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Research Paper

Prevalence of multidrug resistance bacterial isolates from infected wound patients in Dhaka, Bangladesh: A cross-sectional study

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ABSTRACT

Introduction: Multidrug resistance (MDR) is threatening the adequate coverage of antibiotics. This study aimed to analyze the antimicrobial resistance pattern of bacterial isolates from wound infection and the scenario of multidrug resistance.

Methods: Microbiological culture results scripts of Medinova Medical Services LTD, representing non-repetitive various wound samples (post-surgical, trauma, superficial skin, burn) reported between January 2017 and March 2018, were retrieved and analyzed for pathogens and their antimicrobial resistance patterns using R version 3.5.3.

Results: Overall, 1266 bacterial isolates were obtained, and 850 (67.1%) were identified as MDR. The percentage of MDR among gram-positive and gram-negative bacterial isolates were 68.8% and 66.0%, respectively. Among isolates *Staphylococcus aureus* (n = 401), *Pseudomonas aeruginosa* (n = 200), and *Escherichia coli* (n = 193) were predominant. Vancomycin followed linezolid showed most activity against gram-positive bacteria. Whereas, Colistin was found to be the most active against most of the gram-negative bacterium except for the *Proteus* spp in sensitivity test. Although, carbapenem group was determined to be the best against Proteus spp. About 82% *Enterococcus* spp and 76% *Proteus* spp were MDR. Isolates from patients aged >60 years (AOR = 1.774 95%CI: 1.089–2.892) were more prone to becoming MDR in compared to other age group and was a significant determinant *(P = 0.02)* of MDR.

Conclusions: Our study revealed that the presence of MDR pathogens in wound infection was noteworthy. The findings of this study would assist in decision making of wound infection treatment.

1. Introduction

Bacterial infections caused by multidrug resistance (MDR) bacteria are a growing threat worldwide, including Bangladesh [1,2]. The World Health Organization (WHO) has already proclaimed antimicrobial resistance (AMR) as a public health threat and has urged different countries to develop an action plan to combat the imminent crisis [3].

Bacteria species isolated from various body samples have shown one or more resistance mechanisms to each of the major classes of antimicrobial agents [4,5]. However, wound provides a moist, warm, and nutritious environment conducive to microbial colonization, proliferation, and infection [6,7]. Infected wounds are characterized by the bacterial burden, chronic inflammation, and an unbalanced cellular defense mechanism [8]. The common bacterial pathogens associated with wound infection include *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, *Streptococcus pyogenes*, Proteus species, Streptococcus species, and Enterococcus species [9]. In developing countries like Bangladesh, wound infections are major health problems; a large

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number of people die daily of preventable and curable wound infections [10,11].

The spectra of bacteria causing infections and their susceptibility pattern have been found to vary from one setting to another [12]. Resistance develops naturally over time, but the misuse of antibiotics in humans and animals is rapidly accelerating the process. Antimicrobial resistance often occurs through the inhibition of specific antimicrobial pathways such as cell wall synthesis, nucleic acid synthesis, ribosome function, protein synthesis, folate metabolism, and cell membrane function [13–15]. The absence of strict regulations in the sales of antimicrobials is also a driving factor in the access and misuse of antimicrobials. In most developing countries, antimicrobials can be purchased without a medical prescription [16].

In Bangladesh, it is also a common practice that antibiotics can be purchased without a prescription from a registered doctor; this leads to misuse of antibiotics by the public, thus, contributing to the emergence and spread of antimicrobial resistance [17]. Few studies have been conducted previously in Bangladesh to see the AMR pattern of the various specimen. However, a study targeting MDR wound infection is very scarce. Therefore, this study aimed to analyze the AMR and MDR pattern of bacterial isolates from wound infections patients.

2. Methods

2.1. Study site and period

From January 2017 to March 2018, microbiological culture results and their sensitivity reports of Medinova Medical Services LTD (secondary data) for various wound infection (surgical incisions, burns, abscess, and traumatic wounds, etc.) were analyzed. The study has been completed in line with the STROCSS criteria [18]. Medinova Medical Services LTD is an approved Medical Check-Up Center of the Executive Board of The Health Minister's Council for G.C.C (Gulf Co-operation Council) States, bearing G.C.C Computer Code No. 05/01/18. It is one of the member medical centers under GAMCA, Dhaka-Bangladesh. GAMCA (GCC approved medical centers association) an association of medical centers, controls all medical centers under GAMCA, and ensures strict compliance of rules, regulations & instructions issued from GCC HQ time to time by all the medical centers. Incomplete filling scripts were excluded from the analysis.

