

ISSN: 2219-410X

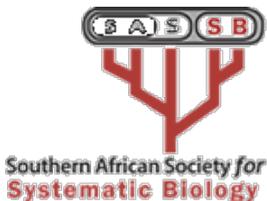
Proceedings
of the
Congresses of the Southern African Society for Systematic
Biology

Organised by the
Southern African Society for Systematic Biology
Grahamstown 19-21st January 2011



**Hosted by the Department of Zoology and Entomology,
Rhodes University**

Edited by Martin H. Villet and Kendall L. Crous

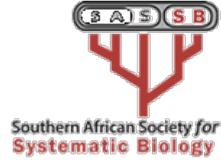


Published by the Southern African Society for Systematic Biology

Published by the Southern African Society for Systematic Biology

©2011

ISSN: 2219-410X



Southern African Society for Systematic Biology

Department of Zoology

P.O. Box 94

Grahamstown

6140 South Africa

Key title: Proceedings of the Congresses of the Southern African Society for Systematic Biology

ORGANISING COMMITTEE

Prof Martin Villet (*Convenor*)

Dr Doug Downie

Prof Nigel Barker

Dr Gavin Gouws

Dr Monica Mwale

Ms Helen Barber-James

Ms Poogendri Reddy

Ms Kendall Crous (*Editor*)

Ms Carolyn Stevenson-Milln (*University Conference Manager*)

EDITORS' PREFACE

The SASSB congresses are about to enter their teens! Perhaps as a sign of this transition, the proceedings are taking on a new format, and have even acquired their own auspicious International Standard Serial Number (ISSN), which features in the prescribed standard place on the cover. While this does not mean that the SASSB has initiated a new journal, it does mean that future proceedings are anticipated, and it may indeed be another step to greater things for southern African systematic biology.

This 9th Congress of the SASSB is another manifestation of this progression, featuring an array of national and international plenary speakers: Peter Weston (Royal Botanical Garden, Sydney), Luciano Beheregaray (Flinders University, Adelaide), Steve Goodman (Field Museum, Chicago), and Tim Crowe (University of Cape Town).

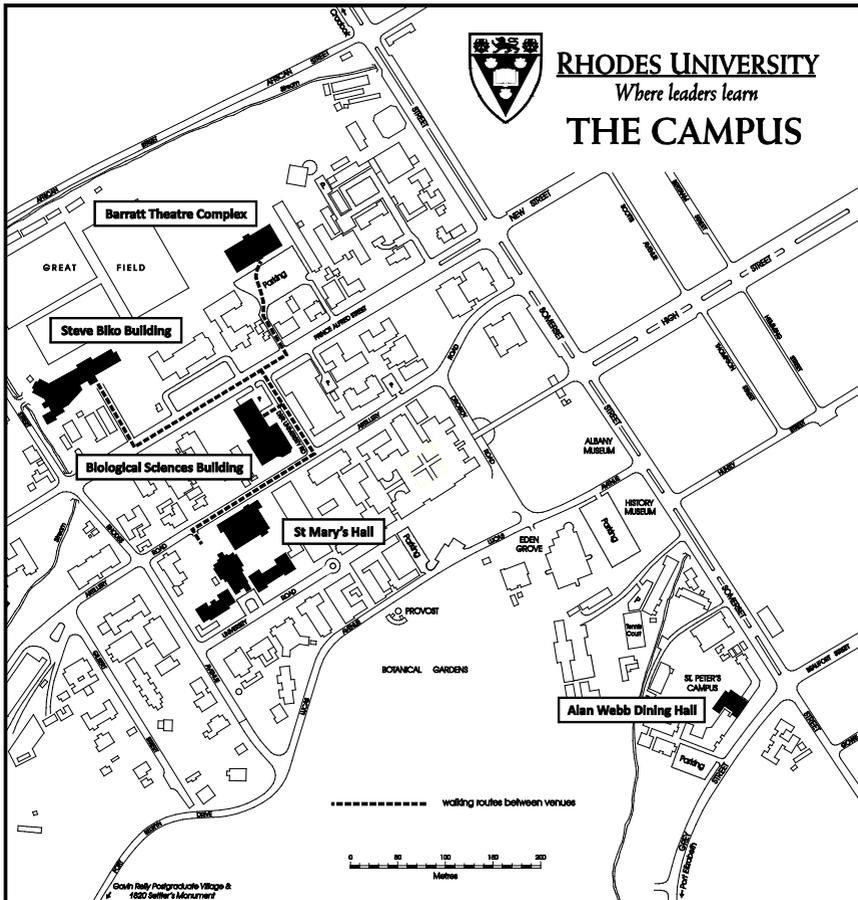
The programme also features special workshops on emerging disciplines such as cybertaxonomy (led by Pavel Stoev, Pensoft Publishers, Bulgaria), national biodiversity research strategy (led by Michelle Hamer, SANBI), Specify6 (led by Willem Coetzer, SAIAB) and statistical phylogeography (led by Alastair Potts, University of Cape Town), and interdigitates with the 37th Congress of the South African Association of Botanists, with a joint symposium on African Biodiversity. There are also 78 oral presentations and a total of 100 presentations that fill 17 sessions about systematics, phylogenetics, and biogeography.

The Organising Committee can't take all of the credit for this conference, and we particularly thank Michele Pienaar (Rhodes University Conference Office) for her part in making this SASSB conference a reality. We also have to thank the delegates, without whom there would be no conference to organise!

