# Prevalence, Antimicrobial Resistance, and Virulence Profiling of Hypermucoviscous Klebsiella pneumoniae in a Cardiac Tertiary Care Hospital in Kathmandu, Nepal

Supriya Sharma<sup>1\*</sup>, Soni Maharjan<sup>1</sup>, Sanjib Adhikari<sup>1</sup>, Sobita Khadka<sup>2</sup>, Komal Raj Rijal<sup>1</sup>, Prakash Ghimire<sup>1</sup>

<sup>1</sup>Central Department of Microbiology, Tribhuvan University, Kathmandu, Nepal <sup>1</sup>Shahid Gangalal National Heart Centre, Tribhuvan University, Kathmandu, Nepal Email: supriya.Sharma@cdmi.tu.edu.np

## BACKGROUND

Hypermucoviscous Klebsiella pneumoniae (hmvKp) is an emerging pathotype associated with severe infections and enhanced virulence, posing growing threat due to multidrug resistance.

However, data from South Asia remain limited, especially in cardiac patients.

## OBJECTIVES

To determine the prevalence, antimicrobial resistance patterns, and virulence gene distribution of hmvKp isolated form clinical specimens at a cardiac tertiary care hospital in Kathmandu, Nepal.

## METHODS

- •Study design: Hospital based cross sectional study from September 2023 to February 2025
- Study population: Clinical specimens from patients submitted for culture at Shahid Gangalal National Heart Centre, Nepal
- **Sample size**: 1576 clinical specimens
- **Ethical approval** from Institutional Review Committee (IRC) of Institute of Science and Technology (Ref. No.: 165/080/081) and Shahid Gangalal National Heart Centre, Bansbari (Ref. No.: SGNHC/IRC No.: 9-2024)

