

XVI SASSB 2023 CONFERENCE

# PROGRAMME & **ABSTRACTS**



Southern African Society for  
**Systematic Biology**

**XVI SASSB 2023 Conference**

5-7 July 2023

STIAS, Stellenbosch



**Stellenbosch**

UNIVERSITY  
IYUNIVESITHI  
UNIVERSITEIT



# **PARTICIPANT INFORMATION**

---

## **Registration Information**

Each participant at SASSB must register in person at the Registration Desk to collect a Conference kit and badge before attending any of the sessions or events.

## **Registration Times**

Wednesday 05 July: 15:00 – 17:00

Thursday 06 July: 08:00 – 09:00

Friday 07 July: 08:00 – 09:00

## **Badges**

Identification badges are required for admission to all sessions, official functions and social events of the Conference. Participants who lose their badges must report to the Registration Desk, presenting proof of identity.

## **Presenters, Chairs & Facilitators**

All speakers are required to report to the Registration Area at least 90 minutes before their presentation to ensure that we have uploaded the correct presentation onto the presentation laptop in the auditorium.

## **Poster Presentations**

Posters will be available for viewing at the back of Auditorium Room 2 for the duration of the Conference. Posters may be setup from Wednesday 15:00, or Thursday morning from 07:00.

## **Contact**

Mrs Melanie Pretorius | +27 (0) 82 410 1202

# **ON-SITE CONFERENCE SUPPORT**

---

## **Emergency Medical assistance and Paramedic Services**

For assistance with any medical emergencies, please visit the Registration area. Medical procedures and medicine will be for the attendee's own account. For any medical emergencies, please contact +27 (0) 82 925 9241 during conference hours.

## **Guide to logging onto the wireless network:**

Username: Stias2

Password: Conference22!

## **Meals and Snacks**

Meals and beverages will be provided to attendees as indicated in the programme, during conference times. All additional meals will be for the attendees' own account.

## **Safety and Security**

In the interest of personal safety and security, attendees should only display their identity tags on the STIAS premises and within the restricted Conference areas.

Lost property can be handed in at the Registration Desk. Any losses should be reported to the Conference Secretariat. Although every effort will be made to retrieve lost personal belongings, the responsibility for securing his/her personal belongings remains that of each person attending the Conference.

### **Accommodation and Transport**

IMPORTANT: All accommodation and transport arrangements will be for your own account. It is quite safe to book an Uber while in Cape Town, details can be found [here](#).

### **Flights**

Should you require any assistance with flights, please approach Melanie Pretorius at the Registration Desk area.

### **Dress Code**

The suggested dress code for the conference is business casual, but please do bring something warm along as weather is quite cold and the rooms will be air-conditioned.

### **Liability**

Neither the Conference Secretariat nor any of its contracted service providers will be responsible for the safety of articles of any kind brought into the Conference facilities by attendees, whether registered or not, their agents, contractors, visitors and/or any other person/s whatsoever. The Conference attendee shall indemnify and not hold the organisers and associates of the organisers and their subcontractors liable in respect of any cost, claims, demands and expenses as a result of any damage, loss or injury to any person howsoever caused as a result of any act or default of the Conference Secretariat or a person representing the Conference Secretariat, its contractors or guests. In addition, the Conference attendee shall take all necessary precautions to prevent any loss or damage to his/her property with special regard to mobile phones, carry or handbags and computing equipment.

## **ABOUT THE SASSB**

---



**Southern African Society for  
Systematic Biology**

### **History**

The SASSB was formally established at the Inaugural Conference of the SASSB in January 1999. The formation of the Society was initially proposed by Professor Peter Linder, formerly of the Botany Department of the University of Cape Town. There was concern that, following global trends, in South Africa systematics was a discipline that was in decline in terms of capacity and resources, mainly as a result of the lack of understanding of the critical role of taxonomy, systematics and natural history collections play in science and society.

### **Objectives of SASSB**

To promote and represent the activities and interests of all biological systematists, evolutionary biologists, curators and managers of natural history collections in South Africa. To increase appreciation in the general community of the importance of systematics and natural history collections. To lobby government agencies and granting agencies for funding for research and training. To foster the training of systematists / taxonomists. To hold meetings that deal with issues in systematic biology.

# PROGRAMME OF PRESENTATIONS

## WEDNESDAY, 5 JULY 2023

Time	Description
15h00	SASSB Registration opens at STIAS
15h00	Posters to be placed on poster boards
17h00	SASSB Welcome Reception @ STIAS for all SASSB Conference Attendees

## THURSDAY, 6 JULY 2023

Time	Abstract	Description	Speaker
08h00	SASSB Registration - arrival coffee and tea		
<b>THEME: TAXONOMY AND MORPHOLOGY   SYSTEMATICS AND PHYLOGENETICS (Chair: Conrad Matthee)</b>			
08h30	<b>Keynote: The use of phylogenetic trees to reveal environment history</b>		Tony Verboom, University of Cape Town
09h15	072	What is Myzostomids parenchyma?	Alexander Tzetlin, M.V.Lomonosov Moscow State University
09h30	131	Current knowledge of the family Capitellidae (Annelida) in Brazil: what has been done and next steps	Camila F. Silva, Oceanographic Institute of the University of São Paulo ( <i>presented by: Wagner Magalhães, Federal University of Bahia</i> )
09h45	069	Clarifying the identity of beach dwelling polychaetes of the genus <i>Scolecopsis</i> (Annelida: Spionidae) from the Atlantic coast of North America, previously confused with the European species <i>Scolecopsis squamata</i> (O.F. Müller, 1806)	Jason D. Williams, Hofstra University
10h00	035	Revisiting the evolution of annelid larval forms	Greg Rouse, Scripps Oceanography, University of California San Diego
10h15	103	Species diversity of the pelagic polychaete family Tomopteridae in the eastern Indian and Pacific Oceans	Kanako Amei, Atmosphere and Ocean Research Institute, the university of Tokyo
10h30	Mid-morning refreshments		
<b>THEME: SYSTEMATICS AND PHYLOGENETICS (Chair: Torsten Struck)</b>			
11h00	074	Dating the annelid tree of life	Torsten H. Struck, University of Oslo
11h15	107	An update on the phylogeny of scale worms (Aphroditiformia, Polychaeta)	Yu Wang, Hainan University
11h30	118	The <i>Syllis prolifera</i> species complex: a morphological and molecular approach	Irene del Olmo, Universidad Autónoma de Madrid
11h45	119	Integrative taxonomy to study syllid annelids of Bermuda with reorganization of the genus <i>Megasyllis</i>	Paula Moreno Martín, Universidad Autónoma of Madrid
12h00	085	Phylogeny of Orbiniidae (Annelida) based on genome skimming	Miguel A. Meca, University Museum of Bergen
12h15	066	Orbiniidae (Annelida, Sedentaria) - does morphology match molecular data?	Anna Zhadan, M.V.Lomonosov Moscow State University, biological faculty
12h30	Lunch   International Polychaetology Association Advisory Council meeting		
<b>THEME: SYSTEMATICS AND PHYLOGENETICS / INVASIVE SPECIES (Chair: Tammy Robinson)</b>			
13h30	132	Capturing cryptic diversity of Andaman coral reefs with Autonomous Reef Monitoring Structures (ARMS): First initiative in Indian waters	Tejal V. Vijapure, Centre for Ecological Sciences, Indian Institute of Science (IISc)
13h45	127	Evaluation of the presence of mitochondrial sequences in Annelida nuclear genomes	Joana Zanol, Museu Nacional, Federal University of Rio de Janeiro
14h00	Change venues – SASSB delegates moves to Manor Library		

IPC14 – AUDITORIUM				SASSB 2023 – MANOR LIBRARY		
Time	Abstract	Description	Speaker	Abstract	Description	Speaker
14h15	017	Colonization patterns of the invasive species <i>Ficopomatus enigmaticus</i> (Fauvel, 1923) in a shallow coastal lagoon in Greece	Sarah Faulwetter, University of Patras	Session chair: Martin Coetzee		
				001	A description of a new species of a paederine staphylinid beetle from a Cretaceous crater lake at Orapa, Botswana	Sandiso Mnguni, University of the Witwatersrand
14h30	039	Polychaete diversity in New England marinas after two decades of rapid biodiversity assessment surveys: challenges and future plans	Andrew A. Davinack, Wheaton College	002	Genome size variation in Cape schoenoid sedges (Cyperaceae: Schoeneae) and its ecophysiological consequences	Ruan van Mazijk, University of Cape Town
14h45	033	“Cosmopolitan” species as gateways for cryptic invasions: integrative taxonomy to the rescue	Elena K. Kupriyanova, Australian Museum Research Institute	005	Exploring <i>Penicillium</i> diversity in South Africa	Cobus Visagie, University of Pretoria
15h00	018	The European Research Infrastructure LifeWatch ERIC and its potential for supporting the Polychaete Community	Christos Arvanitidis, LifeWatch ERIC	006	Assessing Introgressive hybridization of native <i>O. mossambicus</i> in South Africa	Tonna Mojekwu, University of Pretoria
15h15	Q&A Session			Q&A Session		
15h35	All to move back to Plenary Auditorium					
15h40	Short presentation from Delheim Wine Estate					
16h00	Dedicated poster session + wine & cheese					

## FRIDAY, 7 JULY 2023

08h00	Arrival coffee and tea					
THEME: EDUCATION   DEVELOPMENTAL MORPHOLOGY (Chair: Patricia Álvarez-Campos)						
Time	Abstract	Description	Speaker	Abstract	Description	Speaker
08h30	154	<b>Keynote 4: Building up STEAM: Innovative approaches to engage undergraduate students in investigations of morphology</b>	Sara M. Lindsay, University of Maine			
09h15	Change venues – SASSB delegates moves to Manor Library					
IPC14 – AUDITORIUM				SASSB 2023 – MANOR LIBRARY		
Time	Abstract	Description	Speaker	Abstract	Description	Speaker
09h30	151	Inspiring young polychaetologists in the molecular age	Paul D. Rawson, University of Maine	Session chair: Muthama Muasya		
				008	Acclaimed but poorly named: A new molecular phylogeny unveils evolutionary relationships in the charismatic South African daisy genus <i>Dimorphotheca</i>	Thaabiet Parker, University of Cape Town
09h45	138	Single cell sequencing for evolutionary and developmental biology in annelids	Patricia Álvarez-Campos, Universidad Autónoma de Madrid	009	Systematics of the Sub-Saharan Perilidae	Abigail Kirkaldy, Rhodes University

