# Impact of thermal treatment on the nutritional quality of pea protein ingredients produced by dry and wet fractionation processing

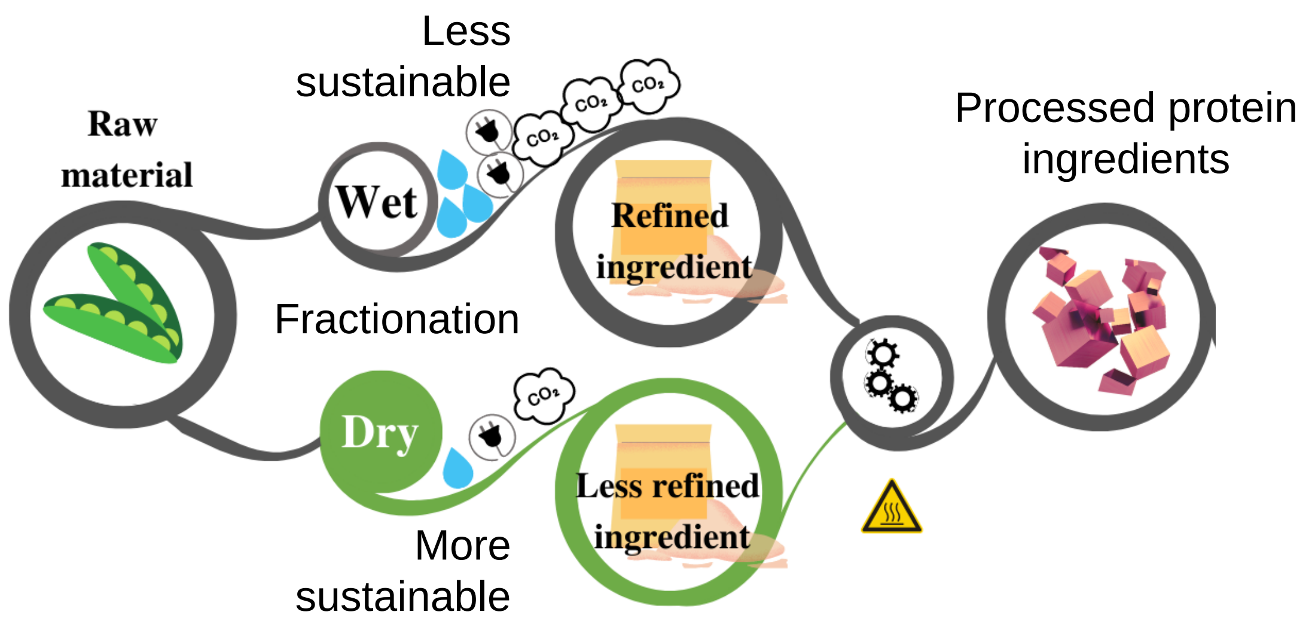
**Patrícia Duque-Estrada**[1], Maarten A. I. Schutyser[2], Atze Jan van der Goot[2], Iben L. Petersen[1]

1. Department of Food Science, Food Analytics and Biotechnology Section, University of Copenhagen, Denmark.
2. Food Process Engineering, Wageningen University & Research, The Netherlands.

**patricia.estrada@food.ku.dk**

## 1. Background

A strategy commonly used to enhance the protein digestibility in plant protein ingredients is to apply thermal treatment to reduce antinutritional factors. However, depending on the conditions applied, the processing can also negatively impact protein structures and compositions, resulting in reduced protein digestibility.



Different levels of processing can yield varying degrees of protein nutritional quality in the final food product.

