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

Lucile Chauvet, Alexy Brunel, Olivia Ménard, Yann Le Gouar, Julien Jardin, Thomas Croguennec, Isabelle Luron Le Huërou-Luron, Didier Dupont, Marion Lemaire, Amélie Deglaire

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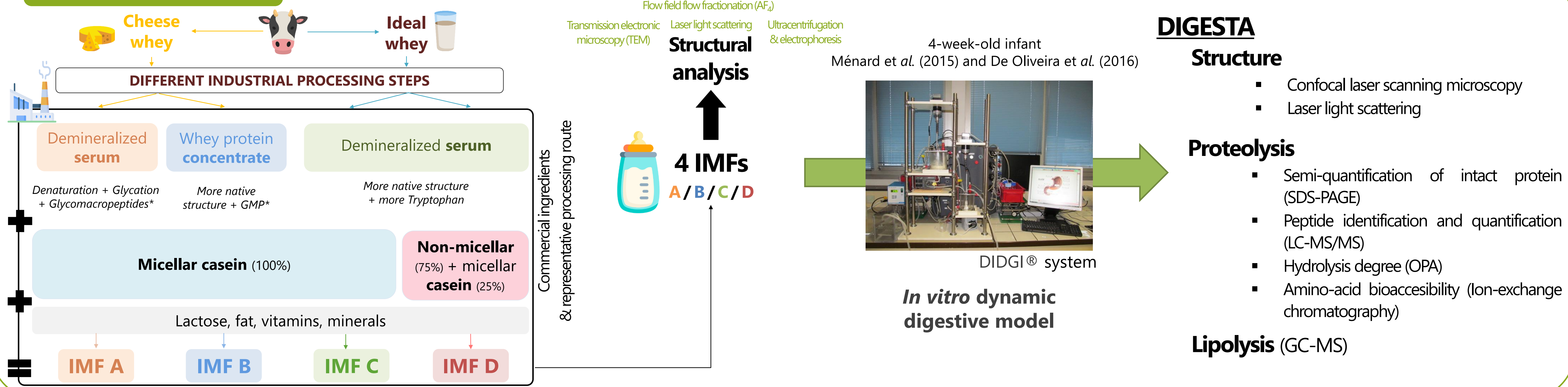
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CHAUVET L.^{1,2}, MÉNARD O.¹, LE GOUAR Y.¹, JARDIN J.¹, HENNETIER M.³, CROGUENNEC T.¹, VAN AUDENHAEGE M.², DUPONT D.¹, LEMAIRE M.², DEGLAIRE A.¹

