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Trends in the assessment of multidrug efficiency against identified bacterial strains isolated from wounds at El-Demerdash Hospital, Egypt

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Abstract:

Multidrug-resistant (MDR) bacteria is a severe problem for universal public health which increases morbidity and mortality rate. These resistant bacteria lead to ineffective treatment of drugs resulting in the spreading and persistence of infections. So, the major target of this study is to estimate the competence of multidrug antibacterial agents against bacterial strains isolated from wound samples and then identify the most potent Multidrug-resistant (MDR) bacteria. Fifty wound swab specimens were gathered from various wounds and several patients from the Central Microbiology Laboratory of El-Demerdash Hospital, Cairo, Egypt. Eighty- nine bacterial isolates were isolated from fifty wound samples then cultured on different media and tested for their susceptibility to different thirty antibiotic discs using the agar disc diffusion method. After recording the results of the susceptibility test, the post potent resistant bacterial isolates recorded 3 bacterial isolates which resistant to 30 different antibiotic types. These resistant bacterial isolates were identified using morphological, biochemical, and molecular techniques. The results recorded that the post potent resistant bacterial isolates identified as *Klebsiella oxytoca, Pseudomonas aeruginosa, and Escherichia coli.* This study concluded that with the increase in the random use of antibiotic drugs resulted in the presence of multi-antibacterial resistant strains. There are bacterial strains that were isolated from wounds in patients at El-Demerdash Hospital, Egypt, and identified. They can resist about thirty different antibiotic discs.

Abbreviation**:** Multiple antibiotic resistance **(**MAR).

Keywords: Wound infection, Multi-drug resistant (MDR) bacteria, Antibiotic drugs, *Klebsiella oxytoca, Pseudomonas aeruginosa, and Escherichia coli.*

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1. Introduction

The skin considers as the defense partition versus the presence of different pathogens. So, any disorder of the natural anatomic composition via mechanical, chemical, thermal and physical, events or by surgical operations with a change of skin functions, leads to the wound formation [1]. It is prone to the lesion, abrasion and in touch with the outer environment, consequently it is the most liable to colonization via pathogens [2–4]. The wounds are classified as chronic and acute wounds, acute wound, such as surgical wounds, cuts, burns, and abrasions. The infected wounds weaken the wound's healing rate and affect the human life [5]. The infections of wounds act as one-third of nosocomial infections in surgical patients and also responsible for 70–80% of the death rate among people [5, 6]. Wound contagions are related with morbidity and death rate in patients, particularly in developing lands, in spite of the kind of injury [6]. The fail in the treatment leads to a rise in healthcare expenses because of the increased use of antimicrobial agents, diagnostic tests as well as invasive operation [7]. The detection of infection needs the right equipment's, qualified professionals and long time [8, 9] and it is often depend on wound checkups, microbiological analysis and infection biomarker determination. Antibiotic therapy as well as wound sponsorship are two crucial agents for the controlling of the infection [10]. On the other hand, chronic wounds, such as leg or arterial ulcers, need prolonged time to treat. These wounds happen as a result of inner factors which can be related to illnesses such as immune deficiency diseases or diabetes [4, 8]. Gram-negative bacteria have become an important factor in wound infection because of their antimicrobial resistance which is one of the three greatest threats to human health [11] and also possesses high therapeutic challenges [12]. The overuse or misuse of antimicrobial agents has led to the development of multi-drug resistant bacteria [13]. Different researches have been done around the world that have identified *Proteus mirabilis, , Klebsiella pneumoniae Pseudomonas aeruginosa, Acinetobacter baumannii* and *Escherichia coli* as the most widespread multidrug-resistant Gram-negative bacteria [14]. A bacterial strain is assumed multi-drug resistant if it shows resistance to antibiotics from different classes such as aminoglycosides, quinolones, cephalosporins and Chloramphenicol [15]. Normal resistance is probably innate as it's mostly expressed in the creatures, or the gene is naturally found in bacteria however it is stimulated only to resistance levels by the antibiotic therapy which is considered mediated [16]. On the other hand, acquired resistance is probably because the bacteria acquire genetic substances via transposition, translation, coupling [17], and mutations

in the chromosomal DNA [18]. Antimicrobial resistance mechanisms are probably divided into four classes: drug target modification, drug uptake limitation, efflux of the drug, and inactivation of drug [19]. Because of the structural variations and others, Gram-negative bacteria are able to use whole mechanisms, in contrast, Gram-positive bacteria can use only the drug uptake limitation and drug efflux mechanisms [20]. WHO reported that multidrug resistant bacteria are accountable for around 23 thousand deaths and 25 thousand deaths yearly in the United States and Europe, respectively [21]. Moreover, the most common bacterial infections recorded *S. aureus, K. pneumonia, P. aeruginosa* and *E. coli* indicated resistance against the most effective antimicrobial agents like third-generation cephalosporin [5, 21 and 22]. Finally, the target of this study was to estimate the efficiency of different antibiotics drugs against microbial pathogens isolated from different wound samples, then select the most potent multidrug-resistant bacterial isolates to identify them morphologically, biochemically, and molecularly to control them with affordable drugs in the future prospective.

2. Materials and Methods

2.1. Swab samples collection

About 50 wound swabs were collected from the Central Microbiology Laboratory of El-Demerdash hospital with GPS 30.072848º, 31.276755º, Cairo, Egypt, the collected swabs were obtained from different types of wounds (20 swabs from burns, 15 swabs from diabetic foot, 10 swabs from surgery and 5 swabs from bed ulcers).

2.2. Media used

Nutrient agar [23], Mannitol salt agar [24], MacConkey agar [25], Blood agar [26] and Mueller-Hinton agar [27]. All chemicals, as well as media used in this work, were bought from Sigma-Aldrich, Egypt.

Central Microbiology Laboratory precautions; before sample collection, the wounds were washed with ordinary saline solution. Then wound swab samples were aseptically gathered from the deepneath of the wound by rotating sterile cotton swabs with adequate pressure. Then, wound swabs were took to the microbiology laboratory within 15 minutes by putting the swabs into the sterilized test tubes containing 0.5 ml of sterile saline solution [28]. Bacteriological culture and screening were made according to typical microbiological methods [29].

2.3. Isolation of multidrug-resistant microorganisms

According to **Puca *et al.*, [6]** 50 swab samples from different types of wounds were streaked on various media such as Nutrient agar, Mannitol salt agar, MacConkey agar and Blood agar to detect bacterial pathogens. Then plates were incubated at 37°C for 24 hours for bacteria [6]. Purification of the isolated bacteria was then achieved via sub-culturing. All plates for isolation were made in (3 replicates). Results were recorded as observation of bacterial colonies.