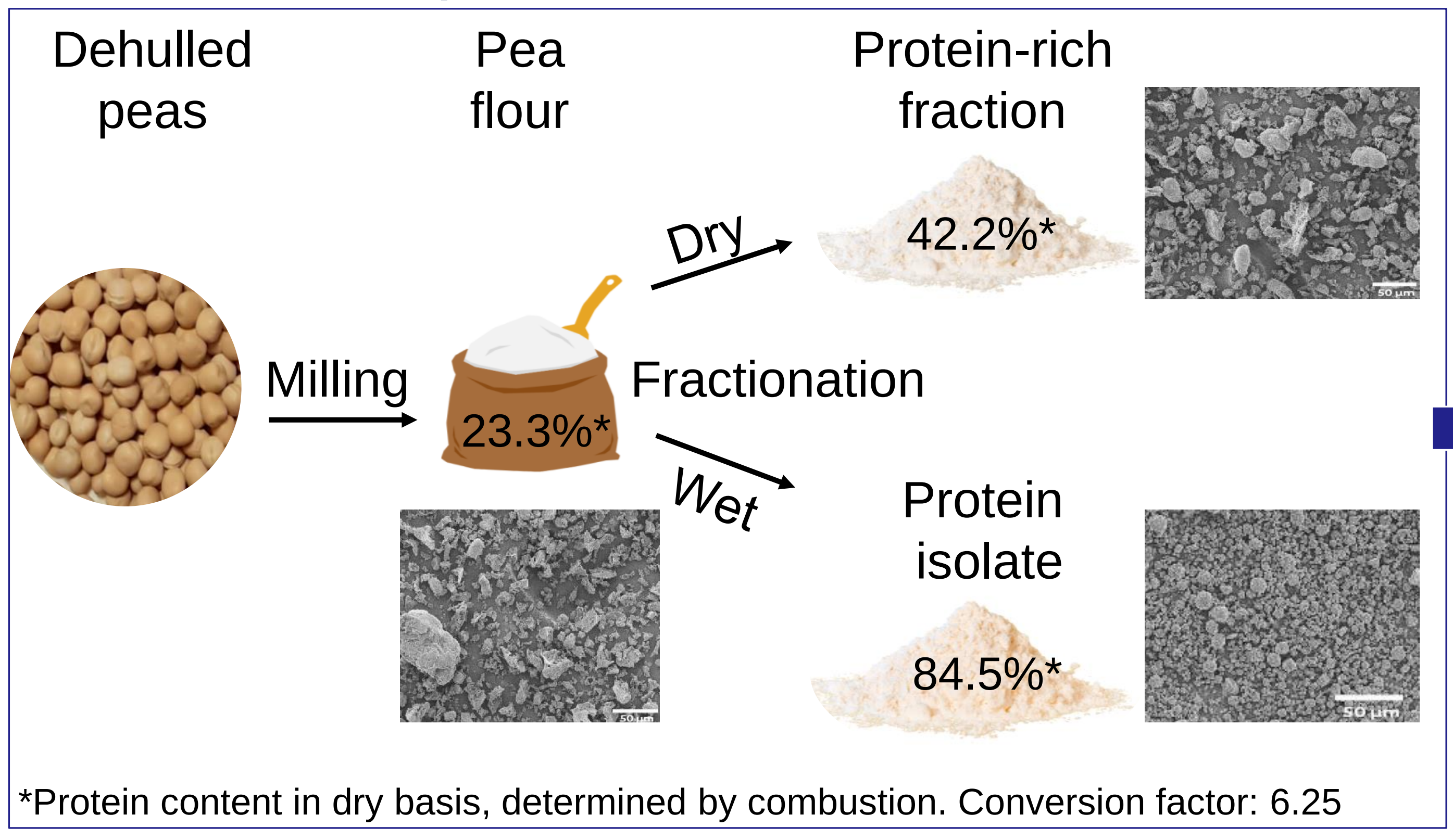
## 2. Aim & Perspectives

**Aim:** to determine the effect of thermal treatment on the *in vitro* digestibility of pea protein ingredients produced by dry and wet fractionation.

**Perspectives:** contribute to establish optimal processing conditions that simultaneously prioritize high protein nutritional quality and sustainability of plant-based foods.

