

Metataxonomic analysis of microbial community changes in *Fusarium* wilt-infected banana crops from Colombia

Jeanneth Mosquera-Rendón, Diana López-Alvarez, Juan M. Pardo, Elizabeth Alvarez



Abstract

Fusarium wilt disease, caused by the fungus *Fusarium oxysporum* f. sp. *ubense* (FOC), is one of the most destructive diseases of banana worldwide. Our aim was to compare and evaluate microbial communities in soils and roots of Gros Michel banana cultivar plants with and without the disease. Bacterial 16S rRNA gene and fungal ITS metabarcoding were used to study the microbial community composition of 26 soils and 15 roots from banana crops.

Results

16S rRNA analysis showed that Acidobacteria, Proteobacteria, Verrucomicrobia, Actinobacteria, Chloroflexi, Nitrospirae, Firmicutes, Bacteroidetes, Planctomycetes and Gemmatimonadetes were the most abundant phyla in soils and roots, comprising 58.3% of all read sequences. Comparative microbiome analyses performed between healthy and diseased banana plants in *Fusarium* wilt-infested fields in Colombia revealed significant shifts in Chloroflexi, Firmicutes, Bacteroidetes, which were the most abundant in healthy plants, while Nitrospirae was more abundant in diseased plants. ITS analysis showed that Ascomycota, Basidiomycota, Glomeromycota and Zygomycota were the most abundant phyla in soils and roots, comprising 9.44% of all read sequences. (Figure 2).

