Prevalence of Antimicrobial Resistance of Common Bacterial Isolates Before and During COVID-19 Pandemic in Armed Forces Hospital Jazan, Saudi Arabia

Manal AlDiba, Ahmad Mohammad Hassan Daghriri, Essa Mohammed Essa Jamali, Ahmed Alzahrani, Ahmed Bijad Alsharif, Haider Ghalip Almudeer, Hassan Mosa Ahmed Khobrani, Nabil Turki Madhi Hakami, Wagih Mommtaz Ghannam, and Hassan Mohamed Alasy

ABSTRACT

Background: Antimicrobial resistance (AMR) is one of the top global public health issues. After the pandemic of corona virus 2019 (COVID-19), AMR became a challenging complex that needs to be addressed during the corona pandemic.

Objectives: Evaluating the prevalence of antimicrobial resistance (AMR) before and during COVID-19 pandemic.

Methods: This is a retrospective cross-sectional study that was conducted at Armed Forces Hospital Jazan, Saudi Arabia using positive cultures' results from microbiology department.

Results: Escherichia coli, Pseudomonas aeruginosa, Staphylococcus aureus and Klebsiella pneumoniae were the most prevalent microorganisms isolated from the patients. E. coli was the most isolated organism from patients with infections such as: COVID-19 fever, sepsis, urinary tract infections and wound infection. There was no significant change between 2019 and 2020 regarding AMR prevalence.

Conclusion: There was no significant difference in the AMR before and during the COVID-19 era thus other large population studies must be conducted to evaluate worldwide evolution of AMR during COVID-19 pandemic.

Keywords: Antibiotics, antimicrobial resistance, coronavirus critical illness, COVID-19 pandemic, drug resistance, KSA, sepsis, urinary tract infection.

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M. AlDiba

Microbiology Department, Armed Forces Hospital Jazan, Saudi Arabia.

(e-mail: manalaldiba@yahoo.com)

A. M. H. Daghriri

Microbiology Department, Armed Forces Hospital Jazan, Saudi Arabia.

(e-mail: a.vip.1402@gmail.com)

E. M. E. Jamali

Microbiology Department, Armed Forces Hospital Jazan, Saudi Arabia.

(e-mail: saudi_code@hotmail.com)

A. Alzahrani

Preventive Medicine Department, Armed Forces Hospital, Saudi Arabia.

(e-mail: ahmedsaudsaad@gmail.com)

A. B. Alsharif

Armed Forces Hospital Jazan, Saudi Arabia.

(e-mail: dr.a.b.r3@hotmail.com)

H. G. Almudeer

Microbiology Department, Armed Forces Hospital Jazan, Saudi Arabia.

(e-mail: hyder1818@gmail.com)

H. M. A. Khobrani

Microbiology Department, Armed Forces Hospital Jazan, Saudi Arabia.

(e-mail: mrr.ok@hotmail.com)

N. T. K. M. Hakami

Microbiology Department, Armed Forces Hospital Jazan, Saudi Arabia.

(e-mail: nabeelt33@gmail.com)

W. M. Ghannam*

Mansoura Faculty of Medicine, Mansoura University, Egypt.

(e-mail: wghnnam@gmail.com)

H. M. Alasy

Tanta Faculty of Medicine, Tanta University, Egypt.

(e-mail: drhassanalasy@yahoo.com)

**Corresponding Author*

I. BACKGROUND

The improper and increased usage of antibiotics have led to development and spreading of antimicrobial resistance (AMR), which is considered a major worldwide health problem. According to the antimicrobial stewardship programs, adjusting the proper usage of antibiotics with correct dose and duration could outcome or at least limit the AMR side effects [1].

Recently, studies showed a significant increase in AMR resulting from COVID-19 pandemic [2]-[4]. Although the world is suffering to control COVID-19 pandemic, the AMR outbreaks development should be considered. Also, multidrug resistant organisms (MDROs) were noticed during that pandemic as carbapenem resistant Enterobacteriaceae (CRE) and methicillin resistant *Staphylococcus aureus* (MRSA) Frontiers in microbiology. Several studies in Europe showed an increase in MDROs infections during COVID-19 pandemic but other studies in France and Spain did not show increase in MDROs infections. Therefore, the impact of COVID-19 pandemic on AMR will only become clear in the coming years as a lot of published data would become available [5].

