

# Use of FT-IRS to detect in-patient diversity of vancomycin-resistant *Enterococcus faecium*

Miriam Cordovana<sup>1</sup>, Lena Biehl<sup>2,3</sup>, Harald Seifert<sup>3,4</sup>, Kyriaki Xanthopoulou<sup>3,4</sup>, Paul G. Higgins<sup>3,4</sup>

<sup>1</sup>Bruker Daltonics GmbH & Co. KG, Bremen, Germany, <sup>2</sup>University of Cologne, Faculty of Medicine and University Hospital Cologne, Department I for Internal Medicine, Cologne, Germany,

<sup>3</sup>German Center for Infection Research, Partner site Bonn-Cologne, Cologne, Germany, <sup>4</sup>Institute for Medical Microbiology, Immunology and 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.
- We have previously found using core-genome multi-locus sequence typing (cgMLST) that a subset of patients can be colonized with more than one strain of VREfm.
- Fourier Transform-Infrared spectroscopy (FT-IRS) is a phenotypical method that has been demonstrated to show a high degree of typing resolution in different hospital associated pathogens.

## AIM

- To compare cgMLST clustering of VREfm against FT-IRS clustering, to determine if FT-IRS can detect in-patient diversity.

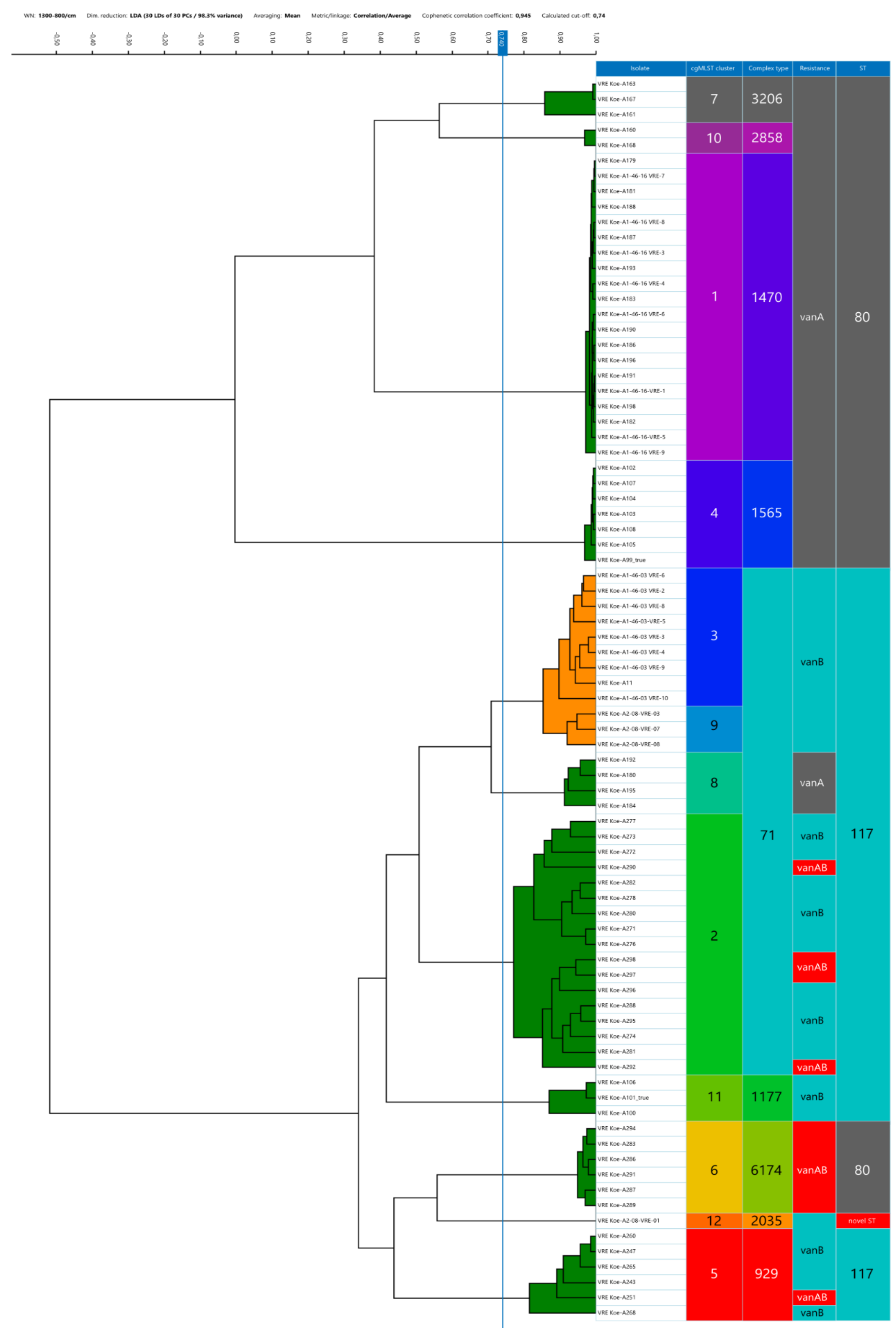
## METHODS

1. To determine strain variation within a patient, from seven VRE-colonized patients, six to twenty-five colonies were picked from screening agar plates. From this, a total of 81 isolates were sequenced (Illumina) and analysed by cgMLST (Ridom SeqSphere+) where twelve clusters of related isolates were identified.
2. FT-IRS analysis was performed using the IR Biotyper® (IRBT -Bruker Daltonics, Germany). Spectra were acquired from dried spots of bacterial suspensions in ethanol solution from bacteria cultured on Columbia sheep blood agar, in three technical replicates of three independent cultures on different days. Exploratory data analysis was performed by Hierarchical cluster analysis, using the IR Biotyper software V4.0.

## Results

- By cgMLST, each patient except one had two distinct clones of VREfm.
- Each cluster was specific to each patient, except cluster 1 where isolates from two patients clustered together.
- This cgMLST clustering was mirrored in the IR Biotyper clustering, with a few minor differences (Figure 1).
- cgMLST cluster 2 shows a higher intra-cluster variance in comparison with the other clusters, which required a clustering cut-off, whereby clusters 3 and 9, despite separated, look merged.

Figure 1. Dendrogram showing FT-IRS results. in the column to the right cgMLST cluster, complex type, vancomycin resistance variant, and MLST sequence types are shown



## CONCLUSIONS

These data suggest that FT-IRS has the potential to identify VRE strain variation within a patient, 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 cluster identification using FT-IRS.

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