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Continuing Evolution of USA300 (CMRSA10) Community-Associated Methicillin-Resistant *Staphylococcus aureus* (CA-MRSA) in Canadian Hospitals from 2007-2011

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ABSTRACT

Background: As part of the CANWARD surveillance study, we compared the epidemiology of CA-MRSA and healthcare-associated (HA)-MRSA genotypes in Canadian hospitals.
Methods: Between 2007 and 2011, 1266 MRSA were collected from patients attending tertiary-care medical centres across Canada. Susceptibility testing was performed by CLSI broth microdilution. Isolates were characterized by *spa* typing and PCR of the Panton-Valentine leukocidin (PVL) gene. Detection of hVISA was performed by the Etest macromethod and confirmed by population analysis profile-area under the curve.
Results: The annual prevalence of MRSA genotypes is shown below.

MRSA Type	Study Year					P-value*
	2007	2008	2009	2010	2011	
All MRSA (% of all *S. aureus*)	26.1	27	21	21.2	19.3	0.0002
HA-MRSA (% of all MRSA)	79.2	69.1	65.5	58.7	59.7	<0.0001
CMRSA1 [USA600]	2.3	1.1	0	1.8	0.6	0.2951
CMRSA2 [USA100/800]	64.9	56.3	58.6	49.8	55.8	0.0613
CMRSA3/6	10.6	8.8	4.7	3.1	0.6	<0.0001
CMRSA4 [USA200]	0	0.4	0	0.9	0	1
CMRSA5 [USA500]	1	1.5	0	1.3	1.3	1
CMRSA8	0	0.7	1.7	1.8	1.3	0.0813
CMRSA9	0.3	0.4	0.4	0	0	1
CA-MRSA (% of all MRSA)	19.7	27.6	31.9	38.1	36.4	<0.0001
CMRSA7 [USA400]	6.5	5.5	8.2	6.7	7.8	0.576
CMRSA10 [USA300]	13.2	22.1	23.7	31.4	28.6	<0.0001
Unique	1	3.3	2.6	3.1	3.9	0.0362

*P-value determined by Fisher's exact test comparing 2007 vs. 2011 data.

Conclusions: CA-MRSA were significantly more susceptible to CIP, CLR, CLD and SXT than HA-MRSA. The majority of CA-MRSA were PVL(+) and belonged to epidemic type CMRSA10/USA300 while most HA-MRSA were PVL(-) and belonged to epidemic type CMRSA2/USA100/800. CA-MRSA represented 27.8% of all MRSA and is increasing in prevalence in CANWARD hospital sites.

BACKGROUND

Community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) account for an increasing proportion of MRSA isolates in hospitals and long-term care facilities across North America. While skin and soft tissue infections are the most common infections caused by CA-MRSA, invasive disease such as bacteremia associated with sepsis and necrotizing pneumonia can occur. The individuals most often affected by CA-MRSA typically lack established risk factors for MRSA acquisition/infection. CA-MRSA differ from health care-associated MRSA (HA-MRSA) in that they are generally more susceptible to a variety of non-beta-lactam antimicrobial agents. Of particular concern, however, is the emergence of isolates with reduced susceptibility or heterogeneous resistance to vancomycin, an important antimicrobial for the empiric treatment of severe infections. In addition, the majority of CA-MRSA strains harbor virulence determinants such as the Panton-Valentine leukocidin (PVL) as well as other toxins that may contribute to the increasing morbidity and mortality associated with CA-MRSA infections.

PURPOSE

The purpose of this study was to compare the demographics, antimicrobial susceptibilities and molecular epidemiology of community-associated and health care-associated MRSA genotypes in Canada from 2007 to 2011, inclusive.

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MATERIALS & METHODS

Methicillin-Resistant *S. aureus* Isolates
1266 isolates of MRSA were collected between 2007 and 2011 as part of the ongoing CANWARD surveillance study assessing antibiotic resistance in Canadian hospitals. Isolates were received from tertiary-care medical centres (12 in 2007, 10 in 2008, 15 in 2009, 14 in 2010, 15 in 2011) that were geographically distributed in a population-based fashion in 9 of the 10 Canadian provinces. All *S. aureus* were identified at the originating centre using local site criteria. Resistance to methicillin was confirmed at the coordinating laboratory (Health Sciences Centre, Winnipeg, Canada) using the CLSI-approved disk diffusion method with cefoxitin, as well as by growth on MRSA*Select* chromogenic media.

