXT**	**CIP**	**CAZ**	**CT**	**CFM**	**PIP**	**IPM**	**AZM**	**V**	**CRO**	**CTX**	**CZ**
E. coli (N=2)	0 (0)	1 (50)	2 (100)	1 (50)	0 (0)	1 (50)	2 (100)	0 (0)	0 (0)	0 (0)	NA	1 (50)	1 (50)	NA
***Klebsiella*spp.** (N=3)	0 (0)	2 (66.6)	3 (100)	2 (66.6)	2 (66.6)	1 (33.3)	3 (100)	1 (33.3)	1 (33.3)	1 (33.3)	NA	2 (66.6)	2 (66.6)	NA
P. aeroginosa (N=1)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	0 (0)	0 (0)	1 (100)	NA	1 (100)	1 (100)	NA
***Acinetobacter*spp.** (N=1)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	1 (100)	NA	1 (100)	1 (100)	NA
S. typhi (N=1)	0 (0)	0 (0)	1 (100)	1 (100)	0 (0)	0 (0)	1 (100)	0 (0)	0 (0)	0 (0)	NA	0 (0)	NA	0 (0)
CoNS* (N=1)	0 (0)	0 (0)	1 (100)	0 (0)	0 (0)	0 (0)	1 (100)	NA	NA	NA	0 (0)	0 (0)	0 (0)	0 (0)
S. aureus (N=2)	0 (0)	1 (50)	2 (100)	0 (0)	1 (50)	0 (0)	2 (100)	NA	NA	NA	0 (0)	0 (0)	0 (0)	1 (50)
S. viridans (N=1)	0 (0)	0 (0)	1 (100)	0 (0)	1 (100)	0 (0)	1 (100)	NA	NA	NA	0 (0)	0 (0)	0 (0)	0 (0)
S. pneumonia (N=1)	0 (0)	0 (0)	1 (100)	0 (0)	0 (0)	0 (0)	1 (100)	NA	NA	NA	0 (0)	0 (0)	0 (0)	0 (0)

Table 3: Antibiotic susceptibility profile of organisms isolated from CSF infections.
AN, amikacin; GEN, gentamicin; TMP-SXT, trimethoprim-sulfamethoxazole; CIP, ciprofloxacin; CAZ, ceftazidime; CT, ceftizoxime; CFM, cefixime; PIP,piperacillin; IPM,imipenem; AZM, azithromycin; V, vancomycin; CRO-ceftriaxone; CTX, cefotaxime; CZ, cefazolin. *CoNS, Coagulase-Negative *Staphylococci*; NA, not applicable.

Table 4. Antibiotic susceptibility profile of organisms isolated from lower respiratory infections.

Organism	Resistance Rate (%)													
	AN	GEN	TMP-SXT	CIP	CAZ	CT	CFM	PIP	IPM	AZM	V	CRO	CTX	CZ
E. coli (N=31)	11 (35.5)	18 (58)	27 (87.1)	20 (64.5)	22 (70.9)	23 (74.2)	25 (80.6)	9 (29)	10 (32.2)	18 (58)	NA	22 (70.9)	24 (77.4)	NA
***Klebsiella*spp.** (N=68)	50 (73.5)	44 (64.7)	63 (93)	46 (67.6)	54 (79.4)	41 (60.3)	57 (83.8)	26 (38.2)	26 (38.2)	31 (45.6)	NA	57 (83.8)	53 (77.9)	NA
P. aeroginosa (N=110)	42 (38)	66 (60)	83 (75.4)	62 (56.3)	69 (62.7)	80 (72.7)	89 (80.9)	43 (39)	45 (40.9)	41 (37.3)	NA	91 (82.7)	79 (71.8)	NA
***Enterobacter* spp.** (N=13)	4 (30.7)	7 (53.8)	10 (76.9)	8 (61.5)	7 (53.8)	8 (61.5)	10 (76.9)	4 (30.7)	2 (15.4)	6 (46.1)	NA	9 (69.2)	8 (61.5)	NA
Proteus spp. (N=32)	18 (56.2)	21 (65.6)	20 (62.5)	19 (59.3)	21 (65.6)	21 (65.6)	23 (71.8)	11 (34.3)	11 (34.3)	15 (46.8)	NA	21 (65.6)	23 (71.8)	NA
***Acinetobacter*spp.** (N=63)	53 (84.1)	61 (96.8)	(100)	6363 (100)	(100)	۶۳63 (100)	63 (100)	56 (88.9)	57 (90.5)	(66.6)	42NA	63 (100)	63 (100)	NA
***Citrobacter*spp.** (N=11)	5 (45.4)	7 (63.6)	9 (81.8)	7 (63.6)	7 (63.6)	8 (72.8)	8 (72.8)	4 (36.3)	3 (27.3)	3 (27.3)	NA	8 (72.8)	8 (72.8)	NA
S. marcescens (N=18)	4 (22.2)	7 (38.9)	14 (77.8)	6 (33.3)	8 (44.4)	6 (33.3)	12 (66.6)	4 (22.2)	3 (16.6)	7 (38.9)	NA	11 (61.1)	9 (50)	NA
Alcaligenesfaecalis (N=4)	1 (25)	2 (50)	4 (100)	3 (75)	2 (50)	2 (50)	3 (75)	1 (25)	1 (25)	1 (25)	NA	3 (75)	2 (50)	NA
CoNS* (N=8)	1 (12.5)	2 (25)	2 (25)	2 (25)	3 (37.5)	1 (12.5)	5 (62.5)	NA	NA	NA	۰1 (0)	1 (12.5)	1 (12.5)	3 (37.5)
S. aureus (N=23)	10 (43.5)	8 (34.8)	7 (30.4)	6 (26.1)	13 (56.5)	7 (30.4)	15 (65.2)	NA	NA	NA	1 (4.3)	8 (34.8)	5 (21.7)	9 (39.1)
***Enterococcus* spp.** (N=14)	7 (50)	9 (64.3)	11 (78.6)	5 (35.7)	6 (42.8)	2 (14.3)	11 (78.6)	NA	NA	NA	1 (7.1)	3 (21.4)	4 (28.6)	8 (57.1)
S. viridans (N=10)	4 (40)	4 (40)	6 (60)	4 (40)	4 (40)	2 (20)	5 (50)	NA	NA	NA	0 (0)	4 (40)	3 (30)	5 (50)
S. pneumonia (N=3)	0 (0)	0 (0)	1 (33.3)	0 (0)	1 (33.3)	0 (0)	1 (33.3)	NA	NA	NA	0 (0)	0 (0)	0 (0)	1 (33.3)

