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P2668 Genomic epidemiological investigation of globally disseminated clonal lineage *Acinetobacter baumannii* ST195

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Background: Whole-genome sequencing (WGS) has revolutionized the genotyping of bacterial pathogens and is expected to become the new gold standard for tracing the transmissions of bacterial infectious diseases for public health purposes. However, it is still unexpectedly demanding to employ WGS for global epidemiological surveillance because of the high degree of similarity between the genomes of intercontinental isolates. The aim of this study was to utilize genomically derived bioinformatics analysis to identify globally distributed clonal groups and differentiation outbreaks to address this issue.

Materials/methods: The genomic sequences and their related epidemiological metadata of 2850 *A. baumannii* isolates were recruited from NCBI Genbank database. Classification to species and assignment into sequence type (Oxford scheme) and lineage (International clone II/CC92) were performed using an in house developed bioinformatics pipeline. A total of 91 ST195 *A. baumannii* isolates were subsequently classified to perform the bacterial source tracking analysis by implementing both core genome MLST (cgMLST) and core genome SNP (cgSNP) strategy that were integrated in our recently updated BacWGSTdb 2.0 server. Antibiotic resistance genes were identified using the ResFinder database.

Results: The ST195 *A. baumannii* isolates distributed widely in eight different countries and harboured multiple antimicrobial resistance genes simultaneously, including β-Lactamase (bla_{OXA-66}, bla_{OXA-23}, bla_{TEM-1}, bla_{ADC-25}); Aminoglycoside [*aadA1*, *strA*, *aph(3'')-Ib*, *aph(6)-Id*, *aph(3')-Ia*, *ant(3'')-Ia*, *armA*, *aac(3)-Ib*, *aac(3)-Ia*]; Macrolide [*msr(E)*, *mph(E)*]; Phenicol (*catB8*, *catB4*); Sulphonamide (*sul1*, *sul2*); Tetracycline (*tetB*) and Rifampicin (*ARR-3*). In most cases, the bacterial isolates recovered from geographically distant sources may present less genomic sequence similarity, i.e., the phylogenetic relationship between these ST195 isolates worldwide was roughly congruent with that with their country of isolation. However, a few isolates collected from distant geographic regions were revealed to possess smaller genetic distances (less than 10 loci or 20 SNPs) than the threshold without an observable epidemiological link.

Conclusions: Our study highlights the emerging challenges entailed in the WGS-powered epidemiological surveillance of globally distributed clonal groups. Standardization is urgently required before WGS can be routinely applied to infectious diseases outbreak investigations.