

## Global Change Research Plan (GCRP) Programmes and Projects OVERVIEW July 2021

Programme	Title of the Project and research team	Project Overview	Objectives/ Outcomes
		<p><b>Foundational Biodiversity Information Programme (FBIP)</b> Foundational biodiversity Information is considered to be fundamental to all biodiversity-related disciplines and forms the base of a value chain which ultimately delivers economic development through the bioeconomy, and ensures that ecological infrastructure that provides essential services is sustained. However, the biodiversity information required for this foundation or base is scattered and in many cases inaccessible to users of the data. In addition, critical gaps exist in exiting knowledge and so strategic research is required. In 2013, the Department of Science &amp; Technology integrated its previously supported programmes (the South African Biosystematics Initiative (SABI), the South African Biodiversity Information Facility (SABIF) and those national projects that had requested funding in the discipline by establishing the Foundational Biodiversity Information Programme (FBIP).</p> <p>The FBIP is a long-term programme to enable the generation and dissemination of foundational biodiversity knowledge, and to ensure that the knowledge and data generated by the programme will contribute to improved decision-making, service delivery and the creation of new economic opportunities. The FBIP is positioned as the basis for decision-making which will promote human well-being, and as a catalyst for the bio-economy which will promote sustainable development. The main themes of the programme align with those of two of the DSI Grand Challenges, i.e. Global Change and the Bio-economy. The primary focus of the programme is to generate knowledge relevant to essential biodiversity variables (EBVs) which include species occurrence, species identity, population abundance, and phylogenetic / DNA information. These data sets are critical for ecosystem mapping, monitoring and reporting on the state of biodiversity, for sustainable use of biodiversity, and for understanding and mitigating the impacts of global change on biodiversity.</p> <p>The programme includes the funding of large, collaborative projects which align with knowledge needs, or which involve participants along the entire value chain from knowledge generation to application for decision-making. A number of smaller grants are also available for researchers to address strategic gaps in information not aligned with any of the larger funded projects. The outputs of the programme are foundational to protecting South Africa’s ecological infrastructure on which many industries and communities depend for their livelihood and to support the sustainable use of components of biodiversity. The funded projects will generate species occurrence data, DNA barcode and phylogenetic data, descriptive information on species, and will ensure that the knowledge is coordinated, managed and disseminated through a comprehensive web-based system. Monitoring of the uptake and impact of the knowledge generated will allow the development of an understanding of best practice for ensuring that research outputs do have an impact on global change understanding and decision-making relating to biodiversity and sustainable livelihoods. These projects also include postgraduate students and emerging researchers, and up-skilling of researchers and practitioners who use the data generated.</p>	

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<b>Foundational Biodiversity Information Programme (FBIP)</b>	<p><b><u>Large Projects</u></b></p> <p>1. Defining functional microbiomes of two major crops in South Africa for improved productivity.</p> <p><b><u>Research Team:</u></b>            Prof Shayne Jacobs, Stellenbosch University (<a href="mailto:sjacobs@sun.ac.za">sjacobs@sun.ac.za</a>)            Dr Marcellous Le Roux, Stellenbosch University (<a href="mailto:mrl@sun.ac.za">mrl@sun.ac.za</a>)            Prof Hugh Patterton, Stellenbosch University (<a href="mailto:hpatterton@sun.ac.za">hpatterton@sun.ac.za</a>)            Dr Jan Greyling, Stellenbosch University (<a href="mailto:jancg@sun.ac.za">jancg@sun.ac.za</a>)            Dr Johann Strauss, Elsenburg Agricultural Research Centre (<a href="mailto:JohannSt@elsenburg.com">JohannSt@elsenburg.com</a>)            Dr Thulani Makhalanyane, University of Pretoria (<a href="mailto:thulani.makhalanyane@up.ac.za">thulani.makhalanyane@up.ac.za</a>)            Prof Angel Valverde, University of the Free State (Bloemfontein Campus) (<a href="mailto:ValverdePortalA@ufs.ac.za">ValverdePortalA@ufs.ac.za</a>)            Dr Riana Jacobs-Venter, Agricultural Research Council (South Africa), Plant Protection Research Institute (<a href="mailto:JacobsR@arc.agric.za">JacobsR@arc.agric.za</a>)            Dr Cobus Visagie, Agricultural Research Council (South Africa), Plant Protection Research Institute (<a href="mailto:VisagieC@arc.agric.za">VisagieC@arc.agric.za</a>)</p>	<ul style="list-style-type: none"> <li>- Agriculture significantly contributes to the South African economy and has been recognized as a sector, which could potentially drive economic growth. However, less than 12% of the country's land mass is suitable for use as arable land. Alarming, substantial proportions of soils are subject to increased desertification, reducing the proportion of productive lands. Given South Africa's increasing population, increasing the productivity of arable lands is crucial for sustenance. Over the last few years, there has been a significant demand on the farming sector to alter agricultural practices while simultaneously improving yield. It is increasingly recognized that soil microbiomes play crucial roles in nutrient cycling, soil formation, plant growth and ultimately in the production of food.</li> </ul>	<ul style="list-style-type: none"> <li>- Understanding the microbiome has clear and very practical applications. It provides us with a tool to measure and monitor changes. Knowledge of microbiome dynamics will allow stakeholders to assess practices that may encourage or disrupt these communities. It will allow for precision/smart farming on a micro scale to better manage inputs and practices. Developments in analytical approaches, such as high throughput sequencing and culture methods, helped to reduce the knowledge deficit around microbial diversity and their specific roles. The power of this approach has been evident in the study of the human microbiome, which revolutionized our perception, diagnosis and treatment of diseases. This study has a direct impact on the bioeconomy as it informs managing inputs and.</li> </ul>