Table 4: Antibiotic susceptibility profile of organisms isolated from lower respiratory infection
AN, amikacin; GEN, gentamicin; TMP-SXT, trimethoprim-sulfamethoxazole; CIP, ciprofloxacin; CAZ, ceftazidime; CT, ceftizoxime; CFM, cefixime; PIP,piperacillin; IPM,imipenem; AZM, azithromycin; V, vancomycin; CRO-ceftriaxone; CTX, cefotaxime; CZ, cefazolin. *CoNS, Coagulase-Negative *Staphylococci*; NA, not applicable.

Table 5. Antibiotic susceptibility profile of organisms isolated from wound infections.

Organism	Resistance Rate (%)													
	AN	GEN	TMP-SXT	CIP	CAZ	CT	CFM	PIP	IPM	AZM	V	CRO	CTX	CZ
E. coli (N=18)	8 (44.4)	9 (50)	12 (66.6)	7 (38.9)	9 (50)	9 (50)	11 (61.1)	5 (27.8)	2 (11.1)	7 (38.9)	NA	5 (27.8)	6 (33.3)	NA
***Klebsiella*spp.** (N=15)	7 (63.6)	11 (73.3)	14 (93.3)	8 (53.3)	11 (73.3)	10 (66.6)	13 (86.6)	4 (26.6)	4 (26.6)	3 (20)	NA	10 (66.6)	10 (66.6)	NA
P. aeroginosa (N=22)	12 (54.5)	15 (68.2)	20 (90.9)	14 (63.6)	14 (63.6)	15 (68.2)	19 (86.3)	10 (45.4)	9 (40.9)	13 (59.1)	NA	16 (72.7)	17 (77.3)	NA
***Enterobacter* spp.** (N=5)	0 (0)	1 (20)	3 (60)	1 (20)	0 (0)	2 (40)	3 (60)	1 (20)	0 (0)	1 (20)	NA	2 (40)	1 (20)	NA
***Proteus* spp.** (N=8)	1 (12.5)	2 (25)	6 (75)	2 (25)	4 (50)	4 (50)	6 (75)	3 (37.5)	0 (0)	4 (50)	NA	2 (25)	3 (37.5)	NA
***Acinetobacter*spp.** (N=8)	7 (87.5)	8 (100)	8 (100)	8 (100)	8 (100)	8 (100)	8 (100)	6 (75)	7 (87.5)	7 (87.5)	NA	8 (100)	8 (100)	NA
S. marcescens (N=3)	0 (0)	1 (33.3)	3 (100)	1 (33.3)	1 (33.3)	1 (33.3)	2 (66.6)	1 (33.3)	0 (0)	1 (33.3)	NA	1 (33.3)	0 (0)	NA
CoNS* (N=14)	1 (7.1)	1 (7.1)	7 (50)	2 (14.3)	4 (28.6)	1 (7.1)	8 (57.1)	NA	NA	NA	۰ (0)	1 (7.1)	۰ (0)	2 (14.3)
S. aureus (N=30)	8 (26.6)	9 (30)	8 (26.6)	7 (23.3)	12 (40)	3 (10)	18 (60)	NA	NA	NA	1 (3.3)	5 (16.6)	4 (13.3)	9 (30)
***Enterococcus* spp.** (N=11)	3 (27.3)	5 (45.4)	7 (63.6)	6 (54.5)	6 (54.5)	2 (18.2)	7 (63.6)	NA	NA	NA	1 (9.1)	2 (18.2)	2 (18.2)	5 (45.4)
S. viridans (N=13)	5 (38.5)	6 (46.1)	8 (61.5)	5 (38.5)	8 (61.5)	1 (7.7)	10 (76.9)	NA	NA	NA	0 (0)	4 (30.7)	1 (7.7)	3 (23.1)

