Background: The co-existence of carbapenemase and 16S rRNA methyltransferase (16S-RMTase) can cause serious difficulty in treating infections with multidrug-resistant Gram-negative pathogens in cancer patients. We investigated the prevalence of carbapenemase genes in 16S-RMTase-producing Enterobacteriaceae isolated from cancer patients in Bulgaria.

Material/methods: One hundred 16S-RMTase-producing isolates collected consecutively during 2006-2015 at the Cancer hospital of Sofia were studied. Multiplex polymerase chain reaction (PCR) using nine sets of carbapenemase specific primers (VIM, IMP, SIM, GIM, SPM, NDM-1, KPC, GES, OXA-48) followed by sequence analysis of PCR amplicons were used to identify carbapenemase genes. Screening for associated ESBL and AmpC-type genes was carried out by PCR-based assays and PCR products were sequenced. Genotyping, by pulse-field gel electrophoresis (PFGE) of genomic DNA was performed to determine genetic relatedness of carbapenemase-producing isolates.

Results: Among the one hundred 16S rRNA methyltransferase-producing enterobacterial isolates, 16 were positive for carbapenemase genes. VIM-1 carbapenemase gene was detected in 15/16 armA-positive Proteus mirabilis isolates, and co-existence with blaSHV-12 and blaCMY-99 was observed in all of them. These isolates were identical by PFGE, suggesting clonal dissemination of multidrug-resistant P. mirabilis strain. In addition, the NDM-1 carbapenemase gene was identified in one E. coli strain harboring rtmB methyltransferase gene in association with blaCTX-M-15 and blaCMY-4. The remaining 84 enterobacterial isolates, which were armA-positive did not possess any of the carbapenemase genes studied.

Conclusions: This study reports on the relatively low prevalence (16%) of carbapenemase genes among 16S rRNA methyltransferase-producing enterobacterial isolates at the cancer hospital in Sofia, and on the co-existence of VIM-1 carbapenemase gene and ArmA methyltransferase gene in Proteus mirabilis isolated in Bulgaria.