

**P1351 Investigation of *oxa-48*-like genes in carbapenemase-producing producing *Klebsiella* spp. isolates**Elmas Pinar Kahraman<sup>1</sup>, Hande Toptan<sup>1</sup>, Baris Otlu<sup>2</sup>, Mehmet Koroglu<sup>1</sup>, Mustafa Altindis\*<sup>1</sup><sup>1</sup> Medical school, Sakarya University, Sakarya, Turkey, <sup>2</sup> Medical school, Inonu University, Sakarya, Turkey

**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.

