

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](#).

#### P44- Vertical transmission of Microbiota and Metabolites: Impact of Maternal obesity on Neonate

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Obesity is a significant public health concern in Mexico, and several factors, including gut microbiota, are contributing to its prevalence. Maternal obesity affects the microbiota of breast milk, resulting in a higher risk of obesity and metabolic diseases in newborns. This study aimed to identify the specific bacteria and metabolites associated to dysbiosis in newborns. We collected samples, including mother stool, human milk with normal weight, overweight, and obesity (Class 1, 2, 3) and neonatal stool, from both obese and normal-weight mothers for DNA extraction. We analyzed the V3-16S ribosomal DNA gene libraries using next-generation sequencing (Ion-torrent) and characterized the microbiota using both differential analysis (DESeq2) and metagenome prediction (PICRUST). The metabolites were analyzed using FT-ICR Mass Spectrometry. The study found that microbiota and metabolites are transmitted through breastfeeding, with *Patescibacteria* and *Firmicutes* being the most dominant bacterial phyla in human milk. *Firmicutes* dominate the neonatal stool of mothers with obesity, while *Lactobacillus* and *Staphylococcus* genera are higher in neonatal stool and human milk from obese mothers. The alpha diversity index did not show any difference in BMI classification among the samples. However, a subset of metabolites was linked to maternal weight and neonate health. The study highlights that maternal and neonatal obesity can be vertically transmitted through milk during breastfeeding. The research findings can be leveraged to develop interventions that reduce the risk of obesity and metabolic diseases in newborns. This work was supported by CONACyT 163235 INFR-2011-01 and CONACyT FORDECYT-PRONACES/6669/2020\_Programa Presupuestario F003-Ciencia de frontera 2019.

#### P45- Broad distribution and rampant horizontal transmission of new *Wolbachia* supergroups in a dipteran family

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*Wolbachia* are among the most widespread insect symbionts, infecting nearly half of all known insect species. They are known to significantly influence the biology of their hosts through a wide range of mechanisms such as reproductive manipulations, nutritional provisioning, anti-viral protection, and modulation of behaviour and preferences. These bacteria can profoundly impact insect communities and alter species distributions. Despite their importance, the distribution, diversity, and phylogeny of *Wolbachia* in wild insect communities remains poorly characterised, with research primarily focused on a few model species. Our goals were to understand the distribution of *Wolbachia* genotypes across natural insect communities and characterise phylogenetic relationships among the identified strains. To address these objectives, we conducted amplicon sequencing analysis of a part of the cytochrome oxidase I gene (COI) from 1842 scuttle flies (Diptera: Phoridae) from northern Sweden, representing 186 fly species. We identified 259 distinct COI genotypes of *Wolbachia*, displaying specific distribution patterns across host species and genotypes. Additionally, for most of the host species-bacteria genotype combinations, we generated target enrichment data of *Wolbachia* genes that provided genome-level phylogenetic resolution and insight into symbiont functions. Within the phorid fly





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## Certificate of Attendance

This certificate presented to:

***Aparna Krishnakumar***

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



*Luís Teixeira*

*(Project Coordinator)*