

TITLE: COMPOSITION OF MICROBIAL COMMUNITY IN MIDGUT OF *Anticarsia gemmatalis* FED WITH DIFFERENT SOYBEAN GENOTYPES

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ABSTRACT:

Ecosystems are shaped by complex communities of mostly unculturable microbes. The microbiota plays an important role in insect development and fitness. The gastrointestinal tract of animals harbors a diversity microbial community, and the composition of this community ultimately reflects the co-evolution of microorganisms with their animal host and the diet adopted by the host. Understanding the gut microbiota composition is essential for the development of pest management strategies. The midgut microbiota of *Anticarsia gemmatalis* was isolated after being submitted to different diets with soybean cultivars. This study aimed to characterize the microbiota of the midgut of *A. gemmatalis* under the influence of different cultivars resistant and susceptible soybean. It was used next-generation Illumina MiSeq platform to sequence the V3–V4 hypervariable regions of 16S rRNA gene evaluate the diversity associated with bacterial communities in four groups (Control susceptible (C); susceptible, under water stress (S) and insect resistance (IAC 17 and IAC 24); n = 8). Also using the same sequencing platform was used for the ITS region sequence fungi and V6-V8 Archaea region to identify diversity. There were differences ($P > 0.05$) for the symbiont microbiota fed with different soybean cultivars (C, S, IAC 17 and IAC 24). It noted the predominance of phyla Proteobacteria and Firmicutes for bacteria and Ascomycota and Chytridiomycota for fungi, what to fungi has few reports. In all groups, were observed 210 operational taxonomic units (OTUs) to bacteria and 110 OTUs for fungi, with an average of 52 and 27 OTUs for bacteria and fungus, respectively. The diversity and richness of data show that the diet is determining the composition of the microbiota, being grouped into different quadrants. When analyzed by non-Metric Multidimensional Scaling (nMDS), well established OTUs for each type of diet. The insects have the ability then to modulate their microbiota in order to get the best out of your diet. According to the literature, this is only possible with the contribution of its microbiota in symbiosis with the host. So, for effective control of herbivorous insects becomes necessary modulation of the microbial community that could even be acting in induced plant response.

Keywords: gut microbiota, herbivores, host–microbe interactions, Next-generation sequencing (NGS), symbionts

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