Abstract

Background: *Pseudomonas aeruginosa* is a gram-negative, Obligate aerobe, non-fermenting and catalase-positive oxidase bacillus. This bacterium is one of the most common and important opportunistic pathogens causing nosocomial infections, which can infect almost all tissues of the human body.

A wide range of acute and chronic infections are caused by the *Pseudomonas aeruginosa*: including; Urinary tract infections, sepsis, pneumonia, wound infections, and soft tissue infections, especially in patients with weakened immune systems, burn patients, and long-term hospitalization. Today, approximately 13% of hospital-acquired infections are caused by multidrug-resistant strains of *Pseudomonas aeruginosa*.

Pseudomonas aeruginosa infections are difficult to treat due to their innate and acquired resistance mechanisms, and only a limited class of antibiotics is effective in treating these infections. Among antibiotics, carbapenems (imipenem, meropenem) are the most commonly used drugs for the treatment of multidrug-resistant Pseudomonas aeruginosa infections. Strains of *Pseudomonas aeruginosa* show high resistance to carbapenems by producing the enzyme metallobetalactamase, especially simultaneous resistance to several drugs. Carbapenem-resistant strains of *Pseudomonas aeruginosa* are rapidly spreading, posing a major threat to human health worldwide. Therefore, understanding the mechanisms of drug resistance in clinical isolates of *Pseudomonas aeruginosa* seems necessary.

Aim: The current study aimed to determine the prevalence of imipenem-resistant *P. aeruginosa*, detect metallo-B-lactamase (MBL) -producer isolates, and evaluate their clonal relationships in strains isolated from patients referring to the hospitals of Ardabil city, Iran.

Material and Methods: The resistance rate to imipenem was evaluated using the disk diffusion method. Double-disk synergy test and PCR technique were used for phenotypic and genotypic screening of MBL-positive *P. aeruginosa*, respectively. Ultimately, enterobacterial repetitive intergenic consensus-polymerase chain

reaction (ERIC-PCR) and multilocus sequence typing (MLST) methods were used for assessing clonal relatedness among the isolates.

Results: The prevalence of imipenem-resistant *P. aeruginosa* strains was estimated at 57.1% (48 out of 84 isolates). In addition, 45 (93.7%) out of 48 imipenem-resistant *P. aeruginosa* isolates were phenotypically screened as MBL positive, among which 16 (35.5%) and three (6.6%) isolates harbored blaIMP and blaVIM-1 genes, respectively. However, blaNDM, blaSIM-2, blaSPM, and blaGIM-1 genes were not detected in this study. MBL-producing *P. aeruginosa* strains were divided into 42 ERIC-PCR types. Based on the results of MLST, P. aeruginosa ST235 was the only identified sequence type.

Conclusions: Our results revealed a high and alarming prevalence of imipenem-resistant and blaIMP-positive *P. aeruginosa* ST235 at Ardabil hospitals. Continuous monitoring is essential to control the further spread of this highly virulent and drug-resistant clone.

Keywords: *Pseudomonas aeruginosa*, Imipenem, Drug Resistance, Metallo-Beta- Lactamase, Clonal Relation