

Phenotypic and Genotypic Detection of Hypervirulent *Klebsiella pneumoniae* Isolated from Clinical Samples at a Tertiary Care Hospital

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Abstract

Background: Hypervirulent *Klebsiella pneumoniae* (hvKp) is an emerging pathogen capable of causing severe invasive infections and is increasingly associated with antimicrobial resistance. This study aimed to evaluate the demographic and clinical distribution, hypermucoviscous phenotype, antimicrobial susceptibility profile, and molecular virulence markers among clinical *K. pneumoniae* isolates.

Methods: A hospital-based prospective observational study was conducted in the Department of Microbiology, NIMS Medical College and Hospital, Jaipur. A total of 110 non-duplicate clinical *K. pneumoniae* isolates were identified using standard microbiological methods and the VITEK-2 Compact system. Demographic characteristics, clinical specimen distribution, and ward-wise distribution were analyzed. Hypermucoviscosity was assessed using the string test. Antimicrobial susceptibility testing was performed according to CLSI 2023 guidelines. String-test-positive isolates were further subjected to polymerase chain reaction (PCR) for detection of *rmpA* and *iucA* virulence-associated genes.

Results: Of the 110 isolates, 69 (62.73%) were recovered from male patients and 41 (37.27%) from female patients. The highest proportion of isolates was observed among patients aged 51–60 years (22.73%), followed by 61–70 years (20.91%), with the age distribution showing statistical significance ($p < 0.001$). Endotracheal tube specimens constituted the largest proportion (31.82%), followed by blood (27.27%), urine (14.55%), and pus (14.55%) ($p < 0.001$). The majority of isolates were obtained from the MICU (30.0%), followed by NICU (15.45%) and SICU (10.91%). Overall, 11 (10.0%) isolates were string-test positive, with positivity varying significantly according to specimen type ($p = 0.015$). Among the 11 string-test-positive isolates, **10 (90.9%) demonstrated simultaneous detection of both *rmpA* and *iucA* genes by PCR**. Among string-test-positive isolates, the highest susceptibility was observed to ciprofloxacin and piperacillin/tazobactam (81.8% each), whereas resistance was highest to ampicillin/sulbactam, cefotaxime, cefepime, meropenem, and ceftazidime (63.6% each). No statistically significant association was observed between string-test positivity and antimicrobial susceptibility ($p > 0.05$).

Conclusion: The findings demonstrate a significant clinical and demographic burden of *K. pneumoniae*, particularly among older patients and critically ill individuals. The high frequency of *rmpA* and *iucA* detection among string-test-positive isolates highlights the importance of molecular characterization for confirmation of hvKp. The lack of a significant association between hypermucoviscosity and antimicrobial susceptibility further indicates that the string test should not be used as a surrogate marker for antimicrobial resistance. A combined phenotypic, molecular, and antimicrobial susceptibility approach is recommended for reliable identification and surveillance of hvKp.

Keywords

Klebsiella pneumoniae, Hypervirulent *Klebsiella pneumoniae*, Hypermucoviscosity, String test, *rmpA*, *iucA*, Polymerase chain reaction, Antimicrobial resistance.