CONCISE COMMUNICATION

Methicillin-Resistant *Staphylococcus aureus* in Canadian Aboriginal People

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We describe 279 hospitalized Canadian aboriginals in whom methicillin-resistant *Staphylococcus aureus* (MRSA) was detected. They were identified in 38 Canadian hospitals from 1995 through 2002. Compared with nonaboriginals, aboriginals were more likely to be younger than 18 years of age (OR, 1.8; $P < .0001$), to have had an MRSA infection (OR, 3.8; $P < .0001$), and to have had MRSA isolated from specimens of skin or soft tissue (OR, 4.1; $P = .016$). The clinical features of MRSA infection in aboriginals are distinct from those in the general patient population with MRSA infection in Canadian hospitals, and the genetic background of MRSA isolates from aboriginals also varies from that of strains from the non-aboriginal population.

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In the past few years there has been an increasing awareness that community-associated methicillin-resistant *Staphylococcus aureus* (MRSA) infection is occurring in native or aboriginal populations in many countries.[1-5] In this report, we describe the epidemiology of MRSA infection in Canadian aboriginals identified through a national hospital-based surveillance network, the Canadian Nosocomial Infection Surveillance Program (CNISP).

METHODS

Surveillance for MRSA has been conducted by 38 hospitals participating in the CNISP since January 1995. Surveillance methods have been described elsewhere.[6] When a new case of MRSA infection or colonization in an inpatient was identified, the infection control practitioner used a standardized data collection form to abstract demographic and clinical information from the medical records. Aboriginal ethnicity was defined by federal registration as status or nonstatus Indian, Metis, or Inuit, or by self-identification of individuals as "First Nations People" or "aboriginal." The presence of infection caused by MRSA was defined according to standard definitions.[7] MRSA colonization was defined as the presence of MRSA without clinical signs or symptoms of infection. For MRSA to be considered to have been acquired in a hospital or healthcare facility there had to be no evidence that the organism was present at the time of admission, or there had to be evidence that it was likely acquired during a previous hospitalization. The organism was assumed to have been community-acquired or community-associated if there was no evidence of acquisition in a hospital or a long-term care or other healthcare facility.

MRSA isolates were typed with pulsed-field gel electrophoresis (PFGE) after extraction of DNA and digestion of the extract with *Sma*I, as described elsewhere.[8] Electrophoretically generated DNA profiles were digitized and analyzed using GelCompar software, version 4.1 (Applied Maths). Isolates with certain specific DNA profiles were grouped into 1 of 6 Canadian epidemic strains of MRSA (designated "CMRSA-1, CMRSA-2," etc),[8] and compared with MRSA clones described in the United States.[9] For SCC*mec* typing, PCR was done using 9 primer pairs targeting loci of the 4 different SCC*mec* cassettes.[10] Detection of the Panton-Valentine leukocidin (PVL) gene locus was done with PCR as described elsewhere.[11]

Data were analyzed using SAS software, version 6.12 (SAS Institute). Categorical variables were compared using the Fisher exact test or the χ^2 test, as appropriate. Continuous variables were compared using Student's t test. All P values were 2-tailed, and a P value of .05 or less was considered to be statistically significant. Variables found to be significant in univariate analysis were included in a backward logistic regression model. Effect modification between factors was searched for by testing appropriate interaction terms for statistical significance.

RESULTS

In the years 1995-2002, a total of 279 aboriginals in whom MRSA was detected were hospitalized in CNISP hospitals, representing 2.2% of all detected persons with MRSA who were identified in the surveillance, and 3.5% of those for whom ethnicity was reported. Although the incidence of MRSA colonization or infection in these hospitals increased from 0.5 cases per 1,000 admissions in 1995 to 4.5 cases per 1,000 admissions in 2002 ($P < .001$), the proportion of cases in aboriginals did not vary over time.