2.4. Multidrug-resistance test

The sensitivity of bacterial isolates (89) versus various antibiotics was done by the disk diffusion method (modified Kirby- Bauer method) on Mueller-Hinton agar according to typical steps recommended by the Clinical and Laboratory Standards Institute (CLSI) [14, 30]. To achieve this target, the next antibiotics with specific concentrations were used according to the protocol of El- Demerdash hospital in treatment of wound infection: Trimethoprim-sulfamethoxazole/Cotrimoxazole (**SXT 25*μ*g**), Amoxicillin/ Clavulanic acid (**AMC 30*μ*g**), Cefepime **(FEP 30*μ*g)**, Cefotaxime **(CTX 30*μ*g)**, Ceftriaxone **(CRO 30 *μ*g)**, amikacin (**AK 30 *μ*g**), levofloxacin (**LEV 5*μ*g**), Meropenem **(MEM 10 *μ*g**), Doxycycline **(DOX 30*μ*g)**, Penicillin **(P 10μg),** Rifampin **(RA 5*μ*g),** Vancomycin (**V 30*μ*g**), Polymixin B (**PB 30*μ*g**), Imipenem (**IMP 10*μ*g**), Clindamycin (**DA 2*μ*g**), Ampicillin - Sulbactam(**SAM 20*μ*g**), Gentamycin **(CN 10μg),** Erythromycin (**E 15*μ*g**), Metronidazole (**MET 5*μ*g),** Streptomycin (**S 10*μ*g**), Neomycin (**N 30*μ*g**), Bacitracin (**B 10*μ*g),** Tetracycline (**TE 30*μ*g**), Fusidic acid (**FA 10*μ*g**), Oxcillin (**OX 1*μ*g**), Norfloxacin (**NOR 10*μ*g**), Chloramphenicol (**C 30*μ*g**), Amoxicillin (**AX 25*μ*g**), Cefoperzone/ Sulbactam (**CES 105*μ*g),** Kanamycin **(K 30*μ*g),** Azithromycin **(AZM 15*μ*g),** Cefaclor **(CEC 30*μ*g),** Ceftazidime (**CAZ 30*μ*g)**, Ampicillin (**AM 10*μ*g),** Cefoperazone **(CEP 75*μ*g).** Explanation of antibiotic sensitivity results was determined following the instruction of interpretative zone diameters of CLSI. [31]. Results were recorded as inhibition zones (mm) around antibiotic discs.

2.5. Identification of multidrug-resistant bacteria

2.5.1. Morphological and biochemical identification

The most potent MDR was done according to Bergey's Manual of Systematic Bacteriology [32]. Also, biochemical tests were done by the automated Vitek 2 system (bioM´erieux, Marcy l'Etoile, France).

2.5.2. Molecular identification of the most potent multidrug-resistant bacteria

Pure cultures of bacterial isolates were cultured in Lauria Bertani (LB) broth and genomic DNA was separate according to the protocol by **Sambrook *et al.*,** [33]. PCR amplification of the 16S rRNA was done using the universal primers.

F 5′- AGA GTT TGA TCC TGG CTC AG-3′ and R 5′- GGT TAC CTT GTT ACG ACT T- 3 from Sigma Scientific Services Co. The reaction mixture (50µL) of Maxima Hot Start PCR Master Mix (2x), 25µl, 20µl mole of each primer. PCR reaction condition were 1 cycle of 95^{o}C for 10 min, 35 cycles of (95^{o}C for 30 sec, 65^{o}C for 1 min, 72^{o}C for 1 min) and 1 cycle of final extension at 72^{o}C for 10 min.

2.6. Statistical analysis.

All statistical analysis results of our work were made by SPSS, sigma plot, and excel. All results obtained were recorded in 3 replica, mean, standard deviation and standard error were done for all results.

3. Results and discussion

3.1. Isolation of multidrug-resistant microorganisms

About 89 bacterial isolates were obtained from different types of wounds in the central microbiology laboratory of El-Demerdash hospital. These isolates were subjected to further study. In other studies, some authors collected About 50 bacterial isolates from diabetic patients in Zagazig University Hospitals [34].

3.2. Screening to evaluate the efficiency of antibiotic drugs and select the most potent multidrug-resistant bacterial pathogen

3.2.1. Screening to evaluate the activity of ten antibiotic drugs against isolated bacteria

Table (1) and Figures (1a& 1b) showed that about 51 bacterial isolates isolated from El-Demerdash hospital were sensitive and 38 bacterial isolates were resistant to 10 antibiotics with different degrees. According to Multiple antibiotic resistance % with 100% the following bacterial isolate codes SD22, SD31, SD32, SD5, SD7, SD92, SD153, SD162, SD17, SD19, SD24, SD28, SD29, and SD210 were selected. Multiple antibiotic resistance (MAR) index was determined for each isolate by using the formula **MAR = a/b**, where a represents the number of antibiotics to which the test isolate depicted resistance and b represents the total number of antibiotics to which the test isolate has been evaluated for susceptibility.

3.2.2. Screening to evaluate the efficiency of twenty antibiotic discs against isolated bacteria

The selected 14 bacterial isolates from the previous results were tested against further twenty antibiotic discs as shown in Table (2) and Figure (2a& 2b) to select the most potent MDR bacterial isolates According to MAR % with 100% of obtained results, the following bacterial isolate codes, SD22, SD28, and SD31 were selected. All selected bacterial isolates were gram-negative bacteria. According to **Puca *et al.***, [6] the thirty four bacterial species were separated from wounds with a symptom of contagions were (57.9%) Gram-negative bacteria and (36.6%) Gram-positive bacteria. **Mohamed *et al.*,** [34] found that only 4 bacterial isolates were resistant to all 7 antibiotics used.

Table (1) Screening to evaluate the efficacy of ten antibiotics discs against isolated bacteria.

