

S6-ST02 PDO and non-PDO Roccaverano cheeses: Exploring microbiome diversity and correlations

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Roccaverano Protected Designation of Origin (PDO) is a fresh soft cheese produced in the Roccaverano area (AT), using raw whole goat's milk or with the addition of raw whole cow's and/or ewe's milk in a variable ratio.

The research aims to enhance understanding of the microbiome composition of PDO and non-PDO cheeses exploring potential correlations with the production area.

The sampling consisted of 15 Roccaverano cheeses produced exclusively with goat milk from various producers and 15 non-PDO cheeses of similar type from the same area and from large-scale distribution. The DNA was subject to Illumina shotgun sequencing to reveal insights into bacteria and fungi. Microbiota composition was assessed using MetaPhlAn and bowtie2. Metagenome-Assembled Genomes (MAGs) were generated utilizing SPAdes and metabat2.

Lactococcus lactis emerged as the predominant species in PDO and non-PDO cheese groups. Comparable levels of bacterial α -diversity were noted across both groups, while a noteworthy positive correlation was noted between *Acinetobacter* spp. and *Pseudomonas* spp. in PDO and non-PDO cheeses, respectively. Conversely, *Streptococcus thermophilus* was negatively correlated to PDO cheeses (p -value < 0.05). The bacterial β -diversity revealed PDO cheeses clustering closely with certain non-PDO cheeses on the same plot area, suggesting a degree of similarity between PDO and artisanal cheeses. Notably, no significant clustering between PDO and non-PDO MAGs was observed (Roary).

In terms of fungi, the two predominant species identified in both groups were *Kluyveromyces lactis* and *Kluyveromyces marxianus*. Seventy species were correlated with either PDO or non-PDO cheeses, with *K. lactis* demonstrating a positive correlation with PDO (p -value < 0.05). Additionally, fungal α -diversity was higher in PDO cheeses exhibiting greater stability across samples compared to non-PDO cheeses, indicating a heightened diversity within PDO varieties.

Despite the selection of cheeses based on their technological similarities, notable differences were observed between PDO and non-PDO, particularly in fungal composition. The next phase of this study will concentrate on volatile organic compounds analysis, integrating statistical studies with sensory analysis data to explore potential correlations with cheese microbiome. This approach promises to shed further light on the intricate relationships between cheese microbial composition and sensory characteristics.