Klebsiella pneumonia carbapenemase (KPC) is a β-lactamase that confers resistance to all β-lactam antibiotics, including carbapenems. This enzyme is encoded by a high mobility and dissemination plasmid that can be found in different enterobacteria. The aim of this study was to evaluate K. pneumoniae isolates resistant to carbapenems from four hospitals in northwestern Paraná, as the presence of carbapenemase and clonality. Eighteen samples of K. pneumoniae were selected for the study (three from hospital A, two from hospital B, four from hospital C and nine from hospital D) with resistance to both imipenem as meropenem (automated and disc-diffusion methods) isolated in the period from November 2014 to May 2015, for carbapenemase production detection. Phenotypic tests were the modified Hodge test (HTM) and inhibition by phenylboronic acid (AFB) second technical note 01/2013 of ANVISA. Regarding the genotypic methods, blaKPC and blaNDM genes were researched using the polymerase chain reaction methodology - multiplex PCR. Molecular typing was determined by the technique of Enterobacterial Repetitive Intergenic Consensus - ERIC-PCR. All samples showed positive HTM and inhibition before the AFB. It was detected the presence of blaKPC gene in all isolates, and none tested positive for blaNDM. All samples from different hospitals that belongs in the same cluster pattern similarity greater than 93%, analyzed by BioNumerics software version 6.5 with clonality Dice coefficient of ≥ 0.93, showing the existence of inter and intra-hospital transmission. Patients were not allowed simultaneously while at the same institution and there is no concrete epidemiological links between the hospitals that justify such dissemination, however, the presence of the same support staff in different hospitals cannot be ruled out. It concludes that the rapid spread intra and inter-hospital of the same pattern of clonal KPC reveals the need to intensify efforts to reduce the transmission preventing the spread of this cluster to other institutions.

Palavras-chave: Klebsiella pneumoniae; drug-resistance; KPC; molecular typing