Isolates code	CN 10 µg	SXT 25µg	FEP 30 µg	CTX 30 µg	AMC 30 µg	CRO 30 µg	AK 30 µg	LEV 5µg	MEM 10µg	DOX 30 µg	MAR%
SD1	R	R	R	R	21±0.577	R	17.3±0.915	R	R	R	80
SD21	R	R	20.3±0.43	20.3±0.713	17.7±0.713	15.3±0.71	R	R	19±0.577	22.3±0.915	40
SD22	R	R	R	R	R	R	R	R	R	R	100
SD31	R	R	R	R	R	R	R	R	R	R	100
SD32	R	R	R	R	R	R	R	R	R	R	100
SD4	20.3±0.713	R	R	R	23±0.577	R	16±0.577	18.7±0.713	13.3±0.713	13±0.577	40
SD5	R	R	R	R	R	R	R	R	R	R	100
SD6	20.6±0.713	R	15±0.577	R	R	R	R	R	R	R	80
SD7	R	R	R	R	R	R	R	R	R	R	100
SD8	R	17.3±0.713	20±0.57	R	19±0.577	R	R	R	13±0.577	15.7±0.713	50
SD91	18.6±	R	R	R	R	R	14±0.577	R	R	17.3±0.438	70
SD92	R	R	R	R	R	R	R	R	R	R	100
SD10	23.6±	R	R	R	R	R	16.7±0.438	16±0.577	R	18.3±0.713	60
SD11	R	R	R	R	17.7±0.438	17.3±0.438	R	19±0.577	R	17.3±0.438	60
SD12	20.6±0.438	R	R	14.7±0.713	24.3±0.713	21±1.478	19.7±0.713	17.3±0.438	16.7±0.833	25.7±0.915	20
SD13	R	R	20.3±0.915	17.3±0.438	R	R	16.3±0.438	22.3±0.438	14.7±0.438	19.7±0.915	40
SD14	18±0.577	R	18.6±0.833	R	R	R	21±0.577	16.7±0.438	19.7±0.438	21.7±1.081	40
SD151	R	R	15.6±0.713	R	R	R	17±0.577	18.3±0.438	R	15.3±0.713	60
SD152	18.3±0.713	20.3±0.713	R	21.7±0.713	16.7±0.833	R	R	19.7±0.438	18.7±1.009	16±0.939	30
SD153	R	R	R	R	R	R	R	R	R	R	100
SD161	R	R		R	19.7±0.438	R	R	15.7±0.438	20.7±0.438	19.3±0.713	50
SD162	R	R	R	R	R	R	R	R	R	R	100
SD17	R	R	R	R	R	R	R	R	R	R	100
SD18	R	16.6±0.43	18.6±0.438	16.7±0.438	20±0.577	R	13.3±0.438	13.7±0.43	12.3±0.438	17.3±0.833	20
SD19	R	R	R	R	R	R	R	R	R	R	100

SD20	R	16.3±0.71	R	20.7±0.833	19.3±0.833	R	12.7±0.438	17.7±0.833	R	16.3±0.713	40
SD210	R	R	R	R	R	R	R	R	R	R	100
SD220	21.6±0.438	16.3±0.833	R	24.3±0.713	17.3±0.713	R	R	18.7±0.833	R	23.3±0.438	40
SD23	12.3±0.621	23.3±0.71	R	R	R	R	R	16.7±0.438	R	R	70
SD24	R	R	R	R	R	R	R	R	R	R	100
SD25	R	R	15.3±0.43	17.7±0.438	19.3±0.438	R	R	20.3±0.438	15.7±0.438	13.7±0.438	40
SD261	R	R	19.3±0.71	16.3±0.713	15.7±0.713	R	16.7±0.438	R	21.7±1.03	21.7±0.83	30
SD262	R	R	18.3±0.438	R	19.7±0.438	R	R	R	20.3±0.438	16.7±0.43	60
SD27	22.6±0.438	22.6±0.438	R	22.3±0.833	18.3±0.71	R	R	R	17.7±0.833	21.3±1.081	40
SD28	R	R	R	R	R	R	R	R	R	R	100
SD29	R	R	R	R	R	R	R	R	R	R	100
SD30	16.3±0.43	R	17.6±0.438	18.3±0.713	17.7±0.621	18.3±0.713	16.3±0.438	R	19.3±0.438	21.3±0.713	20
SD31	14± 0.577	14± 0.577	R	R	R	R	19.3±0.438	R	R	16.7±0.438	70

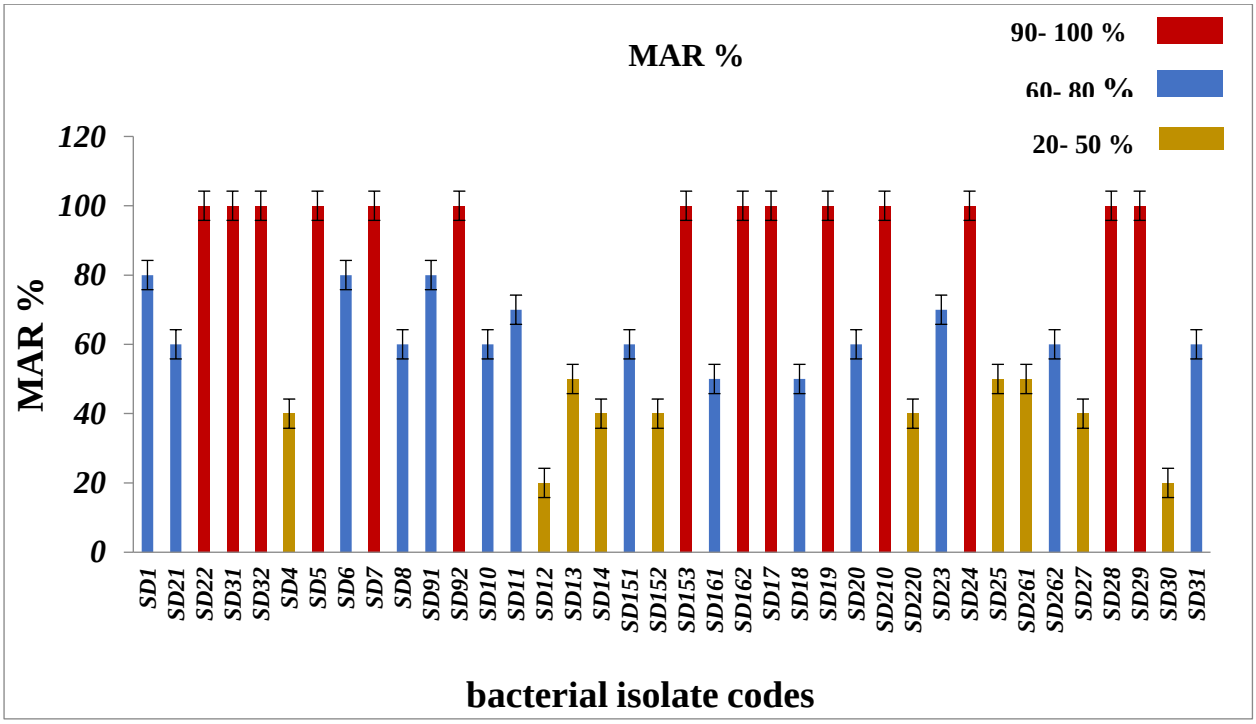


Figure (1a): Multiple-Antibiotic Resistant % of bacterial isolates from El-Demerdash hospital against ten antibiotic discs.