2.2. Data collection

All microbiological tests, result collection, and report maintenance were done by trained microbiologist of Medinova Medical Services LTD [19]. The antibiotic susceptibility examination was done using the disc diffusion method (Kirby-Bauer Method) according to the National Committee for Clinical Laboratory Standards. Samples with colony counts <105 cfu/mL were omitted. Quality assurance has been strictly controlled by the Clinical and Laboratory Standards Institute (CLSI) according to the "Performance Standards for Antimicrobial Susceptibility Testing" (i.e., the CLSI M100-S24 manual) [20]. As there are no agreed international standards for disc diffusion method for colistin, test was done by following Etest and disk diffusion methods as the standard [21].

Antibiotic susceptibility was tested for Azithromycin (15 μg), Amoxyclav (20 + 10 μg), Amikacin (30 μg), Gentamycin (10 μg), Cotrimoxazole (1.25 + 23.75 μg), Cephradine (30 μg), Cefuroxime (30 μg), Ceftazidime (30 μg), Cefixime (5 μg), Ceftriaxone (30 μg), Ciprofloxacin (5 μg), Colistin Sulphate (10 μg), Imipenem (10 μg), Meropenem (10 μg), Vancomycin (30 μg), Linezolid (30 μg), Piperacillin + Tazobactam (100 + 10 μg). Antibiotics discs were supplied by Mast group Ltd. Merseyside, UK. Intermediate susceptibility results were considered as resistant in the analysis.

We were not able to find any standard definition of multidrug-resistance (MDR). We observed that many previous studies had used the definition of MDR as resistance against three or more classes of antibiotics both for Gram-positive [22–24] and Gram-negative [25–28] bacteria. Seven frequently used classes of antibiotics were used to analyze MDR.

2.3. Data analysis

Data were checked for completeness and consistency. Data were entered, cleaned, and analyzed using R version 3.5.3. Descriptive statistics like frequencies and percentages were used to determine the pattern of AMR and MDR. Multinomial logistic regression was done to find out the strength of association, and P-value ≤ 0.05 was considered as statistically significant.

3. Result

3.1. Distribution of wound infections

In this study, microbiological culture result scripts for various types of wound samples were screened, and their antibiotic sensitivity reports were analyzed. After the screening of culture result script 1266 isolates of 12 types of Bacteria. Of them, 738 isolates contained eight types of gram-negative [*Acinetobacter Spp* (n = 82), *Citrobacter* spp (n = 32), *Enterobacter* spp (n = 53), *Escherichia coli* (n = 193), *Klebsiella* spp (n = 110), *Proteus* spp (n = 58), *Pseudomonas aeruginosa* (n = 200), *and Serratia* spp (n = 8)] (Fig. 1) and 528 isolates contained four types of gram-positive bacteria [*Enterococcus* spp (n = 60), *Staphylococcus aureus* (n = 401), *Coagulase-negative Staphylococci* (n = 54), *and Streptococcus pyogenes* (n = 13)] (Fig. 2). Among the gram-negative bacterial wound infections *Pseudomonas aeruginosa* (27.1%) and *Escherichia coli* (26.2%) were the most predominant and, among the gram-positive bacteria *Staphylococcus aureus* (75.9%) infection was found to be the most (Figs. 1 and 2).

3.2. Antibiotic resistance pattern of gram-negative bacteria

Overall, 13 types of antibiotics were tested against gram-negative bacteria. Of them, colistin (CST) retained most activity against most of the gram-negative bacteria except *Proteus* spp. The carbapenem group (imipenem and meropenem) followed by piperacillin-tazobactam were found to be most active antimicrobials in sensitivity test against *Proteus* spp. isolates from wound infection (Table 1).

3.3. Antibiotic resistance pattern of gram-positive bacteria

On the other hand, a total of 11 types of antimicrobials were tested against gram-positive bacterial isolates. From those, vancomycin (VAN) followed by linezolid (LZD) showed most activity against the isolates. No vancomycin-resistant *Enterococcus* spp were observed in our study. However, 3 (0.7%) *Staphylococcus aureus* were found resistant to vancomycin. Moreover, 2 (3.3%) isolates of *Enterococcus* spp and 4 (1%) of *Staphylococcus aureus* were found resistant to linezolid (Table 2). Other than antimicrobials of Table 2, *Staphylococcus aureus* was tested against methicillin, and we observed that 137 (34.16%) isolates were Methicillin-resistant *Staphylococcus aureus* (MRSA).

