



# Antimicrobial Susceptibility of 49,319 Pathogens Isolated from Patients in Canadian Hospitals: 12 Years of the CANWARD Study 2007-2018

G. G. ZHANEL<sup>1</sup>, M. BAXTER<sup>1</sup>, K. NICHOL<sup>1</sup>, A. GOLDEN<sup>1</sup>, R. HINK<sup>1</sup>, P. LAGACÉ-WIENS<sup>1</sup>, J. FULLER<sup>3</sup>, J. A. KARLOWSKY<sup>1</sup>,  
A. WALKTY<sup>1</sup>, M. GILMOUR<sup>1,2</sup>, D. BAY<sup>1</sup>, F. SCHWEIZER<sup>1</sup>, R. DOMALAON<sup>1</sup>, T. IDOWU<sup>1</sup>, A.S. HENNI<sup>1</sup>, M. R. MULVEY<sup>1,2</sup>, G. R. GOLDING<sup>1,2</sup>,  
the CANADIAN ANTIMICROBIAL RESISTANCE ALLIANCE (CARA) and H. ADAM<sup>1</sup>



Dr. George G. Zhanel  
Microbiology, Health Sciences Centre  
MS673-820 Sherbrook Street  
Winnipeg, MB R3A 1R9  
Email: ggzhanel@pcsc.mb.ca

<sup>1</sup>University of Manitoba and <sup>2</sup>National Microbiology Laboratory, Winnipeg, Manitoba, Canada; <sup>3</sup>University of Alberta, Edmonton, Alberta, Canada

## Introduction

Antimicrobial resistant Gram-positive organisms such as methicillin-resistant *Staphylococcus aureus* (MRSA, community associated [CA] and healthcare associated [HA]), vancomycin-resistant *Enterococcus species* (VRE), penicillin-resistant *Streptococcus pneumoniae*, and Gram-negative bacilli such as extended spectrum β-lactamase (ESBL) producing *Escherichia coli* and *Klebsiella* species as well as fluoroquinolone-resistant and carbapenem-resistant Enterobacteriaceae and *Pseudomonas aeruginosa* are increasing in prevalence in Canada and around the world (1, 2). Available therapeutic options for the treatment of these antibiotic resistant organisms are limited as these organisms frequently display a multidrug resistant (MDR) and potentially an extremely drug resistant (XDR) phenotype (1, 2).

CANWARD (a collaboration between the Canadian Antimicrobial Resistance Alliance and the National Microbiology Laboratory) is a national ongoing surveillance study which assess pathogens associated with antimicrobial resistance patterns in respiratory, bacteraemic, urinary, and wound/IV site infections in Canadian hospitalized patients on medical/surgical wards, intensive care units, emergency rooms and outpatient clinics.

## Materials and Methods

### Participating Sites

From January 2007 to October 2018, tertiary-care medical centres in major population centres in 8 of the 10 provinces in Canada were recruited (1, 2). These sites were geographically distributed in a population based fashion.

### Bacterial Isolates

Tertiary-care medical centres submitted pathogens from patients attending hospital clinics, emergency rooms, medical and surgical wards, and intensive care units. Each study site was asked to submit clinical isolates (consecutive, one per patient, per infection site) from inpatients and outpatients with respiratory, urine, wound, and bloodstream infections. Isolate identification was performed by the submitting site and confirmed at the reference site as required, based on morphological characteristics and antimicrobial susceptibility patterns. Isolates were shipped on Amies semi-solid transport media to the coordinating laboratory (Health Sciences Centre, Winnipeg, Canada), subcultured onto appropriate media, and stocked in skim milk at -80°C until minimum inhibitory concentration (MIC) testing was carried out. From 2007-2018, 7718, 5283, 5373, 4960, 3785, 2802, 3511, 3172, 3206, 3126, 3420 and 2963 isolates were collected in each study year (1, 2).

### Antimicrobial Susceptibilities

The *in vitro* activity of selected antimicrobials was determined by broth microdilution in accordance with (CLSI) guidelines (3). Antimicrobial minimum inhibitory concentration (MIC) interpretive standards were defined according to CLSI breakpoints (4). The MICs of the antimicrobial agents were determined using 96-well custom designed microtitre plates. These plates contained doubling antimicrobial dilutions in 100µL/well of cation adjusted Mueller-Hinton broth and inoculated to achieve a final concentration of approximately 5 x 10<sup>5</sup> CFU/mL then incubated in ambient air for 24 hours prior to reading. Colony counts were performed periodically to confirm inocula. Quality control was performed using ATCC QC organisms including *S. pneumoniae* 49619, *S. aureus* 29213, *E. faecalis* 29212, *E. coli* 25922, and *P. aeruginosa* 27853.

## Results

Table 1. Antimicrobial activity against the most common Gram-positive cocci isolated from Canadian hospitals

