

**Clinical implications of hypermucoviscosity
phenotype in *Klebsiella pneumoniae* isolates:
association with invasive syndrome in patients with
community-acquired bacteremia.**

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摘要

Abstract

Background. *Klebsiella pneumoniae*, a Gram-negative bacillus usually forming glistening mucoid colonies with viscid consistency on the culture plate, is a common pathogen causing various clinical infection patterns. However, little is known about the clinical implications of this mucoid character. Objective. The purposes of this study, therefore, were to investigate the frequency of hypermucoviscosity (HV) in bacteraemic isolates of *K. pneumoniae*, and determine the significance of any association between HV and various clinical manifestations. Design. Retrospective observational study. Patients. Patients diagnosed with *K. pneumoniae* bacteraemia at a community-based university hospital between June 1999 and June 2001 were enrolled in this analysis. Measurements. Clinical data concerning comorbid diseases and infection patterns was collected. *K. pneumoniae* bacteraemic isolates were examined for the presence of HV using a modified string test. The clinical impact of HV and risk factors for the invasive syndrome were assessed using statistical analysis. Polymerase chain reaction (PCR) was performed to detect *magA*, a gene related to HV phenotype. Results. Overall, 200 (64.9%) of the 308 cases of *K. pneumoniae* bacteraemia were community-acquired infections. Compared with hospital-acquired *K. pneumoniae* bacteraemia (HA-KpB), community-acquired *K. pneumoniae* bacteraemia (CA-KpB) was more likely to be monomicrobial in nature (83.5% vs. 64.8%; $P < 0.001$) and caused by HV strains (41.5% vs. 14.8%; $P < 0.001$). The prevalence rate of *magA* among HV phenotypical *K. pneumoniae* strains was 24.1%. Patients infected with HV-positive strains were more likely to have the distinctive

invasive syndrome (i.e. liver abscess, meningitis, pleural empyaema or endophthalmitis) than those infected with HV-negative variants (37.3% vs. 6.8%; $P < 0.001$). Multivariate logistic regression analysis, adjusted for age, showed that HV phenotype in *K. pneumoniae* strains (OR 8.86; 95% CI, 3.70-21.25; $P < 0.001$) was positively associated with the development of the invasive syndrome in CA-KpB cases. Conclusions. The HV phenotype of *K. pneumoniae* bacteraemic isolates was associated with the development of a distinctive invasive syndrome. Identification of the HV phenotype should prompt clinicians to initiate aggressive investigations for invasive diseases..

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