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#### Dissemination of *Enterococcus* spp. across One Health Settings: Insights from fingerprinting analysis

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#### **INTRODUCTION & AIM**

**ECM** 

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Enterococcus spp. are ubiquitous Gram-positive bacteria present in the gastrointestinal tract of humans and animals. as well as a widely distributed in the environmental sector, being present in the soil, plants, food, water and sewage through faecal contamination.

Over recent decades, enterococci have emerged as significant opportunistic pathogens in healthcare-associated infections, due to their rapid adaptation to their host and high tendency to acquire both virulence and antibiotic resistance genes. Among the species of this genus, the vancomycin-resistant E. faecium were identified as a critical health threat. In this context, the One Health concept underscores the interconnection of human, animal and environmental health, highlighting the importance of intervention fields such as antimicrobial resistance and food safety.

This study aims to isolate and analyse the genetic diversity of Enterococcus spp. recovered from a diverse range of samples across One Health sectors, using RAPD-PCR.

## **METHOD**



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#### Collection of enterococcal isolates 148 Enterococcus isolates 16 Enterococcus from vancomycin supplemented media SBAvan (12%) 8 VRE from human infections (44% of infection isolates) (presumptively confirmed in BEA) Environment n = 82 enterococcal isolates 60 from surface water (55 SBA, 5 SBAvan) 11 from public transports (11 SBA, 0 SBAvan) 11 from food (9 SBA, 2 SBAvan) Humans n = 35 enterococcal isolates 18 from sick humans with enterococcal infections (NA, **8 VRE**) 17 from healthy humans (11 SBA, 6 SBAvan) ŤŤ 1 Animals 27 enterococcal isolates 14 from sick animals (12 SBA, 2 SBAvan) 13 from healthy animals (12 SBA, 1 SBAvan) n **RAPD-PCR Genetic diversity analysis** Clustering by sample type - isolates from different samples at the same setting share similar profiles (>76% similarity). Sample origin Sample Source Community Surf. Onboard Handles Public transports Isolate code Media TT.I04-1 SBA Community Surf. Boarding Handle Public tra Sick Humans Unknown Hospital Community Surf. Boarding Handle Public tra TT.I05-2 SBA HFM-200 TTJ15-1 SRA Cluster containing isolates from healthy humans. Isolates highlighted belong to related individuals (>85% similarity). 8 8 8 8 8 8 8 8 9 0PC15 Sample origin Sample Healthy Humans Human feces AE-MZ-03 SBA Voluntee 4E-PM7-01 SRA AE-IF-02VRE SBAve ratory FS-20-02VRE SBAve Clinical analysis la 11 Cluster of isolates from enterococcal infections (clinical), healthy humans and surface water (purple) (>85% similarity). Custer composed of on VRE clinical isolate and surface water (green) (>84% similarity). Cluster containing isolates from a healthy and a sick human (blue) (>81% similarity), Cluster of two clinical VRE isolates from the same hospital, but different patients and dates (>79% similarity). GTG5 OPC15 Sample origin Urine VRE Sick Humans SL-170 Bathing Water Bathing Water Envr. analysis laboratory AF19-3 Sick Humans Blood Hospital 1 HFAR-136 Healthy Humans Human feces Clinical analysis laboratory FS-82-02V Pus Biopsy Sick Humans Hospital 1 HFAR-89 HEM-83 111 Cluster formed of isola es from surface water and a clinical VRE isolate from a blood infection (70% similarity). GTG5 OPC15 8 8 8 8 8 Sample origin Sample Bathing Water Bathing Water Source Envr. analysis laboratory AF38-1 SBA Bathing Water Bathing Water Envr. analysis laboratory AF38-3 SBA ШĬ Blood Hospital 2 HEM-106 Sick Humans Bathing Water Bathing Water Envr. analysis laboratory AF35-4 SRA Cluster containing isolates from healthy domestic animals from different households (>84% genetic similarity). <u>8 8 8 8 8 8 8 8 6 8 8 6 0PC15</u> Sample origin Sample Healthy Animals Cat feces Source Volunteer tutor Isolate code Media CAT-PT-01 SBA 67.4 Healthy Animals Dog feces DOG-JM-01 Cluster containing an isolate from a healthy domestic cat and a sick dog (not related) (>86% genetic similarity). Cluster containing an isolate iron a nearing contact of the second state of the second Source Volunteer tutor Isolate code Media AD-E7-2V SBAvan 1 Sick Animals Dog's rectal swab Veterinary hospita DOG130-1 SBA 66.3 Cluster containing isolates from healthy domestic dogs and public transports and spaces (up to 95% genetic similarity). 8 8 9 8 8 8 8 8 Sample origin Sample Healthy Animals Cat feces solate code Media Volunteer tuto CAT-JM-II-01 SBA 25.0 unity Surf. ATM Machine Public transports Public transports TTJ02-2 SBA TTJ02-3 SBA Community Surf. ATM Machine Community Surf. ATM Machine Public transport TTJ02-1 SBA III I 65.2 CAT-IM-05 SRA

**RESULTS & DISCUSSION** 

\* Column only applicable for clinical isolates of enter Reproducibility level was set at 70% (red line).

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#### CONCLUSION

This study used RAPD-PCR to analyze the genetic relatedness of *Enterococcus* isolates across settings and explore their dissemination and foresee potential reservoirs of vancomycin resistance in clinical isolates.

- Overall, no significant clusters by sample type or One Health sector were highlighted in the dendrogram, suggesting the dissemination of genetically diverse enterococci across settings. However. RAPD analysis suggested that similar Enterococcus were found in surface water and clinical isolates, isolates
- estic animals and public transports and spaces, and healthy and sick animals This study confirmed the widespread dissemination of similar enterococci across specific One Health sectors, including presumptive vancomvcin-resistant enterococci

### FUTURE WORK / REFERENCES

Characterize the pathogenic potential of these isolates: - Antibiotic susceptibility testing and resistance gene confirmation by Multiplex PCR

- Presence of virulence factors
 Selection of isolates for WGS based on pathogenicity and genetic relationship between One Health sectors

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