# RESULTS

**RES-391** 

**Presentation Date: 2-4 Nov, 2025** 

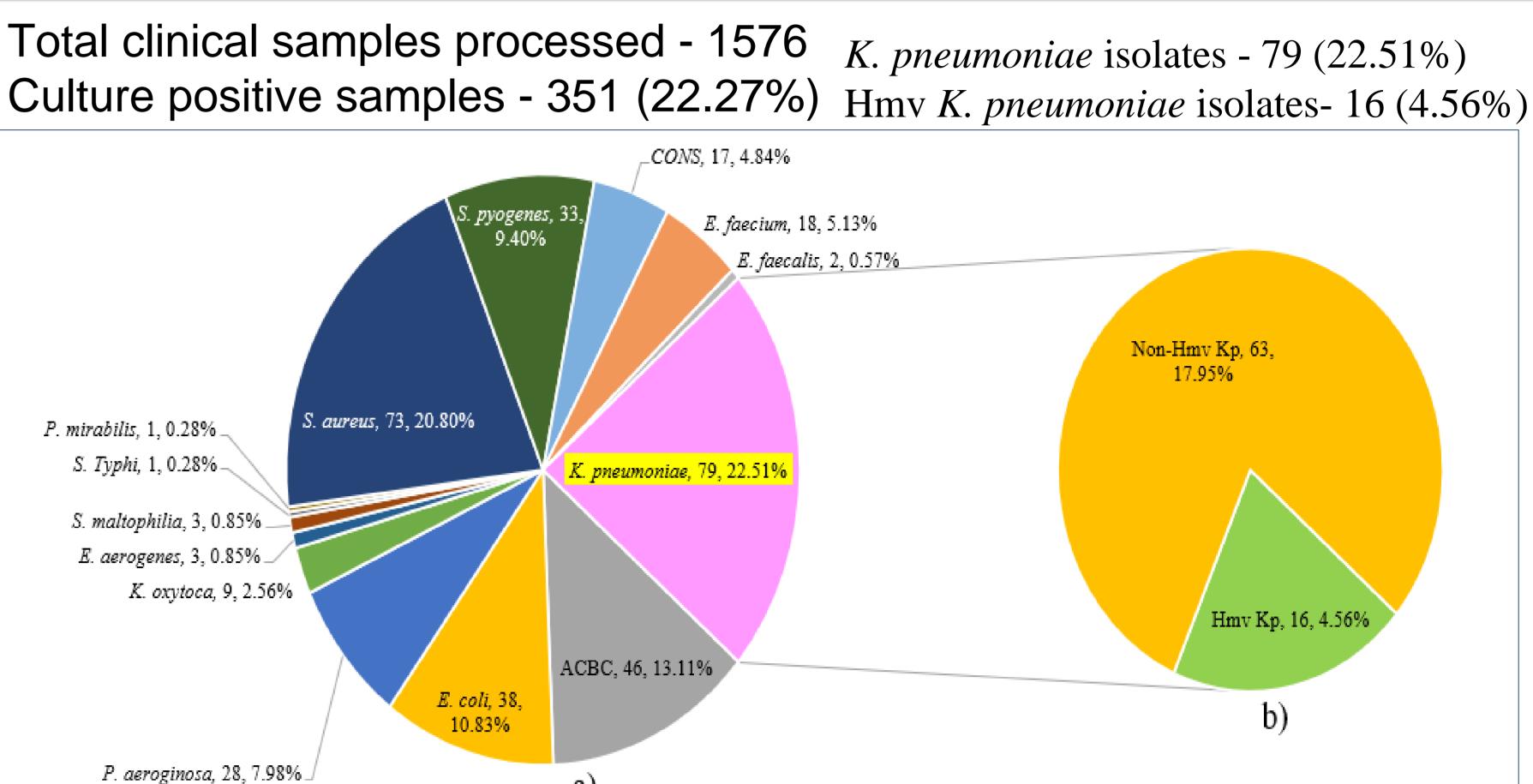


Figure 1: a) Bacterial profile from clinical isolates; b) prevalence of Hmy Kp among K. pneumoniae isolates

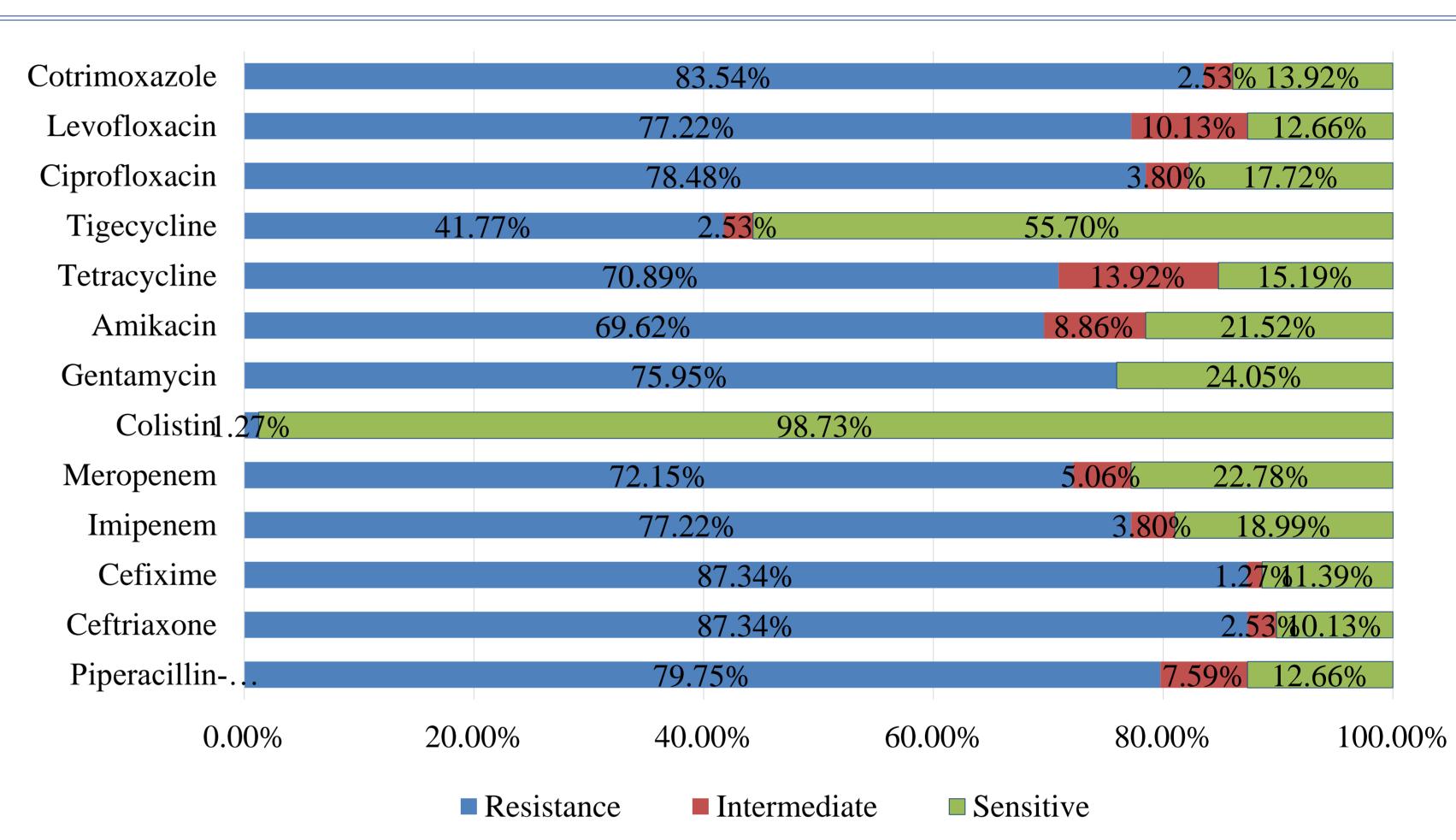


Fig 2. Antibiotic susceptibility pattern of *K. pneumoniae* 

#### Prevalence of MDR K. pneumoniae isolates among HmV Kp and non- Hmv Kp

Category	Total N=79		Hmv Kp N=16		Non- Hmv Kp N=63	
	No.	%	No.	%	No.	%
MDR	64	81.01%	14	87.5%	50	79.37%
Non- MDR	15	18.99%	2	12.5%	13	20.63%