## 3. Material & Methods

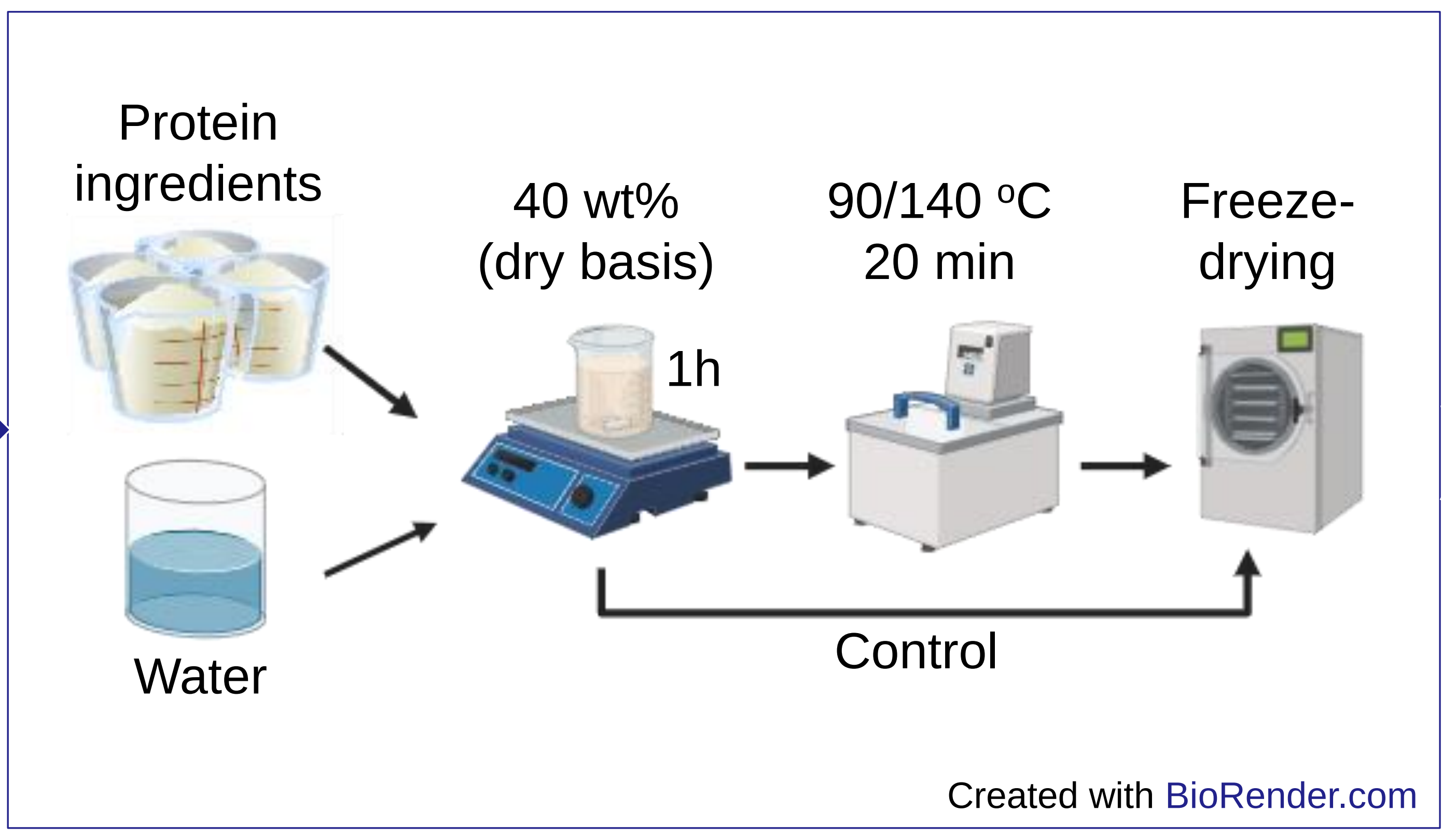
### Fractionation process



*Protein content in dry basis, determined by combustion. Conversion factor: 6.25

Air classification (dry fractionation)[1]: classifier wheel speed of 5000 rpm and airflow of 52 m$^3$/h. Wet fractionation: aqueous acid extraction followed by isoelectric precipitation.

