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Antimicrobial Resistance in 13,163 Pathogens from Canadian Hospitals: CANWARD Study 2007 and 2008

G. G. ZHANEL*, M. DeCORBY, K. NICHOL, N. LAING, B. WESHNOWESKI, R. VASHISHT, F. TAILOR, A. WIERZBOWSKI, P. BAUDRY, P. LAGACE-WIENS, A. WALKTY, H. ADAM, J. A. KARLOWSKY, M. McCRACKEN, M. R. MULVEY, CANADIAN ANTIMICROBIAL RESISTANCE ALLIANCE (CARA), and D.J. HOBAN

University of Manitoba, Health Sciences Centre, and National Microbiology Laboratory, Winnipeg, Manitoba, Canada

Dr. George G. Zhanel
MS673-820 Sherbrook Street
Winnipeg, Manitoba, Canada
R3A 1R9
Phone: (204) - 787 - 4902
Fax: (204) - 787 - 4699
Email: ggzhanel@pcs.mb.ca

ABSTRACT (REVISED)

Background: The CANWARD study assessed the pathogens causing infections in Canadian hospitals as well as their antimicrobial resistance patterns.

Methods: In a prospective, national surveillance study Jan to Dec 2007 and 2008, inclusive, 12 hospitals (10 in 2008) across Canada submitted clinical isolates from patients attending hospital clinics (C), emergency rooms (ER), medical/surgical wards (W) and intensive care units (ICU). Susceptibility testing was performed by CLSI methods.

Results: 13,163 isolates, 44.3%, 29.8%, 17.5%, and 8.4% from blood, respiratory, urine and wound specimens, respectively were collected. Patient demographics were 53.7%/46.3% male/female, 12.8% ≤ 17yrs, 46.3% 18-64 yrs and 40.9% ≥ 65yrs. Isolates were obtained from patients on W 38.7%, ER 27.9%, C 17.1% and ICU 16.2%. Most common pathogens were: *E. coli* 21.6%, *S. aureus* (MSSA) 13.9%, *S. pneumoniae* (SPN) 9.5%, *P. aeruginosa* 7.7%, *K. pneumoniae* 7.2%, MRSA 5.0%, *H. influenzae* 4.2% and *Enterococcus* spp. 3.1%. Resistance rates (RR) for *E. coli* were: 0% ertapenem (ERT), 0% tigecycline (TGC), 0.2% amikacin (AMK), 1.3% piperacillin/tazobactam (P/T), 7.1% ceftriaxone (CTR), ciprofloxacin (CIP) 23.5% and 27.0% with cotrimoxazole (T/S). RR for *P. aeruginosa* were: 1.2% colistin, 6.1% AMK, 7.2% MER, 7.6% P/T, 10.0% cefepime, and 21.8% CIP. RR for MRSA were: 0% ceftobiprole (BPR), daptomycin (DAP), linezolid (LZD), and TGC, 11.4% T/S, 59.2% clindamycin, 88.6% CIP and 89.0% for clarithromycin.

Conclusions: *E. coli*, MSSA, SPN, *P. aeruginosa*, *K. pneumoniae*, *Enterococcus* spp. and MRSA are the most common pathogens in Canadian hospitals. RR for *E. coli* were lowest with ERT, TGC, AMK and P/T. RR for *P. aeruginosa* were lowest with colistin, AMK, MER and P/T. No resistance occurred in MRSA to BPR, DAP, LZD, and TGC.

INTRODUCTION

Infections caused by antibiotic resistant pathogens is a Canadian and global crisis. Antibiotic resistant pathogens including methicillin-resistant *Staphylococcus aureus* (MRSA, community associated and hospital associated), vancomycin-resistant *Enterococcus* species (VRE), penicillin-resistant *Streptococcus pneumoniae* (PRSP), extended spectrum β-lactamase (ESBL) producing *Escherichia coli* and *Klebsiella* species and fluoroquinolone-resistant and carbapenem-resistant Enterobacteriaceae and *Pseudomonas aeruginosa* are increasing in prevalence in Canada and around the world. Available therapeutic options for the treatment of these antibiotic resistant organisms are severely limited as these organisms frequently display a multidrug resistant (MDR) phenotype.

The goal of the CANWARD study was to assess pathogens associated with and antimicrobial resistance patterns in respiratory, bacteremic, urinary, and wound/IV site infections in Canadian hospitalized patients on medical/surgical wards (W), emergency rooms (ER), outpatient clinics (C) and intensive care units (ICU).

