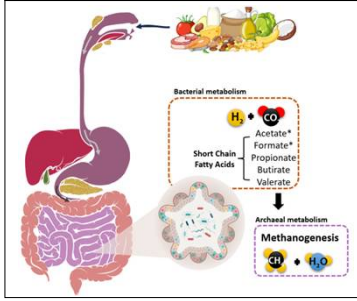
Diversity of immunoglobulin-coated archaea in human colostrum and neonatal stool from Mexican individuals

Diana Laura Rojas-Guerrero[1], Karina Corona-Cervantes[1], Carmen Josefina Juárez-Castelán[1], Alberto Piña-Escobedo[1], Bulmaro Cisneros-Vega[1], Leopoldo Santos-Argumedo[2], Tito Ramírez-Lozada[3], Gustavo Acosta-Altamirano[4], Mónica Sierra-Martínez[5], Paola Berenice Zárate-Segura[6] and Jaime García-Mena[1].

[1]Departamento de Genética y Biología Molecular, Cinvestav, [2]Departamento de Biomedicina Molecular, Cinvestav, [3]Unidad de Ginecología y Obstetricia, Hospital Regional de Alta Especialidad de Ixtapaluca, [4]Dirección de Planeación, Enseñanza e Investigación, Hospital Regional de Alta Especialidad de Ixtapaluca, [5]Unidad de Investigación en Salud, Hospital Regional de Alta Especialidad de Ixtapaluca, [6]Laboratorio de Medicina Traslacional, Escuela Superior de Medicina, Instituto Politécnico Nacional.

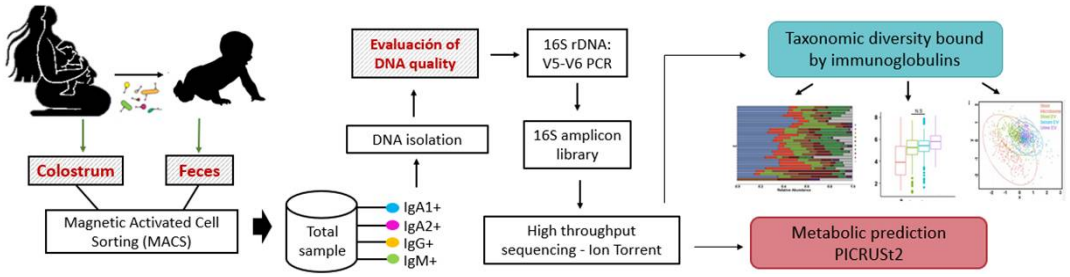
Introduction



Methanogenic archaea have been widely associated with the human gut[1], where they interact with byproducts generated through bacterial fermentation, facilitating important bacterial metabolic processes, such as the production of short-chain fatty acids (SCFAs). In a recent study[2], *Methanobrevibacter smithii* was cultured from human colostrum, prompting intriguing questions about the potential transfer of these archaea, possibly coated by maternal immunoglobulins, to infants during breastfeeding. In the present study we aimed to describe the diversity of immunoglobulin-bound archaea present in human colostrum and newborn stool.

Figure 1. Bacteria produce SCFAs in the human gut. Archaea then utilize them for methanogenesis. "*": SCFAs used for methane production.

