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Clinical microbiology laboratory isolates: prevalence and gender variation

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ABSTRACT

Data archives of clinical microbiology laboratory (CML) are a rich source of valuable information. In this study, CML data from two tertiary care hospitals in Jordan were reviewed, in order to identify the source prevalence of microorganisms and the dissemination of Extended Spectrum Beta-Lactamase (ESBL) bacteria. The association between gender and the microorganism or specimen source was investigated. Data collected from each hospital was screened and filtered according to predetermined exclusion criteria. Of 20726 records screened, 5547 valid specimens with positive growth were considered. From these specimens 7143 isolates were identified to genus or species level. The most common specimens were identified and their association with gender was statistically determined and discussed. The prevalence of microorganisms in different specimens was compared with the literature, and variation from the expected results was explained. In addition, some associations were observed between gender and the predominating microorganisms. High dissemination rate of ESBL-producing bacteria was observed among Gram-negative bacteria (57%), indicating serious challenges facing clinicians in finding suitable treatments. Reviewing CML data can aid in the study of trends in the dissemination of microorganisms in specific population groups and can aid clinicians in amending their treatment protocols.

Keywords: Enterococcus, Streptococcus agalactiae, ESBL, gender, prevalence, laboratory, urine culture, vaginal swab.

1. INTRODUCTION

Infectious diseases are known to cause a large burden on the health sector and economy of many countries. They are responsible for a substantial proportion of morbidities and mortalities among the population. The causative agents of these infections vary from bacterial and viral infections to fungal and parasitic ones. In order to treat or manage these illnesses, diagnosis is a crucial step in order to identify the pathogen and to commence a suitable treatment protocol. Diagnosis involves many aspects including clinical manifestation, physical examination, medical history, travel history, imaging and an important confirmative tool, laboratory testing [1]. Although some infections can be identified clinically (ie: the so-called "frank" pathogen), others require clinical microbiology laboratory to identify the causative agent [1]. Besides identifying the etiologic agent of the disease, clinical microbiology laboratories provide *in vitro* information about the susceptibility of the isolated microorganisms towards antimicrobial drugs. The retrospective review of microbiology laboratory data can be a valuable tool in estimating the prevalence of certain microorganisms among specific population groups or under certain conditions, and also helps in tracing the trends in the microorganism's dissemination throughout a host population [2–4].

Variation in gender could predispose a sub-section of a

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host population to some specific infectious diseases more than the opposite gender. Due to anatomical and physiological differences between males and females, the microbiota in certain areas in the body vary and consequently, the incidence of some infections will vary between the two genders [5]. Some studies have shown that patient's gender could be a risk factor for some microbial infections [5,6]. Furthermore, the WHO has issued a report indicating the effect of sex and gender on population health in emerging infectious diseases and epidemic-prone diseases [7]. In this report, biological differences between males and females, and the physiological changes women undergo during pregnancy are observed to have an effect on the immune response and hence, upon overall vulnerability and susceptibility towards infections and subsequent disease. Similarly, the report also made reference to observed gender differences in physical activity patterns, which could lead to different levels of exposure towards different infectious agents and gender differences in accessibility to economic resources, which could act as a barrier to access effective health care. Such differences will undoubtedly result in gender variations in responses to emerging infectious diseases [7].

Over several years, bacteria have developed mechanisms to resist antibiotics. In fact, antimicrobial resistance has become a public health crisis with the emergence of multiple drug resistance (MDR) in several clinically important species of bacteria. This crisis is taking the world into what is called the *"post antibiotic era"*, where previously minor infections might no longer be curable and may result in fatality due to lack of effective antibiotics [8]. Among these MDR microorganisms are the Extended Spectrum Beta Lactamase producing bacteria. These bacteria produce a group of enzymes called Extended Spectrum Beta Lactamases (ESBLs). ESBLs confer resistance to a broad range of β-lactams, such as penicillins and first-, second- and third-generation cephalosporins; and azotreonam [9]. These enzymes are primarily produced by Gram-negative bacteria, mainly Enterobacteriaceae, *Acinetobacter*, and *Pseudomonas aeruginosa* [9]. Recent studies indicated that the spectrum of antibiotic resistance of the ESBL-producing bacteria is expanding to include multiple antibiotic classes, leaving the clinician with very limited treatment options and the patient with poorer prospective outcomes [10,11].