Objectives of CANWARD:

1. To determine the pathogens associated with respiratory, urinary, bacteremic and wound/IV site infections in Canadian patients affiliated with hospitals.
2. To determine the prevalence of antimicrobial resistance in pathogens associated with respiratory, urinary, bacteremic and wound/IV site infections in Canadian patients affiliated with hospitals.
3. To assess the activity of antimicrobials against respiratory, urinary, bacteremic and wound/IV site pathogens in Canadian patients affiliated with hospitals.

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MATERIALS AND METHODS

Participating Sites: From January 2007 to December 2008, 12 sentinel hospital sites (10 in 2008) in major population centres in 7 of the 10 provinces in Canada were recruited. These sites were geographically distributed in a population based fashion: (BC [1 site], Alberta [1 site], Saskatchewan [1 site], Manitoba [1 site], Ontario [4 sites], Quebec [3 sites], Maritimes [1 site]).

Isolate Collection: Each study site was asked to collect and submit pathogens (one per patient) as detailed below:
Respiratory Tract Infections: 150 consecutive isolates per site from patients hospitalized with respiratory tract infections (community or nosocomial). Specimen sources included sputums, tracheal secretions, BAL, bronchoscopy washes/protective brush specimens.
Skin/Skin Structure Infections (wounds): 50 consecutive isolates per site from patients with wound/IV site infections. Specimen sources included high quality swabs, biopsies and aspirates.
Urinary Tract Infections: 100 consecutive isolates per site from patients (inpatients or outpatients) with urinary tract infections.
Blood Stream Infections: 20 consecutive blood stream infection isolates/site/month (240 per year).

All isolates were deemed clinically significant by that site. All organisms were identified at each site using local site criteria and at the reference site, where indicated. At study sites, isolates were subcultured on appropriate solid media and incubated overnight. Amies semi-solid transport media containing charcoal (Difco Laboratories, Detroit, MI) were inoculated with the isolate and sent to the coordinating laboratory (Health Sciences Centre, Winnipeg, Manitoba, Canada), where isolates were subcultured on appropriate media and stocked in skim milk at –70°C.

Antimicrobial Susceptibility Testing: A custom designed microtitre panel was designed with a variety of antimicrobials. Antimicrobials were obtained as laboratory grade powders from their respective manufacturers. Stock solutions were prepared and dilutions made as described by the Clinical Laboratory Standards Institute (2006 CLSI). Following two subcultures from frozen stock, the MICs of the antimicrobial agents for the isolates were determined by the CLSI approved broth microdilution method. Briefly, 96-well custom designed microtitre plates containing doubling antibiotic dilutions in 100 µl/well of cation adjusted Mueller-Hinton broth (eg. for Enterobacteriaceae) with or without lysed horse blood (2-5% V/V) [eg. for *S. pneumoniae*) was inoculated to achieve a final concentration of approximately 5×10^5 CFU/mL and incubated in ambient air for 24 hours prior to reading. Colony counts were performed periodically to confirm inocula. Quality control was performed every two weeks using a variety of ATCC QC organisms. For all antimicrobials tested, MIC interpretive standards were defined according to CLSI breakpoints (M100-S16, 2006). The following interpretive breakpoints (FDA) were used for tigecycline: susceptible (S), intermediate (I) and resistant (R) (µg/mL): *S. aureus* (MSSA and MRSA) ≤ 0.5 (S); *Enterococcus* spp., ≤ 0.25 (S); Enterobacteriaceae, ≤ 2 (S), 4 (I), and ≥ 8 (R). Health Canada breakpoints were used for ceftobiprole: susceptible (S), intermediate (I) and resistant (R) (µg/mL): *S. aureus* (MSSA and MRSA) 4 (S); *Streptococcus* spp. other than *S. pneumoniae* ≤ 0.5 (S); Enterobacteriaceae, ≤ 1 (S), 2 (I), and ≥ 4 (R).