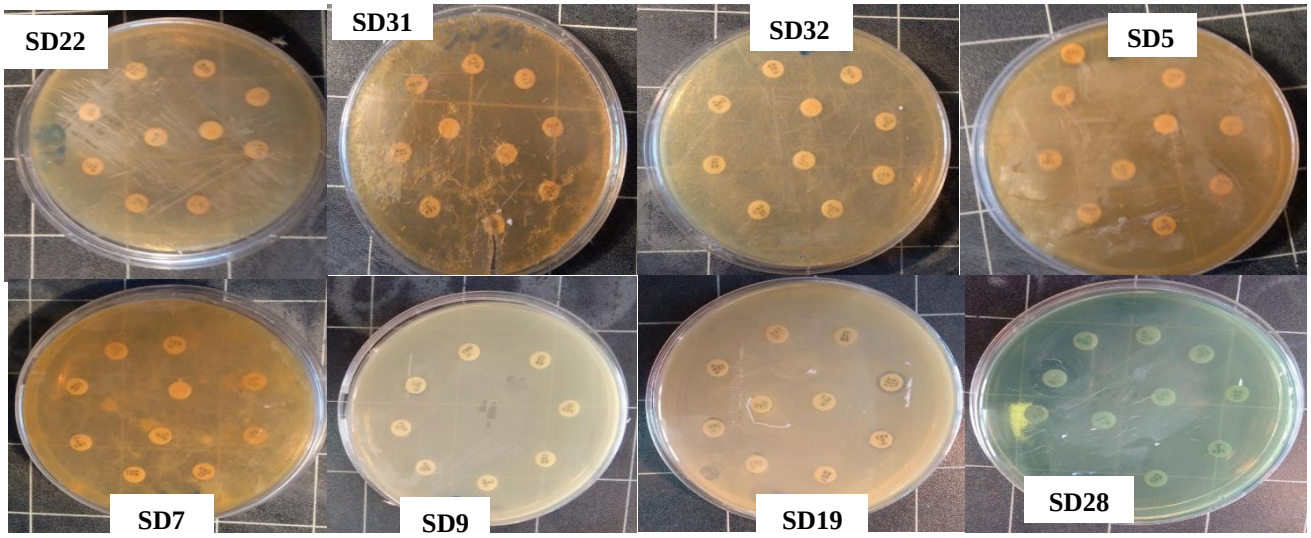


Figure (1b): Antibiotic sensitivity test of bacterial isolates from El- Demerdash hospital against 10 antibiotic discs.

Table (2): Screening to evaluate the efficacy of twenty antimicrobial agents against isolated bacteria.

Sample code	FA 10µg	C 30 µg	CAZ 30 µg	Ox 1 µg	CES 105 µg	CEP 75 µg	AX 25 µg	DA 2µg	TE 30 µg	MET 5µg	NOR 10 µg	AM 10 µg	E 15µg	B 10 µg	AZM 15 µg	K 30 µg	S 10µg	N 30µg	SAM 20µg	CEC 30µg	MAR %
SD22	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100
SD31	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100
SD32	15± 0.57	20.6± 0.62	R	R	R	13 ±0 .57	10.6± 0.438	R	18 .3 ±0 .438	R	R	R	R	R	R	R	10.7±1 .009	R	R	R	70
SD5	R	R	10 ±0 .4	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	95
SD7	R	R	R	R	R	R	14 ±0 .438	R	R	R	R	R	R	R	R	R	R	R	R	R	95
SD92	22± 1.527	16 ± 0.57	R	R	R	R	R	R	14 .6 ± 0. 438	R	R	R	R	R	R	R	R	24.7 ± 1.081	12. 3±0 .438	R	75
SD153	R	R	R	R	R	R	R	R	R	R	R	R	R	R	10. 7± 0.438	R	R	R	R	R	95

SD162	10.3 ±0.4 3	15 ±0 .57	R	R	R	R	15. 6± 0.8 33	R	R	R	R	R	R	R	11 ±0. 57 7	R	R	R	R	R	80
SD17	R	R	R	R	10.3 ±0.4 38	11. 6± 0.4 38	R	R	R	R	R	R	R	R	R	10 .3 ±0 .4 38	R	R	R	R	85
SD19	R	R	R	R	R	R	R	12.7 ± 0.43 8	R	R	R	R	R	R	R	R	R	R	R	R	95
SD21 ….	26± 0.57	15. 6± 0.6 2	R	R	R	R	15. 6± 0.6 20	R	R	R	R	R	R	R	R	R	R	30± 1.09 6	R	R	80
SD24	R	11. ± 0.4 3	R	R	R	R	10. 3± 0.4 38	R	R	R	R	10. 7± 0.4 8	R	R	R	R	R	R	11. 7±0 .43 8	R	80
SD28	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	100
SD29	R	15. 3± 0.4 3	R	R	11.3 ±0.4 3	12. 6± 0.4 3	R	15.3 ±0.4 38	R	R	18. 7± 0.7 1	R	20. 3±0 .43 8	R	17 ±0. 57 7	12 .7 ± 0. 43 8	17± 0.5 77	18.7 ±0.7 13	R	R	45