Antimicrobial Susceptibility Testing
The *in vitro* activities of cefazolin, clarithromycin, clindamycin, ciprofloxacin, daptomycin, levofloxacin, linezolid, moxifloxacin, telavancin, tigecycline, trimethoprim-sulfamethoxazole and vancomycin were determined by broth microdilution in accordance with CLSI guidelines (M7-A8, 2009). MIC interpretive standards were defined according to CLSI breakpoints (M100-S21, 2011). The following interpretive breakpoints (FDA) were used: telavancin susceptible, ≤1 μg/ml; tigecycline susceptible, ≤0.5 μg/ml.

Molecular Characterization of MRSA
MRSA status was confirmed by real-time PCR of the *mecA* and *nuc* genes (McDonald et al. 2005. J. Clin. Microbiol. 43:6147-6149). This triplex PCR assay also included primers for the detection of the *lukF-PV* and *lukS-PV* genes encoding the Panton-Valentine leukocidin (PVL) toxin (McDonald et al. 2005. J. Clin. Microbiol. 43:6147-6149).
MRSA strains were characterized by staphylococcal protein A (*spa*) typing as previously described (Golding et al. 2008. Can. J. Infect. Dis. Med. Microbiol. 19:273-281). For the purpose of this study, community-associated (CA)-MRSA and healthcare-associated (HA)-MRSA were defined genotypically (ie. on the basis of their *spa* type) and not epidemiologically as per CDC criteria for distinguishing CA-MRSA from HA-MRSA, because epidemiologic information was not available. There has previously been shown to be good correlation between *spa* types and Canadian epidemic PFGE strain types CMRSA1-10 (Golding et al. 2008. Can. J. Infect. Dis. Med. Microbiol. 19:273-281), allowing for classification of strains as either CA-MRSA or HA-MRSA. Any MRSA with a *spa* type associated with a CMRSA7 (USA400) or CMRSA10 (USA300) genotype were labeled as CA-MRSA while all other *spa* types corresponding to a characterized epidemic type (eg. CMRSA1 [USA600], CMRSA2 [USA100/800], CMRSA4 [USA200], CMRSA5 [USA500], CMRSA3/6, CMRSA8, CMRSA9, etc.) were labeled as HA-MRSA. MRSA with a *spa* type not associated with one of the known Canadian epidemic types were labeled as unique (non-CMRSA).

Detection of Heterogeneous Vancomycin-Intermediate *S. aureus* (hVISA)
All MRSA isolates with a vancomycin MIC of 2 μg/ml (n=27) were screened for the presence of the hVISA phenotype using the Etest macromethod. A randomly selected subset (25% each) of MRSA with vancomycin MICs of 1 μg/ml (n=230) and 0.5 μg/ml (n=31) were included for comparison. MRSA identified as hVISA by the Etest macromethod were further evaluated by population analysis profile-area under the curve (PAP-AUC).

CONCLUSIONS

1. Overall, 28.9% and 68.6% of MRSA strains from Canadian hospitals were identified by *spa* typing as CA-MRSA and HA-MRSA, respectively. The prevalence of CA-MRSA increased significantly from 19.7% in 2007 to 36.4% in 2011 while HA-MRSA decreased from 79.2% to 59.7% during this same period (*P*<0.0001).
2. CA-MRSA genotypes CMRSA7 (USA400) and CMRSA10 (USA300) represented 6.8% and 22.1% of all MRSA, respectively. The prevalence of CMRSA10 (USA300) increased significantly from 13.2% in 2007 to 28.6% in 2011 (*P*<0.0001).
3. CMRSA2 (USA100/800) was the predominant HA-MRSA genotype, accounting for 58.1% of all MRSA and 84.8% of HA-MRSA.
4. The majority (89.6%) of CA-MRSA were PVL(+). 10.4% of CA-MRSA and 99.3% of HA-MRSA were PVL(-).
5. CA-MRSA strains were more susceptible to clarithromycin, clindamycin, fluoroquinolones and trimethoprim-sulfamethoxazole than HA-MRSA.
6. Only 0.5% of CA-MRSA had a vancomycin MIC of 2 μg/ml compared to 3.0% of HA-MRSA (*P*=0.009). Intermediate resistance (MIC, 4 μg/ml) to vancomycin was observed in one MRSA with a PVL-negative CMRSA2 (USA100/800) genotype. No MRSA were resistant to daptomycin, linezolid or telavancin.
7. Detection of hVISA by PAP-AUC was rare overall (2.8%), but was common in isolates with a vancomycin MIC of 2 μg/ml (25.9%).