Martin H. Villet and Kendall L. Crous
Grahamstown, January 2011



MAP OF CENTRAL CAMPUS



CONTENTS

Editors' Preface.....	iii
Map of Central Campus.....	iv
Programme.....	vi
Wednesday talks.....	vii
Thursday talks.....	x
Friday talks.....	xiv
Abstracts.....	1
Plenaries.....	1
Workshops.....	5
Research presentations (<i>alphabetical order</i>)....	8
Delegates' addresses.....	111
Index of Autors.....	114

	Wednesday 19 th		Thursday 20 th		Friday 21 st	
8.15	SASSB Welcome					
8.30	Joint Plenary - Peter Weston		Plenary - Luciano Beheregary		Plenary - Tim Crowe	
9.30	Joint Session Centres of Endemism	POPULATIONS B. van Vuuren	BIOGEOGRAPHY H.M. Barber-James	DIVERSITY A.J.F.K. Craig	EVOLUTION M. Mwale	BIODIVERSITY F.P.D. Cotterill
11.00	Tea & Posters					
11.30	Joint Session Centres of Endemism	PHYLOGEOGRAPHY J. Bishop	BIOGEOGRAPHY & PHYLOGENY G. Hofmeyer	DIVERSITY C.A. Matthee	IDENTIFICATION K.A. Williams	PHYLOGENETICS B.W. Price
13.00						
14.00	Joint Session Centres of Endemism	Workshop - Michelle Hamer	Plenary - Steve Goodman		Digital Taxonomy Workshop - Pavel Stoev	SPECIFY6 Databse Workshop - Willem Coetzer
15.00	Tea & Posters					
15.30	Joint Session Centres of Endemism	PHYLOGEOGRAPHY G. Gouws	PHYLOGENY S. Willows-Munro	DIVERSITY J.M. Masters	Digital Taxonomy Workshop	SPECIFY6 Databse Workshop
17.00						
18.00	Welcome cocktails - Zoology Foyer		SASSB AGM & Gala Dinner - Allan Webb Dining Hall		Spit Braai - Oppidan Dining Hall	

WEDNESDAY 19TH JANUARY - JOINT SESSION WITH SAAB (BARRATT COMPLEX)

8.30: **PLENARY:** *P. Weston*. Cenozoic environmental change and the systematics of southern hemisphere plants

N.P. Barker & V.R. Clark. Centres of endemism: overview, analyses and the future

S.J. Perera, D. Ratnayake-Perera & Ş. Procheş. A greater Maputaland-Pondoland-Albany region of vertebrate endemism

J. Burrows & J. Timberlake. Mozambique's centres of endemism, with special reference to the Rovuma Centre of Endemism of NE Mozambique and SE Tanzania.

V.R. Clark, N.P. Barker & L. Mucina. On-ramps and off-ramps: the phytogeography of the southern Great Escarpment, South Africa

N. Helme. The Kamiesberg Centre of Endemism

L.M. Loffler. Swaziland plant endemism

D. McCallum. Rare plants and serpentine soils

R.A. Reddy, T. McLellan & K. Balkwill. Ecotype formation - a stepping stone towards endemism

J.H.J Vlok. Phytogeographic affiliation of the flora of the Klein Karoo - a unique pattern or a model of regional phytogeographic assemblage?

S.D. Williamson & K. Balkwill. Endemism and diversity hotspots within the serpentine outcrops of the Barberton Greenstone Belt, Mpumalanga

WEDNESDAY 19TH JANUARY - ZOOLOGY MINOR 2

Barratt	8.15	SASSB WELCOME
	8.30	PLENARY: <i>P. Weston</i> . Cenozoic environmental change and the systematics of southern hemisphere plants
Zoo Minor 2	9.45	<i>C. Berthouly-Salazar</i> , B.J. van Rensburg, C. Hui, J. Le Roux & B. van Vuuren. Understanding population dynamics of invasive birds: a landscape genetics approach
	10.00	<i>M. Karsten</i> , B. van Vuuren, P. Goodman & A. Barnaud. History and management of black rhino in KwaZulu-Natal: a population genetic approach to assess the past and guide the future
	10.15	<i>M.N. Britton</i> & G.A. Verboom. Variables, variance, variation and variants: speciation in the Cape Fold Mountains
	10.30	<i>M. Cooper</i> , M. van der Bank, M. Powell & A. Moteete. DNA fingerprinting (AFLP's) in <i>Colophospermum mopane</i> and <i>Imbrasia belina</i>
	10.45	<i>B. van Vuuren</i> & S. Goodman. Population structure in <i>Mungotictis decemlineata</i> , a mysterious Malagasy mongoose
	11.00	TEA & POSTERS
	11.30	<i>T.V. Reynolds</i> , S. von der Heyden & C.A. Matthee. Pleistocene climatic changes and ocean currents influence the phylogeography of the South African barnacle, <i>Tetraclita serrata</i> (Thoracica; Cirripedia)
	11.45	<i>N. Springbok</i> , M. Mwale, G.Gouws & O. Gon. A molecular genetic approach to consider regional connectivity and differentiation of three goatfishes (<i>Parupeneus</i> spp.) in the Western Indian Ocean
	12.00	<i>M.L. de Jager</i> & A.G. Ellis. Phylogeography of a pollinator from the GCFR: genetic structure and its ecological relevance
	12.15	<i>N. Cangi</i> , I. Horak, L. Neves & C. Matthee. Phylogeography of <i>Amblyomma hebraeum</i> and <i>Hyalomma rufipes</i> (Acari: Ixodidae) in southern Africa
	12.30	<i>N. du Toit</i> , B. van Vuuren, S. Matthee & C.A. Matthee. Comparative phylogeography of the four-striped mouse, <i>Rhabdomys pumilio</i> and its specific parasitic louse, <i>Polyplax arvicanthis</i>
	12.45	<i>J.M. Bishop</i> , C. O'Ryan & G.N. Bronner. Pleistocene fragmentation shapes contemporary genetic structure in a forest endemic, the giant golden mole
	13.00	LUNCH
	14.00	WORKSHOP: M.Hamer. Developing a national strategy for zoological systematics in South Africa (VENUE: ZOO MINOR 2)