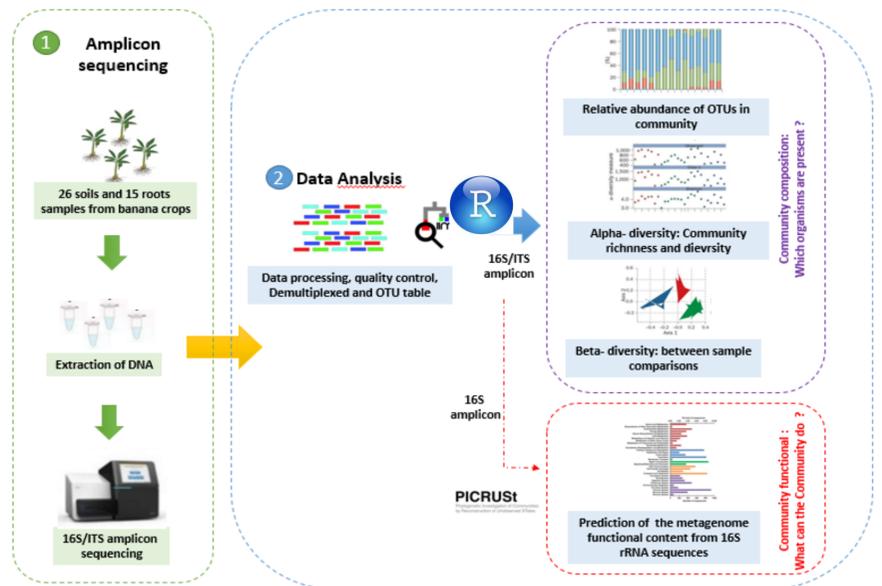


Figure 1: Methodology

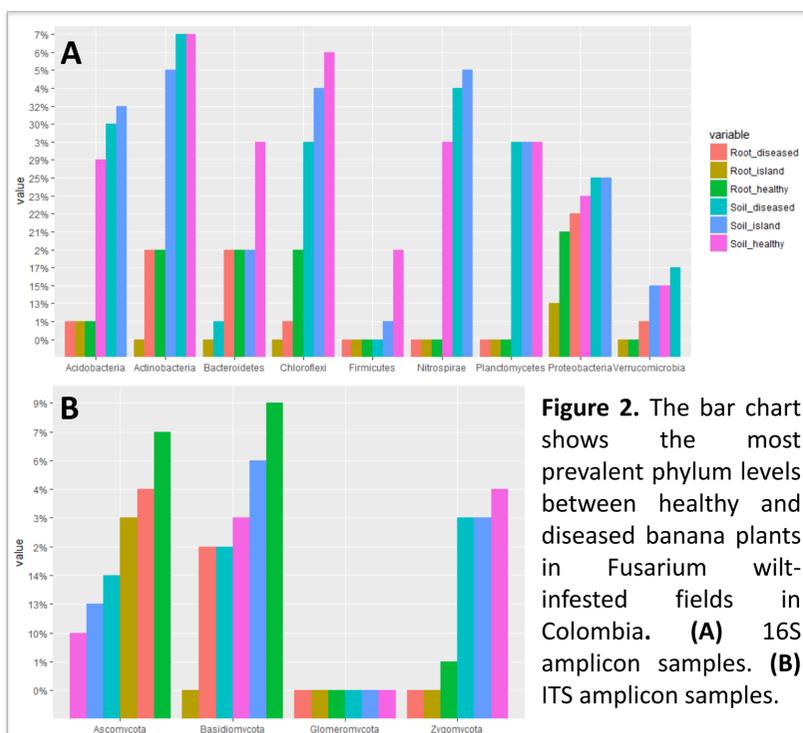


Figure 2. The bar chart shows the most prevalent phylum levels between healthy and diseased banana plants in *Fusarium* wilt-infested fields in Colombia. (A) 16S amplicon samples. (B) ITS amplicon samples.

Moreover, we used PICRUSt to predict the functional composition of each microbial community metagenome based on its 16S profile. When healthy and diseased soil samples were compared, the results showed a decrease of the subcategories carbohydrate, amino acid and energy metabolism pathways, membrane transport, and replication and repair, respectively (Figure 3). In contrast, the comparison between healthy and diseased root samples showed an increase of the subcategories membrane transport, energy, carbohydrate, amino acid, cofactors and vitamins metabolism pathways, in addition to replication and repair (Figure 3).

