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UMR INRAE – L'Institut Agro Rennes Angers
Science et technologie du lait et de l'œuf

MicroBio team
Microbiology of milk and egg sectors

Keywords
Human milk microbiota
Gut homeostasis
Immunity
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Intestinal microbiota

Funding

Région Bretagne
Région Pays de la Loire
Bba Milk Valley

Collaborators

numecan nutrition•métabolismes•cancer
Valorial OSONS L'ALIMENT PLUS INTELLIGENT

STLO
L'institut agro Rennes Angers
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Role of breast milk bacteria on gut homeostasis

Socio-economic context

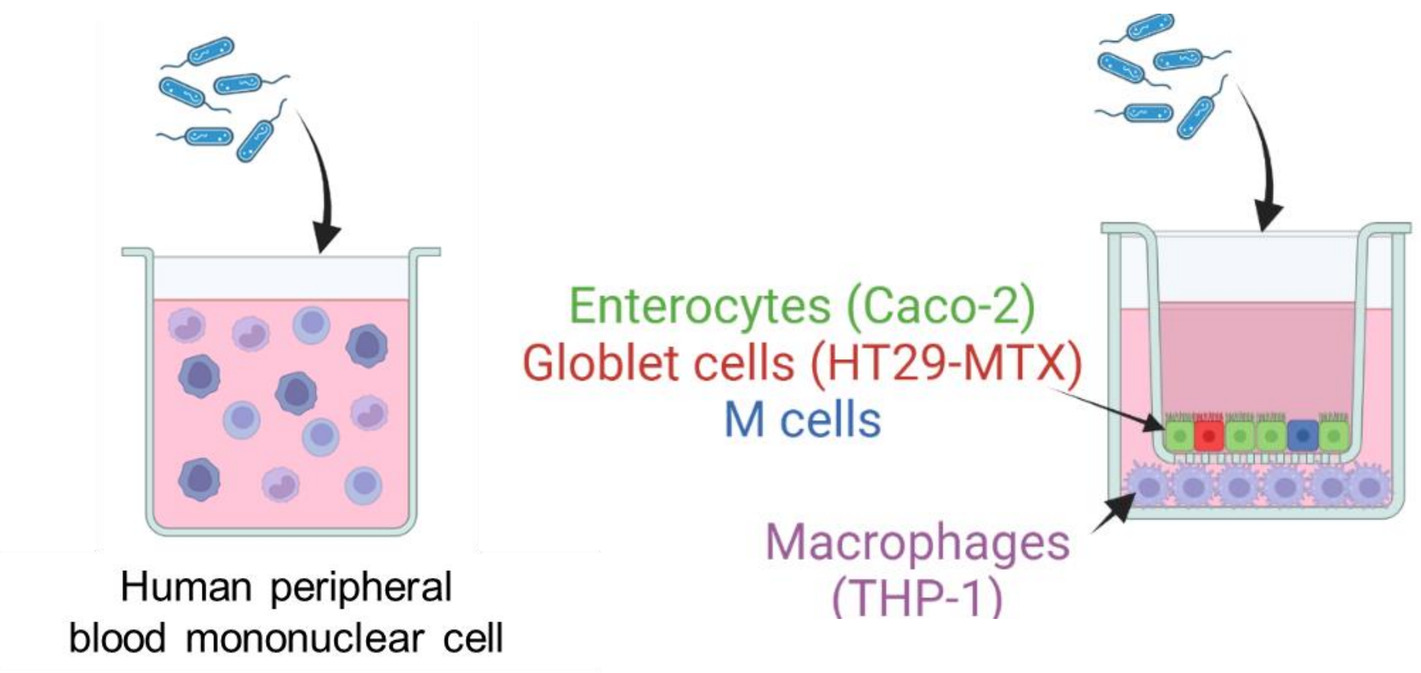
- Human milk (HM) promotes optimal growth and health benefits for infants
- Several differences in composition between infant formulas (IF) and HM, including a complex bacterial community present in HM and absent in IF
- Improvement of IF is needed, to mimic the HM composition and confer similar health benefits

Scientific context

- The HM microbiota is a very diverse community that contributes to the infant gut microbiota
- This HM microbiota is assumed to participate to the HM health benefits
- Some HM genera, such as *Bifidobacterium* and *Lactobacillus* are able to impact intestinal immune and barrier functions, but the role of HM microbiota as a complex community has been poorly explored so far

Research questions

Could HM microbiota influence the gut homeostasis (i.e. the gut immune and barrier functions and the intestinal microbiota)?

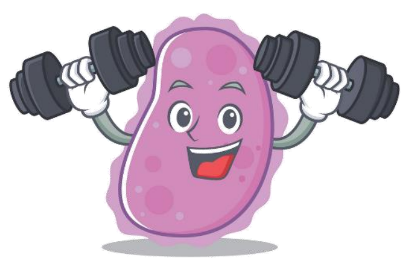


***In vitro* cellular models**

***In vivo* model: Yucatan mini-piglets**

Expected results

- Establishing an HM bacterial collection covering a maximum of HM taxonomic diversity
- Characterisation of the HM bacteria properties-: immunomodulatory profiles and impact on the intestinal barrier
- Design of synthetic bacterial communities representative of the HM microbiota and *in vitro* characterisation of their properties
- Modulation of early gut development of Yucatan mini-piglets with the supplementation of infant formula with HM-based synthetic bacterial communities



Perspectives

- A better understanding of the interactions between bacteria assembled in synthetic communities and impact on the global properties of the community
- Focus on the strict anaerobic bacteria of HM microbiota (poorly included in the HM collection)
- Improving IF with the addition of a complex bacterial component composed of bacteria from HM