

**Title:** Impact of 2,4-D Exposure on Microbial Community Structure in a Brazilian soil

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**Abstract:**

The intensive use of pesticides to eradicate pests and weeds has resulted in increased world agricultural production; however, this practice has environmental, social and economic impacts. Soil is a natural resource of great importance; it is a dynamic, heterogeneous and complex system, harboring a large number of ecological niches. Hence, this study aimed to verify whether the selective pressure exerted by the presence of the herbicide 2,4-Dichlorophenoxyacetic acid (2,4-D) has the potential to change the composition of the local microbiota. The Denaturing Gradient Gel Electrophoresis (DGGE) technique was performed in order to evaluate changes in the composition of the soil microbiota after application of different concentrations of 2,4-D. Furthermore, the study determined the soil microbiota before and after exposure to 2,4-D by sequencing of the 16S *rRNA* gene, which it was performed at Michigan State University using the Illumina MiSeq platform. Through DGGE and the profile of bands it was possible to state that the bacterial community changed according to the persistence time and concentration of the herbicide applied on soil. These results also were confirmed by the 16S *rRNA* gene sequencing. In addition, it was observed that the microbial community of the Brazilian soil is predominantly composed of Acidobacteria and Proteobacteria. These phyla have already been correlated with the application of herbicides and also reported as the most abundant phyla in environments contaminated by agrochemicals and several herbicide-degrading microorganisms are part of these phyla. Herbicides can hinder the

growth of some organisms due to toxicity, but they may also stimulate other specific groups that already use it as a source of nutrient. In conclusion, it was possible to observe the persistence time had more influence in soil microbiota than herbicide application and the Acidobacteria and Proteobacteria were the most abundant phyla due to their correlation with biodegradation of pesticides.

**Key-words:** 16S rRNA; 2,4-D; Microbiota; Sequencing; Soil.

**Development agency:** Capes and Capes-PDSE.