Bacterial co-infection during viral infections are significant cause of morbidity and mortality but the clinical evidence suggests that bacterial co-infections rates for the COVID-19 patients are very low but antibiotic prescribing remain high [4]. It was noted that about 72% of COVID-19 patients were treated with antibiotic even when not clinically indicated and this heavy use of empiric antibiotics led to high rate of AMR [6].

The hypothesis of this study suggests that the more prevalence of COVID-19 patients', the more inappropriate use of antibiotics could occur which may lead to significant increase in AMR. Most of the published data were from Europe and Western countries but to our knowledge no similar studies have been conducted at local or national level in KSA till to date, therefore, our study is important to detect the prevalence of AMR before and during COVID-19 pandemic at local level in Jazan, Saudi Arabia.

II. METHODS

A. Study Design and Area

Two years retrospective cross sectional study was conducted at Armed Forces Hospital Jazan (AFHJ), Kingdom of Saudi Arabia (KSA). The hospital is about 70 bedded hospitals, and it is Central Board for Accreditation of Healthcare Institutions (CBAHI) accredited hospital.

B. Study Population

All patients (inpatients and outpatients) who were suspected to have bacterial infections and samples were collected from them and cultured for possible pathogen. Full two years data of all positive culture results between 1 January 2019 and 31 December 2020 were obtained from AFHJ microbiology laboratory including full bacterial identification and susceptibility tests results. The inclusion criteria were all positive cases with complete data and Clinical and Laboratory Standards Institutes (CLSI) states that an organism of more than or equal to 30 is optimal for

annual antibiogram inclusion [7].

C. Sample Collection

Positive bacterial cultures were collected from different types of samples such as urine, respiratory sources, wounds swab, and blood. All samples collected from inpatients and outpatients who visited AFHJ in Jazan using standard laboratory procedures between January 2019 and December 2020 [7].

D. Study Tools

1) Identification of Bacterial Etiology

All the specimens were processed according to the CLSI guidelines [8]. Samples were inoculated on different types of agar plates (Saudi Prepared Media Laboratory Company, Riyadh) according to sample type using sterile disposable loops. Plates were incubated at 35- 37 °C for 24-48 hours.

Primary identification of growth was done by the manual methods such as colony morphology, Gram staining and culture characteristics on the plates. Further identification of bacterial species was done using BD phoenix M50 automated system using appropriate panels for the Gram-negative bacteria and for the Gram-positive bacteria according to the manufacturer instructions.

2) Antimicrobial Susceptibility Testing

Identified bacteria were screened for their antimicrobial susceptibility patterns using BD phoenix M50 automated system according to the manufacturer's instructions then for the confirmation, the epsilometer (E-test) was conducted.

3) Antimicrobials Resistance Patterns

The data of antimicrobials resistance patterns are presented in terms of total numbers of isolate and their percentage. Multidrug resistance was defined as the resistance of isolate to two or more antimicrobials.

4) Internal Quality Control Assurance

E. coli American Type Culture Collection (ATCC 25922), *E. faecalis* (ATCC 51299), *S. aureus* (ATCC 29213), and *P. aeruginosa* (ATCC 27853) were used as quality control strains.

5) Data Collection

Electronically completed results from the microbiology laboratory computer system in AFHJ in Jazan. Those positive results had been obtained using some tools such as agar plate, Gram staining, and automated machine for bacterial identification and antimicrobial susceptibility testing (AST).

E. Ethical Considerations

Ethical approval was obtained from Evidence Based and Research Ethics Committee at AFHJ. The collected data will be safe and confidential for research purposes.

F. Statistical Analysis

The data were fed up into windows and analyzed using SPSS V.22. The data were shown as distributions and percentages. Chi square test was used to calculate p-values.

III. RESULTS

A. Demographics of the Included Subjects

Table I showed the demographics of the included subjects n=249 and 264 in 2019 and 2020 respectively including age, gender, and hospital units. Most of the subjects were males

61.4% and 71.2% during 2019 and 2020, respectively. The age of included subjects ranged from younger than 12 years old to 80 years old. During 2019, 26.5% of the patients were admitted to intensive care units (ICU) unit followed by male ward (MW) and female ward (FW) unit while in 2020 the highest percentage was for MW followed by ICU.