CONCLUSIONS

- Isolates were obtained from patients on W 38.7% (29.6% medical/9.1% surgical), ER 27.9%, C 17.1% and ICU 16.2%.
- The most common pathogens were: *E. coli* 21.6%, *S. aureus* (MSSA) 13.9%, *S. pneumoniae* 9.5%, *P. aeruginosa* 7.7%, *K. pneumoniae* 7.2%, MRSA 5.0%, *H. influenzae* 4.2% and *Enterococcus* spp. 3.1%.
- Susceptibility rates for *E. coli* were: 100% ertapenem and meropenem (MER), 99.8% tigecycline (TGC), 99.5% amikacin (AMK) and 97.3% piperacillin/tazobactam (P/T) and 95.0% ceftobiprole, 91.4% ceftriaxone (CTR), 89.3% gentamicin (GEN), 73.0% trimethoprim/sulfamethoxazole (T/S) and 76.2% ciprofloxacin (CIP).
- Susceptibility rates for *P. aeruginosa* were: 92.5% P/T, 88.8% MER, 88.2% ceftazidime, 88.6% AMK, 64.2% GEN and 69.5 % CIP.
- Susceptibility rates for MRSA were: 100% ceftobiprole, DAP, LZD and TGC, 99.8% vancomycin, 88.6% T/S, 40.6% clindamycin, 11.3% CIP and 10.8% for clarithromycin.

RESULTS

Demographics of CANWARD 2007-2008

Gender	n	% of Total
Female	6014	45.7
Male	7149	54.3
	13,163	

Age Group	n	% of Total
17 and under	1686	12.8
18 to 64	6096	46.3
65 or greater	5381	40.9
	13,163	

Specimen Source	n	% of Total
Blood	5825	44.3
Respiratory	3918	29.8
Urine	2310	17.5
Wound / IV Site	1110	8.4
	13,163	

Ward Type	n	% of Total
Clinic	2249	17.1
ER	3676	27.9
ICU	2137	16.2
Medical	3900	29.6
Surgical	1201	9.1
	13,163	

Most Common Pathogens Overall (n=13,163)

Rank	Organism	n	% of Total
1	*E. coli*	2837	21.6
2	*S. aureus* – MSSA	1830	13.9
3	*S. pneumoniae*	1246	9.5
4	*P. aeruginosa*	1007	7.7
5	*K. pneumoniae*	945	7.2
6	*S. aureus* – MRSA	657	5.0
7	*CNS/ S. epidermidis*	600	4.6
8	*H. influenzae*	556	4.2
9	*Enterococcus* spp.	413	3.1
10	*E. cloacae*	280	2.1
11	*E. faecalis*	262	2.0
12	*P. mirabilis*	204	1.5
13	*S. pyogenes*	202	1.5
14	*S. agalactiae*	189	1.4
15	*S. marcescens*	177	1.3
16	*K. oxytoca*	176	1.3
17	*S. maltophilia*	164	1.2
18	*M. catarrhalis*	145	1.1
19	*S. viridans*	110	0.8
20	*E. faecium*	108	0.8
	Other	1055	8.0
		13,163	

Most Common Pathogens by Infectious Site

Blood

Rank	Organism	n	% of Total
1	*E. coli*	1316	22.7
2	*S. aureus* - MSSA	786	13.5
3	*CNS / S. epidermidis*	517	8.9
4	*K. pneumoniae*	404	7.0
5	*S. pneumoniae*	355	6.1
6	*S. aureus* - MRSA	278	4.8
7	*E. faecalis*	243	4.2
8	*P. aeruginosa*	228	3.9
9	*E. cloacae*	136	2.3
10	*C. albicans*	118	2.0
11	*S. pyogenes*	111	1.9
12	*S. viridans*	108	1.9
13	*S. agalactiae*	103	1.8
14	*E. faecium*	100	1.7
15	*K. oxytoca*	83	1.4
16	*S. marcescens*	75	1.3
17	*P. mirabilis*	67	1.2
18	*C. glabrata*	39	0.7
19	*S. mitis*	36	0.6
20	*BHS gr G*	32	0.6
	Other	690	11.9
		5825	

Respiratory

Rank	Organism	n	% of Total
1	*S. pneumoniae*	895	22.9
2	*S. aureus* - MSSA	619	15.8
3	*P. aeruginosa*	597	15.2
4	*H. influenzae*	523	13.4
5	*S. aureus* - MRSA	215	5.5
6	*E. coli*	162	4.1
7	*M. catarrhalis*	143	3.7
8	*K. pneumoniae*	127	3.2
9	*S. maltophilia*	121	3.1
10	*S. marcescens*	83	2.1
11	*E. cloacae*	68	1.7
12	*K. oxytoca*	47	1.2
13	*P. mirabilis*	29	0.7
14	*H. parainfluenzae*	28	0.7
15	*S. agalactiae*	25	0.6
16	*S. pyogenes*	21	0.5
17	*Enterococcus* spp.	19	0.5
18	*E. aerogenes*	18	0.5
19	*Haemophilus* spp.	14	0.4
20	*C. freundii*	11	0.3
	Other	153	3.9
		3918	

