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

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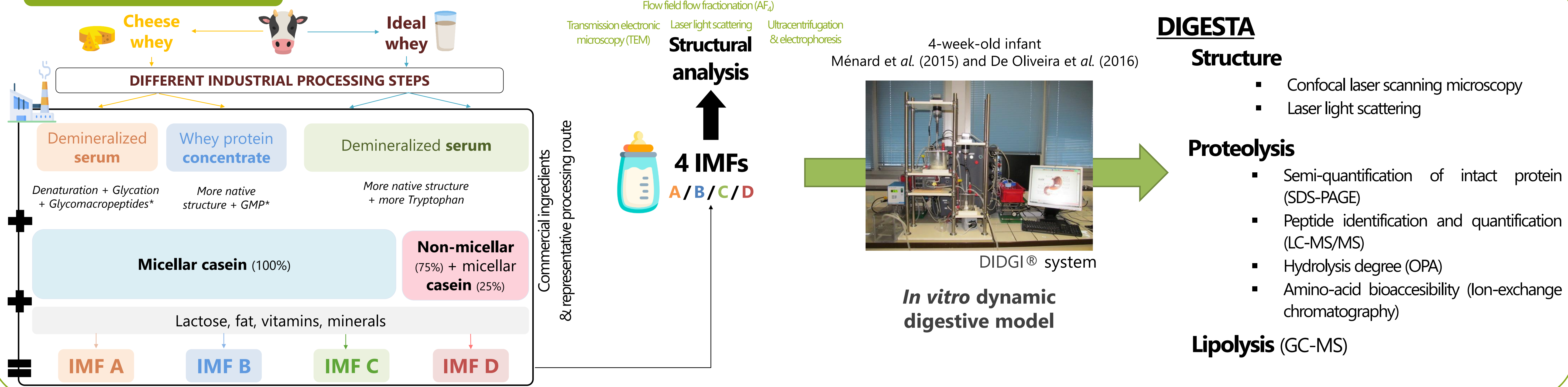
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## INTRODUCTION and OBJECTIVE

