

Dynamic of an Invasive Insect Gut Microbiome When Facing to Abiotic Stress

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Abstract : The emerald ash borer (EAB) is an exotic wood borer insect native from China, which is associated with important environmental and economic damages in North America. Beetles are known to be vectors of microbial communities related to their adaptive capacities. It is now established that environmental stress factors may induce physiological events on the host trees, such as phytochemical changes. Consequently, that may affect the establishment compartment of herbivorous insect. Considering the number of insects collected on ash trees (insects' density) as an abiotic factor related to stress damage, the aim of our study was to explore the dynamic of EAB gut microbial community genome (microbiome) when facing that factor and to monitor its diversity. Insects were trapped using specific green Lindgren® traps. A gradient of the captured insect population along the St. Lawrence River was used to create three levels of insects' density (low, intermediate, and high). After dissection, total DNA extracted from insect guts of each level has been sent for amplicon sequencing of bacterial 16S rRNA gene and fungal ITS2 region. The composition of microbial communities among sample appeared largely diversified with the Simpson index significantly different across the three levels of density for bacteria. Add to that; bacteria were represented by seven phyla and twelve classes, whereas fungi were represented by two phyla and seven known classes. Using principal coordinate analysis (PCoA) based on Bray Curtis distances of 16S rRNA sequences, we observed a significant variation between the structure of the bacterial communities depending on insects' density. Moreover, the analysis showed significant correlations between some bacterial taxa and the three classes of insects' density. This study is the first to present a complete overview of the bacterial and fungal communities associated with the gut of EAB base on culture-independent methods, and to correlate those communities with a potential stress factor of the host trees.

Keywords : gut microbiome, DNA, 16S rRNA sequences, emerald ash borer

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