Urine

Rank	Organism	n	% of Total
1	*E. coli*	1259	54.5
2	*Enterococcus* spp.	318	13.8
3	*K. pneumoniae*	210	9.1
4	*P. mirabilis*	95	4.1
5	*P. aeruginosa*	78	3.4
6	*CNS / S. epidermidis*	46	2.0
7	*E. cloacae*	41	1.8
8	*S. aureus* - MSSA	36	1.6
9	*K. oxytoca*	36	1.6
10	*S. agalactiae*	33	1.4
11	*S. aureus* - MRSA	30	1.3
12	*C. freundii*	24	1.0
13	*M. morganii*	18	0.8
14	*C. koseri*	11	0.5
15	*S. marcescens*	9	0.4
16	*E. aerogenes*	8	0.3
17	*Klebsiella* spp.	8	0.3
18	*S. saprophyticus*	7	0.3
19	*P. vulgaris*	4	0.2
20	*S. maltophilia*	3	0.1
	Other	36	1.6
		2310	

Wound / IV Site

Rank	Organism	n	% of Total
1	*S. aureus* - MSSA	387	34.9
2	*S. aureus* - MRSA	134	12.1
3	*P. aeruginosa*	103	9.3
4	*E. coli*	97	8.7
5	*S. pyogenes*	69	6.2
6	*Enterococcus* spp.	47	4.2
7	*CNS / S. epidermidis*	36	3.2
8	*E. cloacae*	35	3.2
9	*K. pneumoniae*	31	2.8
10	*S. agalactiae*	28	2.5
11	*P. mirabilis*	13	1.2
12	*K. oxytoca*	10	0.9
13	*S. marcescens*	10	0.9
14	*S. maltophilia*	10	0.9
15	*E. faecalis*	9	0.8
16	*C. freundii*	8	0.7
17	*BHS gr G*	8	0.7
18	*E. faecium*	7	0.6
19	*M. morganii*	6	0.5
20	*H. influenzae*	6	0.5
	Other	56	5.0
		1110	

Most Common Pathogens by Ward Type

Hospital Clinic

Rank	Organism	n	% of Total
1	*E. coli*	445	19.8
2	*S. aureus* - MSSA	392	17.4
3	*P. aeruginosa*	270	12.0
4	*S. pneumoniae*	215	9.6
5	*H. influenzae*	152	6.8
6	*CNS / S. epidermidis*	99	4.4
7	*K. pneumoniae*	77	3.4
8	*S. aureus* - MRSA	71	3.2
9	*Enterococcus* spp.	64	2.8
10	*S. maltophilia*	49	2.2
11	*M. catarrhalis*	48	2.1
12	*E. cloacae*	36	1.6
13	*S. marcescens*	30	1.3
14	*S. agalactiae*	27	1.2
15	*P. mirabilis*	26	1.2
16	*E. faecalis*	25	1.1
17	*S. pyogenes*	23	1.0
18	*K. oxytoca*	23	1.0
19	*C. freundii*	14	0.6
20	*H. parainfluenzae*	11	0.5
	Other	152	6.8
		2249	

Emergency Room

Rank	Organism	n	% of Total
1	*E. coli*	1101	30.0
2	*S. aureus* - MSSA	512	13.9
3	*S. pneumoniae*	400	10.9
4	*K. pneumoniae*	206	5.6
5	*P. aeruginosa*	155	4.2
6	*S. aureus* - MRSA	154	4.2
7	*H. influenzae*	144	3.9
8	*S. pyogenes*	120	3.3
9	*CNS / S. epidermidis*	107	2.9
10	*S. agalactiae*	76	2.1
11	*Enterococcus* spp.	69	1.9
12	*P. mirabilis*	67	1.8
13	*E. faecalis*	60	1.6
14	*E. cloacae*	43	1.2
15	*K. oxytoca*	43	1.2
16	*S. viridans*	42	1.1
17	*BHS gr G*	27	0.7
18	*M. catarrhalis*	25	0.7
19	*M. morganii*	21	0.6
20	*S. marcescens*	20	0.5
	Other	284	7.7
		3676	