Demographic and clinical characteristics of patients with MRSA isolated are summarized in Table 1. In the logistic regression analysis, variables that were found to be independently associated with isolation of MRSA from aboriginals included the following: age of less than 18 years (odds ratio [OR], 11.0; 95% confidence interval [CI], 7.5-16.0; $P < .0001$), female sex (OR, 1.7; 95% CI, 1.3-2.2; $P < .0001$), hospitalization in western Canadian provinces (OR, 11.4; 95% CI, 4.7-27.8; $P < .0001$), MRSA infection at any anatomical site (OR, 3.8; 95% CI, 2.1-7.2; $P = .006$), and MRSA infection or colonization involving skin and soft tissues (OR, 4.1; 95% CI, 1.7-9.9; $P = .016$).

TABLE 1. Demographic and Clinical Characteristics of Patients Infected With Methicillin-Resistant *Staphylococcus aureus* (MRSA) in Canadian Hospitals, 1995-2002

Characteristic	Aboriginals (n = 279)	Nonaboriginals (n = 7,647)	P
Sex			
Male	142 (51)	4,560 (60)	.01
Female	136 (49)	3,068 (40)	
Unknown	1 (0)	19 (0.2)	
Age			
⩽18 years	54 (19)	181 (2)	<.0001
⩾19 years	213 (76)	7,330 (96)	
Unknown	12 (4)	136 (2)	
Median, in years	45	71	<.0001
Region of Canada[a]			
West	230 (82)	2,494 (33)	<.0001
Central	45 (16)	4,690 (61)	
East	4 (1)	463 (6)	
Hospital admission in previous 12 months	157 (56)	4,551 (60)	.31
Reason culture performed			
Clinical indication	197 (71)	3,379 (44)	<.0001
Surveillance or screening	57 (20)	2,811 (37)	
Outbreak investigation	19 (7)	1,339 (18)	
Unknown	6 (2)	118 (2)	
MRSA infection	171 (61)	2,560 (33)	<.0001
Site of MRSA infection[b]			
Skin or soft tissue	94 (34)	1,012 (13)	<.0001
Surgical site	30 (11)	582 (8)	.07
Respiratory tract	45 (16)	825 (11)	.01
Urinary tract	9 (3)	293 (4)	.72
Bloodstream	23 (8)	396 (5)	.03
Other	16 (6)	307 (4)	.20
Location of MRSA acquisition			
Community	73 (26)	331 (4)	<.0001
Long-term care facility	3 (1)	449 (6)	
Hospital	102 (37)	5,542 (72)	
Unknown	101 (36)	1,325 (17)	

NOTE. Data are no. (%) of subjects, unless indicated otherwise. Percentages may not sum to 100% because of rounding.

[a] West: Manitoba, Saskatchewan, Alberta, or British Columbia. Central: Ontario or Quebec. East: Nova Scotia, New Brunswick, or Newfoundland.

[b] Some patients had infection at more than 1 anatomical site.

A total of 148 MRSA isolates from aboriginals and 3,589 isolates from nonaboriginals were available for antimicrobial susceptibility testing and molecular typing by PFGE. Isolates from aboriginals were less likely to be resistant to erythromycin or clindamycin, compared with MRSA isolates from nonaboriginals (72% vs 94% of isolates; $P < .0001$), as well as to trimethoprim-sulfamethoxazole (22% vs 49%; $P < .0001$) and ciprofloxacin (46% vs 90%; $P < .0001$). However, MRSA isolates from aboriginals were more likely to be resistant to mupirocin than were isolates from nonaboriginals (10% vs. 4%; $P = .001$). Resistance to glycopeptides was not detected in any MRSA isolates. Only 64% of the isolates from aboriginals could be grouped into 1 of 6 previously described Canadian epidemic clones, compared with 92% of the strains from nonaboriginals ($P < .0001$) (Table 2).[8] More than half (59%) of the MRSA isolates from aboriginals were SCC*mec* type IV. Fifteen (10%) of 149 isolates from aboriginals contained the PVL gene locus.