15.00

TEA & POSTERS

15.30

P.A. Maake, E. Swartz, B. Kramer & O. Gon. Phylogeography of *Marcusenius pongolensis* (Mormyridae: Teleostei) in South Africa

15.45

B.W. Price, M.H. Villet & N.P. Barker. From tree to tree: comparative phylogeography of two forest-dwelling cicada (Hemiptera: Cicadidae) lineages in South Africa

16.00

C.M.R. Kelly, W.R. Branch, M.H. Villet & N.P. Barker. Adders and afro-montane phylogeography: the Great Escarpment and Cape Fold Mountains as a speciation hot-bed for dwarf Bitis (Serpentes: Viperidae)

16.15

A.J. Potts, T.A. Hedderson, R.M. Cowling & J.H.J. Vlok. River drainage basins channel genetic diversity in the Albany Subtropical Thicket: a comparative phylogeographic study of three plant species

16.3

G.P. Keevey, M.H. Villet & N.P. Barker. Phylogeography and genetic diversity of the Mountain beauty butterfly (*Aeropetes tulbaghia*)

16.45

G. Gouws, M. Mwale, J. Bourjea, D. Muths, J. Mwaluma, A. Mwandya & O. Gon. Many fish and many genes: what are they saying about Western Indian Ocean connectivity and biogeography?

G. Gouws

THURSDAY 20TH JANUARY - ZOOLOGY MINOR 1

Zoo Minor 1

- 8.30 **PLENARY:** *L.B. Beheregaray*. A review of phylogeography and the integration between biologists and earth scientists (**VENUE: ZOOLOGY MAJOR**)
- 9.30 *T.E. Moore*, G.A. Verboom, M.D. Cramer & F. Forest. The phylogenetics and biogeography of the parasitic genus *Thesium* L. (Santalaceae s.l.), and the role of the edaphic environment in shaping divergence in heterotrophy-associated traits
- 9.45 *V.C. van der Merwe*. The vicariance biogeography of terrestrial gamebirds (Galliformes)
- 10.00 *E. Uys*. Relationships and evolution in the Drakensberg near-endemic genus, *Craterocapsa* (Campanulaceae)
- 10.15 *A. Biccard* & C.L. Griffiths. Systematics, taxonomy and biogeography of South African barnacles
- 10.30 *O.R. Davies*, T.M. Crowe & R. Bowie. Taxonomy, systematics and biogeography of 'marsh cisticolas', *Cisticola* spp.
- 10.45 *H.M. Barber-James*. Fossils, molecules and morphology: an in-depth look at the historical biogeography of the mayfly family Prosopistomatidae (Insecta: Ephemeroptera)
- 11.00 **TEA & POSTERS**
- 11.30 *G.J. G. Hofmeyr*, S.E.E. Plön & P.A. Pistorius. Assessing changes in the distribution of bottlenose and common dolphins on the South African coast
- 11.45 *M. Morallana*, G. Gouws & M. Mwale. Regional genetic differentiation in the Dory Snapper (*Lutjanus fulvivflamma*) in the Western Indian Ocean
- 12.00 *J.M. Olbers*, Y. Samyn, C.L. Griffiths. New distribution records of ophiocomid brittle stars (Echinodermata: Ophiuroidea: Ophiocomidae) from KwaZulu-Natal, South Africa
- 12.15 *P. Rousseau*, P. Vorster & M. van der Bank. A molecular phylogeny and DNA barcoding of African endemic cycads: preliminary findings
- 12.30 *B. Kyalangalilwa*, S. Boatwright, O. Maurin & M. van der Bank. A molecular phylogeny of Acacia (Fabaceae)
- 12.45 *N. Phaliso*, N.P. Barker, R.J. McKenzie & P.-O. Karis. The prickly problem of Berkheya Ehrh. (Asteraceae)
- 13.00 **LUNCH**
- 14.00 **PLENARY:** *S.M. Goodman*. The importance of molecular systematics in advancing measures of biodiversity and its

implications for conservation on Madagascar (VENUE:
ZOOLOGY MAJOR)

15.00

TEA & POSTERS

15.30

M. Martínez-Azorín, M.B. Crespo, A. Juan, M.F. Fay & N.P. Barker. A new taxonomic arrangement of Ornithogaloideae (Hyacinthaceae) - morphological evidence supports molecular-based clades

15.45

W. P. Strümpher, D. Downie, C. L. Sole & C.H. Scholtz. Phylogeny of the family Trogidae (Coleoptera: Scarabaeoidea)

16.00

M. D. Pirie, E.G.H. Oliver & D.U. Bellstedt. A densely sampled ITS phylogeny of the Cape flagship genus *Erica* L. reveals numerous shifts in floral macro-morphology

16.15

S. Mlambo. Phylogeny of the African ball-rolling dung beetle genus *Epirinus* Reiche (Coleoptera: Scarabaeinae): the origin of rolling?

