Supplementary Material

Genotypic identification

Genomic DNA isolation

Bacterial isolates were activated in MRS broths for aerobic bacteria respectively. Cultures were centrifuged to obtain bacterial pellets. DNA isolation was performed using Thermo Scientific GeneJet Genomic DNA Purification Kit (Thermo Fisher Scientific, US). The quantity of DNA obtained after isolation was measured using a NanoPhotometer (Implen, Germany). The isolated DNA was then stored at -20 °C until the next step.

Preliminary identification of LAB isolates by RAPD PCR Sequencing

A total of 25 LAB strains were analyzed for discrimination using random amplification of polymorphic DNA (RAPD) with the M13 primer (5c-GAGGGTGGCG GTTC T-3c), as described by Rossetti and Giraffa (2005). For this procedure, sterile water, the M13 primer, master mix, and DNA template were combined in 100 µl PCR tubes to achieve a final reaction volume of 50 µl, and all components were thoroughly mixed using a micropipette. DNA fragments were amplified in a thermal cycler (Bio-Rad Laboratories, Hercules, CA) under the following conditions: initial denaturation at 94°C for 3 minutes, followed by 30 cycles of denaturation at 95°C for 30 seconds, annealing for 30 seconds, extension at 72°C for 1 minute, and a final extension step at 72°C for 10 minutes. The PCR products were loaded onto a 1% agarose gel stained with ethidium bromide, and DNA separation was carried out at 90 V for 1 hour. The resulting gel was visualized using a gel imager (Bio-Rad Laboratories, Hercules, CA).

Genetic identification of LAB isolates by 16S rRNA Sequencing

16S rRNA analysis was performed on 25 bacterial strains identified through RAPD-PCR. For the 16S rRNA analysis, a PCR mixture targeting a 1,500 bp product was prepared by adding 1 µl of DNA from the relevant bacterium, 25 µl of Q5 High-Fidelity 2X Master Mix (New England Biolabs), 20 mmol of the forward primer AMP_F (5'GAGAGTTTGATYCTGGCTCAG − 3') and reverse primer AMP_R (3'AAGGAGGTGATCCARCCGCA − 5'). The mixture was completed with 50 µl of sterile water. The PCR program used for 16S rRNA analysis included 2 minutes at 98°C, followed by 30 seconds at 98°C, 20 seconds at 57°C, and a final 5-minute extension at 72°C, repeated for 25 cycles. The resulting PCR products were loaded onto a 1% agarose gel and separated by electrophoresis at 90 V for 40 minutes. The gel was then visualized using the Bio-Rad Gel Doc EZ Imager. The PCR products were sequenced, and the sequences were identified by Medsantek (Istanbul, Turkey). Sequences showing 97-100% similarity were compared using the BLAST algorithm.

Table S1. Identified LAB strains and their amounts

Strain	**Amount**
L.rhamnosus	25
L.casei	11
L.paracasei	8
L.fermentum	4
L.brevis	7