TITLE: Phenotypic and molecular characterization of KPC-producing *Pseudomonas aeruginosa*

AUTHORS: Ivson Cassiano de Oliveira Santos[1], Juliana Brito Martins de Oliveira[1], Natacha Ferreira Pereira[1], Cláudio Marcos Rocha de Souza[1], Marise Dutra Asensi[1], Ana Paula D´Alincourt Carvalho-Assef[1]

INSTITUTION: [1] *IOC – FIOCRUZ. - Instituto Oswaldo Cruz, Fundação Oswaldo Cru (Av. Brasil No. 4365, Manguinhos - Rio de Janeiro, RJ – Brasil);*

Carbapenemase production is an important mechanism of resistance in the world, compromising the therapy by the use beta-lactam. The KPC-type is one of the most widespread carbapenemases, mainly in Enterobacteriaceae. This gene is present in mobile genetic elements that are responsible for its spread among different genera and species. During the period from 2015 to 2017, the Laboratório de Pesquisa em Infecção Hospitalar (IOC/fiocruz) detected 30 KPC-producing *Pseudomonas aeruginosa* isolates from the states of Bahia, Espírito Santo, Goiás, Minas Gerais, Piauí, Rio de Janeiro and Rio Grande do Norte. The isolates were submitted to susceptibility determination by agar diffusion method, the detection of phenotypic carbapenemase was performed by Carba NP, Blue Carba, Modified Carbapenem Inativation Method (mCIM) and confirmed by PCR. The clonality was evaluated by PFGE and one isolate was submitted to whole genome sequencing (WGS) on an Illumina MiSeq system for more information. All isolates carried the *bla*$_{KPC-2}$ allele. Resistance to carbapenems was observed in all isolates, 28 of them with MIC above 32 µg/ml for imipenem and meropenem, two intermediates for imipenem (4-6ug/ml) and a one with MIC 8ug/ml. The KPC-producing isolates showed Multidrug-resistance phenotype being more susceptibility for fluoroquinolones (31%) and aminoglycosides (24%). A 93% agreement was observed between the phenotypic tests and the PCR, two isolates were negative in the mCIM and another isolate was negative in all the phenotypic tests, but positive in the PCR. KPC-producing isolates belonged to 14 clonal groups by PFGE. The isolate submitted to WGS (CCBH17347) belonged to clonal group B that was present in Rio de Janeiro and Minas Gerais. This isolate belonged to a new ST (ST2584), carrying IncQ1 plasmid with *bla*$_{KPC-2}$ associated to transposon Tn*4401* and *aph*(3')-VI. Other resistance genes found in the genome were: *bla*$_{OXA-50}$, *bla*$_{PAO}$, *fos*A, *cat*B. This study showed the potential risk of dissemination KPC in different clonal and new ST of *P. aeruginosa*. In addition to calling attention to the possibility of not detecting phenotypically the production of KPC in *P. aeruginosa*.

Key words: *Pseudomonas aeruginosa, KPC,* carbapenemases, genome

Development Agency: CAPES, CNPq