TABLE I: DEMOGRAPHIC OF INCLUDED SUBJECTS

		2019		2020		Total		Chi-square	
		N	%	N	%	N	%	X ²	P-value
Age	<12	29	11.6%	14	5.3%	43	8.4%	13.263	0.039
	12-35	23	9.2%	40	15.2%	63	12.3%		
	35-50	46	18.5%	44	16.7%	90	17.5%		
	50-60	37	14.9%	39	14.8%	76	14.8%		
	60-70	48	19.3%	67	25.4%	115	22.4%		
	70-80	42	16.9%	36	13.6%	78	15.2%		
Sex	>80	24	9.6%	24	9.1%	48	9.4%	5.491	0.019
	Female	96	38.6%	76	28.8%	172	33.5%		
	Male	153	61.4%	188	71.2%	341	66.5%		
UNITS	fw	52	20.9%	41	15.5%	93	18.1%	29.760	0.000
	icu	66	26.5%	63	23.9%	129	25.1%		
	msw	36	14.5%	43	16.3%	79	15.4%		
	mw	56	22.5%	67	25.4%	123	24.0%		
	Out Patient	9	3.6%	38	14.4%	47	9.2%		
	Pedia	30	12.0%	12	4.5%	42	8.2%		

B. Distribution of the Studied Samples regarding to Sample Type, Isolated Organisms and Diagnosis

TABLE II: DISTRIBUTION OF THE STUDIED SAMPLES REGARDING SAMPLE TYPE, ISOLATED ORGANS AND DIAGNOSIS IN 2019 AND 2020

Unit		2019		2020		Total		Chi-square	
		N	%	N	%	N	%	X ²	P-value
Sample Type	Blood	29	11.6%	31	11.7%	60	11.7%	10.738	0.057
	Ear Swab	4	1.6%	16	6.1%	20	3.9%		
	Sputum	46	18.5%	36	13.6%	82	16.0%		
	Urine	88	35.3%	100	37.9%	188	36.6%		
	Wound Swab	82	32.9%	80	30.3%	162	31.6%		
	Eye Swab	0	0.0%	1	0.4%	1	0.2%		
Isolated Organisms	<i>Acinetobacter baumannii</i>	27	10.8%	7	2.7%	34	6.6%	54.547	0.000
	<i>Barkholderia cecacia complex</i>	0	0.0%	1	0.4%	1	0.2%		
	<i>Citrobacter braakii</i>	0	0.0%	1	0.4%	1	0.2%		
	<i>Citrobacter freundii</i>	4	1.6%	0	0.0%	4	0.8%		
	<i>Enterobacter cloacae</i>	8	3.2%	9	3.4%	17	3.3%		
	<i>Enterobacter aerogenes</i>	1	0.4%	0	0.0%	1	0.2%		
	<i>Enterococcus faecalis</i>	6	2.4%	2	0.8%	8	1.6%		
	<i>Enterococcus faecium</i>	0	0.0%	1	0.4%	1	0.2%		
	<i>Escherichia coli</i>	69	27.7%	79	29.9%	148	28.8%		
	<i>Haemophilus influenzae</i>	0	0.0%	1	0.4%	1	0.2%		
	<i>Klebsiella pneumoniae</i>	31	12.4%	67	25.4%	98	19.1%		
	<i>Klebsiella aerogenes</i>	1	0.4%	0	0.0%	1	0.2%		
	<i>Morganella morganii</i>	1	0.4%	0	0.0%	1	0.2%		
	<i>Proteus mirabilis</i>	6	2.4%	3	1.1%	9	1.8%		
	<i>Providencia stuartii</i>	2	0.8%	1	0.4%	3	0.6%		
	<i>Pseudomonas aeruginosa</i>	48	19.3%	52	19.7%	100	19.5%		
	<i>Stenotrophomonas maltophilia</i>	3	1.2%	7	2.7%	10	1.9%		
	<i>Salmonella species</i>	2	0.8%	1	0.4%	3	0.6%		
	<i>Serratia marcescens</i>	4	1.6%	0	0.0%	4	0.8%		
	<i>Serratia spp</i>	0	0.0%	1	0.4%	1	0.2%		
	<i>Staphylococcus aureus</i>	36	14.5%	31	11.7%	67	13.1%		
Type of Resistance	CRE	6	5.4%	26	22.4%	32	14.0%	33.683	0.000
	CR-ESBL	0	0.0%	4	3.4%	4	1.8%		
	ESBL	63	56.3%	61	52.6%	124	54.4%		
	MDR	6	5.4%	1	0.9%	7	3.1%		
	MRSA	18	16.1%	20	17.2%	38	16.7%		
	XDR	19	17.0%	4	3.4%	23	10.1%		
Diagnosis	COVID-19	0	0.0%	3	1.1%	3	0.6%	21.395	0.003
	Ear Infection	4	1.6%	16	6.1%	20	3.9%		
	Eye Infection	0	0.0%	1	0.4%	1	0.2%		
	Fever	0	0.0%	4	1.5%	4	0.8%		
	Pneumonia	46	18.5%	34	13.0%	80	15.7%		
	Sepsis	29	11.6%	25	9.5%	54	10.6%		
	Uti	88	35.3%	100	38.2%	188	36.8%		
	Wound Infection	82	32.9%	79	30.2%	161	31.5%		

