

# Significant overlap in disease phenotype between genotypically defined hypervirulent and classical *Klebsiella pneumoniae* among bacteraemic patients in endemic area

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## Introduction

Hypervirulent *Klebsiella pneumoniae* (hvKP) has been described as an invasive syndrome of liver abscess and/or metastatic infection in Asia, and this syndrome is emerging as a global disease.

## Methods

This study investigated the relationship between disease phenotypes and genotypic hypervirulence markers in 273 patients with *Klebsiella pneumoniae* (KP) bacteraemia or meningitis from three hospitals in Hong Kong from 2019 to 2023. WGS were analysed by Kleborate and Kaptive. Epidemiological background, disease phenotype, virulence genes, and antimicrobial susceptibility were analysed. Genotypically defined hvKP (g-hvKP) are defined as having *iucA*, *iroB*, *rmpA*, *rmpA2*, and *peg-344*. Others are defined as classical *Klebsiella pneumoniae* (cKP).

## Results

The mean age was 72.2 years. The M:F ratio was 1.33:1. The 14-day mortality rate was 19.8%. 20.8% were g-hvKP. g-hvKP has a sensitivity of 46% and a specificity of 86% in detecting liver abscesses or metastatic infections. g-hvKP caused only 51% of liver abscesses. g-hvKP was not associated with mortality, disease severity, or metastatic infection. g-hvKP were more susceptible to cephalosporins ( $p = 0.02$ ) and fluoroquinolones ( $p = 0.01$ ).

The commonest K types were K2 (13.9%) and K1 (10.6%). The commonest ST was ST 23 (8.8%). The ESBL phenotype was more likely in cKP than g-hvKP (22% vs 9%,  $p = 0.04$ ).

## Conclusion

Significant overlap in disease phenotype exists between cKP and g-hvKP. Currently proposed genotypic definition of hvKP does not correlate with clinical outcomes.