Assessment of microbial diversity of the dominant microbiota in fresh and mature PDO Feta cheese made at three mountainous areas of Greece

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ABSTRACT

The aim of the present study was to assess the dynamics and the diversity of dominant microbiota in fresh and mature traditional Feta cheese produced in three mountainous areas and for that purpose a combined approach of culture-independent examination with conventional genotypic typing of the predominant NSLAB microbiota were applied. The microbial communities were monitored by PCR-DGGE on seven fresh and nine mature Feta cheese samples made by three artisanal producers. DGGE profiles suggested variability in the microbial composition of cheeses within the production area and distinctive differences in band profile of NSLAB in cheeses between the areas. PCR-DGGE analysis showed that Lactococcus spp. were the most widespread bacteria, Streptococcus macedonicus was detected often and, among lactobacilli, Lactobacillus plantarum prevailed. The diversity of NSLAB isolates from fresh and mature cheeses was assessed by RAPD-PCR and PFGE. Typing data indicated intraspecies genetic heterogeneity and specificity to the production area. Our results point to the conclusion that the manufacturing environment influence the dynamic and the diversity of microbial groups developed in the cheese and possibly the cheese flavour. In addition, the traditional Feta cheese may be a source of different NSLAB genotypes to make cheese with sensorial peculiarities appropriate for each area.

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