



BIODIVERSITY IN A TRADITIONAL RAW EWE'S MILK CHEESE MICROBIAL CONSORTIUM - CONTRIBUTION FOR THE PROTECTION OF AN AUTOCHTHONOUS MICROBIAL ECOSYSTEM

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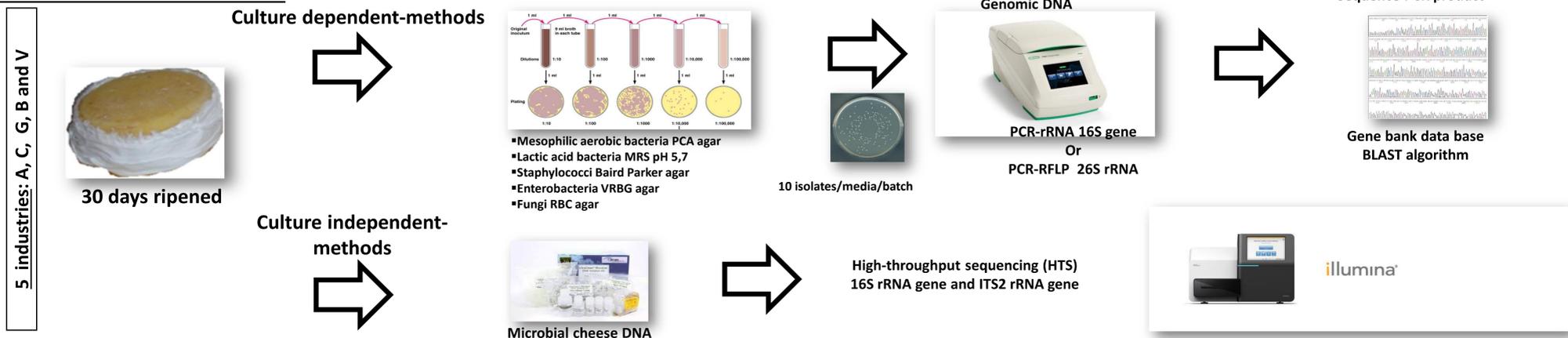
OBJECTIVE

The aim of this research was to assess the specificity and biodiversity of the endogenous microbial consortium associated with the traditional Portuguese cheese Serpa, thus contributing to the preservation of an autochthonous microbial ecosystem and a Portuguese dairy heritage.

INTRODUCTION

Serpa cheese is known as a high quality cheese with Protected Designation of Origin (PDO), as provided for in Regulation (EEC) 2081/92 of the European Commission. This cheese exemplifies a ripened cheese made from raw ewe's milk using as rennet dried flowers of the plant *Cynara cardunculus* L.. The absence of any thermal process of standardization and commercial starter, makes this cheese a complex natural ecosystem created by the interaction of autochthonous microbes coming mainly from raw milk but also from the surrounding environment, shaped by the conditions that cheesemakers build to obtain specific flavors and textures. In fact, the microbial diversity of this type of cheese is the secret of its specificity and quality, and even of its safety, but little is known about it. Thus, precise identification of their microbial population seems crucial. For this, the microbial population of the cheese was characterized by culture-dependent and independent-methods. The results obtained can contribute to the rational optimization of its production and quality, but also to the preservation of this Portuguese dairy heritage.

MATERIAL AND METHODS



RESULTS

Culture dependent-methods

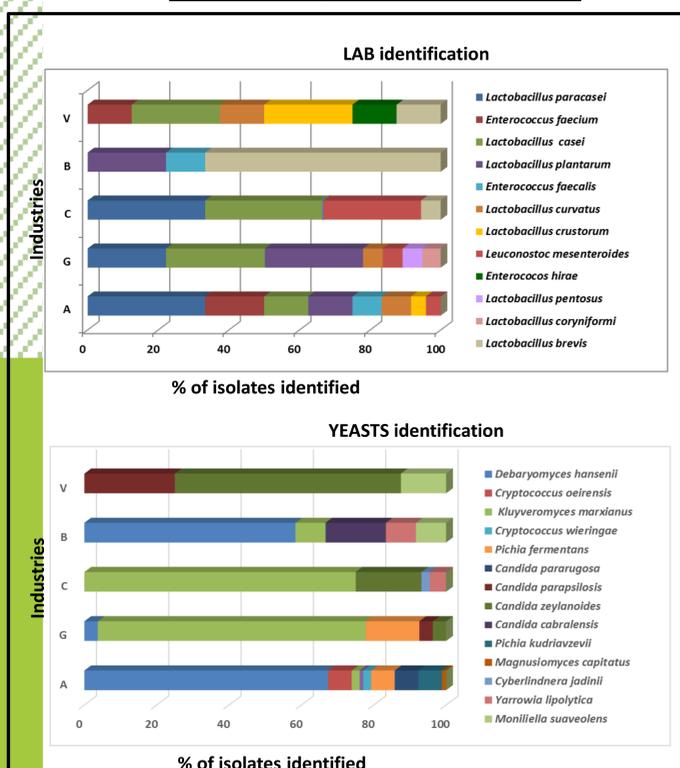


Figure 1. Prevalence of lactic bacteria (LAB) and yeasts species in Serpa cheeses from five industries (A, G, C, V and B) at the end of the ripening (30 days) by culture dependent methods.