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	<p>Prof J Dames, Rhodes University (j.dames@ru.ac.za)            Dr Bronwyn Kirby-McCullough, University of the Western Cape (bkirby@uwc.ac.za)</p> <p><b><u>Project Start Date:</u></b>            2019</p> <p><b><u>Contact Details for Project Leader:</u></b>            Prof Karin Jacobs (kj@sun.ac.za)</p> <p>2. Biodiversity of the Waterberg Mountain Complex</p> <p><b><u>Research Team:</u></b>            Prof Catherine Sole, University of Pretoria (<a href="mailto:cathrine.sole@up.ac.za">cathrine.sole@up.ac.za</a>)</p>	<p>- The Waterberg Mountain Complex (hereafter WMC) is a discrete geological entity situated in Limpopo Province. Previously an agricultural area, there have been considerable changes in land use to conservation and eco-tourism activities, and one third of the region has been declared a UNESCO Waterberg Biosphere Reserve (WBR). In addition, the Marakele National Park is also situated in the WMC and is part</p>	<p>- Propose the establishment of a multidisciplinary foundational baseline biodiversity data gathering project in the WMC, which will provide much needed data and information for the management of the various Waterberg conservation areas and bordering regions. The data generated through this project will support the conservation and</p>

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	<p>Dr Darragh Woodford, University of the Witwatersrand (<a href="mailto:darragh.woodford@wits.ac.za">darragh.woodford@wits.ac.za</a>)</p> <p>Dr Albert Chakona, South African Institute for Aquatic Biodiversity (SAIAB) (<a href="mailto:a.chakona@saiab.ac.za">a.chakona@saiab.ac.za</a>)</p> <p>Mr Werner Conradie, Port Elizabeth Museum at Bayworld (<a href="mailto:werner@bayworld.co.za">werner@bayworld.co.za</a>)</p> <p>Prof Peter le Roux, University of Pretoria (<a href="mailto:peter.leroux@up.ac.za">peter.leroux@up.ac.za</a>)</p> <p>Mr Pieter Bester, South African National Biodiversity Institute (SANBI) (<a href="mailto:p.bester@sanbi.org.za">p.bester@sanbi.org.za</a>)</p> <p>Dr Teresa Kearney, Ditsong National Museum of Natural History (<a href="mailto:kearney@ditsong.org.za">kearney@ditsong.org.za</a>)</p> <p>Prof Dan Parker, University of Mpumalanga (<a href="mailto:tjobosa@gmail.com">tjobosa@gmail.com</a>)</p> <p>Prof Martin Potgieter, University of Limpopo (<a href="mailto:martin.potgieter@ul.ac.za">martin.potgieter@ul.ac.za</a>)</p> <p>Dr Angelique Kritzinger, University of Pretoria (<a href="mailto:angelique.kritzinger@up.ac.za">angelique.kritzinger@up.ac.za</a>)</p> <p>Prof Paulette Bloomer, University of Pretoria (<a href="mailto:paulette.bloomer@up.ac.za">paulette.bloomer@up.ac.za</a>)</p> <p>Dr Mark Keith, Institution University of Pretoria (<a href="mailto:mark.keith@up.ac.za">mark.keith@up.ac.za</a>)</p>	<p>of the WBR, as are some of the Limpopo Department of Economic Development, Environment and Tourism (LEDET) reserves. While thus enjoying some environmental protection, proposed coal mines and related infrastructure projects on the northern borders of this area represent a major potential environmental conflict, and will impact the ecological integrity of the WMC. The WMC is a region of special conservation concern. However, despite being situated a mere 2 to 3 hours from Pretoria where there is a hub of plant and animal biodiversity scientists, and the fact that it includes a large part of the Waterberg Biosphere Reserve, there has never been a comprehensive and structured biodiversity survey of the WMC</p>	<p>management activities of numerous stakeholders in the region.</p>

