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Title : Genomic Adaptation in Antimicrobial Resistance: Elucidating the Route and Effects in *Acinetobacter Baumannii*

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Antimicrobial resistance has been a looming threat ever since its conception and it has become one of the greatest global problems of the current era. Although various studies have been conducted to better understand the mutational triggers leading to antimicrobial resistance, the specific genomic path towards it have yet to be discerned. Here, we aim to elucidate the pathway of genomic evolution throughout the resistance induction of an *A. baumannii* strain towards ciprofloxacin, erythromycin, meropenem and imipenem, as well as comparing the mutations acquired clinically versus *in vitro*. Twenty-five (25) local clinical *A. baumannii* strains were isolated and screened for antimicrobial susceptibility, and their genome were sequenced using the Illumina GAIIx genome sequencer. The susceptible parent was then challenged with ciprofloxacin, erythromycin, meropenem and imipenem separately until growth is still possible beyond the Minimum Inhibitory Concentration (MIC) as defined by EUCAST standards. Once the resistance stability was confirmed, another sequencing run was done on the isogenic. Variant analysis was carried out using CLC Bio, and primers were designed to target the mutations of interest. PCR was then carried out on aliquots of the resistant mutants, each taken at increasing levels of antimicrobial tolerance throughout the challenging process. Phylogenomics and wgMLST analyses were carried out between the parent and resistant strain, as also the remaining isolates. Stable low and high-level resistant strains were successfully generated. Several genomic variants were identified in the high-level resistant strains. Validation of variant calling via PCR removed all miscalled variants. Comparative genome annotation revealed a high consistency in the genome structures of the clinical strains, despite non-consistent phylogenetic and synteny profiles. The mutation validation revealed several variations arising in genes responsible for signaling (*yihG bvgS* and *srrA*), metabolic activities (*atpD, ribonuclease I*, and *epsL*) and cell structure maintenance (*ftsI* and *yceG*) in addition to targeted mutations (*mexB, acrB* and *gyrA*). Analysis of the mutation chronology shows that when exposed to *erythromycin*, *A. baumannii* incurs modifications to genes *bvgS* and *srrA*, on days 4, 6, and to *ftsI* and its ribonuclease I encoding gene on day 67. When exposed to ciprofloxacin, mutations developed in *gyrA* and *yihG* on days 28 and 48. Meropenem exposure on the other hand has led to variations in *epsL*, *mexB*, and *atpD* on days 4, 10 and 70. In contrast, meropenem exposure resulted in mutations to *acrB* on day 38, and two mutations in *ftsI* occurred on day 19 and 67. From the results it is deduced that the chronology of intrinsic mutations is dependent on the types and intensity of selective pressures enacted, even on the same bacteria. Antibiotic pressure under *in vitro* and *in vivo* conditions has also resulted in development of different mutations leading to similar resistance profiles. It was also found that a prolonged exposure to the drugs used in this study plays as much of a role as the sub-inhibitory concentration.