16.30

B.H. Daru, O. Maurin, N. Maclean, B. Bayer & M. van der Bank. Molecular phylogeny of *Haworthia* (Asphodelaceae): evidence from plastid and nuclear DNA sequences

16.45

S. Willows-Munro, M.J. Morgan, J.C. Santos, D.M. Hillis & D.C. Cannatella. The relative utility of 20 nuclear markers in assembling the Amphibian Tree of Life

S. Willows-Munro

THURSDAY 20TH JANUARY - ZOOLOGY MINOR 2

Zoo Minor 2

- 8.30 **PLENARY:** *L.B. Beheregaray*. A review of phylogeography and the integration between biologists and earth scientists **(VENUE:ZOOLOGY MAJOR)**
- 9.30 *C.M. Francis*, J.J. Bolton, T. Mandiwana-Neudani & R.J. Anderson. Molecular systematics of the red seaweed genus *Laurencia* in South Africa
- 9.45 *M. P.A. Coetzee*, M.J. Wingfield & B.D. Wingfield. Species diversity within the *Ganoderma lucidum* species complex in southern Africa
- 10.00 *K. Naidoo*, B.D. Wingfield & M.J. Wingfield. Mitochondrial genomics: developing tools to characterize sibling species in fungi
- 10.15 *O. Gon*, G.R. Allen & G. Gouws. Revision of the cardinalfish genus *Siphamia* (Perciformes, Apogonidae): final report
- 10.30 *M. Cole*. Chondrocyclus - small, forest-dwelling land snails
- 10.45 *A.Craig*, M. Louette & M. Hasson. *Ploceus* weavers (Aves: Ploceidae) in central Africa: revisiting old taxa may revise diversity
- 11.00 **TEA & POSTERS**
- 11.30 *C.A. Matthee* & C. Montgelard. Tempo of genetic diversification in southern African rodents: what role does climate really play?
- 11.45 *B.W. Price*, F.C. de Moor & M. H. Villet. Who are you? A DNA-based approach to linking the life-cycle stages of Afrotropical Megaloptera
- 12.00 *M. Kraai* & O. Gon. Systematics of the '*Apogon unicolor*' species group (Pisces: Apogonidae: Apogon)
- 12.15 *E. Swartz* & R. McDowall. How does African *Galaxias* diversity compare with global patterns?
- 12.30 *A.K. Switala*, C.H. Scholtz & C.L. Sole. Beetle relicts of the Western Cape: evaluating species delineation within *Colophon* (Coleoptera: Scarabaeoidea: Lucanidae)
- 12.45 *P.J. Taylor*, S. Stoffberg, A. Monadjem, M.C. Schoeman & F.P.D. Cotterill. Cryptic species of horseshoe bats in the *Rhinolophus hildebrandtii* complex: a taxonomic jigsaw puzzle
- 13.00 **LUNCH**
- 14.00 **PLENARY:** *S.M. Goodman*. The importance of molecular systematics in advancing measures of biodiversity and its implications for conservation on Madagascar **(VENUE: ZOOLOGY MAJOR)**

A.J.F.K. Craig

C.A. Matthee

TEA & POSTERS

15.00

15.30

J.Masters, M. DelPero, D. Silvestro & F.Génin. Seeing the wood for the trees: over-estimation of family-level diversity in Malagasy lemurs

15.45

M. Kraai & O. Gon. Discovery and investigation of the occurrence of spinoid scales in the cardinalfish family Apogonidae (Pisces: Perciformes)

16.00

R. Groenewald, B. van Vuuren & S. Chown. Systematics of the flightless moths (Genus: Pringleophaga) on islands in the sub-Antarctic

16.15

A. Channing, A. Hillers, S. Lötters, M-O. Rödel, S. Schick, V. Mercurio & D. Rödder. Not all green jewels are the same: cryptic species of African reedfrogs

16.30

A. Chakona, E. Swartz, G. Gouws & P. Bloomer. Vicariance or dispersal: does the distribution of genetic diversity in *Galaxias 'nebula'* conform to previous biogeographic hypotheses?

16.45

J.L. Fearon, N.P. Barker and D.G. Herbert. The genetic diversity and conservation biology of the rare terrestrial snail genus *Prestonella*

J. Masters

FRIDAY 21ST JANUARY - ZOOLOGY MINOR 1

Zoo Minor 1

- 8.30 **PLENARY:** *T. Crowe*. What kind of fowl am I? Poultry in motion
(**VENUE: ZOOLOGY MAJOR**)
- 9.30 *J. Bentley*, G.A. Verboom & N.G. Bergh. The evolution of the Afrotropical-endemic genus *Macowania* (Asteraceae) in the Drakensberg region of South Africa
- 9.45 N.G. Bergh & G.A. Verboom. Anomalous capitulum structure and monoecy confer flexible sex allocation and life history evolution in the *Ifloga* lineage of paper daisies (Compositae: Gnaphalieae)
- 10.00 *V. Hoffmann*, F.P.D. Cotterill & G.A. Verboom. Tracking geobiological linkages between speciation and landscape evolution through space and time - are plants timekeepers of formative events in the geomorphic history of the Cape Fold Belt?
- 10.15 *P. Kaleme*, B. van Vuuren, R. Bowie, J. Bates, E. Solano & C. Born. The Albertine Rift region of Africa: evolution and conservation of small mammals
- 10.30 *L.J. Odendaal*, D.S. Jacobs & J.M. Bishop. Of bats and accents: gene flow and the evolution of local acoustic signatures in bats
- 10.45 *M. Mwale*, C. Mavimbela, N. Mjacu & O. Gon. A molecular phylogeny and evolution of goby species of *Caffrogobius*
- 11.00 **TEA & POSTERS**
- 11.30 *R. Kabongo*, O. Maurin & M. van der Bank. The development of an accurate DNA-based identification tool for traded and protected tree species in Africa
- 11.45 *M. Ramoeljane**, E. Swartz & O. Weyl. Morphological evidence of hybridisation between *L. capensis* and *L. umbratus* (Cyprinidae)
- 12.00 *M.T. Sethusa*, I.M. Millar & M. van der Bank. Towards DNA barcoding scale insects of economic importance in South Africa
- 12.15 *L.T. Mankga*, A. Moteeteete, O. Maurin & M. van der Bank. DNA barcoding medicinal plants of South Africa
- 12.30 *L.P. Snyman*, M.W. Mansell & C.H. Scholtz. Solving the Mantispidae puzzle: generating a key to the genera of South Africa
- 12.45 *K.A. Williams* & M.H. Villet. The challenges of using molecular techniques for identifying *Lucilia* blowflies
- 13.00 **LUNCH**
- 14.00 **WORKSHOP:** L. Penev, *P. Stoev*, W.J. Kress, S. Knapp & T. Erwin. Cybertaxonomy, semantic markup and semantic enhancements: the PhytoKeys and ZooKeys experience (**VENUE: JACARANDA COMPUTER LABS**)
- 15.00 **TEA & POSTERS**
- 15.30 Digital taxonomy workshop (continued)