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	<p><b><u>Project Date:</u></b> 2021</p> <p><b><u>Contact Details of the Project Leader:</u></b> Prof Nigel Barker (<a href="mailto:nigel.barker@up.ac.za">nigel.barker@up.ac.za</a>)</p> <p><b><u>Small Grants Projects</u></b></p> <ol style="list-style-type: none"> <li>1. Barcoding of Forest Birds of the Eastern Cape</li> </ol>	<ul style="list-style-type: none"> <li>- Forests make up only 0.56% of SA but display unusually high biodiversity. Naturally patchy, they have been further fragmented by human activities: nearly 50% of indigenous forests are estimated to have experienced anthropogenic fragmentation, which together with the introduction of alien plantations, has led to range changes in dependent faunal species. Recent work has shown that half of SA forest dependent bird species have experienced range declines since 1992, mostly in the Eastern Cape. The primary causes of these declines appear to have been forest degradation, as forest cover has increased over this period. Forests are important in terms of the bio-economy as they have traditionally been harvested by local rural communities. Post-democracy they have experienced increased pressure from informal harvesters, particularly for timber for building and crafts; and bark for medicine. Degradation occurs where utilization of particular tree species leads to declining</li> </ul>	<ul style="list-style-type: none"> <li>- Proposed area of study forms part of the Maputaland-Pondoland-Albany Biodiversity Hotspot. Eastern Cape forest faunal diversity has been poorly documented, despite the province containing 46% of SA's natural forests.</li> </ul>

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		<p>forest condition, although boundaries may remain intact. Our proposed area of study forms part of the Maputaland-Pondoland-Albany Biodiversity Hotspot. Eastern Cape forest faunal diversity has been poorly documented, despite the province containing 46% of SA's natural forests. Forests make up only 0.56% of SA but display unusually high biodiversity. Naturally patchy, they have been further fragmented by human activities: nearly 50% of indigenous forests are estimated to have experienced anthropogenic fragmentation, which together with the introduction of alien plantations, has led to range changes in dependent faunal species. Recent work has shown that half of SA forest dependent bird species have experienced range declines since 1992, mostly in the Eastern Cape. The primary causes of these declines appear to have been forest degradation, as forest cover has increased over this period. Forests are important in terms of the bio-economy as they have traditionally been harvested by local rural communities. Post-democracy they have experienced increased pressure from informal harvesters, particularly for timber for building and crafts; and bark for medicine. Degradation occurs where utilization of particular tree species leads to declining</p>	

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	<p>2. Diversity and DNA barcodes of Succulent Karoo spiders</p>	<p>forest condition, although boundaries may remain intact.</p> <ul style="list-style-type: none"> <li>- Spiders (Araneae) are important arthropods in all terrestrial ecosystems, where they contribute significantly to the regulation of prey populations. South Africa has a rich fauna of spiders, with 2253 spp. recorded (4.6% of global diversity), with approximately 60% of the species endemic to the country. Although the South African National Survey of Arachnida (SANSA) was very successful in identifying gaps in the distribution of South African spiders, large parts of the Succulent Karoo (SKB) and Desert biomes (DB) remain poorly sampled. This study aims to sample in five degree-squares in western South Africa. We will use a standardized protocol to collect in four biotopes per degree-square (e.g. open plain, riparian vegetation, eastern and western slopes of a hill), in both summer and winter, to generate comparable datasets to determine local species richness, as well as species turnover between sites. Further, we will provide DNA barcodes of 95 specimens per degree square to aid in identification of species and matching sexes, particularly for rare or understudied taxa.</li> </ul>	<ul style="list-style-type: none"> <li>- Through this work, we hope to make a considerable contribution towards understanding the biodiversity and conservation importance of non-acarine arachnids in the western parts of the SKB and the DB.</li> </ul>

