TITLE: GENOMIC CHARACTERIZATION OF A KPC-2-PRODUCING *Pseudomonas aeruginosa* IN A COVID-19 PATIENT ADMITTED TO A REFERENCE HOSPITAL IN SÃO PAULO, BRAZIL

AUTHORS: YAMADA, A. Y.[1]; ADIWARDANA, N. S.[2]; DE SOUZA, A. R[1]; BERTANI, A. M. de J.[1]; CAMPOS, K. R.[1]; SACCHI, C. T.[1]; CUNHA, M. P. V.[3]; CASAS, M. R. T.[1]; CAVALCANTE, N. J. F.[2]; CAMARGO, C. H.[1]

INSTITUTION: 1. INSTITUTO ADOLFO LUTZ (AVENIDA DR. ARNALDO, 355, CEP 01246-902, SÃO PAULO – SP, BRAZIL)
2. INSTITUTO DE INFECTOLOGIA EMÍLIO RIBAS (AVENIDA DR. ARNALDO, 165, CEP 01246-902, SÃO PAULO – SP, BRAZIL)
3. FACULDADE DE MEDICINA VETERINÁRIA E ZOOTECNIA, UNIVERSIDADE DE SÃO PAULO (AV. PROF. DR. ORLANDO MARQUES DE PAIVA, 87, CEP 05508-270, SÃO PAULO – SP, BRAZIL)

ABSTRACT:
As a consequence of the pandemic COVID-19, an increase in hospital admissions was observed, as well as the use of antimicrobial therapy and length of the patient's stay. COVID-19 infections lead to poor clinical conditions that demand invasive procedures, facilitating the occurrence of hospital-acquired infections. Here we report a fatal case of co-infection with SARS-CoV-2 and KPC-producing *Pseudomonas aeruginosa* in a patient without previous comorbidities admitted to an infectious disease reference hospital in the city of São Paulo, Brazil. The patient was admitted for a COVID-19 diagnosis with severe acute respiratory syndrome, with positive SARS-CoV-2 PCR result. Patient was undergone to hemodialysis after 2 weeks, and developed bloodstream infection, ending with multiorgan disfunction syndrome and death. Catheter tip was cultured and revealed the presence of *P. aeruginosa*, identified by biochemical and molecular test (MALDI-TOF MS, Bruker Daltonics), named PA36721. The susceptibility test was performed by disk-diffusion and showed resistance to the amikacin, tobramycin, aztreonam, ceftazidime, cefepime, and to the carbapenems imipenem and meropenem, but broth microdilution showed susceptibility to polymyxin B (MIC 0.5mg/L). Multiplex PCR, targeting the main carbapenemase genes (KPC, NDM, OXA-48, SPM, IMP, VIM), was positive only for the bla_{KPC} gene. Isolate PA36721 had its whole genome sequenced (Illumina MiSeq platform) and further analysed. The resistome analysis (ResFinder and CARD databases) detected genes conferring resistance to aminoglycosides (*aph(3')-IIb*), phenicols (*catB7*) and fosfomycin (*fosA*). The bla_{KPC} allele was identified as *bla*KPC-2, flanked by IS*Kpn*6 and Tn3 in a structure compatible with a IncQ plasmid, according to PlacNetW assembly. The most similar sequence found in NCBI database match with the plasmid pMS14403, recovered from a clinical isolate of a polymyxin-resistant *P. aeruginosa* ST979, from Australia, but without the bla_{KPC} gene. MLST analysis found that PA36721 strain belong to ST803, never reported before in Brazil, identified only in Australia until our finding. After this infection, no other cases by the same strain were reported. This case recalls for the recurrence of uncommon antimicrobial resistance mechanisms in opportunistic pathogens and reinforces the need of continuous molecular surveillance for detection of unusual genotypes in well-recognized pathogens causing hospital acquired infections.

Keywords: co-infection, COVID-19, KPC-producing, *Pseudomonas*, whole genome sequencing

Development Agency: Secretaria de Saúde do Estado de São Paulo