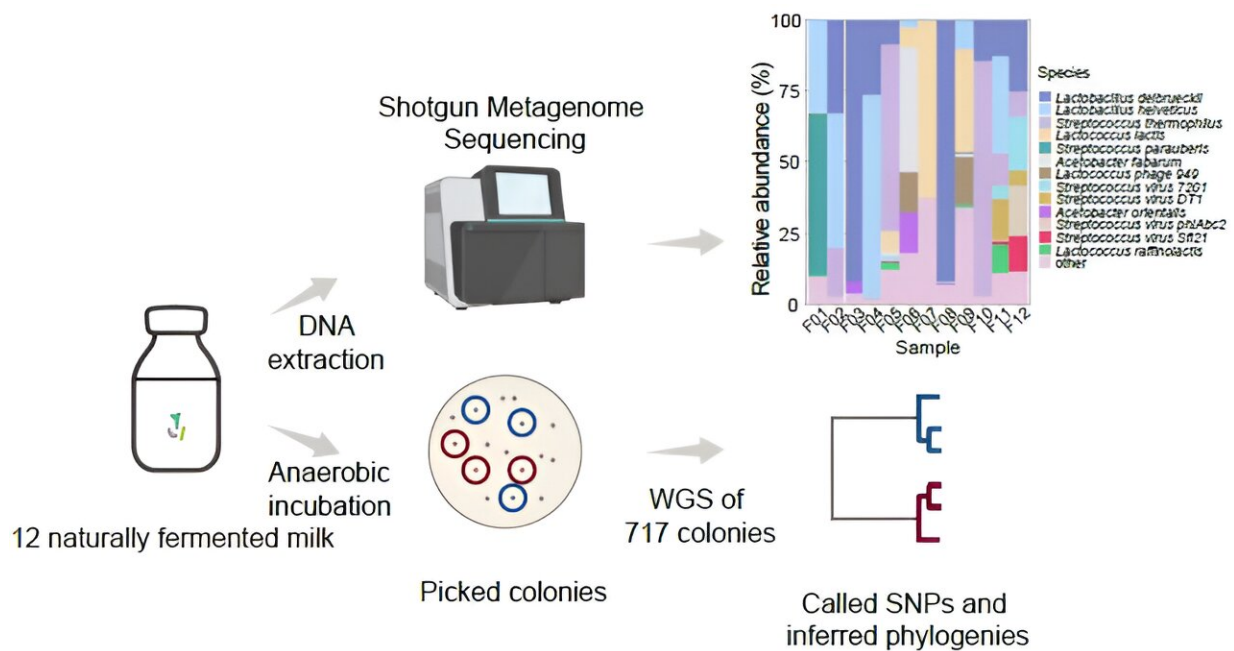


Intraspecific microdiversity and ecological drivers of lactic acid bacteria in naturally fermented milk ecosystem

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This graphical abstract includes metagenomic sequencing of natural fermented dairy products and whole-genome sequencing of isolated strains. Credit: Science China Press

Traditional fermented milks are produced by the inoculating technique, which selects well-adapted microorganisms that have been passed on through generations. Few reports have used naturally fermented milks as

model ecosystems to investigate the mechanism of formation of intra-species microbial diversity.

In a new study, researchers led by Prof. Heping Zhang and Wenjun Liu at the Inner Mongolia Agricultural University, China, isolated and whole-genome-sequenced a total of 717 [lactic acid](#) bacterial isolates obtained from 12 independent naturally fermented milks collect from 12 regions across five countries. The research is [published](#) in the journal *Science Bulletin*.

The researchers further analyzed the within-sample intra-[species](#) phylogenies of 214 *Lactobacillus helveticus* isolates, 97 *Lactococcus lactis* subsp. *lactis* isolates, and 325 *Lactobacillus delbrueckii* subsp. *bulgaricus* isolates. The team observed a high degree of intra-species genomic and functional gene diversity within-/between-sample(s). Single nucleotide polymorphism-based phylogenetic reconstruction revealed great within-sample intra-species heterogeneity, evolving from multiple lineages.

Further phylogenetic reconstruction (presence-absence gene profile) revealed within-sample inter-clade functional diversity (based on carbohydrate-active enzyme- and peptidase-encoding genes) in all three investigated species/subspecies.

By identifying and mapping clade-specific genes of intra-sample clades of the three species/subspecies to the respective fermented milk metagenome, the team found extensive potential inter-/intra-species horizontal gene transfer events.

The microbial composition of the samples is closely linked to the nucleotide diversity of the respective species/subspecies. Overall, the team's results contribute to the conservation of lactic acid bacteria resources, providing ecological insights into the microbial ecosystem of

naturally fermented [dairy products](#).

More information: Lijun You et al, Intraspecific microdiversity and ecological drivers of lactic acid bacteria in naturally fermented milk ecosystem, *Science Bulletin* (2023). [DOI: 10.1016/j.scib.2023.09.001](https://doi.org/10.1016/j.scib.2023.09.001)

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