ICU

Rank	Organism	n	% of Total
1	*S. aureus* - MSSA	288	13.5
2	*S. pneumoniae*	249	11.7
3	*E. coli*	235	11.0
4	*P. aeruginosa*	171	8.0
5	*CNS / S. epidermidis*	150	7.0
6	*K. pneumoniae*	143	6.7
7	*S. aureus* - MRSA	122	5.7
8	*H. influenzae*	97	4.5
9	*E. cloacae*	82	3.8
10	*Enterococcus* spp.	49	2.3
11	*S. marcescens*	48	2.2
12	*E. faecalis*	47	2.2
13	*S. maltophilia*	44	2.1
14	*K. oxytoca*	43	2.0
15	*C. albicans*	40	1.9
16	*M. catarrhalis*	32	1.5
17	*E. faecium*	24	1.1
18	*S. agalactiae*	21	1.0
19	*P. mirabilis*	20	0.9
20	*E. aerogenes*	18	0.8
	Other	214	10.0
		2137	

Medical Ward

Rank	Organism	n	% of Total
1	*E. coli*	852	21.9
2	*S. aureus* - MSSA	465	12.0
3	*P. aeruginosa*	325	8.4
4	*S. pneumoniae*	316	8.1
5	*K. pneumoniae*	263	6.8
6	*S. aureus* - MRSA	222	5.7
7	*CNS / S. epidermidis*	201	5.2
8	*Enterococcus* spp.	165	4.2
9	*H. influenzae*	124	3.2
10	*E. faecalis*	94	2.4
11	*E. cloacae*	79	2.0
12	*S. marcescens*	66	1.7
13	*P. mirabilis*	62	1.6
14	*S. agalactiae*	57	1.5
15	*C. albicans*	53	1.4
16	*K. oxytoca*	51	1.3
17	*S. maltophilia*	43	1.1
18	*E. faecium*	42	1.1
19	*S. viridans*	42	1.1
20	*S. pyogenes*	30	0.8
	Other	348	9.0
		3900	

Surgical Ward

Rank	Organism	n	% of Total
1	*E. coli*	201	16.8
2	*S. aureus* - MSSA	171	14.3
3	*S. aureus* - MRSA	88	7.3
4	*P. aeruginosa*	85	7.1
5	*K. pneumoniae*	83	6.9
6	*S. pneumoniae*	70	5.8
7	*Enterococcus* spp.	64	5.3
8	*CNS / S. epidermidis*	48	4.0
9	*H. influenzae*	41	3.4
10	*E. cloacae*	40	3.3
11	*E. faecalis*	31	2.6
12	*P. mirabilis*	29	2.4
13	*E. faecium*	22	1.8
14	*C. albicans*	18	1.5
15	*K. oxytoca*	16	1.3
16	*S. pyogenes*	16	1.3
17	*S. marcescens*	13	1.1
18	*S. maltophilia*	12	1.0
19	*M. catarrhalis*	12	1.0
20	*C. glabrata*	12	1.0
	Other	129	10.8
		1201	

Activity of various antimicrobials against select pathogens from the CANWARD Study

***E.coli* (2833)**

	Susceptibility					Range	
	% Sus	% Int	% Res	MIC_{50}	MIC_{90}	Minimum	Maximum
Amikacin	99.5%	0.3%	0.2%	≤ 2	4	≤ 2	> 64
Amoxicillin Clavulanate	95.4%	3.9%	0.8%	4	8	0.5	> 32
Cefazolin	84.4%	3.1%	12.5%	2	64	0.5	> 128
Cefepime	96.0%	2.2%	1.8%	≤ 1	≤ 1	≤ 1	> 32
Cefoxitin	91.3%	3.7%	5.0%	4	8	≤ 0.06	> 32
Ceftazidime	95.9%	0.6%	3.5%	≤ 0.5	1	≤ 0.5	> 32
Ceftobiprole*	95.0%	0.4%	7.6%	≤ 1	≤ 1	≤ 1	> 32
Ceftriaxone	91.4%	1.5%	7.1%	≤ 1	2	≤ 1	> 64
Ciprofloxacin	76.2%	0.3%	23.5%	≤ 0.06	> 16	≤ 0.06	> 16
Colistin	No breakpoints defined			0.5	1	≤ 0.06	> 16
Ertapenem	100.0%			≤ 0.06	≤ 0.06	≤ 0.06	1
Gentamicin	89.3%	0.4%	10.3%	≤ 0.5	16	≤ 0.5	> 32
Levofloxacin	76.5%	0.7%	22.8%	≤ 0.06	16	≤ 0.06	> 32
Meropenem	100.0%			≤ 0.06	≤ 0.06	≤ 0.06	0.12
Moxifloxacin	No breakpoints defined			≤ 0.06	> 16	≤ 0.06	> 16
Nitrofurantoin	96.5%	2.4%	1.1%	16	32	0.25	> 256
Piperacillin Tazobactam	97.3%	1.4%	1.3%	2	4	≤ 1	256
Tigecycline*	99.8%	0.2%		0.5	1	0.12	4
Trimethoprim Sulfa	73.0%		27.0%	≤ 0.12	> 8	≤ 0.12	> 8