Table II showed the distribution of the studied samples regarding to sample type, isolated organisms, and diagnosis as the majority of the samples were taken from urine, wound swabs followed by sputum and blood. The most isolated organisms in 2019 were *Escherichia coli* (27.7%), *Pseudomonas aeruginosa* (19.3%), and *Staphylococcus aureus* (14.5%) while in 2020 the isolated organisms were *Escherichia coli* (29.9%), *Klebsiella pneumoniae* (25.4%), *Pseudomonas aeruginosa* (19.7%), and *Staphylococcus aureus* (11.7%). Extended Spectrum Beta-Lactamase (ESBL) was the most frequent resistance type in 2019 (56.3%) and in 2020 (52.6%). It was followed by Extensive drug resistance (XDR) (17%) and methicillin-resistant *Staphylococcus aureus* (MRSA) (16.1%) in 2019 and Carbapenem-resistant *Enterobacteriaceae* (CRE) (22.4%) and MRSA (17.2%) in 2020. The diagnosis of the type of infection showed that urinary tract infection (UTI), wound infection, pneumonia and sepsis were prevalent during 2019 and 2020. On the other hand, COVID-19 and eye infection were the least frequent infections either in 2019 or 2020.

C. Antibiotic Sensitivity Test

The microorganisms were very sensitive to Amikacin,

Daptomycin, Ertapenem, Erythromycin, clindamycin, Imipenem, Linezolid, Meropenem, Moxifloxacin, Mupirocin, Rifampin, Teicoplanin and Vancomycin. There was a moderate sensitivity to Ciprofloxacin, Nitrofurantoin, Piperacillin-tazobactam, Tigecycline, and Trimethoprim/sulphamethoxazole. They showed a high resistance pattern to Amoxicillin-clavulanic, Ampicillin, Cefotaxime, Cefoxitin, Ceftazidime, Ceftriaxone, Cefuroxime, Oxacillin, and Penicillin-g (Table III and Fig. 1).

Table IV and Fig. 2 showed that the antibiotics' resistance and sensitivity pattern showed no significant change between 2019 and 2020 except for Amoxicillin-clavulanic which showed significant decrease in the resistance pattern to such antibiotic.

D. Association between the Isolated Organisms and Resistance Pattern

Antimicrobial susceptibility patterns of bacterial strains isolated in association with antibiotic resistance is presented in Table V.

Fig. 1. Antibiotic sensitivity test.

TABLE III: ANTIBIOTIC SENSITIVITY TEST

	S		R		Total	
	N	%	N	%	N	%
Amikacin	371	85.1%	65	14.9%	436	100.0%
Amoxicillin-clavulanic	118	25.8%	339	74.2%	457	100.0%
Ampicillin	28	5.6%	476	94.4%	504	100.0%
Aztreonam	42	46.7%	48	53.3%	90	100.0%
Cefepime	207	47.7%	227	52.3%	434	100.0%
Cefotaxime	28	36.8%	48	63.2%	76	100.0%
Cefoxitin	44	34.9%	82	65.1%	126	100.0%
Ceftazidime	203	46.6%	233	53.4%	436	100.0%
Ceftriaxone	122	27.9%	315	72.1%	437	100.0%
Cefuroxime	90	18.0%	411	82.0%	501	100.0%
Ciprofloxacin	295	57.7%	216	42.3%	511	100.0%
gentamycin	365	71.7%	144	28.3%	509	100.0%
Daptomycin	72	100.0%	0	0.0%	72	100.0%
Ertapenem	263	60.7%	170	39.3%	433	100.0%
Erythromycin	46	63.0%	27	37.0%	73	100.0%
clindamycin	53	73.6%	19	26.4%	72	100.0%
Imipenem	366	73.1%	135	26.9%	501	100.0%
Levofloxacin	246	56.7%	188	43.3%	434	100.0%
Linolid	72	97.3%	2	2.7%	74	100.0%
Meropenem	349	80.4%	85	19.6%	434	100.0%
Moxifloxacin	70	95.9%	3	4.1%	73	100.0%
Mupirocin	70	98.6%	1	1.4%	71	100.0%
Nitrofurantoin	269	53.2%	237	46.8%	506	100.0%
Oxacillin	28	40.6%	41	59.4%	69	100.0%
Pencillin-g	3	4.2%	68	95.8%	71	100.0%
Piperacillin-tazobactam	221	50.6%	216	49.4%	437	100.0%
Rifampin	64	92.8%	5	7.2%	69	100.0%
Tegecycline	210	48.5%	223	51.5%	433	100.0%
Teicoplanin	71	97.3%	2	2.7%	73	100.0%
Trimethoprim/ sulphamethoxazole	220	43.7%	283	56.3%	503	100.0%
Vancomycin	66	98.5%	1	1.5%	67	100.0%
Total	4672	52.0%	4310	48.0%	8982	100.0%

