

Microbial Community Diversity in Larval Insect Gut from Field and Laboratory Populations of the Sugarcane Weevil *Sphenophorus levis* (Coleoptera, Cucurliionidae)

Rinke, R.<sup>1</sup>, Fonseca, F.P.P.<sup>1</sup>, Henrique-Silva, F.<sup>1</sup>

<sup>1</sup> Departamento de Genética e Evolução, Universidade Federal de São Carlos, São Carlos, São Paulo, Brazil

The sugarcane weevil, *Sphenophorus levis*, is an important pest in sugarcane culture in São Paulo state. To complete its life cycle, *S. levis* may depends on microorganisms that inhabit its intestinal tract and play an important key in the insect physiology and nutrition. The objective of this study is to characterize the microbiota from intestinal population of insect larvae from field and laboratory. It is also our objective to search for microorganisms capable to degrade cellulose, an important event in the insect attack. We compared the intestinal microbiota diversity from field and laboratory insect larvae using 16S rRNA marker and culture-dependent methods. 16S rRNA sequences analyses revealed a total of sixteen genera and three unclassified genera in both libraries represented by Alfa-Proteobacteria, Beta-Proteobacteria, Gamma-Proteobacteria, Firmicutes and Bacteroidetes phylum. Microorganisms isolated through culture-dependent methods were grouped according morphological parameters and classified in nine bacteria groups and six yeasts groups. Three filamentous fungi were isolated. We found a higher microbial diversity in field than in laboratory according to Shannon-Weaver index (Field H'= 1.6999; Laboratory H'= 0.9133). From the cultivable microorganisms, four groups of bacteria, two groups of yeast and two filamentous fungi presented cellulolytic activity. This is the first study about *S. levis* microbiota which can contribute to understand plant-pathogen interaction and also be useful for future development of new strategies for control of *S.levis* in sugarcane cultivation.

Key-words: Sugarcane, *Sphenophorus levis*, 16S rRNA, intestinal microbiota, cellulolytic activity.

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