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

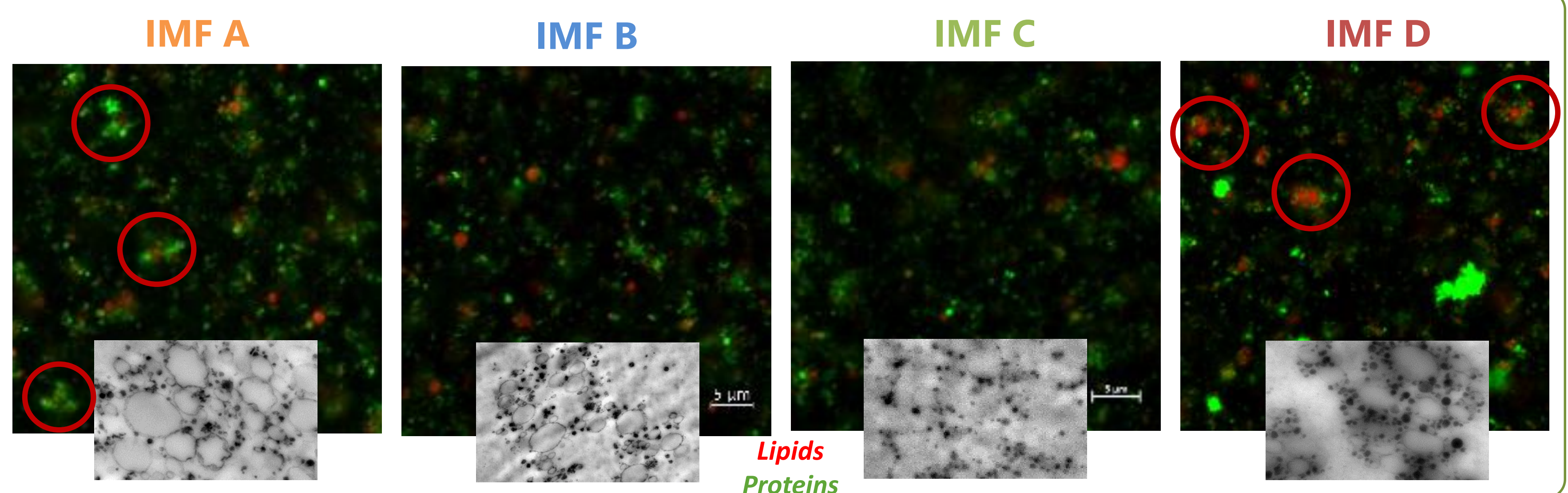


## RESULTS

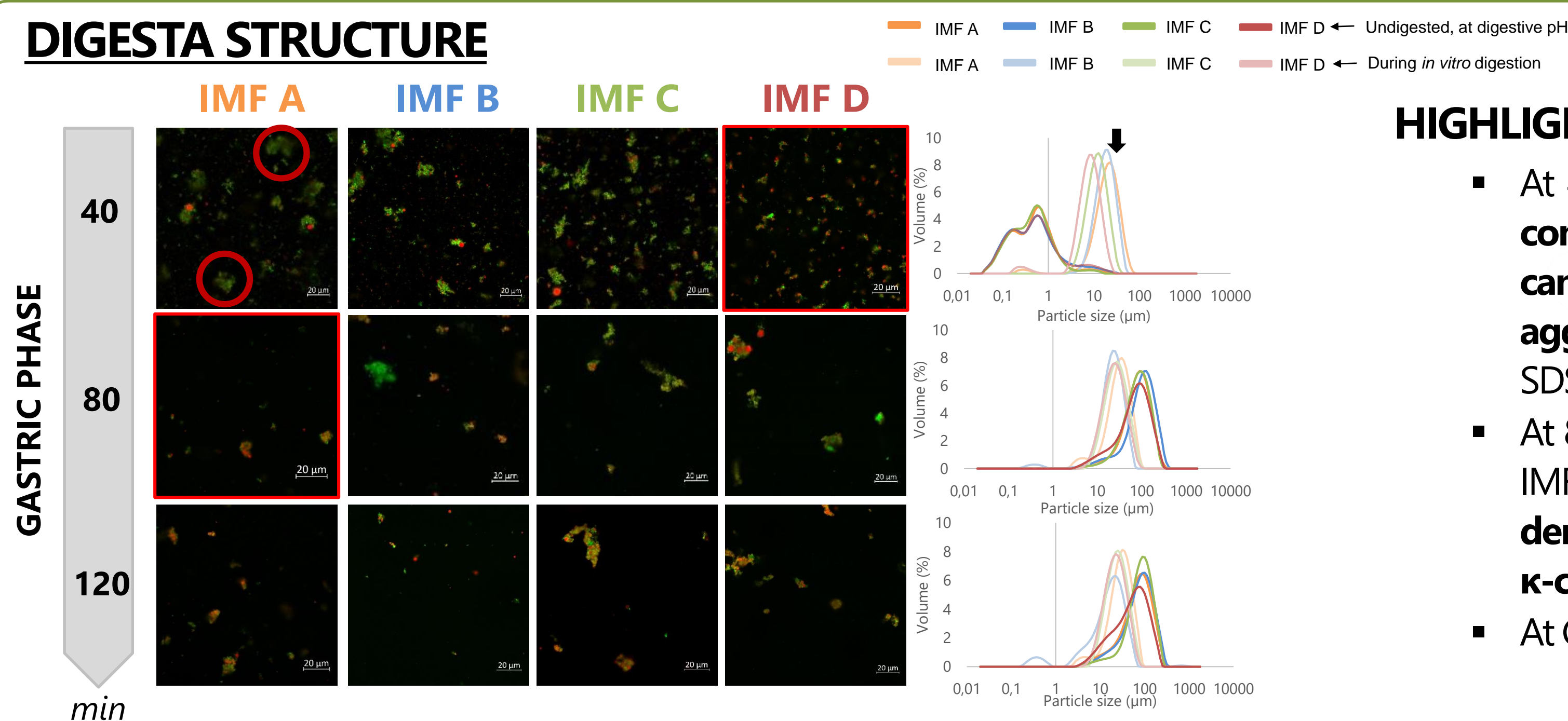
### IMFs STRUCTURE

- IMF A**: star-shape lipoprotein structure, glycosylated 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