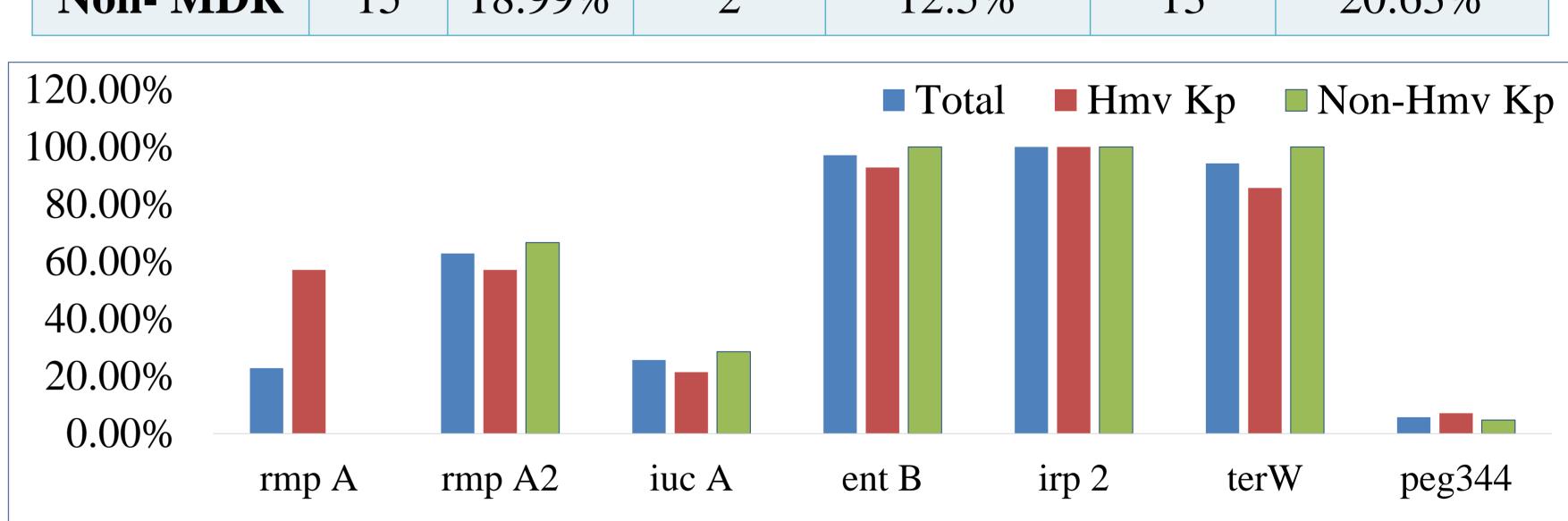


Fig 3. Prevalence of virulence genes among MDR K. pneumoniae

# CLINICAL SPECIMEN PROCESSING

Isolation of *K. pneumoniae* on MacConkey agar

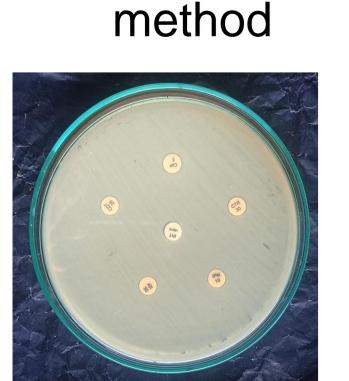
Colony Morphology

Identification of *K. pneumoniae* 

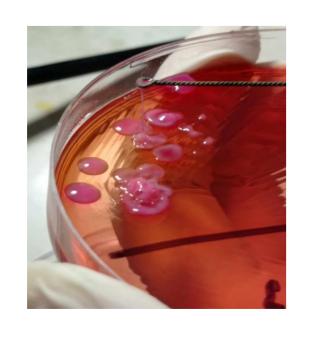


**Biochemical Tests** Gram's staining

Antibiotic Susceptibility Test Kirby Bauer Disc Diffusion



MDR K. pneumoniae



String Test

Detection of virulence genes (rmpA, rmpA2, iucA, iroB, entB irp2, Peg-344 and terW gene)

DNA extraction and PCR

HmvKp

HvKp

# ACKNOWLEDGEMENTS

- Patients for providing specimens
- OWSD Early Career Fellowship for partial support (Laboratory analysis)

## CONCLUSION

- Hypermucoviscous *K. pneumoniae* is present in cardiac care settings in Kathmandu, Nepal, exhibiting high multidrug resistance and notable virulence gene profiles.
- The strong association of rmpA with hmvKp strains highlights the need for robust molecular surveillance and targeted antimicrobial stewardship to prevent public health threats.