Characterization of antimicrobial resistance and hypervirulent traits of Klebsiella variicola isolates collected in South Korea

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Background

- *Klebsiella pneumoniae* complex
  - *K. pneumoniae*
  - *K. quasipneumoniae*
  - ***K. variicola***
  - *K. quasivariicola*
- *K. variicola*
  - Similar biochemical characteristics to those of K. pneumoniae
  - Accurate identification: MALDI-TOF MS
  - ESBL-producing K. variicola have been reported in US, Norway...
  - Carbapenemase-producing K. variicola (KPC-2, NDM-1, NDM-5)
  - Hypervirulent strains
- The aim of study
  - To characterize antimicrobial susceptibility profile
  - Resistance determinants, virulence factors

Methods

- Bacterial strains
  - *K. variicola* isolates collected from Sep 2022 to Oct 2023
  - 8 different districts of South Korea
- Bacterial identification: Bruker Biotyper (DB version 13)
- Antimicrobial susceptibility testing
  - Disk diffusion on Mueller-Hinton agar
  - 18 antimicrobials
- Beta-lactamasea genotyping
  - Chromosomal SHV-OKP-LEN beta lactamase genotyping
  - ESBL, carbapenemase genotyping
- Hypervirulent trait determination
  - String test, *wzi* allelic type
- Whole genome sequence analysis: MDR strains, hypervirulent strains

Results

- A total of 76 *K. variicola* isolates

Table 1. Clinical characteristics of patients with *K. variicola* infection

Variable	Total (N = 76)	Male (N = 21)	Female (N = 55)	*P*-value
Old age (>60)	53 (69.7)	17 (81.0)	34 (61.8)	0.189
Regions				0.432
Gyeonggido	19 (25)	4 (19.0)	15 (27.3)	
Gyeongsangdo	17 (22.4)	3 (14.3)	14 (25.5)	
Jeollado	12 (15.8)	4 (19.0)	8 (14.5)	
Chungcheongdo	8 (10.5)	2 (9.5)	6 (10.9)	
Seoul	8 (10.5)	5 (23.8)	3 (5.5)	
Busan	6 (7.9)	2 (9.5)	4 (7.3)	
Gangwondo	5 (6.6)	1 (4.8)	4 (7.3)	
Type of hospital				0.032
General hospital	42 (55.3)	16 (76.2)	26 (47.3)	
Clinic	20 (26.3)	2 (9.5)	18 (32.7)	
Nursing hospital	4 (5.3)	1 (4.8)	3 (5.5)	
Others	10 (13.2)	2 (9.5)	8 (14.5)	
Specimen				< 0.001
Urine	40 (52.6)	3 (14.3)	37 (67.3)	
Abscess	17 ()	8 (28.6)	9 (16.4)	
Blood	6 (7.9)	5 (23.8)	1 (1.8)	
Sputum	5 (6.6)	1 (1.8)	1 (1.8)	
Others	8 (10.5)	1 (4.8)	7 (12.7)	

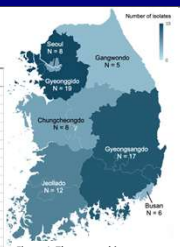

Figure 1. The geographic distribution of *K. variicola* isolates

- Antimicrobial resistance profile
  - Resistance rate: less than 10% in all antimicrobials tested.
  - Resistance rate to CTX: 5.3% (four isolates)
  - One isolate was resistant to carbapenem.

Figure 2. Antimicrobial resistance rates of *K. variicola* isolates.
Abbreviation: AMS, ampicillin-sulbactam; CIP, ciprofloxacin; TMP-SMX, trimethoprim-sulfamethoxazole; CLO, chloramphenicol.

- Hypervirulent traits of *K. variicola* isolates

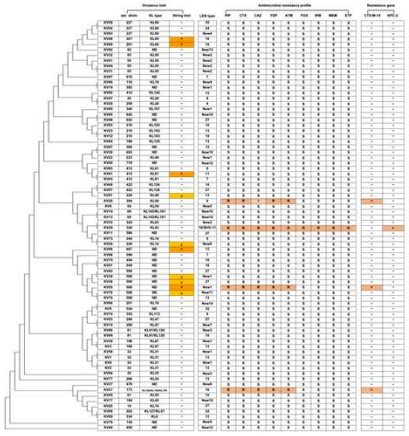

Figure 3. Phylogenetic tree of *K. variicola* isolates based on the sequence of the *wzi* gene. Positive reactions in the string test are highlighted in orange, and weakly positive reactions in light orange. Resistance to antimicrobials is shaded in apricot, with intermediate resistance shown in light apricot. The presence of resistance genes is also indicated in apricot.

- Carbapenemase-producing *K. variicola*

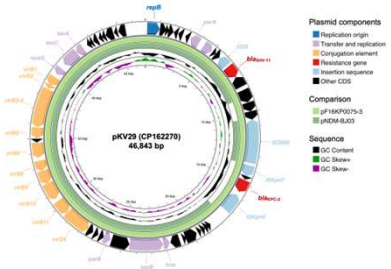

Figure 3. Schematic map of pKV29. From the outside, the outermost circle presents the open reading frames of pKV29. The colors of arrows were classified according to the function of each gene including blue for replication origin, light purple for transfer and replication, yellow for conjugation, red for resistance, and light blue for insertion sequences. The inner two circles with emerald and light green indicate the regions that showed homology (>99% nucleotide similarity) with the plasmids published previously (pF16KP0075-3, GenBank accession: CP052170.1; pNDM-BJ03, GenBank accession: JX104760.1). The innermost circles present GC content and GC skew.

Discussion and Conclusion

- MALDI-TOF MS showed accurate identification of *K. variicola* strains. Whole genome sequencing could be a standard for species-level discrimination within K. pneumoniae complex. Acquisition of bla_{SHV}-harboring plasmid could lead to misidentification in bacterial identification by SHV-OKP-LEN genotyping.
- Resistance rates of *K. variicola* isolates have been still low in South Korea. Only 4 CTX-resistant isolates and one carbapenem-resistant isolate was identified. The bla_{KPC-2} gene was located in the plasmid (pKV-29) which was >99% homology with pF16KP0075-3 originated from K. pneumoniae strain. Possible interspecies dissemination of carbapenemase encoding gene is noted in this study.
- Hypermucovisous *K. variicola* strains are still rare in South Korea.

Reference

- Rodrigues C, Passet V, Rakotondrasoa A, Diallo TA, Criscuolo A, Brisse S. Description of Klebsiella africanensis sp. nov., Klebsiella variicola subsp. tropicalensis subsp. nov. and Klebsiella variicola subsp. variicola subsp. nov. Res Microbiol 2019;170:165-70.
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