Prevalence of hypervirulent *Klebsiella pneumoniae*-associated genes *rmpA* and *magA* in two tertiary hospitals in Houston, TX, USA

*Klebsiella pneumoniae* is a common and well-established pathogen associated with hospital- and healthcare-acquired infections worldwide. A hypervirulent *K. pneumoniae* (hvKP) variant associated with primary pyogenic liver abscesses was initially described in Taiwan (Liu et al., 1986) and was subsequently reported in North America (Fierer et al., 2011; Lederman & Crum, 2005a; McCabe et al., 2010; Nadasy et al., 2007; Pastagia & Arumugam, 2008; Peirano et al., 2013), Australia (Chang et al., 2013) and Europe (Keynan et al., 2007). *magA* (mucoviscosity-associated gene A), which is on the same operon responsible for capsular serotype K1, was the first gene described to lead to a hypermucoviscous phenotype and thought to be related to the ability of hvKP to form pyogenic liver abscesses (Fang et al., 2004; Chuang et al., 2006). Later, a second gene, *rmpA* (regulator of mucoid phenotype A), was reported to be associated with *K. pneumoniae* causing pyogenic tissue abscesses (Yu et al., 2006). More recently, whole-genome sequencing found *rmpA* and genes encoding iron acquisition systems to be conserved in hvKP isolates and that *rmpA* is found in isolates with K1 and non-K1 capsular serotypes (Struve et al., 2015).

Although there are multiple case reports and case series of hvKP in the USA and Canada (Alsaedi et al., 2014; Fierer et al., 2011; Frazier et al., 2009; Keynan et al., 2007; Lederman & Crum, 2005a, b; McCabe et al., 2010; Nadasy et al., 2007; Pastagia & Arumugam, 2008; Patel et al., 2014; Pomakova et al., 2012), none of these studies reported the prevalence of hvKP. The only surveillance study in North America was from Alberta, Canada; an estimated prevalence of 8.2% hvKP was found (Peirano et al., 2013). We used two large tertiary care hospitals in Houston, TX, USA, to measure the baseline prevalence of hvKP-associated genes, *rmpA* and *magA*.

We collected 38 consecutive *K. pneumoniae* bloodstream isolates from different patients from January 2009 to January 2010 at the Ben Taub General Hospital, a large urban hospital, and 26 *K. pneumoniae* isolates from patients from the Michael E. DeBakey Veterans Affairs Medical Center in Houston during the same period. Bacterial DNA was purified from each isolate, and the *magA* and *rmpA* genes were amplified by end point PCR and detected by gel electrophoresis, as previously described by Nadasy et al. (2007). Patient charts were reviewed for clinical and radiographic (ultrasonography or computed tomography) evidence of pyogenic liver abscesses.

From the Ben Taub General Hospital, three (7.9%, n=38) *K. pneumoniae* isolates carried one or both hvKP-associated genes; two isolates were *rmpA+/magA+,* and one isolate was *rmpA+/magA−.* Only one patient had a pyogenic liver abscess, which cultured an *rmpA+/magA+* isolate. The second *rmpA+/magA−* isolate and the *rmpA−/magA−* isolate did not have clinical or computed tomographic evidence of pyogenic liver abscess. One *rmpA−/magA−* isolate (2.9%, n=35) was isolated from a patient with multiple small hepatic abscesses due to acute cholecystitis and appeared more consistent with a classical phenotype; this patient had chronic alcoholism, chronic pancreatitis and biliary stenosis requiring stenting, which were the suspected predisposing factors to biliary infection. Twenty-four other patients with bacteraemia had abdominal imaging, and none had radiographic evidence of pyogenic liver abscess.

From the Veterans Affairs Medical Center, one (3.9%, n=26) *K. pneumoniae* isolate carried both hvKP-associated genes. The isolate was collected during an elective diagnostic bronchoscopy for biopsy-proven hypersensitivity pneumonitis; there was no clinical evidence of infection. None of these patients had clinical evidence of pyogenic liver abscess. Fourteen patient had abdominal imaging, and none had radiographic evidence of pyogenic liver abscess.

Our point estimate for the hospital prevalence of isolates carrying at least one hvKP-associated gene is 6.3% (SE, 3.0%; 95% confidence interval, 0.3–12.2%). While limited to two large hospitals in the fourth largest city in the USA, these data represent the first systematic description of the molecular epidemiology of hvKP-associated genes and the first prevalence study in the USA and can serve as an initial estimate of the prevalence for larger-scale studies.

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Abbreviation: hvKP, hypervirulent Klebsiella pneumoniae.

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References


