Evaluation of a gene-resistance profile testing platform (OpGen) with traditional typing methods as a potential for more accurate and quicker identification of carbapenem-resistant Enterobacteriaceae (CRE) outbreaks

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OBJECTIVES

Carbapenem-resistant Enterobacteriaceae (CRE) outbreaks within healthcare settings have devastating effects and our institution has seen an increasing numbers of CRE positive samples over the years (Figure 1). Identification of linked organisms is key to controlling outbreaks. Currently, potentially linked isolates are sent to the national reference laboratory for VNTR or PFGE testing. We aim to compare traditional methods with the OpGen - ACUITAS® platform (an international genetic analysis service), as a potential for quicker outbreak identification.

METHODS

50 gram negative isolates isolated at Imperial College Healthcare NHS Trust from November 2015 to September 2017 (42 carbapenemase PCR positive and 8 PCR negative,) were tested on ACUITAS Resistome assay (OpGen®). The OpGen® platform detects 46 different genes to cover ESBL, CRE and AmpC related genes (Figure 2). These results were compared to Cepheid® Carba-R and VNTR or PFGE. Notes were also reviewed for risk factors for CPE.

RESULTS

All samples tested on Resistome assay matched the Cepheid® PCR result. 50 samples from 48 patients were identified on Cepheid® PCR as: 18 x OXA48, 5 x IMP-1, 10 x NDM, 4 x VIM, 5 mixed and 8 negative. VNTR was performed on 20 isolates and PFGE on 12. All samples tested on Resistome assay matched the Cepheid® PCR result.

CONCLUSION

Identical profiles were found within known outbreaks, but also in non-outbreak strains separated in time and space and varying VNTR profiles. If these outbreak and non-outbreak isolates are linked, this suggests either an endemic reservoir fixed within the hospital environment or plasmid transmitted across common strains, not picked up by traditional typing. Answering this could provide information to reduce outbreaks.

Unlike current typing methods, data are easily comparable and stored in an online server. Whole genome sequencing could clarify these discrepant results and it could help establishing whether gene resistance profile testing could be a more rapid and accurate tool then VNTR/PFGE.

Figure 1: Increasing numbers of CRE positive samples over the years, from November 2015 to December 2017.

Figure 2: Range of genes identified on the OpGen® platform compared to Cepheid® Carba-R.

Figure 3: Isolates tested with the largest cluster containing 15 isolates.