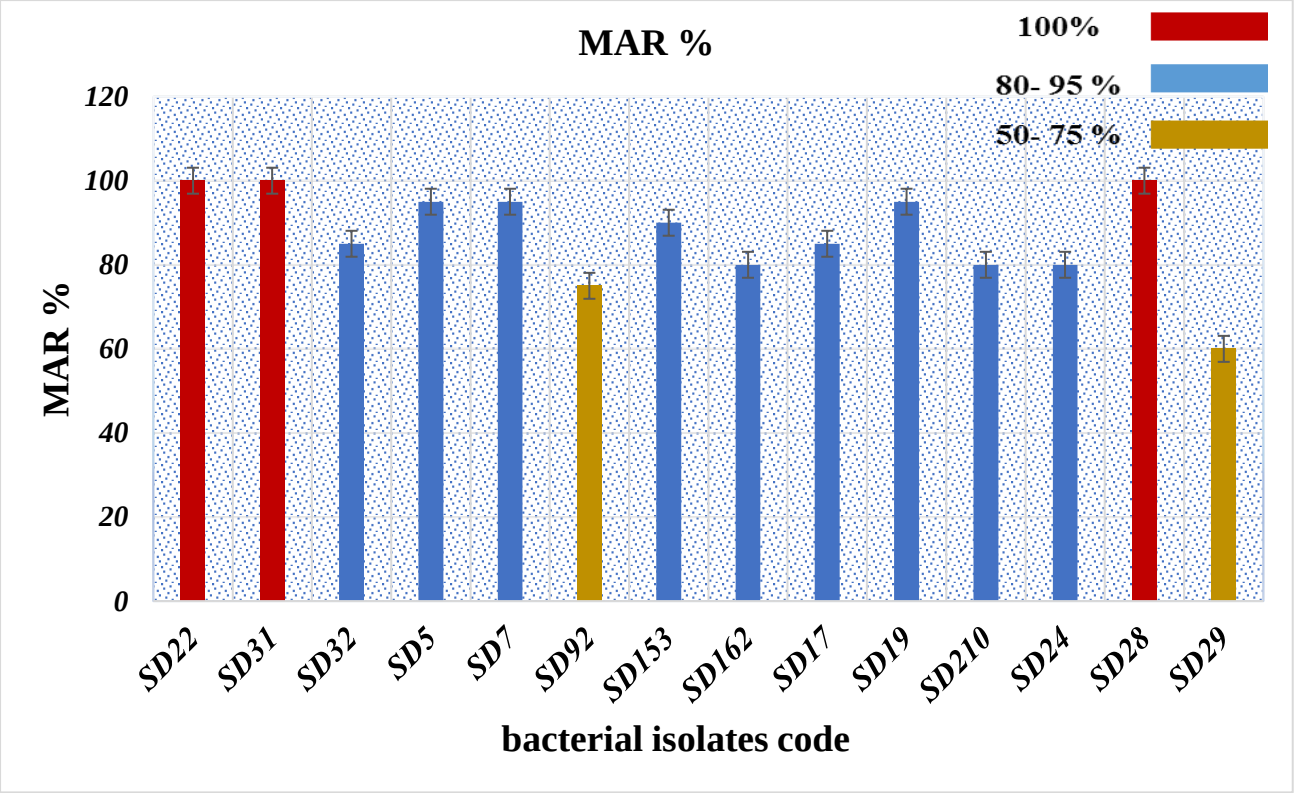


Figure (2a): Multiple-Antibiotic Resistant % of bacterial isolates from El- Demerdash hospital against twenty antibiotic discs.

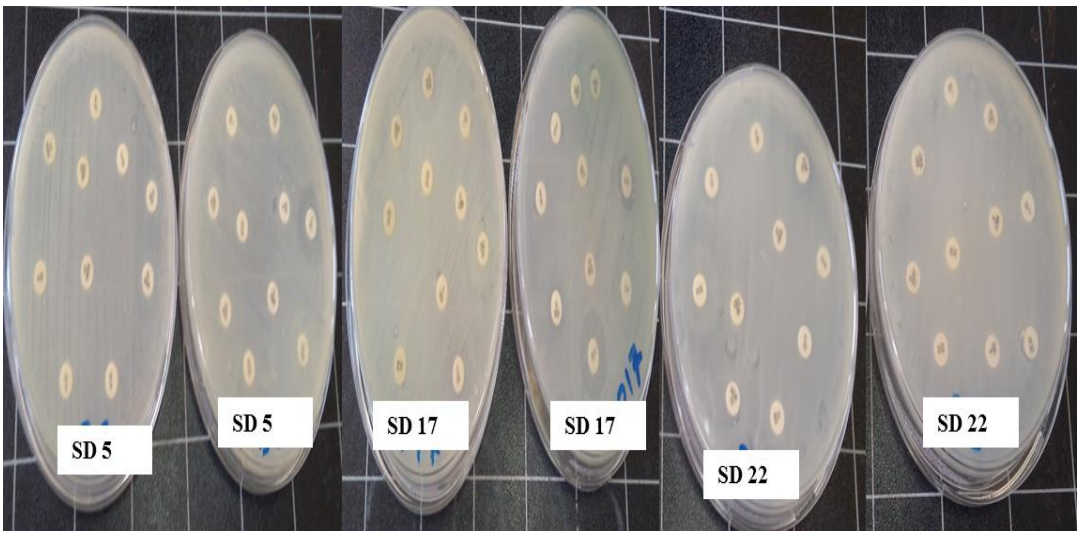


Figure (2b): Antibiotic sensitivity test of bacterial isolates from El- Demerdash hospital against 20 antibiotic discs.

3.3. Select the most potent bacterial isolates and identification them morphologically, biochemically, and molecularly

The most potent MDR isolates code SD22 and SD28 isolated from pus swabs (surgery) and bacterial isolate code SD31 isolated from wound swabs (burns). All isolated bacteria can't grow on mannitol salt agar but can grow on MacConkey agar. All isolates were catalase-positive and Gram-negative bacteria Figure (3). The manual biochemical tests were represented in Table (3). Automated biochemical identification using the automated Vitek 2 system (bioM´erieux, Marcy l'Etoile, France) was done for three isolates and results in Table (4). Also, molecular identification was done for all bacterial isolates showed in figures (4, 5, 6 and 7). The bacterial isolates code SD22, SD28 and SD31 were identified as *Klebsiella oxytoca*, *Pseudomonas aeruginosa,* and *Escherichia coli.* These results agreed with the result recorded by Mohammad *et al*., [35] who indicated that *Staphylococcus aureus* followed by *Escherichia coli* and *Pseudomonas* spp., were the most common bacteria linked to wound contagions.

Table (3): Primary biochemical tests of the most potent MDR bacteri.

organism / Test	SD22	SD28	SD31
Gram stain	-Ve	-Ve	-Ve
Catalase	+Ve	+Ve	+Ve
Citrate	-Ve	+Ve	-Ve
Gelatin	-Ve	+Ve	-Ve
Oxidase	-Ve	+Ve	-Ve
Indol	+Ve	-Ve	+Ve
Urease	-Ve	+Ve	-Ve
Methyl red test	-Ve	-Ve	+Ve
Voges proskour	+Ve	-Ve	-Ve
Nitrate reduction	+Ve	+Ve	+Ve
Motility test	-Ve	+Ve	+Ve

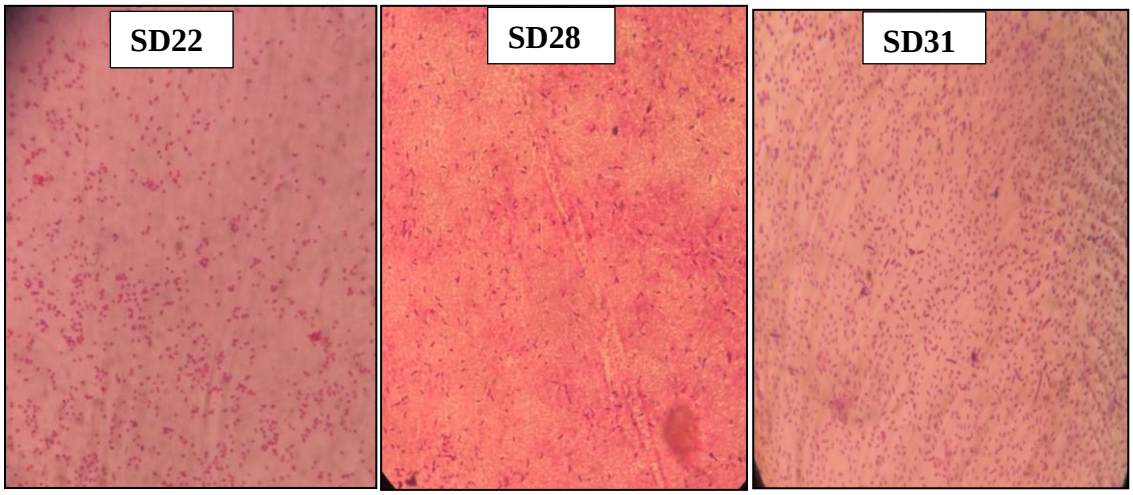


Figure (3): Gram stain of SD22, SD28, and SD31.