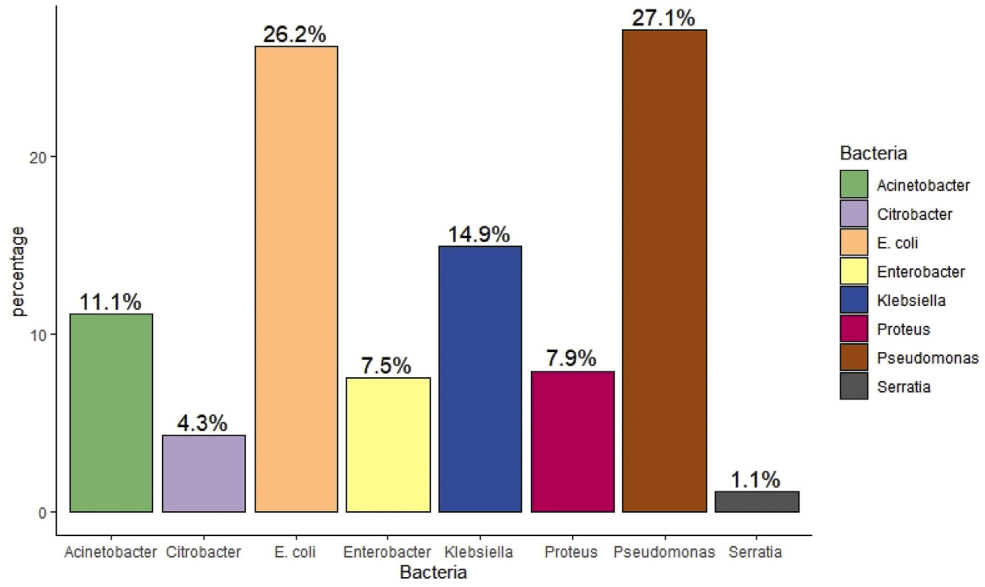

Fig. 1. Distribution of the wound infection by the gram-negative bacteria.

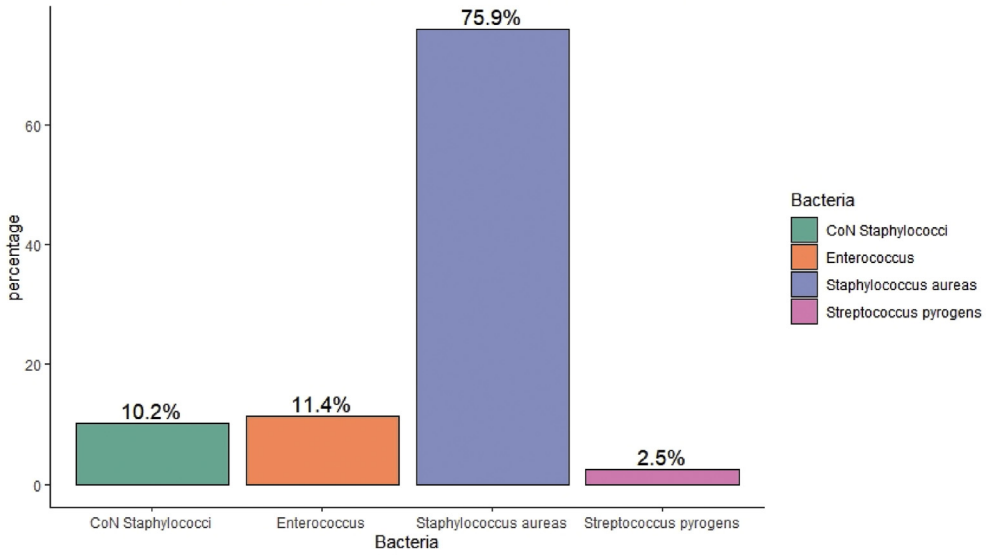

Fig. 2. Distribution of the wound infection by the gram-positive bacteria.