Organism (no. tested)	% S	% I	% R	MIC (µg/mL)			Organism (no. tested)	% S	% I	% R	MIC (µg/mL)			
				MIC <sub>50</sub>	MIC <sub>90</sub>	Range Min					MIC <sub>50</sub>	MIC <sub>90</sub>	Range Max	
<i>Staphylococcus aureus</i> , MSSA (8243)	99.6	0.4	4	4	0.12	> 32	<i>Streptococcus agalactiae</i> (792)	Amox-Clav	< 0.06	< 0.06	0.25	2	4	> 64
Cefotaxime	100.0			≤ 1	≤ 1	2	Cefotaxime	< 0.06	< 0.06	0.06	2	2	> 128	
Ceftobiprole <sup>a</sup>				4	4	256	Cefuroxime	100.0	≤ 0.12	≤ 0.12	0.06	5	8	< 32
Ceftriaxone				≤ 0.25	≤ 0.25	0.5	Chloramphenicol	96.8	2.9	0.2	4	4	16	< 32
Ciprofloxacin	86.5	3.1	10.4	0.5	4	> 16	Ciprofloxacin		0.5	1	0.25	> 16		
Clarithromycin	75.7	0.6	23.7	0.25	> 32	> 0.03	Clarithromycin	66.1	3.6	30.3	0.03	> 32	> 32	
Clindamycin	93.6	0.4	5.9	≤ 0.25	≤ 0.25	> 8	Daptomycin	81.1	0.8	18.1	≤ 0.12	> 64		
Daptomycin	99.9	0.01	0.25	0.5	0.03	2	Daptomycin	100.0	0.25	0.25	0.03	1		
Doxycycline	98.9	0.8	0.4	≤ 0.12	0.25	32	Doxycycline		8	16	> 16	> 16		
Gentamicin	98.4	0.09	1.77	≤ 0.5	0.5	> 32	Ertapenem	100.0	0.06	0.06	0.06	12		
Levofloxacin	90.35	0.00	9.28	0.25	1	> 32	Levofloxacin	96.3	3.7	0.1	0.25	> 32		
Linezolid	99.9	0.01	2	4	0.12	> 16	Linezolid	97.4	2.6	1	2	< 12	4	
Moxifloxacin	90.6	0.8	8.6	≤ 0.06	0.25	0.06	Moxifloxacin	98.8	0.03	0.09	16	16	5.0	256
Nitrofurantoin	98.8	0.03	0.09	16	16	≤ 0.5	Nitrofurantoin	100.0	0.06	0.06	0.06	12		
Telavancin	100.0			0.06	0.06	0.12	Telavancin	100.0	0.06	0.06	0.05	12		
Tigecycline <sup>b</sup>	99.8	0.2	0.12	0.25	0.03	2	Tigecycline	99.8	0.2	0.06	0.12	> 1		
Tobramycin	97.3	0.3	2.5	≤ 0.5	≤ 0.5	> 64	Tobramycin	99.5	0.5	≤ 0.12	≤ 0.12	> 8		
Trimethoprim-Sulfra	99.5	0.5	≤ 0.12	≤ 0.12	≤ 0.12	> 8	Trimethoprim-Sulfra	100.0	1	1	≤ 0.12	2		
Vancomycin	100.0			1	1	≤ 0.12	Vancomycin		0.5	0.5	≤ 0.25	1		

Organism (no. tested)	% S	% I	% R	MIC <sub>50</sub>	MIC <sub>90</sub>	Range Min	Organism (no. tested)	% S	% I	% R	MIC <sub>50</sub>	MIC <sub>90</sub>	Range Max	
<i>Staphylococcus aureus</i> , MRSA (2214)	99.8	0.2	> 32	1	> 32		<i>Escherichia coli</i> (6591)	Amikacin	99.6	0.2	0.1	≤ 2	4	> 64
Cefotaxime	100.0			≤ 1	≤ 1	2	Cefotaxime	83.4	11.7	4.9	4	16	≤ 0.06	
Ceftobiprole <sup>a</sup>				4	4	256	Cefotaxime	69.9	11.7	18.4	2	32	≤ 0.5	
Ceftriaxone				≤ 0.25	≤ 0.25	0.5	Cefotaxime	91.0	6.5	12.5	4	32	≤ 0.25	
Ciprofloxacin	86.5	3.1	10.4	0.5	4	> 16	Cefotaxime	92.0	4.3	3.8	4	8	> 0.06	
Clarithromycin	75.7	0.6	23.7	0.25	> 32	> 0.03	Cefotaxime	92.1	6.1	≤ 0.25	2	32	> 0.06	
Clindamycin	93.6	0.4	5.9	≤ 0.25	≤ 0.25	> 8	Cefotaxime	93.3	0.2	0.5	1	≤ 0.25	> 0.06	
Daptomycin	99.9	0.01	0.25	0.5	0.03	2	Cefotaxime	94.0	0.2	0.5	1	≤ 0.25	> 0.06	
Doxycycline	98.9	0.8	0.4	≤ 0.12	0.25	32	Cefotaxime	94.1	0.3	0.6	≤ 1	≤ 1	> 0.06	
Gentamicin	98.4	0.09	1.77	≤ 0.5	0.5	> 32	Cefotaxime	94.2	1.4	2	4	8	≤ 0.06	
Levofloxacin	90.35	0.00	9.28	0.25	1	> 32	Cefotaxime	94.3	2.2	2.6	4	8	≤ 0.06	
Linezolid	99.9	0.01	2	4	0.12	> 16	Cefotaxime	94.4	2.9	3.6	4	8	≤ 0.06	
Moxifloxacin	90.6	0.8	8.6	≤ 0.06	0.25	0.06	Cefotaxime	94.5	2.9	3.6	4	8	≤ 0.06	
Nitrofurantoin	98.8	0.03	0.09	16	16	≤ 0.5	Cefotaxime	94.6	3.0	3.7	4	8	≤ 0.06	
Telavancin	100.0			0.06	0.06	0.12	Cefotaxime	94.7	3.1	3.8	4	8	≤ 0.06	
Tigecycline <sup>b</sup>	99.8	0.2	0.12	0.25	0.03	2	Cefotaxime	94.8	3.2	3.9	4	8	≤ 0.06	
Tobramycin	97.3	0.3	2.5	≤ 0.5	≤ 0.5	> 64	Cefotaxime	94.9	3.3	4.0	4	8	≤ 0.06	
Trimethoprim-Sulfra	99.5	0.5	≤ 0.12	≤ 0.12	≤ 0.12	> 8	Cef							