# Microbiological dynamics of Serpa cheese during ripening

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## Objectives

The aim of this work was to assess the specificity and biodiversity of autochthonous microbial consortium associated with Serpa cheese by High Throughput DNA Sequencing (HTS), thus contributing to the preservation of the specificity of this Portuguese dairy heritage.

### Introduction

Serpa is a Protected Designation of Origin cheese, as provided for in Regulation (EEC) 2081/92 of the European Commission, as such, it must be manufactured in the defined geographic area. Serpa traditional manufacturing process maintained through the ages in region, requires the use of raw ewe's milk and vegetable coagulant based on dried flowers of *Cynara cardunculus* L., without any commercial starter, which emphasizes the role of the selected autochthonous microbiota. Its proliferation and qualitative composition will play a key role in its specificity. This microflora comes mainly from raw milk, but also from the whole surrounding environment.

### Conclusions

This approach confirms the diversity of the Serpa cheese microbiota and also that microflora mainly corresponded to lactic bacteria and to lesser extent, enterobacteria, estafilococos and yeasts. No pathogenic bacteria were identified in the different samples. The results obtained by HTS identify *Lactococcus* genus contributing to approximately 40% to 60% of the population, followed by *Leuconostoc* and *Lactobacillus*. The culture-independent methods established the prevalence of *Debaryomyces spp*. and *Kluyveromyces spp*. but also of *Galactomyces spp*.

### Culture dependent-methods **Genomic DNA** PCR-rRNA 16S illeula / Datcii 30 days ripened rRNA from 5 cheese manufactures Sequence Mesophilic aerobic bacteria PCA agar **Gene bank data** Lactic acid bacteria MRS pH 5,7 product base Staphylococci Baird Parker agar **BLAST algorithm** •Enterobacteria VRBG agar •Fungi RBC agar LAB identification 4E TOACTERCTE CETECOTTE OFF COOFFICE OR OCCUMENTAL OCTORE TOALAGE GETAA TREAST IN 340 350 400 400 418 **■** Lactobacillus casei halamamanahaamamahaanahamaanahaan ■ Enterococos hirae Lactobacillus brevis % of isolates identified YEASTS identification Pichia fermentans Candida pararugosa Candida zeylanoides ■ Candida cabralensis Yarrowia lipolytica Moniliella suaveolens % of isolates identified

# All days ripened from 5 cheese manufactures Microbial cheese DNA High-throughput sequencing (HTS) 165 rRNA gene and ITS2 rRNA gene \*\*Lindaward Colors of the Colors of

Culture independent-methods

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