TABLE IV: ANTIBIOTIC SENSITIVITY TEST DIFFERENCE BETWEEN 2019 AND 2020

	2019					2020					Chi-square	
	S		R		Total	S		R		Total	X ²	P-value
	N	%	N	%		N	%	N	%			
Amikacin	177	85.5%	30	14.5%	207	194	84.7%	35	15.3%	229	0.054	0.817
Amoxicillin-clavulanic	40	19.3%	167	80.7%	207	78	31.2%	172	68.8%	250	8.480	0.004*
Ampicillin	18	7.2%	231	92.8%	249	10	3.9%	245	96.1%	255	2.658	0.103
Aztreonam	-	-	-	-	-	42	46.7%	48	53.3%	90	-	-
Cefepime	95	45.9%	112	54.1%	207	112	49.3%	115	50.7%	227	0.515	0.473
Cefotaxime	17	40.5%	25	59.5%	42	11	32.4%	23	67.6%	34	0.535	0.464
Cefoxitin	17	43.6%	22	56.4%	39	27	31.0%	60	69.0%	87	1.838	0.175
Ceftazidime	94	45.6%	112	54.4%	206	109	47.4%	121	52.6%	230	0.135	0.713
Ceftriaxone	56	27.1%	151	72.9%	207	66	28.7%	164	71.3%	230	0.146	0.702
Cefuroxime	40	16.2%	207	83.8%	247	50	19.7%	204	80.3%	254	1.037	0.308
Ciprofloxacin	150	60.5%	98	39.5%	248	145	55.1%	118	44.9%	263	1.499	0.221
gentamycin	186	75.0%	62	25.0%	248	179	68.6%	82	31.4%	261	2.589	0.108
Daptomycin	41	100.0%	-	-	41	31	100.0%	-	-	31	-	-
Ertapenem	118	57.6%	87	42.4%	205	145	63.6%	83	36.4%	228	1.649	0.199
Erythromycin	28	68.3%	13	31.7%	41	18	56.3%	14	43.8%	32	1.116	0.291
clindamycin	32	80.0%	8	20.0%	40	21	65.6%	11	34.4%	32	1.885	0.170
Imipenem	178	73.6%	64	26.4%	242	188	72.6%	71	27.4%	259	0.059	0.807
Levofloxacin	123	59.4%	84	40.6%	207	123	54.2%	104	45.8%	227	1.210	0.271
Linolid	41	97.6%	1	2.4%	42	31	96.9%	1	3.1%	32	0.038	0.846
Meropenem	167	81.1%	39	18.9%	206	182	79.8%	46	20.2%	228	0.106	0.744
Moxifloxacin	38	92.7%	3	7.3%	41	32	100.0%	0	0.0%	32	3.561	0.059
Mupirocin	38	97.4%	1	2.6%	39	32	100.0%	0	0.0%	32	1.210	0.271
Nitrofurantoin	134	53.8%	115	46.2%	249	135	52.5%	122	47.5%	257	0.084	0.772
Oxacillin	17	45.9%	20	54.1%	37	11	34.4%	21	65.6%	32	0.957	0.328
Pencillin-g	1	2.6%	37	97.4%	38	2	6.1%	31	93.9%	33	0.517	0.472
Piperacillin-tazobactam	104	50.2%	103	49.8%	207	117	50.9%	113	49.1%	230	0.017	0.896
Rifampin	36	97.3%	1	2.7%	37	28	87.5%	4	12.5%	32	2.567	0.109
Tegecycline	111	53.9%	95	46.1%	206	99	43.6%	128	56.4%	227	4.569	0.033
Teicoplanin	40	95.2%	2	4.8%	42	31	100.0%	0	0.0%	31	2.253	0.133
Trime/sulpham-ethoxazole	114	45.8%	135	54.2%	249	106	41.7%	148	58.3%	254	0.839	0.360
Vancomycin	37	97.4%	1	2.6%	38	29	100.0%	0	0.0%	29	1.146	0.284
Total	2288	53.0%	2026	47.0%	4314	2384	51.1%	2284	48.9%	4668