FRIDAY 21ST JANUARY - ZOOLOGY MINOR 2

Zoo Minor 2

- 8.30 **PLENARY:** *T. Crowe*. What kind of fowl am I? Poultry in motion (**VENUE: ZOOLOGY MAJOR**)
- 9.30 *M. Hamer*. An assessment of the zoological research collections in South Africa
- 9.45 *W. Coetzer* & *O. Gon*. A platform for biodiversity information is a platform for biodiversity science
- 10.00 F.P.D. Cotterill *C. Griffiths*, *T. Robinson* & *L. Lange*. Assessing the state of knowledge of marine biodiversity in South Africa
- 10.15 *K. Yessoufou*, *V. Savolainen*, *O. Maurin* & *M. van der Bank*. Plant survival strategies in a tropical African savanna, Kruger National Park, South Africa
- 10.30 F.P.D. Cotterill & *M.J. de Wit*. Geocodynamics and geobiological fingerprints of tectonism. I. Biotic indicators
- 10.45 F.P.D. Cotterill & *M.J. de Wit*. Geocodynamics and geobiotic fingerprints of tectonism. II. Landscape history
- 11.00 **TEA & POSTERS**
- 11.30 *G.A. Verboom*, *M.L. Herron* & *J.A. Slingsby*. Morphology as an arbiter of gene tree incongruence: phylogenetic relationships and biome history in the African flowering plant genus *Jamesbrittenia* (Scrophulariaceae: Limoselleae)
- 11.45 *C.W. Beukes*, *I.J. Law*, *S.N. Venter* & *E.T. Steenkamp*. Phylogenetic characterisation of root-nodule bacteria associated with indigenous fynbos legumes
- 12.00 B.W. Price *G. Cron*, *M. Bartlett* & *C. Pirone*. Phylogenetic relationships and evolution of the Strelitziaceae
- 12.15 *J. Gere*, *M. van der Bank* & *O. Maurin*. Phylogenetic relationships within subtribe Terminaliinae (Combretaceae)
- 12.30 *P. Spies*, *R. Kleynhans* & *J.J. Spies*. Cytogenetic and phylogenetic studies in the genus *Lachenalia*
- 12.45 *B.W. Price*, *M.H. Villet*, *S.M. Walton* & *N.P. Barker*. The phylogenetic relationships and evolutionary history of the Dirini (Nymphalidae: Satyrinae), a tribe of butterflies endemic to southern Africa
- 13.00 **LUNCH**
- 14.00 **WORKSHOP:** *W. Coetzer*. Database ('Specify6') Workshop (**VENUE: JACARANDA COMPUTER LABS**)
- 15.00 **TEA & POSTERS**
- 15.30 Specify6 workshop (continued)



PLENARY TALKS

A review of phylogeography and the integration between biologists and earth scientists

*L.B. Beheregaray**

School of Biological Sciences, Flinders University, Adelaide, SA 5001, Australia

*Corresponding author: luciano.beheregaray@flinders.edu.au

Phylogeography is a young, vigorous and integrative field of study that has recently expanded into many areas of biodiversity research and also into several historical disciplines of Earth sciences. In the first section of this talk I present a numerical synthesis of the phylogeography literature for 10 major groups of organisms. I summarize the progress, tendencies and deficiencies of the field at both global and regional scales (with a particular focus on the Southern Hemisphere). In the second section I provide examples about how Earth scientists and phylogeographers can mutually benefit from integrating information to fill in temporal and spatial gaps when reconstructing the history of a particular region and its biota.

What kind of fowl am I? Poultry in motion

T. Crowe^{1,*}

¹ DST/NRF Centre of Excellence in Birds at the Percy FitzPatrick Institute, Department of Zoology, University of Cape Town, Private Bag X3, Rondebosch 7701, South Africa

*Corresponding author: timothe.crowe@uct.ac.za

The phylogenetic relationships and biogeography of gamebirds (Aves: Galliformes) are re-investigated. In-group taxa (rooted on representatives of the Struthioniformes and Tinamiformes) include 293 terminal taxa representing all supra-generic galliform taxa and nearly all genera. The characters include 120 morpho-behavioural (M/B) and 62 173 nucleic characters from 13 mitochondrial and 42 nuclear markers. Analysis of the combined character data set yielded a strict consensus tree that supports: a southern origin of gamebirds with several basal lineages predating the 65 myr K-T event; an early Gondwanan split of the three basal lineages to Australasia (Megapodiidae), followed by South America (Cracidae) and then Africa (Numididae); two major 'Out-of-Africa' dispersal events to Asia (giving rise to the balance of Old World galliforms) and North America (giving rise to the New World Quails). The traditional phylogenetic groupings of most phasianine galliforms are shown to be para- or polyphyletic.

