Emergence of an Epidemic Clone of Community-Associated Methicillin-Resistant Panton-Valentine Leuocidin-Negative *Staphylococcus aureus* in Cystic Fibrosis Patient Populations

The article by Moroney et al. (3) documents the increased prevalence of community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) strains in different patient populations. Most of the CA-MRSA strains characterized by carriage of staphylococcal cassette chromosome mec (SCCmec) type IV were also positive for the Panton-Valentine leucocidin (PVL) gene (2). However, this gene association is not necessarily indicative of CA-MRSA strains. We analyzed the prevalence and molecular epidemiology of MRSA from the airways of cystic fibrosis (CF) patients in an Italian multicenter study. One hundred eighty-one (7.6%) out of 2,362 CF patients attending 9 Italian CF centers were infected with MRSA. A high prevalence (36%) of SCCmec IV (suggestive of CA-MRSA strains) was found (5). Pulsed-field gel electrophoresis analysis showed a single MRSA clone colonizing 31 patients in 6 centers. Twenty-four out of 31 strains (77.4%) revealed SCCmec type IV, mostly associated with CA-MRSA. All the SCCmec type IV MRSA isolates belonging to the epidemic clone were negative for the PVL genes, as reported by other authors (4).

The high prevalence of MRSAs strains, suggestive of CA-MRSA in a patient population considered at risk for hospital-associated (HA)-MRSA acquisition, is worrisome evidence supporting current opinions that CA-MRSA strains are replacing HA-MRSA strains in health care settings (1, 6).

The interesting question of whether the CA-MRSA clone infected the CF patients in the community or whether the patients acquired the clone in the hospital which they attended regularly is unclear and needs to be further studied.

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Author’s Reply

I read with interest the letter from Silvia Campana et al. describing an MRSA clone positive for SCCmec type IV yet negative for PVL present in their CF patient population. Numerous studies have shown evidence that CA-MRSA is associated with the genes encoding PVL (1, 4, 5). In addition, there is a concomitant low rate of PVL carriage in HA-MRSA isolates (3, 5). We observed two predominant SCCmec IV CA-MRSA clones in our study, almost all of which were PVL positive. However, we are also aware of several reports of CA-MRSA SCCmec IV strains which do not carry the PVL toxin. I believe these studies, along with the author’s work, demonstrate that the molecular characteristics of CA-MRSA isolates are indeed heterogeneous in nature and may vary among different geographic locations. It is of interest whether the CF patients studied presented with active infection or were merely colonized with the CA-MRSA strain, since PVL has been shown to be present less often in CA-MRSA isolates from asymptomatic colonized individuals (2). Nevertheless, the data represent the migration of CA-MRSA into the health care setting and the presence of CA-MRSA infection in patients with risk factors for HA-MRSA. I agree that the highrepresentation of CA-MRSA, irrespective of PVL presence, in a hospital setting is troublesome and may be rapidly blurring the line of distinction between CA-MRSA and HA-MRSA infections.

REFERENCES

reus lineage from Taipei, Taiwan, that carries either the novel staphylococcal chromosome cassette mec (SCCmec) type V or SCCmec type IV. J. Clin. Microbiol. 43:4719–4730.


Shannon M. Moroney
Esoteric Testing/Department of Pathology
Tampa General Hospital
P.O. Box 1289
Tampa, Florida 33601

Phone: (813) 844-4261
Fax: (813) 844-1312
E-mail: smoroney@tgh.org