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	<p>3. Marine molluscs from KwaZulu-Natal</p> <p>4. Taxonomy</p>	<ul style="list-style-type: none"> <li>- Baseline knowledge in the form of accurately identified occurrence records, supported by a sound taxonomic backbone, underpins robust multidisciplinary research programmes. Such research programmes which inform evidence-based policy and management advice ultimately sustain the effective utilisation of our bio-economies. However, for South Africa's marine benthic invertebrates there is a lack of baseline or foundational knowledge, mostly due to the difficulty of sampling offshore habitats. Traditionally, marine molluscs, South Africa's most specious marine taxa, have been relatively well documented, due to the efforts of the Natal Museum Dredging Programme (NMDP) in the 1980s and 90s. However, much of the expertise on the taxonomy of our marine molluscs will soon be lost. In addition, this programme was conducted before the genome revolution, meaning that critical genomic data was not collected and curated.</li> <li>- Taxonomy has played an important role in diversity assessment. It provides an understanding of biodiversity components that are essential for making decisions on conservation and sustainable use and is also</li> </ul>	<ul style="list-style-type: none"> <li>- To ensure that these skills remain within South Africa's marine biodiversity expertise, this project aims to return to the NMDP sampling sites in the KwaZulu-Natal region and in doing so fulfil other missing foundational biodiversity information needs. In addition to contributing to the sediment database of the South African Marine Research and Exploration Forum, through this project, we aim to produce new occurrence records, new DNA barcodes, and new photoquadrats, and at the same time collect data which will allow us to investigate benthic community change over time, giving insight into global change research. Finally, through engagement with current specialists in marine molluscs' taxonomy, we aim to ensure timeous knowledge transfer and continued research on South Africa's mollusc species.</li> <li>- This project is aiming to 1) resolve taxonomic challenges in two ant groups: Anoplolepis and the Camponotus fulvopilosus species-group including the production of updated identification keys</li> </ul>



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	<p>5. Phylogenetic analysis of Aloe and Sutherlandia root microbiome</p>	<p>a foundation for phylogenetic studies. This field of study has played an important role in identifying and describing biodiversity, but the issue of cryptic species has posed many taxonomic challenges. In most taxonomic groups, species with subtle differences and high intraspecific variation are often misidentified when morphological data is not supported by other methods, for example, genetic data. The misidentification of ecologically important species may have a negative impact in conservation decision-making. In addition, overlooking the presence of a new invasive species could cause ecosystem collapse if not detected and controlled in time.</p> <p>- 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</p>	<p>for the species; and the description of six new species; 2) resolve the taxonomic challenges in these two ant genera using molecular data, with 285 specimens submitted for barcoding; 3) to understand and update the geographical distribution of species within Anoplolepis and the Camponotus fulvopilosus species-group; and 4) to investigate the distribution and abundance of an invasive ant species, A. gracilipes, and its potential impact on indigenous ant populations. A total of at least 1,500 new records will be added to the collection. In summary, this project will develop scarce skills such as the taxonomic identification and the descriptions of new species, the barcoding of specimens, and the overall revision of these two economically and ecologically important ant groups.</p> <p>- 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</p>

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	<p>6. Systematics of the genus <i>Eriosema</i></p>	<p>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, <i>Aloe ferox</i> and <i>Sutherlandia frutescens</i>. 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.</p> <p>- The genus belongs to the large and very diverse flowering plant family Fabaceae and within the subfamily Papilionoideae, tribe Phaseoleae and subtribe Cajaninae. It is</p>	<p>sequence data will be fundamental in understanding these niche environments and assist us to understand various aspects of soil/plant health.</p> <p>- The aim of the study is to undertake a comprehensive taxonomic revision of the genus <i>Eriosema</i> and reconstruct a phylogenetic tree of the relationship</p>