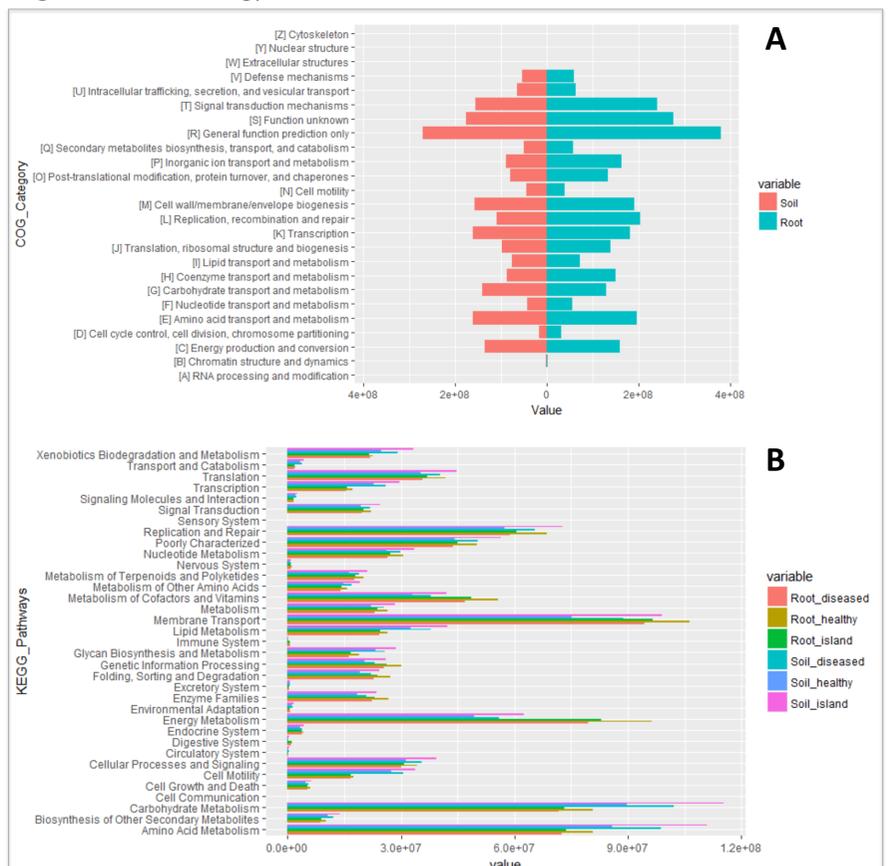


Figure 4: Functional differences, predicted using 16S sequencing data, between healthy and diseased banana plants in *Fusarium* wilt-infested fields in Colombia. (A) Summary of the (values) of COG groups predicted to differ between Root (Pink bars) and Soil (Blue) samples y (B) The bar-plot represents the (values) of KEGG metabolic pathways predicted to be more common among the samples of healthy and diseased banana plants.

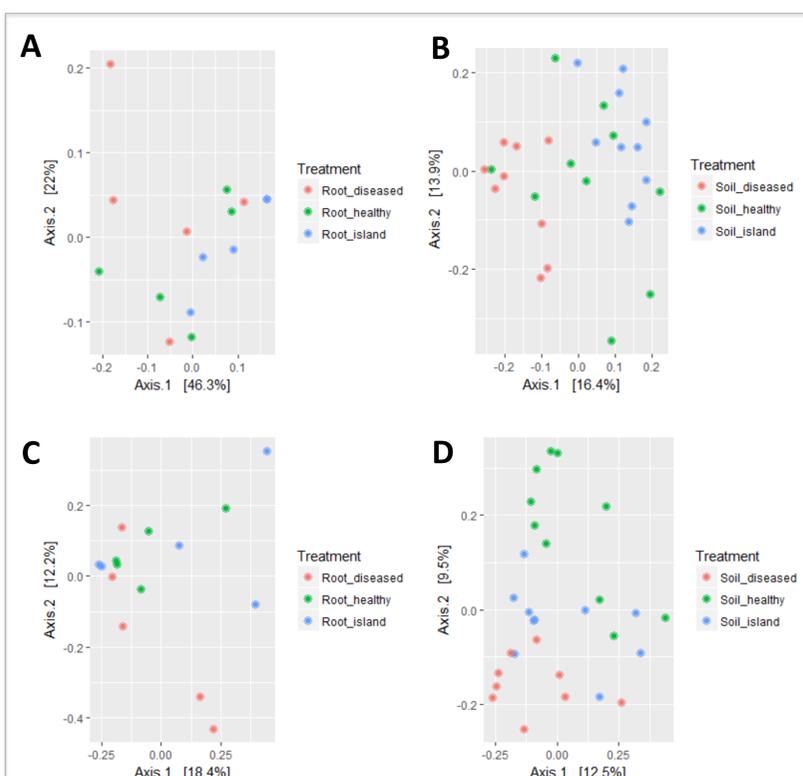


Figure 3. Comparison of beta-diversity between healthy and diseased banana plants in *Fusarium* wilt-infested fields in Colombia, using principal components analysis (PCoA) of Bray-Curtis dissimilarity matrixes. (A-B) PCoA plots of 16S amplicon samples and (C-D) PCoA plots of ITS amplicon samples. For both bacterial and fungal communities, no clear distinction was observed between root (diseased, healthy) and soil (diseased, healthy) samples.

This is the first effort to specifically identify antagonistic and synergistic relationships between microorganisms associated with *Fusarium* wilt disease in Colombia, in order to propose strategies for disease prevention and management. Therefore, metagenomics can represent an important approach for determining crop health.

References

- Shen, Z., Ruan, Y., Chao, X., Zhang, J., Li, R., & Shen, Q. (2015). Rhizosphere microbial community manipulated by 2 years of consecutive biofertilizer application associated with banana *Fusarium* wilt disease suppression. *Biology and fertility of soils*, 51(5), 553-562.
- Shen, Z., Ruan, Y., Xue, C., Zhong, S., Li, R., & Shen, Q. (2015). Soils naturally suppressive to banana *Fusarium* wilt disease harbor unique bacterial communities. *Plant and soil*, 393(1-2), 21-33.

Funding Sources/Acknowledgements