IPC14 – AUDITORIUM				SASSB 2023 – MANOR LIBRARY		
Time	Abstract	Description	Speaker	Abstract	Description	Speaker
10h00	013	Desmosomal connectomics and muscular system innervation in the <i>Platynereis</i> larva	Sanja Jasek, University of Exeter	010	The enigmatic subterranean amphipod genus ( <i>Sternophysinx</i> : Sternophysingidae): Conservation and systematics	Zizile Mlungu, Rhodes University
10h15	112	When something goes wrong: comparative analysis of regeneration processes in annelids	Viktor V. Starunov, Zoological Institute of Russian Academy of Sciences	011	Citizen Scientists apprehend alien stick insect in South Africa	Martin Villet, Rhodes University
10h30	Mid-morning refreshments					
THEME: EDUCATION   DEVELOPMENTAL MORPHOLOGY (Chair: Ekin Tilic)				SASSB 2023		
11h00	070	What (a) nerve! A "sensormotor" neuron in the copulatory organ of <i>Dimorphilus gyrociliatus</i> dwarf males (Dinophilidae) likely orchestrates glands, muscles and multiciliated cells during copulation	Alexandra Kerbl, Centre for Organismal Studies, Heidelberg University	Session chair: Nicola Bergh		
				012	Systematics of the genus <i>Argyrolobium</i> Eckl. & Zeyh. (Genisteae)	Xichavo Mathebula, University of the Western Cape
11h15	135	Insights into molecular pathways underlying development and paedomorphism in the bone eating worm <i>Osedax japonicus</i> (Siboglinidae, Annelida)	Alice Rouan, Marine Biological Section, Department of Biology, University of Copenhagen	013	Evolutionary timeline of rhizobial beta-proteobacteria	Lazarus Mavima, University of Pretoria
11h30	063	Axial differences in regeneration ability and identification of a putative stem cell niche in the annelid <i>Capitella teleta</i>	Elaine Caeia Seaver, University of Florida	014	Can the vegetation units in the GCFR be distinguished based on pollen morphology?	Janaïs Delpont, University of Cape Town
11h45	106	Everlasting tail: organisation and regeneration of <i>Pygospio elegans</i> (Spionidae) nervous system	Zinaida Iadina Starunova, Zoological Institute of the Russian Academy of Sciences	016	Implementing the SeqCode for naming nine new Mesorhizobium species isolated from Vachellia karroo root nodules	Melandre van Lill, University of Pretoria
12h00	043	New Insights into Annelid Chaetogenesis	Ekin Tilic, Senckenberg Research Institute and Natural History Museum	018	Myrmecochory in the Fynbos Biome revisited: origin, occurrence and its implication for the biology of Cape plants	Muthama Muasya, University of Cape Town

IPC14 – AUDITORIUM				SASSB 2023 – MANOR LIBRARY		
Time	Abstract	Description	Speaker	Abstract	Description	Speaker
12h15	134	Insights into male paedomorphosis through postembryonic developmental studies of the sexually dimorphic <i>Osedax</i> (Siboglinidae, Annelida)	Katrine Worsaae, University of Copenhagen	020	The complex dynamics of population divergence in Cape heathers: the case of <i>Erica abietina</i>	Seth Musker, University of Cape Town
12h30	Lunch					
13h30	International Polychaetology Association meeting & next conference bids			Session chair: Conrad Matthee		
14h45				021	Investigating the phylogenetics of <i>Osteospermum</i> section <i>Polygalina</i> and the placement of novel specimens	Lauren James, University of Cape Town
14h00				022	Botryosphaeriaceae associated with three native tree species in South Africa	Martin Coetzee, University of Pretoria
14h15				023	Heteroscleromorph demosponge taxonomy and diversity of the Amathole region (Eastern Cape, South Africa)	Robyn Payne, Anchor Environmental Consultants
14h30				025	Inferring phylogenetic trees under the isolation-with-migration model	Zaynab Shaik, University of Stellenbosch
14h45				026	Resolving tribe Calenduleae Taxonomy: Multilocus Phylogenetic Analysis, generic taxonomy and associations between habitat and dispersal ability	Robert Sadler, University of Cape Town
14h45	Close of Conference & Prize Giving			027	DNA Barcoding and morphological analysis confirm that the Afrotropical <i>Syrirta bulbus</i> is a species complex (Diptera: Syrphidae)	Bonolo Mosime, KwaZulu-Natal Museum
15h15	Mid-afternoon coffee/tea					

IPC14 – AUDITORIUM				SASSB 2023 – MANOR LIBRARY		
Time	Abstract	Description	Speaker	Abstract	Description	Speaker
				Session chair: Muthama Muasya		
15h15				029	Taxonomy, diversification, and evolutionary history of the African laminated toothed rats (Rodentia, Otomyini)	Conrad Matthee, University of Stellenbosch
15h30		Not in use		031	Polyploidy in the Cape Flora: discovery, exploration of origins, and environmental and morphological correlates of polyploidy in the flagship Cape plant species renosterbos ( <i>Dicrothamnus rhinocerotis</i> , Asteraceae, Gnaphalieae)	Nicola Bergh, South African National Biodiversity Institute
15h45				Close of Conference & Prize Giving/Award		

## OFFICIAL CONFERENCE DINNER

Dress code: Business Casual (and something warm)

17:00	Buses depart from STIAS to GOLD Restaurant
18:30	IPC 14 Conference Dinner
22:00	First bus leaves back to STIAS
24:00	Last bus leaves back to STIAS





# POSTER PRESENTATIONS

---

Abstract #	Topic and Speaker	Poster #
003	The cicada genus <i>Tugelana</i> Distant, 1912 (Hemiptera, Cicadidae): phylogenetic position and conservation status <i>Martin Villet, Rhodes University</i>	01
007	Addressing the role of reference databases on marine biodiversity surveys with eDNA metabarcoding: a South African perspective <i>Emma Rossouw, University of Stellenbosch</i>	02
015	Revisiting the Taxonomy of Giant Eunice in the Western Cape, South Africa <i>Robin Lacey, University of Stellenbosch</i>	03
017	Systematics and diversification of the genus <i>Aspalathus</i> L. (Crotalariaeae, Fabaceae) <i>Lydia Madika, University of Cape Town</i>	04
019	Earthworm species in sugarcane <i>Thembeke Nxele, KwaZulu-Natal Museum</i>	05
024	The exploration of abiotic tolerance related traits of the wheat wild relative <i>Thinopyrum distichum</i> <i>Kishalya Haridass, University of Stellenbosch</i>	06
028	eDNA metabarcoding vs metagenomics: an assessment of dietary competition in two estuarine pipefishes <i>Conny Serite, University of Johannesburg</i>	07

# WELCOME MESSAGE

---



A warm word of welcome to the 16<sup>th</sup> Conference of the Systematic Society of Southern Africa. The host, Stellenbosch University, which is also one of the sponsors of this meeting, is wishing you a rewarding experience through fruitful interactions with the attendees interested in evolution. It is also envisaged that you will find the interaction with members of the International Polychaete Conference beneficial. The SASSB council members, who also served as conference organizers, trust that this long overdue meeting will invigorate members and will mark a new growth phase that will highlight the importance of Systematics in the well-being of our planet. We constantly need to remind us of the words of Theodosius Dobzhansky: “Nothing in Biology Makes Sense Except in the Light of Evolution”.

The conference organizers would also like to sincerely thank Prof Tony Verboom (University of Cape Town) who agreed, at very short notice, to present a plenary talk at the meeting. We look forward hearing about “The use of phylogenetic trees to reveal environment history”. Funding towards selected student delegate attendance to the SASSB was provided by GENUS: DSI-NRF Centre of Excellence in Palaeosciences’. The latter will also be used to partly fund a student prize and Stellenbosch University is thanked for partially sponsor the venue at the Stellenbosch Institute for the Advancement of Science (STIAS). The Dean of the faculty of Science, Stellenbosch University, is acknowledged for providing sponsorship that will be utilized to cover the R15 000 travel reward for the best student presentation at the conference.

We wish you all luck with your presentations and enjoy the meeting!

*Conrad Matthee*  
**on behalf of the Council**

## The use of phylogenetic trees to reveal environment history

Associate Professor G Anthony Verboom

*Department of Biological Sciences, University of Cape Town (tony.verboom@uct.ac.za)*

Phylogenetic trees are routinely used to gain insights into the evolution of single biological lineages. Where phylogenetic trees are available for multiple lineages diversifying in a region, these can also be used to draw inferences about environment history. In this talk I show how comparative reconstructions of habitat variables across multiple phylogenies can be used to reveal the timing of key environmental transitions, while the shapes of phylogenetic trees and their correlation to habitat variables can be used to draw inferences about past environmental stability. A comparison of phylogenetic tree shape and habitat reconstructions across 12-14 Cape plant lineages reveals that mountain fynbos environments have been stable for a longer time than the low elevation environments currently occupied by renosterveld and succulent karoo vegetation.



**Biography:** Tony Verboom holds an associate professorship in the Department of Biological Sciences at the University of Cape Town, teaching topics in systematics, evolutionary ecology and land plant diversity. Research-wise he is interested in questions relating to speciation, adaptation and the processes that underpin the spatial organization of biodiversity. Much of his research has involved the use of systematic tools to understand better the assembly of the modern Cape flora. To date, Verboom has published 39 papers in international peer-reviewed journals. He regularly reviews for international journals and currently serves as an associate editor for *Austral Ecology*. He also co-edited a special issue of *Molecular Phylogenetics and Evolution* entitled 'Origins and evolution of a biodiversity hotspot, the biota of the African Cape Floristic Region'.

### Core research interests

Focussing on the southern African flora, especially the hyper-diverse Greater Cape flora, my research is motivated by an interest in patterns of diversity and the historical and contemporary processes by which diversity is generated, maintained and organized. As such, it can be structured into four broad themes:


- documenting the diversity of plant lineages and floristic assemblages;
- understanding the processes by which diversity is generated and maintained;
- exploring the evolution of resource acquisition traits and how such traits define plant niches and distributions; and
- understanding the historical and contemporary factors that determine the distribution and organization of floristic diversity at the community and landscape level.

