

Healthcare-Associated Pneumonia: Where Do We Go Next?

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(See the major article by Chalmers et al on pages 330–9.)

The term “healthcare-associated infections” was first introduced in 2001 with the recognition of bloodstream-infected patients who came from the community with certain multidrug-resistant (MDR) pathogen risk factors (ie, those for methicillin-resistant *Staphylococcus aureus* [MRSA]) that were similar to those generated in the hospital setting [1, 2]. Follow-up studies further defined these healthcare-associated infections in patients with bacteremia, and this was then expanded to other conditions including pneumonia. The American Thoracic Society (ATS)/Infectious Diseases Society of America (IDSA) [3] defined healthcare-associated pneumonia (HCAP) as pneumonia that originates within the community in individuals who have certain healthcare contact risk factors for acquiring MDR pathogens. The list of MDR risk factors included hospitalization for 2 days or more in the preceding 90 days, residence in a nursing home or extended care facility, home infusion therapy (including antibiotics), chronic

dialysis within 30 days, home wound care, and family member(s) with an MDR pathogen [3]. These risk factors were considered to be associated with the risk for MDR pathogens similar to those pathogens reported in hospital-acquired pneumonia (HAP) and ventilator-associated pneumonia (VAP) patients rather than those observed in community-acquired pneumonia (CAP). The most common MDR pathogens associated with HCAP suggested by the guidelines are MRSA, *Pseudomonas aeruginosa*, *Acinetobacter* spp., and extended-spectrum beta-lactamase (ESBL) producing gram-negative bacilli [3]. The landmark study that originated the term “HCAP” was performed in 4543 patients with positive-culture pneumonia in a large, multi-institutional database of US acute-care hospitals [4]. It was suggested that HCAP patients had a unique MDR microbiology pattern that could lead to inappropriate antibiotic selection, as well as increased mortality. The study identified *S. aureus* as a major pathogen in HCAP patients at a level that was much higher than in CAP patients but similar to that observed in HAP and VAP patients. In addition, HCAP patients carried a higher mortality and longer length of hospital stay compared with CAP patients. However, once an effort was made to implement these “HCAP” criteria in clinical practice, there was considerable confusion and serious risk of overprescribing

antimicrobial agents for patients with pneumonia.

Since the creation of the term “HCAP,” several studies from around the globe have confirmed or contradicted the original definition, questioning its validity and generalizability [5]. In this issue of *Clinical Infectious Diseases*, Chalmers and collaborators [6] attempt to clarify the concerns raised by the HCAP definition using a detailed and elegant meta-analysis and systematic review. The authors identified 24 studies; most were retrospective and only 37.5% had a prospective design. The authors concluded that the concept of HCAP does not accurately identify resistant pathogens, nor does it identify a mortality risk related to the presence of MDR pathogens. In addition, these important limitations put into question the validity of the IDSA/ATS clinical practice guidelines and suggest that the HCAP term be revised.

This interesting study reveals questions and areas that require further exploration. First, are patients coming from the community with pneumonia who were considered at risk for MDR pathogens? After more than 10 years of both retrospective and prospective data collection, it seems reasonable to say, yes. However, both the proportion of MDR pathogens and the type of MDR pathogens have a different geographical distribution based on the local healthcare system, which differ from country to

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country as do their antibiotic policies [7]. In view of this, the idea of a single global tool for predicting the presence of MDR pathogens, as with the HCAP classification, would not be feasible. After evaluating the evidence, it seems that the 2 main MDR pathogens that cause pneumonia in the community are MRSA and *P. aeruginosa*. Chalmers et al reveal that a proportion of patients with pneumonia have infections that are secondary to MRSA. In addition, since 2001, the CAP clinical practice guidelines have recommended the stratification of patients with severe structural lung disease who present with severe pneumonia and require intensive care unit–level care for the risk of *P. aeruginosa* [8].

