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Case Report

Multiplex PCR for Detection of a Successful Pathogen; *Acinetobacter baumanni* as a Real Threat in Intensive Care Unit of a University Hospital

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Multidrug resistance in *Acinetobacter baumannii* is a growing public health concern all over the world. In the current study, the isolation and antimicrobial resistance pattern and detection of *blaOXA-51* and *lpxC* genes by multiplex PCR method was performed.
All the isolates demonstrated high levels of resistance rates to amikacin, ciprofloxacin, meropenem, imipenem, ceftriaxone, gentamicin, and colistin. Screening of two resistance genes by multiplex PCR showed that all the isolates contained *blaOXA-51* and *lpxC* genes. As we previously reported, nosocomial infections caused by *A. baumannii* isolates are a major cause of morbidity and mortality in our hospital.

Keywords: Acinetobacter baumannii, Nosocomial infection, Multidrug-resistance, *blaOXA-51* and *lpxC* genes

1.Background

Acinetobacter baumannii is a non-motile gram-negative and aerobic bacterium commonly isolated from the hospital environment and also hospitalized patients. *A. baumannii* is a nosocomial organism and preferentially colonizes aquatic environments. This organism is often cultured from sputum or respiratory secretions, wounds, skin and urine specimens of hospitalized patients.

A. baumannii is commonly associated with serious nosocomial infections worldwide; In this regard, Iran is no exception (1-2). In health care settings, *A. baumannii* is known for its ability to colonize or infect severely ill patients, particularly elderly. Moreover, it is extremely resistant to various antibiotics (3), particularly the carbapenem-hydrolysing Class D b-lactamase, that is intrinsic in this bacterium. Similarly, colistin resistance in *A. baumannii* isolates has been reported from several countries (4).

In Iran, dissemination of *A. baumannii* clones harboring carbapenem as well as colistin was reported (5-6).

2.Context

In this study, we documented eight cases of *A. baumannii* in a teaching hospital, Karaj.

Species identification had been performed previously using biochemical tests (7). The antibiotic susceptibility of the strains was determined by the standard disk diffusion method on Mueller– Hinton agar according to CLSI guideline (8). The following antibiotics were tested: imipenem, amikacin, gentamicin, ciprofloxacin, meropenem, ceftriaxoneand, and colistin.

All the *Acinetobacter* isolates were subjected to multiplex PCR assay in search for *blaOXA-51* and *lpxC* genes using specific primers (9).

Antibiotic susceptibility testing showed that all the isolates under study were resistant to ciprofloxacin, gentamicin, amikacin, meropenem, imipenem, ceftriaxone, and colistin.

Screening for carbapenemase-encoding genes by multiplex PCR showed that all the isolates contained the naturally occurring blaOXA-51 gene. Similarly, molecular analysis of the colistin-resistant isolates showed that all the isolates harbored lpxC resistance genes (Figure 1).

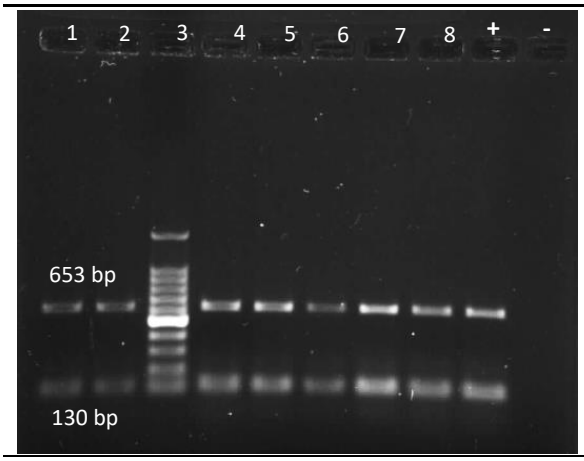

Figure 1: Detection of *blaOXA-51* and *lpxC* genes by multiplex PCR. The molecular size marker (Lane 3), Lane 9 positive control and Lane 10 negative control.

3.Conclusion

Emergence of multidrug resistance among *A. baumannii* strains is a clinical problem affecting people health worldwide, making it as an important nosocomial pathogen which is able to acquire resistance to almost all routin antibiotics, including carbapenems (10). In such cases, colistin is a key antimicrobial agent for treatment, however, increased prescription of this antibiotic has led to the emergence of colistin resistant *A. baumannii* isolates (11).

Our study involved eight unique patients identified with infection due to multidrug resistant *A. baumannii*, which can be supported by the genetic relatedness of colistin- and carbapenem-resistant genes among these isolates. Therefore, in conclusion, it is recommended that the use of antibiotics to

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be well managed, and the establishment of a resistance monitoring system to be warranted.

Conflict of Interest

The authors report no conflicts of interest in this work.

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Authors' Contributions

The authors declare no financial disclosure to report.

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