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Metagenomic approach to identify the complex microbiota in Sicilian cheeses

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The manufacturing process of cheeses, as for most fermented food, involves a complex flora, which is composed of bacteria, yeast and filamentous fungi. They can be directly inoculated as starter culture or developed from the food-chain environment. Further understanding of cheeses ecosystems and control of cheese product's constant quality both require a better characterisation of the cheese flora and precise taxonomic identification. High-throughput DNA sequencing approaches could be used to decipher food microbial ecosystems and have a lot of potential in the field of food microbiology.

The results obtained when identifying the microbiota in Sicilian cheeses were consistent for both taxonomic identification and abundance. Most of the genera detected in this work have often been described as a part of the microbiota of non-pasteurised milk. Two different parts of the cheese were investigated: the core and the cortical zones. The genus *Lactobacillus* is commonly found in both parts of the cheese, mostly in the forms of streptococcus and other lactic bacteria, however *Lactobacillus* was more abundant in the core of the cheeses. This study confirms the distribution of a variety of bacteria species in the different parts of the cheese.

This communication will report on the first metagenomic study for a typical Sicilian cheese production chain. It confirms the applicability of the method on the production chain. The aim of this work was to illustrate how this approach can be a valuable tool to better characterise the microbiota in cheeses during their transformation as they progress from the storage phase to the maturation phase under controlled environmental conditions.

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