Abstract

Carbapenem resistant Enterobacteriaceae are a significant public health concern, and genes encoding the Klebsiella pneumoniae carbapenemase (KPC) have contributed to the global spread of carbapenem resistance. In the current study, we used whole-genome sequencing to investigate the diversity of blaKPC-containing plasmids and antimicrobial resistance mechanisms among 26 blaKPC-containing Escherichia coli, and 13 blaKPC-containing Enterobacter asburiae, Enterobacter hormaechei, K. pneumoniae, Klebsiella variicola, Klebsiella michiganensis, and Serratia marcescens strains, which were isolated from the same patients as the blaKPC-containing E. coli. A blaKPC-containing IncN and/or IncFIIK plasmid was identified in 77% (30/39) of the E. coli and other bacterial species analyzed. Complete genome sequencing and comparative analysis of a blaKPC-containing IncN plasmid from one of the E. coli strains demonstrated that this plasmid is present in the K. pneumoniae and S. marcescens strains from this patient, and is conserved among 13 of the E. coli and other bacterial species analyzed. Interestingly, while both IncFIIK and IncN plasmids were prevalent among the strains analyzed, the IncN plasmids were more often identified in multiple bacterial species from the same patients, demonstrating a contribution of this IncN plasmid to the inter-genera dissemination of the blaKPC genes between the E. coli and other bacterial species analyzed.