Fig. 2. The antibiotic sensitivity difference between 2019 and 2020.

TABLE V: ASSOCIATION BETWEEN THE ISOLATED ORGANISMS AND RESISTANCE PATTERN (R)

R	Isolated Organisms							
	<i>Escherichia coli</i>		<i>Klebsiella pneumoniae</i>		<i>Pseudomonas aeruginosa</i>		<i>Staphylococcus aureus</i>	
	N	%	N	%	N	%	N	%
Amikacin	0	0.0%	24	24.5%	5	5.0%	-	-
Amoxicillin-clavulanic	90	60.8%	56	57.1%	100	100.0%	15	71.4%
Ampicillin	135	91.2%	97	99.0%	100	100.0%	57	96.6%
Aztreonam	11	52.4%	13	41.9%	18	69.2%	-	-
Cefepime	97	65.5%	51	52.0%	28	28.3%	-	-
Cefotaxime	-	-	-	-	-	-	39	58.2%
Cefoxitin	2	18.2%	11	61.1%	17	100.0%	39	60.0%
Ceftazidime	102	68.9%	56	57.1%	26	26.0%	-	-
Ceftriaxone	102	68.9%	55	56.1%	99	99.0%	-	-
Cefuroxime	114	77.0%	76	77.6%	99	99.0%	35	58.3%
Ciprofloxacin	82	55.4%	40	40.8%	30	30.0%	10	14.9%
gentamycin	41	27.9%	27	27.6%	15	15.0%	4	6.1%
Daptomycin	-	-	-	-	-	-	0	0.0%
Ertapenem	7	4.7%	27	27.8%	85	87.6%	-	-
Erythromycin	-	-	-	-	-	-	19	29.2%
clindamycin	-	-	-	-	-	-	12	18.5%
Imipenem	6	4.1%	28	28.6%	22	22.0%	39	60.0%
Levofloxacin	80	54.1%	39	40.2%	32	32.0%	-	-
Lincolid	-	-	-	-	-	-	0	0.0%
Meropenem	6	4.1%	25	25.8%	17	17.0%	-	-
Moxifloxacin	-	-	-	-	-	-	0	0.0%
Mupirocin	-	-	-	-	-	-	0	0.0%
Nitrofurantoin	9	6.1%	57	58.8%	97	98.0%	1	1.5%
Oxacillin	-	-	-	-	-	-	39	58.2%
Pencillin-g	0	0.0%	-	-	-	-	65	97.0%
Piperacillin-tazobactam	95	64.2%	53	54.1%	21	21.0%	0	0.0%
Rifampin	1	100.0%	-	-	-	-	2	3.1%
Tegecycline	15	10.2%	49	50.0%	97	98.0%	-	-
Teicoplanin	-	-	-	-	-	-	0	0.0%
Trime/sulphamethoxazole	85	57.4%	52	53.1%	94	94.0%	8	12.9%
Vancomycin	-	-	-	-	-	-	0	0.0%

