Protein structure within infant milk formulas impact their in vitro dynamic digestion.

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DO PROTEIN STRUCTURE AND COMPOSITION WITHIN INFANT MILK FORMULAS IMPACT DIGESTIVE KINETICS ?

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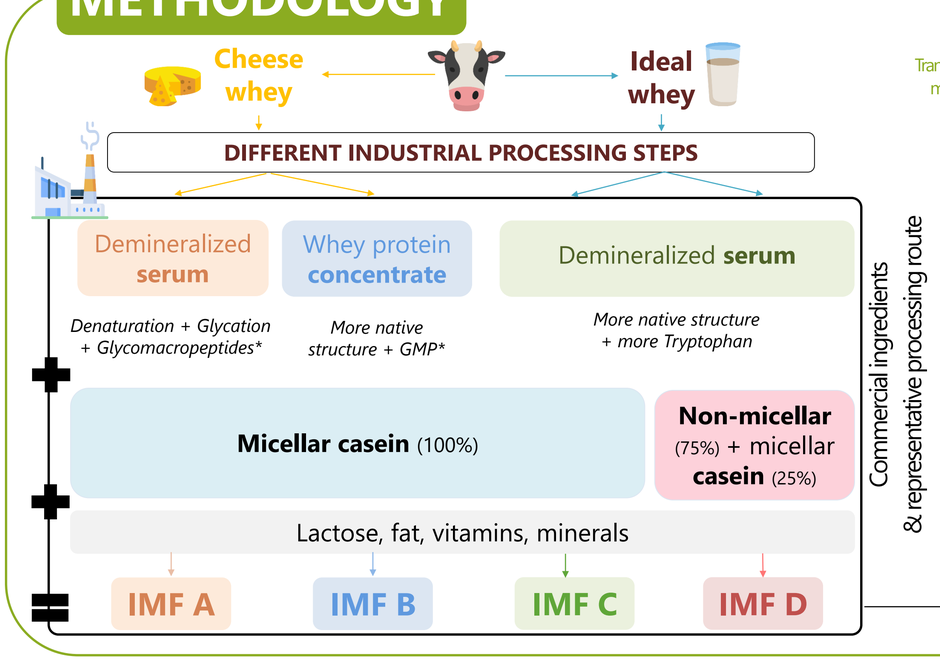
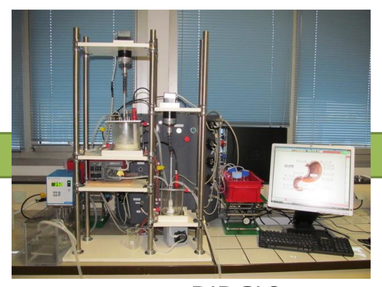
INTRODUCTION and OBJECTIVE

Infant formulas, the only **adequate substitute** to **breastmilk**, are complex matrices that require **numerous ingredients and processing steps** that both can vary among manufacturers and affects IF quality. A part of this thesis aims to understand **how protein structure** and **composition within dairy ingredients impact Infant Milk Formulas** (IMFs) **structure and digestive kinetics** using *in vitro* model mimicking infant stage.

METHODOLOGY



4-week-old infant
Ménard et *al.* (2015) and De Oliveira et *al.* (2016)



DIDGI® system

***In vitro* dynamic digestive model**

DIGESTA

Structure
- Confocal laser scanning microscopy
- Laser light scattering

Proteolysis
- Semi-quantification of intact protein (SDS-PAGE)
- Peptide identification and quantification (LC-MS/MS)
- Hydrolysis degree (OPA)
- Amino-acid bioaccesibility (Ion-exchange chromatography)

