

Development of a peptidomic workflow to apprehend dynamic digestion of a mix of proteins:
application of meat product for elderly

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Meat is known to be a source of protein of good nutritional quality in terms of composition in essential amino acids and digestibility. Evaluation of meat proteins digestibility is a critical issue in regard of various meat product, industrial process and according the digestive physiological status of the consumer. The peptidomic analysis is of a great interest to evaluate this digestibility. The major difficulties of these studies are related to the complexity of meat protein composition and kinetics of the digestion. Therefore, creating a workflow of various techniques (*in vitro* digestion model, mass spectrometry, statistic and bioinformatics) would allow to access to a multivariate proteolysis model.

The main objective of this work was to create a workflow relevant for analysing peptides from a complex meal during digestion. Meat product was chosen as an example

Dynamic digestive conditions: Two *in vitro* gastric physiological conditions of digestion were applied using DIDGI©: adult / elderly. Three repetitions of digestion were done. Five samplings were realized in gastric phase at 30, 60, 90, 120 and 150 min to analyze the kinetics of peptide production of meat.

Mass spectrometry analysis: Identification and quantification of peptides generated by gastric digestion of meat model were performed using LC-MS/MS analysis (Q Exactive plus ThermoFisher) and Progenesis Q1 (Waters) and/or Mascot (www.matrixscience.com).

Statistics/Bioinformatics: Analysis of kinetic were realized using hierarchical clustering non-supervised method and a fitting method was tested to compare proteins kinetics. Peptigram a web application was used to visualize protein hydrolysis.

This combined approach permitted to analyse senior and adult protein digestion. Specific protein hydrolysis kinetic were obtained.