Prevalence and Antimicrobial Susceptibility of Hypervirulent Klebsiella pneumoniae Isolates in China

To the Editor—Recently, Li et al reported that an increasing proportion of hypervirulent Klebsiella pneumoniae (hvKP) among clinical K. pneumoniae isolates has been identified in China and that the hvKP strains exhibited an increasing antimicrobial resistance [1]. Our concern is that their study may have significant impact on the empiric anti-infection treatment of serious infections caused by hvKP. Therefore, we performed this study to clarify the hypermucoviscosity (HV) and antimicrobial susceptibility of clinical K. pneumoniae isolates causing pyogenic liver abscess (PLA) and metastatic infectious disease (MID). In contrast to the findings from Li et al [1], we did not find an increasing prevalence of HV and antimicrobial resistance among those isolates. Thus, there are several issues of concern that need to be discussed.

First, the genetic relatedness of clinical isolates should be further identified by molecular analysis. Li et al stated that “cases of MID were diagnosed in patients with K. pneumoniae–positive culture obtained from 1 or more sites in addition to a clear infection site, even if the abscess fluid culture was negative for K. pneumoniae” [1]. We analyzed 67 patients who suffered from blood and other infections simultaneously. Comparisons of their pulsed-field gel electrophoresis profiles revealed that 16.4% (11/67) of the patients were infected by different clones. Therefore, it is unreliable to identify MID-causing isolates just by isolating K. pneumoniae from different sites, not to mention the negative cultures for some abscesses.

Second, in the study reported by Li et al, the K. pneumoniae strains with a positive string test were designated as hvKP [1]. In this study, only 70.6% (35 of 51) of PLA-causing and 32.1% (18 of 56) of MID-causing K. pneumoniae isolates exhibited HV. Because the factors other than HV are required for the systemic dissemination of K. pneumoniae [2], and because whether all hvKP are hypermucoviscous remains unclear [3], hvKP should be defined by genomic background, rather than by HV [4, 5]. Therefore, defining hvKP only by HV likely leads to a biased result. For example, contrary to the findings from Li et al [1], we found that the PLA-causing K. pneumoniae isolates exhibited an absolute susceptibility to the commonly used antibiotics.

Finally, Li et al conducted their study with only 88 patients from a single hospital in 3 years, and the average annual number of case patients is <30 [1]. Therefore, the sample size of that study cannot be considered to be the true reality even with a large sample size. From a statistical point of view, it is not suitable for an annual proportion analysis of hvKP. Meanwhile, on the epidemiological aspect, it is very unreliable to conclude that “hvKP strains are being isolated from patients in China” just by a single-center study with a small sample size in a special hospital.

In conclusion, a truly objective and scientific conclusion should be obtained from a multicenter study with a large number of samples collected from patients in the representative regions/hospitals nationally.

Notes

Financial support. This study was supported by the China Mega-Project on Infectious Disease Prevention (grant number 2013ZX10004202-002). Potential conflicts of interest. All authors: No reported conflicts.

All authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

Youjiang Zhang, a Yanning Ma, a Liyan Ye, Yanping Luo, and Jiyong Yang

Department of Microbiology, Chinese PLA General Hospital, Beijing, China

References


*Y. Z. and Y. M. contributed equally to this work.

Correspondence: Jiyong Yang, PhD, Microbiology Department, 301 Hospital, No. 28 Fuxing Road, Beijing 100853, China (yangjy301@hotmail.com).