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Antimicrobial Resistance of the Most Common Bacterial Pathogens Isolated from Skin, Mucosal, and Wound Swabs in Outpatients in Sarajevo Canton (March–June 2024)

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Abstract

Background: Antimicrobial resistance (AMR) is one of the greatest challenges of modern medicine and significantly affects the successful treatment of bacterial infections. Continuous surveillance of resistance patterns enables more rational antibiotic use and improvement of empirical therapy.

Objective: To analyze the prevalence of the most common bacterial pathogens isolated from skin, mucosal, and wound swabs, and to determine their antimicrobial resistance patterns in outpatients in Sarajevo Canton.

Materials and Methods: A retrospective analysis was performed on microbiological data from skin, mucosal, and wound swabs collected from outpatients in Sarajevo Canton. Identification of bacterial isolates and antimicrobial susceptibility testing were conducted using standard microbiological methods in accordance with EUCAST guidelines. The analysis included the most frequently isolated bacterial species and their resistance patterns to tested antibiotics.

Results: *Staphylococcus aureus* was the dominant pathogen in skin (73.5%) and wound swabs (52.1%), while *Escherichia coli* was most frequently isolated from mucosal swabs (34.7%). MRSA accounted for 7.2% of skin isolates and 5.3% of wound isolates. *S. aureus* showed very high resistance to penicillin G (92.3%) but retained high susceptibility to cefoxitin (99.5%) and trimethoprim-sulfamethoxazole (99.7%). All analyzed MRSA isolates were resistant to cefoxitin and penicillin G, while full susceptibility was observed for trimethoprim-sulfamethoxazole. ESBL- and carbapenemase-producing *Klebsiella pneumoniae* isolates were also detected in wound swabs.

Conclusion: *Staphylococcus aureus* remains the leading causative agent of skin and wound infections in outpatients, while the emergence of multidrug-resistant organisms highlights the need for continuous AMR surveillance and rational antibiotic use.

Keywords: antimicrobial resistance, *Staphylococcus aureus*, MRSA, *Escherichia coli*, antibiogram, outpatients

Introduction

Antimicrobial resistance (AMR) represents one of the most significant global public health challenges of the 21st century. The increasing prevalence of resistant bacterial isolates significantly complicates infection treatment, prolongs hospitalization, increases healthcare costs, and contributes to higher mortality. According to the World Health Organization (WHO), AMR threatens the effectiveness of standard antibiotic therapy and poses a serious risk to patient safety.

Skin, soft tissue, and wound infections are among the most common indications for microbiological diagnostics in outpatient healthcare. The most frequent causative agents include *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Klebsiella spp.*, *Proteus spp.*, and other opportunistic microorganisms. Their ability to develop multiple resistance mechanisms, including extended-spectrum β-lactamases (ESBL) and carbapenemases, represents an increasing therapeutic challenge.

Of particular epidemiological importance is methicillin-resistant *Staphylococcus aureus* (MRSA), one of the most important pathogens causing skin, wound, and soft tissue infections. Monitoring MRSA prevalence and resistance patterns is essen-

tial for selecting appropriate empirical therapy and implementing infection control measures.

Local AMR data are of special importance because resistance patterns vary between geographic regions and healthcare settings. Regular surveillance enables the development of local antibiotic guidelines, supports antimicrobial stewardship, and helps preserve antibiotic effectiveness.(1,2,3,4)

Aim of the Study

The aim of this study was to analyze the prevalence of the most common bacterial pathogens isolated from skin, mucosal, and wound swabs in outpatients in Sarajevo Canton and to determine their antimicrobial resistance patterns, with special emphasis on *Staphylococcus aureus* and MRSA isolates.

