Comparaison of dynamic in vitro digestion of human milk vs standard infant formula to better understand their digestive kinetics

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COMPARISON OF DYNAMIC *IN VITRO* DIGESTION OF HUMAN MILK VS. STANDARD INFANT FORMULA TO BETTER UNDERTAND THEIR DIGESTIVE KINETICS

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INTRODUCTION and OBJECTIVE

Human milk (HM) is an **optimal** bioactive fluid, which **meets** infant **requirement** and is frequently **substituted** by **infant formula** (IF).
These two infant diets are assumed to have **different digestion kinetics** although they are **rarely** directly **compared**.
The present study aimed to **evaluate the digestion kinetics** and **the structure evolution** using the DIDGI® **dynamic digestion** system at the infant stage

METHODOLOGY

***In vitro* digestion**

DIDGI® system

Human Milk: Pool of 50 **raw** milk samples
Lactation time: 1.8 - 2 months post-delivery
1.0% true proteins, 2.8% lipids

Infant formula: NativIF basic IF powder (Yu et al. 2021)
Rehydrated at **1.4% true proteins, 3.2% lipids**

Parameters based on literature (Roman et al. 2007.; Bourlieu et al 2014):

- Gradual decrease of gastric pH → $pH = 8 \times 10^{-5} \times time^2 - 0{,}031 \times time + pH_{meal}$
- Enzymes: Rabbit Gastric Extract + Porcine pancreatin. Bovine bile
- Gastric emptying by Elashoff fitting (half-time emptying – $T_{1/2\ HM}$ = 47 min ; $T_{1/2\ IF}$ = 78 min).

Sampling times (min of digestion):

- Diet (G0)
- Gastric phase: G20, G40, G80, G120, G180*
- Intestinal phase: I20, I40, I80, I120, I180

**only for IF sampling*

MACROSCOPY Scale → MOLECULAR scale

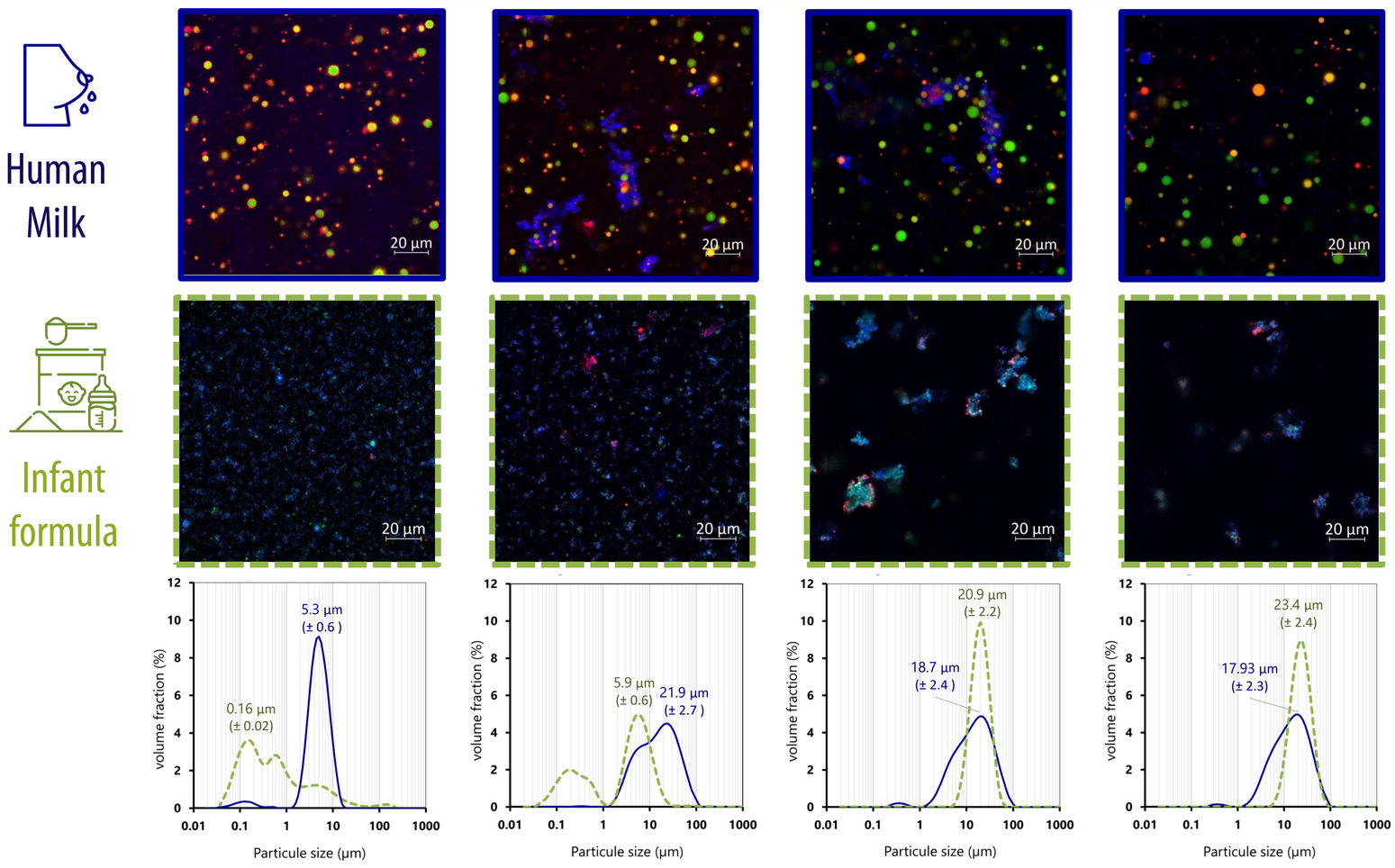
Evolution of the matrix structure
- Laser light scattering
- Confocal microscopy(Confocal Zeiss)

