

Supplementary Material

Link to Elac_AGAR_MF.btmdb database:

https://www.dropbox.com/scl/fi/tvauqqlad3np8d3utoq5g/Elac_AGAR_MF.btmdb?rlkey=8x2n64429yu0ofpa1ju4p9u7p&st=zbpagzhk&dl=0

Supplementary Table 1.

Species identified	Database	TP	FP	FN	TN	Sensitivity	Specificity
<i>E. faecium</i>	BioTyper [®] MBT Compass reference library (2022)	51	38	0	8	100%	17.4%
	BioTyper [®] MBT Compass reference library (2022) + Elac_AGAR_MF database	51	0	0	46	100%	100%
<i>E. lactis</i>	BioTyper [®] MBT Compass reference library (2022)	0	0	38	59	0%	100%
	BioTyper [®] MBT Compass reference library (2022) + Elac_AGAR_MF database	38	0	0	59	100%	100%

TP, true-positive; FP, false-positive; FN, false-negative; TN, true-negative

Supplementary Figure 1. SNP phylogeny of enterococcal isolates aligned with *E. lactis* KCTC 21015

The phylogeny was inferred based on 607 single nucleotide polymorphisms (SNPs) identified after the same set of genomes were aligned to the chromosome of the reference *E. lactis* strain KCTC 21015 (Accession number CP065211.1) using a neighbour-joining algorithm. The scale bar represents the number of SNPs. The non-*faecium* non-*lactis* enterococcal species included *E. avium*, *E. casseliflavus*, *E. cecorum*, *E. durans*, *E. faecalis*, *E. gallinarum*, *E. mundtii*, and *E. raffinosus*. The sequence type (ST) and the multilocus sequence typing (MLST) allele numbers were obtained from the PubMLST website using the MLST scheme designed by Hootman et al. (2002).