Table 1. Bacterial Isolates According to Sample Type

Smear	Causative agent	N	%
Skin	Staphylococcus aureus	1935	73.5%
	Staphylococcus aureus MRSA	189	7.2%
	Pseudomonas species	86	3.3%
	Klebsiella species	53	2.0%
	Escherichia coli	183	6.9%
	Acinetobacter species	7	0.3%
	Proteus species	126	4.8%
	Streptococcus ß haemoliticus-gr. A	16	0.6%
	Enterobacter species	16	0.6%
	Streptococcus grupa C	3	0.1%
	Streptococcus pneumoniae	7	0.3%
	Enterobacter spp. ESBL	13	0.5%
Mucous membrane	Staphylococcus aureus	170	24.1%
	Staphylococcus aureus MRSA	23	3.3%
	Klebsiella species	19	2.7%
	Escherichia coli	245	34.7%
	Proteus species	31	4.4%
	Streptococcus ß haemoliticus-gr. A	20	2.8%
	Enterobacter species	24	3.4%
	Streptococcus ß haemoliticus-gr. B	149	21.1%
	Enterococcus faecium / faecalis	20	2.8%
	Morganella morganii	5	0.7%
Wound	Staphylococcus aureus	963	52.1%
	Staphylococcus aureus MRSA	97	5.3%
	Pseudomonas species	224	12.1%
	Klebsiella species	101	5.5%
	Escherichia coli	104	5.6%
	Acinetobacter species	47	2.5%
	Proteus species	84	4.5%
	Enterobacter species	51	2.8%
	Streptococcus grupa C	4	0.2%
	Enterococcus faecium / faecalis	8	0.4%
	Morganella morganii	6	0.3%
	Klebsiella pneumoniae ESBL	13	0.7%
	Klebsiella pneumoniae CRE	30	1.6%
	Escherichia coli ESBL	10	0.5%
	Klebsiella species KPS (karbapenemaza producing strain)	13	0.7%
	Klebsiella species ESBL	92	5.0%

Materials and Methods

A retrospective study was conducted using laboratory data obtained from microbiological samples collected from outpatients in Sarajevo Canton. Skin, mucosal, and wound swabs yielding the most common bacterial pathogens were included in the analysis.

Bacterial identification was performed using standard microbiological methods, while antimicrobial susceptibility testing was carried out using the disk diffusion method and interpreted according to current EUCAST guidelines. Results were categorized as susceptible (S), intermediate (I), or resistant (R).

Data were analyzed using descriptive statistical methods and presented as absolute and relative frequencies (%).

Results

During the study period, numerous bacterial pathogens were isolated from skin, mucosal, and wound swabs of outpatients. The most frequently identified organisms across all sample types were *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas spp.*, and *Klebsiella spp.*

In skin swabs, *Staphylococcus aureus* was the predominant isolate, accounting for 73.5% of all isolates. MRSA was detected in 7.2% of cases, while *Escherichia coli* (6.9%), *Proteus spp.* (4.8%), and *Pseudomonas spp.* (3.3%) were less frequently isolated. Other pathogens, including *Klebsiella spp.*, *Enterobacter spp.*, *Acinetobacter spp.*, and β-hemolytic streptococci, each accounted for less than 3% of isolates.

In mucosal swabs, *Escherichia coli* was the dominant pathogen (34.7%), followed by *Staphylococcus aureus* (24.1%) and Group B β-hemolytic streptococci (21.1%). Other isolates were significantly less frequent.

In wound swabs, *Staphylococcus aureus* again predominated (52.1%), followed by *Pseudomonas spp.* (12.1%). *Escherichia coli* (5.6%) and *Klebsiella spp.* (5.5%) were present in similar proportions. Notably, multidrug-resistant *Klebsiella pneumoniae* isolates, including ESBL (0.7%), CRE (1.6%), and carbapenemase-producing strains (0.7%), were detected, indicating the presence of highly resistant bacteria in the outpatient population.

Antimicrobial Resistance of *Staphylococcus aureus*

Antibiogram analysis demonstrated that *Staphylococcus aureus* retains high susceptibility to most antibiotics used in the treatment of skin and soft tissue infections.

The highest resistance was observed to penicillin G (92.3%), confirming widespread β-lactamase production among isolates. Elevated resistance was also observed for erythromycin (37.5%) and clindamycin (30.3%).

In contrast, very high susceptibility was recorded for cefoxitin (99.5%), trimethoprim-sulfamethoxazole (99.7%), and chloramphenicol (99.1%). Good activity was also observed for gentamicin (78.7%) and tobramycin (77.4%).