Second, how could we identify MDR pathogens in patients coming from the community with pneumonia and how could we differentiate MRSA from *P. aeruginosa*? Similar to the previous question, we need a better understanding of the MDR risk factors that may suggest specific pathogen risk factors rather than a set that will include them all. Recently, a road has been opened toward analysis of individualized risk factor for MDR pathogens in the single patient in order to prevent overtreatment [9, 10]. MDR-oriented scores could be used to identify these clinical characteristics in order to enable healthcare providers to focus on the modifiable risk factors that could lead to better outcomes. Although we may have tools that can help us predict pneumonia caused by MDR vs non-MDR pathogens, we still do not have secure and validated methods for determining whether pneumonia is due to MRSA or *P. aeruginosa* in hospitalized patients coming from the community. A possible explanation could be found in the overlap between major risk factors for MRSA and those for *P. aeruginosa*, such as nursing home residency and previous hospitalization.

Third, how could this problem be solved? There is hope that in the near future the waiting period for a final

microbiological identification with antimicrobial susceptibility testing could be reduced from 48–72 hours to just a few hours from the time of clinical presentation. Rapid point-of-care testing methodologies may assist clinicians in directing appropriate and adequate antimicrobial therapies for patients with pneumonia.

In the mean time, a reasonable approach should consider the following points: (1) The identification of the probability for a patient with pneumonia coming from the community to have an MDR vs non-MDR pneumonia. Risk factor calculators may assist clinicians in the objective quantification of the risk for MDR pathogens in order to lead to appropriate antimicrobial utilization. However, the need for these tools, along with the risk factors included in them, should be individualized based on local epidemiology. (2) The evaluation of the presence of single risk factors for MRSA, *P. aeruginosa*, or ESBL-positive pathogens. (3) Strong efforts to perform microbiological evaluations at the time of diagnosis of pneumonia with the aim of identifying a possible isolate after 48–72 hours, changing antibiotic therapy, and preventing adverse clinical outcomes.

Finally, it should be clear that risk factor analysis, microbiological approach, and choice of the right antibiotic therapy are just one field of action for preventing mortality in patients with pneumonia. In order to resolve the puzzle of saving the lives of those with pneumonia, we need to integrate this approach with therapeutic measures that are focused on stabilization of the immune response following the infection and better control of decompensation of comorbidities.

Notes

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References

1. Morin CA, Hadler JL. Population-based incidence and characteristics of community-onset *Staphylococcus aureus* infections with bacteremia in 4 metropolitan Connecticut areas, 1998. *J Infect Dis* **2001**; 184:1029–34.
2. Friedman ND, Kaye KS, Stout JE, et al. Health care-associated bloodstream infections in adults: a reason to change the accepted definition of community-acquired infections. *Ann Intern Med* **2002**; 137:791–7.
3. Niederman MS, Craven DE, Bonten MJ, et al. Guidelines for the management of adults with hospital-acquired, ventilator-associated, and healthcare-associated pneumonia. *Am J Respir Crit Care Med* **2005**; 171:388–416.
4. Kollef MH, Shorr A, Tabak YP, Gupta V, Liu LZ, Johannes RS. Epidemiology and outcomes of health-care-associated pneumonia: results from a large US database of culture-positive pneumonia. *Chest* **2005**; 128:3854–62.
5. Ewig S, Welte T, Chastre J, Torres A. Rethinking the concepts of community acquired and health-care-associated pneumonia. *Lancet Infect Dis* **2010**; 10:279–87.
6. Chalmers JD, Rother C, Salih W, Ewig S. Healthcare-associated pneumonia does not accurately identify potentially resistant pathogens: a systematic review and meta-analysis. *Clin Infect Dis* **2014**; 58:330–9.
7. Polverino E, Torres A, Menendez R, et al. HCAP Study investigators. Microbial aetiology of healthcare associated pneumonia in Spain: a prospective, multicentre, case-control study. *Thorax* **2013**; 68:1007–14.
8. Niederman MS, Mandell LA, Anzueto A, et al. American Thoracic Society. Guidelines for the management of adults with community-acquired pneumonia. Diagnosis, assessment of severity, antimicrobial therapy, and prevention. *Am J Respir Crit Care Med* **2001**; 163:1730–54.
9. Aliberti S, Di Pasquale M, Zanaboni AM, et al. Stratifying risk factors for multidrug resistant pathogens in hospitalized patients coming from the community with pneumonia. *Clin Infect Dis* **2012**; 54:470–8.
10. Aliberti S, Cilloniz C, Chalmers JD, et al. Multidrug-resistant pathogens in hospitalised patients coming from the community with pneumonia: a European perspective. *Thorax* **2013**; 68:997–9.