RESULTS

Figure 1. Proportion of *S. aureus* strains identified as MSSA or MRSA.

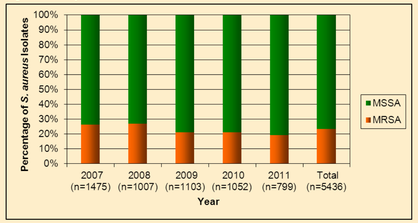

Figure 2. Proportion of MRSA strains identified as CA-MRSA or HA-MRSA.

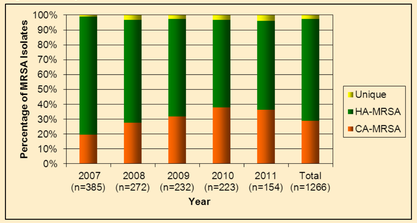

Figure 3. Distribution of CA-MRSA and HA-MRSA PFGE epidemic types.

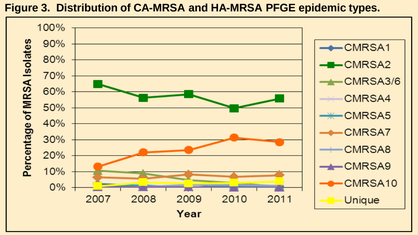

Figure 4. Distribution of PVL(+) and PVL(-) CA-MRSA and HA-MRSA.

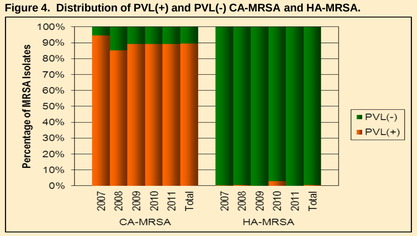

Table 1. Demographics of patients with MRSA infections.

Characteristic	CA-MRSA (n=366)	HA-MRSA (n=868)	Total (n=1266)
Sex, n (%)			
Male	208 (56.8)	520 (59.9)	741 (58.5)
Female	158 (43.2)	348 (40.1)	525 (41.5)
Mean age, years	41.4	65.4	57.7
Median age (range)	43 (1-95)	68 (1-105)	61 (1-105)
Age group, n (%)			
≤ 17	55 (15.0)	10 (1.2)	73 (5.8)
18-64	260 (71.0)	349 (40.2)	627 (49.5)
≥ 65	51 (13.9)	509 (58.6)	566 (44.7)
Region, n (%)			
West	220 (60.1)	226 (26.0)	457 (36.1)
Ontario	108 (29.5)	284 (32.7)	407 (32.1)
Quebec	17 (4.6)	291 (33.5)	313 (24.7)
Maritimes	21 (5.7)	67 (7.7)	89 (7.0)
Hospital ward type, n (%)			
Emergency room	140 (38.3)	133 (15.3)	284 (22.4)
Clinic/office	73 (19.9)	112 (12.9)	191 (15.1)
Intensive care unit	52 (14.2)	170 (19.6)	224 (17.7)
Medical/surgical ward	101 (27.6)	453 (52.2)	567 (44.8)
Infection site, n (%)			
Bloodstream	131 (35.8)	350 (40.3)	492 (38.9)
Respiratory tract	72 (19.7)	331 (38.1)	407 (32.1)
Urinary tract	2 (0.5)	44 (5.1)	47 (3.7)
Wounds/IV sites	161 (44.0)	143 (16.5)	320 (25.3)

Table 2. Vancomycin MIC distributions for CA-MRSA and HA-MRSA.

Genotype, Study Year	Number (%) at each Vancomycin MIC				
	≤0.25	0.5	1	2	4
CA-MRSA					
2007 (n=76)		17 (22.4)	59 (77.6)		
2008 (n=75)		17 (22.7)	58 (77.3)		
2009 (n=74)		8 (10.8)	64 (86.5)	2 (2.7)	
2010 (n=85)		11 (12.9)	74 (87.1)		
2011 (n=56)		22 (39.3)	34 (60.7)		
HA-MRSA					
2007 (n=305)	5 (1.6)	22 (7.2)	274 (89.8)	4 (1.3)	
2008 (n=188)		18 (9.6)	161 (85.6)	8 (4.3)	1 (0.5)
2009 (n=152)		14 (9.2)	131 (86.2)	7 (4.6)	
2010 (n=131)		9 (6.9)	116 (88.5)	6 (4.6)	
2011 (n=92)		13 (14.1)	79 (85.9)		

Table 3. Detection of hVISA in MRSA strains from across Canada.

