PO-03

COMPARATIVE MICROBIOMICS OF TEPHRITID FRUGIVOROUS PESTS (DIPTERA: TEPHRITIDAE) FROM THE FIELD: A TALE OF HIGH VARIABILITY ACROSS AND WITHIN SPECIES

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INTRODUCTION

Tephritid fruit flies demonstrate a wide differentiation in host range and dietary breadth, from specialized monophagy to extreme polyphagy. It is considered that the gut microbiome plays an important role in shaping this dietary range. The present study provides a first comparative analysis of the microbiome profiles of a selection of ten African and Mediterranean fruit flies with different host plant ranges.

MATERIAL & METHODS

We targeted 10 species belonging to three tephritid genera of economic relevance and with different host range breadth: *Bactrocera dorsalis, B. zonata, Ceratitis capitata, C. cosyra, C. flexuosa, C. podocarpi*, *C. quilicii, C. rosa and Zeugodacus cucurbitae*. We used a multi-factorial sampling design to compare the microbiome profiles of wild third instar larvae from different species and replicated sampling sites and host plants.

RESULTS & DISCUSSION

16S rRNA metagenomics allowed recovering 2749 Amplicon Sequence Variants (ASV) that were assigned to 401 genera belonging to 142 different families and 22 phyla. Of the latter, Proteobacteria was the most dominant, following by Firmicutes, Bacteroidetes, Actinobacteria, Epsilonbacteraeota and Tenericutes (Fig. 1). Our results did not suggest the presence of common "core microbiomes" shared within genera (*Ceratitis*, *Bactrocera, Zeugodacus*) or among polyphagous, oligophagous or monophagous species. Conversely, we observed high variability of microbiome profiles with ANOVA and PERMANOVA revealing significant differences across both fruit fly species and host plants (Fig. 2). A number of bacterial genera showed distinct higher relative abundances in particular fruit fly species. These were: *Erwinia* in *Bactrocera oleae*, *Lactococcus* in *B. zonata*, *Providencia* in *Ceratitis flexuosa*, *Klebsiella* and *Rahnella* in *C. podocarpi* and *Acetobacter* and *Serratia* in *C. rosa* (Fig. 3). The present study provides relevant baseline information for future studies that will further investigate the functional role of the observed associations.

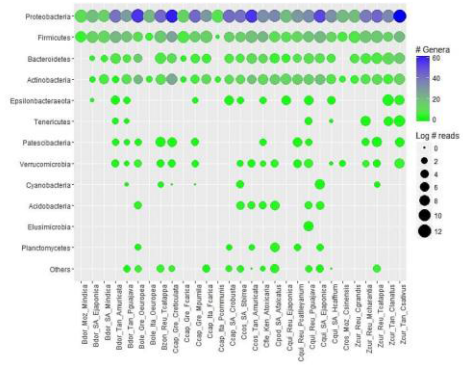

Fig. 1 Bubble plot representing the bacterial phylum composition per sample

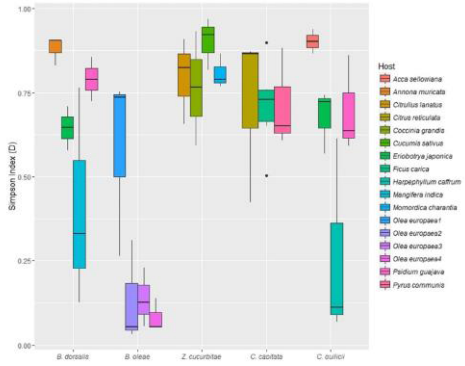

Fig. 2 Alpha diversity of gut microbial assemblages in target fruit fly species sampled in two locations, from two host plants within each location

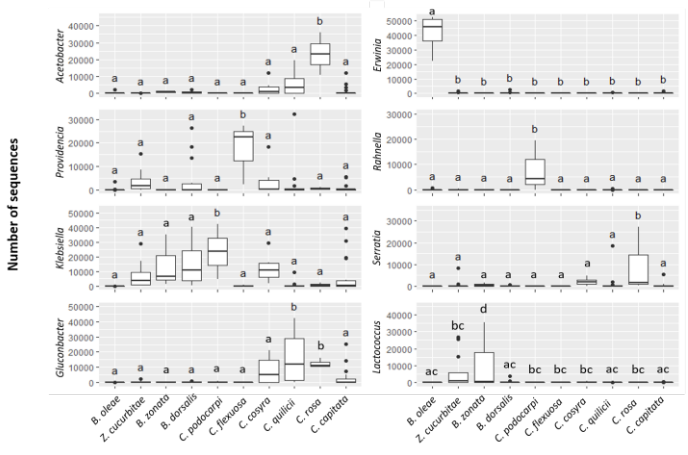

Fig. 3: Abundances of representative bacterial genera in ten targeted fruit fly species. Results are reported for bacterial genera producing significant differences in at least 8 pairwise tests out of 9 (FDR-corrected p value < 0.01) and contributing to >5% of dissimilarity between fruit fly species. Significance letters for pairwise tests are indicated.

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