

Association between *rmpA* and *magA* genes and clinical syndromes caused by *Klebsiella pneumoniae* in

Taiwan

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摘要

Abstract

Background. The association of the *magA* gene with the hypermucoviscosity phenotype relevant to the pathogenesis of *Klebsiella pneumoniae* liver abscess has been reported in Taiwan. Similarly, the *rmpA* gene, known as a positive regulator of extracapsular polysaccharide synthesis that confers a mucoid phenotype, may be another candidate gene causing hypermucoviscosity. However, the association of *rmpA* with *K. pneumoniae* clinical syndromes is unreported. We aimed to investigate the clinical correlation between *rmpA* and primary *Klebsiella* abscess, focusing on sites other than the liver. **Methods.** From July 2003 through December 2004, a total of 151 *K. pneumoniae* isolates recovered from 151 patients with bacteremia were collected from 2 large medical centers in southern Taiwan. Clinical data were collected from medical records. The genes *rmpA* and *magA* were amplified by polymerase chain reaction using specific primers. **Results.** The prevalences of hypermucoviscosity, *rmpA*, and *magA* were 38%, 48%, and 17%, respectively. As determined by statistical multivariate analysis, strains carrying *rmpA* were significantly associated with the hypermucoviscosity phenotype, and there was a significant correlation with purulent tissue infections, such as liver abscess and lung, neck, psoas muscle, or other focal abscess. **Conclusion.** Our data support a statistical correlation between the *rmpA* gene and virulence in terms of abscess formation for these hypermucoviscous *K. pneumoniae* strains. Hypermucoviscosity associated with *rmpA*, together with a thorough physical examination, may be helpful as a guide to carry out appropriate diagnostic tests on patients with an initially unknown source of *K. pneumoniae* bacteremia, particularly when looking for the occurrence of an underlying abscess.