The importance of molecular systematics in advancing measures of biodiversity and its implications for conservation on Madagascar

*S.M. Goodman**

Field Museum of Natural History, 1400 South Lake Shore Drive, Chicago, Illinois 60605, United States of America & Association Vahatra, BP 3972, Antananarivo (101), Madagascar

*Corresponding author: sgoodman@fieldmuseum.org, sgoodman@vahatra.mg

On the basis of classical museum studies, major progress has been made in understanding measures of species richness for the Madagascar biota. In turn, this information has been instrumental in deciphering biogeographic patterns and definitions of species' limits. However, the patterns and measures disclosed by these studies are notably more ambiguous than those uncovered by molecular genetic techniques. These new insights range from the discovery of a myriad of cryptic species to a more precise understanding of the colonization and speciation history of the unique adaptive radiations endemic to the island. Given recent political-social-economic problems on Madagascar, that have had a devastating impact on certain remaining forested areas and the exploitation of natural resources, the implications and importance of uncovering measures of biodiversity is discussed in light of conservation measures.

Cenozoic environmental change and the systematics of southern hemisphere plants

*P.H. Weston**

National Herbarium of New South Wales, Royal Botanic Gardens, Mrs Macquaries Road, Sydney, NSW 2000, Australia

*Corresponding author: Peter.Weston@rbgsyd.nsw.gov.au

Systematists traditionally justify their science on the grounds that it enables other scientific research by providing a logical framework for generalisations about organisms. However, systematists since Linnaeus have also taken a specific interest in reconciling their knowledge of organismal relationships and distributions with theories of environmental change. Joseph Hooker, for instance, armed only with species lists, distributional information and intuitively assessed ideas of interspecific relationships, was able to formulate a remarkably prescient theory explaining disjunct plant distributions in the southern hemisphere as the result of changes in climate and the distribution of land and sea. The development of explicit methods for reconstructing phylogeny in the second half of the twentieth century was the catalyst for significant advances in biogeographic methodology, which allowed systematists to test macroevolutionary hypotheses of vicariance, dispersal, biome shifts and diversification far more rigorously than before. The recent addition of relaxed molecular clock dating techniques to the systematist's tool kit has provided yet another potentially powerful method that allows us to augment knowledge of the relative ages of clades with estimates of their minimum absolute age. These advances have enabled ever more detailed reconciliation of phylogeny with knowledge from earth and climate sciences. The results of this work have been surprising in suggesting that most taxa are more vagile but also more ecologically conservative than many of us had expected. They have also reminded us of the likely inability of most plant groups to adapt successfully to abrupt climate change. Systematic research at and below the species level has also been recently invigorated by the addition of molecular data and new analytical tools from population genetics. The exquisitely detailed descriptions of geographic variation that these advances have enabled suggest how populations have evolved and moved in response to recent climatic change. These studies also give us an insight into likely microevolutionary responses of plant populations to future climate change.

WORKSHOPS

Database ('Specify6') Workshop

*W. Coetzer**

South African Institute for Aquatic Biodiversity, Grahamstown 6140, South Africa

[*Presenter: W.Coetzer@saiab.ac.za](mailto:W.Coetzer@saiab.ac.za)

Ever wondered whether there is a State-of-the-Art system for biodiversity information management? Welcome to Specify6 (www.specifysoftware.org). During this workshop you will see how easy it is to manipulate taxon and specimen records. We will use the exhaustive Catalogue of Afrotropical Bees (Eardley and Urban, 2010) to demonstrate the power of a solid platform for biodiversity information and Biodiversity Science. While assistance can be offered for installing the software on laptops after the workshop, the demonstration cannot be done on laptops. Desktop machines will be supplied for the demonstration. The workshop will be interactive and very "hands-on."

Developing a national strategy for zoological systematics in South Africa

*M. Hamer**

Biosystematics Division, South African National Biodiversity Institute, Private Bag X101, Pretoria, 0001

*Presenter: M.Hamer@sanbi.org.za

The Biodiversity Sector is developing Human Capital Development and Research Strategies, under the auspices of SANBI. This provides an important opportunity for systematics and taxonomy to reposition itself in terms of relevance and alignment to the national investments in Research and Development. More importantly, an integrated, holistic, national approach for systematics and taxonomy will ensure strategic positioning for an ongoing contribution to national agendas, which will strengthen arguments in leveraging funding, thereby ensuring long-term sustainability of the discipline. A national strategy will also identify key priorities, ensuring effective allocation of limited resources. The foundation of any strategy is identification of the current state of the discipline, and harnessing of ideas and possible direction from the stakeholders. This workshop will provide an overview of the current state of zoological systematics in terms of animal diversity, trends in publications, and existing capacity, and will provide an opportunity for participants to provide suggestions for a common vision and goals for the national strategy for zoological systematics.

