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Understanding how the structure of dairy matrices affects protein hydrolysis in the gastrointestinal tract.

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Objectives

Understanding and modeling the influence of food structure and of food constituents interactions (i.e food matrix) on proteolysis (prediction of peptides profiles):

-2 well-studied milk proteins :
β-lactoglobulin and caseins

-2 technological processes tested:
→ thermal treatment(90°C-10min)
→ acid and rennet gelation



Materials & Methods

5 matrices (composition= 50g proteins/L): liquid vs. gel gelation during 24h at 20°C

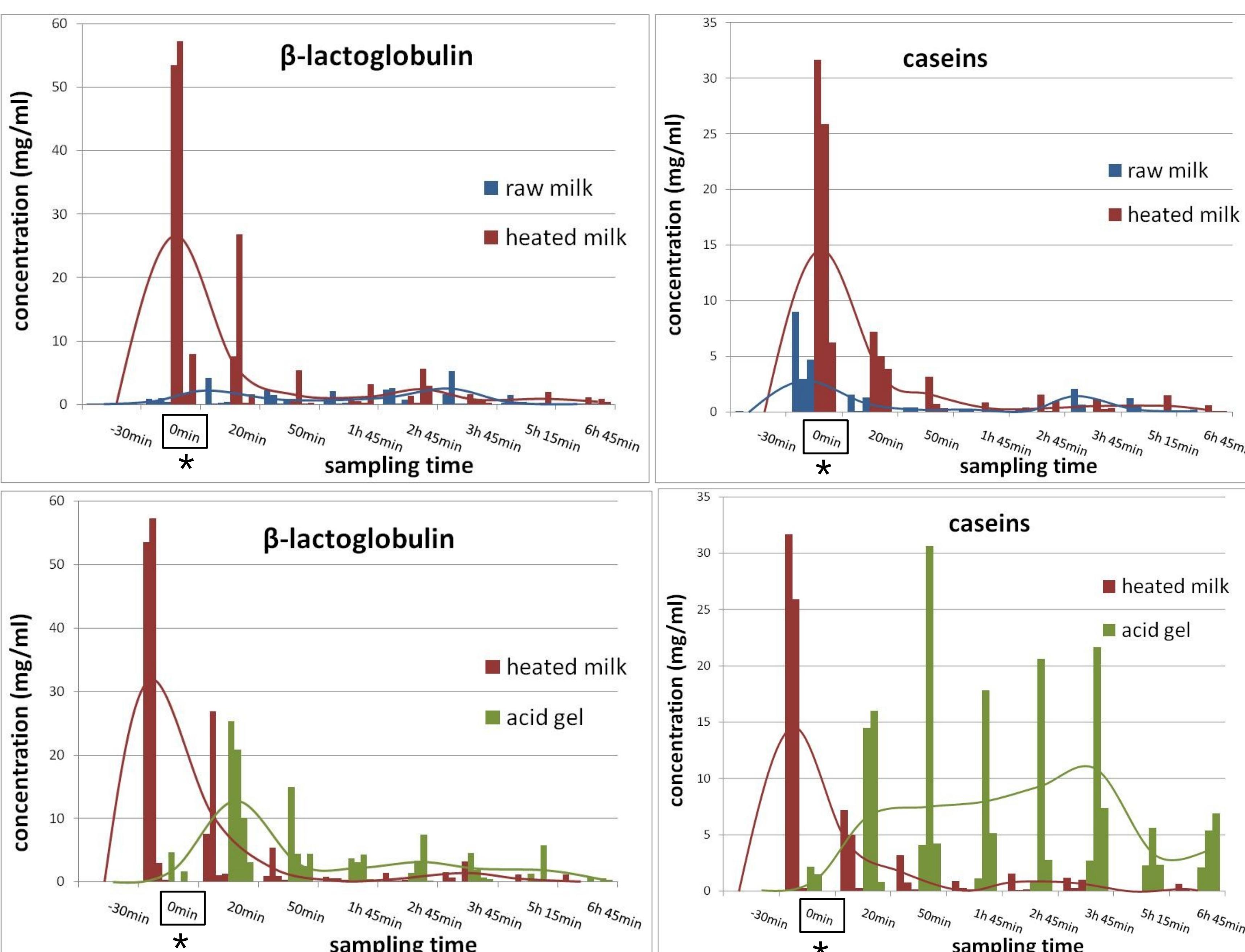
- defatted milk (Ultra Low Heat powder)= raw milk
- defatted milk + rennet= raw rennet gel
- defatted milk+ thermal treatment TT 90°C-10min= heated milk
- defatted milk + TT+ gluconodeltalactone= acid gel
- defatted milk + TT+ rennet= heated rennet gel