My research is integrative, spanning the fields of evolutionary biology, ecology, systematics and biogeography. Current research in my lab is centred around the use of next generation sequencing data to address the mechanistic basis of population and species differentiation in the Greater Cape Floristic Region. I am also embarking on a new program of research, exploring the use of phylogenies and population genetic data to identify climatic refugia in the Greater Cape Floristic Region.



# Welcome to a new era in Palaeoscience.

At GENUS we're breaking down barriers between people, disciplines, industries and borders. We're sharing ideas, resources and skills. Join us in building a future worth preserving.



**We are GENUS.**

**Knowledge centre. Network leader. Explorer.**





GENUS is a collective knowledge hub and inclusive network for Palaeosciences in Africa. Dedicated to studying the origins of species, we see beyond science to inspire researchers and citizens to find meaning in the past and inform our decisions for a better future.

With South Africa's unmatched fossil and archaeological record at our feet, we enable ground-breaking discoveries that move Palaeosciences forward, encourage cross-discipline collaboration, and make knowledge accessible to all.

Through our broad international and local network, we provide access to a valuable repository of tools, information, funding, technology and support. This empowers emerging researchers, postdoctoral fellows, and postgraduate students to further their research, grow their network and contribute to discovering sustainable solutions for society and the environment.

## What does it take to make a real difference?

We believe in a world where everyone has a role to play in preserving the future of our planet. From researchers, collaborators and partner institutions to ordinary citizens, aspiring students and young children, we aim to break down barriers and make a real contribution to a more hopeful future.

 <p><b>Igniting Wonder</b> We capture imaginations and spark curiosity, opening minds to the limitless world that still needs to be explored.</p>	 <p><b>Fuelling Discovery</b> We support our network with the resources and partners required to make groundbreaking discoveries.</p>	 <p><b>Driving Inclusivity</b> We create an open culture of collaboration that represents the rich diversity of South Africa.</p>	 <p><b>Enabling Real Impact</b> We empower our network to make a boundless impact – not only in the world of science but the bigger story of life itself.</p>
--	--	---	--

# ORAL PRESENTATIONS

---

## (001) A description of a new species of a paederine staphylinid beetle from a Cretaceous crater lake at Orapa, Botswana

Sandiso Mnguni<sup>1</sup>, Ian James McKay<sup>1</sup> & Shaw Badenhorst<sup>1</sup>

<sup>1</sup>University of the Witwatersrand – [sandiso@gmail.com](mailto:sandiso@gmail.com)

The fossil record of insects is rich in time and space, and insects preserved in lacustrine deposits are found as far back as the Late Carboniferous. The fossil record of Coleoptera dates back to the Late Carboniferous/Early Permian. Staphylinidae is a hyper-diverse family with over 65 561 extant and 450 extinct species, making it the most speciose in the animal kingdom. It has four informal subgroups, viz. omaliine, tachyporine, oxyteline, and staphylinine within which 1 extinct and 33 extant subfamilies belong. A species of rove beetle, *Mesostaphylinus orapa* (incertae sedis) is described and figured based on one well-preserved compression fossil from a crater lake in Orapa Diamond Mine, Botswana. *Mesostaphylinus orapa* is definitively placed in the extant subfamily Paederinae based on general habitus, concealed antennal insertions, and hypomeron with a well-developed post-coxal process. It shares characteristics with other *Mesostaphylinus* spp. such as general habitus, narrow and medium-sized body, elongate head and pronotum, and very distinct neck constriction of the head. Placement of *Mesostaphylinus* in the extant subfamily Paederinae is supported by the combination of the following characters: hypomera of prothorax with sclerotized post-coxal processes, elytra possibly with epipleural ridge, mesothorax elongate with median transverse carina intersecting with mesoventral-pleural sutures, and lateral tergal sclerites IX dorsally contiguous or fused. This is the first fossil paederine staphylinid beetle from Africa. It demonstrates morphological stasis dating back to the Cretaceous. In the Cretaceous, Orapa is reconstructed as being strongly seasonal, with a warm, high humidity, wet summer, and a dry, cold winter. At Orapa, its microhabitat was possibly damp places, under logs, litter or foliage. It was probably an active predator which hunted near the crater-lake.

---

## (002) Genome size variation in Cape schoenoid sedges (Cyperaceae: Schoeneae) and its ecophysiological consequences

Ruan van Mazijk<sup>1,2,3</sup>, Adam G. West<sup>1</sup>, G. Anthony Verboom<sup>1,2</sup>, Tammy L. Elliott<sup>1,2,4</sup>, Petr Bureš<sup>4</sup> & A. Muthama Muasya<sup>1,2</sup>

<sup>1</sup>Department of Biological Sciences, University of Cape Town - [ruanvmazijk@gmail.com](mailto:ruanvmazijk@gmail.com)

<sup>2</sup>Bolus Herbarium, University of Cape Town

<sup>3</sup>C4 EcoSolutions

<sup>4</sup>Department of Botany and Zoology, Masaryk University

Stomatal size and density are important aspects of plant ecophysiology pertaining to water-balance. Thus, increases in genome size, associated with larger, low density stomata and greater water-use efficiency (WUE), could covary with aspects of plant function. Variation in genome size across plants is often due to polyploidy, known to have occurred multiple times in the austral sedge genus *Schoenus* in the Cape Floristic Region (CFR), but not in the other major schoenoid genus in the region, *Tetralix*, which exhibits smaller genomes similar to most Cyperaceae. Comparing these genera is useful as they co-occur in fynbos landscapes, under broadly similar bioclimatic conditions. We hypothesise CFR *Schoenus* species to be more WUE, as a function of lower maximum stomatal conductance (g<sub>w</sub>max) imposed by larger, less dense stomata. To test this, we investigate relationships between genome size and stomatal parameters in a phylogenetic context, reconstructing a phylogeny of CFR-occurring Schoeneae. Species' stomatal and functional traits were measured from field collected and herbarium specimens, informed by existing genome size data used here. Carbon stable isotopes (δ<sup>13</sup>C) were used as an index of WUE. Evolutionary regressions demonstrated that stomatal size and density covary with genome size, positively and negatively respectively, with genome size explaining 72–75% of the

variation in stomatal size. Additionally, gwmax and C:N ratios were lower in larger-genomed species, particularly in culms. We interpret differences in vegetative physiology between the genera to evidence more conservative strategies in CFR Schoenus compared to the more acquisitive Tetraria. As Schoenus species have relatively small, reduced leaves, they likely rely more on culm photosynthesis compared to Tetraria species. Across the CFR Schoeneae, ecophysiology correlates with genome size, though confounding sources of trait variation limit inferences about causal links any given trait.

---

### **(005) Exploring *Penicillium* diversity in South Africa**

Cobus M Visagie<sup>1</sup>

<sup>1</sup>*Forestry and Agricultural Biotechnology Institute, University of Pretoria - [cobus.visagie@up.ac.za](mailto:cobus.visagie@up.ac.za)*

South Africa is a fungal biodiversity hotspot, with many new species discovered annually. This is especially true for *Penicillium*, with 47 of 162 recorded species that was newly described from South Africa during the last decade. *Penicillium* was historically difficult to work with and identify. Recent taxonomic changes included extensive nomenclatural reviews and adoption of a phylogenetic species concept, which resulted in identifications being easier than ever and making for rapid species discovery. To further our knowledge on fungal diversity occurring in South Africa, our next challenge will be to develop novel high-throughput sequencing detection methods that makes use of the modern taxonomies and its associated data for genera like *Penicillium*. This presentation will focus on the modern taxonomy of *Penicillium* and how we are using it to further explore and discover this diverse genus within South Africa.

---

### **(006) Assessing Introgressive hybridization of native *O. mossambicus* in South Africa**

Tonna O Mojekwu<sup>1,2</sup>, Michael J Cunningham<sup>1,4</sup> & Thierry B Hoareau<sup>1,3</sup>

<sup>1</sup>*Department of Biochemistry, Genetics and Microbiology, University of Pretoria - [tonyystone@yahoo.com](mailto:tonyystone@yahoo.com)*

<sup>2</sup>*Nigerian Institute for Oceanography and Marine Research,*

<sup>3</sup>*Boobook Ecology, Australia,*

<sup>4</sup>*Reneco International Wildlife Consultants LLC, Abu Dhabi, United Arab Emirates*

The native Mozambique tilapia *Oreochromis mossambicus* is recognised as vulnerable on the IUCN red list because of the threats linked to hybridization with the introduced Nile tilapia *Oreochromis niloticus* that is invasive in South Africa. The objective of this work was to show the extent of hybridization between *O. mossambicus* and *O. niloticus* in South Africa with genetic makers. We genotyped the mitochondrial DNA (mtDNA) control region (532 bp) of *Oreochromis* species 81 specimens from 43 locations in the wild and 13 specimens from a hatchery. Microsatellites designed from the *O. niloticus* genome linked to targeted genes were used to assess the level introgression using Bayesian approach. Phylogeographic analysis revealed clues of mtDNA introgression with multiple lineages of both *O. mossambicus* and *O. niloticus*. Principal Component and UPGMA analyses separates the two species as different phylogenetic groups while Bayesian evaluation showed the power of the new markers to detect hybrids (*O. mossambicus* × *O. niloticus*) and backcross beyond the fifth generation at an individual membership of  $q < 0.95$ . Two hybrids identified at the Olifants river SA3 and Flagboshielo dam TOM004 shared 1 % of their genome with *O. niloticus*, showing that hybridization has progressed to some tributaries of the lower Limpopo river system. These results indicate that the threat linked to introgressive hybridization is prevalent than previously thought and requires urgent conservation and ecological actions in the region. Furthermore, we suggested using a genomic approach like gene capture, to increase the resolution in the detection of introgressed genes in *O. mossambicus*.