Table (4): Identification of the most potent bacterial isolate SD22, SD28, and SD31 by Vitek 2 system.

Character (test)	abbreviation	SD22	SD28	SD31
Ala-Phe-Pro-Arylamidase	APPA	+	-	-
Adonitol	ADO	+	-	-
L-Pyrrolydonyl- Arylamidase	PyrA	+	-	-
L-Arabitol	lARL	-	-	-
D-cellobiose	dCEL	+	-	-
B-glactosidase	BGAL	+	-	+
H_2S production	H_2S	-	+	-
Beta-N-acetyleglucosaminidase	BNAG	+	-	-
Glutamyle arylea midase pNA	AGLTp	-	-	-
D-glucose	dGLU	+	+	+
Gamma glutamyle transferase	GGT	+	+	-
Fermentation/ glucose	OFF	+	-	+
Beta-glucosidase	BGLU	+	-	-
D-maltose	dMAL	+	-	+
D-manitol	dMAN	+	+	+
D-mannose	dMNE	+	+	+
Beta-xylosidase	BXYL	+	-	-
Beta-alanine arylea midase pNA	BAlap	-	+	-
L-proline arylamidase	ProA	+	+	-
Lipase	LIP	-	+	-
Palatinose	PLE	+	-	-
Tyrosine arylamidase	TyrA	+	+	+
Urease	URE	-	+	-
D-sorbitol Salicin	dSOR	+	-	+
Saccharose/ sucrose	SAC	+	-	+
D-Tagatose	dTAG	-	-	-
D-trehalose	dTRE	+	-	+
Citrate (Sodium)	CIT	-	+	-
Malonate	MNT	+	+	-
5-Keto-Gluconate	5KG	-	-	-
L-lactate alkalinisation	1LATk	+	+	-
Alpha glucosidase	AGLU	-	-	-
Succinate alkalinisation	SUCT	+	+	-
Beta N-acetyl galactoseaminidase	NAGA	-	-	-
Alpha glactosidase	AGAL	+	-	+
Phosphatase	PHOS	+	+	-
Glycine arylamidase	GlyA	-	-	-
Decarboxylase base	ODEC			
Ornithine decarboxylase	ODC	-	-	+
Lysine decarboxylase	LDC	+	-	+
L-histidine assimilation	lHlSa	-	-	-
Coumarate	CMT	+	+	+
Beta- glucoronidase	BGUR	-	-	+
O/129 Resistance	O129R	+	+	+
Glu-Gly-Arg-Aryleamidase	GGAA	-	+	-
L-malate assimilation	lMLTa	-	+	-
ELLMAN	ELLM	-	-	+
L-lactate assimilation	lLATa	-	-	-

