Outbreak of Vancomycin Resistant Enterococcus faecium (VREfm) in a Hematology Unit Identified Through Whole Genome Sequencing

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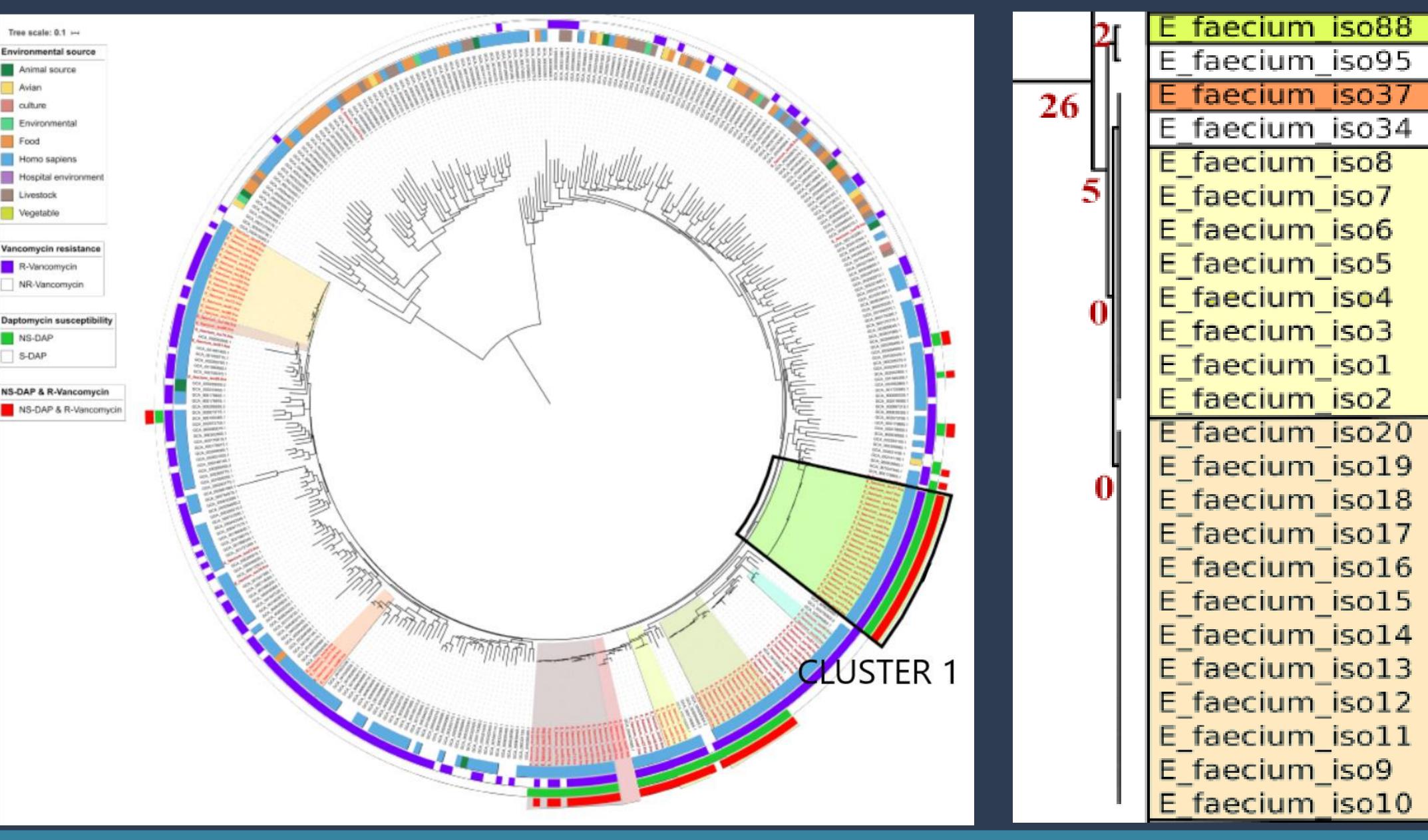
contact gayathrik@wustl.edu with further questions

BACKGROUND

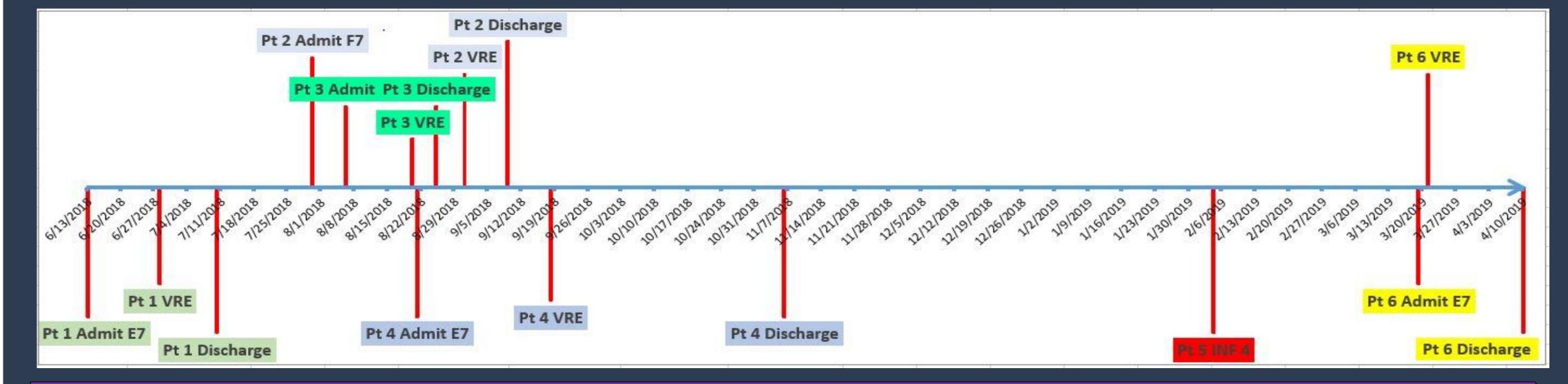
- VREfm is a major cause of Hospital Acquired Infection in the United States.
- We analyzed all the VREfm infections that occurred in our institution between 2018 Whole Genome using (WGS) Sequencing understand to epidemiological relationship between previously unidentified clusters.
- In this study we describe a cluster in our hematology oncology unit.