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	<p>7. Zoonotic disease burdens in rural communities: Rodent microbiome surveillance and cataloguing emerging rickettsial species diversity</p>	<p>characterised by erect or climbing subshrubs or herbs with unifoliolate or trifoliolate leaves and leaflets that often have small glands underneath. The flowers are reflexed, have a 5-lobed calyx and mainly yellow corolla. The genus is distributed worldwide but mostly found in tropical areas and comprises about 150 species, with 100 of them occurring in Africa and 36 in South Africa. The genus has not never been revised neither in its entirety worldwide nor in southern Africa. Therefore, correct identifications have become difficult, compounded by the fact that introgressive hybridisation is common. Furthermore, species distribution ranges are not well-known. The infrageneric and infraspecific phylogenetic relationships of this genus remain unknown due to the fact previous phylogenetic studies have included only one African species or no species from this genus.</p> <p>- As in the rest of Africa, undifferentiated febrile illness is among the most common presenting signs in patients seeking medical care at the health clinics in the Mnisi community, Mpumalanga, South Africa (SA); an area of high rural poverty. Fever is often misclassified as malaria; understanding of</p>	<p>within the genus based on morphological and molecular data.</p> <p>- The aim of the study is to continue cataloguing the bacterial pathogen strain diversity present in rodents trapped in households in the community using a metagenomics approach. We will also molecularly characterize known and hitherto uncharacterized <i>Rickettsia</i> spp. in</p>

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		<p>aetiologies is limited. Recent research suggested that rodent-borne zoonoses may be common aetiologies for febrile illness in Mnisi; patients showed exposure to spotted fever group Rickettsia, Coxiella burnetii, Bartonella and Leptospira spp. Spotted fever rickettsioses are one of the emerging infectious diseases to which little attention has been accorded. A recent study recorded a high diversity of Rickettsia spp. In rodents across SA. Rodents are abundant in the Mnisi community; 76% households see rodents in and around their homes. The potential contribution of rodent pathogen transmission to human febrile illnesses in rural communities is of concern; active surveillance for potential pathogens is of utmost importance to predict and combat emerging diseases. This study will build on our previous study which provided a synoptic insight into the zoonotic bacterial pathogen diversity in rodent blood in Mnisi. We have since also shown that Amblyomma hebraeum, the most abundant tick in the community and known for its aggressiveness and readiness to bite humans, are significantly dominated by zoonotic Rickettsia spp.</p>	<p>rodents, ticks and fleas. We will provide information about zoonotic pathogens in SA, and will generate genomic data that will form the basis for the development of diagnostic tests to be implemented in rural communities ensuring appropriate interventions and benefiting human health and well-being.</p>

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	<p>8. DNA barcoding of ectotherm blood parasites from Southern Africa to provide a genetic and evolutionary perspective.</p>	<ul style="list-style-type: none"> <li data-bbox="1014 292 1612 1149">- It is estimated that more than half of the human population and even more animals suffer from parasitic infections. However, parasites not directly associated with human or livestock disease are often understudied or have limited data available. When trying to understand the phylogenetic placement of these human or livestock infecting parasites, their relationships with other closely related taxa becomes more important. For example, gaining insights from the phylogenetic relationships of ectotherm blood parasites may provide a better perspective of why certain parasites do not produce the same disease severity as seen in their close relatives of mammalian and avian hosts. Research completed on ectotherms blood parasites from South Africa, strongly suggests that besides general biodiversity surveys and describing new species, molecular data specifically for mtDNA barcoding markers are lacking, as most molecular data available for ectotherm blood parasites are from the conservative nuclear 18S rRNA gene.</li> <li data-bbox="1014 1228 1612 1361">- In winemaking processes, there is a growing interest to return to tradition and develop spontaneous fermentations taking advantage of the metabolic diversity derived from the</li> </ul>	<ul style="list-style-type: none"> <li data-bbox="1635 292 2197 790">- The study aims to develop a basis for generating the first COI barcodes of complex and understudied parasite taxa of ectotherm hosts. NGS will be used to initially sequence the full mtDNA genomes for selected parasites, to provide data to develop universal barcoding primers for a broad range of parasite taxa. Furthermore, this study is a joint venture between the Biochemistry and Zoology departments of the North-West University (NWU) and the Department of Zoology and Entomology, of the University of the Free State, Qwaqwa campus.</li> <li data-bbox="1635 1260 2197 1361">- The study aims to perform phylogenetic surveys of Pinotage (a unique South African varietal) from three wine</li> </ul>

