In silico predictions of pepsin released peptides

A. Tonda[1], A. Grosvenor[2], S. Clerens[2], S. Le Feunteun[1*]

[1]UMR GMPA, AgroParisTech, INRA, Université Paris-Saclay, 78850, Thiverval-Grignon, France ; [2]Lincoln Research Centre, AgResearch Ltd, Private Bag 4749, Christchurch 8140, New Zealand

* steven.le-feunteun@inra.fr

☐ For oral presentation ☒ For poster presentation (please tick one)

Pepsin is the first protease encountered within the digestive tract. Unlike other digestive proteases, its specificity is low. It is therefore particularly difficult to determine *a priori* which peptides will be released during gastric digestion. Detailed information about food protein truncation during digestion is however critical to understanding and optimizing the availability of bioactives, or limiting allergen release. In this study, a stochastic model which tries to reproduce the dynamics of protein hydrolysis by pepsin is presented. The model is based on pepsin cleavage frequency tables taken from the literature, and makes use of Monte-Carlo *in silico* simulations to quantitatively predict peptides that are likely to be produced by pepsin during the course of the reaction. The proposed model, which requires the expected hydrolysis kinetics and the amino-acid sequence of the studied protein to run, was applied to bovine lactoferrin. Model predictions were then compared with 89 peptides experimentally observed with a peptidomic approach using isobaric labelling during 2h gastric digestion experiments (Grosvenor *et al*., Food and Function, 2014). The model was found to reproduce many real-world features of the case study, such as the relative peptide abundance summary maps along the protein sequence (peptide patterns) or peptide size distribution. It even appeared that 50% of experimentally observed peptides (45/89) fall within the 164 most abundant predicted peptides (over a total of ~ 1500 predicted peptides). These first results illustrate that *in silico* modelling of pepsin hydrolysis is a promising approach to determine which peptides are likely to be released during gastric digestion of foods.