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**RNA-BASED 16S SEQUENCING REVEALS THE MICROBIOTA DEVELOPMENT DURING RIPENING OF ARTISANAL VS. INDUSTRIAL LARD D'ARNAD**

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“Valle d'Aosta Lard d'Arnad” is a protected designation of origin (PDO) product produced from fat of the shoulder and back of heavy pigs. Its manufacturing process can be very diverse, especially regarding the maturation temperature and the NaCl concentration used for the brine, thereby the main goal of this study was to investigate the impact of those parameters on the microbiota developed during curing and ripening. Three farms producing Lard d'Arnad were selected. Two plants, reflecting the industrial process characterized either by low maturation temperature (plant A [10% NaCl; 2°C]) or by using a low NaCl concentrations (plant B [2.5% NaCl; 4°C]), while the third was characterized by an artisanal process (C [30% NaCl; 8°C]). Lard samples were obtained at time 0 and after 7, 15, 30, 60 and 90 days of maturation. The diversity of live microbiota was evaluated by RNA based amplicon target sequencing. The main OTUs identified by RNA based sequencing were *Acinetobacter johnsonii*, *Psychrobacter*, *Staphylococcus equorum*, *S. sciuri*, *Pseudomonas fragi*, *Brochothrix*, *Halomonas* and *Vibrio* and their relative abundance drove the separation of the samples in function of the plant. The composition of the microbiota was more similar among plants A and B and it was characterized by the higher presence of taxa recognized as undesired bacteria in food processing environments. Oligotype analysis of *Halomonas* and

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*Acinetobacter* revealed the presence of several characteristic oligotypes associated with A and B samples with spoilage potential. The industrial processes, characterized by a reduction of the salt concentration in the brines to address a consumer demand for less salty products, can negatively affect the dynamics and development of the live microbiota and as a consequence can negatively impact the quality of the final product due to the higher abundance of spoilage bacteria.

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**THE STAKA CREAM MICROBIAL ECOSYSTEM: A METAGENOMICS APPROACH**

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Staka, a naturally fermented sheep and/or goat milk cream, is a Greek artisanal product originated from the island of Crete. It has unique taste characteristics and is used in many traditional Cretan recipes like the “gamopilafo”, a special rice dish prepared for the wedding table. In the present study, five Staka samples from two regions in Crete, namely Chania and Sitia, were analyzed. The Staka samples were initially subjected to microbiological analysis using selective growth media. The isolates were grouped using the genotyping technique of rep-PCR. Representative bacterial and yeast isolates from each group were identified at the species level by 16S rDNA and ITS DNA sequencing, respectively. Moreover, total DNA was extracted from the Staka samples and the metagenomics results obtained from the 16S and ITS diversity assays were analyzed. Using culture-dependent approaches, a number of bacteria and yeast species

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