Phenotype	Vancomycin MIC (no. tested)			
	0.5 μg/ml (n=31)	1 μg/ml (n=230)	2 μg/ml (n=27)	Total (n=288)
hVISA+ by Etest macromethod [n (%)]	0 (0)	17 (7.4)	15 (55.6)	32 (11.1)
hVISA+ by population analysis profile [n (%)]	0 (0)	1 (0.4)	7 (25.9)	8 (2.8)

Of the 8 hVISA identified by PAP-AUC, 7 (87.5%) had vancomycin MICs of 2 μg/ml and belonged to healthcare-associated *spa* types.

Table 4. Comparison of antibiotic resistance rates among CA-MRSA and HA-MRSA.

CA-MRSA (n=366)

Antibiotic	MIC_{50}	MIC_{90}	MIC Range	% of Isolates per Category		
				S	I	R
Cefazolin	16	64	1 - >128	-	-	100.0%[a]
Ciprofloxacin	16	>16	0.12 - >16	33.4%	0.8%	65.8%
Clarithromycin	>16	>16	≤0.25 - >16	24.8%	0.3%	74.9%
Clindamycin	≤0.25	>8	≤0.25 - >8	87.0%	0.0%	13.0%
Daptomycin	0.25	0.25	0.12 - 1	100.0%	-	-
Levofloxacin	4	8	0.12 - 32	39.7%	0.0%	60.3%
Linezolid	2	2	1 - 4	100.0%	-	-
Moxifloxacin	2	2	≤0.06 - 16	35.1%	6.8%	58.1%
Telavancin	0.25	0.5	0.12 - 1	100.0%	-	-
Tigecycline	0.25	0.25	0.06 - 0.5	100.0%	-	-
TMP-SMX	≤0.12	≤0.12	≤0.12 - 2	100.0%	-	0.0%
Vancomycin	1	1	0.5 - 2	100.0%	0.0%	0.0%

HA-MRSA (n=868)

MIC_{50}	MIC_{90}	MIC Range	% of Isolates per Category		
			S	I	R
128	>128	1 - >128	-	-	100.0%[a]
>16	>16	0.25 - >16	2.8%	0.0%	97.2%
>16	>16	≤0.25 - >16	4.6%	0.0%	95.4%
>8	>8	≤0.25 - >8	30.4%	0.1%	69.5%
0.25	0.25	0.06 - 1	100.0%	-	-
>32	>32	0.12 - >32	3.0%	0.0%	97.0%
2	4	≤0.12 - 4	100.0%	-	0.0%
8	>16	≤0.06 - >16	2.9%	0.1%	97.0%
0.25	0.5	≤0.06 - 1	100.0%	-	-
0.25	0.5	0.06 - 2	99.6%	-	0.4%
≤0.12	8	≤0.12 - >8	88.6%	-	11.4%
1	1	≤0.25 - 4	99.9%	0.1%	0.0%

All MRSA (n=1266)

MIC_{50}	MIC_{90}	MIC Range	% of Isolates per Category		
			S	I	R
64	>128	1 - >128	-	-	100.0%[a]
>16	>16	0.12 - >16	13.7%	0.3%	85.9%
>16	>16	≤0.25 - >16	12.2%	0.1%	87.7%
>8	>8	≤0.25 - >8	48.2%	0.1%	51.7%
0.25	0.25	0.06 - 1	100.0%	-	-
>32	>32	0.12 - >32	14.1%	0.0%	85.9%
2	2	≤0.12 - 4	100.0%	-	-
8	>16	≤0.06 - >16	14.4%	2.0%	83.6%
0.25	0.5	≤0.06 - 1	100.0%	-	-
0.25	0.5	0.06 - 2	99.8%	-	0.2%
≤0.12	0.25	≤0.12 - >8	92.2%	-	7.8%
1	1	≤0.25 - 4	99.9%	0.1%	0.0%

[a] Based on cefoxitin disk test.

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