

Characterizing fungal diversity associated with maize produced in the Eastern Cape

Fighting world hunger is one of the world's biggest problems and forms part of the United Nations SDG2 of zero hunger. High-quality crops and a reduction of waste is thus of great importance. Unfortunately, South Africa has seen an increase in mycotoxin levels the past three seasons in both white and yellow maize. To better understand this, it is important to identify the fungi present on maize samples. This project thus aims to isolate and identify fungi from stored maize samples collected in the Eastern Cape from commercial, small-scale and emerging farmers. Isolation efforts will target the total community, but efforts focused on the mycotoxigenic genera like *Aspergillus*, *Penicillium* and *Fusarium*. These genera produce the major regulated mycotoxins, namely aflatoxins, zearalenone, trichothecenes, fumonisins and ochratoxin A, at a great cost to the global economy and place food security at risk. Currently, the fungal communities associated with maize is not well characterised. Past diversity studies either did not employ modern species identification methods or focused isolation on specific genera. We do expect diverse communities, but it will be dominated by *Aspergillus*, *Penicillium* and *Fusarium*. These have well defined modern taxonomies with identifications in most cases possible using a single DNA sequence, thanks to recent sequencing efforts. Expansion of these efforts is needed to further capture the diversity and make the database even more robust. The less common genera will present a different challenge as morphology will be needed in many cases to confirm identifications, while we expect to find many new species. This project will thus not only generate baseline knowledge needed for future projects, but will also make valuable contributions to the taxonomy and identification of *Aspergillus*, *Penicillium* and *Fusarium*, and many other less studied or isolated genera.