Data Article

Data on the diversity of lactic acid bacteria isolated from raw and fermented camel milk

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\section*{A B S T R A C T}

Lactic acid bacteria (LAB) are the dominant and advantageous microorganisms of raw and fermented camel milk; these bacteria have the potential to develop functional camel-milk-derived products and can be used in dairy technology. This article presents data on the diversity of LAB, isolated from raw and fermented camel milk. In total, from two samples of raw camel milk and one sample of fermented camel milk, seventeen isolates of LAB were isolated. The data of genetic identification of strains, which was performed through analysis of the 16S rRNA gene sequence, is presented. According to this data, the prevailing number of LAB belong to the \textit{Lactobacillus} genus – 53%. Following species of Lactobacillus bacteria were determined – fermentum, casei, curiae, oryzae, brevis, plantarum, rhamnosus, paracasei. The next prevailing number of lactic acid bacteria belong to the \textit{Pediococcus} genus – 23%, represented by acidilactici and pentosaceus species. Lactic acid bacteria of \textit{Weissella} and \textit{Enteroococcus} genera comprised 12% each from total abundance. These results can be used for a further selection of potential starter cultures for functional camel-milk-derived products.

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Specifications table

| Subject                       | Applied Microbiology and Biotechnology |
|-------------------------------|-----------------------------------------|
| Specific subject area         | Isolation and identification of lactic acid bacteria, isolated from raw and fermented camel milk with future potential in the development of starter cultures |
| Type of data                  | Tables and figure                       |
| How data were acquired        | Microscope MS 300X (MICROS, St. Veit an der Glan, Austria), 3730xl DNA Analyzer (Applied Biosystems, Foster, USA), SeqScape 2.6.0 software (Applied Biosystems, Foster, USA). |
| Data format                   | Raw and analyzed data.                  |
| Parameters for data collection| Data were collected by seeding raw and fermented camel milk samples on plates with MRS agar. |
| Description of data collection| The data were collected by conducting microbiological seeding of raw and fermented camel milk samples on nutrient media, followed by isolation of LAB and identification. |
| Data source location          | Nur-Sultan, Kazakhstan                  |
| Data accessibility            | Data is included in this article.       |

The sequences of the fragments of the 16S rRNA gene are deposited in the NCBI database, under accession numbers MT598199.1, MT598200.1, MT598201.1, MT598202.1, MT598203.1, MT598204.1, MT598205.1, MT598206.1, MT598207.1, MT598208.1, MT598209.1, MT598210.1, MT598211.1, MT598212.1, MT598213.1, MT598214.1, MT598215.1. (https://www.ncbi.nlm.nih.gov/nuccore/)

Value of the Data

- The right starter culture plays a crucial role in the success of the fermented milk product. This data would be valuable for further studies to select beneficial LAB with unique biotechnological properties.
- The value of the data is on the possibility of finding the novel species of LAB among the LAB, isolated from raw and fermented camel milk.
- This data can be an impetus for the development of a new domestic starter for camel milk.
- Researchers who are engaged in studying of new strains of the LAB could use this data.

1. Data

Camel milk and fermented camel milk are popular drinks among the population of Kazakhstan. Due to the unique therapeutic potential and absence β-LG, camel milk has a focus area of research in health science and nutrition [1]. Fermented camel milk, named shubat, is also known for its medicinal and dietary properties [2]. LAB is the dominant population in raw and fermented milk; they produce various antimicrobials such as organic acids and hydrogen peroxide, antifungal peptides and bacteriocins and play a crucial role in food fermentation processes [3]. The isolation and characterization of resident LAB in raw and fermented camel milk are essential for further development starters of functional camel-milk-derived products.

The data of this article provides data on the isolation of LAB from raw and fermented camel milk and their identification. In total, three samples were used for data collection (two samples of raw camel milk and 1 sample of shubat – traditional fermented camel milk in Kazakhstan). From two samples of camel milk, eight LAB were isolated, from fermented camel milk, nine LAB were isolated. Table 1 presents the data of microscopic characteristics of isolates. By molecular identification based on the analysis of the 16S rRNA gene’s partial sequence, the isolates were assigned to the genus Lactobacillus, Pediococcus, Weissella, and Enterococcus. Table 2 presents the nucleotide sequences of isolate’s 16S rRNA gene and their similarity to available nucleotide se-
| Isolate | Sample          | Place of sample isolation | Microscopical characterization | Gram stain | Cell morphology |
|---------|----------------|---------------------------|--------------------------------|------------|----------------|
| L-001   | camel milk     | Turkestan region          | positive                       | rod        |                |
| L-002   | camel milk     | Turkestan region          | positive                       | rod        |                |
| L-008   | fermented camel milk | Turkestan region      | positive                       | rod        |                |
| L-004   | fermented camel milk | Turkestan region      | positive                       | rod        |                |
| L-003   | camel milk     | Kyzylorda region         | positive                       | rod        | small cocci    |
| L-007   | camel milk     | Kyzylorda region         | positive                       | rod        |                |
| L-009   | camel milk     | Kyzylorda region         | positive                       | rod        |                |
| L-010   | camel milk     | Kyzylorda region         | positive                       | rod        |                |
| L-014   | camel milk     | Kyzylorda region         | positive                       | rod        | small cocci    |
| L-015   | camel milk     | Kyzylorda region         | positive                       | rod        |                |

