

**TITLE:** Genotypic characterization of *Klebsiella pneumoniae* isolated from tracheal secretion in patients from a university hospital with outcome of hospital discharge and death.

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#### **ABSTRACT:**

*Klebsiella pneumoniae* is an opportunistic gram-negative pathogenic bacterium that has the ability to cause infections in the community and hospital environment. This pathogen is known for the high frequency and diversity of genes for antimicrobial resistance and virulence factors, which can impact its treatment. The objective of the present study was to characterize the genotypes of the main mechanisms of virulence and resistance to beta-lactam antimicrobials in *K. pneumoniae* isolated from tracheal secretion of patients admitted to a University Hospital in Western Sao Paulo that concluded to death and hospital discharge. The project was approved by the Research Ethics Committee with CAAE 01767418.2.0000.5515. Samples were collected from October 2018 to December 2019. The isolates were evaluated for the presence of virulence and resistance to antimicrobial genes through DNA extraction and amplification of virulence genes for K1 and K2 capsular antigens, type 1 and 3 fimbriae encoded by *fimH* (type I fimbria) and *mrkD* (type 3 fimbria) genes. It was also evaluated the *mpa* and *magA* genes indicate the phenotypic of hypermucoviscosity, the *Kfu* gene which is related to the iron uptake system, the *wabG* gene involved in the biosynthesis of lipopolysaccharide A and the genes encoding  $\beta$ -lactamases in *K. pneumoniae* (*blaTEM*, *blaOXA*, *blaCTX-M*, *blaSHV*). The presence or absence of the gene was confirmed by visualization of the PCR products, which were subjected to agarose gel electrophoresis. A total of 56 isolates were collected, where 36 were obtained from patients who concluded in death and 20 who were discharged. The *Wab* gene was predominant among virulence genes, (100% of the isolates in the death group and 90% in the discharge group). The *mpa* and *magA* genes had a lower prevalence (3.6% in both group of patients). Among the genes coding for  $\beta$ -lactamase, the *blaSHV* gene was found to be more prevalent (94% in death group and 90% discharge group). The *blaOXA* gene was present only in isolates from patients with death outcome. The multiple presence of resistance genes was also analyzed, and 100% of the isolates that presented four antimicrobial resistance genes were related to patients who died. Data analysis demonstrated that multiple presence of resistance genes and *blaOXA* resistance gene isolated from *K. pneumoniae* is strongly associated with the group of deaths, while most other genes have no significant difference between groups.

**Keywords:** Virulence, beta-lactam antimicrobials, death, hospital discharged

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