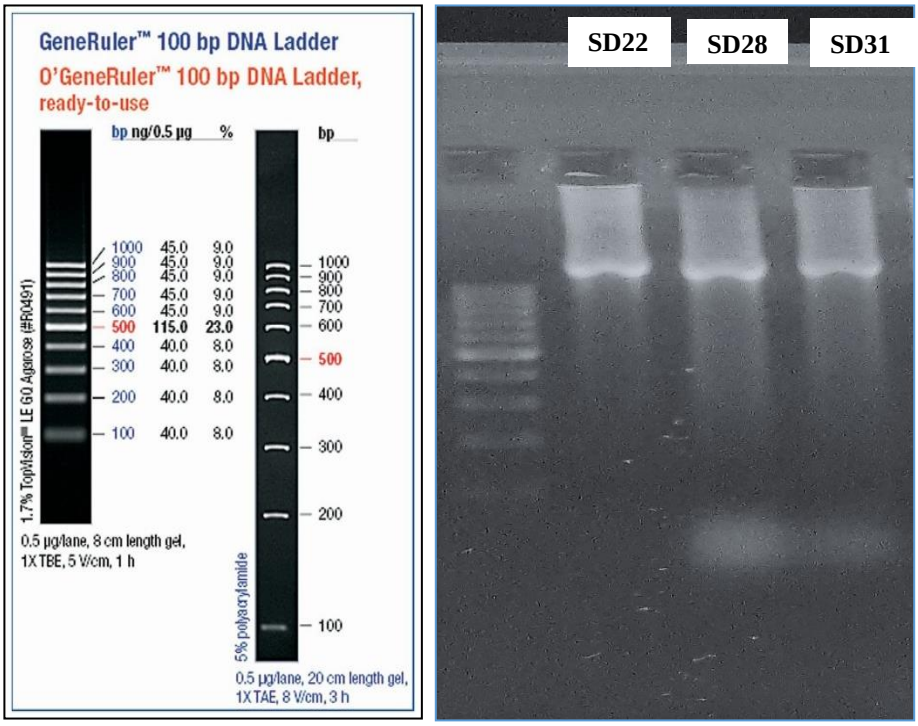
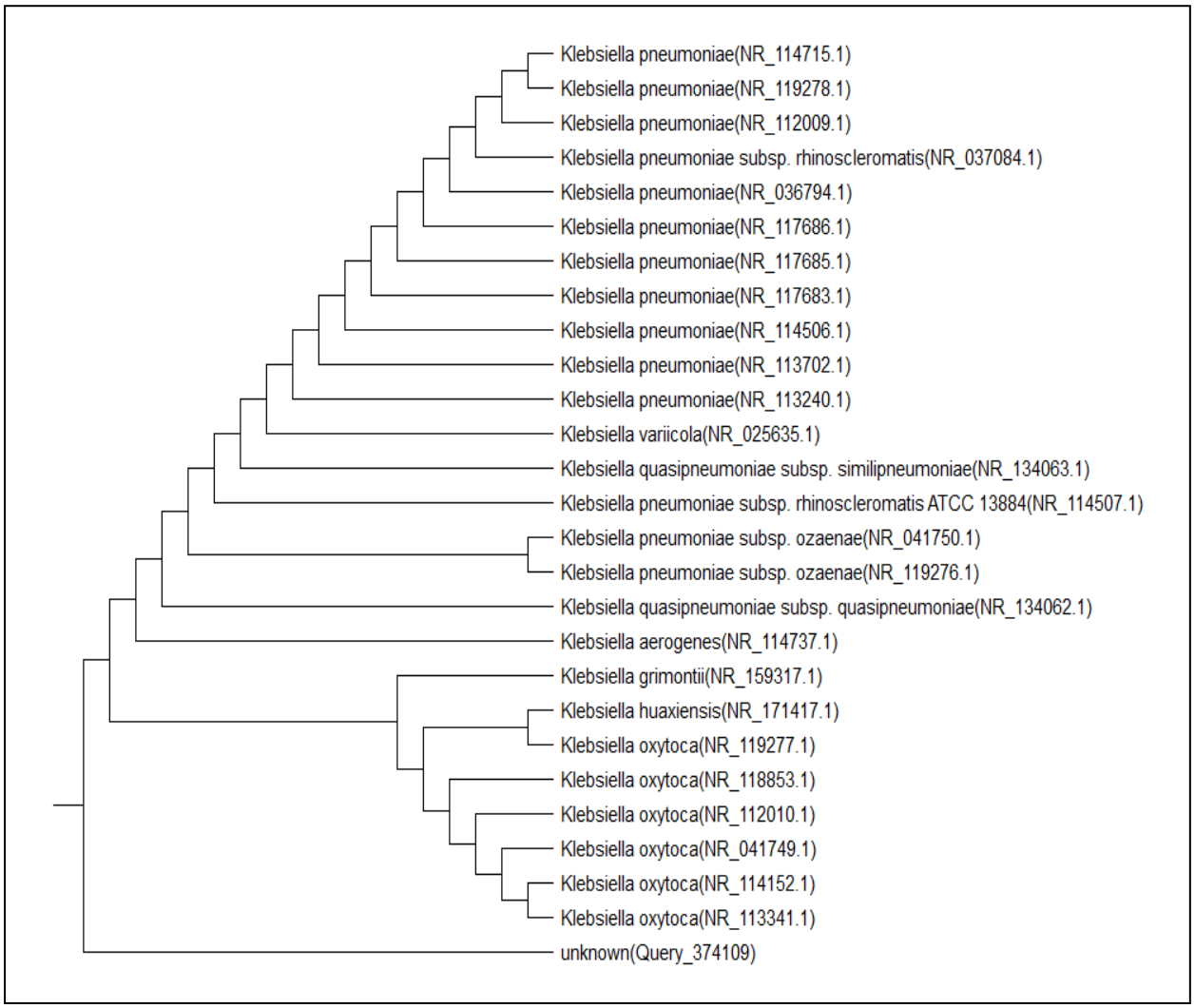
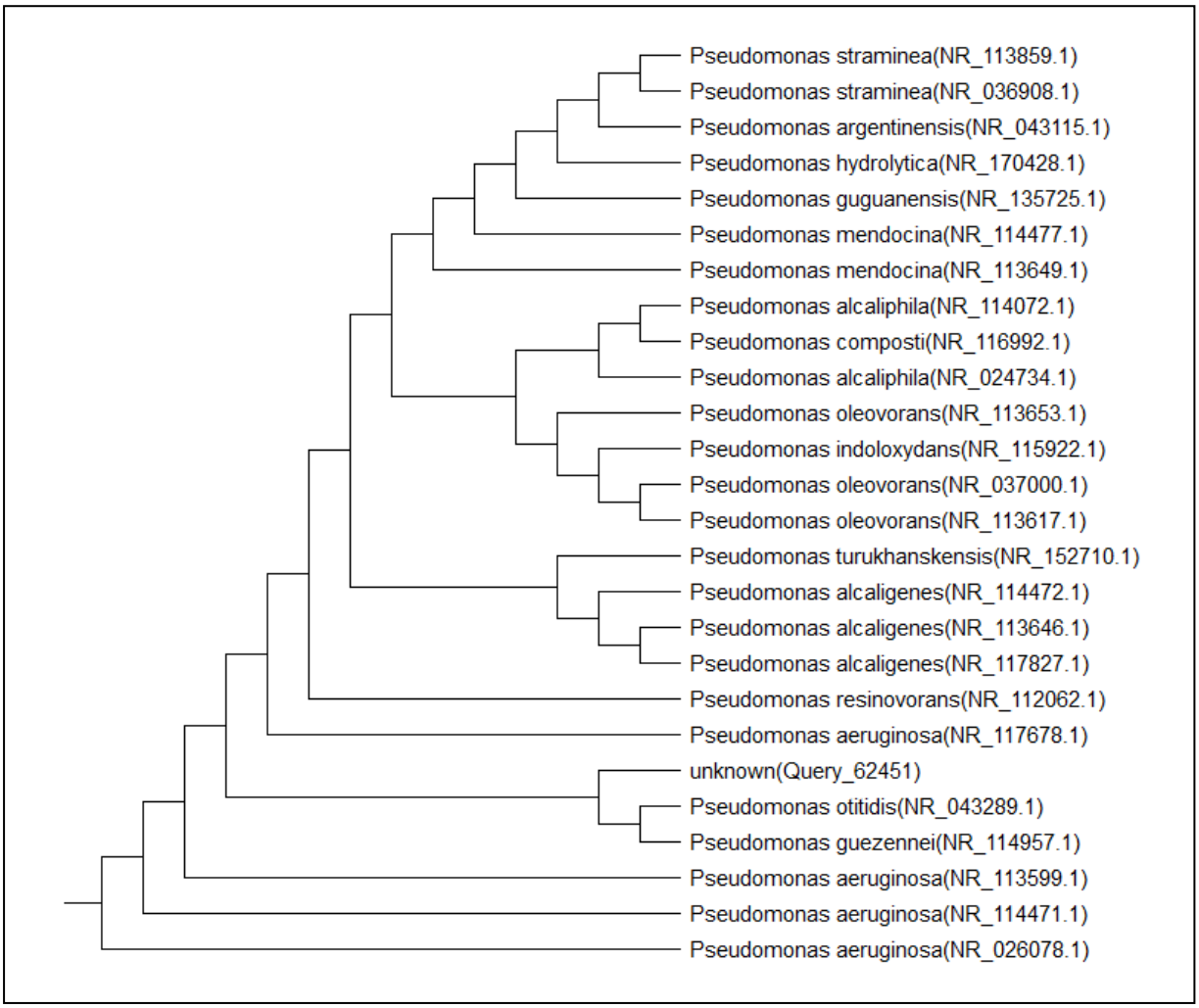


Figure (4): Gelelectrophorosis of the most potent bacterial isolate SD22, SD28, and SD31 with ladder.