### Thermal treatment



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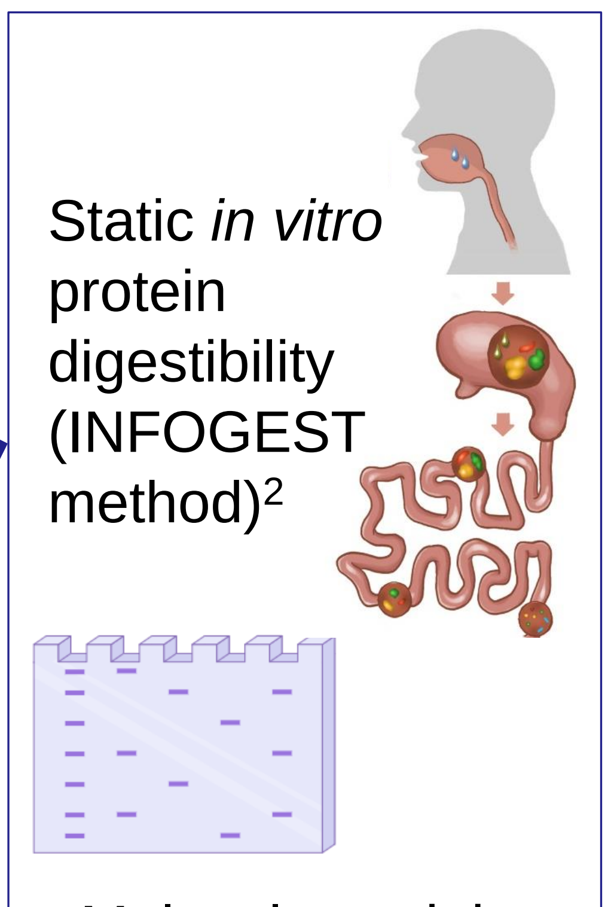
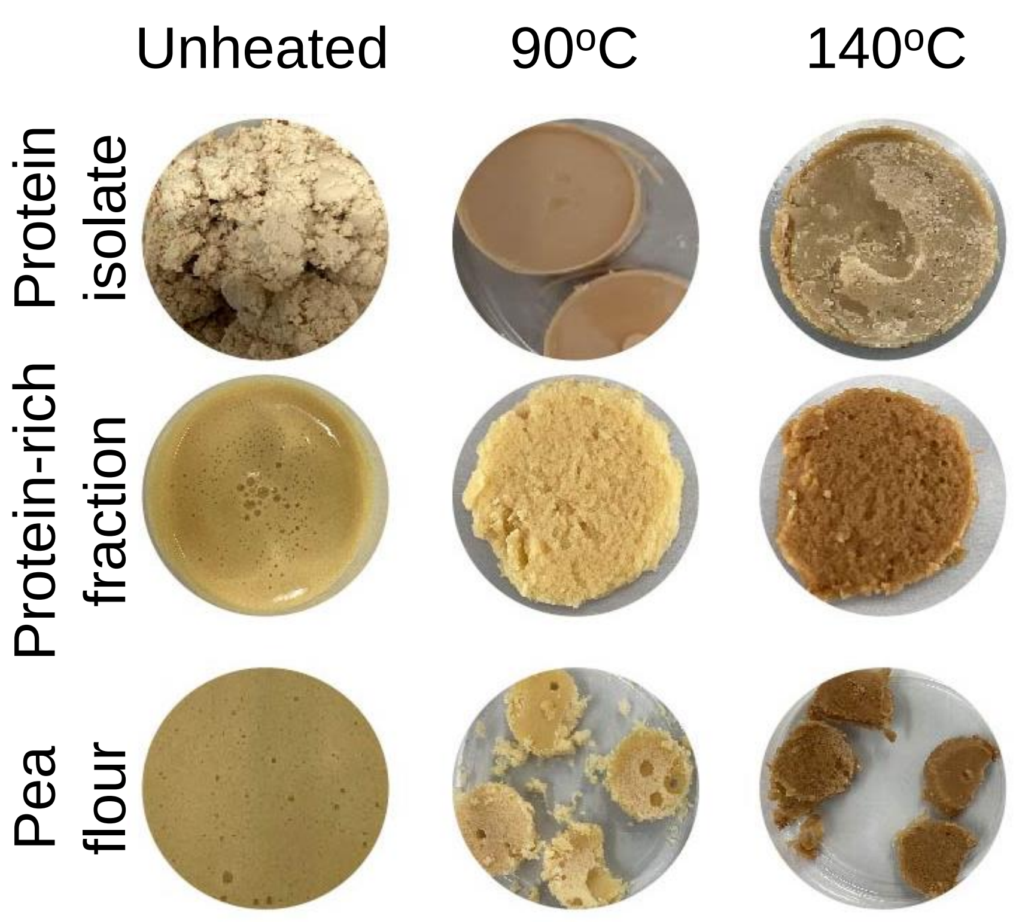
### Analyses



