## TLP-398. Rhizosphere bacterial community composition in wild and modern common bean

Stalin Wladimir Sarango F.\*, Lucas William Mendes\*, Josiane Barros Chiaramonte\*, Rodrigo Mendes\*

> \*Luiz De Queiroz College Of Agriculture (Esalq), University Of São Paulo, Piracicaba SP, Brazil.

Introduction. Modern cultivars were obtained through breeding programs focusing on productivity increase based on selection of best vegetable phenotypic traits. This manipulation is likely to have neglected the rhizosphere microbiota's role on the agricultural production systems. In this research we studied whether wild materials of common bean are able to recruit a more diverse and abundant community of beneficial bacteria when compared with modern cultivars. Objective. Determine the rhizosphere bacterial community in a wild and modern cultivar of common bean by using cultivation-dependent approach and metagenomic sequencing.

**Materials and methods.** The common bean cultivar iac alvorada and the ancient wild mex were grown on Amazon dark earth under greenhouse conditions considering two replicates. Rhizospheric soil was collected in iac alvorada flowering stage and wild mex in the foliar renewal stage. The total DNA was extracted and followed by shotgun sequencing using illumina miseq platform. In addition, bacteria were isolated from rhizosphere on tsba, psa and ga selective medium and isolates were screened for antagonism against the soil borne pathogens *Rhizoctonia solani* (rs) and *Fusarium oxysporum F SP. Phaseoli* (fo).

**Results.** Approximately 2.5 million sequences were obtained with average length of 226 bp. An average of 58% of sequences were classified into bacteria and archaea using rdp database. Proteobacteria represented the most abundant phyla (20% of sequences), followed by *Actinobacteria* (15%), *Firmicutes* (14%) and *Bacteroidetes* (12%). Pcoa analysis showed that while bulk soil and wild mex samples clustered, the iac alvorada samples did not. The frequency of bacterial antagonists isolated from wild plants was higher when compared with modern cultivar. Out of 68 bacterial isolates, six inhibited rs and five fo growth.

**Conclusions.** The preliminary sequencing data showed that rhizosphere bacterial community of wild mex is more homogeneous than in the iac alvorada cultivar suggesting a more selective recruitment by wild plants.