**SUPPLEMENTARY MATERIAL**

Performance Evaluation of Selenite (SeO$_3^{2-}$) Reduction by *Enterococcus spp*

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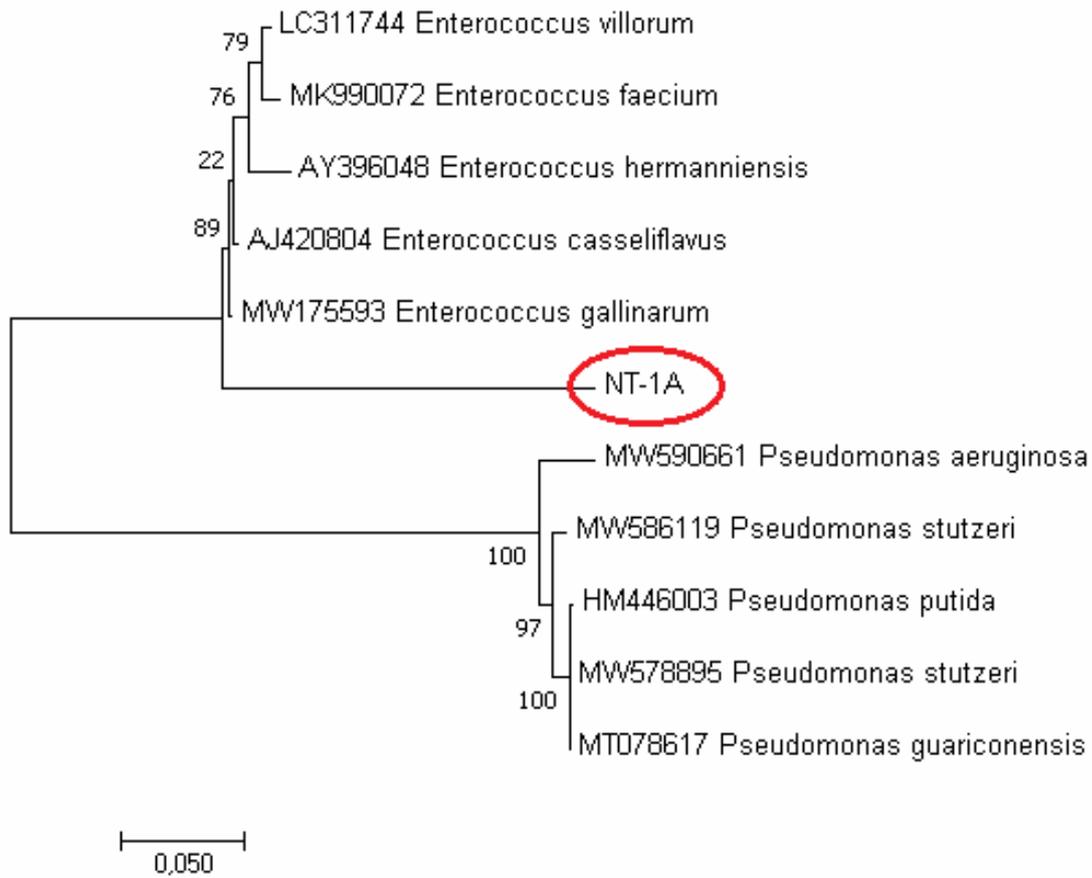
**Figure S1: Phylogenetic tree for the microbial culture results**
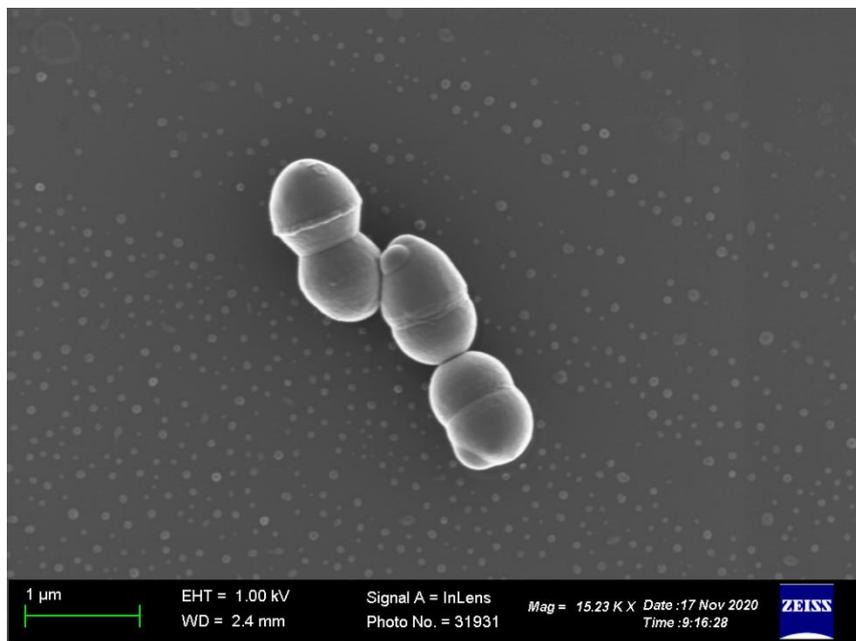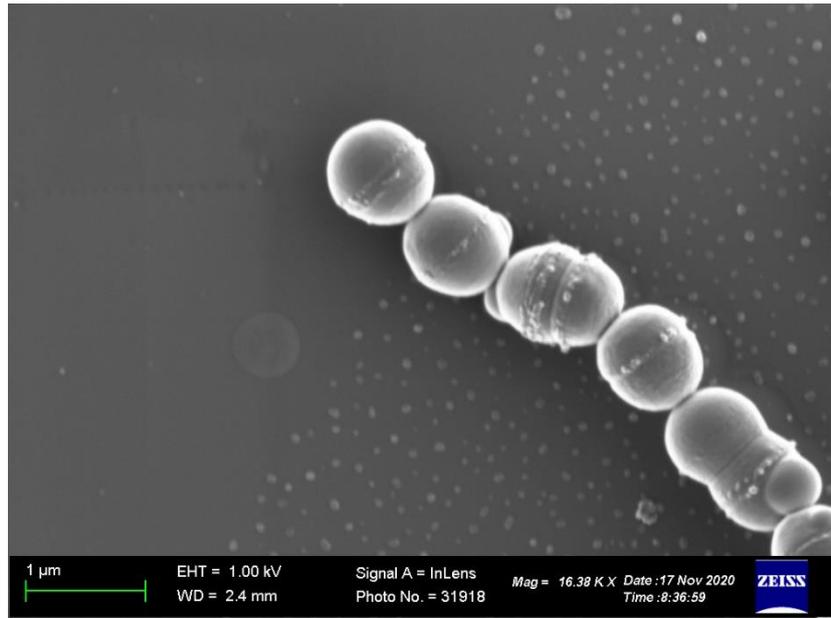
Figure S2: SEM micrographs depicting the morphology of *Enterococcus spp*

