

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.

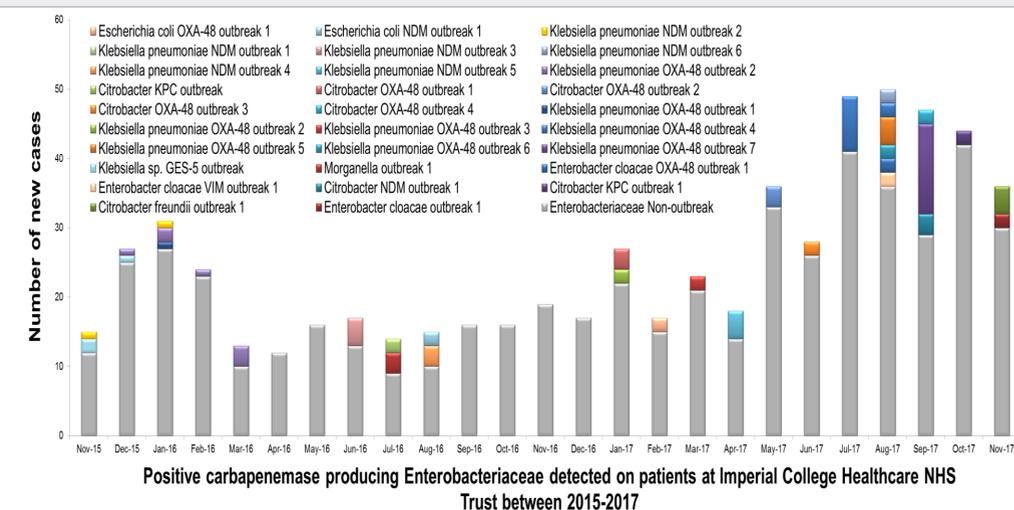


Figure 1: Increasing numbers of CRE positive samples over the years, from November 2015 till December 2017.

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.

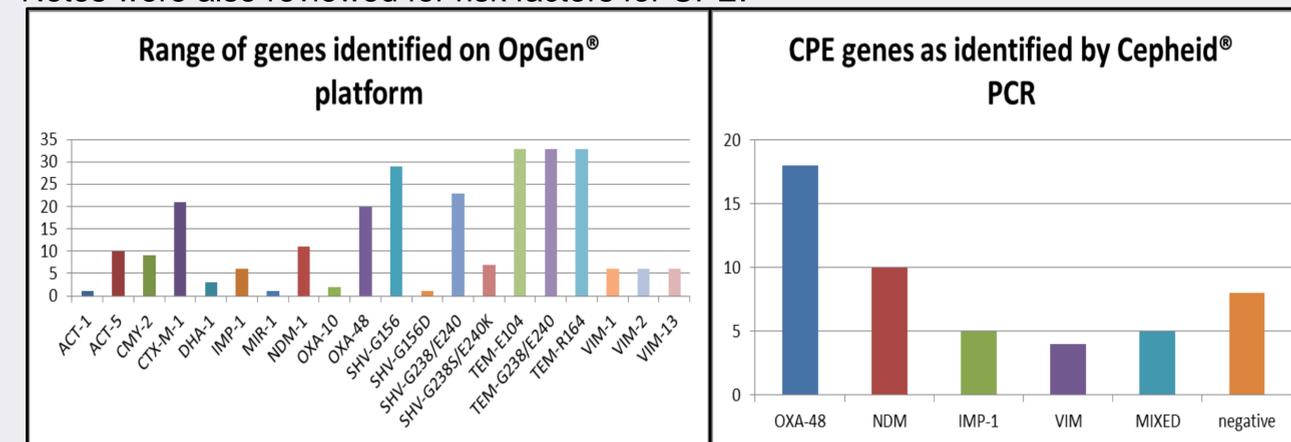


Figure 2: Range of genes identified on the OpGen® platform compared to Cepheid® Carba-R.

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.

19 isolates had an identical Acuitas Lighthouse® genetic profile when analysed in OpGen's Acuitas Lighthouse. Within the largest group, there were 15 isolates and VNTR was performed on 14. There were 4 different VNTR profiles. This group included 11 from a known 2017 outbreak, but included 4 other isolates from 2015-16, originally not thought to be linked (Figure 3).

11 isolates were different by one gene only. One pair of these isolates was found to be linked by VNTR testing. The other 9 were not linked, nor was there an obvious risk factor link.

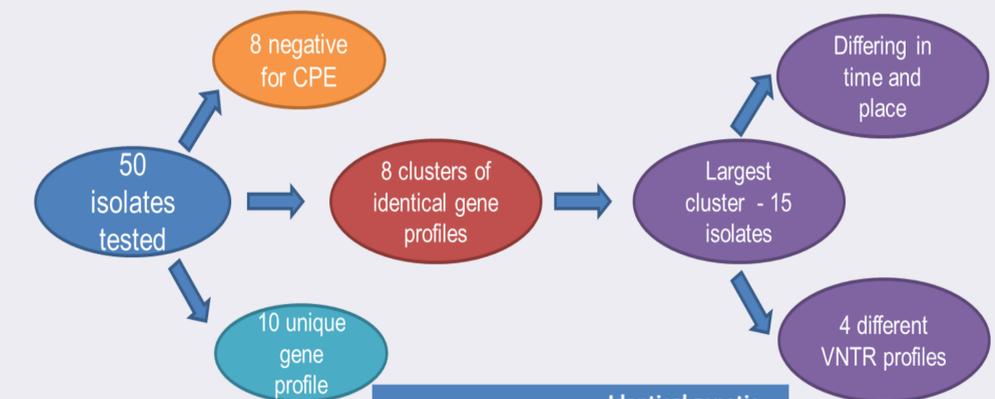


Figure 3: Isolates tested with the largest cluster containing 15 isolates

VNTR Profiles	Identical genetic profile expression
3, 3, 3, 0, 1, 1, 4, 1, 5, 2, 7	CTX-M-1
	OXA-48
4, 4, 4, 5, 2, 1, 1, 2, 4, 2, 3	SHV-G156
	SHV-G238/E240
5, -, 4, 1, 2, 1, 1, 3, 1	TEM-E104
	TEM-G238/E240
6, 3, 4, 0, 1, 1, 4, 1, 1	TEM-R164

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 than VNTR/PGFE.