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Analysis of koumiss microbiome in Akmola region

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Introduction: Koumiss is a low-alcohol product made from fermented mare's milk. Today it is popular in Kazakhstan, Russia and other countries of the Central Asia, China and Mongolia. Natural mare's milk is fermented in symbiosis of two types of microorganisms (lacto-bacteria and yeast). Koumiss microbial composition varies depending on the geographical, climatic and cultural conditions. For example Wu, R. and coauthors, on the basis of phenotypic characteristic from samples, isolated in Inner Mongolia and autonomous region of China identified following bacteria: *L. casei, L. helveticus, L. plantarum, L. coryniformis subsp. coryniformis, L. paracasei, L. kefiranofaciens, L. curvatus, L. fermentum* and *W. kandleri*. Studies of yeast composition in koumiss also showed significant differences. Thus, from 87 isolated yeast cultures to *Saccharomyces unisporu* related 48.3% of isolates, to *Kluyveromyces marxianus* (27.6%), *Pichiamembranae faciens* (15.0%), *Saccharomyces cerevisiae* (9.2%).

Methods: To extract DNA from the koumiss, 1.8 ml of fermented milk was centrifuged to generate a pellet which was suspended in 450 µl of lysis buffer P1 from the Power food Microbial DNA Isolation kit (MoBio Laboratories Inc., USA). To determine the composition of the microflora was used to amplification a fragment of the gene 16S rRNA and ITS1. Plasmid library with target insertion were obtained on the basis of hight copy plasmid vectors produces high pGem-T. The definition of direct nucleotide sequence was performed by the method of Sanger using a set of "BigDyeTerminanor v 3.1 Cycle sequencing Kit with automatic genetic analyzer ABI 3730xl (Applied Biosystems, USA). For the analysis were used the software package Informax Vector NTI Suite 9, Sequence Scanner v 1.0.

Result: Studies showed, that in the most samples of koumiss isolated from Akmola region (The Central Kazakhstan) prevailed following bacteria species: *Lactobacillus diolivorans, Lactobacillus acidophilus, L. casei, L. curvatus,* yeast strain *Torula* (62.4%) and *Saccharomyces cerevisiae* (37.6%).

Conclusions: Thus, there was conducted the first metagenomic research of koumiss in Kazakhstan, which showed significant differences in microbial composition of koumiss.

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