Lipolysis & Proteolysis
- GC : Gas chromatography
- SDS-Page
- OPA

RESULTS

Human milk — Infant formula

Structure: G0 G40 G80 G120 Time (min)

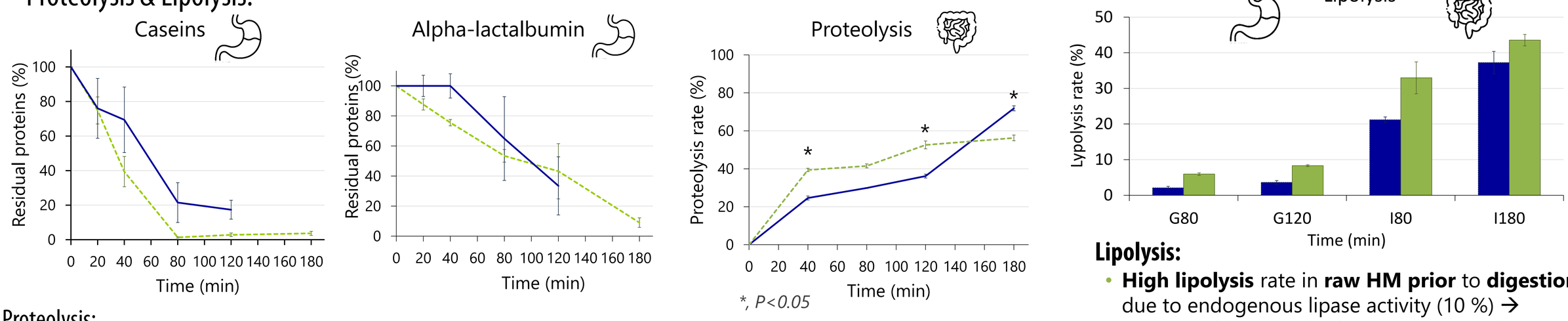


- Apolar lipid
- Proteins
- Amphiphilic molecules

Highlights :

- **HM fat globules** were sized around **5 µm** while **IF fat droplets** were sized under 1 µm. HM fat globules remained present across time.
- **Particle aggregation** specifically protein one was **faster in stomach** during **HM** digestion (40 min) than in IF (80 min).
- **Final** aggregate **sizes** were more **heterogenous** for **HM**.
  - For **HM**, particle size was due to protein aggregation and **remaining native fat globules**.
  - For **IF**, **high** particle **size** observed **after 80 min** was due to **protein aggregation**.

Proteolysis & Lipolysis: Representation corrected by meal dilution and emptying (*Mean ± SEM*)



Proteolysis:
- **No** significant **difference** between **caseins** and **alpha-lactalbumin release** between diets, although HM proteins tended to be more resistant in the gastric phase.
- **Proteolysis** was significantly **lower** in **HM** at **I40** and **I120**. Faster proteolysis for IF during the first digestion times.

Lipolysis:
- **High lipolysis** rate in **raw HM prior** to **digestion** due to endogenous lipase activity (10 %) → subtracted here for lipolysis rate during digestion
- **Lipolysis** was **not** significantly **different** although it tended to be faster for IF during the early intestinal digestion phase.

CONCLUSION

Despite nutritional similarity, this study highlights that the **influence** of the **matrix** on the **structure of the digesta** and on the **digestion kinetics** and gives some **further understanding** to the **global value of digestibility**, such as determined *in vivo*.

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