---

## **(008) Acclaimed but poorly named: A new molecular phylogeny unveils evolutionary relationships in the charismatic South African daisy genus *Dimorphotheca***

Thaabiet Parker<sup>1,2</sup>, George A. Verboom<sup>1</sup>, John C. Manning<sup>2</sup>, Allan G. Ellis<sup>3</sup> & Nicola G. Bergh<sup>1,2</sup>

<sup>1</sup>University of Cape Town - [PRKTHA005@myuct.ac.za](mailto:PRKTHA005@myuct.ac.za),

<sup>2</sup>South African National Biodiversity Institute

<sup>3</sup>University of Stellenbosch

Evolutionary relationships in the South African daisy genus *Dimorphotheca* have long been problematic, with historical taxonomy based on single morphological traits – most prominently floret fertility (i.e. fruit type) and ray colour – which are not evolutionarily conserved. Here we present the first well-sampled molecular phylogeny of the genus, based on nuclear ribosomal (ITS and ETS) and plastid trnL-trnF region DNA sequences from multiple accessions per species. We also reconstruct the evolution of fruit type and ray colour within the genus. We find support for the monophyly of the genus, with the exception of the recently transferred *O. polypterum*, and thus support for the genus in its modern enlarged circumscription. We find the overall phylogenetic structure (i.e. major subclades) of the genus matches geographical distribution, and can potentially be grouped into sections supported by morphological traits. Most species are supported as monophyletic but there are several possible cases of introgression, and polyphyletic species which represent potential species complexes. We describe two new species from the tree and discuss evidence supporting the elevation of at least one variety to species level, based on phylogenetic position. We find that fruit type and ray colour are not evolutionarily conserved within lineages in the genus, and consequently neither trait can be used to delimit major lineages. Our findings highlight the need for a formal taxonomic revision of the genus to reassess species taxonomy.

---

## **(009) Systematics of the Sub-Saharan Perlidae**

Abigail P. Kirkaldy<sup>1</sup>, Martin H. Villet<sup>1</sup> & Helen M. Barber-James<sup>1,2</sup>

<sup>1</sup>Rhodes University - [abbykirkgeneral@gmail.com](mailto:abbykirkgeneral@gmail.com),

<sup>2</sup>Ulster Museum, National Museums Northern Ireland

Plecoptera is a small order of aquatic insects, that spend most of their life cycle as nymphs inhabiting freshwater habitats, followed by a short-lived flying adult stage. They are highly sensitive to small changes in water quality, and form a useful component of biomonitoring systems worldwide. Perlidae is by far the most diverse (>1000 species) and widespread family of Plecoptera, known from every continent except Antarctica and Australia. However, the Afrotropical Perlidae is presently known only by a single species complex, *Neoperla spio*, that is distributed across the entire continent. This severely limits its usefulness as a biomonitoring tool, as it has been impossible to interpret the biological and ecological significance of the cryptic species within the complex. This study reassessed the systematics of the African Perlidae, particularly in South Africa, using morphological and genetic evidence. This identified nine species of Perlidae from South Africa, Angola and Rwanda, from both adult and nymphal material. A summary of these species, and the relevant characters needed for their identification is presented.

---

## **(010) The enigmatic subterranean amphipod genus (*Sternophysinx*: Sternophysingidae): Conservation and systematics**

Zizile Mlungu<sup>1,2</sup>, Musa Mlambo<sup>1,2</sup>, Samuel Motitsoe<sup>1</sup>, Fatima Parker<sup>3</sup> & Charles Griffiths<sup>4</sup>

<sup>1</sup>Department of Zoology and Entomology - [mlunquzizile@gmail.com](mailto:mlunquzizile@gmail.com),

<sup>2</sup>Rhodes University, Makhanda (Grahamstown), South Africa,

<sup>3</sup>Albany Museum,

<sup>4</sup>Department of Freshwater Invertebrates, Makhanda

Sternophysingidae Holsinger, 1992 is a monotypic subterranean amphipod family endemic to Namibia and South Africa. It currently has eight described species under the genus *Sternophysinx*. The species in this family are considered narrow endemics, having only been identified using morphological characters. However, the apparent wide distribution of certain species, reported in several subterranean waters in different provinces, suggests that our current taxonomic understanding of these species needs to be completed, thus needing revision. This study aimed to use integrative taxonomy to analyse both morphology and molecular biology to study hidden diversity and to further our understanding of the distribution in this taxon. The available morphological keys were used to identify species, and 12S rRNA was also used to investigate the relationships of *Sternophysinx* species and delimit species boundaries. Three delimitation methods, Assemble Species by Automatic Partitioning (ASAP), Bayesian implementation of the Poison Tree Processor (bPTP) and Automatic Barcode Gap Discovery (ABGD), were used to identify cryptic species within *Sternophysinx*. Phylogenetic analyses and three delimitation methods (ASAP, bPTP and ABGD) revealed considerable hidden cryptic diversity within this *Sternophysinx*. Preliminary morphological examination revealed at least two species as undescribed from Bakwena and Sterkfontein caves, and several that were morphologically identified using the current taxonomic keys did not match with the molecular analysis. For example, *S. basilobata* from three different systems, Boesmansgat cave (Northern Cape), Beaufort West (Western Cape) and Potchefstroom (North West), was in genetically different putative species. The same is true for *S. robertsi* and *S. alca* in Ficus and Peppercorn cave in Limpopo. Overall, the results of the current study demonstrate the need for a comprehensive integrative taxonomic revision of *Sternophysinx*. These findings suggest that *S. basilobata* is a complex of distinct lineages and requires further study. On the other hand, species delimitation methods suggested that there are 12- 14 candidate species.

---

## **(011) Citizen Scientists apprehend alien stick insect in South Africa!**

Martin H. Villet<sup>1</sup>, Clarke J.M. van Steenderen<sup>1</sup>, Janaï's Delport<sup>2</sup>, Peter Vos<sup>3</sup>, Suncana Bradley<sup>4</sup> & Riaan Stals<sup>5</sup>

<sup>1</sup>Rhodes University - [m.villet@ru.ac.za](mailto:m.villet@ru.ac.za)

<sup>2</sup>University of Cape Town

<sup>3</sup>Citizen Scientist

<sup>4</sup>Citizen Scientist

<sup>5</sup>Agricultural Research Council

Through the citizen science portal iNaturalist, two populations of the stick insect *Sipyloidea sipyilus* (Westwood, 1859) (Phasmida: Lonchodidae) have been found in South Africa. The KwaZulu-Natal population was probably established before 2015 through the port at Durban, and now has an Extent of Occurrence (EOC) of at least 4925 km<sup>2</sup>; the eastern Limpopo population has been recorded since 2019, but only in the inland town of Tzaneen. Partial COI DNA sequences from specimens from these populations are all identical to a sequence from Singapore and very similar to another from Japan. The current status of a potential third population in the port city of East London in the Eastern Cape is unknown. Apart from being a poor candidate for an eradication programme, *S. sipyilus* apparently does not pose an obvious agricultural, conservation or health threat that would merit such action in South Africa. In the face of growing budgetary and human resource constraints faced by museums, iNaturalist provides a complementary means to discover, record and disseminate information about organisms and their associations, and to fuel early evaluations of threats to biodiversity.



## (012) Systematics of the genus *Argyrolobium* Eckl. & Zeyh. (Genisteae)

Xichavo A. Mathebula<sup>1,2</sup>, M. Marianne le Roux<sup>2,3</sup> & J. Stephen Boatwright<sup>1</sup>

<sup>1</sup>University of the Western Cape - [4114603@myuwc.ac.za](mailto:4114603@myuwc.ac.za)

<sup>2</sup>South African National Biodiversity Institute

<sup>3</sup>University of Johannesburg

*Argyrolobium* Eckl. & Zeyh. is a genus in the tribe Genisteae (Fabaceae), comprised of ca. 97 species that are distributed throughout tropical and northern Africa, Madagascar, the Mediterranean and southern Europe, and west into the highlands of India. The main centre of diversity for the genus is in southern Africa, where about 51 species occur. Previous molecular studies, based on a limited sampling of the genus, have indicated that the genus may not be monophyletic and that the generic concept needs to be revised. In addition, the South African species (47) have only been treated synoptically in recent years based on an unpublished Ph.D. thesis, and the last published comprehensive taxonomic revision of the southern African species dates back to 1862. The present study is aimed at producing high quality morphological and molecular data (including DNA barcodes) for *Argyrolobium* that will contribute towards resolving the generic circumscription and relationships to ultimately inform a revised taxonomy of the genus. It will also inform much needed future revisionary work on the genus. A preliminary phylogenetic analysis of *Argyrolobium* is presented here based on nuclear (ITS) and plastid (trnL-F) DNA sequences to test the monophyly of the genus. These analyses confirm the results of previous studies that *Argyrolobium* is not monophyletic. While a large clade of southern African species is recovered, the remaining tropical African, Middle Eastern, Asian and Malagasy species form at least two separate clades distributed among other genera of the Genisteae. The resolution in the trees is poor, and will be improved by sampling an additional three plastid regions (matK, psbA-trnH and trnS-G).

---

## (013) Evolutionary timeline of rhizobial beta-proteobacteria

Lazarus Mavima<sup>1</sup>, Chrizelle W. Beukes<sup>2</sup>, Marike Palmer<sup>3</sup>, Sofie E. De Meyer<sup>4,5</sup>, Euan K. James<sup>2</sup>, Martin P.A. Coetzee<sup>1</sup>, Emma T. Steenkamp<sup>1</sup> & Stephanus N. Venter<sup>1</sup>

<sup>1</sup>Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria - [mavimalazarus@gmail.com](mailto:mavimalazarus@gmail.com)

<sup>2</sup>The James Hutton Institute, Invergowrie, Dundee DD2 5DA, UK

<sup>3</sup>School of Life Sciences, University of Nevada Las Vegas, Las Vegas, NV, United States of America <sup>4</sup>MALDIID Pty Ltd, Murdoch, Western Australia, Australia

<sup>5</sup>Laboratory of Microbiology, Department Biochemistry and Microbiology, Ghent University, Belgium

The evolutionary timeline of different lifestyles within the beta-proteobacteria is poorly characterized. Here, we investigated the evolutionary history of beta-proteobacteria in the context of 'rhizobia' (i.e., nitrogen-fixing and nodule-forming symbionts of legumes), of which rhizobial beta-proteobacteria ('beta-rhizobia') are housed in only three genera, namely, *Paraburkholderia*, *Trinickia* and *Cupriavidus*. Evolutionary divergence dates as well as ancestral states for the nodulation trait were estimated using over 800 diverse proteobacterial strains. Molecular dating was carried out with the program BEAST (Bayesian Evolutionary Analysis Sampling Trees), and the 'chronopl' function in the R package 'ape'. Our results showed that the most recent common ancestor (MRCA) of the extant beta-rhizobia emerged between 2273 and 1702 million years ago (Ma) and later (around 1702 to 814 Ma) diverged into the extant lineages *Cupriavidus*, *Trinickia* and *Paraburkholderia*. Although beta-rhizobia first diverged long before the super continent Pangaea formed, most beta-rhizobia species diverged in the Permian period (400 – 250 Ma) when Pangaea was fully assembled and its landmass was filled with flora and fauna. Furthermore, based on the evolutionary timeline and the reconstructed ancestral states of the nodulation trait, the beta-proteobacteria acquired the nodulation ability fairly recent, around 500 Ma. Our findings also suggest that this ability was acquired multiple times at different time points throughout the group's evolutionary history. Accordingly, our study describes the evolutionary history of beta-rhizobia, thus enabling a better understanding of what past environmental effects could have shaped the

current geographical distribution of these agricultural important bacteria and potential locations from where to search for more beta-rhizobial members.

