Antimicrobial Stewardship Lessons: Know When to Say No to Vancomycin

To the Editor—O'Horo et al [1] found that negative predictive value of Gram stain for the diagnosis of ventilator-associated pneumonia (VAP) was 91% (for a prevalence between 20% and 30%), suggesting that VAP is unlikely with a negative Gram stain result. Moreover, there was only a fair concordance between organisms on Gram stain and those recovered from culture. However, a remarkable result was the high accordance between Gram stain and culture results for gram-positive organisms. The impact of these later finding on the empirical therapy for gram-positive organisms is worth to be discussed.

Methicillin-resistant *Staphylococcus aureus* (MRSA) prevalence in VAP is quite variable. Several risk factors for MRSA infection are described, but local prevalence is a potential compelling factor for empirical coverage of this pathogen [2]. Episodes of VAP due to MRSA are associated with high rates of inappropriate therapy and worse outcomes [3], mainly when anti-MRSA drugs are not included in empirical therapy. Despite that, strategies to spare exposure to anti-MRSA drugs such as vancomycin or linezolid could be useful to diminish selection pressure and resistance emergence in gram-positive pathogens [4].

We evaluated the accordance of Gram stain and the bacteria recovered from culture of respiratory tract specimens collected from critical patients at Hospital de Clínicas de Porto Alegre, an 845-bed university-affiliated tertiary care hospital located in Brazil. From May 2006 to December 2010 we prospectively evaluated 406 cases of microbiologic confirmed cases of VAP.

Three hundred seventy-six (92.6%) of 406 samples were obtained using endotracheal aspirate (cutoff for positivity of 10^5 colony-forming units [CFU]/mL), and 30 (7.4%) were obtained by bronchoalveolar lavage (cutoff for positivity of 10^4 CFU/mL). *Acinetobacter baumannii* was identified in 22.7% (n = 92), *S. aureus* in 18.0% (n = 73), *Pseudomonas aeruginosa* in 17.0% (n = 69), and *Klebsiella* species in 13.1% (n = 53) of patients.

For patients with gram-positive cocci in clusters (n = 63), 81.0% (n = 51) had *S. aureus* identified by culture results. In contrast, for those patients without gram-positive cocci in cluster, 6.7% (n = 22) had *S. aureus* identified by culture. Therefore, the presence of gram-positive clusters had a sensitivity of 69.8% (95% confidence interval [CI], 57.8–79.7); specificity of 96.2% (95% CI, 93.3–97.9); positive predictive value of 80.9% (95% CI, 68.7–89.3); and negative predictive value of 93.3% (95% CI, 89.8–85.6) for recovery of *S. aureus* on culture.

The incidence of MRSA in our intensive care unit has progressively fallen from 12.4 infections per 1000 patients-days in 2005, to 2.5 infections per 1000 patient-days in 2010. Of the 22 cases of *S. aureus* infection without gram-positive cocci in cluster identification, 15

were MRSA; of these, 5 were identified in 2006, 6 in 2007, 2 in 2008, 1 in 2009, and 1 in 2010.

Considering these results and those by O'Horo et al, together with the risk associated with vancomycin use (see step 7 of the Centers for Disease Control and Prevention's campaign to prevent antimicrobial resistance in healthcare settings, "Know when to say no to vanco" [5]), we suggest that clinicians reconsider the empirical use of anti-MRSA drugs in low-MRSA-prevalence settings when there is no evidence of gram-positive organisms in clusters on Gram stain of respiratory specimens.

Notes

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