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	<p>9. Biogeographical patterns of Pinotage grape microbiomes in South African wine regions</p> <p>10. Reclaiming the guernsey lilies: Phylogeny and vulnerability of endemic bulbous monocots</p>	<p>great microbial diversity present in grape musts. However, in order to successfully manage such processes it is important to have a good grasp of the spatial and temporal distribution of the grape-associated microbiomes. In particular, knowledge of the vintage shifts in fermentative microbiota as well as potential grape and wine spoilage organisms is pivotal towards creating a database which can be a source of information for winemakers. Modelling such microbial data to climatic data can help viticulturalists and winemakers manage their farm practices as well as cellar interventions to produce good quality wines that keep South Africa as a strong competitor in the global market.</p> <p>- In South Africa plant biodiversity is an extremely important source of economic revenue via ecotourism (e.g. the flower season in Namaqualand), traditional medicine, horticulture and agricultural practices, but it is currently under threat. In this project, we will focus on the species from the subtribe Strumariinae (Amaryllidaceae, seven genera, ~87 known species), several of which are endemic to South Africa and used in traditional medicine, while the majority are</p>	<p>producing regions and integrate them with climatic data to generate a database that can be accessible to all wine producers.</p> <p>- This project will consolidate existing biodiversity data in collections and expand it with intensive field surveys of an estimated 60 taxa. Information to be collected includes current distribution ranges, locality data, abundance estimates, morphological traits, herbarium vouchers, photographs and material suitable for DNA studies. We intend to sequence two barcoding regions for the 60 species, generating new</p>

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	<p>11. Characterizing fungal diversity associated with maize produced in the Eastern Cape</p>	<p>of horticultural importance. As a consequence of this cultural and commercial interest, many of the Strumariinae species in South Africa are currently threatened due to habitat loss and over-harvesting. Previous global phylogenetic studies of the family were limited to one specimen per species and revealed non-monophyletic relationships within genera, most obviously in Nerine, Hessea and Strumaria.</p> <ul style="list-style-type: none"> <li>- This taxonomic ambiguity requires revision using a more comprehensive local sampling scheme to fully assess and document the extant number of species occurring in South Africa.</li> <li>- 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.</li> <li>- These genera produce the major regulated mycotoxins, namely aflatoxins, zearalenone, trichothecenes, fumonisins and ochratoxin A,</li> </ul>	<p>barcoding data for up to 200 specimens, with multiple samples per taxa, to help disentangle the evolutionary relationships within this group. The findings of this project will greatly aid in understanding current patterns of distribution of plant biodiversity in South Africa, as well as in the establishment of future conservation plans to ensure the long-term persistence of this valuable and iconic group of plants.</p> <ul style="list-style-type: none"> <li>- The 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.</li> <li>- 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</li> </ul>

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	12. DNA barcoding zooplankton	<p>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 <i>Aspergillus</i>, <i>Penicillium</i> and <i>Fusarium</i>. 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.</p> <ul style="list-style-type: none"> <li>- Zooplankton play an essential role as secondary producers in marine pelagic food webs and typically exhibit rapid responses to environmental change making them suitable as indicators of ecosystem health and biodiversity. However, they are notoriously difficult to identify using taxonomic keys. DNA barcoding and metabarcoding have been proposed to rapidly characterize</li> </ul>	<p>and <i>Fusarium</i>, and many other less studied or isolated genera.</p> <ul style="list-style-type: none"> <li>- The project will generate DNA barcode records (COI) and 16S rDNA sequences for zooplankton groups focusing on the Euphausiidae (krill), Amphipoda and Chaetognatha (arrow worms). These groups have thus far been neglected for DNA barcoding studies. The potential impacts of this study will be contributions to generating a comprehensive DNA</li> </ul>



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	<p>13. An integrative morphological-molecular taxonomic study of marine copepods: building a DNA reference library of metabarcoding studies</p>	<p>biodiversity but require taxonomically complete and geographically comprehensive reference databases of DNA sequences to accurately identify organisms to species level. There is a paucity of DNA barcode records for marine zooplankton taxa occurring in South African waters.</p> <p>- The recent development of DNA metabarcoding protocols has the potential to transform marine biodiversity research, by enabling rapid and accurate species identification of bulk zooplankton samples. Metabarcoding protocols require that robust DNA barcode reference libraries are developed, in which DNA barcodes of individual species are linked with validated taxonomic descriptions of morphospecies. To date, few or no molecular records are</p>	<p>barcode reference library for zooplankton. It will also provide unique opportunities for discovery of new species, for revision of taxonomic ambiguities, and highlight key species for further phylogenetic studies using suites of molecular markers. The reference library will greatly enhance the potential of using DNA metabarcoding for swiftly surveying biodiversity and as a tool for long-term monitoring of zooplankton assemblages at selected sentinel sites. Rapid and long-term monitoring surveys of zooplankton diversity will be important for benchmarking present biodiversity so that future shifts in species distribution due to climate change can be measured.</p> <p>- The study aims to bridge this knowledge gap by establishing a validated DNA barcode reference library for calanoid copepods. The project will contribute data towards the basic understanding of marine biodiversity in South African waters, contribute to the global databases on marine biodiversity (i.e. Genbank, BOLD).</p>

