TITLE: COLISTIN RESISTANCE IN Klebsiella pneumoniae ISOLATES MEDIATED BY mgrB INSERTIONAL INTERRUPTION


INSTITUTION: UNIVERSIDADE FEDERAL DE PERNAMBUCO, RECIFE, PE (DEPARTAMENTO DE GENÉTICA, AVENIDA DA ENGENHARIA, 420, CIDADE UNIVERSITÀRÍA, PRÉDIO DO CENTRO DE CIÊNCIAS DA SAÚDE, 1º ANDAR, CEP 50730120, RECIFE – PE, BRASIL) ; UNIVERSIDADE DE PERNAMBUCO, RECIFE, PE (INSTITUTO DE CIÊNCIAS BIOLÓGICAS, RUA ARNÔBIO MARQUÊS, 310, SANTO AMARO, CEP 50100130, RECIFE – PE, BRASIL) ; UNIVERSIDADE FEDERAL RURAL DE PERNAMBUCO, RECIFE, PE (DEPARTAMENTO DE BIOLOGIA, RUA MANUEL DE MEDEIROS, 97, DOIS IRMÃOS, CEP 52171260, RECIFE – PE, BRASIL)

ABSTRACT:
Infections caused by carbapenem-resistant Klebsiella pneumoniae lead to limitations of therapeutic options. Therefore, polymyxins were reintroduced into clinical practice and its increased use led to emergence of resistant bacterial isolates. Recently, an increase in prevalence of K. pneumoniae colistin-resistant was observed in a public university hospital in Recife, Brazil. This study aimed to evaluate the genetic relationship and mechanisms involved in colistin resistance in these isolates. The MIC values were determined by automated system and interpreted according to CLSI (2017). The clonal relationship was analyzed by PFGE and sequence types were determined through MLST. Resistance to colistin was evaluated regarding to the presence of mcr gene and mgrB gene integrity, by PCR followed by sequencing. Sixteen isolates of K. pneumoniae were identified, which were collected from 2013 to 2016, from different samples and anatomical sites. Among them, nine isolates (56.25%) were extensively resistant (XDR), six isolates (37.5%) were pandrug resistant (PDR) and one isolate (6.25%) was multidrug resistant. Most showed susceptibility to amikacin and tigecycline. The PFGE indicated three major clonal groups (A, B and C) and two smaller groups (A1 e A2). Group A and subgroups A1 and A2 comprised 12 isolates and accounted for ten ST11, one for ST340 and one for a new ST (ST3990). ST11 and ST340 are part of the clonal complex 258 (CC258), which is known to be widespread in the world and closely associated to carbapenem-resistant strains. Groups B and C included the remaining four isolates, which belonged to ST25 and ST423, respectively. Regarding to colistin resistance, the presence of insertion sequences (IS) interrupting the mgrB gene was observed in ten isolates. The ISs identified (ISKpn13, IS903 and IS903b) belong to the IS5 family, which have already been reported in isolates of K. pneumoniae resistant to colistin. In the six isolates that showed intact mgrB, resistance to colistin is probably mediated by other mechanisms, such as changes in Two Component Systems (pmrAB and phoPQ), which will be evaluated later. The mcr gene was not detected in any of the isolates. These results highlight the high frequency of insertional interruption of mgrB mediating the resistance to colistin in K. pneumoniae isolates belonging to different STs, indicating this is probably the most common and easily stablishing mechanism to colistin resistance in this species.

Keywords: Klebsiella pneumoniae, colistin, MDR, mgrB insertional interruption, IS5 family

Development Agency: FACEPE, CAPES and CNPq