Cybertaxonomy, semantic markup and semantic enhancements: the PhytoKeys and ZooKeys experience

L. Penev¹, P. Stoev^{1,*}, W.J. Kress², S. Knapp³ & T. Erwin²

¹ Pensoft Publishers, Sofia, Bulgaria

² Smithsonian Institution, Washington DC, United States of America

³ Natural History Museum, London

*Presenter: pavel.e.stoev@gmail.com

Cybertaxonomy is a new approach in support of classical taxonomy that encompasses a variety of methods to provide digitalisation, online presence and comprehensive linking of taxonomic information. Cybertaxonomy addresses four challenges of the Internet era: (1) Electronic publications as amendments/alternatives of the conventional paper-based ones; (2) Open Access as a new publishing model; (3) Linkage of biological information through taxonomic names or their Life Science Identifiers (LSIDs); (4) Web 2.0 semantic markup and enhancement technologies. To address these challenges, Pensoft has launched two high-tech, cybertaxonomic, peer-reviewed, open-access journals *ZooKeys* (www.zookeys.org) and *PhytoKeys* (www.phytokeys.com). Both journals apply cutting-edge technologies in publication and dissemination of biodiversity information, while at the same time strictly following the requirements of the botanical and zoological codes of nomenclature. The journals appear in four different formats: (1) high-resolution, full-colour print version; (2) PDF identical to the printed version; (3) HTML format providing links to external resources and semantic enhancements for interactive reading; (4) XML format (based on the TaxPub schema) providing machine-readable copy for future re-use and digital archiving in PubMedCentral. *PhytoKeys* and *ZooKeys* are more than just journals. They are linked environments built upon content management software and an XML-based editorial workflow. The journals register new taxonomic names in IPNI and ZooBank, taxon treatments in Plazi (www.plazi.org) and provide descriptions and images to the EOL. The content is linked at various levels within the article and to external resources (GBIF, BHL, NCBI, EOL, Morphbank, IPNI, ZooBank, PLANTS, Wikipedia, etc.) through a dynamic web profile of each taxon (www.ptp.pensoft.eu). Geo-referenced localities for each taxon treatment are mapped online. The journals can be followed on Twitter, Facebook, Mendeley and several other social networks. The journals participate in a new EU-funded project, VIBRANT (www.vbrant.eu), that is expected to develop an entire cybertaxonomic e-infrastructure to serve the needs of systematists.

RESEARCH PRESENTATIONS

Fossils, molecules and morphology: an in-depth look at the historical biogeography of the mayfly family Prosopistomatidae (Insecta: Ephemeroptera)

H.M. Barber-James^{1,2,*}

¹ Department of Freshwater Invertebrates, Albany Museum, Grahamstown 6140, South Africa

² Department of Zoology and Entomology, Rhodes University, Grahamstown 6140, South Africa

*Corresponding author: H.James@ru.ac.za

The Prosopistomatidae is an enigmatic family of mayflies (Ephemeroptera) whose stem-group lineage can be traced back to Mesozoic fossils. Comparison of wing venations of fossil insect lineages with those of modern mayfly species has led to a hypothesis that the Prosopistomatidae and their sister group, the Baetiscidae, separated earlier than other mayflies from the stem-group lineage that led to the remaining extant mayfly families, probably during the late Jurassic. This was tested by calibrating a molecular phylogeny using mitochondrial 16S rRNA, and nuclear 18S rRNA and Histone 3 genes, with a relaxed Bayesian clock method, using Odonata as the outgroup. Other mayfly sequences included from GenBank represented a selection of the more prominent extant mayfly families. Calibrations used Aeshnidae (Odonata) and Siphonuridae, Oligoneuriidae, Leptophlebiidae and Baetiscoidea (Ephemeroptera) fossil dates. While this did not show the predicted earlier lineage splitting, it clearly showed the antiquity of the family. Crown group species were shown to be late Cretaceous, with the oldest of species occurring in Asia, suggesting dispersal from this region via the Pacific Islands as far as northern Australia and via Europe and the Middle East to Africa. The Madagascan species are of similar age, or younger than the African species, but not old enough to have been the product of variance due to post-Gondwanan continental drift. The European species are younger than most of the African species (less than 2 Myr old) and show a close relationship with some of the African species, suggesting re-colonisation of Europe following Pleistocene glaciations.

Centres of endemism: overview, analyses and the future

*N.P. Barker** & V.R. Clark

Department of Botany, Rhodes University, Grahamstown 6140, South Africa

*Corresponding author: n.barker@ru.ac.za

Centres of plant endemism (CoE) in South and southern Africa have been variously defined and redefined. While some CoE coincide with hotspots, biomes or some other concept of vegetation unit, others are less discrete, and might merely represent local nodes of sampling intensity in a poorly sampled background. However, with few exceptions, these have been subjective assessments based on experience, field observations and specialist expertise. In some instances the boundaries of some CoE vary from author to author. Furthermore there has been almost no hypothesis-driven form of testing of these CoE. An overview of the current CoE is presented, and examples of the above problems are provided. Biogeographic methods that could improve the delimitation and recognition of CoE are discussed, and their strengths and weaknesses assessed. The effects of factors such as mapping scale, the role of geology, soils and climate are discussed. Finally, links to faunistic diversity are discussed.

The evolution of the Afrotemperate-endemic genus *Macowania* (Asteraceae) in the Drakensberg region of South Africa