3.4. Multi-drug resistance pattern of the gram-positive and gram-negative bacteria

Of the total 1266 bacterial isolates, 850 (67.1%) were identified as multidrug resistance (MDR) according to the definition of MDR used in our study. Among the isolated gram-negative bacteria, *Proteus* spp (75.9%) followed by *Pseudomonas aeruginosa* (72.5%) showed the highest percentage of MDR and *Klebsiella* spp *(59.1%)* followed by *Escherichia coli* (59.6%) exhibited the lowest rate. A total of 54 (7.5%) gram-negative isolates were found sensitive to all seven classes of antibiotics used to determine MDR. However, 2 (0.3%) were identified resistant against all of the seven classes, and 94 (12.7%) were found resistant to six classes of antimicrobials. In the case of gram-positive bacteria, *Enterococcus* spp (81.7%) and *Staphylococcus aureus* (68.3%) exhibited a high percentage of MDR. Only, 2 (0.5%) isolates of *Staphylococcus aureus* were detected resistant to all seven classes of antimicrobials. In this study, it was also observed that gram-positive bacteria (68.8%) from wound infection are slightly more prone to become MDR compared to the gram-negative bacterial isolates (66.0%) (Tables 3 and 4).

3.5. Logistic regression analysis of independent variables and MDR status

We have fitted a multinomial logistic regression model to find out the predictors of Multidrug resistance in our study settings (see Table 4). Isolates from patients aged >60 years (AOR = 1.774 95% CI: 1.089–2.892) were more prone to becoming MDR in compared to other age group and was a significant determinant *(P = 0.02)* of MDR. Moreover, wound sample isolates from children also showed a relatively higher percentage (72.8%) of MDR (Table 5).

Table 1
Antibiotic Resistance pattern of Gram-negative bacteria from Wound infection (Antimicrobials with their frequency and percentage of resistance).

Bacteria	Isolates (n) Resistance to Antibiotics												
	AMK	AMC	CFM	CAZ	CRO	CXM	CIP	CST	GEN	IMP	MEM	TMP/SMX	TZP
Acinetobacter spp *(n = 82)*	34	64	75	56	68	65	57	4	45	30	33	49	40
Resistance Percentage (%)	41.5	78.0	91.5	68.3	82.9	79.3	69.5	4.9	54.9	36.6	40.2	59.8	48.8
Citrobacter spp *(n = 32)*	7	29	31	24	26	29	22	0	17	4	5	21	15
Resistance Percentage (%)	21.9	90.6	96.9	75.0	81.3	90.6	68.8	0.0	57.1	12.5	15.6	65.6	46.9
Enterobacter spp *(n = 55)*	12	52	51	43	43	49	41	3	36	4	5	38	28
Resistance Percentage (%)	21.8	94.5	92.7	78.2	78.2	89.1	74.5	5.5	65.5	7.3	9.1	69.1	50.9
Eschwerichia coli (n = 193)	20	151	149	135	139	143	148	7	67	11	13	117	65
Resistance Percentage (%)	10.4	78.2	77.2	69.9	72.0	74.1	76.7	3.6	34.7	5.7	6.7	60.6	33.7
Klebsiella spp *(n = 110)*	25	86	82	71	74	80	82	1	42	14	15	65	35
Resistance Percentage (%)	22.7	78.2	74.5	65.5	67.3	72.7	74.5	0.9	38.2	12.7	13.6	59.1	31.8
Proteus spp *(n = 58)*	25	34	32	27	31	38	44	56	30	1	1	42	4
Resistance Percentage (%)	43.1	58.6	55.2	46.6	53.4	65.5	75.9	96.6	51.7	1.7	1.7	72.4	6.9
Pseudomonas aeruginosa (n = 200)	107	195	197	127	196	196	139	7	124	56	64	193	82
Resistance Percentage (%)	53.5	97.5	98.5	63.5	98.0	98.0	69.5	3.5	62.0	28.0	32.0	96.5	41.0
Serratia spp *(n = 8)*	4	6	4	4	4	4	0	0	1	0	0	5	0
Resistance Percentage (%)	50.0	75.0	50.0	50.0	50.0	50.0	0.0	0.0	12.5	0.0	0.0	62.5	0.0

AMK: Amikacin; AMC: Amoxiclav; CFM: Cefixime; CAZ: Ceftazidime; CRO: Ceftriaxone; CXM: Cefuroxime; CIP: Ciprofloxacine; CST: Colistin; GEN: Gentamycin; IMP: Imipenem; MEM: Meropenem; TMP/SMX: Cotrimoxazole; TZP: Piperacillin-Tazobactam.

