Published in final edited form as:

JAMA Intern Med. 2014 May ; 174(5): 825. doi:10.1001/jamainternmed.2014.37.

Identifying livestock-associated methicillin-resistant *Staphylococcus aureus* (MRSA) in the United States – Reply

Joan A. Casey, MA and Brian S. Schwartz

Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA (J. Casey, B. Schwartz); Johns Hopkins Center for a Livable Future, Baltimore, MD, USA (J. Casey); Johns Hopkins School of Medicine, Baltimore, MD, USA (B. Schwartz); Geisinger Health System, Danville, PA, USA (B. Schwartz)

RESPONSE

We appreciate the opportunity to respond to Perencevich et al. We emphasize several differences between our work and that of Feingold et al., to which they refer. We studied MRSA infection in a general population representative group and compared them to patients without MRSA infection. Feingold et al. studied MRSA colonization and compared people with ST398 to people with other strains. The inferences that can be made from these two studies are substantially different.

We too were surprised we did not find any ST398. Many have equated ST398 and livestock-associated MRSA.¹ This designation certainly applies to MRSA colonization in Europe, but perhaps less so to MRSA infection in the US. Because of its adaptation to livestock, ST398 may have a limited ability to cause infection in humans² and other strains may arise from livestock in the US. ST398 exists on swine farms in the US,³ but two studies identified ST5 (a common healthcare strain) as the primary colonizer of swine and swine farmers.^{4,5}

We would like to clarify several of the concerns raised regarding our Table 4. First, patients from whom we had isolates and patients in our epidemiologic analysis were not the same because Geisinger does not bank isolates. Second, the two *spa* types that Perencevich et al. state never have been found in swine were only found in one patient each. Third, the community and healthcare groups were defined molecularly, so the fact that 98.5% of community *spa* types in the table were PVL-positive is not surprising.

Perencevich et al. express concern for how we identified MRSA infection patients. We identified 73.9% (n = 2123) using positive laboratory cultures from non-colonization body sites and our results did not change when analysis was restricted to laboratory-confirmed cases. Over 80% of CA-MRSA cases had skin and soft tissue infections (SSTI), so these are not what would be classified as “severe” infections. While it may be true that in this clinical setting only patients whose SSTI was not responding to treatment would have a culture performed, we note that we also found associations of livestock operations with the larger

Corresponding author: Brian S. Schwartz, Professor of Environmental Health Sciences, Epidemiology, and Medicine, Johns Hopkins Bloomberg School of Public Health, 615 N. Wolfe Street, Room W7041, Baltimore, Maryland 21205, 410-955-4158, bschwartz@jhsph.edu.

group of SSTIs independent of MRSA culture. Since most high-density livestock operations in our region are located along major roads, Geisinger has over 40 accessible outpatient clinics, and all patients had a Geisinger primary care provider, we do not think that distance or access to care were large sources of selection bias. We agree that we cannot exclude confounding by occupation, but note that adjusting final models for the percent of agricultural workers in communities did not alter results.

Finally, after completing analysis of the 200 patients with isolates from 2012 with molecular data in relation to our livestock exposure models, we found associations of community-onset PVL-negative MRSA isolates ($n = 23$) with swine livestock production.⁶ We thus believe that these two papers have raised new concerns about risk of human infection, but agree that replication is needed, particularly studies with concurrent epidemiologic and molecular data on patients and livestock.

References

1. Price LB, Stegger M, Hasman H, et al. *Staphylococcus aureus* CC398: host adaptation and emergence of methicillin resistance in livestock. *mBio*. 2012; 3(1):e00305–00311. [PubMed: 22354957]
2. Graveland H, Wagenaar JA, Bergs K, Heesterbeek H, Heederik D. Persistence of livestock associated MRSA CC398 in humans is dependent on intensity of animal contact. *PLoS One*. 2011; 6(2):e16830. [PubMed: 21347386]
3. Smith TC, Male MJ, Harper AL, et al. Methicillin-resistant *Staphylococcus aureus* (MRSA) strain ST398 is present in midwestern U.S. swine and swine workers. *PLoS One*. 2009; 4(1):e4258. [PubMed: 19145257]
4. Frana TS, Beahm AR, Hanson BM, et al. Isolation and characterization of methicillin-resistant *Staphylococcus aureus* from pork farms and visiting veterinary students. *PLoS One*. 2013; 8(1):e53738. [PubMed: 23301102]
5. Molla B, Byrne M, Abley M, et al. Epidemiology and genotypic characteristics of methicillin-resistant *Staphylococcus aureus* strains of porcine origin. *J Clin Microbiol*. 2012; 50(11):3687–3693. [PubMed: 22972820]
6. Casey JA, Shopsin B, Cosgrove SE, et al. High-density livestock production and molecularly characterized MRSA infections in Pennsylvania. *Environ Health Perspect*. 2014 in press.