Infection and Drug Resistance

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RESPONSE TO LETTER

Long Term Characteristics of Clinical Distribution and Resistance Trends of Carbapenem-Resistant and Extended-Spectrum β-Lactamase *Klebsiella pneumoniae* Infections: 2014–2022 [Response to Letter]

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Dear editor

We are glad to receive comments on our recent publication in Infection and Drug Resistance from three authors.[1] They gave professional suggestions and comments on the article, which will guide our follow-up research. As they suggested, although it is appropriate for us to conduct phenotypic screening experiments on carbapenem-resistant *Klebsiella pneumoniae* (CRKP) through the MIC values of imipenem and meropenem, we should add confirmation experiments on carbapenem enzyme in our experiments, which will help improve the accuracy of laboratory reports.

The emergence of hypervirulent and multi-drug resistance *Klebsiella pneumoniae* has become a hot topic for clinicians and researchers around the world. Recent research has found that the potential of pK2606-like conjugative virulence plasmids to spread worldwide.[2] This combination of high virulence and drug resistance has posed a severe challenge to our medical environment. It has been reported that carbapenem-resistant hypervirulent *Klebsiella pneumoniae* (CR-hvKP) has caused fatal hospital infection.[3] And hyperglycemia increases the gene expression of RmpA and ompA in hvKP through cAMP signaling pathway,[4] which will increase the cost of treatment and extend the length of hospital stay.

Our laboratory has been committed to the research on the resistance and virulence mechanism of pathogenic microorganisms. It will preliminarily screen the virulent strains of *Klebsiella pneumoniae* through mucus phenotype and String test, and verify the in vitro virulence of *Klebsiella pneumoniae* through the infection model of Greater Wax Moth Larvae and Serum Killing test. In addition, the drug resistance gene, virulence gene and capsular serotype of CRKP are detected, and the homology analysis is carried out by detecting the sequence typing of multiple sites. The typical strains are selected for whole genome sequencing, to find mutation sites, to carry out targeted treatment, and to establish a multidisciplinary cooperation mechanism to jointly manage the spread of multidrug resistant strains. In recent years, the microbiological laboratory of our hospital is building a collection of pathogenic microbial strains. At present, more than 10,000 strains of bacteria are stored, and the storage of strains is carried out every day, which will provide a solid guarantee for our subsequent experiments.

Disclosure

The authors report no conflicts of interest in this communication.

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