The aim of this study was to explore clinical microbiology laboratory results in two tertiary care hospitals in Jordan during 2017 and 2018, in order to identify the most common specimens provided, the predominating microorganisms in different specimens and the prevalence of ESBL-producing bacteria in these clinical specimens. In addition, the possibility of gender-association with the specimens and microorganisms was also investigated. It is proposed that such information will inform our knowledge of the distribution and host-susceptibility of different microorganisms among the general population, in addition to the extent of dissemination of ESBL-producers.

2. Methodology

This is a retrospective study, in which the microbiology laboratory results from two hospitals in Amman, Jordan were evaluated for the years 2017 and 2018. The first hospital is a public sector academic tertiary care hospital with 600 beds. On an annual basis, this hospital receives more than 600,000 patients in the outpatient clinics and more than 40,000 patients are admitted for treatment. The second hospital is a private sector tertiary care hospital with 160 beds. On an annual basis this hospital deals with about 100,000 patients as outpatients and in-patients.

The study received an ethical approval from the Ethics Committee of Scientific Research, Ministry of Health, Jordan (code: MOH REC 1900018). All necessary approvals were also obtained from the administration of each hospital. The clinical laboratories of the two hospitals relied on Vitek®-2 systems (bioMérieux, France) for microbial identification. The laboratory data was retrieved from the servers of the microbiology laboratory with the help of the hospital's information technology departments.

The following information was obtained: Patient's file number (a unique number of each patient), age, gender, sample date, sample source, microbial culture result (microorganism type and whether it is ESBL-producer or non-ESBL producer).

The data collected were obtained as raw data and screened based upon exclusion criteria. The criteria included the exclusion of any duplication in data entry (e.g same patient's file number on the same date and same sample), invalid data entry or missing information, and any specimen showing no microbial growth or the result was reported as *"no significant growth"* or *"normal flora"*. Moreover, whenever the same microorganism was isolated from a specimen that was cultured within three weeks of the previous culture it was excluded, because it was assumed that the microorganism isolated in the second specimen is the same causative agent of the first culture. Hence, three weeks were considered a suitable cut-off in most treatment guidelines, since the majority of infections are expected to resolve with treatment within 14 days [12,13].

2.1 Statistical analysis

Statistical analysis of the data was performed using SPSS version 20.0 (SPSS Inc., Chicago, IL). Descriptive statistics was used to describe the specimens tested. Categorical variables were presented as valid percentages. Non parametric Chi square test was used to test for association between the categorical variables. A *P*-value of < 0.05 was considered significant

3. Results and discussion

The total number of raw laboratory results screened from in-patients and out-patients from the two hospitals was 20726; 14498 from the first hospital and 6228 from the second hospital. After filtering the data according to the exclusion criteria, the total number of specimens with valid laboratory results and significant microbial growth was 5547; 3775 and 1772 from the first and second hospitals respectively. For these specimens, the age of the patients ranged from 3 days to 102 years. From the specimens reported, 7143 microorganisms were isolated and identified to the genus or species level, except for 146 isolates which were reported as coliforms (Table 1). Gram-positive bacteria were the predominant group of isolated microorganisms (52%) followed by Gram-negative bacteria (45.3%), and then yeast and fungi (2.7%). The most common Gram-positive bacteria isolated were Enterococci (18.8%), followed by Staphylococci (17.5%) and Streptococci (15.7%). The majority of Streptococci belonged to Group B (*S. agalactiae*) which constitutes 95.1% of all Streptococci. For Gram-negative bacteria, the Enterobacteriaceae family was the predominating one, where the most common bacteria isolated were *Escherichia coli* (32.1%), followed by *Klebsiella* (8.6%).