TABLE VI: ASSOCIATION BETWEEN THE TYPE OF INFECTION AND STUDY VARIABLES

		DIAGNOSIS								Chi-square	
		COVID-19	Ear Infection	Eye Infection	Fever	Pneumonia	Sepsis	UTI	Wound Infection	X ²	P-value
		N=3	N=20	N=1	N=4	N=80	N=54	N=188	N=161		
Age	<12	0.0%	5.0%	0.0%	25.0%	0.0%	13.0%	12.2%	6.2%	119.145	0.000
	12-35	33.3%	15.0%	100.0%	0.0%	2.5%	5.6%	11.2%	19.3%		
	35-50	0.0%	35.0%	0.0%	0.0%	13.8%	5.6%	11.7%	29.2%		
	50-60	66.7%	30.0%	0.0%	0.0%	20.0%	20.4%	10.1%	13.7%		
	60-70	0.0%	10.0%	0.0%	75.0%	33.8%	29.6%	22.3%	15.5%		
	70-80	0.0%	5.0%	0.0%	0.0%	18.8%	16.7%	18.1%	11.8%		
	>80	0.0%	0.0%	0.0%	0.0%	11.3%	9.3%	14.4%	4.3%		
Sex	Female	33.3%	25.0%	0.0%	25.0%	31.3%	24.1%	48.4%	22.4%	31.458	0.000
	Male	66.7%	75.0%	100.0%	75.0%	68.8%	75.9%	51.6%	77.6%		
	fw	33.3%	0.0%	0.0%	0.0%	8.8%	13.0%	27.7%	16.1%		
Units	icu	66.7%	0.0%	0.0%	25.0%	68.8%	44.4%	19.7%	6.2%	410.800	0.000
	msw	0.0%	0.0%	0.0%	0.0%	1.3%	0.0%	0.5%	47.2%		
	mw	0.0%	0.0%	0.0%	50.0%	21.3%	29.6%	30.9%	18.6%		
	Out Patient	0.0%	100.0%	100.0%	0.0%	0.0%	0.0%	9.6%	5.0%		
Sample Type	Pedia	0.0%	0.0%	0.0%	25.0%	0.0%	13.0%	11.7%	6.8%	1428.488	0.000
	Blood	0.0%	0.0%	0.0%	100.0%	0.0%	100.0%	0.5%	0.0%		
	Ear Swab	0.0%	100.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%		
	Sputum	66.7%	0.0%	0.0%	0.0%	100.0%	0.0%	0.0%	0.0%		
	Urine	33.3%	0.0%	0.0%	0.0%	0.0%	0.0%	99.5%	0.0%		
	Wound Swab	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	100.0%		
	Eye Swab	0.0%	0.0%	100.0%	0.0%	0.0%	0.0%	0.0%	0.0%		
	<i>Acinetobacter baumannii</i>	0.0%	0.0%	0.0%	0.0%	20.0%	7.4%	2.1%	6.2%		
	<i>Barkholderia cebacia complex</i>	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.6%		
	<i>Citrobacter braakii</i>	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.6%		
Isolate d Organisms	<i>Citrobacter freundii</i>	0.0%	0.0%	0.0%	0.0%	0.0%	1.9%	1.1%	0.6%	315.815	0.000
	<i>Enterobacter cloacae</i>	0.0%	10.0%	0.0%	0.0%	1.3%	1.9%	2.7%	5.0%		
	<i>Enterobacter aerogenes</i>	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.6%		
	<i>Enterococcus faecalis</i>	0.0%	0.0%	0.0%	0.0%	0.0%	1.9%	0.5%	3.7%		
	<i>Enterococcus faecium</i>	0.0%	0.0%	0.0%	0.0%	0.0%	1.9%	0.0%	0.0%		
	<i>Escherichia coli</i>	33.3%	0.0%	0.0%	25.0%	5.0%	27.8%	54.3%	15.5%		
	<i>Haemophilus influenzae</i>	0.0%	0.0%	0.0%	25.0%	0.0%	0.0%	0.0%	0.0%		
	<i>Klebsiella pneumoniae</i>	0.0%	15.0%	0.0%	50.0%	21.3%	24.1%	21.3%	14.3%		
	<i>Klebsiella aerogenes</i>	0.0%	0.0%	0.0%	0.0%	1.3%	0.0%	0.0%	0.0%		
	<i>Morganella morganii</i>	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.6%		
	<i>Proteus mirabilis</i>	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	1.1%	4.3%		
	<i>Providencia stuartii</i>	0.0%	0.0%	0.0%	0.0%	1.3%	0.0%	0.5%	0.6%		
	<i>Pseudomonas aeruginosa</i>	0.0%	65.0%	100.0%	0.0%	33.8%	5.6%	14.9%	16.8%		
	<i>Stenotrophomonas maltophilia</i>	33.3%	0.0%	0.0%	0.0%	7.5%	0.0%	0.5%	1.2%		
	<i>Salmonella species</i>	0.0%	0.0%	0.0%	0.0%	0.0%	5.6%	0.0%	0.0%		
	<i>Serratia marcescens</i>	0.0%	0.0%	0.0%	0.0%	1.3%	0.0%	1.1%	0.6%		
	<i>Serratia spp</i>	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.6%		
	<i>Staphylococcus aureus</i>	33.3%	10.0%	0.0%	0.0%	7.5%	22.2%	0.0%	28.0%		
Type Of Resistance	CRE	0.0%	0.0%	0.0%	0.0%	16.3%	24.0%	19.1%	1.6%	121.210	0.000
	CR-ESBL	0.0%	0.0%	0.0%	0.0%	4.7%	0.0%	1.1%	1.6%		
	ESBL	100.0%	0.0%	0.0%	0.0%	27.9%	48.0%	76.6%	43.5%		
	MDR	0.0%	0.0%	0.0%	0.0%	4.7%	4.0%	2.1%	3.2%		
	MRSA	0.0%	100.0%	0.0%	0.0%	11.6%	24.0%	0.0%	38.7%		
		XDR	0.0%	0.0%	0.0%	34.9%	0.0%	1.1%	11.3%		