---

#### **(014) Can the vegetation units in the GCFR be distinguished based on pollen morphology?**

Janais Delpo<sup>1</sup>, A. Muthama Muasya<sup>1</sup>, Paula Strauss<sup>2</sup>, Nanike Esterhuizen<sup>3</sup>, Theresa Wossler<sup>4</sup> & Saúl Manzano<sup>5,6,7</sup>

<sup>1</sup>*Bolus Herbarium, Department of Biological Sciences, University of Cape Town - [janaisdelpo@gmail.com](mailto:janaisdelpo@gmail.com)*

<sup>2</sup>*Grootbos Foundation, Grootbos Private Nature Reserve, Gansbaai*

<sup>3</sup>*Hortgro Science, Department of Conservation Ecology and Entomology, Stellenbosch University,*

<sup>4</sup>*Department of Botany and Zoology, Stellenbosch University*

<sup>5</sup>*Área de Botánica, Dept. Biodiversidad y Gestión Ambiental, Facultad de Ciencias Biológicas y Ambientales, Universidad de León (Spain)*

<sup>6</sup>*The Compton Herbarium, Kirstenbosch Research Centre, South African National Biodiversity Institute (SANBI) Cape Town*

<sup>7</sup>*Quaternary Palynology Lab, Institute for the Environment, Natural Resources and Biodiversity, University of León, Spain*

The incredible species diversity in the Greater Cape Floristic Region (GCFR) has inspired numerous evolutionary, phylogenetic, ecological, and other biological studies. However, one field of research, palynology – the study of pollen and spores – remains underdeveloped in the region. When used in the identification of parent plant species, palynological tools such as pollen atlases and reference collections have supplemented the development of medicine, palaeobotany, taxonomy, and forensic sciences. Yet, South African palynological research is poorly developed, relative to the rich biodiversity, characterized by scattered site studies or piecemeal taxonomic outputs in charismatic plant groups. The geoclimatic conditions of the GCFR has allowed for unique botanical communities to evolve, resulting in the biomes and the distinct vegetation zones we know today. We aimed to evaluate whether the distinctness of the botanical communities (biomes and the vegetation types) in the GCFR could be distinguished in their pollen assembly. In this study the pollen morphology of 354 taxa from the GCFR were recorded, aiming to sample important species characterizing the major vegetation units. The vegetation types can be identified based on pollen morphologies of characteristic taxa. Groups such as the Asteraceae, Ericaceae, Poaceae, Fabaceae, Aizoaceae, and many monocotyledons have very consistent suprageneric morphology, whereas taxa such as *Cliffortia*, *Grielum*, and *Drosera* have unique morphology that allow for genus level identification. Misidentifications of pollen could arise due to the natural variation of morphology within species, method used in processing the pollen, and inaccurate identification of the source from which pollen is collected.

---

#### **(016) Implementing the SeqCode for naming nine new Mesorhizobium species isolated from Vachellia karroo root nodules**

Mel André van Lill<sup>1</sup>, Emma T. Steenkamp<sup>1</sup>, Esther Muema<sup>2</sup>, Marike Palmer<sup>3</sup>, Wai Y. Chan<sup>1</sup>, Chrizelle W. Beukes<sup>4</sup> & Stephanus N. Venter<sup>1</sup>

<sup>1</sup>*Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria - [melandre.vanlill@up.ac.za](mailto:melandre.vanlill@up.ac.za)*

<sup>2</sup>*Department of Soil Science, Faculty of AgriSciences, Stellenbosch University*

<sup>3</sup>*School of Life Sciences, University of Nevada, Las Vegas, United States of America*

<sup>4</sup>*The James Hutton Institute, Invergowrie, Dundee DD2 5DA, United Kingdom*

South Africa is a well-known for the diversity of its legumes and their nitrogen-fixing bacterial symbionts. However, contrast to the plant partners, remarkably few of these microbes (collectively referred to as rhizobia) have been characterized and formally described. Despite being aided by recent technological and taxonomic advances, the rate at which new bacterial species from South Africa are described is unlikely to

---

increase substantially. This is because the rules of the International Code of Nomenclature of Prokaryotes (ICNP) are at odds with South Africa's National Environmental Management: Biodiversity Act (NEMBA) and its associated Regulations. The ICNP requires that a culture of the proposed type strain for a novel bacterial species be deposited in two international culture collections and be made available upon request without restrictions, which is not possible under the current national regulations. Our aim was to formally describe nine new *Mesorhizobium* species (obtained from root nodules of *Vachellia karroo*), which were previously delineated using a polyphasic approach based on various phenotypic, genetic and genomic characters. For this purpose, we used the genome sequences for the respective species as nomenclatural types and employed the rules set out by the newly published Code of Nomenclature of Prokaryotes described from Sequence Data (SeqCode). All the genome sequences for the designated type strains were compliant with the SeqCode's minimum standards regarding quality and public accessibility. Furthermore, genome-based comparison of our new taxa with one another and with known *Mesorhizobium* species all yielded Average Nucleotide Identity (ANI) values <96%, thus supporting their taxonomic novelty. This work therefore constitutes an example of how the SeqCode could allow for a standardized approach to the official naming of cultivated organisms for which the deposit of a type strain in international culture collections is currently problematic.

---

### **(018) Myrmecochory in the Fynbos Biome revisited: origin, occurrence and its implication for the biology of Cape plants**

Muthama A. Muasya<sup>1</sup>, Daniel A. Zhigila<sup>1,2</sup> & Charles H. Stirton<sup>1</sup>

<sup>1</sup>University of Cape Town - [muthama.muasya@uct.ac.za](mailto:muthama.muasya@uct.ac.za)

<sup>2</sup>Gombe State University

Myrmecochory, the dispersal of seeds by ants, is widespread among land plants and occurs in multiple biomes across all continents. Globally, it has been recorded in over 70 families and in nearly 11000 species of angiosperms. The syndrome is most prevalent on nutrient poor soils, such as the Fynbos Biome, mostly among herbaceous and shrubby plants. Yet the timing of the origin of myrmecochory in the hyperdiverse Cape flora has not been investigated, with the most recent focussed study dating to four decades ago. Using the growing phylogenetic resources on Cape plants, we map the occurrence of the syndrome to identify myrmecochorous lineages and the origin of the syndrome in the Fynbos Biome. We further test whether the syndrome is correlated with seed traits and extent of occurrence of the species. Using exemplar Fynbos families with widespread myrmecochory, we establish that the syndrome arose in mid Oligocene in Fabaceae (tribe Podalyriaceae, ~28 Ma) and Restionaceae (2 lineages, ~29-26 Ma) to Miocene for the Santalaceae (*Thesium*, ~20 Ma) and Cyperaceae (*Ficinia*, ~12 Ma). In these families, myrmecochorous species have seeds bearing an elaiosome, which are significantly larger than seeds in sister lineages that are non-myrmecochorous. As ant dispersal is thought to be restricted to few meters from the parent plant, we are investigating whether myrmecochorous species have decreased occurrence ranges and under increased extinction threats.

---

### **(020) The complex dynamics of population divergence in Cape heathers: the case of *Erica abietina***

Seth D. Musker<sup>1,2</sup>, Michael D. Pirie<sup>3</sup> & Nicolai M. Nürk<sup>2</sup>

<sup>1</sup>University of Cape Town - [sethmusker@gmail.com](mailto:sethmusker@gmail.com)

<sup>2</sup>University of Bayreuth, Germany

<sup>3</sup>University of Bergen, Norway

Deciphering the ecological and geographic factors that influence the dynamics of population divergence can aid in understanding why some groups of organisms diversify more prolifically than others. One such group is the heathers (*Erica*, Ericaceae), whose exceptional diversity in the Cape Floristic Region is enigmatic. Here, we study *Erica abietina*, a small but highly variable species complex with four subspecies differing in

geographic range, habitat, and floral characters. We evaluate the status of the subspecies and test for hybridisation, introgression, pollinator-driven divergence, and geographic population structure using genotyping-by-sequencing on samples across the entire distribution. We find that the four subspecies form variably distinct genetic groups, however, the most widespread subspecies exhibits cryptic diversity, comprising two independent lineages that are geographically isolated and occur on different soil types. We find that populations with different pollination syndromes are genetically distinct. However, for one pair of genetically distinct populations ( $F_{ST} \approx 0.06$ ) with different floral phenotypes we uncover several individuals of hybrid origin at a site where they occur sympatrically. Together, these results suggest that floral differentiation acts in concert with geographic isolation to maintain reproductive isolation. Finally, we show that a reticulate history involving "ghost" introgression best explains the group's evolution. Our results reveal a highly dynamic system whose diversity has been shaped by a variety of interacting forces, and we suggest that such systems are likely to have contributed substantially to the diversity of *Erica* and the rest of the Cape flora.

---

### **(021) Investigating the phylogenetics of *Osteospermum* section *Polygalina* and the placement of novel specimens**

Lauren M.C. James<sup>1,2</sup>, Nicola G. Bergh<sup>2</sup>, Allan G. Ellis<sup>3</sup> & Anthony G. Verboom<sup>1</sup>

<sup>1</sup>University of Cape Town - [l.james@sanbi.org.za](mailto:l.james@sanbi.org.za)

<sup>2</sup>South African National Biodiversity Institute

<sup>3</sup>Stellenbosch University

*Osteospermum* L. (Asteraceae) is a genus of ~ 80 species of mainly yellow-flowered annual and perennial daisies distributed throughout temperate Africa, but having most of its diversity in the Greater Cape Floristic Region of South Africa. Apart from the publication of ten new species, the species-level taxonomy of *Osteospermum* has received limited attention since Norlindh's revision in 1943. *Osteospermum* Section *Polygalina* DC is a fynbos-centred clade currently comprising six species and several subspecies and varieties. Several of these taxa, however, display extensive undocumented variation, which frequently renders the assignment of specimens to taxa challenging. In addition, several morphologically distinct specimens, which cannot be confidently placed under the current taxonomy, have recently been collected. This study employs nuclear ribosomal and plastid DNA sequences to assess the monophyly of Section *Polygalina* and examine the phylogenetic placements of the novel specimens. This lays the foundations for a comprehensive revision of the section, which is likely to comprise between nine and sixteen species.

