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P1750 *In vitro* evaluation of various antibiotic combinations for carbapenemase-producing *Enterobacteriaceae*

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Background: In recent years, increase of carbapenem resistant Enterobacteriaceae isolates is known worldwide. The aim of this study is to identify OXA-232, OXA-181, OXA-162, OXA-204, OXA-244, OXA-163 and OXA-245 gene regions in OXA-48 like carbapenemase producing Klebsiella pneumoniae isolates.

Materials/methods: The isolates used for our study were taken from SEAH Medical Microbiology Laboratory collection. Identification and antibiotic sensitivity studies were performed by VITEK 2 automated system. Carbapenemase production of the isolates was determined by Modified Hodge Test. MIC values of each isolate were determined by broth microdilution method. Isolates containing the OXA-48-like gene region were identified by RT-PCR using consensus primers. Isolates showing deviations of melting temperature by HRMA method were selected with the suspicion of being an OXA-48 variant. And in order to determine which variants were present in these isolates, sequence analysis was performed.

Results: In carbapenemase producing K. pneumoniae strains, categorical agreement for VITEK 2 and microdilution were obtained for imipenem, meropenem and ertapenem, 82%, 77%, and 90% respectively. By RT-PCR method, OXA-48 like gene locus was found to be positive in 45 of 100 K. pneumoniae strains. To identify OXA-48 variants, 45 strains that were positive by PCR were evaluated by HRMA method. With Sanger sequencing, the OXA-48 / OXA-245, OXA-181 and OXA-244 gene regions were found to be positive in 41, 2 and 2 isolates, respectively.

Conclusions: As a result of our study, OXA-48 positivity was found to be 45%. 4.4% were found to contain OXA-181 and 4.4% were found to contain OXA-244 regions. Our study is important because it is the first study to investigate OXA-48 variants in our country extensively. With the optimization of our study and considering that different OXA-48 variants may cause different antibiotic susceptibility patterns, detection of OXA-48-like gene regions in laboratories at the time of need will guide the clinician in the selection of antibiotics in critical patient groups.