

POSTER PRESENTATION

Open Access

P072: Genetic environment and phenotypic analysis of a novel bla_{KPC} variant produced by *Klebsiella pneumoniae*

J-J Mu

From 2nd International Conference on Prevention and Infection Control (ICPIC 2013)
Geneva, Switzerland. 25-28 June 2013

Introduction

A novel variant of *klebsiella pneumoniae* carbapenemase (KPC) was found in multidrug-resistant *Klebsiella pneumoniae* clinical isolates from Taiwan. The novel KPC variant differs from existing KPC due to substitution at position 206 (phe→Leu). Genetic environment and phenotypes were analyzed for further understanding the novel KPC variant.

Objectives

The aim of this study is to characterize the detailed genetic environment of the novel bla_{KPC} produced by *klebsiella pneumoniae* and analyze the enzymatic activity of the novel KPC variant.

Methods

The antibiotic susceptibility of the clinical isolates and corresponding transconjugants was determined and interpreted according to the CLSI guidelines. The plasmid carrying novel KPC variant (pKP78) was subjected into whole genome sequencing for resolving the complete sequence. The GST fusion recombinant KPC proteins were expressed for detecting the enzymatic activity.

Results

The antibiotic susceptibility showed the KP producing novel KPC variant was resistant to most of the antibiotics, such as carbapenem (imipenem, ertapenem and meropenem), aztreonam, cephalosporin (cefazolin, cefotaxime and ceftazidime), but susceptible to amikacin and colistin. The whole genome sequencing has been done and resulted in 11 contigs needed to be assembled. The genetic

environment surrounding novel bla_{KPC} flanked by ISKpn8 and ISKpn6-like sequences is similar with pKP048. The sequences upstream of ISKpn8 in pKP78 were, with gene order TniA transposase, IS26 transposase and partial Tn3-resolvase different from Tn3-transposase and Tn3-resolvase in pKP048. The GST-recombinant proteins were expressed and the detection of enzymatic activity is undertaken.

Conclusion

The novel KPC variant differs from existing KPC due to substitution at position 206 (phe→Leu). The chimera of several transposon-associated elements indicated a novel genetic environment surrounding the novel bla_{KPC} gene. This residue seems not to be close to the active site. Whether it will change the activity remains unknown. The surveillance is engaging to monitor possible spreading in Taiwan.

Disclosure of interest

None declared.

Published: 20 June 2013

doi:10.1186/2047-2994-2-S1-P72

Cite this article as: Mu: P072: Genetic environment and phenotypic analysis of a novel bla_{KPC} variant produced by *Klebsiella pneumoniae*. *Antimicrobial Resistance and Infection Control* 2013 **2**(Suppl 1):P72.

Research and Diagnostic Center, Centers for Disease Control, Taiwan, Taipei, Taiwan, Province of China