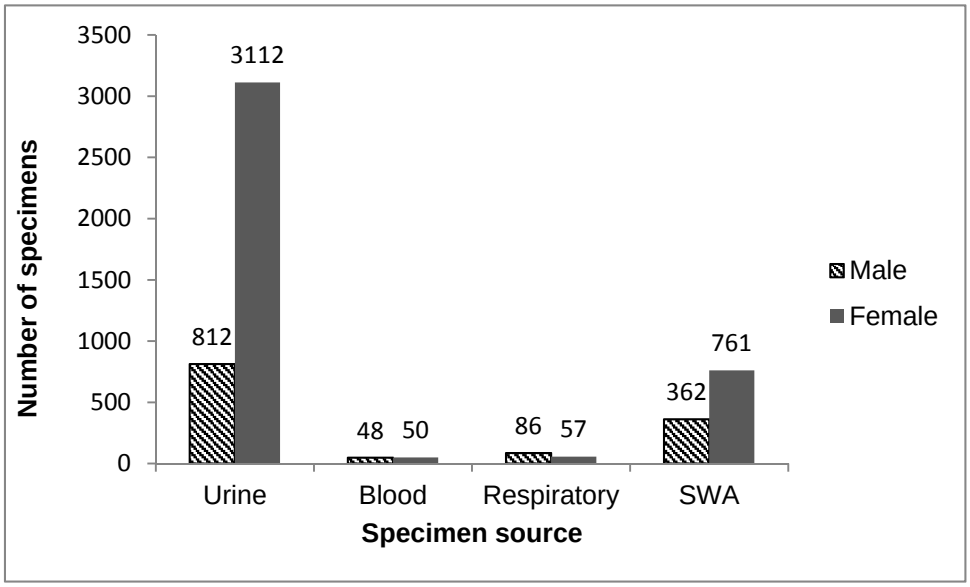

Fig. 1. Numbers of specimens identified between males and females based on specimen source. SWA: Skin, wound and abscess.

Table 2 shows the distribution of the isolates based on the source of specimens. These isolates were detected in the specimens as pure culture or in combination with other microorganisms. Urine samples were the most commonly infected of the specimens cultured (N=3924), followed by skin, wound and abscess (SWA, N=1123), respiratory (N=143), blood (N=98) and vaginal (N=81) specimens.

3.1 Urine Specimens

Urinary tract infections (UTI) are very common worldwide and considered one of the leading causes of visits to primary care clinics. A global study found that in developed countries, UTIs are the second most common infectious disease, after respiratory tract infections, that cause patients to visit clinics [14]. In developing countries, UTIs are the third most numerous reason for clinical visits, preceded by respiratory tract infections and tuberculosis [14]. UTIs account for a significant proportion of antibiotic prescription and dispensing [15,16]. In Jordan, they were found to be the second most numerous infectious disease, after respiratory tract infections, to which antibiotics were dispensed with or without prescription [16].

We suggest that the reason why urine and SWA specimens exceeded respiratory tract specimens in our study is that almost 80% of clinically diagnosed respiratory infections are caused by viruses such as influenza viruses, parainfluenza viruses, adenovirus and rhinoviruses [17]. In addition, even in non-viral respiratory infections, physicians may rely on physical examination, and clinical symptoms or other diagnostic tools (e.g: x-ray) rather than laboratory tests to determine the appropriate treatment [18]. On the other hand, UTIs are known to occur more frequently in females than in males [19], which was obvious in our results where 3112 positive urine specimens from females were reported compared to 812 urine specimens from males (Figure 1).

