

Hypervirulent *Klebsiella Pneumoniae* in a South African Tertiary Hospital - Clinical Profile, Genetic Determinants and Virulence in *Caenorhabditis* *Elegans*

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Abstract : A distinct strain of *Klebsiella pneumoniae* (*K. pneumoniae*), referred to as hypervirulent (hvKp), is associated with invasive infections such as an invasive pyogenic liver abscess in young and healthy individuals. In South Africa, limited information is known about the prevalence and virulence of this hvKp strain. Thus, this study aimed to determine the prevalence of hvKp and virulence-associated factors in *K. pneumoniae* isolates from one of the largest Tertiary hospitals in a South African province. A total of 74 *K. pneumoniae* isolates were received from Pelonomi National Health Laboratory Services (NHLS), Bloemfontein. Virulence-associated genes (*rmpA*, capsule serotype K1/K2, *iroB*, and *irp2*) were screened, and the virulence of hvKp vs. classical *Klebsiella pneumoniae* (cKp) was investigated using *Caenorhabditis elegans* nematode model. The *iutA* (aerobactin transporter) gene was used as a primary biomarker of hvKp. An average of 12% (9/74) of cases were defined as hvKp. Moreover, hvKp was found to be significantly more virulent in vivo *Caenorhabditis elegans* relative to cKp. The virulence-associated genes (*rmpA*, *iroB*, hmv phenotype, and capsule K1/K2) were significantly ($p < 0.05$) associated with hvKp. Findings from this study confirm the presence of hvKp in one large Tertiary hospital in South Africa. However, the low prevalence and mild to moderate clinical presentation suggest a marginal threat to public health. Further studies in different settings are required to establish the true potential impact of hvKp in developing countries.

Keywords : hypervirulent *klebsiella pneumoniae*, virulence, *caenorhabditis elegans*, aerobactin (*iutA*)

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