

Peptide formation from casein by *Lactococcus lactis*: Analysis and development of predictive models

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Foods that are fermented by lactic acid bacteria are known for their enhanced functionality, quality and safety and form an important part of the human diet all over the world. In fermented dairy products balanced degradation of casein, the formation and subsequent breakdown of peptides, is important to prevent accumulation of bitter tasting peptides. Moreover, the proteolysis and peptidolysis of casein (1,2) is prerequisite to generate free amino acids, which is the main pathway to flavour formation (3). Furthermore, a lot of scientific and industrial interests have focused on the production of physiologically active peptides derived from milk proteins (4). A great number of functions have been attributed to such milk-derived peptides including appetite regulation, mineral binding, immunomodulation, and a series of antihypertensive, antithrombotic, antioxidative, antimicrobial and antiviral activities in the human body. For dairy lactic acid bacteria, and *L. lactis* in particular, extensive knowledge is available on the different components of the proteolytic system that are responsible for breakdown of the milk protein casein into peptides (1,2). A validated model, however, predicting peptide formation and peptide stability, which is important for both taste and health beneficial peptides, is lacking. Development of such a model will provide insight in the phenomena occurring, be helpful in developing strategies for the optimization of specific peptide production, and will aid in structured and optimized experimental data generation.

References

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