TOWARDS MECHANISTIC UNDERSTANDING OF GASTRIC DIGESTION OF STRUCTURED PROTEINS

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Proteins are essential macronutrients and the digestion starts in the stomach. Numerous *in vitro* studies on protein digestion are based on experiments with dissolved proteins. However, the majority of protein exists in solid food. Therefore, our research is aimed at understanding how the structure of food affects the digestion of protein. We previously studied the *in vitro* digestion of protein and protein gels by analyzing the peptide distribution after hydrolysis, and found that the kinetics of protein hydrolysis in solution and in gels is different. While the dissolved proteins were hydrolyzed through a 'zipper' type mechanism, the gels followed a slower 'one-by-one' mechanism. We hypothesized that pepsin needs to penetrate the gel microstructure and hydrolyze proteins in gel matrices. Thus the digestion kinetics may be limited by diffusion of pepsin in gel matrices, which can explain the differences in hydrolysis kinetics.

We are currently working on better understanding of the gastric digestion of protein gels. Fluorescence Correlation Spectroscopy (FCS) was applied to investigate the diffusivity of pepsin in gel matrices. Scanning Electron Microscopy (SEM) was used to study the surface of undigested and digested gel. We aim at quantifying the microstructural changes of various protein gels during the digestion process.

Knowledge on the kinetics of the pepsin hydrolysis and modelling of the system, combined with techniques such as SEM and FCS should give us insight in the underlying mechanisms of structured protein digestion. By quantifying the diffusion of pepsin, we gained more insight on the action of pepsin and effect of gel structure in protein digestion. Moreover, this approach makes it possible to bridge the digestion process with established physical-chemistry theories and models, which may lead to better knowledge on the underlying mechanisms of gastric digestion.