The excessive use of β-lactam antimicrobials in hospitalized patients favored the emergence and genetic evolution of Klebsiella pneumoniae strains resistant to carbapenems, being this resistance more related to beta-lactamases production and mediated by conjugative plasmids. Therefore, the objective of this study was to investigate the main plasmidial incompatibility groups (Inc's) and clonal relationship of eleven K. pneumoniae clinical isolates carrying blaKPC, from colonization (culture of surveillance: rectal swab) and infection, in patients of a public hospital in Recife-PE.

The molecular typing by ERIC-PCR showed that two isolates were related with 100% of genetic similarity and another isolate with 80%, these three isolates came from different patients and different hospital sectors, showing clonal dissemination. The other isolates did not showed clonal relationship. The Inc's FIB, Q, A/C, L/M, N, HI2 and HI1B were investigated by PCR and the amplicons were sequenced for Inc's confirmation. The Inc's N and HI2 were not detected. On the other hand, the Inc's FIB, Q, HI1B, A/C and L/M were detected in 10 (90.9%), 10 (90.9%), 3 (27.2%), 3 (27, 2%) and 1 (9.1%) isolates of K. pneumoniae, respectively, showing that most of the isolates had more than one type of plasmid. This is the first report of Inc FIB in Recife-PE, as well as the first report of IncHI1B in Brazil. It should be noted that both the Inc FIB and the IncHI1B are conjugative plasmids. This study showed the high plasmidial variability of K. pneumoniae clinical isolates carrying blaKPC gene and resistant to carbapenems. Highlighting that these plasmids (Inc's FIB, Q, HI1B and A/C) were present in K. pneumoniae from infection and intestinal colonization, indicating the dissemination potential of these mobile genetic elements among K. pneumoniae isolates in the hospital environment.

Keywords: Klebsiella pneumoniae; plasmid; Inc; blaKPC.