Abstract
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Comparative Genomics of a Population of Human, Animal, and Environmental Methicillin-resistant *Staphylococcus aureus* Isolates in Ohio

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Study Objective

- To demonstrate genotypic similarities and differences among a diverse collection of human, animal, and environmental methicillin-resistant *Staphylococcus aureus (*MRSA) isolates.

Background

- MRSA is a cause of serious infections among patients with healthcare-associated risk factors, and in more recent years, infections have increased in community and veterinary settings.
- Antimicrobial drug resistance has added to the complexity of treating infections caused by MRSA.
- The role of the environment as a source of MRSA in hospital and veterinary clinic settings in which endemic cross-infection occurs over an extended period is still not clear; thus, emphasizing the need for a more descriptive examination of the role of environmental surfaces in MRSA transmission.

Methods

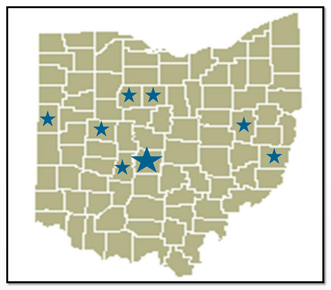

Figure 1: Map of Sampling Areas in Ohio. MRSA isolates were collected from The Ohio State University Wexner Medical Center, Veterinary Medical Center, and seven smaller community hospitals.

Data Collection

- From 2007 to 2010, a total of 1284 human MRSA isolates were collected prospectively and retrospectively from hospitals in the Ohio State Health Network (*see Figure 1*).
- Animal MRSA isolates were collected through canine and equine active surveillance programs. Samples from 41 canine and 7 equine were collected from the nasal cavity, ears, perianal area, and skin lesions.
- A total of 254 environmental MRSA isolates were collected from staff contact areas, general public contact areas, and canine and equine contact areas.

Measures of Interest

- Culture sites were documented for each MRSA isolate.
- Antimicrobial susceptibility profiles were collected, and multi-drug resistance (MDR) was defined as a bacteria resistant to three or more antimicrobial classes.
- MRSA isolates were genotyped using staphylococcal cassette chromosome *mec* (SCC*mec*) A typing and pulsed-field gel electrophoresis (PFGE).

Data Analysis

- Descriptive statistics, including frequency and percentage data, were compiled.
- Genotypic and phenotypic characteristics were compared among human, animal, and environmental MRSA isolates.

Results

Table 1. MRSA Isolates Stratified by SCC*mec* A Type

Culture Type	SCC*mec* II, %	SCC*mec* III, %	SCC*mec* IV, %	SCC*mec* V, %	SCC*mec* VI, %	SCC*mec* VIII, %
Human Blood ¥† *(n = 282)*	141 (50.0)	34 (12.1)	104 (36.9)	1 (0.4)	0 (0.0)	2 (0.7)
Canine † *(n = 39)*	36 (92.3)	0 (0.0)	3 (7.7)	0 (0.0)	0 (0.0)	0 (0.0)
Equine † *(n = 7)*	0 (0.0)	0 (0.0)	6 (85.7)	0 (0.0)	1 (14.3)	0 (0.0)
Hospital Environment *(n = 99)*	49 (49.5)	18 (18.2)	31 (31.3)	0 (0.0)	1 (1.0)	0 (0.0)

¥SCC*mec* A type is only known for blood samples in this population of human MRSA isolates
† Contains missing observations, percentages adjusted

Table 2. MRSA Isolates Stratified by PFGE Type

	USA100, %	USA300, %	USA500, %	USA800, %	Other, % *
Human †					
Blood *(n = 301)*	154 (51.2)	79 (26.2)	8 (2.7)	14 (4.7)	46 (15.3)
Skin *(n = 582)*	106 (18.2)	417 (71.6)	22 (3.8)	13 (2.2)	24 (4.1)
Canine † *(n = 39)*	36 (92.3)	0 (0.0)	1 (2.6)	2 (5.1)	0 (0.0)
Equine † *(n = 5)*	0 (0.0)	1 (20.0)	3 (60.0)	1 (20.0)	0 (0.0)
Environmental †					
Hospital *(n = 94)*	49 (52.1)	25 (26.6)	0 (0.0)	1 (1.1)	19 (20.2)
Canine VTH *(n = 81)*	74 (91.4)	2 (2.5)	1 (1.2)	1 (1.2)	3 (3.7)
Equine VTH *(n = 72)*	4 (5.6)	19 (26.4)	34 (47.2)	0 (0.0)	15 (20.8)

* Includes USA600, 700, 1000, 1100, and Iberian and Portuguese PFGE subtypes
† Contains missing observations, percentages adjusted

Results

Table 3. Distribution of Multi-Drug Resistance among MRSA Isolates

	No. of Antibiotic Classes (%) *			
	3	4	5	6
Human				
Blood *(n = 304)*	115 (37.8)	16 (5.3)	8 (2.6)	32 (10.5)
Skin *(n = 619)*	103 (16.6)	14 (2.3)	2 (0.3)	11 (1.8)
Canine *(n = 41)*	11 (26.8)	2 (4.9)	0 (0.0)	1 (2.4)
Equine *(n = 7)*	0 (0.0)	5 (71.4)	2 (28.6)	0 (0.0)
Environmental				
Hospital (n = 99)	0 (0.0)	0 (0.0)	0 (0.0)	99 (100.0)
Canine VTH (n = 82)	3 (3.7)	1 (1.2)	0 (0.0)	2 (2.4)
Equine VTH (n = 73)	0 (0.0)	33 (45.2)	26 (35.6)	0 (0.0)

* Multi-drug resistance was classified as a bacteria resistant to three or more antimicrobial classes

Conclusions

- Canine and equine MRSA populations had distinct genotypic differences with human strains most common among canine isolates.
- While typically associated with community-associated MRSA, USA300 was detected in the healthcare setting.
- Genotypic environmental MRSA isolate data reflected the distribution of strains circulating in human and animal populations associated with such environments.
- Future surveillance and infection control research should emphasize understanding transmission among human, animal, and environmental populations.

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