It is known that the leading cause of urinary tract infections is *E. coli* [20,21]. It is responsible for 70 to 95% of both upper and lower UTIs. The remainder of UTI infections are caused by *Klebsiella* spp., *Enterococcus faecalis*, *Proteus* spp., *Staphylococcus* spp., other Enterobacteriaceae and yeasts [19,21]. Consistent with

this, several microorganisms were isolated from urine in this study. The most predominant were *E. coli* (51.7%) followed by *Enterococcus* spp. (34%), *Staphylococcus* spp. (30.2%), and then *Klebsiella* spp. (11.8%; Table 2). From the literature it appears that the observed prevalence of the genus *Enterococcus* in urinary tract infections is increasing [22]. It is implicated in urinary tract infections and in asymptomatic bacteriuria. A five year study in a veteran's hospital in the United States identified enterococci in positive culture urine specimens in 22.5 % of the specimens compared to our finding of 34%. The problem with enterococci is their increasing resistance to a broad range of antimicrobials. This has led to the publication of guidelines for the diagnosis and management of UTIs versus asymptomatic bacteriuria caused by enterococci to reduce the overuse of antibiotics [2,3].

The predominating microorganisms identified in urine in our study were also seen in a previous study by Flores-Mireles *et al.* (2015) [19], who found that the prevalence of microorganisms in UTIs varies between complicated and uncomplicated infections. Other than *E. coli*, the top three microorganisms prevailing in uncomplicated UTIs were *K. pneumoniae*, *Staphylococcus saprophyticus* and *Enterococcus* spp. while in complicated UTIs the top three microorganisms excluding *E. coli* were *Enterococcus* spp., *K. pneumoniae* and *Candida* spp.

Interestingly, Gram-positive bacteria, enterococci, staphylococci and streptococci, in relation to other microorganisms exhibited a significantly higher association with female urine specimens than with male urine specimens ($p<0.001$, $p<0.001$, $p=0.043$ respectively). While Gram-negative bacteria (*E. coli* and *Klebsiella* spp.) exhibited a significantly higher association with male urine specimens than with females ($p<0.001$, $p=0.015$). In line with these results, it has been estimated that about 5-25% of uncomplicated urinary tract infections in women are caused by Gram-positive bacteria mainly *S. saprophyticus, Enterococcus faecalis* and Group B Streptococci GBS [23]. These infections are most common in non-pregnant women of child bearing age. Nevertheless, in pregnant women Gram-positive bacteria are more often seen as etiologic agents of UTIs [23]. This was observed in this study where enterococci and staphylococci in urine specimens were significantly more associated with women in the age group 13-50 years than in the other age groups (Pearson's Chi square, $p<0.001$ for both bacteria). However, the presence of streptococci was not significantly different between these age groups.

3.2 Skin, Wound & Abscess Specimens

The second most common specimens in this study were from SWA samples. Specimens tested and reported from females were twice the number of those from males (761 vs 362 specimens, Figure 1). This finding is in agreement with that reported by Shallcross *et al*. (2014). In their study, data collected between 1995 and 2010 in the UK showed that the first time consultation at a general practitioner for a boil or abscess was 512 for females and 387 for males per 100,000 person-years [24].

Bacterial skin infections are mainly caused by staphylococci and streptococci [25]. In this study streptococci comprised the highest proportion of SWA specimens (69.8%), while staphylococci comprised only 3.3% (Table 2). This doesn't necessarily mean that staphylococci play a minor role in these infections. Rather, it could imply that these infections were treated empirically with antibiotics and those not responding were referred to the laboratories to help in diagnosis and treatment regime. As mentioned earlier the vast majority of streptococci isolated in this study were GBS. GBS are known to colonize the human genital and gastrointestinal tracts and to a lesser extent the respiratory tract [26]. This group is a leading cause of morbidity and mortality in neonates and pregnant women [26]. In newborns GBS are responsible for many diseases (such as bacteremia, sepsis, pneumonia, and meningitis), all of which can be fatal in infants. Furthermore, invasive GBS diseases are

increasingly seen in non-pregnant adults, especially among the elderly and people with underlying medical conditions [27]. Of the invasive GBS cases in non-pregnant adults, skin and soft tissue infections are among the most frequently reported cases [27]. This is consistent with our findings, where GBS in SWA infections is significantly higher in the age group >75 years than the other age groups (Pearson's Chi square, p=0.008).

