TITLE: Pathogenic potential and molecular typing of *β*-lactamase-producing *K. pneumoniae* isolated in several countries

AUTHORS: Oliveira-Silva, M. [1]; Nakamura-Silva, R.[1], Moraes, M. A. [1], Goulart, R. S. [2]; Peirano, G. [3]; Pitout, J. D. D [3]; Pitondo-Silva, A. [1,2 *].

INSTITUTIONS: [1] Postgraduate Program in Environmental Technology, University of Ribeirão Preto, Ribeirão Preto, SP, Brazil (Avenida Costábile Romano, 2201 - Ribeirânia, CEP 14096-900, Ribeirão Preto - SP, Brasil)
[2] Postgraduate Program in Dentistry, University of Ribeirão Preto, Ribeirão Preto, SP. Brazil.
[3] Department of Pathology and Laboratory Medicine, University of Calgary, Calgary, AB, Canada (2500 University Drive N.W., Calgary, Alberta, Canada T2N 1N4, Main Switchboard: 403.220.5110).

ABSTRACT:
Klebsiella pneumoniae is among the most important pathogens causing nosocomial and community infections. The emergence of multidrug-resistant *K. pneumoniae* associated with virulence factors is a worldwide concern. This study investigated the pathogenicity of 65 *β*-lactamase-producing *K. pneumoniae*, which were isolated from clinical cases and nosocomial infections from five continents. To investigate the antimicrobial susceptibility, virulence factors, capsular antigen and molecular typing relating and epidemic clones, several phenotypic and molecular techniques were used. The antimicrobial susceptibility profile was performed by disc-diffusion method and the hypermucoviscosity phenotype was characterized by the string test. Virulence genes was investigated by Polymerase Chain Reaction (PCR), the molecular typing and clonal relationships were performed by *Multilocus Sequence Typing* (MLST). Among the 65 isolates, 52% (n=34) were classified as Multidrug-resistant (MDR) and 51% (n=33) showed hypermucoviscosity phenotype. Twenty-one *wzi* alleles were identified being wzi-651, wzi-652, wzi-653, and wzi-654 alleles described for the first time in this study. Virulence factors were found in 83.33% (n=30) of the isolates, including *ent*B, *mrk*D, *fim*H, *ycfm*, *kp*N and *mrk*A. The MLST results showed 29 different STs among the strains, including ST11, ST23, ST340, ST17, ST20. The ST4672, ST4673 and ST4674 were described for the first time in this study. The majority of STs (96,3%) were associated with the clonal group 258(CG258) which is frequently associated with international high-risk clones. In conclusion, this study showed high prevalence of multirresistante *K. pneumoniae* strains isolated from countries from the five continents with high pathogenic potential, including PDR high-risk international clones belonging to CG258.

Keywords: *K. pneumoniae*, virulence, antimicrobial resistance, molecular epidemiology, capsular antigen.

Funding: This study was supported by the Foundation for Research Support of the State of São Paulo (FAPESP) [grant no.2013/22581-5].