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	14. Taxonomy of sponges	<p>available for calanoid copepods occurring in South African marine waters. Calanoida is central to trophic links between phytoplankton and commercially important fish stocks, but their taxonomy is still poorly understood with the validity of some species questioned by genetic data.</p> <ul style="list-style-type: none"> <li>- Sponges are important as habitat forming organisms, indicators of environmental health, known sources of biomedical compounds and amongst the top taxa that contribute to fouling. The available literature indicates that at present 327 sponge species are known from South Africa. The majority of these species have been described during the last century with sampling effort focused on the deep-waters of the south-east coast and shallow waters of the west coast of South Africa (see Samaai et. al., 2005). More recently, research by partner institutions and programmes such as DEFF, SAEON, SANBI and ACEP has been focused on broadening sampling effort and focusing on deeper water in order to gain a better understanding of the diversity of benthic invertebrate taxa with the South African EEZ. However, beyond the capacity of the current applicant no</li> </ul>	<ul style="list-style-type: none"> <li>- The project aims to provide modern e-taxonomy tools that include online image rich keys, genetic barcodes and high quality specimen occurrence data of South African sponge species that are collated from local and international natural history collections.</li> </ul>

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	<p>15. Horse fly taxonomy: an integrated approach</p>	<p>appropriate tools exist for the biodiversity applied researcher to identify sponge species (or more specifically those sponge species of interest).</p> <ul style="list-style-type: none"> <li>- Tabanidae, commonly known as horse flies, are a diverse family of flies, comprising approximately 4400 species distributed worldwide. They are both pollinators and vectors of viruses, bacteria, protozoans and filarial worms. Despite their importance as pollinators and vectors of disease-causing pathogens, the taxonomy of this family is complicated and not well resolved - this is particularly true of the Afrotropical fauna. Efforts regarding the higher classification have revealed paraphyly in the classification of subfamilies and tribes alike. The Tabaninae, comprising over 70% of described horse fly species are especially misunderstood with regards to the taxonomy. This is mostly due to a single genus, <i>Tabanus</i> which is in special need of reclassification. As <i>Tabanus</i> species have been shown to be vectors of pathogens, it is important for farmers and veterinarians to be able to identify these species. This is not possible with the current taxonomic confusion.</li> </ul>	<ul style="list-style-type: none"> <li>- The project aims to clarify the taxonomy of <i>Tabanus</i> by phylogenetic analysis, providing new occurrence records and producing species pages which will assist with identification of these flies. Baseline knowledge in the form of accurately identified occurrence records, supported by a sound taxonomic backbone, have the potential to reduce financial losses experienced by farmers due to pathogens spread by tabanids.</li> </ul>

Programme	Title of the Project and research team	Project Overview	Objectives/ Outcomes
	16. Microbial diversity	<ul style="list-style-type: none"> <li>- The ocean microbial community (microbiome) is vital to its overall function. Its diversity, however, is not well investigated. In the Southern Benguela upwelling region, in particular, it is virtually unknown. Yet, this knowledge is vital in order to properly assess ocean ecosystem health and, more importantly, provide accurate input into ecosystem models. Our lab is finishing up a three-year NRF study focusing on the Southern Benguela microbiome, which has generated more samples than we can afford to sequence. This study, if funded, will sequence key members of the ocean microbiome in the Southern Benguela upwelling region and elucidate their overall functioning alongside those already sequenced in the current study. The availability of new next-generation sequencing technology (a MinION ion torrent sequencer, recently acquired in our lab) allows for in-depth, multiplexed sampling in real time, quickly and relatively cheaply. This funding would allow us to further sequence existing samples using the MinION. The resulting data would allow us to use the information from the samples to their full potential. It would also contribute key knowledge to AtlantECO, a European Commission funded H2020 project.</li> </ul>	<ul style="list-style-type: none"> <li>- The aim of the project is to further sequence existing samples using the MinION. The resulting data would allow us to use the information from the samples to their full potential. It would also contribute key knowledge to AtlantECO, a European Commission funded H2020 project. The aim of AtlantECO is to determine the structure and function of the Atlantic microbiome in the context of ocean circulation and presence of pollutants, to assess its role in driving the dynamics of Atlantic ecosystems at basin and regional scales. We will contribute to AtlantECO.</li> </ul>