A remarkable proportion of SWA specimens harbored Gram-negative bacteria (~20%). Skin infections with Gram-negative bacteria occur mainly in diabetic patients or the immunocompromised [25]. In fact diabetes is wide spread among Jordanians and in 2016 it was estimated that 46% of Jordanians who are above 25 years are diabetic, whether diagnosed or not [28], which could explain the high occurrence of Gram-negative bacteria in these specimens.

Other than bacteria as a cause of skin and soft tissue infections, fungal infections are on the rise [29]. In these fungal infections, cutaneous and soft tissue infections are usually caused by *Candida* spp. [30,31]. The role of *Candida* spp. can be detected in our results where *Candida* was isolated from 5.2% of the SWA specimens comprising the fourth most dominant microorganism in these specimens (Table 2). *Candida* spp. was found to be associated with females more than with males (p=0.01). This association has been reported previously in a study by Heidrich *et al.* (2016). In their sixteen-year retrospective study in Brazil, they found that dermatomycoses caused by the genus *Candida* were more predominant in women than in men [32].

3.3 Respiratory Specimens

Respiratory tract specimens were the third most common group in this study. Specimens from males were one and a half times greater in number than those for females (86 versus 57, Figure 1) indicating a higher incidence of respiratory infections among males than among females. One of the reasons for this could be linked to smoking, which is more prevalent among males than females in Jordan. Smoking is considered a major risk factor for respiratory diseases [33]. Jordan, has one of the highest smoking prevalence in the world. Males from different sample groups (eg: health care workers, college students, youths etc.) were found to significantly outnumber females in smoking [34].

It is known that among the most common bacterial cause of respiratory tract infections are streptococci [35]. *S. pneumoniae* is considered the most common cause of community acquired acute bacterial pneumonia [35]. In general, some Streptococci are part of the normal human oral microflora. Some species, such as *Streptococcus pyogenes* and *Streptococcus pneumoniae*, are considered to be occasional respiratory tract residents [36]. In line with this, the microorganism isolated in greatest numbers from the respiratory system specimens in this study were the streptococci. However, the vast majority of the isolated streptococci were GBS, which was unexpected and requires further investigation. Nevertheless, this high prevalence of GBS could imply that their occurrence in infections is increasing as they also comprised the majority of streptococci in SWA infections. One suggestion for this high prevalence of GBS is that these isolates could have high resistance to antimicrobials, which enables them to survive empirical treatment given to patients.

In our results, the second most frequently isolated microorganism from respiratory specimens was *Candida* spp., in 16.8% of specimens (Table 2). *Candida* spp. is part of the normal human flora of the oral cavity and its detection in the respiratory system has often been thought to be the result of re-localisation of this normally commensal microorganism [37]. Unfortunately, there is no test or criteria to define the isolation of *Candida* from respiratory tract specimen as being a contamination, commensalism, colonization or infection. However, in recent years it has been recognized that the interpretation of the detection of *Candida* spp. in the respiratory tract should be based on clinical and microbiological context [37].

3.4 Blood Specimens

In this study *E. coli* and *Klebsiella* spp. were the most predominant bacteria in the blood cultures (34.7% and 30.6% respectively, Table 2). Compared to a multicenter study in Hubei Province, China, between 2014 and 2016, *E. coli*, *Staphylococcus aureus* and *Klebsiella pneumoniae* were reported as the most common pathogens responsible for nosocomial blood stream infections [38]. In another study, it has been shown that Gram-negative bacteria, in particular Enterobacteriaceae, were among the main causative agents of bacteremia [39].