METHODS

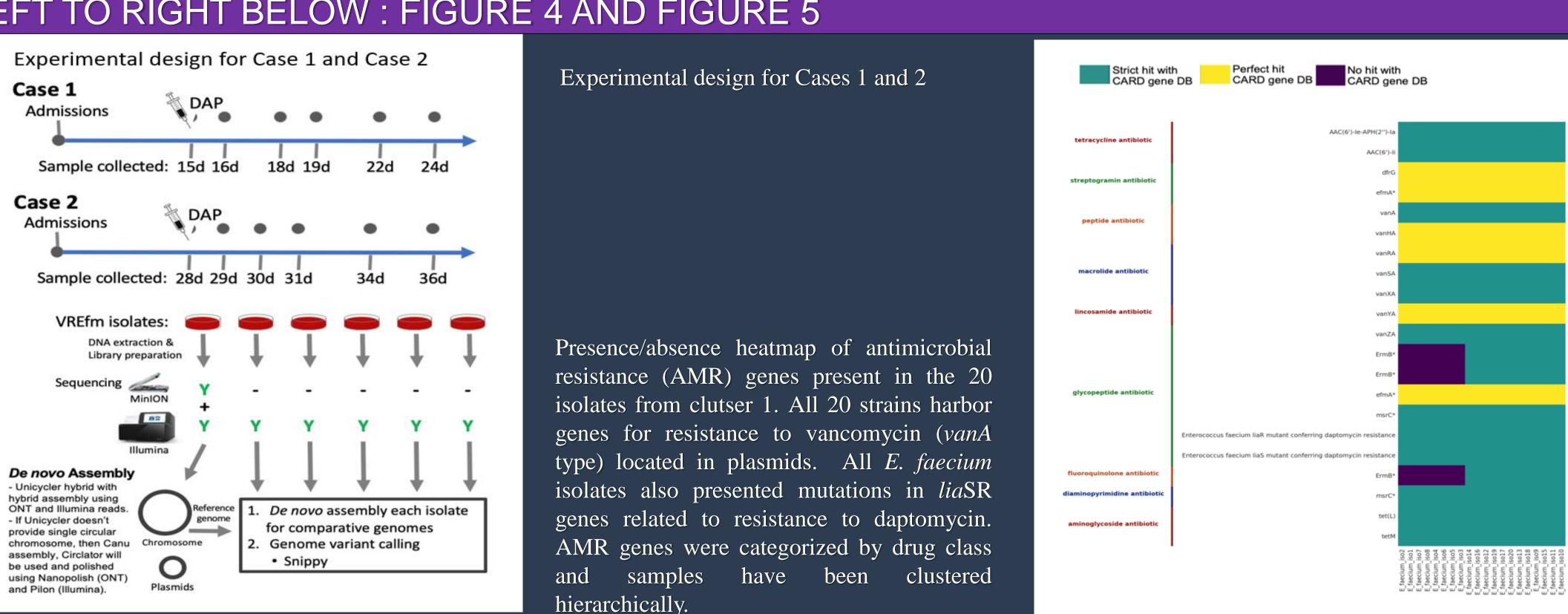
- A total of 106 discrete VREfm isolates from 66 patients were analyzed.
- VREfm isolates used in this study were identified from positive blood and urine cultures.
- Genomic deoxyribonucleic acid was extracted from pure cultures. The and integrity of extracted DNA determined using appropriate assays.
- Library construction and sequencing were conducted, and Multi Locust Sequence Typing (MLST) obtained.
- Sequencing Whole Genome was performed using Illumina Next Seq
- Phylogenomic tree was plotted using the Interactive Tree of Life.







LEFT TO RIGHT BELOW: FIGURE 4 AND FIGURE 5



RESULTS

- 7 clusters were identified.
- Here we describe Cluster 1 which had the highest genetic similarity (0-5 single nucleotide polymorphisms)
- The cluster is composed of 24 clinical strains of VREfm from 6 patients, over a 9 month time period.
- patients hematologic had malignancies; 4/6 patients had received recent chemotherapy and 5/6 patients were neutropenic.
- 4 patients were admitted in a single unit (labelled E7), 1 patient was on a sister unit (labelled F7); and 1 patient was in the cancer infusion center.
- All patients had central venous access placed by radiology at the time of diagnosis of infection and had visited our outpatient infusion center multiple times during this time frame.

CONCLUSION

- The prolonged period in our cluster argues in favor of an environmental niche in the hospital unit.
- It is difficult to ascribe causality to any without these exposures concomitant surveillance cultures of environment personnel. Retrospective WGS is of limited value in infection control.
- third generation have sequencing with the MinION device to do real time sequencing with which we also validated some of our samples.