Fusarium spp associated with soils in the greater Karoo area of South Africa

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South Africa as a mega-diverse country has invested significant resources in documenting its aboveground flora and fauna. However, similar research on soil organisms, specifically soil fungi, has been fragmented and poorly integrated. The soil ecosystem plays host to some of the most important plant, human, and animal fungal pathogens. In the past, these have been mainly identified based on morphology. This is time consuming, and commonly leads to erroneous identifications and do not provide a platform for different research sectors to use. Expanding our understanding of the soil fungal communities in South Africa is of great strategic importance. Efforts towards this has been made in the NCF during the past five years as soil forms the basis for the vast majority of our agricultural production and an essential ecosystem service for rural communities. The benefits of soil ecosystem research to improving agricultural productivity, conservation planning, the management of global change, and the maintenance of ecosystem services have been demonstrated internationally (Pimentel et al., 1995) This project will contribute information regarding the distribution of Fusarium as a plant pathogenic genus in the great Karoo area, ear marked for shale gas exploration. This will link in with three projects namely the existing FBIP project on the greater Karoo area, a concluded survey on fungal diversity in the Namaqua National Park and our current survey in the grassland biome of South Africa. Both these biomes are currently under pressure from human developments. It will also contribute to the internet portals for South African soil and plant pathogenic fungal biodiversity, and will be available for research sectors in agriculture and forestry, health, and industry. It will furthermore increase support for the quarantine lists needed by the DAFF to impose agricultural import-export regulations, as our knowledge of the known distribution of this plant pathogenic genus is expand.