Over time, Enterobacteriaceae have become resistant to antibiotics with the emergence of ESBL and carbapenemase producing strains [39,40]. This can be seen in our results where the predominance of ESBL-producing *E. coli* and *Klebsiella* in blood specimens was 33.7% and 28.7% respectively (Table 3), which is very close to the predominance of these two bacteria as both non-ESBL and ESBL-producers (34.7% and 30.6% respectively, Table 2). This indicates that the vast majority of the bacteria isolated from blood specimens are ESBL-producers. These bacteria are highly resistant to many antibiotics and are extremely difficult to eradicate [39,40]. Thus, their associated infections have a high potential to predispose to blood infections due to the invasion of the bacteria into blood, which explains their predominance in blood specimens.

3.5 Vaginal Specimens

The colonization of the vagina is affected partly by estrogen levels, which change with the female's age, menstrual cycle and pregnancy [5]. In some cases commensal microorganisms such as *Gardnerella vaginalis*, *E. coli* and GBS can cause vaginal infections and subsequent disease [41]. In our study the most predominant vaginal isolates were streptococci and *Candida* spp. GBS colonization in the genital tract [26] could explain its predominance in the high vaginal swabs in our study (45%, Table 2). This predominance in the vagina is consistent with a previous study in Jordan, where nearly 20% of specimens collected from the vagina of pregnant women were colonized with GBS [42]. In another study on non-pregnant women in Oregon USA, Leclair *et al*. [37], found that GBS prevalence was 22.8% and that there was a significant relationship between vaginitis and GBS colonization in the vagina.

The second predominating microorganism in high vaginal swabs is *Candida* spp. (32.1%). Although *Candida* can be found normally in the vagina in many women where it exists as a unicellular commensal under normal circumstances, changes in the vaginal environment, such as hormonal change, diabetes, use of oral contraceptives, etc, can encourage the growth of *Candida* in a non-commensal and pathogenic form, thus predisposing to vulvovaginal candidiasis [5]. Vaginal candidiasis is one of the most common fungal vaginal infections [5], which is in agreement with our findings where *Candida* is the most predominant fungus/yeast isolated.

Of the 3236 Gram-negative bacteria isolated, 1843 (57%) were phenotypically identified as ESBL-producers (Table 1). ESBLs are mainly associated with the family Enterobacteriaceae, of which *E. coli* and *Klebsiella pneumoniae* are the main ESBL producers [43]. This was obvious in our results where *E. coli* was by far the most predominant bacteria in all specimen types, followed by *Klebsiella* spp. and to a lesser extent *Enterobacter* spp. (Table 3). A study on hospitalized patients in Jordan found that from 121 *E. coli* isolated from urinary tract, 62% were ESBL producers [44]. Another study reviewed 1718 published studies worldwide, and reported the prevalence of ESBL-producing bacteria in pediatric blood stream infections to range from 4% in Europe to 15% in Africa [4]. This study observed an annual increase in the prevalence of ESBL-producing bacteria over the period 1996 to 2013 to be 3.2% [4]. In the past, infections complicated by ESBL were restricted to hospitals, nowadays they have spread to the community [43]. ESBL-producer dissemination is not only limited to clinical cases, it has also been detected in hospital environments,

household settings and even in vegetables and meat [45,46].

4. Conclusions

Clinical laboratory data is a vital tool in identifying the causative agents of infections and their associated resistance to antimicrobials. Retrospective review of clinical microbiology laboratory data can be a rich source of information to study the dissemination of microorganisms in specific population groups or certain body systems. This can aid epidemiologists in identifying trends in the isolation of specific microorganisms and it helps clinicians in revising their treatment protocols and guidelines to a more appropriate ones.

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Table 1: Details of the specimens tested and their distribution within gender, age, source and type.

