TITLE: Epidemiological characterization of KPC-2-producing *Klebsiella pneumoniae* in a reference pediatric hospital

AUTHORS: Barroso, M.V.; Benfatti, L.R.; Silva, C.R.; Gozi, K.S.; de Andrade, L.K.; Nogueira, M.C.L; Casella, T.

INSTITUTION: FACULDADE DE MEDICINA DE SÃO JOSÉ DO RIO PRETO - FAMERP, SÃO JOSÉ DO RIO PRETO, SP (AV. BRG. FARIA LIMA, 5416 - VILA SAO PEDRO, CEP 15090-000 SÃO JOSÉ DO RIO PRETO - SP, BRAZIL)

ABSTRACT:

KPC-producing *Klebsiella pneumoniae* (KPKp) infections are considered a threat to public-health. Children and newborn are among the most affected groups since therapeutic options for treating the disease in this population is limited. Despite the clinical relevance, studies focusing on the epidemiological background of KPKp colonizing or causing infections in pediatric wards are scarce worldwide. Hence, the aim of this study was to investigate and characterize the phenotypic, molecular and epidemiological profiles of KPKp isolated from children in a reference pediatric hospital in Brazil. A retrospective study was carried out from November 2016 to March 2021, and 26 KPKp isolates were selected. Identification and antimicrobial susceptibility were performed, and antimicrobial resistance and virulence genes were identified. Molecular typing was performed by *Xba*I-PFGE, MLST and K-typing. The KPKp isolates were obtained from surveillance swabs (65.4%, 17/26), blood (11.5%, 3/26), urine (11.6%, 3/26), bronchial lavage (3.8%, 1/26), pleural fluid or abdominal purulent liquid (3.8%, 1/26 each). Most isolates were resistant to all classes of antibiotic tested, except for polymyxin B. The $bla_{\text{KPC-2}}$ was the only allele found, but $bla_{\text{CTX-M-1}}$, $bla_{\text{CTX-M-2}}$, and $bla_{\text{CTX-M-15}}$ were also responsible for beta-lactam resistance. Eight isolates presented resistance to polymyxin B due to the absence, disruption (IS*1*-like or IS*5*-like) or punctual mutation resulting in amino acid substitution (W20L or I12F) of the *mgr*B gene. All KPKp isolates carried genes encoding for fimbrial adhesin (*fim*H and *mrk*D) and the siderophore enterobactin receptor *ent*B. However, genes traditionally associated with the hypervirulence profile were not detected. Fifteen isolates clustered in 7 distinct groups based on *Xba*I-PFGE. In general, 10 different sequence types (ST) were identified and the clonal complex 258 was the prevalent. Regarding to K-typing, a total of 11 KL-type were identified and the allele 50 was the most recurrent. This study provides the first epidemiology characterization of KPC-producing *K. pneumoniae* in a reference pediatric hospital in Brazil. Despite the high genetic diversity among the non-

typically virulent MDR isolates, KPC-2-producing *K. pneumoniae* ST 11-KL64 strains were the most detected lineage among patients admitted to the institution.

Keywords: *Klebsiella pneumoniae*, KPC-2, molecular typing, pediatrics

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