BRAIN-be
Belgian Research Action through Interdisciplinary Networks

SYMDIV

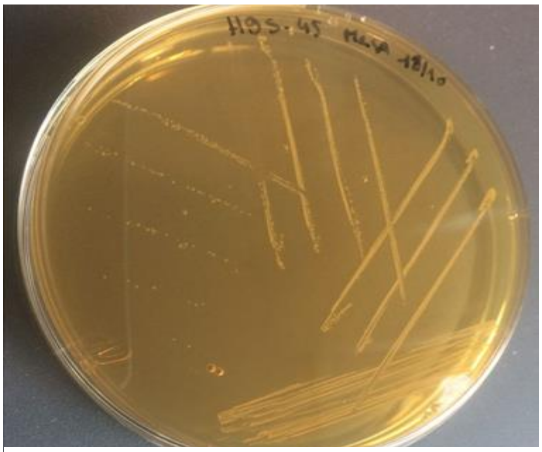
Symbiont diversity and feeding strategies in insect agricultural pests

DURATION
15/12/2015 – 15/03/2018

BUDGET
146 956 €

PROJECT DESCRIPTION

Insects are extremely versatile in exploiting a large range of nutritional niches. This is not so much the result of their metabolic flexibility but heavily depends on intimate relationships between insects and associated gut microbionts. Insects feeding on largely indigestible plant tissues of low nutritional value rely on their gut microbiome to convert these into essential nutrients. Insects in turn can develop metabolic pathways that overcome plant defence mechanisms, including toxins. There is growing evidence that bacteria play a major role in these detoxification processes, making plant tissue edible for the insect and even modifying plant compounds into chemicals such as pheromones used by the insect. Hence, microbial mutualistic symbioses enable insects to manipulate the plant physiology for their own benefit and have a major role in determining insect host plant ranges. Shifts in the composition of insect gut microbiome represent a main adaptive process promoting coevolution and speciation of phytophagous insects and their host plants.



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This project focuses on the relationships between insect microbiont diversity and host plant adaptation in tephritid fruit flies. About half of the 4500 fruit fly species worldwide feed on fruits with the larval stages developing inside a wide variety of fruits. They include some of the world's most notorious horticultural and agricultural pests. Fruit flies can be monophagous (attacking plants belonging to a particular species), stenophagous (a particular genus), oligophagous (a particular family) or polyphagous. Fruit fly larval feeding is thought to depend heavily on activities of gut microbiota, yet symbiotic relationships between microbiota and fruit flies have been studied to a limited extent.

Our aim is to investigate the association between fruit flies and their gut microflora by comparing gut microbial assemblages across closely related fruit flies with diverse feeding strategies, from strict monophagy to extreme polyphagy. The project focusses on bacteria because recent studies have indicated that they play an important role in the adaptive evolution of their hosts, for example through metabolic interactions contributing to nutrition, detoxification and protection. The main hypothesis is that gut microbiome diversity and composition will be correlated with the insect niche breadth. This study will provide the necessary baseline data for innovative research on relationship between insect microbionts, host range spectrum, and metabolic processes.

We will use 16S rRNA metagenomic sequencing to sample the gut bacterial assemblages of widespread agricultural pests because this approach (1) targets microbial genomes directly without the need for culturing, thus giving access also to uncultivable taxa and (2) it permits to sample these assemblages in an unprecedented detail. The metagenomic survey will generate a comprehensive overview of gut microbiomes in tephritid fruit flies. This information will be used to guide isolation and cultivation strategies for gut microbionts. Cultivation of bacteria is important because (1) it allows a more precise identification and will permit the description of novel diversity which is expected, and (2) the cultured microbiota will be preserved for future research in the BCCM/LMG Bacteria Collection.

While the Royal Museum for Central Africa (RMCA) has extensive knowledge on fruit fly systematics and phylogeny, the Laboratory of Microbiology at Ghent University (GU), who is also in charge of the BELSPO financed BCCM/LMG Bacteria Collection, has solid experience in the study of microbial diversity. Bringing these two fields of expertise together, while exploring new technologies, is a synergetic collaboration that aims to provide a significant contribution to research on insect pests.

SYMDIV

Our results will impact several important areas. Scientifically, the role of symbionts in host evolution and diversity is recognized, yet relatively underexplored. With relation to agriculture, fruit flies are a major pest group that includes potentially invasive species threatening plant health and crop production worldwide. A better understanding of the relation between gut microbiome composition and insect host choices may provide useful information for pest control strategies targeted on selected microbial activities. Furthermore, similarity between detoxification of plant chemicals and detoxification of insecticides by gut bacteria suggests there may be a link between host plant adaptation and pesticide resistance which has consequences for agriculture, pesticide use and food security. Although the project is too limited in time and resources to explore this link, it can provide useful baseline data for such further studies.

Deliverables produced will include: datasets on molecular inventories of bacterial microbiota in fruit flies with different feeding strategies made available in public databases, identified bacterial isolates cryo-preserved and deposited in the BCCM/Bacteria collection, available for further research, peer-reviewed scientific papers. Future prospects include the detailed characterization of bacterial strains for their genome sequence and metabolic capacities and antibiotic resistance, knowledge that can be used to set up experiments with host species to verify hypotheses on the nature of the interactions in controlled conditions.

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