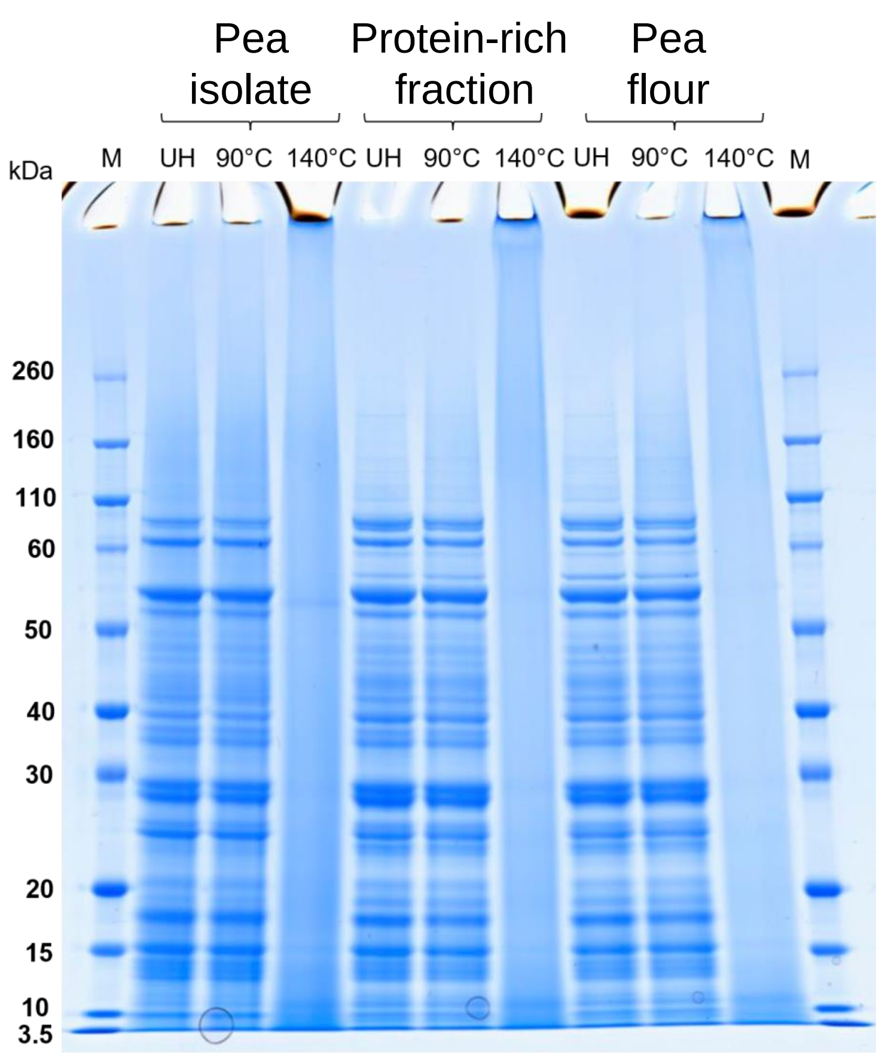
Molecular weight distribution by electrophoresis