Overall, the resistance pattern indicates that narrow-spectrum β-lactams, particularly penicillin G, have lost therapeutic value in *S. aureus* infections, while trimethoprim-sulfamethoxazole and aminoglycosides remain effective treatment options.

Antimicrobial Resistance of MRSA Isolates

All analyzed MRSA isolates were resistant to cefoxitin and penicillin G (100%), confirming their methicillin-resistant phenotype.

Discussion

Staphylococcus aureus showed high resistance to penicillin G (92.3%) while maintaining high susceptibility to cefoxitin (99.5%) and trimethoprim-sulfamethoxazole (99.7%). MRSA isolates demonstrated 100% resistance to cefoxitin and penicillin G.

ESBL- and CRE-producing *Klebsiella pneumoniae* isolates were also detected in wound swabs, indicating the presence of highly resistant strains in the outpatient population.

The results confirm that *Staphylococcus aureus* is the leading cause of superficial bacterial infections in outpatients, consistent with reports from the European Centre for Disease Prevention and Control (ECDC) and the World Health Organization (WHO). Its high prevalence in skin and wound samples highlights its dominant role in skin and soft tissue infections.

Table 2. Antimicrobial Resistance in Staphylococcus aureus

Causative agent			resistance			Total
			I	R	S	
antibiotic	Cefoxitin	Count	1	1	374	376
		Expected Count	44.7	93.1	238.1	376.0
		% Within antibiotic	0.3%	0.3%	99.5%	100.0%
		Standardized Residual	-6.5	-9.5	8.8	
	Chloramphenicol	Count	0	1	113	114
		Expected Count	13.6	28.2	72.2	114.0
		% Within antibiotic	0.0%	0.9%	99.1%	100.0%
		Standardized Residual	-3.7	-5.1	4.8	
	Ciprofloxacin	Count	362	11	2	375
		Expected Count	44.6	92.9	237.5	375.0
		% Within antibiotic	96.5%	2.9%	0.5%	100.0%
		Standardized Residual	47.5	-8.5	-15.3	
	Clindamycin	Count	0	96	221	317
		Expected Count	37.7	78.5	200.8	317.0
		% Within antibiotic	0.0%	30.3%	69.7%	100.0%
		Standardized Residual	-6.1	2.0	1.4	
	Erythromycin	Count	1	141	234	376
		Expected Count	44.7	93.1	238.1	376.0
		% Within antibiotic	0.3%	37.5%	62.2%	100.0%
		Standardized Residual	-6.5	5.0	-.3	
	Gentamicin	Count	0	80	295	375
		Expected Count	44.6	92.9	237.5	375.0
		% Within antibiotic	0.0%	21.3%	78.7%	100.0%
		Standardized Residual	-6.7	-1.3	3.7	
	Penicillin G	Count	0	347	29	376
		Expected Count	44.7	93.1	238.1	376.0
		% Within antibiotic	0.0%	92.3%	7.7%	100.0%
		Standardized Residual	-6.7	26.3	-13.6	
	Rifampicin	Count	0	0	8	8
		Expected Count	1.0	2.0	5.1	8.0
		% Within antibiotic	0.0%	0.0%	100.0%	100.0%
		Standardized Residual	-1.0	-1.4	1.3	
	Tetracycline	Count	0	0	8	8
		Expected Count	1.0	2.0	5.1	8.0
		% Within antibiotic	0.0%	0.0%	100.0%	100.0%
		Standardized Residual	-1.0	-1.4	1.3	
	Tobramycin	Count	0	83	285	368
		Expected Count	43.8	91.2	233.1	368.0
		% Within antibiotic	0.0%	22.6%	77.4%	100.0%
		Standardized Residual	-6.6	-.9	3.4	
	Trimethoprim - Sulfamethoxazole	Count	1	0	374	375
		Expected Count	44.6	92.9	237.5	375.0
		% Within antibiotic	0.3%	0.0%	99.7%	100.0%
		Standardized Residual	-6.5	-9.6	8.9	
	Total	Count	365	760	1943	3068
		Expected Count	365.0	760.0	1943.0	3068.0
		% Within antibiotic	11.9%	24.8%	63.3%	100.0%

