

COMPREHENSIVE ANALYSIS OF PROTEOLYSIS IN CHEESE

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In the present study, proteolysis as one of the most important biochemical events during cheese ripening (Fox & McSweeney, 1996) was analyzed in long-ripened Old Saare cheese, applying capillary electrophoresis (CE), liquid-chromatography coupled with tandem mass-spectrometry (LC-MS/MS), and ultra-performance liquid chromatography (UPLC).

Altogether, a number of proteolysis fractions, including intact caseins and their hydrolysis products, were identified, and the cleavage site analysis of caseins provided a comprehensive picture of proteolysis evolution in Old Saare cheese. Progressive degradation of the casein network with simultaneous involvement of chymosin, milk indigenous proteinases, as well as proteolytic systems of mesophilic and thermophilic LAB was observed during cheese ripening.

This work presents the selection of methods and *in silico* tools that allows a detailed characterization of the dynamics of different protein fractions during ripening. The application of this set of tools provided a better understanding how proteolysis evolves in Old Saare cheese. Such complex approach for monitoring of cheese ripening contributes to a better estimation of the role of different proteolytic enzymes in the ripening of certain cheese varieties, and can be used for optimization of the choice of appropriate ripening starters and fine-tuning of cheese manufacturing parameters, and thus texture and flavor of final product.

References

1. Fox, P. F., and P. L. H. McSweeney, 1996, Proteolysis in cheese during ripening, *Food Rev. Int*, 12:457–509.



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