

HOST PLANT DETERMINES MICROBIOME COMPOSITION AND STRUCTURE IN WILD MELON FLY LARVAE (DIPTERA, TEPHRITIDAE: ZEUGODACUS CUCURBITAE)

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INTRODUCTION

MATERIAL & METHODS

The diversity observed in phytophagous insects seems to have arisen from plant-insect interactions. Microbial symbionts play a relevant role in host plant choice and adaptation of phytophagous insects. In this study we investigated the effects of intergenerational shifts between conventional and unconventional host plants on the microbiome diversity and composition of the oligophagous cucurbit feeder *Zeuqodacus cucurbitae*.

Zeugodacus cucurbitae adults were (a) reared from infested ivy gourds ('Co': ivy gourd) collected in two locations in La Réunion ('BP': Bassin Plat and 'M': Manapany) and (b) allowed to oviposit on two conventional cucurbit host plants (ivy gourd; 'Cu': squash) and one unconventional non cucurbit host ('Au': eggplant, Solanaceae) (Fig. 1). The microbiomes of the emerging third instar larvae were subjected to 16S rRNA metagenomic profiling and compared.

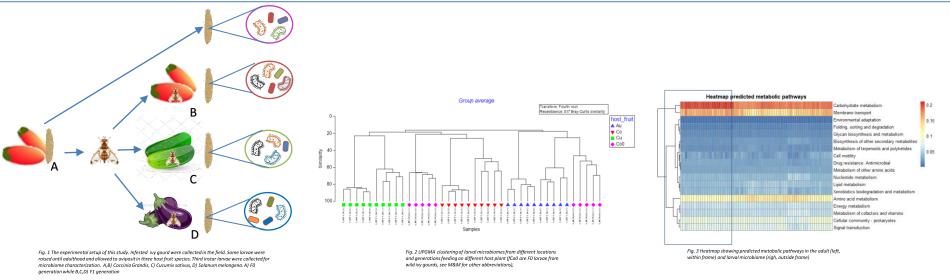
RESULTS & DISCUSSION

We recovered 2949 Amplicon Sequence Variants (ASV) belonging to 527 microbial genera in 204 different families and 26 phyla. Our results show complex differences between the microbiome profiles of larvae from different generations and sampling locations feeding on different host fruits and, to a less extent, between larvae originating from different locations (Fig. 2). The results also showed differences between the predicted metabolic pathways of the microbial symbionts associated with adults and larvae (Fig. 3). These preliminary results suggest a possible role of *Z. cucurbitae* associated microbiomes in host plant utilization and host switching to unconventional host plants.

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