



Molecular Analysis of *Acinetobacter baumannii* Strains Isolated in Lebanon Using Four Different Typing Methods

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This study analyzed 42 *Acinetobacter baumannii* strains collected between 2009–2012 from different hospitals in Beyrouth and North Lebanon to better understand the epidemiology and carbapenem resistance mechanisms in our collection and to compare the robustness of pulsed field gel electrophoresis (PFGE), multilocus sequence typing (MLST), repetitive sequence-based PCR (rep-PCR) and *bla*_{OXA-51} sequence-based typing (SBT). Among 31 carbapenem resistant strains, we have detected three carbapenem resistance genes: 28 carried the *bla*_{OXA-23} gene, 1 the *bla*_{OXA-24} gene and 2 strains the *bla*_{OXA-58} gene. This is the first detection of *bla*_{OXA-23} and *bla*_{OXA-24} in Lebanon. PFGE identified 11 types and was the most discriminating technique followed by rep-PCR (9 types), *bla*_{OXA-51} SBT (8 types) and MLST (7 types). The PFGE type A'/ST2 was the dominant genotype in our collection present in Beyrouth and North Lebanon. The clustering agreement between all techniques was measured by adjust Wallace coefficient. An overall agreement has been demonstrated. High values of adjust Wallace coefficient were found with followed combinations: PFGE to predict MLST types = 100%, PFGE to predict *bla*_{OXA-51} SBT = 100%, *bla*_{OXA-51} SBT to predict MLST = 100%, MLST to predict *bla*_{OXA-51} SBT = 84.7%, rep-PCR to predict MLST = 81.5%, PFGE to predict rep-PCR = 69% and rep-PCR to predict *bla*_{OXA-51} SBT = 67.2%. PFGE and MLST are gold standard methods for outbreaks investigation and population structure studies respectively. Otherwise, these two techniques are technically, time and cost demanding. We recommend the use of *bla*_{OXA-51} SBT as first typing method to screen isolates and assign them to their corresponding clonal lineages. Repetitive sequence-based PCR is a rapid tool to access outbreaks but careful interpretation of results must be always performed.

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