Hypermucoviscosity: An Extremely Sticky Phenotype of *Klebsiella pneumoniae* Associated with Emerging Destructive Tissue Abscess Syndrome

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(See the article by Yu et al. on pages 1351–8)
with the hypermucoviscosity phenotype, a mutant library of K. pneumoniae was constructed using transposon mutagenesis. The mutation in magA and other genetic loci, including the cps cluster [12], the wb cluster [13], and rmpA [14], resulted in a deficiency in the hypermucoviscosity phenotype. However, only magA had a significantly higher incidence in invasive strains than in noninvasive clinical isolates of K. pneumoniae (98% vs. 29%). The magA mutants lost the hypermucoviscosity phenotype and became extremely serum sensitive, phagocytosis susceptible, and avirulent to mice [11].

Yu et al. [10] discovered an article published in 1989 [14] demonstrating that rmpA (regulator of the mucoid phenotype A) is a regulatory gene for the synthesis of extracapsular polysaccharide and positively controls the mucoid phenotype of K. pneumoniae. It is the overproduction of polysaccharide, not capsule production, that is responsible for the mucoid phenotype of K. pneumoniae. Although the rmpA gene is encoded by the chromosome, the mucoid phenotype is regulated by rmpA located in a plasmid [14]. Knockout and restoration of the rmpA gene showed the loss and recovery of the mucoviscosity phenotype [14]. On the basis of these lines of evidence, Yu and colleagues hypothesized that the mucoid phenotype regulated by the rmpA gene may correspond to the hypermucoviscosity phenotypes of K. pneumoniae isolated from tissue abscess. They further demonstrated that the frequency of the rmpA gene positively correlates with the incidence of tissue abscess formation due to K. pneumoniae with the hypermucoviscosity phenotype [10]. Of interest, the experiments using transposon mutagenesis by Fang et al. [11] also revealed that rmpA is associated with the hypermucoviscosity phenotype. In contrast to the study by Fang and colleagues, in which magA-positive strains were most frequently isolated from liver abscess, Yu and colleagues found relatively low frequencies of magA, as well as kfu, in their isolates from liver abscess. An iron-uptake system encoded in the kfu gene is highly correlated with magA expression in K. pneumoniae [15]. The discrepancy between the 2 studies, both performed in Taiwan, may be related to the geographic distribution of the genes that correlate with the genotypes of K. pneumoniae. In fact, the clinical isolates studied by Yu et al. [10] were from the southern region of Taiwan, whereas the isolates studied by Fang et al. [11] were almost all from northern Taiwan.

The geographic distribution of K. pneumoniae strains that cause liver abscess seems to be restricted to East and Southeast Asian countries, with the exception of some reports of cases from South Africa and the United States [2, 6, 7]. If rmpA and/or magA are responsible for the pathogenesis of K. pneumoniae tissue abscess, then expression of these genes should be identified only in clinical isolates of K. pneumoniae in East and Southeast Asian countries. The geographic restriction of K. pneumoniae tissue abscess also suggests that susceptibility to infection with the K. pneumoniae strains that cause tissue abscess may be attributed to a certain host genetic background that is distinct to the geographic region. During the period of 1993–2003, for example, 23 cases of K. pneumoniae liver abscess were recorded at 2 hospitals in New York. Of note, 18 (78.3%) of the patients were of Asian ethnicity, indicating a possible genetic linkage to disease susceptibility [6]. Meanwhile, future global etiology studies may elucidate the possible engagement of rmpA and/or magA in the context of K. pneumoniae tissue abscess.

In an additional observation, the possession by K. pneumoniae of resistance plasmids that express genes conferring antibiotic resistance may account for the rapid spread of this organism in communities and may lead to nosocomial outbreaks. For instance, epidemics of gentamicin-resistant K. pneumoniae in hospitals were frequently reported in the late 1970s [16]. K. pneumoniae is naturally resistant to ampicillin and amoxicillin because of the production of SHV-1 β-lactamase encoded on the chromosome or on a transferable resistance plasmid [17]. Therefore, it is crucial to know whether it is the rmpA or magA gene that is expressed in resistance plasmids.

Irrespective of the conflicting results between the frequencies of rmpA- and magA-positive strains, the consensus of the 2 studies carried out in Taiwan is that the hypermucoviscosity phenotype of K. pneumoniae appears to be associated with purulent infection with K. pneumoniae. Both rmpA and magA genes are requisite for the induction of the hypermucoviscosity phenotype by K. pneumoniae. Thus far, K. pneumoniae strains with the hypermucoviscosity phenotype have been identified only in Taiwan, except for 1 case reported from the United States [18]. However, it is still unclear whether the hypermucoviscosity phenotype is critically related to the pathogenesis of K. pneumoniae. The problem arises because a number of genetic loci appear to be associated with the hypermucoviscosity phenotype of K. pneumoniae [11], and hypermucoviscosity-negative strains have also been isolated from the abscesses of liver and other organs [10]. Therefore, not only hypermucoviscosity phenotypes but also other characteristics may be involved in purulent infection along with those presented in K. pneumoniae.

In summary, the hypermucoviscosity phenotype, as well as the rmpA and magA genes, can be used in the diagnosis of bacteremia due to K. pneumoniae strains with putative virulence. This can, perhaps, result in the early detection and prevention of tissue abscess disease that results from K. pneumoniae infection.

Acknowledgments

Potential conflicts of interest. T.K: no conflicts.

References


