

Identifying indispensable proteins and pathways for *Acinetobacter baumannii* virulence

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Nosocomial infections have become alarming with the increase of drug resistant bacterial strains of *Acinetobacter* spp. These pathogenic gram-negative species are resistant to most antibiotics and are the root cause of various types of opportunistic infections including but not limited to septicemia, endocarditis, meningitis, pneumonia, skin and wound sepsis and urinary tract infection. Primarily infecting an immuno-compromised system, the illness causes severe pneumonia and infections of the urinary tract, bloodstream and other parts of the body. Conventional and modern methods of typing methods had been adopted to differentiate outbreak strains. However, identifying indispensable proteins for causing virulence of *Acinetobacter* has remained an ever challenging task. Here, we focus on the 3790 proteins from the whole genome of *Acinetobacter baumannii* from where we targeted down the most indispensable protein from the 28 Pathogenicity Alien Islands (PAI) responsible for the virulence. Our method is the first of its kind to figure out, albeit theoretically, the most significant proteins which might be involved in the resistance to antibiotics of the *Acinetobacter* sp. Besides proposing a hierarchy of the proteins involved in the total infection process, interaction studies helped to identify unique pathways responsible for virulence in *Acinetobacter baumannii*. An understanding of the above will provide insight into conditions which are encountered by this pathogen during the course of infection which will further contribute in identifying new targets for antimicrobial agents.

Biography

Indhuja obtained her M.Tech. degree from Karunya University, Coimbatore, India in 2012. She has been the recipient of Canadian Commonwealth Scholarship for pursuing research currently at York University, Toronto, Canada.

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