6 mini-pigs : 2 T-shaped cannulas
(end of stomach and mid-jejunum)

sampling kinetics: 9 samples until 7 hours after matrix ingestion

analyses: SDS-PAGE and ELISA

Preliminary results (end of stomach) & Discussion



raw milk/heated milk:

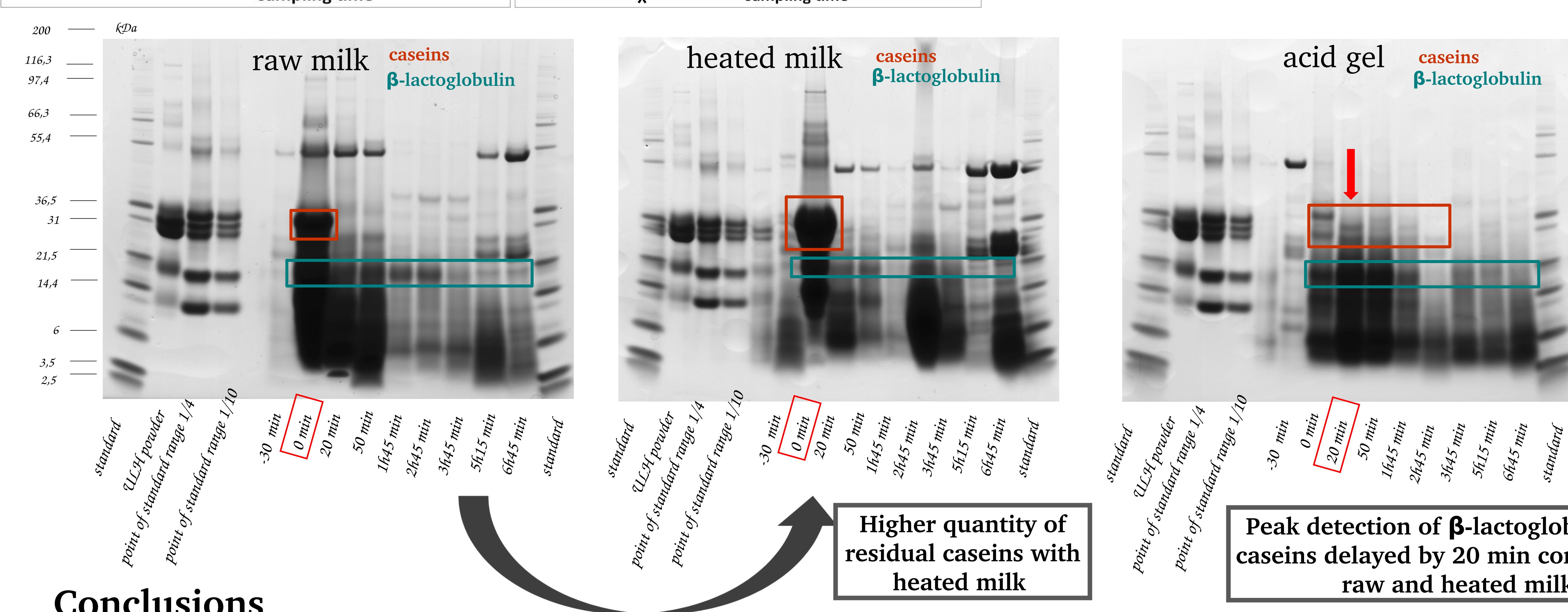
thermal treatment (90°C-10min) → β-lactoglobulin and caseins become resistant to proteolysis until 2h45 min after matrix ingestion

heated milk/acid gel:

acid gelation → the peak of β-lactoglobulin and caseins immunodetection is delayed (20 min) compared to that observed with heated milk

hypothesis:

acid gel ingestion → formation of a denser coagulum in the stomach with slowing down of gastric emptying



ELISA results confirmed by SDS-PAGE

Conclusions

These preliminary results show an influence of the food matrix (structure and microstructure) on the kinetics of milk protein digestion *in vivo*.