| Isolate | Accession number in GenBank | Accession number to an identical sequence in GenBank | Species affiliation             | Percent identity (%) |
|---------|----------------------------|------------------------------------------------------|---------------------------------|----------------------|
| L-001   | MT598199.1                 | MH532286.1                                           | Lactobacillus fermentum        | 100                  |
| L-002   | MT598200.1                 | MF179633.1                                           | Pediococcus acidilactici      | 100                  |
| L-011   | MT598201.1                 | MH473167.1                                           | Pediococcus pentosaceus       | 99                   |
| L-008   | MT598202.1                 | MH398517.1                                           | Weissella confusa             | 99                   |
| L-013   | MT598203.1                 | MK418664.1                                           | Lactobacillus plantarum       | 100                  |
| L-003   | MT598204.1                 | MF405178.1                                           | Lactobacillus curiae          | 89                   |
| L-004   | MT598205.1                 | NR041893.1                                           | Lactobacillus casei           | 100                  |
| L-005   | MT598206.1                 | GU983698.1                                           | Enterococcus lactis           | 100                  |
| L-006   | MT598207.1                 | MG462090.1                                           | Lactobacillus oryzae          | 93                   |
| L-007   | MT598208.1                 | MH817736.1                                           | Lactobacillus paracasei       | 100                  |
| L-009   | MT598209.1                 | FR873980.1                                           | Pediococcus pentosaceus       | 97                   |
| L-010   | MT598210.1                 | KY466904.1                                           | Pediococcus acidilactici      | 98                   |
| L-014   | MT598211.1                 | MH346266.1                                           | Enterococcus faecium          | 99                   |
| L-015   | MT598212.1                 | MH398517.1                                           | Weissella confusa            | 95                   |
| L-017   | MT598213.1                 | MK418585.1                                           | Lactobacillus rhamnosus       | 98                   |
| L-018   | MT598214.1                 | MK408481.1                                           | Lactobacillus brevis          | 100                  |
| L-019   | MT598215.1                 | MK418666.1                                           | Lactobacillus plantarum       | 99                   |
sequences deposited in the Gene Bank databases. For three strains of lactic acid bacteria L-003, L-006, L-015, the percent of identity to their affiliations were 89%, 93%, 95%, respectively. It could indicate that novel species of LAB possibly were isolated from raw and fermented camel milk. On Fig. 1 presented the diversity of LAB, isolated from raw and fermented camel milk.

2. Experimental design, materials, and methods

2.1. Source for isolation LAB

For data producing, two samples of raw camel milk were collected: from Social Entrepreneurship Corporation «Zhelmaya» in Turkestan region and private compound in the Kyzylorda region. Also, a sample of fermented camel milk – shubat, collected from Social Entrepreneurship Corporation «Zhelmaya», was used for data-producing. The samples of fresh raw and fermented camel milk were collected to the sterile glass tubes and delivered to the laboratory at 4 °C.

2.2. Isolation of LAB cultures

One milliliter from each sample was transferred to the tubes with 7 mL of MRS broth (HiMedia Lab Pvt., Mumbai, India) and inoculated at 37 °C under microaerophilic conditions. After 24 h of incubation 0.1 mL of suspension spread-plated onto MRS agar (HiMedia Lab Pvt., Mumbai, India) to isolate the LAB. The plates were incubated at 37 °C for three days. Colonies with morphological differences in color, shape, and size were picked and purified by streaking. Pure cells of isolates were maintained at −20 °C in the culture broth, which was supplemented with 10% glycerol, also the cultures stored in a hermetically sealed form in the refrigerator at +4–8 °C.

2.3. Microscopical characterization

Smears of the LAB strains were prepared on a clean glass slide. The air-dried smears were fixed by heating. The fixed smears were washed with water after flooding with crystal violet.
Then were flooded with mordant Gram's iodine, decolorized with ethanol, washed with water, and counterstained with safranin for 45 s. Then the glass slides were washed with water, dried with tissue paper and examined under oil immersion (100 ×) [4].

2.4. Molecular identification of bacterial isolates

Genomic DNA was isolated from pure LAB cultures using Wizard Genomic DNA Purification Kit A11125 (Promega Corporation, Madison, USA) following the manufacturer's protocol. The genotyping was performed using amplification of the fragment of the 16S rRNA gene according to the following protocol by Shevtsov A. B. et al. [5]. The PCR reaction was performed with universal primers – (5′-agagtgttgcctggctcag-3′) and (5′-ggactacccggattcata-3′) in a total volume of 30 μl. Purification of PCR products from unbound primers was performed using Exonuclease I enzymes (Fermentas, Vilnius, Lithuania) and alkaline phosphatase (Fermentas, Vilnius, Lithuania). The sequencing reaction was carried out using the BigDye® Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems, Foster, USA) according to the manufacturer's instructions, followed by fragment separation on a 3730xl DNA Analyzer (Applied Biosystems, Foster, USA). The nucleotide sequences of the 16S rRNA gene of LAB cultures were analyzed and aligned into a common sequence in SeqScape 2.6.0 software (Applied Biosystems, Foster, USA). After that, terminal fragments (nucleotide sequences of primers with fragments having a low-quality index) were removed, which allowed us to obtain a nucleotide sequence of more than 650 bp in length. The later was identified in GeneBank using the BLAST algorithm.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships which have or could be perceived to have, influenced the work reported in this article.

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.dib.2020.105956.

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