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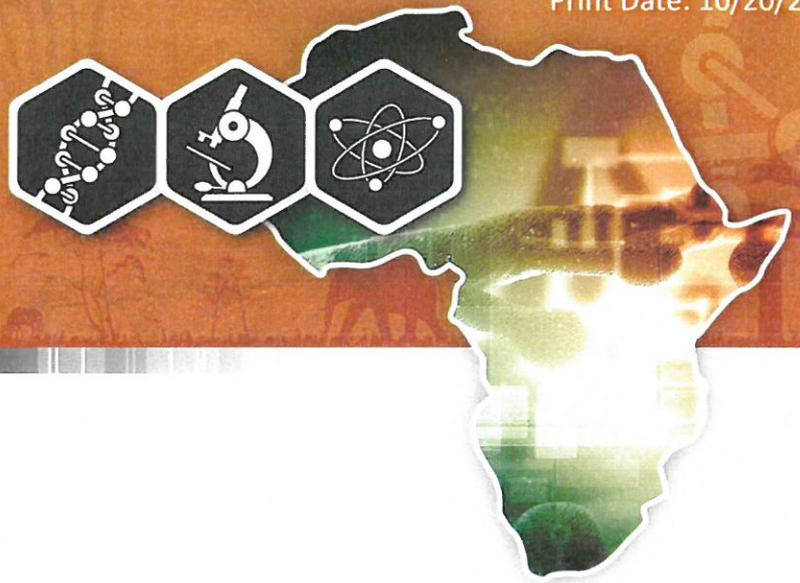
16S REPORT

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BACKGROUND:

Some bacterial isolates cannot be taxonomically identified from phenotypic characteristics. Bacterial isolates can be characterised by sequencing the 16S rDNA. The universal primers 27F and 1492R are used to amplify the 16S target region (Lane et al 1991; Turner et al 1999).

