High Resolution Clonality of Outbreak-Causing Acinetobacter baumannii studied by Whole Genome Mapping

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Introduction

Whole Genome Mapping (WGM) is a valuable molecular tool for high resolution clonality of microbial pathogens1. WGM has been successfully employed in epidemiological outbreak studies when strains needed to be rapidly typed, and in a high throughput manner, for comparisons to related outbreak/non-outbreak strains. Here we employed WGM to study clonality of 16 isolates of A. baumannii isolated from Greek patients during an outbreak (2008) and in a ‘non-outbreak’ situation (2008-2013) at Tzaneio Hospital, Athens and University Hospital of Larissa, Greece.

Figure 1A: Comparison of whole genome maps of typed A. baumannii in Bionumerics

Methods

Non-outbreak (n=13, NO1-NO13) and outbreak (n=3, O1-O3) A. baumannii strains were typed by multi-locus sequence typing (MLST) prior to mapping by WGM. For WGM, high molecular DNA was prepared using agarose plugs. NcoI restriction maps were generated on the Argus® system (OpGen, Gaithersburg, USA) and analysed using Bionumerics (Applied Maths, Belgium). Antimicrobial resistance profiles were determined by disc diffusion.

Conclusions

This study revealed high genomic heterogeneity of the typed A. baumannii clinical isolates (SR of ≥44%) with only marginal differences detected between the closest typed outbreak and non-outbreak strains. Transition of A. baumannii from a non-outbreak to an outbreak strain is thus likely to involve acquisition of plasmids, SNPs and/or other point chromosomal or plasmid-encoded mutations, with all of these changes not detectable by WGM.

Figures

Figure 1: (B) Map similarity cluster generated from the whole genome maps. (C) Antibiograms of typed strains with resistance (in red) intermediate resistance (brown) and sensitivity (green) to (from left to right): piperacillin, piperacillin-tazobactam, cefepime, ceftazidime, meropenem, ciprofloxacin, trimethoprim-sulfamethoxazole, gentamycin, cefotaxime and cefoxitin.

Results

According to MLST, all typed A. baumannii belonged to CC2 (http://www.pasteur.fr/recherche/genopole/PFB/mlst/). According to WGM, the strains formed three distinct clusters: C1 (outbreak-causing O1, O2, and O3, non-outbreak NO1-NO5), C2 (non-outbreak NO7-NO13) and C3 (non-outbreak NO6) (Fig.1A). The inter-cluster similarity rate (SR) was 74% for isolates belonging to C1 and C2, whereas only 44% of inter-cluster SR was detected for C3 as compared to C1/C2 clusters (Fig. 1A). The intra-cluster SR was 93% and 95% for C1 and C2, respectively (Fig. 1A). Moreover, C1 was composed of three distinct sub-clusters with sub-C1 (intra-cluster SR=94%), sub-C2 (intra-cluster SR=97%), sub-C3 (intra-cluster SR=94%) with sub-C2 exclusively composed of outbreak strains. C2 cluster was composed of two sub-clusters, sub-C4 (intra-cluster SR=96%) and sub-C5 (intra-cluster SR=96%) (Fig. 1B). Most of the typed A. baumannii strains shared multidrug resistance phenotype with resistance to most antibiotics tested, apart from O2, NO2 and NO3 exhibiting sensitivity to aminoglycosides and NO9, NO11 and NO13 to trimethoprim/sulfamethoxazole (Fig. 1C).

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References