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

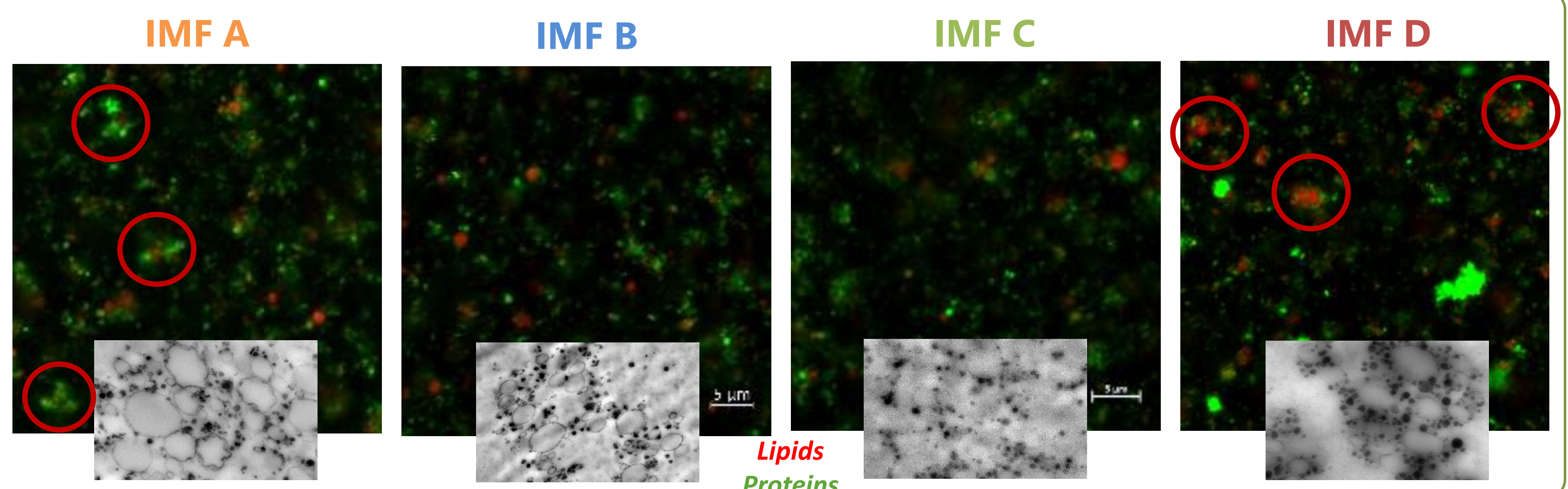


RESULTS

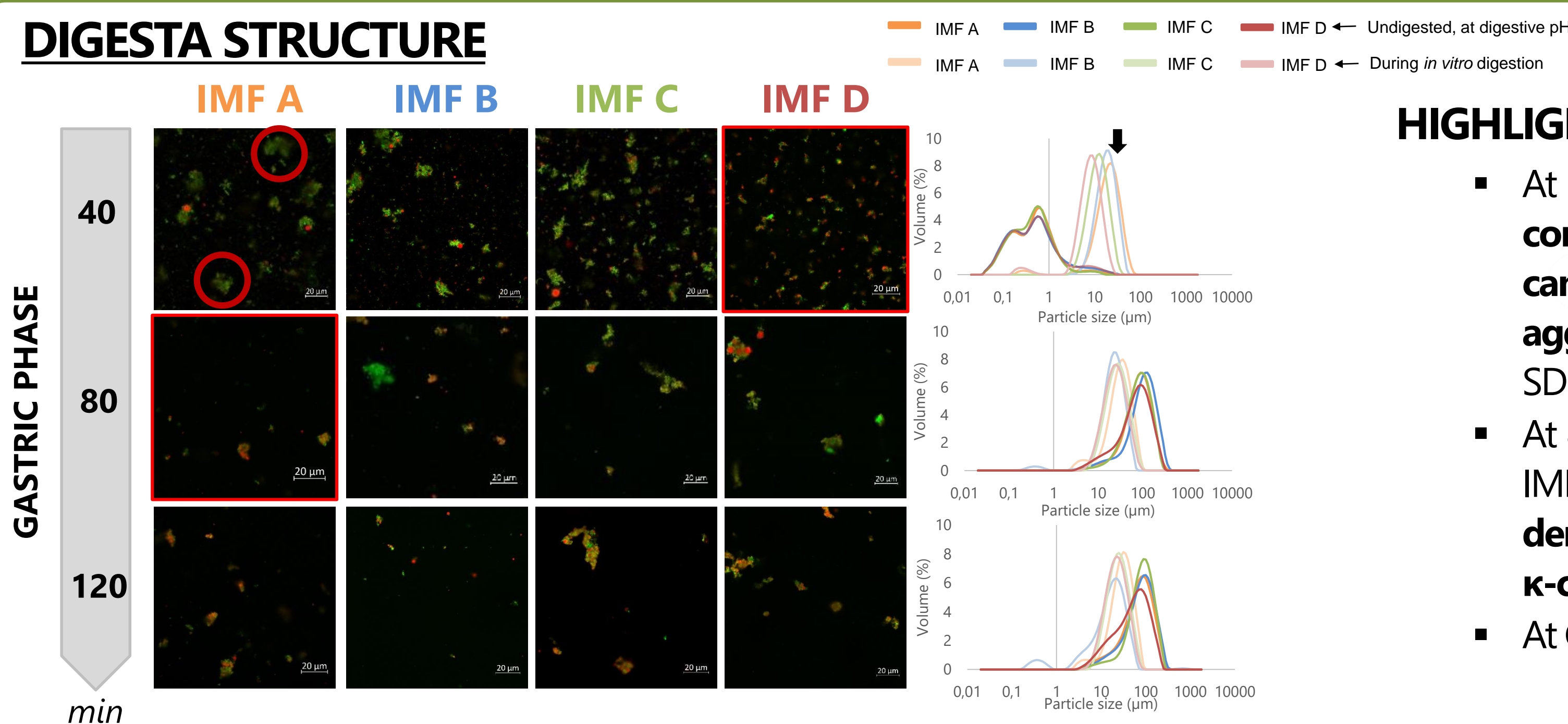
IMFs STRUCTURE

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

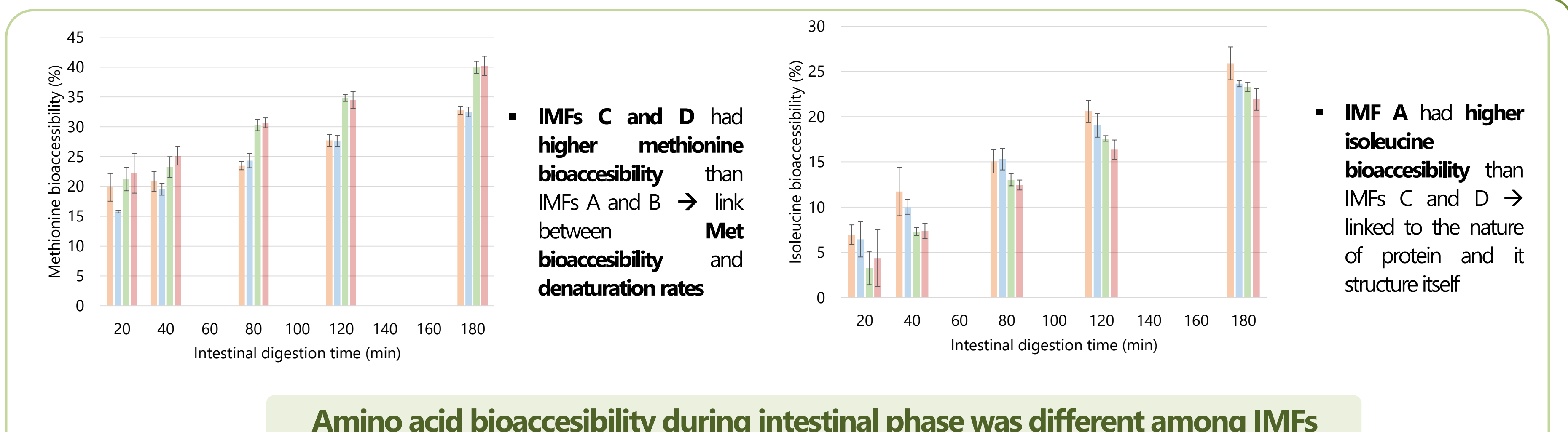
