Biochem. Cell. Arch. Vol. 21, No. 1, pp. 857-864, 2021	www.connectjournals.com/bca	*ISSN 0972-5075*
DocID: https://connectjournals.com/03896.2021.21.857		*eISSN 0976-1772*

PHENOTYPIC AND GENOTYPIC DETECTION OF SOME VIRULENCE FACTOR FOR MULTI-DRUG RESISTANT *ACINETOBACTER BAUMANNII* ISOLATED FROM DIFFERENT CLINICAL SPECIMENS

Zainab Hussein Mahdi, Abbas Abboud Farhan and Ammar Ahmed Sultan

Department of Biology, College of Education for Pure Science, University of Diyala, Iraq.

(Received 30 November 2020, Revised 11 February 2021, Accepted 27 February 2021)

ABSTRACT : *Acinetobacter baumannii* is one of the emerging pathogens that causes concern in general and hospital environments during the last two years, and has various virulence factors that contribute to its pathogenicity. This study was conducted during the period from the beginning of November 2019 to the end of May 2020, during which it were collected 420 specimens from different clinical sources including Blood , wounds, burns, sputum and urine. Depending on the diagnostic methods using: conventional, VITEK2 system and molecular detection of *16S rRNA* and *blaOXA-51,* 43 (10.23%) *A. baumannii* isolates were obtained. All isolates were MDR, so they showed complete resistance to seven antibiotics used and at the same time, all of them were sensitive to colistin and Tigecycline. All isolates showed adherence ability to adhere to epithelial cells and form a strong biofilm by the TM, while they were 29(67.44%), 13(30.23%), 1(2.33%) of which strong, moderate and weak biofilm production respectively when used MTP method. In addition, all isolates have no capsule. The results of genotypic detection were 42(97.7%) for *ompA*, 24(55.8%) for *Bap* and no isolates possesse gene *KpsMII*. There was a relationship between the phenotype and genotype of the studied virulence factors of *A. baumannii*. The genetic sequences were recorded origin sequence in NCBI for tow isolates carrying accession number LC576834.1, LC576831.1 for *ompA* gen and LC576828.1 for *Bap* gene.

Key words : *A. baumannii*, biofilm production, *Bap*, *ompA*, *KPSMTII*.

How to cite : Zainab Hussein Mahdi, Abbas Abboud Farhan and Ammar Ahmed Sultan (2021) Phenotypic and genotypic detection of some virulence factor for multi-drug resistant *Acinetobacter baumannii* isolated from different clinical specimens. *Biochem. Cell. Arch.* **21**, 857-864. DocID: https://connectjournals.com/03896.2021.21.857

INTRODUCTION

A. baumannii is one of the most challenging pathogens due to its particular multi-drug resistance (MDR) characteristics. Rrecently, World Health Organization is considered *A. baumannii* as number one critical priority pathogen for which new therapeutics are urgently required (WHO, 2017). It is also classified as important Gram-negative opportunistic bacterial pathogens that are responsible for 2–10% of all Gram negative and mortality rates can reach 35% (Antunes *et al*, 2014).

During the last decade, this pathogen has become increasingly resistant to most antimicrobials. There are several resistance mechanisms contribute to the MDR phenotype include decreased outer membrane protein (OMP) permeability, overexpression of efflux pumps, and acquisition of genetic elements carrying resistance determinants, such as plasmids, integrons, transposons, and resistance islands (Smani *et al*, 2014). On the other hand, it can also persist for a prolonged period in harsh environments (walls, surfaces, and medical devices in the hospital settings, so it become one of the most important species associated with nosocomial infections (Asif *et al*, 2018). *A. baumannii* causes a range of infections in both the hospital and community, including skin and soft tissue, urinary tract infections, meningitis, bacteremia, and pneumonia with the latter being the most frequently (Dexter *et al*, 2015). Pathogenesis in *A. baumannii* infections is an outcome of multiple virulence factors, including porins, capsules, and cell wall lipopolysaccharide, enzymes, biofilm production, motility, and iron-acquisition systems. Such virulence factors help the organism to resist stressful environmental conditions and enable development of severe infections (Moubareck and Halat, 2020). OmpA was the first *A. baumannii* virulence factor and the most abundant to be described and confirmed *in vivo* (Antunes, 2013). The interaction of OmpA with eukaryotic cells induces cytotoxicity, through binding and adhesion to