---

### **(022) Botryosphaeriaceae associated with three native tree species in South Africa**

Martin P.A. Coetzee<sup>1</sup>, Cindy Ramokgano<sup>1</sup> & Elelwani Ramabulana<sup>2</sup>

<sup>1</sup>Forestry and Agricultural Biotechnology Institute (FABI) University of Pretoria - [martin.coetzee@fabi.up.ac.za](mailto:martin.coetzee@fabi.up.ac.za)

<sup>2</sup>University of Venda

The Botryosphaeriaceae include various endophytic species. Some of these species are known phytopathogens. Little is, however, known regarding the diversity and occurrence of these fungi on indigenous *Berchemia discolor* (brown ivory) (Rhamnaceae), *Lannea schweinfurthii* and *Sclerocarya birrea* (marula) (both Anacardiaceae) in South Africa. These trees play a role in the socio-economic well-being of small-scale farmers and people living in rural communities. They are valued for their medicinal properties and nutritional values, and *B. discolor* and *S. birrea* are used in the production of liquor. The aim of our study was to explore the diversity of Botryosphaeriaceae on these trees at sampling sites in agricultural and natural ecosystems. Several species were identified based on analyses of DNA sequence data of the ITS rDNA region and portions of the  $\beta$ -tubulin, TEF-1 $\alpha$  and Rpb2 genes. The fungi identified included four potentially new species, designated as *Alanphillipsia* sp. 1, *Dothiorella* sp. 1, *Oblongocollomyces* sp. 1 and *Oblongocollomyces* sp. 2,, which await morphological descriptions and formal naming. In addition, isolates of *Diplodia allocellula*,

---

*Dothiorella brevicollis*, *Do. diospyricola*, *Do. dulcispinae*, *Do. viticola*, *Lasiodiplodia crassispora*, *L. exigua*, *L. gonubiensis*, *L. mahajangana*, *L. margaritacea*, *L. pseudotheobromae* and *Neofusicoccum parvum* and various isolates with uncertain identity, belonging to Botryosphaeria and Dothiorella were identified. Overall our results showed that native tree species are rich reservoirs for the Botryosphaeriaceae in the sampling sites.

---

### **(023) Heteroscleromorph demosponge taxonomy and diversity of the Amathole region (Eastern Cape, South Africa)**

Robyn Payne<sup>1</sup>, Toufiek Samaai<sup>2</sup>, Mark J. Gibbons<sup>3</sup>, Sven Kerwath<sup>2</sup>, Denham Parker<sup>4</sup> & Aiden Biccard<sup>1</sup>

<sup>1</sup>Anchor Environmental Consultants - [robyn@anchorenvironmental.co.za](mailto:robyn@anchorenvironmental.co.za)

<sup>2</sup>Department of Forestry, Fisheries and the Environment

<sup>3</sup>University of the Western Cape

<sup>4</sup>Commonwealth Scientific and Industrial Research Organisation, Australia

Sponges are functionally important and ubiquitous components of the global marine benthos. South Africa accounts for roughly 4% of the global marine sponge diversity, comprising 374 described species and seven varieties/forms, with elevated apparent endemism (59%). However, an estimated 900 sponge species are thought to be undescribed, and much work is needed to update and expand our knowledge of the South African sponge fauna. The Amathole region is situated offshore of the Amathole District, around the city of East London, on the south-east coast of South Africa. This area has been historically unexplored and was thus the focus of the Imida Frontiers Project initiated in 2015, under the auspices of the African Coelacanth Ecosystem Programme (phase IV). As a component of this larger project, the research presented here focuses exclusively on the diversity, depth distribution and biogeographic affinities of the heteroscleromorph demosponge fauna. This study included 474 specimens, from four expeditions comprising 48 sites across depths of 3–229 m. Non-random-stratified sampling was undertaken during two cruises onboard the R/V Ellen Khuzwayo in 2016, with 457 specimens collected from 42 sites using an epibenthic dredge. An additional 11 specimens were included from three dredge sites in 2015, as were six specimens from three SCUBA sites sampled by the Coral Reef Research Foundation in 1999. Underwater visual surveys were undertaken onboard the R/V Phakisa using a Remotely Operated Vehicle during two expeditions in 2017, with in situ images used for species accounts. The Amathole region was found to support elevated heteroscleromorph demosponge diversity, with the fauna dominated by two orders (Poecilosclerida, Tetractinellida), and three families (Geodiidae, Isodictyidae, Latrunculiidae). Of the 74 species obtained, 47 were known, while 27 are likely new to science. Twenty-three species were further described, eight as new. This study also documented an additional 35 species and 11 genera for South Africa, and three genera for the Indian Ocean. Consequently, the number of marine sponge species from South Africa will increase to 410 with six varieties/forms. Assemblages did change with depth, and taxa-specific depth restrictions were observed. However, low average similarities and a relatively high number of unique species were indicative of heterogeneity within each depth zone, possibly driven by habitat type. Species richness peaked in the mesophotic zone, which was likely an artefact of the collection effort. Finally, faunal affinities were primarily with southern Africa, with additional influence from the Western Indian Ocean region. Species were shared with every ecoregion in South Africa, but the fauna was most similar to that found in the Agulhas and southern Benguela ecoregions. Findings were limited by the exclusion of aspiculate demosponges, and specimens from the other classes, as well as under-sampling in the shallow and sub-mesophotic depth zones. Nevertheless, this study supports the position of the region within the Algoa to Amathole Ecologically or Biologically Significant Marine Area, and formation of the Amathole Offshore Marine Protected Area in 2019. Sixty-three (85%) of the recorded species fall within the latter, and thus receive some level of protection. In 2022, further opportunistic sponge collections were carried out in Saldanha Bay and offshore Namibia, with specimens sent for sequencing. Preliminary findings from these sampling events will also be detailed.

---

## (025) Inferring phylogenetic trees under the isolation-with-migration model

Zaynab Shaik<sup>1,3,5</sup>, Nicola G. Bergh<sup>2,4</sup>, Anthony G. Verboom<sup>2</sup> & Bengt Oxelman<sup>1,5</sup>

<sup>1</sup>University of Gothenburg - [zshaik@sun.ac.za](mailto:zshaik@sun.ac.za)

<sup>2</sup>University of Cape Town

<sup>3</sup>Stellenbosch University

<sup>4</sup>South African National Biodiversity Institute

<sup>5</sup>Gothenburg Global Biodiversity Centre

Postspecciation gene flow is widespread across the Tree of Life but is ignored as a cause of gene tree discordance under the standard multispecies coalescent. Where interspecific migration has occurred but is not modelled explicitly, effective population sizes, divergence times and topology can be seriously misestimated. Isolation-with-migration models explicitly model migration but include additional parameters that limit their computational viability with even moderately sized molecular data sets. We assess phylogeny inference and computational performance under the isolation-with-migration model DENIM (Jones et al. 2019) and the standard multispecies coalescent program StarBeast3 (Douglas et al. 2022) using sequences simulated under the coalescent with empirically realistic time-decaying patterns of migration. Despite having many additional parameters, DENIM achieves convergence up to an order of magnitude faster than StarBeast3 per-processor in the presence of tree-wide migration. Additionally, we show that rapidly decaying migration and longer sequences are associated with improved topology and divergence time estimates under DENIM. Our work demonstrates that DENIM can deliver accurate phylogeny estimates in the presence of both deep coalescence and empirically realistic patterns of migration with as few as 30 loci with single-CPU runtimes on the order of several days.

---

## (026) Resolving Tribe Calenduleae Taxonomy: Multilocus Phylogenetic Analysis, Generic taxonomy and associations between habitat and dispersal ability

Robert Sadler<sup>1,2,3</sup>

<sup>1</sup>University of Cape Town

<sup>2</sup>University of Stellenbosch

<sup>3</sup>South African National Biodiversity Institute - [SDLROB002@myuct.ac.za](mailto:SDLROB002@myuct.ac.za)

The Tribe Calenduleae, comprising approximately 120 species, is arguably the most taxonomically unstable tribe in the Asteraceae. Recent studies revealed widespread non-monophyly and have led to the collapse of several genera into an expanded definition of *Osteospermum*, resulting in only three extant genera: *Osteospermum*, *Dimorphotheca*, and *Garuleum*. Our multilocus phylogenetic analysis, covering over 80% of the tribe's diversity, supports the monophyly of these three genera but reveals that *Osteospermum*'s subgeneric taxonomy does not reflect natural groupings. By integrating novel morphological and genetic evidence, we propose a new sectional classification for *Osteospermum* and highlight an association between vegetation type and dispersal potential across its two major clades. This study provides a robust framework for future research on the evolution and ecology of Tribe Calenduleae.

---

## **(027) DNA Barcoding and morphological analysis confirm that the Afrotropical *Syritta bulbus* is a species complex (Diptera: Syrphidae)**

Bonolo Mosime<sup>1,2</sup>, Kurt Jordaens<sup>3</sup>, Timotheus van der Niet<sup>2</sup> & John Midgley<sup>1,4</sup>

<sup>1</sup>Department of Natural Sciences, KwaZulu-Natal Museum - [mosimebf@gmail.com](mailto:mosimebf@gmail.com)

<sup>2</sup>Centre for Functional Biodiversity, School of Life Sciences, University of KwaZulu-Natal

<sup>3</sup>Department of Biology, Royal Museum for Central Africa, Belgium

<sup>4</sup>Southern African Forensic Entomology Research Group, Department of Zoology and Entomology, Rhodes University

The hoverfly species *Syritta bulbus* Walker (Diptera: Syrphidae: Eristalinae) is widely distributed in the Afrotropical region, from South Africa to Senegal. While *S. bulbus* currently is considered a single species, it was already suggested by others that it may represent a complex. The aim of this study was to resolve the taxonomy of the species complex. An integrative taxonomic approach combining an analysis of the DNA barcode region of the mitochondrial cytochrome c oxidase subunit I (COI) gene with morphological descriptions of the external morphology and morphometric patterns of the head, wing, thorax and male genital morphology was implemented. All datasets confirmed the existence of genetic and morphological variation that is indicative of 16 putative species. Species descriptions, images, DNA barcodes and an identification key to selected species from the 16 identified in the *S. bulbus* complex are presented.