Table 5: Antibiotic susceptibility profile of organisms isolated from wound infections.
AN, amikacin; GEN, gentamicin; TMP-SXT, trimethoprim-sulfamethoxazole; CIP, ciprofloxacin; CAZ, ceftazidime; CT, ceftizoxime; CFM, cefixime; PIP,piperacillin; IPM,imipenem; AZM, azithromycin; V, vancomycin; CRO-ceftriaxone; CTX, cefotaxime; CZ, cefazolin. *CoNS, Coagulase-Negative *Staphylococci*; NA, not applicable.

Our findings indicate of 408 microorganisms isolated from respiratory tract infections samples, 58 (14.2%) were Gram positive and 350 (85.8%) were Gram negative. In this study, 100% of the trachea specimens were obtained from inpatients (hospital-acquired infections).

Among Gram negative bacteria, *P. aeroginosa* 110 (31.4%), and among Gram positive bacteria, *S. aureus* 23 (39.6%) were the commonest pathogens followed with other isolated bacteria including *Klebsiella* spp., *Acinetobacter* spp., *Proteus* spp., *E. coli*, *S. aureus*, *S. marcescens*, *Enterococcus* spp., *Enterobacter* spp., *Citrobacter* spp., *S. viridans*, CoNS, *Alcaligenes faecalis*, and *S. pneumonia* respectively. The resistance levels for the both Gram negative and Gram positive pathogens were varying from 0 to 100%. The results at the present study revealed high resistance of *Acinetobacter* spp. to all antimicrobial drugs tested in urinary tract, blood stream, cerebrospinal fluid, and wound infections.

Finally, investigation on wound infection specimens indicates that *S. aureus* 30 (20.4%), *P. aeroginosa* 22 (15%), *E. coli* 18 (12.2%),*Klebsiella* spp. 15 (10.2%), CoNS 14 (9.5%), *S. viridans* 13 (8.9%), *Enterococcus* spp. 11 (7.4%), *Proteus* spp. 8 (5.4%), *Acinetobacer* spp.8 (5.4%), *Enterobacter* spp. 5 (3.4%), and *S. marcescens* 3 (2%) were most prevalence bacterial pathogens respectively. Among Gram positive bacteria level of resistance of *Enterococcus* spp. to vancomycin (9.1%) was higher than other bacteria.

6. Conclusion

The high resistance rate was observed in our study to most of used antibiotics for treatment of all bacterial infections. Therefore, these results suggest setting up a comprehensive surveillance system in order to collect comparable data, 1) to evaluate the distribution of organisms isolated and their drug resistance patterns over different period of time and place of Iran, 2) to prevent the antibiotic resistance, 3) to determine the most effective antibacterial regimen 4) to assess the effectiveness of prevention programs.

Conflict of Interests

The authors declare there is no conflict of interest regarding the publication of this paper.

Acknowledgements

The authors are grateful to the microbiology laboratory personnel of Besat Hospital in Hamadan for their sincerely cooperation.

Authors' Contribution

Farzad Khademi designed the study, Arshid Yousefi-Avarvand wrote the manuscript, Pezhman and Fahimeh performed the experiments and Kiarash Ghazvini analyzed data.

Funding/Support

The authors declare that there is no financial support from the project.

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How to cite this article: Ghiamati Yazdi F, Yavarmanesh M, Khomeiri M, Mahdavi M. Microbial Safety of Masske: A Traditional Butter from South of Khorasan, Genetic Similarity of Pathogenic Bacteria Indicators. Infection, Epidemiology and Medicine. 2016; 2(3): 8-13