

A multi-center peptidomic investigation of simulated gastrointestinal food digestion

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Background: Mass spectrometry has become the technique of choice for the simultaneous assessment of a high variety of molecules in complex food matrices. For this reason, it is best suited for precisely monitoring the evolution of digestive processes *in vivo* and *in vitro*. However, due to the variety of equipment available in different laboratories as well as settings, statistical evaluations, and interpretations, it is difficult to predict a priori the ideal parameters for best results.

Methods: The present work addressed that gap by executing an inter-laboratory study with samples collected during *in vitro* digestion and presenting an overview of the state of the art mass spectrometry applications and analytical capabilities available for studying food digestion.

Results: Three representative high-protein foods, skim milk powder, chicken breast and tofu, were digested according to the INFOGEST protocol with sample collection at five time points during gastric and intestinal digestion. Nine laboratories analyzed all digesta with their in house equipment, conventional sample treatment procedure, data evaluation methods, and graphical representation tools.

Conclusions: The compiled results demonstrate a strong consensus among labs in terms of major protein degradation for the three foods matrices and present suitable methodical and statistical approaches for representing the analytical results.



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