Table 2
Antibiotic Resistance pattern of Gram-positive bacteria from Wound infection (Antimicrobials with their percentage of resistance).

Bacteria	Isolates (n) Resistance to Antibiotics										
	AMC	AZM	CFM	CRO	CXM	RAD	CIP	GEN	TMP/SMX	VAN	LZD
Enterococcus spp *(n = 60)*	13	43	36	27	26	32	54	29	51	0	2
Resistance Percentage (%)	21.7	71.7	60.0	45.0	43.3	53.3	90.0	48.3	85.0	0.0	3.3
Staphylococcus aureus (n = 401)	98	309	398	204	79	122	315	81	130	3	4
Resistance Percentage (%)	24.4	77.1	99.3	50.9	19.7	30.4	78.6	20.2	32.4	0.7	1.0
CoNS (n = 54)	19	43	53	23	3	7	40	3	19	0	0
Resistance Percentage (%)	35.2	79.6	98.1	42.6	5.6	13.0	74.1	5.6	35.2	0.0	0.0
Streptococcus pyogenes (n = 13)	0	8	1	0	0	0	9	6	8	0	0
Resistance Percentage (%)	0.0	61.5	7.7	0.0	0.0	0.0	69.2	46.2	61.5	0.0	0.0

CoNS: *Coagulase-negative Staphylococci*; AMC: Amoxiclav; AZM: Azithromycin; CFM: Cefixime; CRO: Ceftriaxone; CXM: Cefuroxime; RAD: Cephradine; CIP: Ciprofloxacin; GEN: Gentamycin; TMP/SMX: Cotrimoxazole; VAN: Vancomycin; LZD: Linezolid.

4. Discussion

Our study has depicted the list of microorganisms commonly associated with wound infection in Dhaka city and identified the prevalence of MDR bacteria in wound infection. Age, Sex, and Gram staining were considered as independent variables. However, without patients' age (>60 years), no other variable was found as a significant determinant for Multidrug resistance by bacterial isolates. Our study revealed that bacteria isolated from children and older aged patients with wound infection are more prone to become MDR than bacteria from other age groups. Isolates from patients aged >60 years (AOR = 1.774 95% CI: 1.089–2.892) had 1.77 times more chance of becoming MDR in comparison to bacteria isolated young-adults patient (20–39 years). Moreover, wound sample isolates from children also showed a relatively higher percentage (72.8%) of MDR.

We have found that *Staphylococcus aureus* followed by *Pseudomonas* spp., and *Escherichia coli* were the most prevalent organisms associated with wound infection, which is supported by several studies conducted previously [29,30].

Our investigation revealed that colistin (CST) is the most active antimicrobial in sensitivity test for most of the gram-negative bacteria except *Proteus* spp. More than 96% of *Proteus* spp. were found resistant against colistin. For other gram-negative bacterial isolates, it was ranging from 1% to 5.5%. Carbapenem group (imipenem & meropenem) followed by piperacillin-tazobactam showed the most activity against *Proteus* spp. in sensitivity test. Several other types of bacteria also showed a low percentage of resistance against carbapenems. These findings are also comparable to a previously conducted Systematic Review and Meta-analysis [31].

In our analysis, it was also observed that vancomycin (VAN) followed linezolid (LZD) were the most active antimicrobials in sensitivity against gram-positive bacterial species includes *Enterococcus* spp. and *Staphylococcus aureus*. There was no vancomycin-resistant enterococcus (VRE) observed in our study; however, 3 (0.7%) *Staphylococcus aureus* were resistant to vancomycin. Moreover, 3.3% *Enterococcus* spp. and 1% *Staphylococcus aureus* were found resistant against linezolid. Studies recently conducted in India and Colombia also revealed similar findings [32,33].

This study also revealed that gram-positive bacteria from wound infection show a higher percentage (69%) of MDR in compared to gram-negative (66%) bacteria. The overall MDR rate of gram-positive bacteria in our study is slightly lower than the research conducted in Ethiopia [29] but higher than 65.2% [34] and 52.7% [35] the study was carried out several years before. The possible explanation for such unevenness might be the variety in study population where previous studies solely included hospitalized inpatients where higher MDR strains are expected. On the other hand, our study consists of both hospitalized and non-hospitalized patients. Among the gram-negative bacteria isolated, *Proteus* spp. (75.9%) followed by *Pseudomonas aeruginosa* (72.5%) Showed the highest percentage of MDR and *klebsiella* spp. (59.1%) followed by *Escherichia coli* (59.6%) exhibited the lowest percentage. The overall MDR rate in the case of gram-negative bacteria in our study is higher than the previously conducted studies [28,34].