DISCUSSION

In the past decade, the dissemination of MRSA in native aboriginal populations has been reported in parts of the United States, Australia, New Zealand, and islands of the south Pacific.[1-4] Infections caused by MRSA have also been reported among First Nations People in Canada, most often from the

TABLE 2. Strains of Methicillin-Resistant *Staphylococcus aureus* (MRSA) Isolates Recovered From Aboriginals and From Nonaboriginals in Canada, 1995-2002

Strain[a]	No. (%) of Isolates		
	From Aboriginals (n = 148)	From Nonaboriginals (n = 3,589)	P
CMRSA-1	16 (11)	1,527 (43)	<.0001
CMRSA-2	32 (22)	592 (16)	.03
CMRSA-3	7 (5)	275 (8)	.24
CMRSA-4	8 (5)	185 (5)	.89
CMRSA-5	23 (16)	265 (7)	.0005
CMRSA-6	8 (5)	475 (13)	.008
Other	54 (36)	270 (8)	<.0001

[a] Isolates were grouped into 1 of 6 Canadian epidemic strains of MRSA (CMRSA) on the basis of DNA profiles determined by pulsed-field gel electrophoresis (PFGE), as described elsewhere.[8] CMRSA-1 most closely resembles PFGE type USA500; CMRSA-2 most closely resembles PFGE type USA100; CMRSA-4 most closely resembles PFGE type USA200; CMRSA-5 strains from aboriginals most closely resemble PFGE type USA300.

prairie provinces.[5,12,13] Aboriginal Canadians comprise approximately 3% of the Canadian population and are known to have higher rates of many respiratory, enteric, and bloodborne infectious diseases.[14] To our knowledge, this is the first study in Canada to determine the clinical and epidemiologic features of MRSA colonization and infection in hospitalized aboriginals, using data obtained from national surveillance.[6]

In this study, aboriginals in whom MRSA was detected were almost twice as likely to be infected (61%) than were nonaboriginals (33%) ($P < .0001$). This may not be surprising, given that the majority of cultures that yielded MRSA for aboriginals were performed to confirm suspected infection, rather than for screening or surveillance. This could bias the results, if criteria for MRSA screening were applied differently to hospitalized aboriginals and nonaboriginals, although we do not believe this was likely to have occurred. Most of these infections involved skin and soft tissues, as reported elsewhere.[2,4,15]

In previous studies, it was assumed that the majority of MRSA isolates from aboriginal patients were community associated.[1-5,12,15] In several of these studies, transmission of a single clone of MRSA was thought to have occurred in the community.[1,2,15] In the present study, we used stringent criteria to define community acquisition, and we considered that most MRSA isolates from hospitalized aboriginals were associated with a hospital or healthcare facility. Nevertheless, Canadian aboriginals were 6 times more likely to have had community-associated MRSA isolated than were nonaboriginals (26% vs. 4%; $P < .0001$). A lower rate of healthcare-associated MRSA colonization and infection among Canadian aboriginals may be explained, in part, by reduced access to healthcare facilities. Further evidence of community acquisition of at least a subset of MRSA strains isolated from aboriginals may also be provided by laboratory characterization of these isolates. MRSA isolates from Canadian aboriginals tended to be more susceptible to antimicrobial agents and to possess the SCC*mec* type IV locus and the PVL gene locus. These findings are typical of community-acquired MRSA strains internationally, even when strains are of diverse genetic backgrounds.[16-19]

The results of this study are similar to those of previous reports from Canadian prairie provinces,[5,12,13] indicating that MRSA is being transmitted within native communities. These observations may be explained, in part, by socioeconomic and demographic factors. Several markers for poorer health status among First Nations People in Canada have been identified, including lower life expectancy, higher infant mortality, and higher hospitalization rates.[14,20] Overcrowded housing on native reserves has been a recognized problem for many years; in 1999, nineteen percent of dwellings had more than 1 person per room, and only 57% of the housing units were considered to be adequate.[20] Overcrowding, as reflected by large household size, was recently found to be associated with MRSA carriage in a rural American Indian population in Washington state.[21]

The results of this study indicate that the epidemiology and clinical characteristics of MRSA infection in Canadian aboriginals is similar to that reported in other native or aboriginal populations around the world. However, they are distinct from those of the general patient population with MRSA infection in Canadian hospitals. The genetic background of the MRSA isolates from aboriginals also varies from that of nonaboriginal strains. Further investigations are required to determine the incidence of MRSA infection in aboriginals in Canada and to define risk factors associated with the acquisition of this organism in native communities.

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