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Biodiversity of Native Lactic Acid Bacteria in Three Artisanal Lebanese Fermented Goat Dairy Products: Ambriss, Serdaleh and Labneh El Darff

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Introduction and Objectives

In Lebanon, the production of traditional fermented goat dairy products is carried out at small scale, and only in a limited number of production units. As a result, there is a real risk of extinction of these products and loss of corresponding microbial resources (Serhan & Mattar 2013). The recovery, enhancement and valorization of their microbial ecosystems are becoming necessary and urgent. This may be a good potential for Geographical Indications (SRVA, 2005). The aim of this work was to isolate and characterize representative strains of Lactic Acid Bacteria (LAB) of three Lebanese traditional fermented goat dairy products, namely "Ambriss", "Serdaleh" and "Labneh El Darff" and to provide an overview of their microbial biodiversity.

Materials and Methods

Selection of three artisanal fermented goat milk

Serdaleh in Chouf

Production in small caves, in old Amphora filled with 60L of raw goat milk, together with whey evacuation and surface salting



Ambriss in Bekaa valley

In-house production in small jars filled with 13L raw goat milk, together with whey evacuation and surface salting



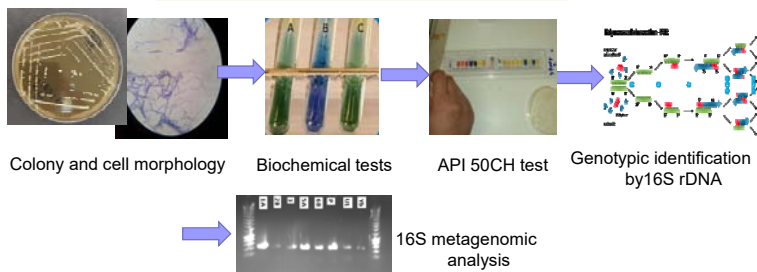
Labneh El Darff

In south Lebanon Goat skin (Darff) filled with fermented milk (Laban) and hung to be strained



14 samples of the 3 fermented products and their respective raw materials (raw milk and Laban) were collected from 6 producers located in the selected regions.

LAB isolation and identification



Results and discussion

1. Microbial enumeration in samples

| Genus | Media | T °C | Ambriss | | | Serdaleh | | | Labneh El Darff | | | | |
|--------------|-------|------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|----------------------|----------------------|----------------------|---------------------|---------------------|
| | | | P1 | P2 | P3 | P4 | P5 | P6 | | | | | |
| Lactobacilli | MRS | 30 | 8.0*10 ⁸ | 1.5*10 ⁹ | 1.3*10 ⁹ | 7.9*10 ⁸ | 1.2*10 ⁹ | 8.8*10 ⁸ | 3.46*10 ⁸ | 1.80*10 ⁸ | 1.10*10 ⁸ | 3.2*10 ⁸ | 1.7*10 ⁸ |
| | MRS | 42 | <10 | 1.8*10 ⁸ | 2.0*10 ⁸ | 66*10 ⁶ | 2.2*10 ⁸ | <10 | <10 | <10 | 6.4*10 ⁶ | <10 | 4.7*10 ⁶ |
| Lactococci | M17 | 30 | 1.3*10 ⁹ | 2.3*10 ⁹ | 4.8*10 ⁹ | 2.5*10 ⁹ | 2.5*10 ⁹ | <10 | 1.87*10 ⁹ | <10 | 1.02*10 ⁹ | 1.1*10 ⁹ | 2.6*10 ⁹ |
| | KF | 37 | 1.8*10 ⁹ | 3.4*10 ⁹ | <10 | 2.9*10 ⁹ | 2.0*10 ⁹ | <10 | 3.2*10 ⁹ | <10 | <10 | <10 | 1.3*10 ⁹ |
| Streptococci | count | PCA | 2.3*10 ⁸ | 2.0*10 ⁸ | 2.5*10 ⁸ | 2.8*10 ⁸ | 1.9*10 ⁸ | 5.5*10 ⁷ | 3.3*10 ⁷ | 1.3*10 ⁷ | 2.6*10 ⁷ | 1.4*10 ⁷ | 2.9*10 ⁷ |

Table 1: Bacterial counts (CFU/ml) on selective media from the Ambriss, Serdaleh and Labneh El Darff and their raw materials

Results show a dominance of mesophilic *Lactobacilli* (3.46×10^8 - 8.8×10^8 UFC/mL) over *Lactococci* in Serdaleh, whereas in Ambriss, *Lactococcus* and *Streptococcus* were most present on M17.

2. Physico-chemical characteristics of the products

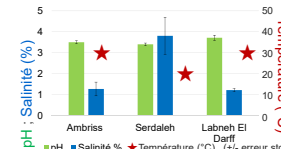


Fig 1: Physico-chemical characteristics (pH and salinity %) of Ambriss, Serdaleh and Labneh El Darff

pH and salinity varied between 3.40 - 3.71 and 1.22 - 3.80% respectively in the three products. High levels of salinity (3.84%) and acidity (pH = 3.40) were observed in Serdaleh in comparison to its counterpart Ambriss, which might have affected bacterial composition of the two products.

3. Microbial biodiversity by 16 S gene sequencing and metagenomics



Fig 2: LAB compositions (%) of Ambriss, Serdaleh and Labneh El Darff samples as determined by 16S rDNA gene sequencing

Enterococcus durans was the most abundant species in Ambriss, followed by *Lactobacillus rhamnosus* and *Pediococcus acidilacti*. *Lactobacillus brevis* was predominant in Labneh El Darff, followed by *L. delbrueckii ssp bulgaricus*. Serdaleh had the lowest biodiversity with *Lactobacillus kefirii* and *L. diolivorans* as the main species.

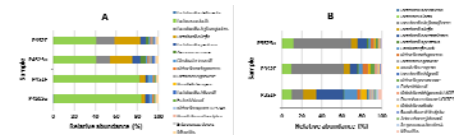


Fig 3: Microbial community structures of Serdaleh samples at two fermentation time intervals (S1 and S2) at the top (Su) and the bottom (F) layers of the jar producers (A) and (B), as determined using 16S metagenomic sequencing, expressed as relative abundance (%) of the microorganisms identified.

Metagenomics allowed better characterization of Serdaleh microbial composition, showing that *Lactococcus lactis* and *Lactobacillus kefirianofaciens* were the most abundant, followed by *L. kefirii* and *L. acetotolerant*. Bacterial composition varied with producing location and time of fermentation, with no difference between the top and the bottom layers of the jar.

Conclusion et perspectives

Our study indicates that microbial ecosystems of "Ambriss", "Serdaleh", and "Labneh El Darff" differ significantly. The physico-chemical characteristics of the products may play an important role in these differences, where Serdaleh presents the lowest biodiversity. 16S Metagenomic analysis allowed us to better characterize microflora diversity of Serdaleh, showing a clear effect of location and fermentation time. Further studies focusing on the technological characterization of LAB strains will be very important step in development of starters and probiotics for use in dairy application.

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