

TLP-218. Quantification of bacteria and archaea in rhizosphere of wild and modern common bean

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Introduction. Rhizosphere microbiome has received ample attention in research considering that distinct crops harbor a rich and diverse rhizobacterial community. Recently was postulated that due to genetically improvement plants may have lost their ability to recruit beneficial bacteria. In this context, the comparison of wild and modern materials is key to understand the selection of microbes in the rhizosphere by the host plant. In this study we aimed to quantify bacterial and archaeal 16s rRNA gene by using QPCR and compare their abundance in bulk soil and rhizosphere of wild plants and modern cultivars of common bean.

Materials and methods. The experiment was performed using two cultivars, i.e. midas and iac-alvorada and two wild plants, i.e. g12873 and wild mex. Plants were grown in greenhouse conditions considering four replicates and sampled during the flowering stage. Total DNA was extracted and bacteria and archaea 16s rRNA gene was quantified using QPCR.

Results. In two independent experiments the amount of bacteria or archaea in the rhizosphere ranged from 2- to 8 fold when compared with bulk soil. No significative difference in abundance was observed when g12873 (wild) and midas (cultivar) were compared. However, in the second experiment, which included wild mex and iac alvorada, the wild plant was able to harbor higher abundance of bacteria ($p=0,0001$) when compared with the modern cultivar iac alvorada. Interestingly, the abundance of archaea was higher ($p=0,0019$) in the midas rhizosphere when compared with the wild plant g12873.

Conclusions. The plant is able to attract and enrich bacteria and archaea in the rhizosphere when compared with bulk soil. The results obtained from iac alvorada and wild mex experiment, suggests that ancestral materials communicated with microbes resulting in a higher quantity of bacteria in its rhizosphere than improved cultivars.