Molecular Detection of MBL Encoding Genes Among Carbapenemase-Producing *Pseudomonas Aeruginosa* Isolated from Sulaimaniyah Hospitals

Kosar Ali Omer, MSc*,** Sehand Kamaluldeen Arif, PhD** Hemin Esmael Othman, PhD***

ABSTRACT

Background: *Pseudomonas aeruginosa* can quickly develop antibiotic resistance mainly through chromosomal mutations, and its carbapenem-resistant resulting from metallo-β-lactamases (MBL) has been reported to be a significant cause of nosocomial infection. Objectives: To characterize the antibiotic resistance profiles, detect carbapenemase production, and identify MBL encoding genes in *P. aeruginosa* isolates.

Materials and Methods: *P. aeruginosa* was isolated (n=59) from patients at Hiwa Hematology/Oncology (n=31) Hospital and High-Quality Hospital (n=28) from June 2022 to January 2023. An antimicrobial susceptibility test, a CarbaNp test, and a combination detection test (CDT) were used to identify MBL producer isolates. Additionally, PCR targeting MBL-encoding genes for blaVIM, blaVIM, blaIMP, blaSPM, blaSIM and blaGIM was performed to provide additional confirmation.

Results: Approximately 37% of the isolates exhibited multi-drug resistance (MDR), while 22% showed extensive drug resistance (XDR). About 30% of the isolates were resistant to carbapenem. Among carbapenem-resistant *P. aeruginosa* (CRPA), 61% and 56% had positive results for imp/EDTA combined disc and RAPIDEC® CARBA NPs, respectively, while 67% harbored MBL-encoding genes. blaVIM-2 was identified as the most prevalent gene (66.6%), followed by blaIMP-1 (16.6%), and then blaSIM-1 (11.1%).

Conclusions: Multiplex PCR is a rapid and accurate technique to detect MBL-encoding genes. The blaVIM gene has been identified as the primary genetic determinant associated with carbapenemase production.

Keywords: *P. aeruginosa,* antibiotic resistance, metallo-β-lactamase genes, carbapenemase production.

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* Hiwa Hematology, Oncology Hospital
Sulaimani Directorate of Health
Sulaimaniyah, Iraq.
E-mail: sehand.arif@univsul.edu.iq

** Department of Biology
College of Science
University of Sulaimani
Sulaimaniyah, Iraq.

*** Department of Biology
College of Science
University of Duhok, Duhok, Iraq.