Recognition of Antibiotic Resistance Preponderance and Correlated Virulence Factors in *Acinetobacter Baumannii* Clinical Isolates from Karachi

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ABSTRACT

Introduction: *Acinetobacter baumannii* are non-fermenter gram negative coccobacilli which mainly cause infection in immune compromised patients often associated with catheters, ventilator and individuals linked with previous antibiotic therapy in healthcare centers. In recent years, *A. baumannii* has gained importance and it has been recognized as one of the most resilient pathogens having ability to produce extended spectrum beta- lactamases. Infectious Disease Society of America categorized it among the six highly virulent and resistant pathogens, referred to as ESKAPE (*Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa*, and Enterobacter species) pathogens and ranks second for causing opportunistic infection in hospital surroundings after *Pseudomonas aeruginosa*.

Aim Of Study: The core target of this research is to emphasis on the virulence related genotypic factors and their association with Multidrug resistance among the clinically isolated strains of *A. baumannii*.

Methodology: Total of 54 *A. baumannii* clinical isolates were collected from various leading Microbiology Diagnostic Laboratories of Karachi. Their identification was confirmed by performing standard biochemical and molecular tests. Disc diffusion method was used for determination of antibiotic susceptibility and Polymerase Chain Reaction (PCR) was performed for molecular detection of resistance and virulence genes.

Result: For evaluation of antibiotic profile, a panel of 10 antibiotics were used and *A. baumannii* were found to be highly drug resistant to all the groups of antibiotics. 96.2% strains were resistant to Ceftriaxone, followed by 90.7% resistance against Piperacillin/Tazobactam, Ceftazidime and Cefepime, 88.8% against Imipenem, Meropenem and Ciprofloxacin, 87% to Amikacin, 79.6% against Sulphamethoxazole/ Trimethoprim and 77.7% against Gentamicin. While the virulence genotypic profile exhibited that 87% strains possessed OmpA genes followed by Bap (74%), 57% harboured EpsA and 55.5% isolates Csu A/B genes.

Conclusion: *A. baumannii* are known as Multidrug resistant (MDR) organism due to presence of various resistance and virulence genes which help them to survive under harsh environmental and host conditions. Our investigation on *A. baumannii* provides the data about the frequency, level of drug resistance, its prevalence and various virulence markers associated with them. The high frequency of MDR strains emphasizes the intense need for development of new therapeutic options for the treatment purpose.

Keywords: Acinetobacter baumannii, Immune compromised, ESKAPE pathogens, MDR, Opportunistic infection, Prevalence.

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