

P1702

Abstract (poster session)

Comparison of matrix-assisted laser desorption/ionisation-time of flight (MALDI-TOF) mass spectra with variable nucleotide tandem repeats profiles (VNTR) of *Pseudomonas aeruginosa* in an outbreak scenario

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Objectives: *Pseudomonas aeruginosa* (PAER) is one of the more common nosocomial pathogens and is an increasing cause of outbreaks on augmented care units. It is frequently found in water sources both inside and outside hospitals and has been implicated with increased morbidity and mortality. During outbreak scenarios PAER isolates require typing to confirm similarity. The current typing method in the UK is VNTR, a highly skilled and specialist method usually performed in reference laboratories. This results in a time delay in results receipt and crucial information to the infection control team. Matrix Assisted Laser Desorption/Ionisation-Time of Flight Mass Spectrometry (MALDI-TOF MS) is becoming more widespread in microbiology laboratories as a method of identification. Spectra can be achieved within minutes and would provide a quick way to confirm outbreak isolates. Here we compare cluster analysis of MALDI-TOF MS spectra with VNTR types. **Methods:** VNTR typing was performed at the Antimicrobial Resistance and Healthcare Associated Infections (AMRHAI) Reference Unit on 47 PAER clinical or screening isolates from patients. In addition, all PAER were extracted using Manufacturers' standard extraction method and MS analysis performed using FlexAnalysis and BioTyper 3.0 (Bruker Daltonik GmbH). Hierarchical analysis on the spectra by the Euclidean distance was performed using the PCA dendrogram tool. VNTR types and spectra dendrograms were compared for correlation. A similarity cut off of 4 was chosen arbitrarily for the MALDI group definition. **Results:** MALDI-TOF MS spectra clustered into 3 main groups compared with 9 main VNTR groups. Within the 9 groups, VNTR showed 16 distinct subpopulations based upon differences at the final locus. The MS spectra clustered the majority of the 9 main VNTR types together (Table), with 15/17 "11,4,5,5,4,3,8,1,8" VNTR types in MS group 1 and 12/12 "11,6,2,2,1,3,8,2,W" clustering in MS group 2. **Conclusions:** Results suggest better discrimination when using VNTR when compared with MALDI-TOF MS. However MS may provide useful infection control information within hours of PAER isolation and warrants further study using a larger number of isolates.

Table: MS validation direct from blood cultures

| VNTR profile | Numbers of isolates in VNTR | MS GROUP | Numbers of isolates in MS group |
|---------------------|-----------------------------|----------|---------------------------------|
| 11,4,5,5,4,3,8,1,8 | 17 | Gp 1 | 15 |
| | | Gp 2 | 2 |
| 11,5,4,3,4,2,-,6,7 | 1 | Gp 1 | 1 |
| 11,3,5,5,3,4,3,2,13 | 3 | Gp 1 | 1 |
| | | Gp 2 | 2 |
| 11,6,2,2,1,3,8,2,W | 12 | Gp 2 | 12 |
| 11,6,2,2,1,3,7,2,10 | 1 | Gp2 | 1 |
| 11,4,5,2,2,1,8,2,X | 6 | Gp 1 | 1 |
| | | Gp 2 | 5 |
| 10,3,2,4,2,1,6,6,9 | 1 | Gp 2 | 1 |
| 12,2,1,-,5,2,4,5,Y | 2 | Gp 2 | 1 |
| | | Gp 3 | 1 |
| 12,5,3,2,6,1,6,4,Z | 4 | Gp 1 | 2 |
| | | Gp 2 | 1 |
| | | Gp3 | 1 |

W=8, 12 or 17, X=7, 8 or 12, Y=9 or 13, Z=9, 12 or 14