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SIMTREA 

Preliminary Study of Microbial Dynamics in a Traditional Italian Cheese: Castelmagno DOP.

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The aim of this work was to study microbial evolution in Castelmagno DOP cheese during manufacturing and ripening processes, in order to acquire preliminary information about the different microbial groups involved.

Milk, curd, and cheese samples at subsequent ripening stages, were collected from three manufacturing batches in one small size traditional dairy plant, and submitted to microbiological analysis on selective media for mesophilic and thermophilic lactococci, mesophilic and thermophilic lactobacilli, enterococci, micrococcaceae, coliforms, yeasts and moulds. Lactococci and lactobacilli isolates were identified by the combined use of PCR 16S-23S rDNA spacer analysis, species-specific probes and 16S rDNA sequencing. Lactic and acetic acid production, and lactose consumption, were HPLC monitored.

Presumptive lactococci and lactobacilli reached the highest levels (10^9 cfu/g) in the curd after 3 days rest in whey, a typical stage in the manufacture of this cheese. Lactic acid bacteria resulted to be the prevailing microflora at one month aged cheeses, although enterococci, *Micrococcaceae* and fungi also showed considerable viable counts. Coliforms, however, progressively decreased in number as a consequence of pH drop during ripening process. Lactic species most frequently isolated were *Lactococcus lactis*, *Lactobacillus plantarum* and *L. paracasei*. Lactic and acetic acid production, and lactose consumption were strongly related to lactic bacteria growth trend. The highest peaks of lactic and acetic acid production, 28.58 and 1.13 g/Kg of curd respectively, coincided with the maximum growth of lactic bacteria. Lactose amount and pH values decreased with the increasing growth of lactic microflora.

The results of the present work represent, to our knowledge, the first approach to the understanding of microbial dynamics in Castelmagno DOP. Further studies are in progress.