00552 Global emergence of Multi-Drug Resistance (MDR) Genomic Island in Acinetobacter baumannii and Its Horizontal Gene Transfer Into Enterobacteriaceae

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Aims: Acinetobacter baumannii is a gram-negative opportunistic nosocomial pathogen. Over the years, carbapenem-resistant A. baumannii has been reported worldwide and listed by World Health Organisation as a pathogen of critical importance. This study aims to characterize the antibiotic resistance genes (ARG) in A. baumannii.

Methodology: We analysed the ARG present in the 3518 genomic sequences of A. baumannii from NCBI Pathogen Detection database on 12-Nov-2017. We sought correlations between ARG and antibiotic sensitivity testing (AST) for 1013 isolates which had both genotypic and phenotypic data. Arrays of ARG cassettes (integrons) were analysed using BLASTN to compare between the isolates and other bacterial species in the NCBI database.

Result: Beta-lactamase genes, blaADC and blaOXA-51 family, were found to be intrinsic in all A. baumannii genomes. There were statistically significant correlations between certain pairs of ARG, and between certain pairs of antibiotic resistance phenotypes, suggesting linkage and genotype sharing. Sequence analysis revealed a 17kb integron present in 438/3512 (12.5%) of Acinetobacter baumannii genomes, but absent in other Acinetobacter spp. It comprised transposases, integrases, and resistance genes against aminoglycosides (aadA1, ArmA), chloramphenicol (CatB8), sulfonamides (sul1), macrolides (MsrE, MphE) and for multiple drugs (QacEdelta1). Comparative genome analysis revealed that this multidrug resistance array of genes are present in plasmids of other bacteria, including Klebsiella pneumoniae, Salmonella enterica and Escherichia coli. This suggested that the resistance integron could have been part of a horizontal gene transfer event between A. baumannii and other gram-negative bacteria.

Conclusion: Whole genome sequencing of isolates in published studies and from routine surveillance offers large genome datasets to study genotypes, phenotypic profiles and genomic organisation of the antibiotic resistance genes. Novel integrons and putative mechanisms for their horizontal transfer have been identified. Further investigations into the phylogenetic relationships and origins of antibiotic resistance integrons may help in preventing and predicting the emergence of drug resistance.