

Abstract Book

MICROBIOME: HUMAN, PLANT AND ENVIRONMENTAL HEALTH applications and challenges



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The Book of Abstracts

**International conference on
MICROBIOME: HUMAN, PLANT AND ENVIRONMENTAL HEALTH
applications and challenges**

(UAE Microbiome 2023)

November 21 – 22, 2023

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P29: Microbiome and metabolome of the Entero-Mammary Pathway

Vélez-Ixta JM¹, Juárez-Castelán, CJ¹, Benitez-Guerrero T¹, Piña-Escobedo A¹, Cruz-Narváez Y², Gómez-Cruz CY², Hoyo-Vadillo C³, Rico-Arzate E², Castro-Arellano JJ², Romero-Maldonado S⁴, Pizano-Zárate ML⁵, García-Mena J¹#

¹ Departamento de Genética y Biología Molecular, Cinvestav, Mexico.

² Laboratorio de Posgrado de Operaciones Unitarias, Escuela Superior de Ingeniería Química e Industrias Extractivas, Instituto Politécnico Nacional, Mexico.

³ Departamento de Farmacología. Cinvestav, México.

⁴ Unidad de Cuidados Intermedios al Recién Nacido, Instituto Nacional de Perinatología, Mexico.

⁵ Departamento de Nutrición y Bioprogramación, Instituto Nacional de Perinatología, Mexico

Contact Email: jgmena@cinvestav.mx

ABSTRACT

The entero-mammary pathway is a specialized route that facilitates the transfer of immune components from the intestine to the mammary gland. This pathway has been hypothesized to selectively translocate bacteria, leading to their ingestion by the newborn, potentially playing a crucial role in neonatal development. Previous studies have successfully identified common bacterial and archaeal taxa shared between human milk and the neonatal intestine. However, the functional implications of this process in neonatal development are still not fully understood due to limited evidence. Therefore, this study aims to identify and characterize these features by assessing the microbiota diversity and the metabolome profile of colostrum, mother, and neonate stool samples using high-throughput DNA sequencing and FT-ICR MS methodology, respectively. Preliminary results from our study have shown promising findings. Spearman's correlation analysis has revealed features that may be associated with distinct metabolic pathways. Discriminatory analysis (LIM-LRT) demonstrated differential expression of metabolites across sample types. Our comprehensive analysis of the microbiota revealed unique microbial communities in each sample type, interestingly, we also identified several bacterial taxa consistently shared between human milk and neonate intestine, supporting the notion of bacterial transfer through the entero-mammary pathway and vertical transmission. In conclusion, these findings contribute to a broader understanding of the role played by the early acquisition of microbiota from human milk in neonatal development. Our study highlights the importance of considering the microbiota composition and its implications for neonatal health. Based on the current evidence, these results suggest implications for developing targeted interventions or recommendations aimed at optimizing infant health and well-being. This work was supported by CONACyT 163235 INFR-2011-01 and CONACyT FORDECYT-PRONACES/6669/2020_Programa Presupuestario F003-Ciencia de Frontera 2019.

Keywords: metabolome, microbiome, 16S RNA gene, Mass spectrometry, Entero-mammary pathway.



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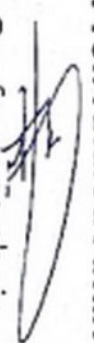
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