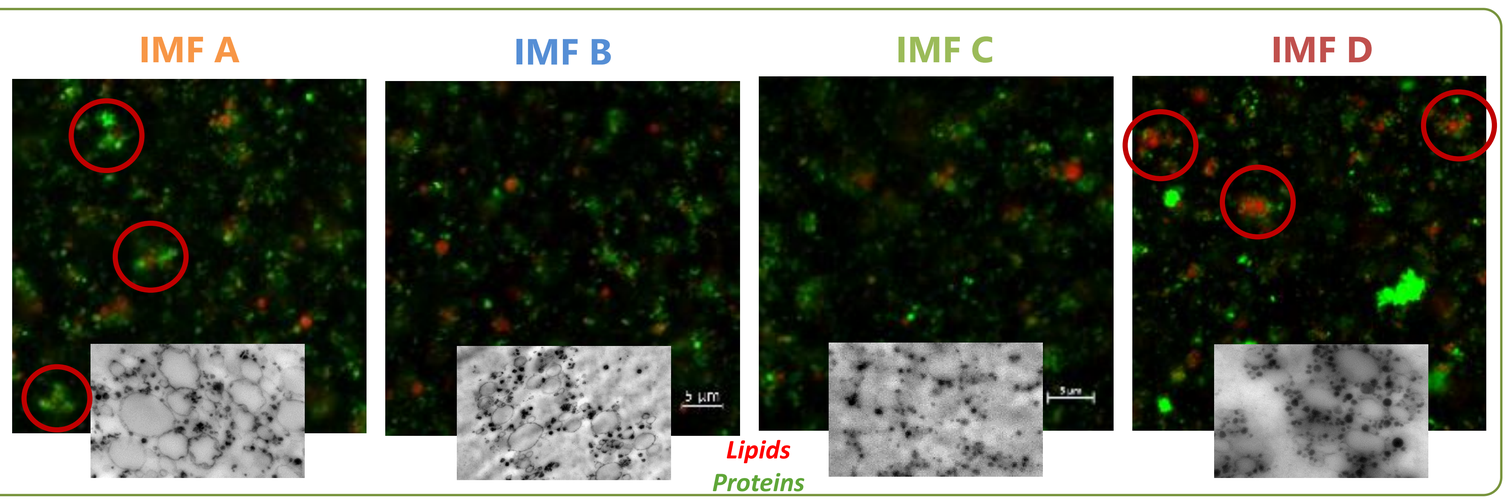
Lipolysis (GC-MS)

RESULTS

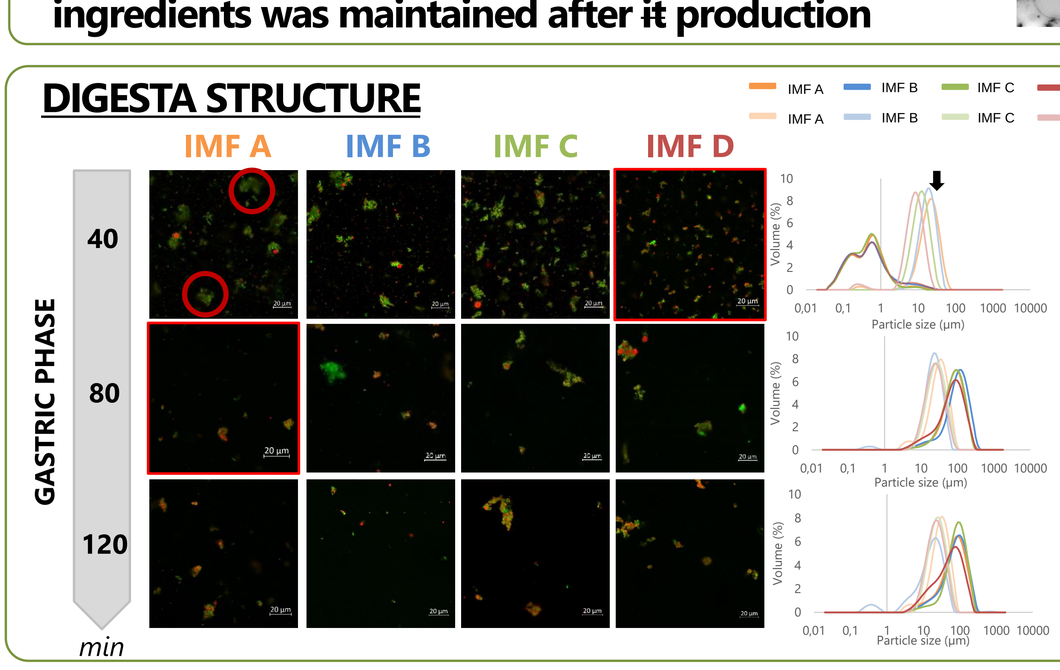
IMFs STRUCTURE

- **IMF A :** star-shape lipoprotein structure, glycated whey proteins
- **IMF B :** no particular shape or size of the lipoprotein structures
- **IMF C :** no particular shape or size of lipoprotein structures
- **IMF D :** large lipoprotein structures covered by numerous caseins structures

