

Phylogenetic analysis of *Klebsiella pneumoniae* isolates recovered from hospitalized patients in Semnan, Iran

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Introduction and objectives The objectives of our study were to determine the distribution of phylogenetic groups among *K. pneumoniae* isolates recovered from hospitalized patients in Kosar hospital in Semnan city and to investigate the relationship between the antibiotic resistance patterns and phylogenetic groups.

Materials and methods We obtained 125 *K. pneumoniae* isolates between April 2014 to March 2015 from hospitalized patients. The sample sources were urine (80, 64%), respiratory secretion (38, 30.4%), wound (5, 4%) and blood (2, 1.6%). The samples collected from patient ages between 9 and 93 years old (63.1 ± 21.6). Seventy (56%) patients were female while 55 (44%) were male. Most of our isolates recovered from hospitalized patients in internal (39, 31, 2%) and internal-ICU wards (37, 29.6%). Antimicrobial susceptibility testing was performed for different classes of antimicrobial agents. The phylogenetic group of isolates were determined using RFLP-PCR method. Furthermore, the prevalence of TEM and SHV was assessed using PCR. **Results** The most susceptibility rate was observed against amikacin ($n=107$, 85.6%), meropenem ($n=102$, 81.6%), imipenem ($n=100$, 80%), and ertapenem ($n=88$, 77.4%). RFLP-PCR method separated the isolates phylogenetically as follows: 92 (73.6%) isolates were identified as KpI, 29 (23.2%) isolates as KpII, 3 (2.4%) isolates as KpIII, and one (0.8%) isolate as unknown. The highest resistance percentages were seen in KpI, followed by KpII and KpIII. There were no significant association between phylogenetic group and resistance profile. Sixty-five (52%) and 82 (65.6%) isolates were carried TEM and SHV ESBL, respectively. More than 80% of KpI isolates were positive for at least one of the ESBLs mentioned before in which resistance against cefotaxime was revealed.

Conclusion Not only was KpI the most predominant phylogenetic group, but the highest rate of resistance was also observed in KpI group. High prevalence of TEM and SHV which may favor their survival in the hospital setting raise additional concern in limiting therapeutic options.

Keywords: *Klebsiella pneumoniae*, phylogenetic group, TEM, SHV, Iran