---

## **(029) Taxonomy, diversification and evolutionary history of the African laminated toothed rats (Rodentia, Otomyini)**

Claudine Montgelard<sup>1,2</sup>, Tanguy Muller<sup>1</sup>, Véronique Arnal<sup>1</sup>, Sarita Maree<sup>3</sup>, Peter Taylor<sup>4</sup>, Arthur Sands<sup>6</sup>, Terence Robinson<sup>5</sup>, [Conrad Matthee](mailto:Conrad.Matthee@sun.ac.za)<sup>5</sup>

<sup>1</sup>CEFE, PSL-EPHE (Biogéographie et Ecologie des Vertébrés), CNRS, Univ. Montpellier, Univ. Paul Valéry Montpellier 3, IRD, Montpellier, France

<sup>2</sup>Centre for Ecological Genomics and Wildlife Conservation, Department of Zoology, University of Johannesburg, Johannesburg, South Africa

<sup>3</sup>Department of Zoology and Entomology, University of Pretoria, Pretoria, South Africa

<sup>4</sup>Department of Zoology and Entomology, Afromontane Research Unit, University of the Free State, Qwa Qwa campus, Phuthaditjhaba, South Africa

<sup>5</sup>Evolutionary Genomics Group, Department of Botany and Zoology, Stellenbosch University Stellenbosch, South Africa - [cam@sun.ac.za](mailto:cam@sun.ac.za)

<sup>6</sup>Area of Ecology and Biodiversity School of Biological Sciences, The University of Hong Kong, Hong Kong, Hong Kong SAR

The African continent was subjected to periodic climatic shifts during the Pliocene and Pleistocene and these greatly affected the evolutionary processes and tempo of diversification in numerous, widely distributed mammals. The Otomyini (Family Muridae) comprises three African rodent genera, *Parotomys*, *Otomys* and *Myotomys*, characterized by unique laminated-shaped molars. Species within this tribe generally prefer open-habitat and show low dispersal capabilities, with previous studies indeed suggesting that their diversification was closely associated with climatic oscillations over the last four million years. Phylogenetic reconstructions, based on three mitochondrial (mtDNA) genes (Cytb, COI and 12S) and four nuclear introns (EF, SPTBN, MGF and THY), identified eight major genetic clades that are distributed across Africa. Our results question the taxonomic validity of the three genera. Multiple mtDNA species delimitation methods incorporating 168 specimens estimated the number of Otomyini species to be substantially higher than the ~30 recognized, suggesting that the current intraspecific taxonomy will necessitate an integrative approach to delimit extant species diversity within the Otomyini. The origin of the Otomyini was estimated to date back to ~5.7 million years ago (Ma) and was most likely in southern Africa. The distribution and phylogenetic associations among the eight major otomyine evolutionary lineages can best be explained by several waves of northward colonization from southern Africa, complemented by independent reversed dispersals from

eastern back to southern Africa at different time periods. There is strong support for the hypothesis that the radiation, dispersion, and diversification of the otomyine rodents is closely linked to recent Plio-Pleistocene climatic oscillations.

---

**(031) Polyploidy in the Cape Flora: discovery, exploration of origins, and environmental and morphological correlates of polyploidy in the flagship Cape plant species renosterbos (*Dicerotheramnus rhinocerotis*, Asteraceae, Gnaphalieae)**

Zuzana Chumová<sup>1</sup>, Zafar Monier<sup>2</sup>, Kristýna Šemberová<sup>1</sup>, Eliška Havlíčková<sup>1,3</sup>, Douglas Euston-Brown<sup>4</sup>, A. Muthama Muasya<sup>2</sup>, [Nicola G. Bergh](mailto:N.Bergh@sanbi.org.za)<sup>2,5</sup> and Pavel Trávníček<sup>1\*</sup>

<sup>1</sup>*Institute of Botany of the Czech Academy of Sciences, Zámek 1, Průhonice, 252 43, Czech Republic*

<sup>2</sup>*Bolus Herbarium, Department of Biological Sciences, University of Cape Town, Cape Town, 7707, South Africa - [N.Bergh@sanbi.org.za](mailto:N.Bergh@sanbi.org.za)*

<sup>3</sup>*Department of Botany, Faculty of Science, Charles University, Benátská 2, Prague, 120 00, Czech Republic*

<sup>4</sup>*Independent botanist, Scarborough, 7975, Cape Town, South Africa*

<sup>5</sup>*The Compton Herbarium, Kirstenbosch National Botanical Gardens, Cape Town, 7735, South Africa*

The GCFR is one of the world's temperate floristic hotspots, with low documented levels of polyploidy. An initial flow cytometric survey of the Cape shrub species *Dicerotheramnus rhinocerotis* (renosterbos), an unusually widespread member of the Cape Flora, indicated the presence of both diploids and tetraploids. Assignment to cytotype was confirmed using chromosome counts. Further measurement, totalling 2370 individuals from 171 populations across the distribution range, indicated widespread diploid and more localised tetraploid populations, with no evidence of triploids and most populations comprising just a single cytotype. Genome size varies within each cytotype category, with mean 2C-values for diploids of 1.80–2.06 pg, and for tetraploids of 3.48–3.80 pg, with very similar monoploid genome sizes. Climatic and environmental niches were compared between cytotypes using a range of environmental layers and a soil model. Intra-cytotype variation showed significant positive correlation with altitude and longitude in both cytotypes and with latitude in diploids. Although niches of both cytotypes are highly equivalent and similar, their optima and breadth are shifted due to differences mainly in isothermality and available water capacity. Morphometric analyses of leaf, capitulum, guard cell, and floral traits showed significant differences between cytotypes in the leaves and corolla traits, in the number of florets per capitulum, and in cypsela dimensions, indicating that they may be distinguishable with a multivariate framework. A RADseq-derived genomic SNP dataset of 90 individuals, including both cytotypes, recovered *D. rhinocerotis* as monophyletic in relation to its (uniformly diploid) sister species, and revealed five genetic clusters within the species. These clusters are largely geographically coherent, and three of the five house tetraploids, indicating multiple independent origins of polyploids out of diploid ancestors. The different regional genetic groupings and their cytotypic variants occupy a wide range of environmental conditions. This study raises questions regarding the importance of ploidy in the megadiverse Cape flora and exemplifies the need for population-based studies with an emphasis on ploidy variation across geographic ranges.

---



# POSTER PRESENTATIONS

---

## **(003) The cicada genus *Tugelana* Distant, 1912 (Hemiptera, Cicadidae): phylogenetic position and conservation status**

Martin Villet<sup>1</sup>, Shelley Edwards<sup>1</sup>

<sup>1</sup>Rhodes University - [m.villet@ru.ac.za](mailto:m.villet@ru.ac.za)

The cicada genus *Tugelana* Distant, 1912 is monotypic and endemic to south-eastern Africa. Material was not available for a recent molecular phylogeny of its tribe, so its precise phylogenetic placement is unestablished. Consequently, a 627 bp sequence of the cytochrome oxidase gene was obtained and its candidate relatives identified as several species of *Platypleura* Amyot & Audinet-Serville, 1843 using the BOLD Identification System and NCBI GenBank's BLAST. Bayesian inference analyses indicated that the type species, the Maputaland Orangewing Cicada *Tugelana butleri* Distant, 1912, is closely related to the Dune Koko Orangewing Cicada *Platypleura zuluensis* Villet, 1989, which has a geographical distribution that is parapatric with *T. butleri* and which has aberrant genitalia for a member of *Platypleura*. This pair of species is placed fairly deep within the African clade of *Platypleura*. We therefore formally recognized *Platypleura* Amyot & Audinet-Serville, 1843 as a senior synonym of *Tugelana* Distant, 1912, syn. nov., and assign *T. butleri* Distant, 1912 to *Platypleura* as *Platypleura butleri* (Distant 1912), comb. nov. The species occurs on the wooded grasslands of the Maputaland coastal plateau east of Lebombo Mountains and south of Maputo Bay. Its Extent of Occurrence is about 6360 km<sup>2</sup>, which would qualify it as Vulnerable under the IUCN's classification criteria for conservation status.

---

## **(007) Addressing the role of reference databases on marine biodiversity surveys with eDNA metabarcoding: a South African perspective**

Emma Rossouw<sup>1</sup>, Sophie von der Heyden<sup>1</sup>

<sup>1</sup>University of Stellenbosch - [21872708@sun.ac.za](mailto:21872708@sun.ac.za)

Environmental DNA metabarcoding is a powerful biomonitoring tool that allows for the broad characterization of marine communities, with enormous potential for marine biomonitoring. However, the success of eDNA metabarcoding is heavily dependent on a reliable and well resolved reference database. Environmental DNA metabarcoding was used to investigate marine biodiversity from a shallow-water kelp forest in Rooi Els, Western Cape, and a deep-sea site ~180 km off Childs Bank, Northern Cape in South Africa. Water and sediment samples were collected from each site respectively and metabarcoding was used to target the CO1 mitochondrial gene (targeting broader eukaryotic community, in both sites) and the 12S rRNA gene (targeting fish, in the kelp forest site). In the kelp forest, metabarcoding detected 880 OTUs representing 75 families in the broader eukaryotic community and 44 OTUs representing 24 fish families. In the deep-sea site, 444 OTUs representing 71 families in the broader eukaryotic community were detected. However, despite the diversity of OTUs that were detected only approximately 3% could be resolved to species level with standard online reference database (BOLD, NCBI). This study highlights the need for more comprehensive reference databases, that are relevant to region, in order to harness the true capabilities of eDNA metabarcoding as a biomonitoring tool.