Table: 3
MDR pattern of Gram-negative bacteria isolated from infected wounds.

Bacteria	R0 (%)	R1 (%)	R2 (%)	R3 (%)	R4 (%)	R5 (%)	R6 (%)	R7 (%)	MDR (%)	Antimicrobial class used to define MDR
Acenetobacter spp	4 (4.9)	11 (13.4)	16 (19.5)	8 (9.8)	12 (14.6)	10 (12.2)	20 (24.4)	1 (1.2)	51 (62.2)	Penicillin (piperacillin),
Citrobacter	1 (3.1)	4 (12.5)	4 (12.5)	11 (34.4)	6 (18.8)	4 (12.5)	2 (6.3)	0 (0.0)	23 (71.9)	Aminoglycosides
Enterobacter spp	2 (3.6)	6 (6.9)	8 (14.5)	15 (27.3)	15 (27.3)	4 (7.3)	4 (7.3)	1 (1.8)	39 (70.9)	(Amikacin), Cephalosporin
Escherichia coli	24 (12.4)	20 (10.4)	34 (17.6)	57 (29.5)	37 (19.2)	16 (8.3)	5 (2.6)	0 (0.0)	115 (59.6)	(Cefixime),
Klebsiella spp	21 (19.1)	8 (7.3)	16 (14.5)	28 (25.5)	17 (15.5)	7 (6.4)	13 (11.8)	0 (0.0)	65 (59.1)	Quinolone (Ciprofloxacin),
Proteus spp	0 (0.0)	10 (17.2)	4 (6.9)	13 (22.4)	9 (15.5)	21 (36.2)	1 (1.7)	0 (0.0)	44 (75.9)	Sulfonamides
Pseudomonas aeruginosa	0 (0.0)	5 (2.5)	50 (25.0)	30 (15.0)	30 (15.0)	36 (18.0)	49 (24.5)	0 (0.0)	145 (72.5)	(Cotrimoxazole), Colistin
Serratia spp	2 (25.0)	1 (12.5)	0 (0.0)	3 (37.5)	2 (25.0)	0 (0.0)	0 (0.0)	0 (0.0)	5 (62.5)	(Polypeptide), Carbapenem
Gram-negative Bacteria	54 (7.3)	65 (8.8)	132 (17.9)	165 (22.4)	128 (17.3)	98 (13.3)	94 (12.7)	2 (0.3)	487 (66.0)	(Meropenem)

R0: Sensitive against all selected antibiotic class; **R1:** Resistant to at least one antibiotic class; **R2**: Resistant to two antibiotic class; **R3:** Resistant to three antibiotic class; **R4:** Resistant to four antibiotic class; **R5:** Resistant to five antibiotic class; **R6:** Resistant to six antibiotic class; **R7:** Resistant to all seven antibiotic class; **MDR:** Resistant to at least three antibiotic class.

Table 4
MDR pattern of selected Gram-positive bacteria isolated from infected wounds.

Bacteria	R0 (%)	R1 (%)	R2 (%)	R3 (%)	R4 (%)	R5 (%)	R6 (%)	R7 (%)	MDR (%)	Antimicrobial class used to define MDR
CONS	0 (0.0)	4 (7.4)	14 (25.9)	18 (33.3)	18 (33.3)	0 (0.0)	0 (0.0)	0 (0.0)	36 (66.7)	Glycopeptide (Vancomycin),
Enterococcus spp	1 (1.7)	3 (5.0)	7 (11.7)	14 (23.3)	20 (33.3)	14 (23.3)	1 (1.7)	0 (0.0)	49 (81.7)	Aminoglycosides (Gentamycin),
Streptococcus pyogenes	0 (0.0)	2 (15.4)	7 (53.8)	0 (0.0)	4 (30.8)	0 (0.0)	0 (0.0)	0 (0.0)	4 (30.8)	Cephalosporin (Cefixime),
Staphylococcus aureus	1 (0.2)	27 (6.7)	99 (24.7)	140 (34.9)	82 (20.4)	48 (12.0)	2 (0.5)	2 (0.5)	274 (68.3)	Quinolone (Ciprofloxacin),
Gram- positive Bacteria	2 (0.4)	36 (6.8)	127 (24.1)	172 (32.6)	124 (23.5)	62 (11.7)	3 (0.6)	2 (0.4)	363 (68.8)	Sulfonamides (Cotrimoxazole), Oxazolidinones (Linezolid), Macrolides (Azithromycin)

