

# COMPARATIVE GENOMIC AND MOLECULAR CHARACTERISATION OF HYPERVIRULENT (hvKp) AND CLASSICAL KLEBSIELLA PNEUMONIAE (cKp) FROM CLINICAL ISOLATES



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## INTRODUCTION

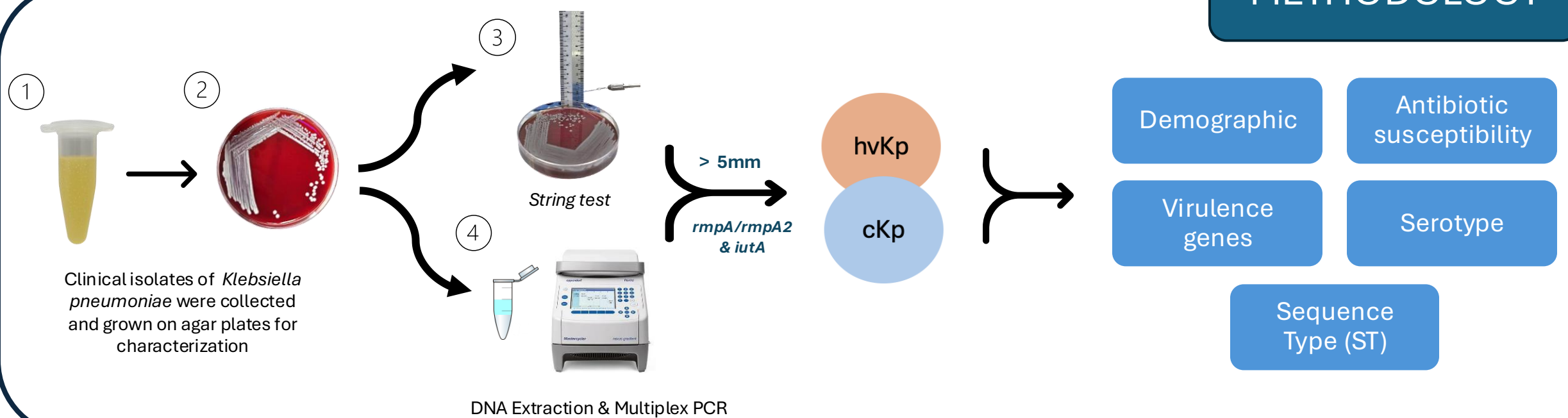


*Klebsiella pneumoniae* is a clinically significant pathogen in both healthcare and community settings. These species have evolved, acquiring resistance and virulence, enhancing their pathogenicity. Hypervirulent *K. pneumoniae* (hvKp) is recognised as a distinct strain associated with severe and invasive infections. Compared to classical *K. pneumoniae* (cKp), hvKp is often identified by elevated expression of virulence markers

## OBJECTIVES

This study aims to comparatively analyze the virulence of hvKp and cKp via molecular genomic approaches

## METHODOLOGY



## FINDINGS

- Among 241 isolates collected, 60 (25%) were identified as hvKp and 181 (75%) were cKp
- HvKp was predominantly isolated from blood and associated with bloodstream infections
- CKp was mainly isolated from urine and linked to other infections
- Both strains were **susceptible** to most antibiotics, though cephalosporin resistance was observed

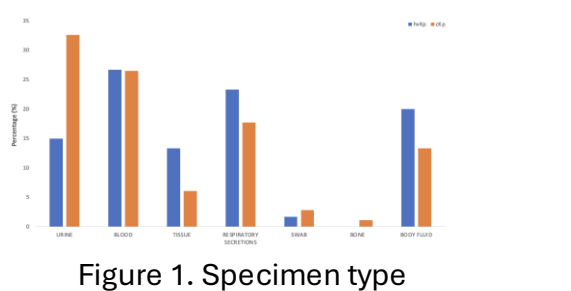


Figure 1. Specimen type

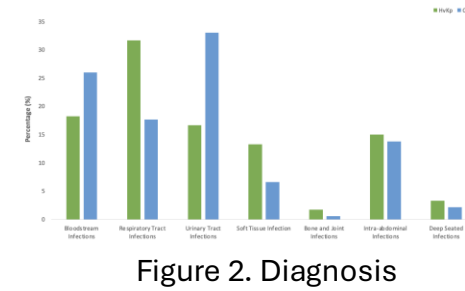


Figure 2. Diagnosis

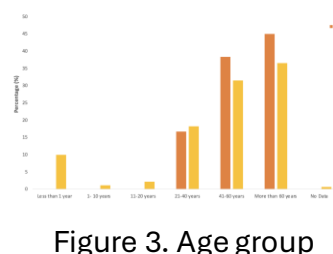


Figure 3. Age group

- HvKp demonstrated higher expression of virulence markers, including **rmpA2**, **iutA**, and **wcaG**, in comparison to cKp
- HvKp was also confined to K1 and K2 serotypes, whereas cKp displayed a diverse serotype distribution, including K5 and K54

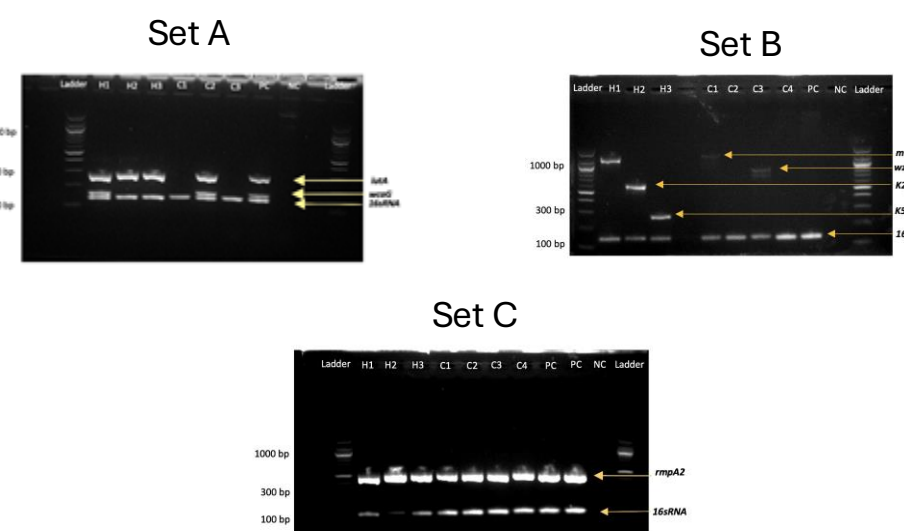


Figure 4, 5, 6. Amplicons on 1.7% agarose gel

## CONCLUSION

HvKp expressed higher virulence markers than cKp and is predominantly isolated from bloodstream infections, posing a serious clinical concern. Bacterial phenotypic and genotypic identification are critical for effective patient care and management. Continuous surveillance is crucial to monitor the emergence and spread of hvKp