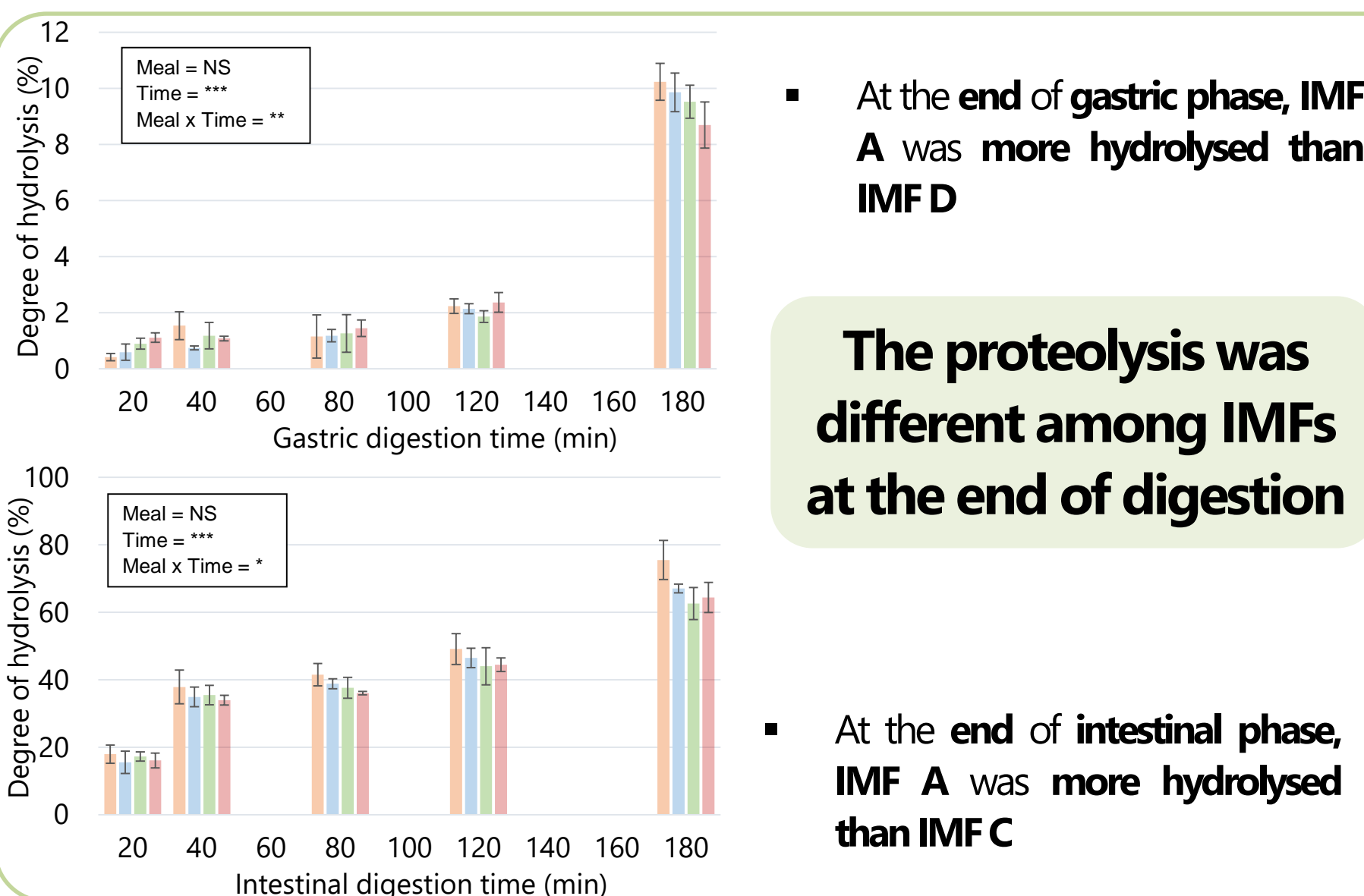
Differences of structure among protein ingredients was maintained after its production



DIGESTA STRUCTURE



PROTEOLYSIS



Amino acid bioaccessibility 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.

¹ UMR STLO, INRAE, Institut Agro-Rennes Angers, Rennes

² SODIAAL International, Direction Recherche & Innovation, Rennes

³ Université de Toulouse, Institut National Polytechnique de Toulouse – Ecole d'ingénieur de Purpan, Département Sciences Agronomique et Agroalimentaire, Toulouse.