## 4. Results

### Protein ingredients before and after thermal treatment

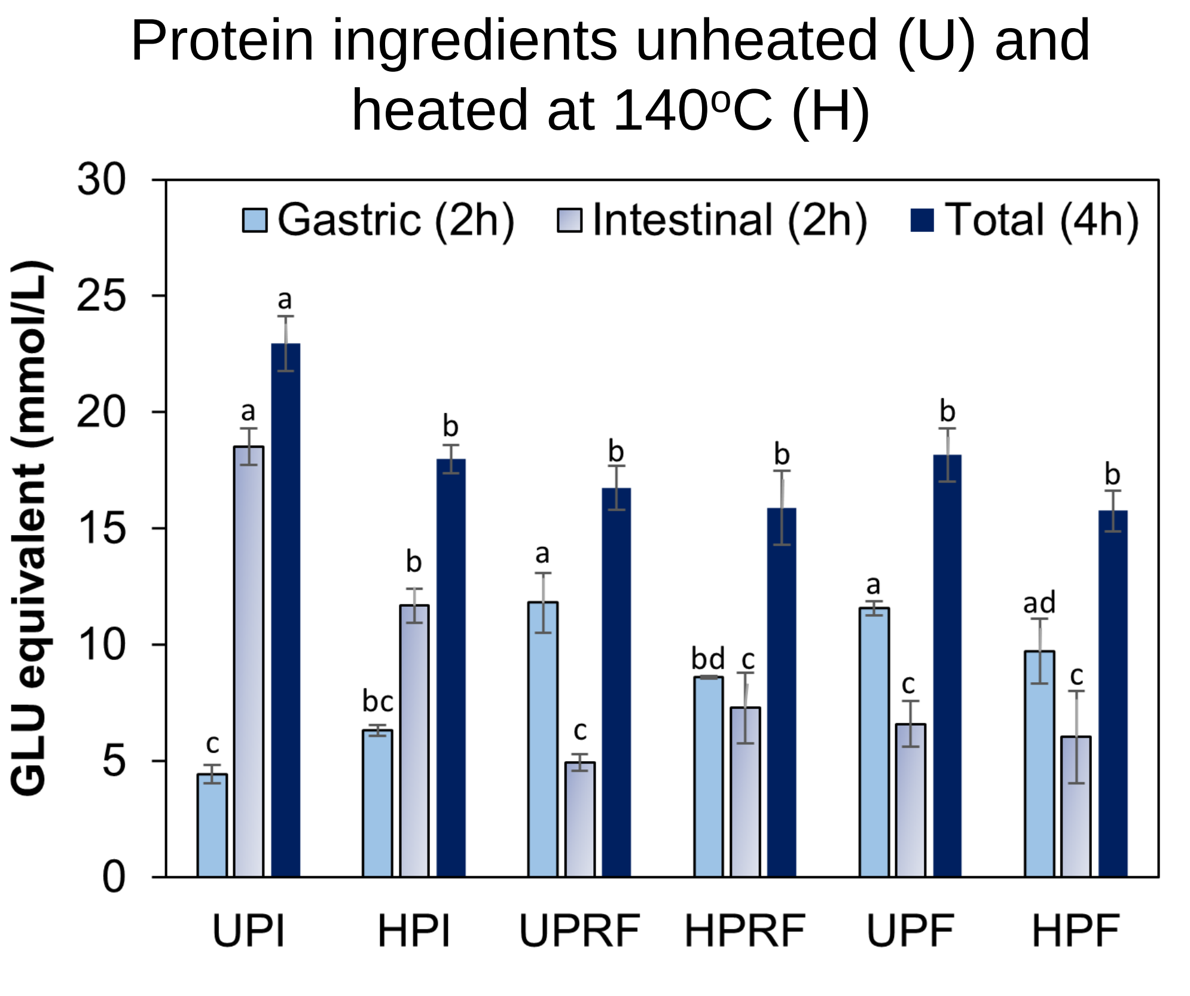


### SDS-PAGE



Molecular weight distribution of protein ingredients unheated (UH) and heated obtained by Sodium Dodecylsulfate Polyacrylamide Gel Electrophoresis (SDS-PAGE) under reducing conditions. M: molecular marker.

### *In vitro* protein digestion using INFOGEST



Release of free amino groups during *in vitro* digestion shown as glutamic acid (GLU) equivalent. Results were corrected with a protein-free cookie. Total digestion represents gastric and intestinal phase (4h). Error bars represent standard deviation of three independent measurements. Values within the same digestion phase with different letters are significantly different (One-way ANOVA followed by Tukey´s post hoc test, $p < 0.05$). PI: pea isolate. PRF: protein-rich fraction. PF: pea flour.

## 5. Conclusions

- Thermal treatment at 140ºC induced protein aggregation in all protein ingredients.
- Heating pea isolate at 140ºC decreased the release of free amino groups after 4h digestion.
- Pea flour and protein-rich fraction showed similar digestion pattern before and after the thermal treatment.

**Reference:**

1. Pelgrom, P. J. M. et al. (2013). Dry fractionation for production of functional pea protein concentrates. *Food Research International*, *53*(1), 232–239.

2. Sousa, R. et al. (2023). *In vitro* digestibility of dietary proteins and *in vitro* DIAAS analytical workflow based on the INFOGEST static protocol and its validation with *in vivo* data. *Food Chemistry*, 404, 134720.

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