Factor	Frequency (%)
Gender (N=5547)	
Male	1393 (25.1)
Female	4154 (74.9)
Age (Years; N=5547))	
≤1	250 (4.5)
1<Age<5	150 (2.7)
5-12	400 (7.2)
13-17	169 (3.0)
18-50	2515 (45.3)
51-70	1184 (21.3)
≥71	879 (15.8)
Specimen source (N=5547)	
Blood	98 (1.8)
High vaginal swab	81 (1.5)
Respiratory system	143 (2.6)
Skin, wound, abscess	1123 (20.2)
Urine	3924 (70.7)
Other sources including unidentified sample source	178 (3.2)
Isolates (N=7143)	
Gram-positive bacteria N=3714 (52.0%)	
Enterococcus	1342 (18.8%)
Staphylococcus	1249 (17.5%)
Streptococcus	1123 (15.7%) (*Strep* GpB n=1069)
Gram-negative bacteria N=3236 (45.3%)	9 (0.1%)
Acinetobacter	5 (0.07%)
Citrobacter	146 (2.0%)
Coliform	20 (0.3%)
Enterobacter	2290 (32.1%)

Escherichia coli	611 (8.6%)
Klebsiella	61 (0.9%)
Proteus	74 (1.0%)
Pseudomonas	20 (0.3%)
Others	154 (2.2%)
Yeast (*Candida*)	39 (0.5%)
Fungus	
ESBL-producing Bacteria N=1843	**Number (%) of ESBL producers**
	11 (0.6%)
Enterobacter	1481 (80.4%)
Escherichia coli	338 (18.3%)
Klebsiella	8 (0.4%)
Proteus	

Table 2: The distribution of the microorganisms amongst the specimens and gender and the association of the microorganisms with gender, if present, p< 0.05. The number of isolates of each microorganism obtained from females (F) or males (M) is shown.

Microorganism	Urine (N=3924) n (%)	SWA N=1123 n (%)	Respiratory (N=143) n (%)	Blood (N=98) n (%)	High vaginal swab (N=81) n (%)
***Enterococcus* spp. (N=1342)**	1334 (34%)	5 (0.02%)	0	1	0
Gender distribution	F= 1133, M=201 p<0.005 (F)*	F= 2, M= 3 -	-	F=0, M=1 -	-
Streptococci (N=1123)	194 (4.9%)	784 (69.8%)	68 (47.6%)	15 (15.3%)	37 (45%) all GBS
Gender distribution	F=165, M=29, p=0.043 (F)*	F=486, M=198, p<0.005 (M)*	F=29, M=39 p= 0.517	F=6, M=9 p=0.409	-
Staphylococci (N=1249)	1186 (30.2%)	37(3.3%)	7 (4.9%),	10 (10.2%),	0
Gender distribution	F=997, M=189 p<0.005 (F)*	F=24, M=13 p=0.701	F=3, M=4 p=1.00	F=3, M=7 p=0.195	-
***Escherichia coli* (N=2290)**	2028 (51.7%)	146(13.0%)	17 (11.9%)	34(34.7%)	16 (19.8%)
Gender distribution	F=1570, M=458 p<0.005 (M)*	F=125, M=21 p<0.005 (F)*	F=3, M=14 p=0.064	F=17, M=17 p=1.00	-
***Klebsiella* spp. (N=611)**	464 (11.8%)	60 (5.3%),	14 (9.8%),	30 (30.6%)	5 (6.2%)
Gender distribution	F=348, M=116 p=0.015 (M)*	F=51, M=9, p<0.005 (F)*	F=8, M=6 p=0.25	P=0.05 -	-