Methodology



Results

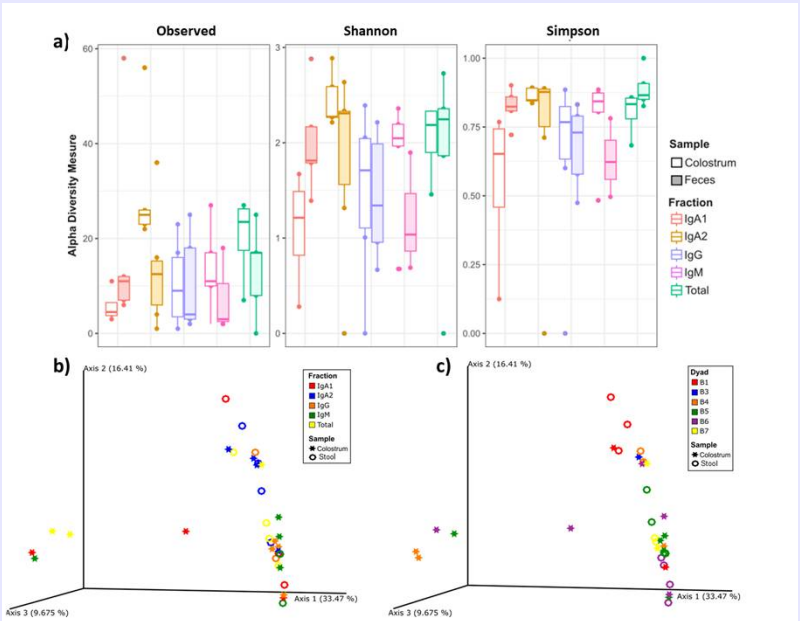


Figure 2. Diversity of archaea bound by immunoglobulins in human colostrum and neonatal stool. **(a)** Alpha diversity boxplots estimated as specific richness (Observed), diversity by the Shannon Index, and as dominance by the Simpson Index. Coefficients are indicated by the median of each group according to the Y-axis. **b,c,** Beta diversity estimated by UniFrac distance metric and represented according to fractions **(b)** or dyads **(c)** in a Non-Metric Multidimensional Scaling (NMDS) scatter plot.

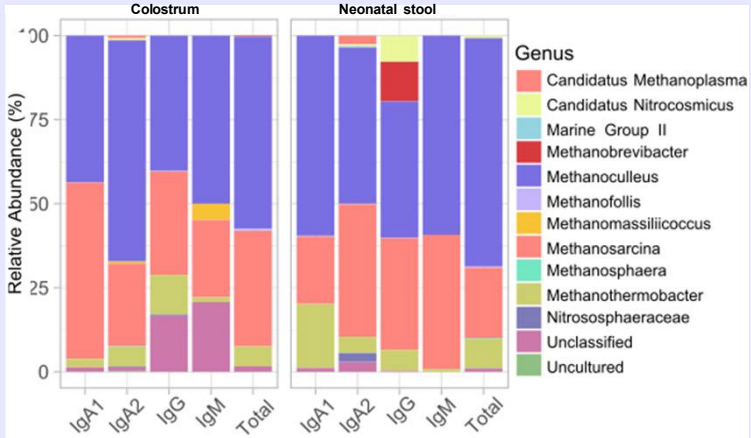


Figure 3. Taxonomic composition of archaea genera detected in colostrum and neonatal stool samples. Values on the X-axis indicate relative abundance (%) and different color represent different genera as shown in the legend.

Table 1. Metabolic pathways expressed differently between pairs of colostrum fractions.

Metabolic pathway	IgA1	IgA2	IgG	IgM	Total
Polyisoprenoid biosynthesis (E. coli)					*
NAD salvage pathway II		*			
Formaldehyde assimilation II (RuMP Cycle)		*			
Incomplete reductive TCA cycle		*			
Factor 420 biosynthesis			*		
L-arginine biosynthesis III (via N-acetyl-L-citrulline)		*		*	
Pyruvate fermentation to isobutanol				*	
Mevalonate pathway II (archaea)				*	
TCA cycle VI (obligate autotrophs)					

Table 2. Metabolic pathways expressed differently between pairs of neonatal stool fractions.

Metabolic pathway	IgA1	IgA2	IgG	IgM	Total
Inosine-5'-phosphate biosynthesis III		*		*	
Chorismate biosynthesis from 3-dehydroquinate		*			
Pyrimidine deoxyribonucleotides de novo biosynthesis I		*			
Pyrimidine deoxyribonucleotides biosynthesis from CTP		*			
TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase)		*			
TCA cycle I (prokaryotic)		*			
Factor 420 biosynthesis			*		
L-arginine biosynthesis III (via N-acetyl-L-citrulline)		*			
Phosphopantothenate biosynthesis III				*	
Superpathway of L-isoleucine biosynthesis I				*	
Superpathway of L-threonine biosynthesis				*	

Conclusions

- IgA2 is associated to a greater diversity of archaea than any of the other immunoglobulins.
- IgG binds to rare taxa in the newborn's gut; these taxa were detected by less tan 1% in total colostrum but more than 5% in stool.
- The archaea found in stool might be early colonizers of the newborns gut, since pathways for the synthesis of isoprenoid compounds and amino acids are activated.

References

1.Chibani et al. Nat Microbiol. 2022 Jan;7(1):48-61. doi: 10.1038/s41564-021-01020-9.
2.Togo AH et al.. Sci Rep. 2019 Dec 9;9(1):18653. doi: 10.1038/s41598-019-54759-x.

Aknowledgments

Work supported by CONACyT 163235 INFR-2011-01 and CONACyT FORDECYT-PRONACES/6669/2020_Programa Presupuestario F003-Ciencia de Frontera 2019.