MATERIAL AND METHODS:

Genomic DNA was extracted from the cultures received using the Quick-DNA™ Fungal/Bacterial Miniprep Kit (Zymo Research, Catalogue No. D6005). The 16S target region was amplified using OneTaq® Quick-Load® 2X Master Mix (NEB, Catalogue No. M0486) with the primers presented in Table 1. The PCR products were run on a gel and gel extracted with the Zymoclean™ Gel DNA Recovery Kit (Zymo Research, Catalogue No. D4001). The extracted fragments were sequenced in the forward and reverse direction (Nimagen, BrilliantDye™ Terminator Cycle Sequencing Kit V3.1, BRD3-100/1000) and purified (Zymo Research, ZR-96 DNA Sequencing Clean-up Kit™, Catalogue No. D4050). The purified fragments were analysed on the ABI 3500xl Genetic Analyzer (Applied Biosystems, ThermoFisher Scientific) for each reaction for every sample, as listed in Section 1. CLC Bio Main Workbench v7.6 was used to analyse the .ab1 files generated by the ABI 3500XL Genetic Analyzer and results were obtained by a BLAST search (NCBI).

BLASTN 2.2.31+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Table 1: 16S Primers sequences

Name of Primer	Target	Sequence (5' to 3')
16S-27F	16S rDNA sequence	AGAGTTTGATCMTGGCTCAG
16S-1492R	16S rDNA sequence	CGGTTACCTTGTTACGACTT

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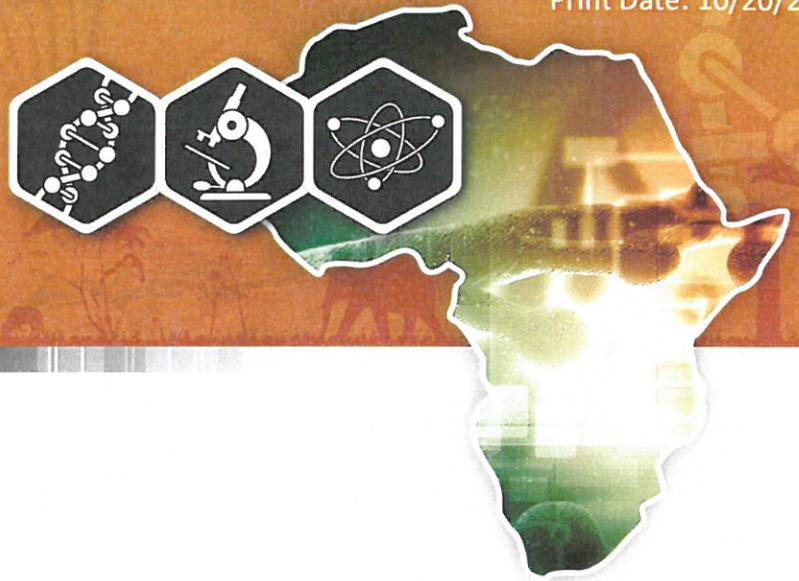
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RESULTS:

Figure 1: A photographic image of an agarose gel indicating the amplification of the 16S target region.

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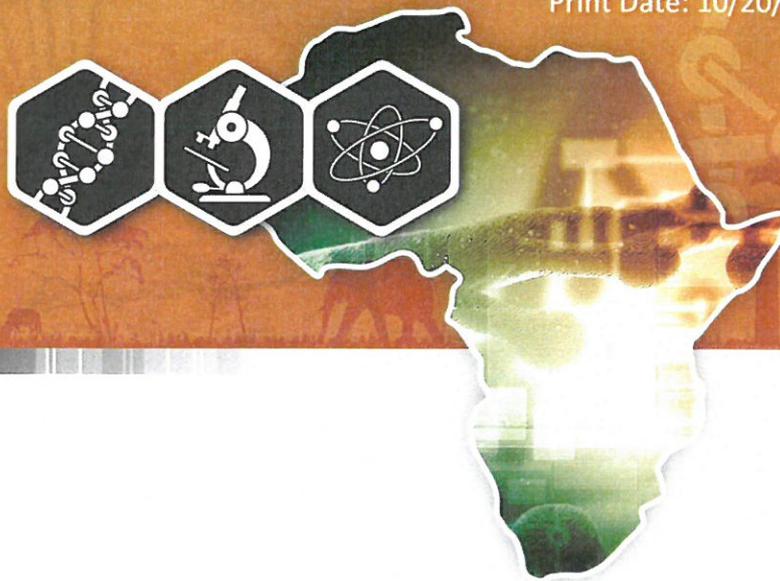
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RESULTS:

BLAST: The BLAST results correspond to the similarity between the sequence queried and the biological sequences within the NCBI database.

Name of sample	NT-1A
Request ID	SK65N3FT014
Predicted Organism	*Enterococcus hermanniensis, Enterococcus gallinarum*
GenBank Accession	AY396048.1, CP050485.1

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CONCLUSION:

Name of sample	BLAST prediction
NT-1A	*Enterococcus hermanniensis, Enterococcus gallinarum*

Dr Simon Lashmar
Genomics Scientist

20/ 10/ 2020.
Date

Dr Erika Viljoen
Genomics Scientist

20/10/2020
Date