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Acinetobacter in Coming Era: Antimicrobial Resistance World

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Editorial

Acinetobacter genus are widespread in nature. Human skin was considered as a normal habitat of some *Acinetobacter* sp. Treatment strategy failure as a result of antibiotic resistance in this genus is focus attention now, where gain its opportunity and cause hospital acquired infections, *Acinetobacter* genus are a non-fermentative, Gram negative bacillus, oxidase negative and catalase positive. This genus currently contains many species that is 33 named and unnamed genomic species. *Acinetobacter* identification very important where genotypically *A. baumannii*, *A. calcoaceticus*, unnamed genospecies 3 and 13 TU are considered closely related but phenotypically, they are difficult to distinguish. Thereby, there were classified as *Acinetobacter* calcoaceticus–baumannii complex (Acb). *Acinetobacter* responsible for almost 75% of nosocomial infection, particularly in intensive care units (ICUs). Hospital environment are the main source for infection where they were transmitted by staff's hands, surfaces and surgical tools resulting in cross-transmission cases. *A. baumannii* was considered as famous species widespread. The risk factors for colonization and infection of *Acinetobacter* are prolonged hospital stay, intensive antibiotic therapy that resulted in the emergence of antibiotic resistance. *Acinetobacter* have remarkable virulence factors play an important role in its pathogenicity as outer membrane proteins A (OmpA), CsuA/BABCDE chaperone-usher pili assembly system, siderophore-mediated iron acquisition system, Biofilm-associated protein (Bap), Two-component regulatory system (BfmRS), Penicillin-binding protein 7/8 (PBP-7/8) PNAG-constituted biofilm, capsule, Lipopolysaccharide and Phospholipase D and C that help to escape from the host defense and implicated in the mechanism of pathogenesis of a variety of infectious diseases.

In recent years, there are an increasing in the emergence of multi-drug resistant *A. baumannii* (MRAB) to carbapenems that was considered as a last resort for antibiotic resistance treatment. The reason behind this emergence was production of carbapenem-hydrolysing ß-lactamase enzymes of Ambler molecular class B (metallo-ß-lactamases) and D (oxacillinases) as a main cebapenems mechanism of resistance. Additionally, overexpression of varieties of efflux pumps was contributed with carbapenems resistance alongside modification of outer membrane proteins (CroD). Consequently, colistin and tigcyline have been reported as treatment option, unfortunately, colistin and tigcyline resistance isolates have been evolved due to the modification of lipid A biosynthesis and Two-component regulatory system (BfmRS). Nowdays, there is an urgent need to find a problem solution for drug resistance in *Acinetobacter* sp. by search for new source or restore the antibiotics to be effective.