R0: Sensitive against all selected antibiotic class; **R1:** Resistant to at least one antibiotic class; **R2**: Resistant to two antibiotic class; **R3:** Resistant to three antibiotic class; **R4:** Resistant to four antibiotic class; **R5:** Resistant to five antibiotic class; **R6:** Resistant to six antibiotic class; **R7:** Resistant to all seven antibiotic class; **MDR:** Resistant to at least three antibiotic class.

Table 5
Logistic regression analysis of independent variables and MDR pattern.

Variable	Category	Resistance Type		Estimate	AOR (95% CI)	*P*-value
		MDR	Non-MDR			
Age	0–9 years	83 (72.8%)	31 (27.2%)	0.356	1.428 (0.904–2.257)	0.13
	10–19 years	113 (66.5%)	57 (33.5%)	0.057	1.059 (0.728–1.541)	0.76
	20–39 years	294 (65.0%)	158 (35.0%)	Reference	Reference	Reference
	40–60 years	278 (65.7%)	145 (34.3%)	0.038	1.038 (0.785–1.374)	0.79
	>60 years	82 (76.6%)	25 (23.4%)	0.573	1.774 (1.089–2.892)	**0.02***
Sex	Female	355 (68.4%)	164 (31.6%)	0.101	1.106 (0.868–1.408)	0.42
	Male	495 (66.3%)	252 (33.7%)	Reference	Reference	Reference
Gram stain	Negative	487 (66.0%)	251 (34.0%)	−0.103	0.902 (0.708–1.149)	0.40
	Positive	363 (68.8%)	165 (31.3%)	Reference	Reference	Reference

*P $\leq$ 0.05 was considered as statistically significant (indicated in bold).

Gram-positive bacteria *Enterococcus* spp. (81.7%) and *Staphylococcus aureus* (68.3%) possesses a high percentage of MDR. Moreover, an isolate of both *Acinetobacter* spp. and *Enterobacter* spp. showed all seven classes of antibiotics examined against gram-negative organisms in our study. *Staphylococcus aureus* isolated from 2 different patients also showed resistance to all seven classes of antibiotics tested against gram-positive bacteria, which is a concerning factor for the authorities of our health sector. The percentage of MRSA in wound infection was determined at 34.16%, which is in line with the previously conducted studies in Bangladesh [36]. The deviation we have found that could result in the difference of our geography and the source of our specimens along with other things.

Besides several important outcome the study has several limitations including the use of disk-diffusion method for the antimicrobial susceptibility testing, which have limited reliability. Moreover, study was conducted based on the data of one diagnostic center in Dhaka city. The would be much more generalized if more geographical area was covered. A multi-level analysis with several districts (geographical variation) would help to assess the overall situation.

5. Conclusions

This study revealed that *Acinetobacter* spp, *Enterobacter* spp, *Escherichia coli*, *Klebsiella* spp, *Proteus* spp, *Pseudomonas* spp, and *Staphylococcus aureus* were the most common isolates from infected wound samples. Isolates showed high levels of resistance to most of the commercially available antibiotics. Antibiotics such as glycopeptide (vancomycin) and oxazolidinones (linezolid) found effective against gram-positive isolates. Whereas carbapenems and polypeptides found effective against predominant gram-negative isolates. A high percentage of MDR among commonly isolated bacteria were found in this study would be a serious, alarming

issue. Children and older aged people were found more prone to MDR infection and should be an issue of concern.

Informed consent

Not Applicable.

Availability of data and materials

The data used and/or analyzed in this study are available from the corresponding author on reasonable request.

Provenance and peer review

Not commissioned, externally peer-reviewed.

Ethical approval

Ethical approval for the study was obtained from the North South University Ethics Review Committee. Official permission was received from the Department of microbiology, Medinova Medical Services Ltd. This research was in compliance with the Helsinki Declaration.

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Author contribution

MMA contributed to Study design, statistical analysis, and manuscript preparation. MNI and KMRU involved in the process of data collection and entry. SA, MI and AW helped in drafting the manuscript. MDHH and AH read and approved the final version.

Conflict of interest statement

The authors declare no conflicts of interest.

Guarantor

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ijso.2020.12.010.

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