Microorganism	Urine (N=3924) n (%)	SWA N=1123 n (%)	Respiratory (N=143) n (%)	Blood (N=98) n (%)	High vaginal swab (N=81) n (%)
***Pseudomonas* spp. (N=74)**	45 (1.1%)	17 (1.5%)	8 (5.6%)	0	0
Gender distribution	F= 34, M= 11, p=0.532	F= 13, M=4 p=0.603	F= 4, M= 4 p=0.71		-
***Proteus* spp. (N=61)**	50 (1.3%)	6 (0.5%)	2 (1.4%)	0	1 (1.2%)
Gender distribution	F= 41, M=9 p=0.728	F= 6, M= 0 P= 0.185	F= 1, M= 1 -		-
***Candida* spp. (N=154)**	36 (0.9%)	59 (5.2%)	24 (16.8%)	1 (1%)	26 (32.1%)
Gender distribution	F= 29, M=7 p= 1.00	F= 49, M= 10, p=0.01 (F)*	F= 11, M= 13, p=0.648	F= 0, M=1 -	-
***Acinetobacter* spp. (N=9)**	0	4 (0.4%)	3 (2%)	0	0
Gender distribution	-	F=1, M=3 -	F=0, M=3 -	-	-
***Citrobacter* spp. (N=5)**	2 (0.05%)	2 (0.2%)	0	0	0
Gender distribution	F=2, M=0 -	F=2, M=0 -	-	-	-
***Enterobacter* spp. (N=20)**	7 (0.2%)	7 (0.6%)	1 (0.7%)	0	0
Gender distribution	F=4, M=3 p=0.16	F=5, M=2 p=1.00	F=0, M=1 -	-	-

* Statistically significant association was found with females (F) or males (M)

Table 3: The distribution of ESBL producing bacteria in the specimens collected based on the specimen source.

Microorganism	Urine (N=3924)	Blood (N=98)	High vaginal swab (N=81)	Respiratory (N=143)	SWA (N=1123)
***E. coli* (N=1481)**	1350 (34.4%)	33 (33.7%)	7 (8.6%)	16 (11.2%)	28 (2.5%)
***Klebsiella* spp. (N=338)**	236 (6.0%)	28 (28.6%)	2 (2.5%)	9 (6.3%)	25 (2.2%)
***Enterobacter* spp. (N=11)**	6 (0.2%)	0	0	0	1 (0.1%)
***Proteus* spp. (N=8)**	6 (0.2%)	0	0	0	1 (0.1%)

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عزلات المختبرات السريرية الجرثومية: إختلاف هيمنتها وإرتباطها بجنس المريض

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ملخص

يعتبر أرشيف البيانات للمختبرات السريرية الجرثومية مصدر مهم وقيم للمعلومات. في هذه الدراسة، تم مراجعة بيانات هذه المختبرات من مستشفيين متخصصين في الأردن من أجل تحديد مصدر العينات للجراثيم الأكثر انتشاراً ولمدى تفشي بكتيريا المنتجة للبيتالاكتيميز الواسع الطيف. كذلك، تم تقصي وجود علاقة بين جنس المريض والجراثيم المعزولة منه أو مصدر هذه الجراثيم. بعد الإطلاع على البيانات من المستشفيات وفرزها بناء على مواصفات محددة ، تم تحديد 5547 عينة فيها نمو جرثومي مؤكد من أصل 20726 ملف تمت دراستهم. بهذه العينات، وجد 7143 عزلة تم التعرف عليها لمستوى الجنس والنوع. تم تحديد أكثر العينات شيوعاً مع إجراء دراسة إحصائية لوجود إرتباط لها بجنس المريض، ومناقشة النتائج .تم مقارنة هيمنة جراثيم معينة بعينات معينة ومحاولة تفسير هذه النتائج وتوضيحها من خلال المعلومات والأبحاث المنشورة. بالإضافة لذلك، وجدت بعض العلاقات بين جنس المريض ونوع الجراثيم المهيمنة بمصادر معينة للعينات. وجد انتشار عالي للبكتيريا المنتجة للبيتالاكتيميز الواسع الطيف (57%) ضمن البكتيريا سالبة الجرام، ما يدل على خطورة التحديات التي تواجه الأطباء بإيجاد علاجات مناسبة. إن مراجعة بيانات المختبرات السريرية الجرثومية يساعد في دراسة التوجه في إنتشار الجراثيم ضمن فئات بشرية معينة وكذلك يساعد الأطباء في تعديل البروتوكولات العلاجية.

الكلمات الدالة: إنتيروكوكس، ستربتوكوكس أجالاكتي، بكتيريا المنتجة للبيتالاكتيميز الواسع الطيف، جنس، هيمنة، مختبر، زراعة البول، مسحة المهبل.

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