

Evaluating FT-IRS in outbreak detection of vancomycin-resistant *Enterococcus faecium*

Miriam Cordovana¹, Kyriaki Xanthopoulou^{2,3}, Janine Zweigner⁴, Paul G. Higgins^{2,3}

¹Bruker Daltonics GmbH & Co. KG, Bremen, Germany, ²Institute for Medical Microbiology, Immunology and Hygiene, Faculty of Medicine and University Hospital Cologne, University of Cologne, Cologne, Germany, ³German Center for Infection Research, Partner site Bonn-Cologne, Cologne, Germany, ⁴Department of Infection Control and Hospital Hygiene, Faculty of Medicine and University Hospital Cologne, University of Cologne, Cologne, Germany

BACKGROUND

- Vancomycin-resistant *Enterococcus faecium* (VREfm) are increasingly isolated in the hospital setting, particularly in vulnerable patient groups, where they cause a variety of infections.
- Core-genome multi-locus sequence typing (cgMLST) has proven invaluable in typing VREfm and to determine bacterial transmissions, however, the time to result leads to several days delay.
- Fourier Transform-Infrared spectroscopy (FT-IRS) is a phenotypical method that has been demonstrated, within two hours, to show a high degree of typing resolution in different hospital associated pathogens.

AIM

To compare cgMLST clustering of VREfm against FT-IRS to determine its usefulness as a rapid screen to rule in/out epidemiological relatedness of bacterial isolates prior to cgMLST analysis.

METHODS

1. Sixty-four VREfm from colonized patients were selected for this study. Isolates were sequenced (Illumina) and analysed by cgMLST (Ridom SeqSphere+) where eight clusters of related isolates, belonging to 5 sequence types (ST), were identified.
2. FT-IR analysis was performed using the IR Biotyper® system (IRBT - Bruker Daltonics, Germany). Spectra were acquired from dried spots of bacterial suspensions in ethanol solution, in three technical replicates of three independent cultures. Exploratory data analysis was performed by Principal Component Analysis (PCA) and Linear Discriminant Analysis (LDA) using the IR Biotyper software V4.0.

Results

IRBT showed a high correspondence with sequence types (Figure 1). Within each ST, a different degree of heterogeneity between isolates was observed, which led to a partial correspondence between IRBT clustering and cgMLST results.

CONCLUSIONS

These data suggest that FT-IRS has the potential to rule-in/rule-out clonality, yields a quick answer to the infection control team regarding the potential transmission of VREfm, and can be utilized as a pre-screen before sequencing. Future studies including more isolates are necessary to confirm these findings and to determine the optimum threshold for calling a potential transmission using FT-IRS.