Differences of structure among protein ingredients was maintained after it production



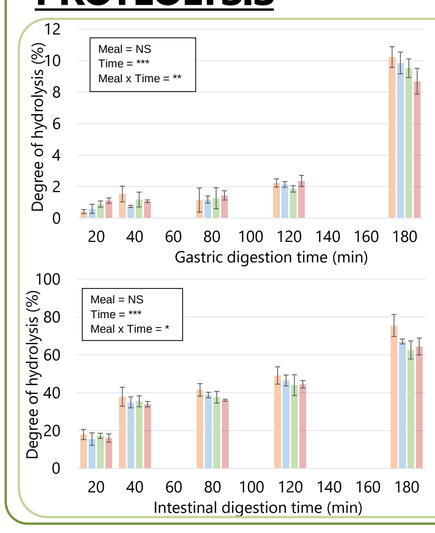
DIGESTA STRUCTURE



HIGHLIGHTS :

- At 40 minutes of gastric phase, **IMFs A and B** showed **larger** lipoprotein **structures compared to IMFs C and D. IMF D** presented **smaller particles than IMF C which can be attributed to the presence of modified casein form. At G40,** the **aggregation** observed **was caused by fat droplets flocculation** since the addition of SDS allowed to return to initial particle size distribution.
- At 80 minutes of gastric phase, **IMF A** had **smaller lipoprotein** particles than the other IMFs which could be **due to hindered casein coagulation caused by the binding of denatured WPs aggregates** at the interface of casein micelles **impairing hydrolysis of κ-casein**
- At G120, IMFs **B, C and D** still had **smaller lipoprotein structures than IMF A.**

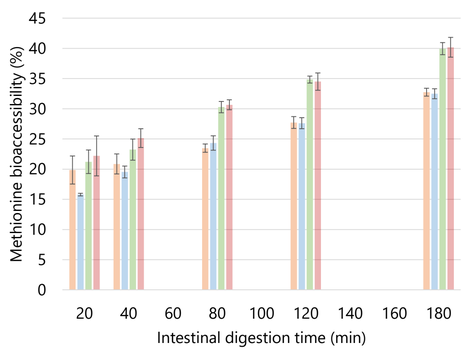
PROTEOLYSIS



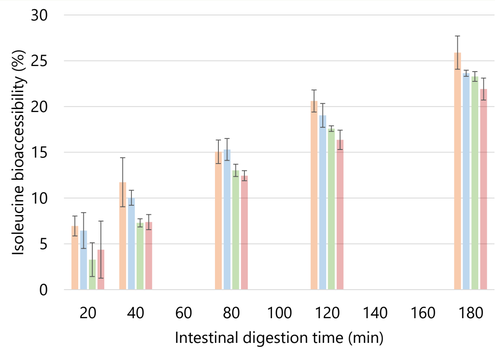
- At the **end** of **gastric phase, IMF A** was **more hydrolysed than IMF D**

The proteolysis was different among IMFs at the end of digestion

- At the **end** of **intestinal phase, IMF A** was **more hydrolysed than IMF C**



- **IMFs C and D** had **higher methionine bioaccesibility** than IMFs A and B → link between **Met bioaccesibility** and **denaturation rates**



- **IMF A** had **higher isoleucine bioaccesibility** than IMFs C and D → linked to the nature of protein and it structure itself

Amino acid bioaccesibility during intestinal phase was different among IMFs

Peptides (including bioactive ones) release kinetics were also different among IMFs

CONCLUSION and PERSPECTIVES

Dairy protein ingredient quality (structure and composition) was shown to have an **impact on IMF structure** and **their hydrolysis** using a *in vitro* dynamic model of infant digestion. **Further investigations** will be performed to determine postprandial **plasma amino acid kinetics** and **physiological impacts** using an *in vivo* model of infants.

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