BURNS XXX (2014) XXX–XXX

Available online at www.sciencedirect.com

ScienceDirect

journal homepage: www.elsevier.com/locate/burns

Letter to the Editor

Reply to: Molecular methods require for confirmation bla_{AIM} (Adelaide imipenemase) producing *Pseudomonas aeruginosa*

We appreciated the comments by Dr. Banerjee and Dr. Singh about our recent paper [1].

In our study, 80 out of 92 isolates of *Pseudomonas aeruginosa* that were typed via RAPD-PCR had identical patterns which were nominated as pattern A and other patterns included only one or two isolates. Frequencies of ESBL and MBL genes of *P. aeruginosa* isolates possessing pattern A have been shown in Table 1. Among assessed isolates, 26 (32.5%) had *OXA-10*, *TEM* and *VIM* genes, 14 (17.5%) had *OXA-10* and *TEM* genes and 14 (17.5%) had *OXA-10* and *VIM* genes and due to presence of producing OXA-10, VIM, PER and IMP beta-lactamases among isolates with pattern A, the mentioned conclusion has been cited in the study. On the other hand, in typing methods, isolates may be similar for genetic patterns but different for phenotypic characteristics or variety of genes that this phenomenon may occur due to gene acquiring horizontally [2].

There is not any difference between CLSI 2011 and CLSI 2013 for performing antibiogram, MIC, ESBLs via combinational disk with clavulanic acid and carbapenemase via MHT methods [3,4]. All conditions for identification of resistance to polymyxin, ceftazidime, azteronam, cefotaxime, cefepime, ciprofloxacin and gentamicin are identical between CLSI 2011 and CLSI 2013 [3,4]. Also, since the diameter of clear zone around disks, in disk diffusion method, for all *P. aeruginosa* isolates resistant to carbapenem was zero for imipenem, meropenem and ertapenem and has been reported as resistant in this study, therefore there is no difference between interpretation of results via CLSI 2011 and CLSI 2013 [1,3,4]. The issues raised by Dr. Banerjee and Dr. Singh are important and should have been addressed in our paper. However, in all PCR reactions in this study, control isolates were used but were not cited in the study. Meanwhile, bla_{AIM} gene with special primer was traced and sequenced (but was not cited in the study) [5] which possessed 100% similarity with gene bla_{AIM} recorded as AM998375.1 in GenBank [6].

Table 1 – Distribution of the ESBL and MBL genes among carbapenem-resistant *Pseudomonas aeruginosa* RAPD type A isolates.

Resistance genes	Number of isolates
OXA-10	14
IMP	1
TEM + VIM	1
OXA-10 + IMP	2
OXA-10 + TEM	14
OXA-10 + VIM	15
OXA-10 + TEM + PER	2
OXA-10 + TEM + VIM	26
OXA-10 + PER + VIM	3
OXA-10 + TEM + PER + VIM	2

1. Conflict of interest statement

None declared.

REFERENCES

[1] Neyestanaki DK, Mirsalehian A, Rezagholizadeh F, Jabalameli F, Taherikalani M, Emaneini M. Determination of extended spectrum beta-lactamases, metallo-beta-lactamases and AmpC-beta-lactamases among carbapenem resistant *Pseudomonas aeruginosa* isolated from burn patients. Burns)2014;(April). pii:S0305-4179(14)00070-9.

[2] van Belkum A, Struelens M, de Visser A, Verbrugh H, Tibayrenc M. Role of genomic typing in taxonomy, evolutionary genetics, and microbial epidemiology. Clin Microbiol Rev 2001;14(3):547–60.

[3] Clinical Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. Twenty-First Inform Suppl 2011;31(1):M100–S121.

[4] Clinical Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. Twenty-Third Inform Suppl 2013;33(1):M100–S123.

[5] Poirel L, Walsh TR, Cuvillier V, Nordmann P. Multiplex PCR for detection of acquired carbapenemase genes. Diagn Microbiol Infect Dis 2011;70:119–23.

[6] http://www.ncbi.nlm.nih.gov/nuccore/Am998375.

Please cite this article in press as: Jabalameli F, Kalantar-Neyestanaki D. Reply to: Molecular methods require for confirmation bla_{AIM} (Adelaide imipenemase) producing *Pseudomonas aeruginosa*. Burns (2014), http://dx.doi.org/10.1016/j.burns.2014.05.020

Fereshteh Jabalameli
Davood Kalantar-Neyestanaki
Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran

Khairollah Asadollahi
Morovat Taherikalani
Clinical Microbiology Research Center, Ilam University of Medical Sciences, Ilam, Iran

Mohammad Emaneini*
Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran

*Corresponding author at: Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, 100 Poursina Street, Keshavarz Boulevard, Tehran, Iran.
Tel.: +98 021 8895 5810; fax: +98 021 8895 5810
E-mail address: emaneini@tums.ac.ir ((M. Emaneini)

26 May 2014

http://dx.doi.org/10.1016/j.burns.2014.05.020

Please cite this article in press as: Jabalameli F, Kalantar-Neyestanaki D. Reply to: Molecular methods require for confirmation bla_{AIM} (Adelaide imipenemase) producing *Pseudomonas aeruginosa*. Burns (2014), http://dx.doi.org/10.1016/j.burns.2014.05.020