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MOLECULAR ANALYSIS OF EFFLUX PUMPS AND QUORUM SENSING GENES IN MDR *ACINETOBACTER BAUMANNII*

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ABSTRACT : ***Acinetobacter baumannii*** **(MDR-Ab) are common among clinical isolates worldwide and are a major therapeutic challenge. Identification of *Acinetobacter* species is complicated due to lack of standard identification techniques, the isolates were confirmed as *Acinetobacter* by PCR which was performed by housekeeping gene *16sRNA* gene and confirmed as *A. baumannii* by $bla_{Oxa\ 51}$ genes. All of clinical isolates indicated multidrug resistant (MDR). The antibiogram typing represent the importance indicator to distinguish and differentiate between bacterial isolates according to origin of infection beside multidrug resistance pattern. *A. baumannii* isolates were typed genotypically by using antibiotic resistance genes, screen showed all 30 (100%) isolates were positive for $bla_{CTX\ and}$ bla_{Oxav51}, 9(30%) were positive for bla_{IMP-1} and bla_{TEM}, 5 isolates (16.6%) were positive for bla_{VIM}, 12(40%) isolated were positive for bla_{SHV} and bla_{ParC} and only one isolate (3.3%) were positive for bla_{OXa23} and bla_{Oxa24}, while no isolate positive for bla_{gyrA}. Whereas, Efflux pump genes screen showed all (100%) isolates were positive for *AdeM*, 12 (40%) isolates were positive for *AdeL*, 10(33.3%) isolates were positive for *AdeH*, 8(826.6%) isolates were positive for *AdeG* and *AdeF* and only one isolates were positive for *Bap* gene (biofilm associated gene). While, Quorum sensing genes screen showed 13 isolates (43.3%) isolates were positive for *RhlI* gene, 12 (40%) isolates were positive for *LasI* gene, 10(33.3%) isolates were positive for *Las R* while 8 isolates were positive for *RhlR* gene. Five(16.6%) isolates were positive for *Las R* and *RhlI* genes and only one isolate isolates were Carrying for *LasR* and *RhlI, LasI, RhlR* genes.The virulence of the *A. baumannii* does not require, carrying full set of QS genes,*AdeM* predominance than other MATE Efflux Pumps genes, indicated have important role of resistance against many antibiotics in Iraqi *A. baumanii*.**

Key words : *Acinetobacter baumannii*, quorum sensing genes, efflux pump genes, antibiogram typing.

INTRODUCTION

*Acinetobacter baumannii*is an opportunistic pathogen that is responsible for a variable nosocomial infections, such as bacteremia, UTI, meningitis and pneumonia, especially in patients in the ICU (Antunes *et al*, 2014). *Acinetobacter* infections is broad and includes infection associated with tropical environments, wars and natural disasters and hospital outbreaks in humid climates, it naturally inhabitssoil and water and other possible reservoirs include arthropods and animals food (Leung *et al*, 2006). In humans, can colonize on skin, burn, the respiratory and gastrointestinal tracts (Kanafani and Kanj, 2013). Tay and Yew (2013) reported the regulation of virulence behavior such asbiofilm formation and antibiotics resistance accrue due to AHL signallis of Q.S that regulatory mechanism among Gram-negative bacteria, and plays important role inexpression of virulence genes, antibiotic resistance in *A.baumannii*. Rahmati *et al* (2002) showed *A. baumannii* protecting themselves from toxic effects of organic chemicals by efflux pump. Efflux-based mechanisms are responsible for resistance against many different antibiotics classes *by* ridding or pumping the drugs for reduction accumulation endogenous antibiotics. In the same manner He *et al* (2015) noticed correlation between quorum sensing and efflux pump.The major objectives of this study were there is Diagnostic technique to characterize *A.baumannii* for test the antimicrobial susceptibility and for study the relationship between Quorum sensing and Efflux pump genes dendrogram analysis.

MATERIALS AND METHODS

Specific primers were used and prepared according to the manufacture company information by adding deionized distilled water to obtain stock solution equal to 100pmol/ìM. From the previous stock, 10ìl was diluted by adding 90 ìl distilled water to get a secondary stock concentration equal to 10pmol. PCR mixture for this gene composed from 12.5ìl of GoTaq®Green Master Mix,