

## Phylogenetic analysis of *Aloe* and *Sutherlandia* root microbiome

One of the major challenges of the twenty-first century is global food insecurity. Climate change is predicted to result in extended periods of drought, where crops will be faced with increased temperatures, decreased water availability, and increased salinity. Scientists have identified the need to find sustainable, environmentally friendly approaches to enhance the growth of commodity crops. The use of plant growth promoting bacteria (PGPB) has been identified as a potential "bio-solution". PGPB are microorganisms that colonise plants and establish symbiotic relationships with the host. Actinobacteria are the dominant microbial taxa in terrestrial environments and are known to colonise root surfaces and associated soils, where they establish a beneficial relationship with the plant. During a previous Thuthuka funded project actinobacteria were isolated from two commercially valuable indigenous South African plants, *Aloe ferox* and *Sutherlandia frutescens*. These isolates displayed various plant growth promoting properties. While over 300 actinobacteria were isolated, they were found to belong to a limited number of genera, and therefore are likely not be a true reflection of the full bacterial diversity present in the rhizosphere - it is known that in any environment the 'culturable' organisms are likely to account for less than 1% of the total microbial diversity. Therefore, the aim of the proposed research project is to extend the screening to include full phylogenetic analysis which will identify both the culturable and non-culturable organisms associated with these plants. 16S rRNA gene metagenomic analysis will be performed using both universal- and actinobacteria specific primer sets. This sequence data will be fundamental in understanding these niche environments and assist us to understand various aspects of soil/plant health.