

Two human milk synthetic bacterial community (SynCom) exhibited contrasted impacts in vitro on intestinal barrier and immune function

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STLO & NuMeCan





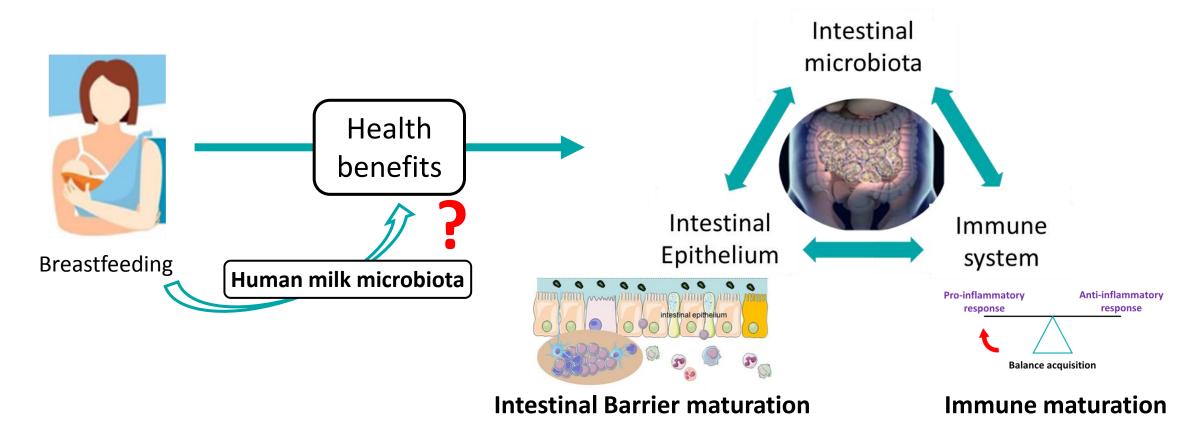




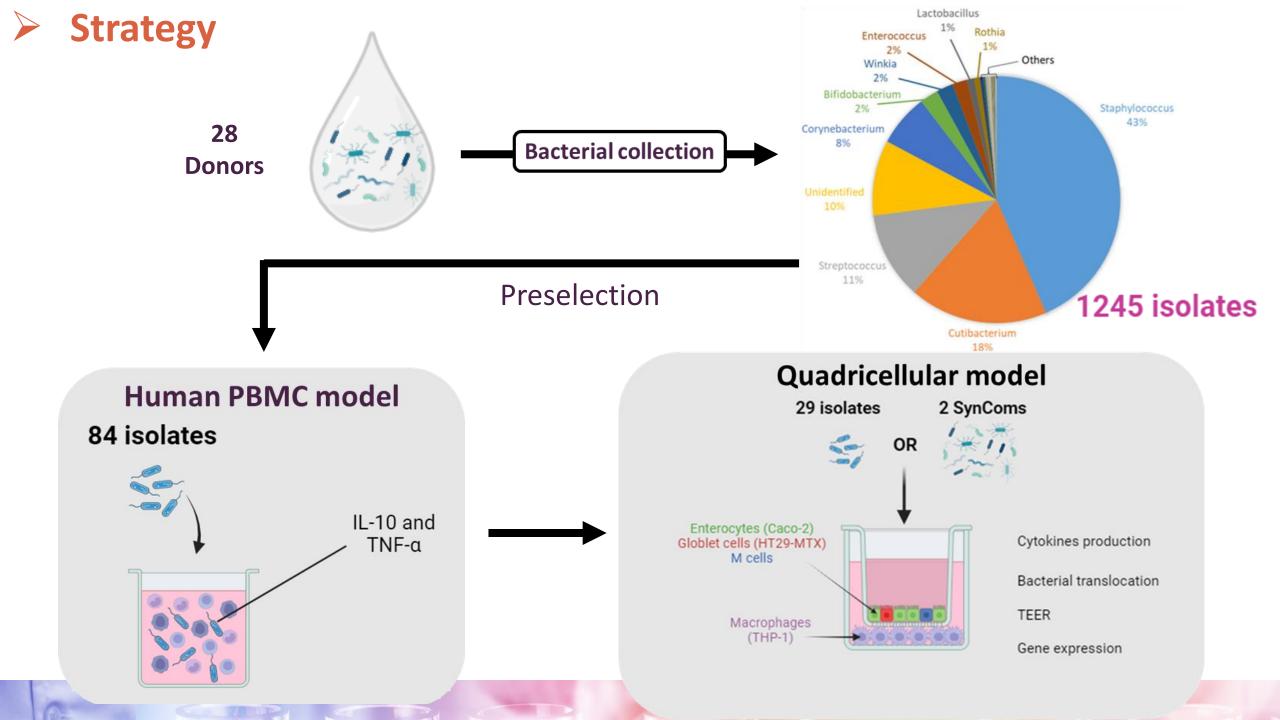


Introduction

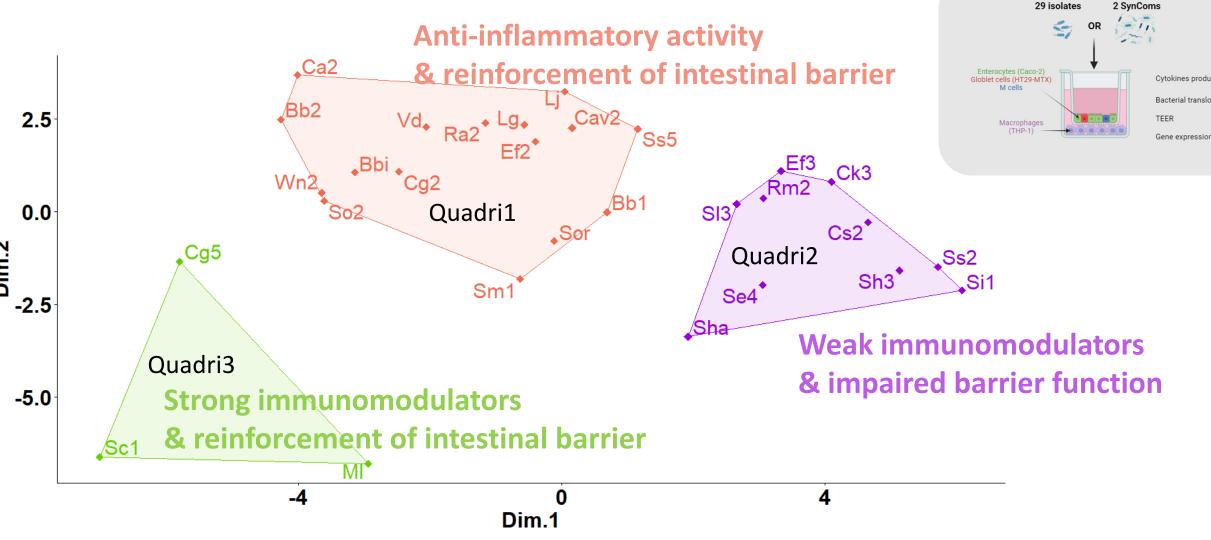
Intestinal homeostasis



Our hypothesis is that the microbiota of human breast milk contributes to the health benefits of breast milk



Individual impact of HM bacteria on immune and barrier functions Classification by MultiDimensionate Scaling Quadricellular model **Anti-inflammatory activity** & reinforcement of intestinal barrier 2.5



Great variability of functional profiles of HM bacteria



Immune and barrier properties of the 2 SynComs

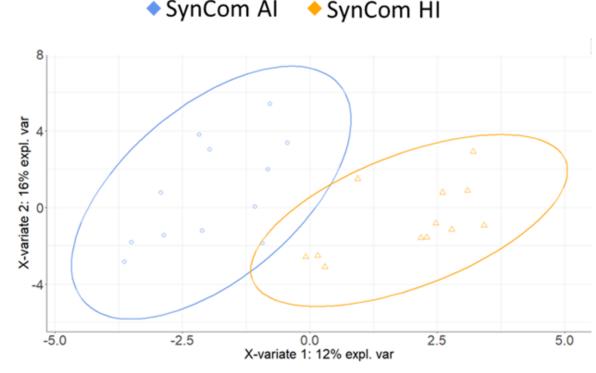
sPLS-DA analysis

Design of 2 Synthetic Communities:

- **→** Mimicking HM microbiota
- **→** With different functional properties

SynCom HI SynCom Al Cutibacterium granulosum (Cg2) Cutibacterium granulosum (Cg5) Strong Staphylococcus haemolyticus (Sha) Staphylococcus capitis (Sc1) Antiimmunomodulatory inflammatory Winkia neuii (Wn2) Micrococcus luteus (MI) Streptococcus infantis (Si1) Staphylococcus epidermidis(Se4) inflammatory Cutibacterium acnes (Ca2) Streptococcus salivarius(Ss2) Corynebacterium simulans (Cs2) Corynebacterium kroppenstedtii (Ck3) Bifidobacterium breve (Bb1) Bifidobacterium breve (Bb2) Lactobacillus gasseri (Lg) Lactobacillus jensenii (Lj) Rothia mucilaginosa (Rm2) Common Veillonella dispar (Vd) strains

Bifidobacterium bifidum (Bbi)



- Contrasted immunomodulatory properties as expected from the assembly
- New properties that differed from those of the individual bacteria

Conclusion

• The profile of HM bacterial SynComs reflected the coexistence of specific bacterial profiles that comprise the HM microbiota, leading to its role in driving gut homeostasis

 The functional properties of the HM bacterial community relied on a combination of strain-specific features rather than on the taxonomic composition itself

Questions & Answers