*Interpretive breakpoints defined by Health Canada (ceftobiprole) or FDA (tigecycline) where applicable

***P. aeruginosa* (1006)**

	Susceptibility					Range	
	% Sus	% Int	% Res	MIC_{50}	MIC_{90}	Minimum	Maximum
Amikacin	88.6%	5.4%	6.1%	8	32	≤ 2	> 64
Cefepime	72.4%	17.6%	10.0%	4	32	≤ 1	> 32
Ceftazidime	88.2%	2.7%	9.1%	2	16	≤ 0.5	> 32
Ceftobiprole	No breakpoints defined			4	16	0.25	> 32
Ciprofloxacin	69.5%	8.8%	21.8%	0.5	8	≤ 0.06	> 16
Colistin	90.8%	8.0%	1.2%	2	2	0.5	> 16
Gentamicin	64.2%	18.1%	17.7%	4	16	≤ 0.5	> 32
Levofloxacin	62.6%	12.6%	24.8%	1	16	≤ 0.06	> 32
Meropenem	88.8%	4.1%	7.2%	0.5	8	≤ 0.06	> 32
Piperacillin Tazobactam	92.5%		7.5%	4	64	≤ 1	> 512

***S. aureus* - MRSA (657)**

	Susceptibility					Range	
	% Sus	% Int	% Res	MIC_{50}	MIC_{90}	Minimum	Maximum
Cefazolin			100.0%**	128	> 128	2	> 128
Cefepime			100.0%**	> 32	> 32	4	> 32
Cefoxitin			100.0%**	> 32	> 32	1	> 32
Ceftazidime			100.0%**	> 32	> 32	16	> 32
Ceftobiprole*	100.0%			1	2	0.5	4
Ceftriaxone			100.0%**	> 64	> 64	16	> 64
Ciprofloxacin	11.3%	0.2%	88.6%	> 16	> 16	0.25	> 16
Clarithromycin	10.8%	0.2%	89.0%	> 32	> 32	≤ 0.03	> 32
Clindamycin	40.6%	0.2%	59.2%	> 8	> 8	≤ 0.12	> 8
Daptomycin	100.0%			0.12	0.25	0.06	1
Ertapenem			100.0%**	8	> 32	0.5	> 32
Levofloxacin	12.0%		88.0%	> 32	> 32	0.12	> 32
Linezolid	100.0%			2	2	≤ 0.12	4
Meropenem			100.0%**	8	32	0.12	> 32
Moxifloxacin	12.0%	0.3%	87.7%	8	> 16	≤ 0.06	> 16
Nitrofurantoin	100.0%			16	16	8	32
Piperacillin Tazobactam			100.0%**	64	128	≤ 1	512
Tigecycline*	100.0%			0.25	0.25	0.12	0.25
Trimethoprim Sulfa	88.6%		11.4%	≤ 0.12	8	≤ 0.12	> 8
Vancomycin	99.8%	0.2%		1	1	≤ 0.5	4

*Interpretive breakpoints defined by Health Canada (ceftobiprole) or FDA (tigecycline) where applicable

**Based on oxacillin susceptibility

Participating CANWARD Investigators / Sites

Investigator	Site	City	Province
Dr. D. Roscoe	Vancouver Hospital	Vancouver	BC
Dr. R. Rennie	University of Alberta Hospitals	Edmonton	AB
Dr. J. Blondeau	Royal University Hospital	Saskatoon	SK
Drs. Hoban / Zhanel	Health Sciences Centre	Winnipeg	MB
Dr. Z. Hussain	London Health Sciences Centre	London	ON
Dr. C. Lee	St. Joseph's Hospital **(2007 only)**	Hamilton	ON
Dr. S. Poutanen	Mount Sinai Hospital	Toronto	ON
Dr. F. Chan	Children's Hosp. of Eastern Ontario	Ottawa	ON
Dr. M. Laverdiere	Hopital Maisonneuve-Rosemont	Montreal	QC
Dr. V. Loo	Montreal General Hospital	Montreal	QC
Dr. V. Loo	Royal Victoria Hospital **(2007 only)**	Montreal	QC
Dr. R. Davidson	Queen Elizabeth II HSC	Halifax	NS