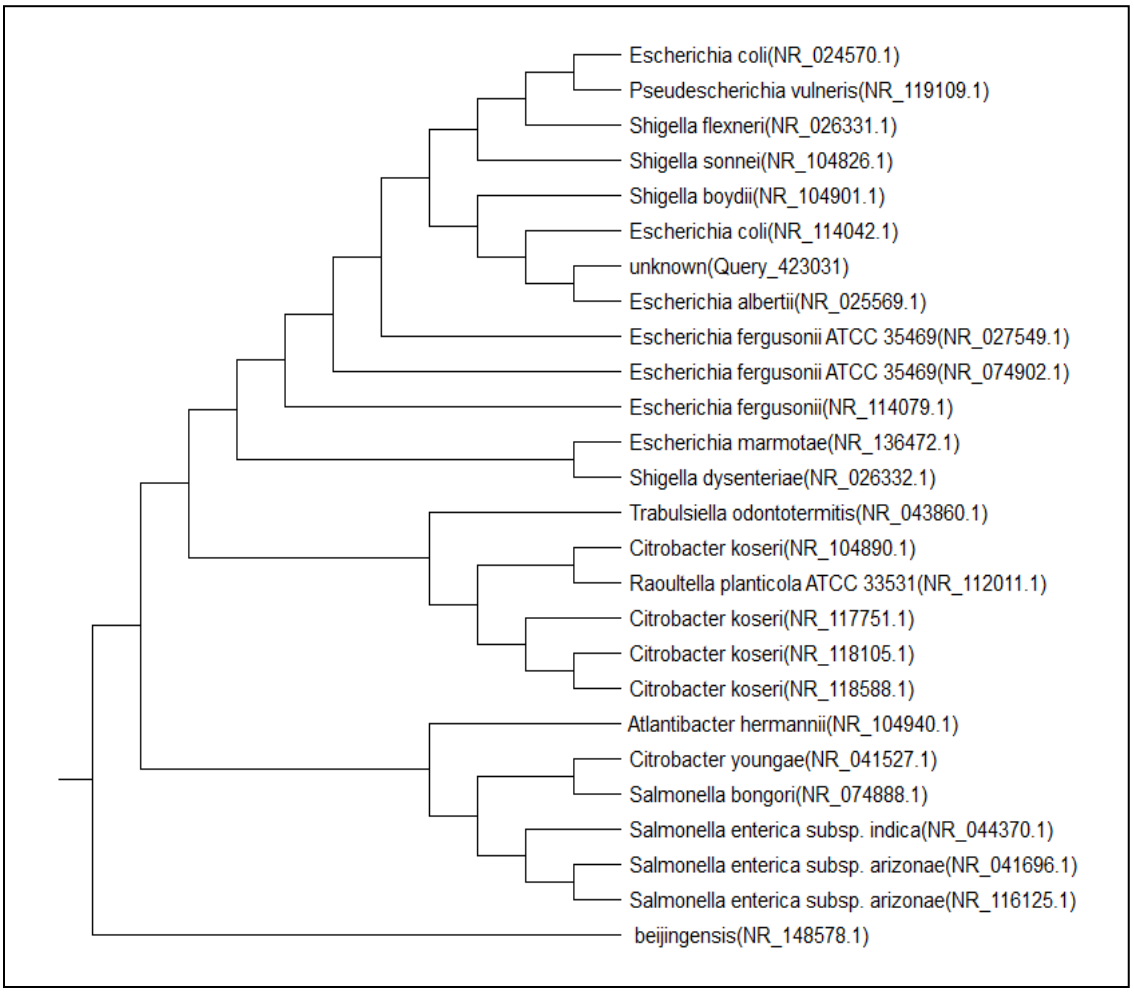
Where query sequence is isolated *Klebsiella oxytoca*

Figure (5): Phylogenetic tree instituted from the 16s rRNA sequence of bacterial isolate code SD22 and their related strains in Gene Bank.



Where query sequence is isolated *pseudomonas aeruginosa*

Figure (6): Phylogenetic tree formed from the 16s rRNA sequence of bacterial isolate code SD28 and their related strains in Gene Bank.



Where query sequence is isolated *Escherichia coli*

Figure (7): Phylogenetic tree constructed from the 16s rRNA sequence of bacterial isolate code SD31 and their related strains in Gene Bank

4. Conclusion

According to the obtained results, it can be concluded that the three bacterial isolates found in wound infection from central lab of El- Demerdash hospital were Gram negative and MDR bacteria as they showed resistance to all 30 antibiotic used from different classes (Aminoglycosides, quinolones, sulfonamides, Macrolides, Carbapenems**,** Tetracyclines, Chloramphenicol, glycopeptides and ß-Lactams). These bacterial isolates were identified as *klebsiella oxytoca, pseudomonas aeruginosa and Escherichia coli.*

5. Conflict of Interest

No conflict of interest exists.

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الملخص العربي

اتجاهات في تقييم كفاءة المضادات الحيوية المتعددة ضد السلالات البكتيرية المعرفة والمعزولة من الجروح في مستشفي الدمرداش، مصر

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الملخص العربي

اصبحت البكتريا المقاومة للعديد من الأدوية من اخطر المشاكل التي تواجه الصحة العامة العالمية حيث أنها تزيد من معدل الأصابة بالمرض وأيضا من معدل الوفيات ، وتؤدي ايضا الي عدم كفاءة المعالجة بإستخدام الأدوية وهذا بدوره يؤدي الي انتشار العدوي وإستمرارها.

لذلك فإن الهدف الرئيسي من هذه الدراسة هو تقييم كفاءة المضادات الحيوية المختلفة ضد السلالات البكتيرية المعزولة من عينات الجروح وتعريف أكثر العزلات المقاومة لهذه المضادات.

ولتحقيق هذا الهدف تم تجميع 50 عينة من مسحات الجروح المختلفة وهذه العينات تم الحصول عليها من المعمل المركزي للميكروبيولوجي بمستشفي الدمرداش.

تم عزل 89 عزلة بكتيرية من مسحات الجروح وزراعتها علي بيئات مختلفة وايضا اختبار حساسيتها ضد 30 نوع من المضادات الحيوية المختلفة بإستخدام طريقة انتشار اقراص المضادات الحيوية في الأجار.

ومن النتائج تم الحصول علي 3 عزلات بكتيرية مقاومة لكل المضادات الحيوية المستخدمة.

وقد تم تعريف هذه العزلات مورفولوجيا وبإستخدام الأختبارات البيوكميائية وايضا جينيا.

وقد عرفت هذه العزلات علي انها ايشرشيا كولاي و سيدوموناس ايروجينوزا و كليبسيلا اوكسيتوكا.

ونستخلص من هذه الدراسة أن الاستخدام العشوائي للمضادات الحيوية أدي الي ظهور سلالات معزولة من مرضي الجروح بمستشفي الدمرداش والمقاومة لثلاثين نوع من المضادات الحيوية المختلفة.