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Differentiation of *Pseudomonas aeruginosa* clinical outbreaks by Fourier transform infrared spectroscopy

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BACKGROUND

- *Pseudomonas aeruginosa* (PA) is an opportunistic pathogen, involved in hospital-acquired infection as well as in community patients with cystic fibrosis, or impaired immune system.
- PA poses a serious public health threat, due to its high prevalence and intrinsic and increasing acquired antibiotic resistance.
- Understanding, tracking, and ending the transmission of PA isolates is a big challenge for infection control.
- Fourier transform infrared spectroscopy (FTIRS) enables microbial typing on different intraspecies levels, relying on the unique FTIRS spectrum of each bacterial strain, which represents a specific fingerprint signature.

AIM

- To compare cgMLST clustering of PA against FT-IRS clustering.

METHODS

1. Seventy-four previously genotyped (cgMLST Ridom SeqSphere+) PA isolates were included in this study, including ST395 (n=13) and ST253 (n=6) obtained in the context of 2 outbreaks[(1,2)].
2. Isolates were analyzed by the FTIRS-based IR Biotyper® system (IRBT; Bruker Daltonics, Germany). The isolates were cultivated on MHA at 37°C for 24±2 h, in three independent biological replicates.
3. IR spectra were acquired from dried spots of bacterial suspensions in ethanol solution on the IR Biotyper sample plate. Exploratory analysis for clustering was performed by Hierarchical Cluster Analysis (HCA).
4. The accuracy of the IR Biotyper system to detect clonality was evaluated by comparison with WGS results, by Adjusted Rand (AR) and Adjusted Wallace (AW) indices.

Results

- HCA showed that IRBT discriminated the isolates in 43 clusters, 6 of them including more than one isolate, and 37 singletons (Figure 1).
- IRBT partitioning was in very good concordance with cgMLST clustering (Figure 2) (AR=0.85, 0.71-0.99 CI; AW=0.99, 0.98-1.00 CI).

Fig. 1. HCA results. In the columns on the right side of the figure, from left to right, isolate and cgMLST cluster designation. The left part of the figure shows the IRBT clusters. Each isolate is represented in the dendrogram by its average spectrum (which is the average of the 9 spectra deriving from the three independent cultures, each one measured in three technical replicates).

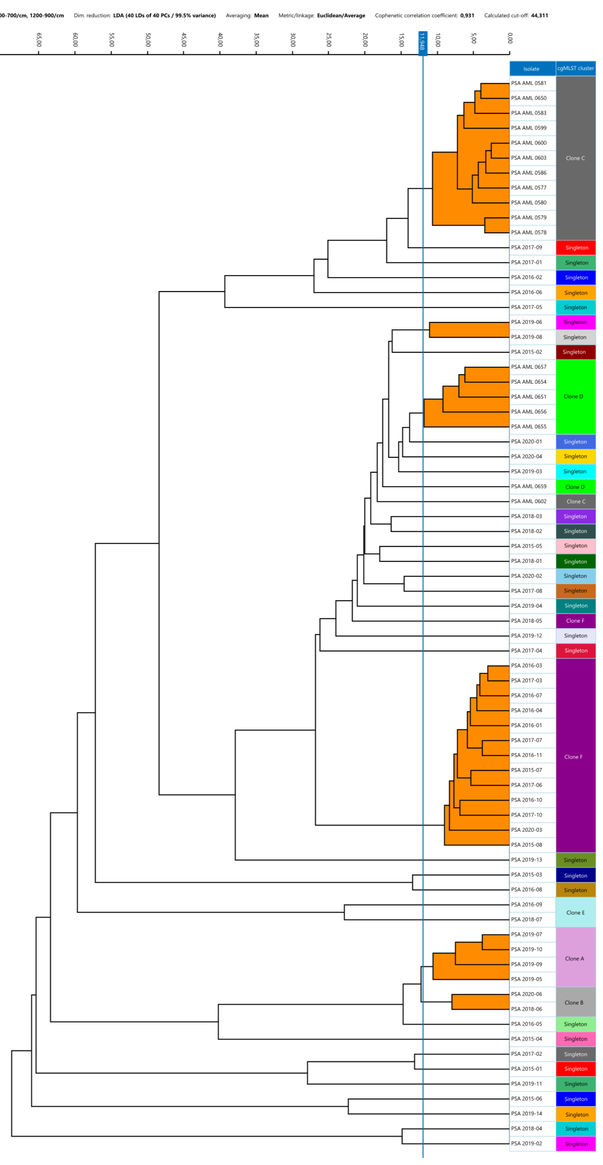
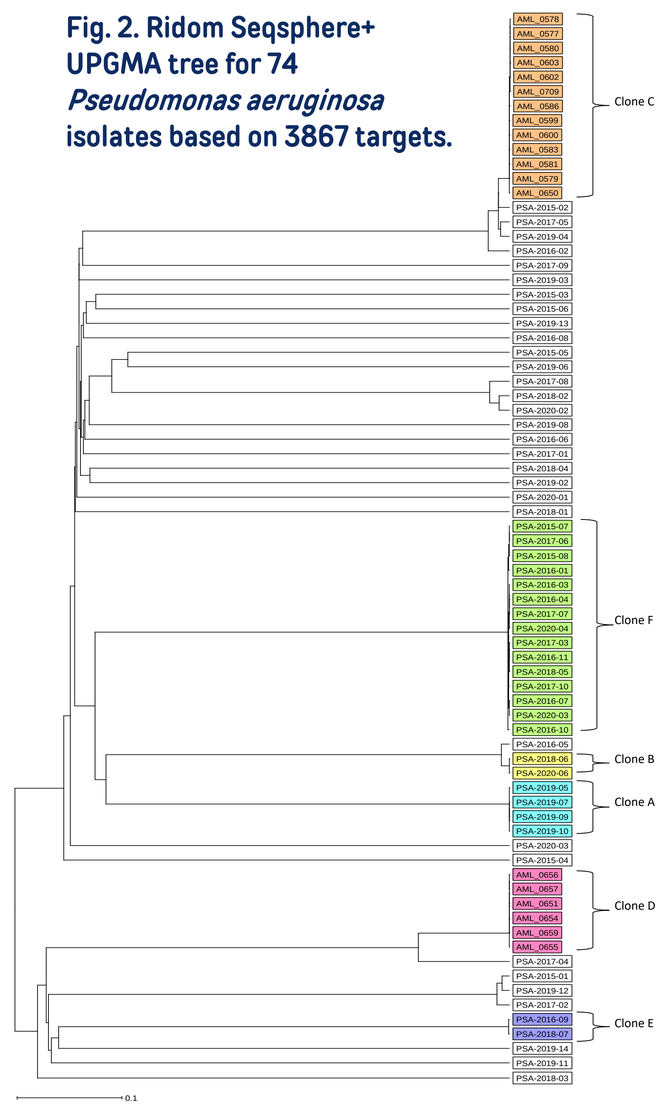


Fig. 2. Ridom Seqsphere+ UPGMA tree for 74 *Pseudomonas aeruginosa* isolates based on 3867 targets.



CONCLUSIONS

- IR Biotyper proved to be a novel, reliable method to reveal clonality among PA isolates and could thus represent a faster, easier, and more cost-effective alternative to molecular methods in the context of hospital hygiene, but also food quality assessment and control.
- Its ease of use and short analytical and handling time could allow to propose this method as a reliable real-time tool.

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References:
1:PMID:34298033
2:PMID:35611260

DZIF German Center for Infection Research