Table 3. Antimicrobial Resistance in MRSA Isolates

Causative agent			resistance			Total
			I	R	S	
antibiotic	Cefoksitin	Count	0	37	0	37
		Expected Count	4.1	15.4	17.5	37.0
		% Within antibiotic	0.0%	100.0%	0.0%	100.0%
		Standardized Residual	-2.0	5.5	-4.2	
	Chloramphenicol	Count	0	1	9	10
		Expected Count	1.1	4.2	4.7	10.0
		% Within antibiotic	0.0%	10.0%	90.0%	100.0%
		Standardized Residual	-1.0	-1.6	2.0	
	Ciprofloxacin	Count	34	3	0	37
		Expected Count	4.1	15.4	17.5	37.0
		% Within antibiotic	91.9%	8.1%	0.0%	100.0%
		Standardized Residual	14.8	-3.2	-4.2	
	Clindamycin	Count	0	12	20	32
		Expected Count	3.5	13.4	15.1	32.0
		% Within antibiotic	0.0%	37.5%	62.5%	100.0%
		Standardized Residual	-1.9	-.4	1.3	
	Erythromycin	Count	0	20	17	37
		Expected Count	4.1	15.4	17.5	37.0
		% Within antibiotic	0.0%	54.1%	45.9%	100.0%
		Standardized Residual	-2.0	1.2	-.1	
	Gentamicin	Count	0	8	29	37
		Expected Count	4.1	15.4	17.5	37.0
		% Within antibiotic	0.0%	21.6%	78.4%	100.0%
		Standardized Residual	-2.0	-1.9	2.8	
	Penicillin G	Count	0	37	0	37
		Expected Count	4.1	15.4	17.5	37.0
		% Within antibiotic	0.0%	100.0%	0.0%	100.0%
		Standardized Residual	-2.0	5.5	-4.2	
	Rifampicin	Count	0	0	4	4
		Expected Count	.4	1.7	1.9	4.0
		% Within antibiotic	0.0%	0.0%	100.0%	100.0%
		Standardized Residual	-.7	-1.3	1.5	
	Tetracycline	Count	0	1	2	3
		Expected Count	.3	1.3	1.4	3.0
		% Within antibiotic	0.0%	33.3%	66.7%	100.0%
		Standardized Residual	-.6	-.2	.5	
	Tobramycin	Count	0	10	27	37
		Expected Count	4.1	15.4	17.5	37.0
		% Within antibiotic	0.0%	27.0%	73.0%	100.0%
		Standardized Residual	-2.0	-1.4	2.3	
	Trimethoprim - Sulfamethoxazole	Count	0	0	37	37
		Expected Count	4.1	15.4	17.5	37.0
		% Within antibiotic	0.0%	0.0%	100.0%	100.0%
		Standardized Residual	-2.0	-3.9	4.7	
	Vancomycin	Count	0	0	1	1
		Expected Count	.1	.4	.5	1.0
		% Within antibiotic	0.0%	0.0%	100.0%	100.0%
		Standardized Residual	-.3	-.6	.8	
	Total	Count	34	129	146	309
		Expected Count	34.0	129.0	146.0	309.0
		% Within antibiotic	11.0%	41.7%	47.2%	100.0%

The increased frequency of *Escherichia coli* in mucosal samples is expected due to its natural colonization of the gastrointestinal tract and its pathogenic potential.

The presence of MRSA in approximately 7% of isolates highlights the need for continuous microbiological surveillance and rational antibiotic use in outpatient settings. (1,2,3,4,5,6)

Conclusion

Staphylococcus aureus is the dominant bacterial pathogen in skin and wound infections among outpatients in Sarajevo Canton.

The most common isolates across all sample types were *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas spp.*, and *Klebsiella spp.*

In skin swabs, *S. aureus* predominated (73.5%), while MRSA accounted for 7.2%. In mucosal swabs, *E. coli* was most frequently isolated (34.7%), whereas *S. aureus* again dominated wound swabs (52.1%).

The distribution of bacterial species varies significantly depending on the sample type, emphasizing the importance of local microbiological surveillance and continuous monitoring of antimicrobial resistance to optimize therapy.

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