Culture independent-methods

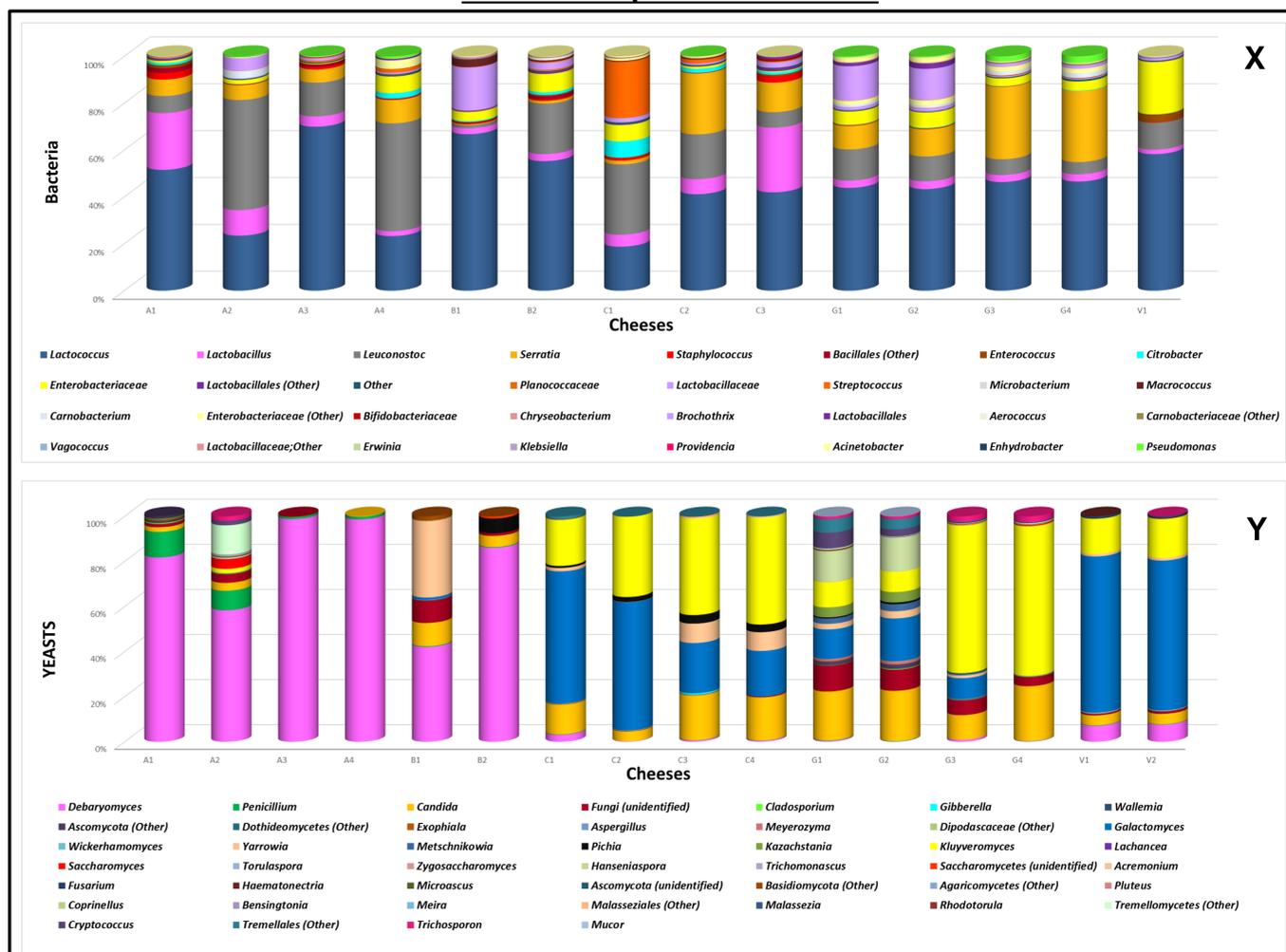


Figure 2. Prevalence of bacteria (X) and yeast (Y) genera in Serpa cheeses (30 days ripened) from five industries (A, G, C, B and V), by culture independent methods (HTS).

CONCLUSIONS

- Both approaches confirm the diversity of the Serpa cheese microbiota. HTS is more efficient in demonstrating this biodiversity.
- Main dominant species identified by conventional 16S rRNA gene sequencing: *Lactobacillus casei/paracasei*, *Lactobacillus brevis*, *Leuconostoc mesenteroides* and *Enterococcus faecium*.
- Main dominant genera identified by HTS : *Lactococcus* (40% to 60% of the population), *Leuconostoc* and *Lactobacillus*.
- The yeast species identified by culture-dependent methods, mainly corresponded to *Debaryomyces hansenii* and *Kluyveromyces marxianus*, with *Candida spp.* and *Pichia spp.* present to a lesser extent. The culture-independent results confirmed but also of *Galactomyces spp.*

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