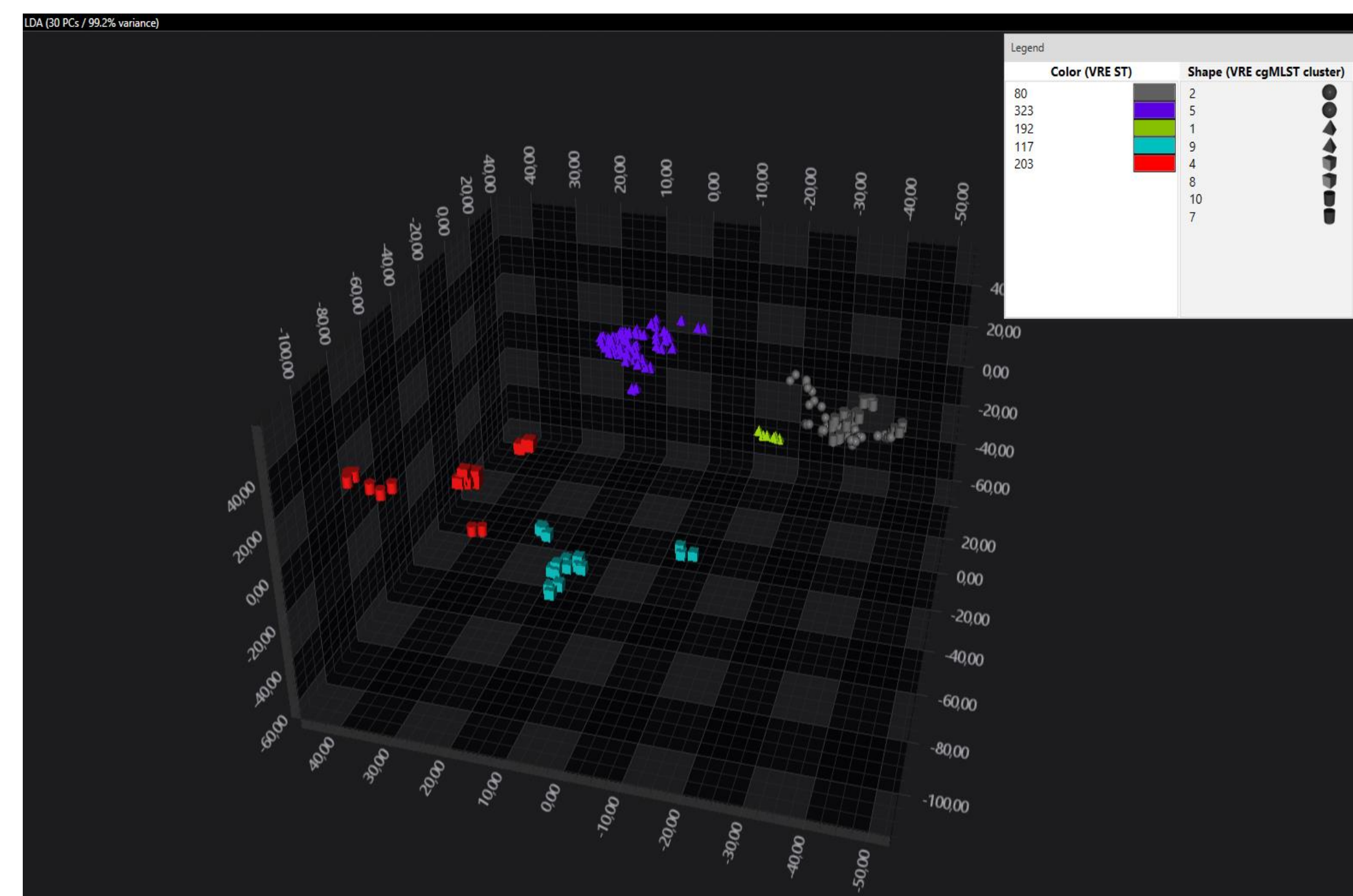


Figure 1. IRBT clustering. Each color represents a sequence type, while the different geometric shapes represent the cgMLST clusters.

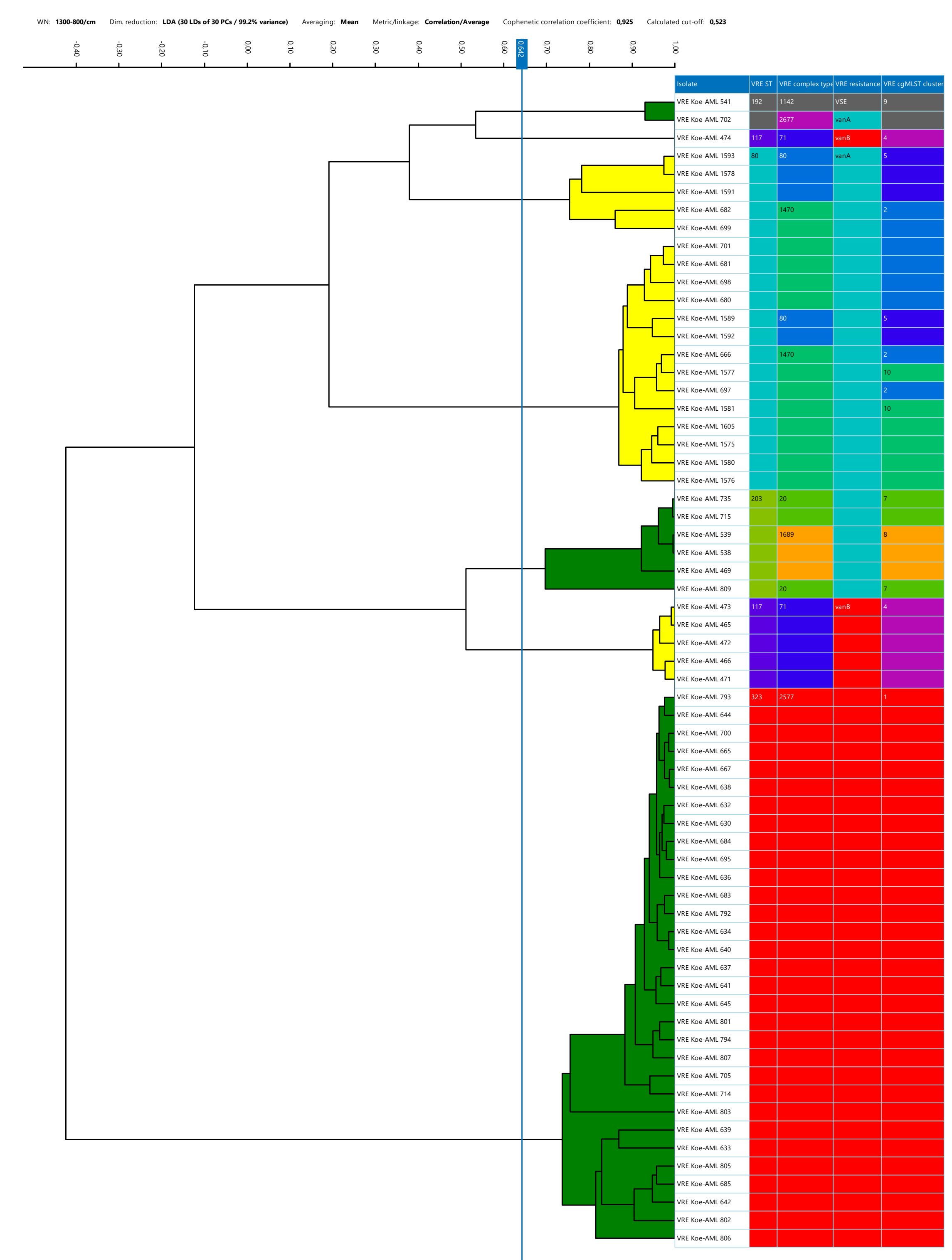


Figure 2. Dendrogram showing FT-IRS results. in the columns to the right are shown the cgMLST cluster, complex type, vancomycin resistance variant, and MLST sequence types