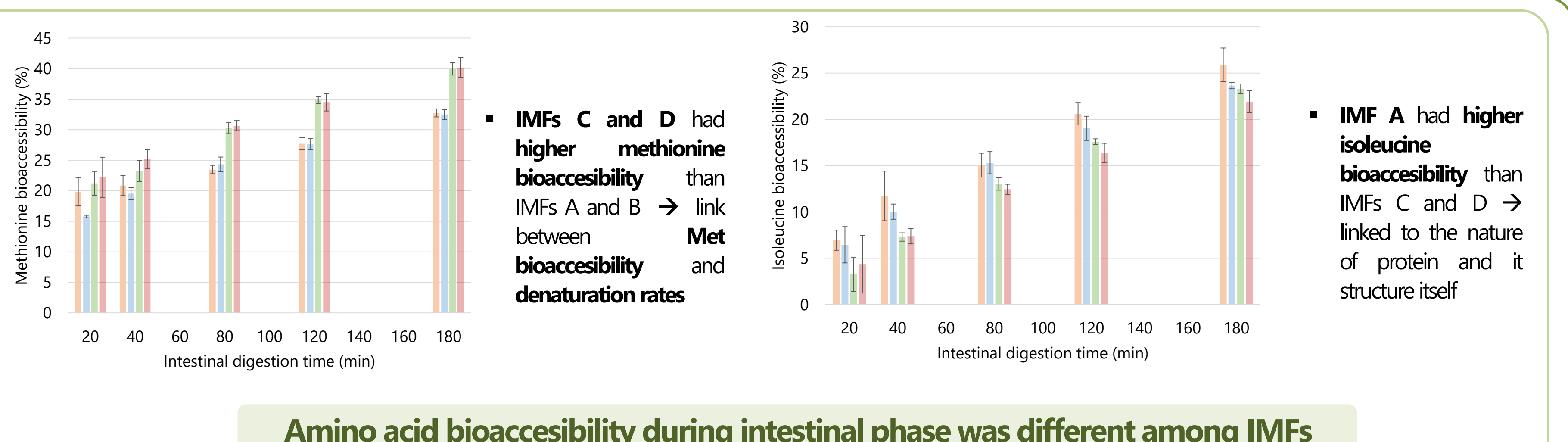
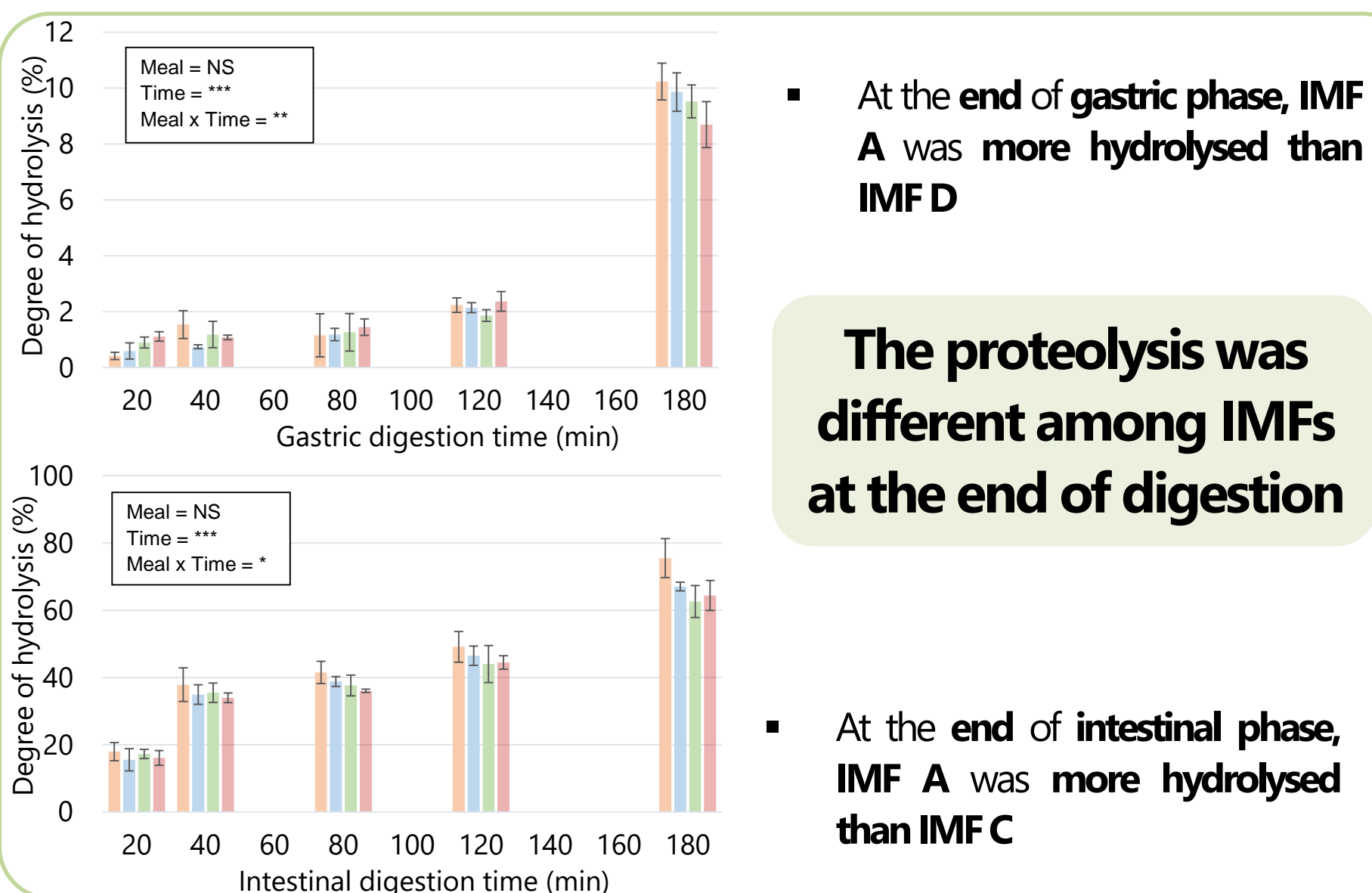
Differences of structure among protein ingredients was maintained after its production



### DIGESTA STRUCTURE



### PROTEOLYSIS



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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