---

## (015) Revisiting the Taxonomy of Giant Eunice in the Western Cape, South Africa

Robin S. Lacey<sup>1</sup>, Jyothi Kara<sup>2</sup>, & Carol A. Simon<sup>1</sup>

<sup>1</sup>Stellenbosch University, Department of Botany and Zoology - [robinlacey0@gmail.com](mailto:robinlacey0@gmail.com)

<sup>2</sup>Department of Research and Exhibitions, Iziko Museums of South Africa

Eunice aphroditois (Eunicidae, Annelida) is the only giant eunicid species reported in South Africa where it is a popular bait species, especially in the Western Cape Province. It is often referred to as the Giant wonderworm, Bobbit, or Sand Striker worm. Although originally described from Sri Lanka, the species was thought to have a cosmopolitan distribution, but recent descriptions of new, morphologically similar, species from within its reported global distribution suggest that there are multiple similar species with restricted distributions. It is therefore probable that the giant Eunice species in South Africa is not *E. aphroditois*. This study investigates the identity of giant Eunice species in South Africa, with special focus on those in the Western Cape Province. Thorough morphological analyses using light, dissecting, and scanning electron microscopy will be conducted on material from throughout the known local distribution (Namibia, Northern Cape, Western Cape, and Eastern Cape). This will be supplemented with molecular analyses of the Cytochrome Oxidase subunit 1 (CO1) sequences generated for recently collected material from the Western Cape Province. Preliminary morphological results show that specimens of different lengths from Strand vary in subacicular hook presence/distribution; prostomial appendage colouration; body colouration from brownish purple to prominent orange banding; in a fixed state the white chaetiger is absent in some or not as prominent in others, and some vary in the white colouration of the head and peristomium. A phylogenetic analysis will be conducted by comparing the sequences of different sized specimens collected in South Africa, with those of giant Eunice from other locations globally.

---

## (017) Systematics and diversification of the genus *Aspalathus* L. (Crotalariaeae, Fabaceae)

Lydia K. Madika<sup>1</sup>, Muthama A. Muasya<sup>1</sup>, Ramagwai J. Sebola<sup>2</sup>, Charles H. Stirton<sup>1</sup> & Daniel A. Zhigila<sup>1,3</sup>

<sup>1</sup>University of Cape Town - [mdklyd001@myuct.ac.za](mailto:mdklyd001@myuct.ac.za)

<sup>2</sup>South African National Biodiversity Institute

<sup>3</sup>Gombe State University

*Aspalathus* L. is the second-most species-rich genus in the Core Cape Subregion (CCR), with around 98% of its species being endemic to the region, accounting for nearly 3% of the region's flora. The most recent taxonomic revision of the genus is Dahlgren's (1988) treatment, which was compiled posthumously. Since then, over 20 new species have been discovered and described, and molecular phylogenetic studies point to a recent (Mioecene) rapid diversification. The goal of this study is to provide a modern systematic treatise that includes phylogenetics and taxonomy of *Aspalathus* and to use this revision to infer macroevolutionary processes within the genus. The specific objectives are to determine the monophyly of the taxonomic groups proposed by Dahlgren, to investigate what drove the 'orgy of speciation' in *Aspalathus*, and to address the taxonomy of the three problematic species complexes in the Adnate group. To build the phylogeny, this study will sample an additional 50 species across all groups, representing morphotypes described by Dahlgren, using four gene regions including ITS, ETS, matK, and trnS-trnG, which will bring the total to more than 60% of the genus. The resulting phylogeny of selected *Aspalathus* species will show the monophyly of the genus, its position in the tribe Crotalariaeae, and its relationship to other genera, i.e., *Lebeckia* Thunb., *Wiborgia* Thunb., and *Wiborgiella* Boatwri. & B.-E. van Wyk. Finally, the phylogeny obtained will be used to reconstruct selected morphological and ecological characters. This study will provide important insights into the evolution of the patterns and processes that have shaped the remarkable biodiversity of the CCR.

---

## **(019) Earthworm species in sugarcane**

Thembeke Nxele<sup>1</sup> & Tarombera Mwabvu<sup>2</sup>

<sup>1</sup>*KwaZulu-Natal Museum* - [tnxele@nmsa.org.za](mailto:tnxele@nmsa.org.za)

<sup>2</sup>*University of Mpumalanga*

Earthworms improve soil quality and structure through nutrient cycling, making chemicals, such as, nitrates and phosphates accessible to plants and other organisms, and improving aeration and drainage in the soil. Earthworms in agroecosystems in South Africa are poorly known, however, few studies have looked at their composition in different crops. This study aims to add on the existing knowledge with a focus on sugarcane. A survey was conducted at kwa Swayimane rural location in grassland and sugarcane fields of small scale farmers. Three different sections of the community, Nomnganga, emaBheleni and Ndlaveleni, were sampled. Three sugarcane fields and a grassland were chosen in each section. Earthworms were sampled in a hectare by digging nine 50 cm X 50 cm X 20 cm deep plots. The plots were 30 m apart and 20 m away from the edge. Only material from the sugarcane fields has been processed (to genera). Four families (Acanthodrilidae: Dichogaster, Megascolecidae: Amynthes, Rhinodrilidae: Pontoscolex and Tritogeniidae: Tritogenia) were collected. Of the four families collected, only Tritogeniidae is native. EmaBheleni section had more individuals collected (363 adults) followed by Ndlaveleni (158 adults) and Nomnganga had the least number of individuals collected (86 adults). Specimens of Amynthes were dominant in all sections. The indigenous specimens of Tritogenia were collected from one sugarcane field that was near a small patch of natural bush. The collection of Amynthes species from sugarcane was expected because of previous collections. Given that sugarcane originated from India, Amynthes may have been introduced with sugarcane. The low number of indigenous earthworms may be because burning of sugarcane occurs during harvest.

---

## **(024) The exploration of abiotic tolerance related traits of the wheat wild relative *Thinopyrum distichum***

Kishalya Haridass<sup>1</sup>, Nicholas Le Maitre<sup>1</sup> & Willem Botes<sup>1</sup>

<sup>1</sup>*Stellenbosch University* - [haridasskishalya@gmail.com](mailto:haridasskishalya@gmail.com)

Wheat is an important socioeconomic food crop. The genetic diversity of the wheat crop has been significantly reduced through the 'domestication bottleneck'. For the continued success of the crop, its genetic diversity must not only be replenished but also increased. *Thinopyrum distichum* is a crop wild relative of wheat. This sea grass thrives in high salinity environments and holds potential to enhance the current wheat crop's tolerance to salinity as well as improve its diversity. This study aims to explore the phylogenetic relationship of *Th. distichum* populations collected from the western, eastern and southern coastal regions of the Western and Eastern Cape provinces of South Africa. Chloroplast markers will be used to assess the phylogenetic relationships of this collection. An environmental niche model will be created with climatic data collected from the Western Cape region as well as data obtained from salinity tests of sand and sea water samples taken at each collection site. Collections have been made from the coastline across the Western Cape province. DNA extractions of the collections have been completed. PCR analysis of DNA and chloroplast marker multiplexes are currently underway as well as quality control of the climatic data collected for the model. PCR products will undergo fragment analysis and a phylogenetic tree will then be created. It is hoped that through understanding the relationship between the climate data and tolerance levels of various *Th. distichum* populations the wheat crop may be improved.

---

## (028) eDNA metabarcoding vs metagenomics: an assessment of dietary competition in two estuarine pipefishes

Conny P. Serite<sup>1</sup>, Arsalan Emami-Khoyi<sup>1</sup>, Ofentse K. Ntshudisane<sup>1</sup>, Nicola C. James<sup>2</sup>, Bettine Jansen van Vuuren<sup>1</sup>, Taryn Bodill<sup>2</sup>, Paul D. Cowley<sup>2</sup>, Alan K. Whitfield<sup>2</sup> & Peter R. Teske<sup>1</sup>

<sup>1</sup>University of Johannesburg - [conny.serite@yahoo.com](mailto:conny.serite@yahoo.com)

<sup>2</sup>South African Institute for Aquatic Biodiversity

Understanding the dietary preferences of endangered species can be useful in implementing conservation strategies, including habitat restoration, translocation, and captive breeding. Environmental DNA (eDNA) from feces provides a non-invasive method for analysing animal diets. Currently, metabarcoding, a PCR-based approach, is the method of choice for analysing such data. However, this method has limitations, specifically PCR bias, which can result in the overestimation of the importance of certain taxa and the failure to detect other taxa because they do not amplify. The present study compared metabarcoding with metagenomics, a PCR-free method, to assess the diversity of prey items in the feces of a critically endangered South African estuarine pipefish, *Syngnathus watermeyeri*, and its widely distributed congener (*S. temminckii*) to investigate potential dietary competition. The metabarcoding results showed a distinct difference between the diets of *S. watermeyeri* and *S. temminckii*, with the former mainly consuming calanoid copepods and the latter preferring caridean shrimp. In each case, a single species dominated the sequences generated by metabarcoding. Metagenomics produced more species identifications, and although the same trend was found regarding the preference of *S. watermeyeri* for copepods and that of *S. temminckii* for shrimp, this approach identified additional, albeit yet unidentified, copepod species as being important in the diet of *S. watermeyeri*. We conclude that the lower number of species identified using metabarcoding was most likely a result of amplification bias, resulting in key copepod species missing from the dietary analysis. These findings suggest that metagenomics is not only a useful complementary method for molecular dietary analysis but may in some cases outperform metabarcoding. However, metagenomics is even more strongly affected by the lack of reference sequences than is metabarcoding, as the majority of sequences originate from genomic regions that have not yet been sequenced for the putative prey species in question.

---

# LIST OF SPEAKERS IN ALPHABETICAL ORDER

---

Presenter	Abstract Nr.	Page
Bergh, Nicola	031	24
Coetzee, Martin	022	20
Delport, Janaïs	014	18
Haridass, Kishalya	024	27
James, Lauren	021	20
Kirkaldy, Abigail	009	15
Lacey, Robin	015	25
Madika, Lydia	017	26
Mathebula, Xichavo	012	16
Mathee, Conrad	029	23
Mavima, Lazarus	013	17
Mlungu , Zizile	010	16
Mnguni, Sandiso	001	13
Mojekwu, Tonna	006	14
Mosime, Bonolo	027	23
Muasya, Muthama	018	19
Musker, Seth	020	19
Nxele, Thembeka	019	26
Parker, Thaabet	008	15
Payne, Robyn	023	21
Rossouw, Emma	007	25
Sadler, Robert	026	22
Serite, Conny	028	27
Shaik, Zaynab	025	22
van Lill, Melandré	016	18
van Mazijk, Ruan	002	13
Verboom, Tony	Keynote	10
Villet, Martin	011, 003	16
Visagie, Cobus	005	14

# Thank you for joining us for the XVI SASSB 2023 Conference



**SAVETCON**  
EVENT MANAGEMENT