

TITLE: Spread of multidrug-resistant high-risk *Klebsiella pneumoniae* clones in a tertiary hospital from southern Brazil

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ABSTRACT:

Klebsiella pneumoniae is among the most important pathogens found in hospitals. The emergence of multiple antibiotic resistant *K. pneumoniae* associated with its virulence factors is a worldwide concern and its early identification is crucial, especially for controlling the spread of emerging clones. In this study, 26 isolates of *K. pneumoniae* isolated from patients admitted to different sectors of a university hospital located in the southern region of Brazil were analyzed. It was determined the antimicrobial resistance profile, followed by investigation of virulence and antimicrobial resistance genes. The clonal relationships were determined by enterobacterial repetitive intergenic consensus PCR (ERIC-PCR) and multilocus sequence typing (MLST). The results indicated a worrying level of antimicrobial resistance among the isolates. Fourteen isolates were classified as multidrug-resistant (MDR), seven as extensively drug-resistant (XDR), and three isolates were resistant to all antibiotics tested and were subsequently classified as pandrug-resistant (PDR). Among the investigated genes encoding carbapenemases, the results indicated a predominance of the *bla*_{KPC} gene, present in 53.8 % of the studied isolates (n = 14), followed by the genes *bla*_{OXA-48-like} present in 26.9 % (n = 7) and *bla*_{VIM} in 23.1 % (n = 6) of the isolates. Six extended spectrum β-lactamases (ESBL) genes were investigated and the most frequent gene was *bla*_{CTXM-Gp9}, present in 84.6 % of the isolates (n = 22). The most frequent virulence genes found were *mrkD* (Adhesion type 3 fimbriae) (92.3 % n=24) and the siderophore *entB* (88.5 % n=23). ERIC-PCR results indicated that the great majority of the isolates presented genetic similarity above 80 %. MLST analysis allowed to detect eight different STs, six of them (ST11, ST15, ST101, ST258, ST340, ST874) belonging to the large clonal complex CC258 (also called CC258/11) and two STs belonging to smaller CCs (ST442 and ST978). In conclusion, the results of the present study indicate a high prevalence of multiresistant *K. pneumoniae* harboring a large number of resistance and virulence genes. Among the isolates, we found three PDR high-risk international clones belonging to CC258. In addition, although the bacteria were isolated from different patients and different sectors of the hospital, they have high genetic similarity (above 80 %) indicating the prevalence of these clones in the hospital environment.

Keywords: *K. pneumoniae*; clonal complex 258; MDR, virulence genes; β-lactamases; MLST

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