



USAID



The African Soil Microbiology project

Don Cowan

**Centre for Microbial Ecology and Genomics
University of Pretoria**

www.up.ac.za/CMEG



BMIF-FBIP workshop, Durban
14-17 August 2017



Centre for Microbial Ecology and Genomics University of Pretoria

3 Academic staff
(Cowan, Makhalanyane, Coutinho)
1 Administrator
1.5 Technicians
14 Postdocs
23 PhDs
15 MSc

“There is no comprehensive survey of the national soil microbiome in South Africa, or across Africa (or anywhere else in the world)”!

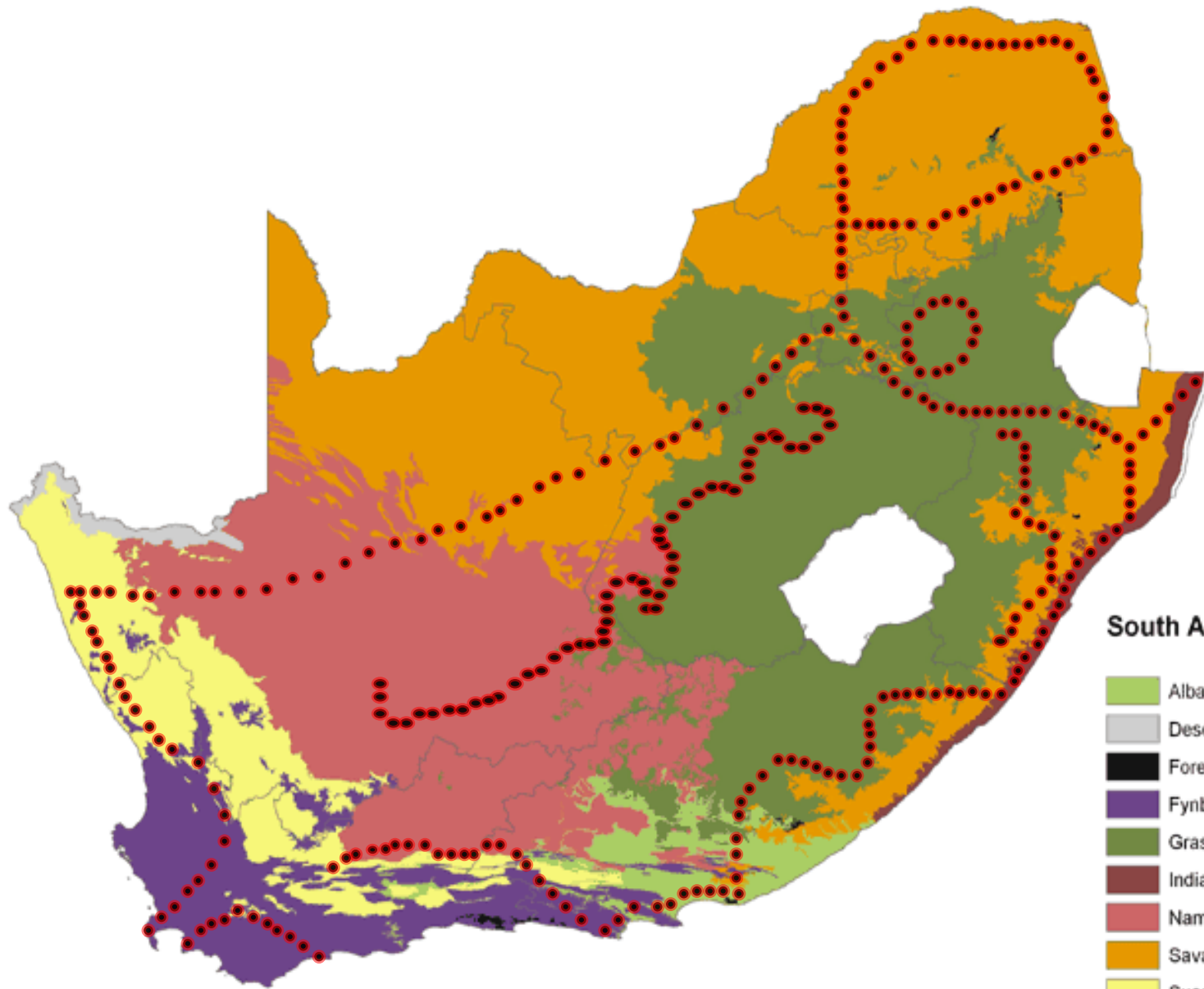


The Project

- A 'low resolution' microbial community survey of soils across sub-Saharan Africa
 - ❖ Acquisition of soil samples from participating nations
 - ❖ Phylogenetic fingerprinting of bacterial communities using NG sequencing of 16S amplicon sets
 - ❖ Physicochemical analysis of soil samples
 - ❖ Interpretation of community composition in terms of soil physicochemical properties and macro-environmental parameters

The basic numbers

- 10 nations: South Africa, Namibia, Botswana, Zimbabwe, Mozambique, Zambia, Kenya, Ethiopia, Cote D'Ivoire, Benin
- Plus a limited number of random samples from Angola, Tunisia
- Total budget: \$435,000
- 1000 samples
- Samples per nation defined by land area
- Sampling intervals: 50 km



South Africa's nine biomes

- Albany Thicket Biome
- Desert Biome
- Forests
- Fynbos Biome
- Grassland Biome
- Indian Ocean Coastal Belt
- Nama-Karoo Biome
- Savanna Biome
- Succulent Karoo Biome

Site data capture

- Sample number/code
- Time and date
- GPS location (decimal degrees)
- Altitude
- Aspect/Slope
- Local vegetation type
- Local ground characteristics
- Other notable characteristics
- Representative photographs of site and location

Analysis; Phylogenetics

- Metagenomic DNA extraction
- DNA concentration and quality
- 16S rRNA gene amplification
- Next Generation Sequencing (Illumina MiSeq)
- Bioinformatics: Phylogenetic assignments
- Correlation analysis with macro- and microenvironmental parameters

Level One Data Generation

- 1000 16S rRNA gene sequence data sets
 - For each data set, 10^5 sequences of 300 bp: 30 million bp
- Total dataset, 30 billion bp
- Representing 10000 to 100000 prokaryotic phylotypes

Data Interpretation

- Phylogenetic assignments (at various taxonomic levels)
- Estimates of α and β diversity, diversity indices
- Correlation analyses with physicochemical properties, regional and national locations, climate zones, biome types, land and agricultural use, etc.
- Identification of differentially abundant taxa (biomarkers)
- Identification of core taxa
- Putative interaction between taxa: Network analysis

Outputs

- The 'first ever' survey of African soil microbiomes
- Correlation of microbiome fingerprints with region, biome, soil type, macroclimate, land-use
- Primary phylogenetic dataset for future re-analysis, comparison etc.
- The role of microbes in ecosystem services, ecosystem sustainability and resilience to climate change
- The soil microbiomic genetic resource

Where next?

- Increase regional coverage (more partner nations)
- Increase survey resolution
- Expand phylogenetic coverage
 - Other taxa
- Extract functional capacity data
 - Full metagenome sequencing
 - Soil health metrics

Thank you.

