Genetic diversity and proteomics analysis of clinical isolates of *Acinetobacter baumannii* complex

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Abstract

Acinetobacter baumannii complex (ACB complex) is the group of rapidly emerging Gram negative coccobacilli including A. baumannii, A. calcoaceticus and Acinetobacter genomic species 13TU which are difficult to differentiate from one another. Among ACB complex, A. baumannii has been documented to be most notorious causing health care associated infections including bacteremia, pneumonia, meningitis, urinary tract infection and wound infection. A. baumannii has intrinsic resistance towards many antibiotics and in recent days it is found to outnumber all other multidrug resistant Gram negative bacteria showing resistance towards complete antibiotic panel posing real health threat. Current study has been designed to find out the common most genetic variants of ACB complex circulating in our community and to further look for their comparative proteome profile to comprehend the role of proteomic and genomic variants in antibacterial resistance demonstrated by these species. The study includes total number of 50 ACB complex strains isolated from clinical specimens like Cerebrospinal fluid, sputum, urine, wound swabs and blood. Genomic DNA was isolated from pure culture of all the 50 isolates. Random Amplified Polymorphic DNA [RAPD-pronounced Rapid] analysis of all 50 samples was done using 3 sets of RAPD primers. These 50 samples were divided into genetically diverse groups based on their RAPD profile combining banding patterns from all three RAPD primers. One representative culture was taken from each genetic variant group including one American Type Culture Collection [ATCC] A. baumannii strain and subjected to mass spectrometry for quantitative proteomics. The study gives clear idea about the genetic diversity among clinical strains and their proteome variability.

Biography

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