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# P2337 Is the WGS genotype for patients with an invasive clinical vancomycin resistant *Enterococcus faecium* infection the same as was found in a preceding screening isolate?

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**Background:** Since 2012, the incidence of Vancomycin Resistant *Enterococcus faecium* (VRE) has increased dramatically in Copenhagen, and *van*A *E. faecium* has become endemic and polyclonal. However, a common *van*A plasmid is present in most clones. The purpose of this study is to determine whether the WGS genotype in the invasive clinical infection was identical to the one from the rectal screening.

**Materials/methods:** We performed a 2-year retrospective register-study from our LIS to identify all VRE screening isolates where patients within 60 days later developed an invasive clinical VRE infection. All invasive clinical isolates were either from blood culture or found in tissue/secretion samples. Only one rectal screening and one clinical isolate were included per patient.

In our department, the first VRE screening isolate or clinical isolate per patient is whole-genome sequenced on a routine basis. All isolates were analyzed in SeqSphere and core genome Multilocus sequence typing (cgMLST) was determined.

**Results:** 27 clinical isolates preceded by a positive rectal screening for VRE were found during the study period.

Of the 27 pairs, we found 15 pairs where both the screening sample and the clinical isolate were whole-genome sequenced. Of these, seven patients had matching cgMLST and eight were mismatches. The matching pairs were cgMLST859 (n=3), cgMLST 1134 (n=2), cgMLST 14 (n=1) and cgMLST 1135 (n=1).

The median number of days between the screening sampling date and the clinical sample was two for matching pairs (range 0-11), and 18 for mismatching pairs (range 0-52). The median allele distance for matching pairs was five out of 1,423 target genes, and 336 for mismatching pairs.

**Conclusions:** From our 15 pairs of clinical VRE isolates with a preceding positive rectal screening, seven were a match in cgMLST, while eight were mis-matches. One explanation for the mis-matches could be the longer interval between colonization and infection. This could allow the vanA plasmid to spread to another E. faecium in the gut of the patient or the patient to be colonized with another VRE clone.