E. Association Between the Type of Infection and Study Variables

The adults (above 12 years and less than 60 years) and elder (above 60 years) ages were significantly associated with increased risk of infection including COVID-19, ear infection, eye infection, fever, pneumonia, sepsis, UTI and wound infection. Males showed high significant susceptibility to all diagnosed infections. COVID-19, pneumonia and sepsis showed a significant association with being admitted to ICU. *Pseudomonas aeruginosa* was significantly associated with pneumonia, ear, and eye infection. *E. coli* was significantly associated with most of the infections as COVID-19, fever, sepsis, UTI and wound infection. *Klebsiella pneumoniae* showed a significant association with pneumonia, sepsis and UTI. The type of resistance was significantly associated with the type of infection as ESBL was associated with COVID-19, pneumonia, sepsis, UTI and wound infection. MRSA was significantly associated with ear and wound infection (Table VI).

IV. DISCUSSION

The world is striving to control COVID-19 pandemic, but on the other hand it is required to be equipped for facing the great influences of outbreak on AMR progression. There was evidence of an increase in the prevalence of multidrug resistant organisms (MDROs) specially during COVID-19 pandemic. Therefore, the impact of COVID-19 pandemic on AMR will only become clear in the coming years.

The present study showed that *Escherichia coli*, *Pseudomonas aeruginosa*, *Staphylococcus aureus* and *Klebsiella pneumoniae* were the most prevalent microorganisms isolated from the patients. Consistently, the most frequently isolated organisms were *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, extended-spectrum beta-lactamase, multidrug-resistant *E. coli*, *Enterococcus*, *Chlamydia pneumoniae*, *Mycoplasma pneumoniae* and *Acinetobacter* [9], [10].

Also, *Pseudomonas aeruginosa* was significantly associated with pneumonia, ear, and eye infection. *E. coli* was significantly associated with most of the infections as COVID-19, fever, sepsis, UTI and wound infection. *Klebsiella pneumoniae* showed a significant association with pneumonia, sepsis and UTI. In contrast, other studies showed that among COVID-19 patients, the bacteria most frequently isolated from were *Mycoplasma pneumoniae*, *Pseudomonas aeruginosa*, and *Haemophilus influenzae*. Over that co-infected patient with influenza showed different percentages of pathogenic isolates including *Streptococcus pneumoniae* and *Streptococcus pyogenes* as well as *S. aureus* [11].

The difference in incidence of resistance to antibiotics showed no significant change between 2019 and 2020. Several studies in Europe showed an increase in MDROs infections during COVID-19 pandemic but other studies in France and Spain did not show increase in MDROs infections. Therefore, the impact of COVID-19 pandemic on AMR will only become clear in the coming years as a lot of published data would become available [5]. It was noted that about 72% of COVID-19 patients were treated with antibiotic

even when not clinically indicated and this heavy use of empiric antibiotics led to high rate of AMR [6].

The usage of more antibiotics showed an increase in the ESBL which was associated with COVID-19, pneumonia, sepsis, UTI and wound infection. MRSA was significantly associated with ear and wound infection. ESBL and CRE were increased in 2019 than 2020. In the same respect, a study showed a wide spread of bacteria producing carbapenemase particularly among hospitalized patients. Also, the rate of carbapenem resistance involved 19.5% MDR cultures and the rate of extended spectrum beta-lactamase was about 50% [12].

V. CONCLUSION

This study showed no significant difference in the AMR before and during the COVID-19 era. There still a debate around the implication of evolving AMR during COVID-19 outbreak thus other large population studies must be conducted to evaluate worldwide evolution of AMR during COVID-19 pandemic.

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