Programme	Title of the Project and research team	Project Overview	Objectives/ Outcomes
	17. Oomycete diversity in three coastal reserves in the Cape Floristic Region	<ul style="list-style-type: none"> <li>- Oomycetes are fungus-like organisms commonly found in soil and aquatic environments. Several oomycetes are known for their devastating impact on food security or naturally occurring flora and fauna; however, many oomycetes are saprophytes that may be important in food webs by decomposing debris or serving as food for other organisms. Surveys of oomycetes on indigenous hosts or in natural environments in South Africa have mainly focused on the genus <i>Phytophthora</i>, indicating a diverse set of <i>Phytophthora</i> spp., including several new species and hybrid species. A recent FBIP funded survey identified 70 oomycete species, including 42 putative new species, in a single nature reserve (Cape Point Nature Reserve). The majority of species (n=56) were of the genus <i>Pythium</i>, while only one <i>Phytophthora</i> species was recovered.</li> </ul>	<ul style="list-style-type: none"> <li>- The project aims to further expand on the diversity and distribution data of oomycetes in South Africa by assessing the diversity of culturable soilborne oomycetes in three additional coastal reserves in the Cape Floristic Region. Soil samples will be taken from coastal, inland, and wetland sites, and sites with increased human activity. Soil will be baited for oomycetes with a variety of baits. Baits will be plated on three selective media for oomycetes and a general medium for fungal growth. Isolates will be grouped based on cultural and morphological characteristics, as well as internal transcribed spacer (ITS) PCR-RFLP profiles. Representative isolates will be identified by sequencing and phylogenetic analyses of the ITS. Cox1 barcodes will be generated for at least one isolate per species. The data gathered will expand the available knowledge on oomycete diversity in South Africa, including the distribution of species previously only identified in Cape Point Nature Reserve. Furthermore, pathogens that could threaten native biodiversity will be identified.</li> </ul>

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	<p>18. Effects of grassland fire intensity on soil microbial ecology</p> <p>19. Revision of two ecologically and economically important ant groups in</p>	<p>- Periodic or seasonal burning of vegetated habitats is a natural process, and is considered to be an important component of ecosystem management and stability. In grassland ecosystems, fire is generally considered to be critical for vegetative species composition and diversity, and is ultimately a driver of biome structure. Anthropogenic activities, which tend to increase burn frequencies, have negative impacts, including loss of the seed bank and long-term losses in key nutrients. While the effects of fire on various vegetated habitats have been extensively studied, less attention has been paid to the effects of fire on the underlying soil microbiome. However, given the widely accepted and critical roles of soil microorganisms in 'soil health', which include biomass degradation and C and N biogeochemical cycling (including diazotrophy), plant-growth promoting effects, and pathogen suppression, the impacts of fire on post-fire ecosystem productivity are of considerable ecological significance.</p> <p>- Natural science collections are a rich source of foundational biodiversity information that is primarily related to spatial, habitat and</p>	<p>- The aim of the study is to use modern metagenomic methods, coupled with functional assays and thermal profiling, to investigate the effects of fire intensity on the structure and function of a grassland soil microbiome, and on plant-microbe interactions in the rhizosphere.</p> <p>- By developing a historical DNA reference barcoding library of polychaete worms for the first time from natural history</p>

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	South Africa AND Historical DNA barcoding library of Polychaete worms	<p>bathymetric parameters. They form the baseline for studies such as biogeography, conservation biology, ecology and the evolutionary history of species. While specimens in natural science collections are known to have DNA degradation and contamination due to preservation methods, modern molecular techniques have enabled the successful amplification of DNA sequences thereby unlocking historical information which can subsequently be used to validate and assign correct taxonomic identities to cryptic species complexes, among other research questions. Although our knowledge of polychaetes in southern Africa is reasonably good, recent molecular evidence has shown that diversity has been significantly underestimated, and that our understanding of the taxonomy and biogeography of many species remains incomplete.</p>	<p>collections, we would be able to validate taxonomically confusing (cryptic) species from type and non-type material of representative specimens. Not only will this enhance our local and global understanding of biodiversity and biogeography of polychaete worms, but such a dataset will form the baseline for subsequent complex research hypotheses such as investigating phylogenetic relationships between species and the historical population connectivity of species. The subsequent molecular techniques used and developed during this project to extract DNA from preserved material can be transferred to other important groups of marine taxa.</p>