

## Rhizosphere Microbial Communities in Fynbos Endemic Legumes during Wet and Dry Seasons

**Authors :** Tiisetso Mpai, Sanjay K. Jaiswal, Felix D. Dakora

**Abstract :** The South African Cape fynbos biome is a global biodiversity hotspot. This biome contains a diversity of endemic shrub legumes, including *Polhillia*, *Wiborgia*, and *Wiborgiella* species, which are important for ecotourism as well as for improving soil fertility status. This is due to their proven N<sub>2</sub>-fixing abilities when in association with compatible soil bacteria. In fact, *Polhillia*, *Wiborgia*, and *Wiborgiella* species have been reported to derive over 61% of their needed nitrogen through biological nitrogen fixation and to exhibit acid and alkaline phosphatase activity in their rhizospheres. Thus, their interactions with soil microbes may explain their survival mechanisms under the continued summer droughts and acidic, nutrient-poor soils in this region. However, information regarding their rhizosphere microbiome is still unavailable, yet it is important for Fynbos biodiversity management. Therefore, the aim of this study was to assess the microbial community structures associated with rhizosphere soils of *Polhillia pallens*, *Polhillia brevicalyx*, *Wiborgia obcordata*, *Wiborgia sericea*, and *Wiborgiella sessilifolia* growing at different locations of the South African Cape fynbos, during the wet and dry seasons. The hypothesis is that the microbial communities in these legume rhizospheres are the same type and are not affected by the growing season due to the restricted habitat of these wild fynbos legumes. To obtain the results, DNA was extracted from 0.5 g of each rhizosphere soil using PowerSoil™ DNA Isolation Kit, and sequences were obtained using the 16S rDNA Miseq Illumina technology. The results showed that in both seasons, bacteria were the most abundant microbial taxa in the rhizosphere soils of all five legume species, with Actinobacteria showing the highest number of sequences (about 30%). However, over 19.91% of the inhabitants in all five legume rhizospheres were unclassified. In terms of genera, *Mycobacterium* and *Conexibacter* were common in rhizosphere soils of all legumes in both seasons except for *W. obcordata* soils sampled during the dry season, which had *Dehalogenimonas* as the major inhabitant (6.08%). In conclusion, plant species and season were found to be the main drivers of microbial community structure in Cape fynbos, with the wet season being more dominant in shaping microbial diversity relative to the dry season. *Wiborgia obcordata* had a greater influence on microbial community structure than the other four legume species.

**Keywords :** 16S rDNA, Cape fynbos, endemic legumes, microbiome, rhizosphere

**Conference Title :** ICPFEB 2021 : International Conference on Plant, Food and Environmental Biotechnology

**Conference Location :** Cape Town, South Africa

**Conference Dates :** November 04-05, 2021