SYMBNET INTERNATIONAL CONFERENCE ON

Host-Microbe Symbiosis

GULBENKIAN
CIÊNCIA

10—13 Jun 2024

Olhão, Algarve
Portugal

ABOUT

Hosts and microbes form long-term symbiotic interactions that shape their biology at multiple levels, from physiology to ecology and evolution. This is a growing field of research which impacts many other areas, from environmental sciences to human health.

The "SymbNET International Conference on Host-Microbe Symbiosis" brings together researchers working on a diverse range of questions, approaches, and model systems. Our meeting, with 6 plenary sessions, will cover different host systems such as plants, animals and humans and different molecular mechanisms, functional understanding and ecological models of the interactions. The purpose is to highlight the most recent advances in the field, common principles between systems, and future directions to explore.

This meeting has 164 participants from 26 countries and it is organized in the context of the EU twinning grant SymbNET, with specific sessions organized by NCCR Microbiomes and CRC Metaorganisms.
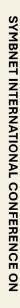
necessitating further research to balance agricultural practices with colony health. However, existing studies yield conflicting findings on the impacts of these substances on honeybee GM composition, compounded by regional variations influenced by genetic and environmental factors. Our objective is to analyze amplicon sequencing data from six geographic locations, supplemented by new data from Armenia, to comprehensively understand honeybee microbiome dynamics. We utilized various diversity measures to assess regional and dietary differences and employed statistical tests and differential abundance analysis to discern treatment effects. Additionally, we constructed maximum weight connected graphs to elucidate bacterial species relationships, identifying specific networks influenced by treatments and regions, subsequently fractionally annotated. Our investigation uncovered drivers of honeybee gut microbiome variance, delineating composition and functional potential responses to geographic location. We established a comprehensive core microbiome and observed significant community-level effects, notably from oxalic acid and manuka honey, which substantially reduced certain community members. By elucidating the intricate interactions between pesticides, herbicides, and honeybee gut microbiomes across diverse regions, our findings contribute valuable insights into preserving bee health amidst agricultural intensification.

P73- Postnatal Microbial and Metabolite Transmission: The Path from Mother to Child

Vélez-Ixta JM[1], Juárez-Castelán CJ[1], Benitez-Guerrero T[1], Piña-Escobedo A[1], Cruz-Narváez Y[2], Gómez-Cruz CY[2], Hoyo-Vadillo C[3], Rico-Arzate E[2], Castro-Arellano JJ[2], Romero-Maldonado S[4], Pizano-Zárate ML[5], García-Mena J[1]

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

The entero-mammary pathway (EMP) is a specialized route that transfers immune components from the intestine to the mammary gland. EMP selectively translocate bacteria, to the newborn´s gut playing a crucial role for neonatal development. Previous studies report shared bacterial and archaeal taxa between human milk and the neonatal intestine. However, the functional implications for neonatal development are not fully understood due to limited evidence. This study aims to identify and characterize the microbiota diversity and the metabolome profile of human milk, mother and infant Stool samples using high-throughput DNA sequencing and FT-ICR MS methodology, at delivery and 4 months post-partum. For the study, 25 mother-infant pairs were included. Our results on bacterial composition (relative mean abundance, alpha and beta diversity) suggest vertical transmission of microbiota through breastfeeding It also seems that major changes in bacterial genera occur during the first 4 months of life (DESEq2). On the other hand, unsupervised machine learning analyses like PCA, partitioning around medoids and hierarchical clustering heatmap of sample m/z peaks, revealed that mother and infant stool clustered together regardless of collection time, and metabolite chemical characterization (Kendric mass defect, Van Krevelen plot and NOSC). Further data integration with multiblock sPLSDA model explored the dynamics between bacteria and metabolites in the samples. A Canonical Correlation Analysis (CCA) network in the model disclosed the interactions between different bacteria and metabolites the biological system.

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Certificate of Attendance

This certificate presented to:

Juan Manuel Vélez-Ixta

for attendance and poster presentation at the SymbNET International Conference on Host-Microbe Symbiosis, held in Olhão, Portugal, during June 10th-13th, 2024.

Luís Teixeira
(Project Coordinator)

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