J. Bentley^{1,*}, G.A. Verboom¹ & N.G. Bergh²

¹ Department of Botany, University of Cape Town, Cape Town, South Africa

² South African National Biodiversity Institute, Cape Town, South Africa

*Corresponding author: bnjoanne@gmail.com

The cosmopolitan Asteraceae tribe Gnaphalieae, or paper daisies/everlastings, form a significant component of both the dry and cool temperate floras of southern Africa. Within this tribe exists a small Afrotemperate genus, *Macowania*, endemic to the grassland biome of South Africa and occurring almost exclusively within the Drakensberg region, apart from two disjunct species in North Africa. The age, relationships and geographic origin of *Macowania* is investigated in order to provide insight into the factors affecting speciation, especially uplift events, on this small Afrotemperate genus. A well-supported phylogenetic hypothesis based on both nuclear and chloroplast genes suggests that *Macowania* is sister to a clade corresponding to the *Relhania* s.s. clade, and that these are in turn sister to a clade containing the genera *Athrixia* and *Pentatrichia*. *Macowania* is monophyletic only with the inclusion of the enigmatic monotypic genus *Arrowsmithia*, resulting in the future synonymy of *Macowania* with *Arrowsmithia*. The anomalous species *M. pinifolia*, previously part of the genus *Athrixia*, is placed in a polytomy with the *Relhania* s.s. clade and the remaining species of *Macowania* and *Arrowsmithia*. DNA sequence data could not be obtained for several *Macowania* species, including the taxa from North Africa. The placement of these species within *Macowania* is confirmed by means of a parsimony analysis of morphological characters against a molecular backbone constraint tree. One species, *M. tenuifolia*, is well-supported in two different placements within *Macowania* by chloroplast and nuclear DNA sequence data. The best position of this species is inferred by Incongruence Decomposition Analysis and morphological affinities. Bayesian relaxed clock methods and ancestral area reconstruction using Maximum Likelihood and Squared Change Parsimony estimate the age and ancestral area of the genus and determine the timing and route of colonisation of the Drakensberg. Diversification within *Macowania* is consistent in timing with the uplift events during the Miocene and Pliocene that resulted in significant vertical movement in eastern South Africa, suggesting that colonisation of the high-elevation Drakensberg grassland by *Macowania* was promoted by uplift. The topographic heterogeneity and increased river action resulting from the uplift may also have promoted evolution into new habitats and potentially mediated the movement of the ancestor of *Macowania* into the Drakensberg region via riparian habitats.

Anomalous capitulum structure and monoecy confer flexible sex allocation and life history evolution in the *Ifloga* lineage of paper daisies (Compositae: Gnaphalieae)

N.G. Bergh^{1,2,*} & G.A. Verboom²

¹ The Compton Herbarium, Kirstenbosch Research Centre, South African National Biodiversity Institute, Private Bag X7, Newlands, Cape Town 7735, South Africa

² Bolus Herbarium, Department of Botany, University of Cape Town, Private Bag 7701, Rondebosch, Cape Town, South Africa

*Corresponding author: N.Bergh@sanbi.org.za

Mechanisms for differential investment in male versus female function in annual and perennial members of southern African Gnaphalieae are explored in a phylogenetic context with particular focus on the *Ifloga* clade, a small group of mainly African daisies that is diverse in life-history duration and capitular sexual system, and possesses an anomalous capitular structure with axillary female florets. Bayesian relaxed clock and ancestral state analysis indicates a monophyletic *Ifloga* clade with an annual ancestor. The anomalous capitulum evolved from a disciform, gynomonoecious ancestor. Two independent switches to monoecy occurred in the clade, and monoecy is associated with a greater range of M/F values (the ratio of flowers with male to those with female function, within a capitulum) than are hermaphrodite or gynomonoecious species. Annual species have significantly lower M/F and possess sexual systems that confer low ratios (gynomonoecy and monoecy), while perenniality is associated with higher M/F, hermaphroditism and monoecy. Two independent gains of perenniality within the monoecious genus *Trichogyne* are accompanied by significant increases in M/F. Since monoecy is equally associated with both life-histories, we suggest that the evolution of monoecy, linked to the anomalous capitulum, may have facilitated flexibility in life-history evolution in the *Ifloga* clade.

Understanding population dynamics of invasive birds: a landscape genetics approach

C. Berthouly-Salazar^{1,*}, B.J. van Rensburg², C. Hui¹, J. Le Roux¹ & B. van Vuuren^{1,3}

¹ Centre for Invasion Biology, Stellenbosch University, Stellenbosch, South Africa

² Centre for Invasion Biology, Pretoria University, Pretoria, South Africa

³ Evolutionary Genomics Group, Department of Botany & Zoology, Stellenbosch University, Stellenbosch, South Africa

*Corresponding author: c.berthouly@gmail.com

Exotic species are non-natives that have been introduced to areas where they do not naturally occur. In some instances exotic species become invasive and represent a major threat to global biodiversity, human health and local economies. South Africa has been subjected to a large number of introductions, some of which have established and became invasive. We adopted a novel research approach for understanding the genetic dynamics of invasive species [our model taxa are the common myna (*Acridotheres tristis*) and common starling (*Sturnus vulgaris*)] and their interactions with landscape features. Our approach is based on landscape genetics; a relatively new field which integrates population genetics, landscape ecology and spatial statistics. Sampling protocols were developed using geographic information systems (GIS); specifically, landscape genetic questions require more continuously distributed sampling within the scale of spatial dependency. Geographic information is integrated when estimating genetic structure and gene flow. Our comparative approach (comparing two species) allows us to assess the relative importance of genetic diversity and landscape features in the actual invasion process including establishment and subsequent spread.

Phylogenetic characterisation of root-nodule bacteria associated with indigenous fynbos legumes

C.W. Beukes^{1,*}, I.J. Law², S.N. Venter¹ & E.T. Steenkamp¹

¹ Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa

² Agricultural Research Council Plant Protection Research Institute (ARC-PPRI), Pretoria, South Africa

*Corresponding author: chrizelle.beukes@fabi.up.ac.za

Rhizobia are gram-negative soil bacteria capable of fixing atmospheric nitrogen in association with legumes. In most of these symbiotic interactions, the plant host forms root nodules in which the rhizobial bacteroids convert nitrogen to ammonia. Currently, little is known regarding the rhizobial symbionts of the diverse fynbos legumes, and most previous studies have focused primarily on legumes of agricultural importance. In our study we considered 69 rhizobial isolates associated with fynbos legumes from the tribes Podalyrieae and Hypocalypteae. Based upon 16S rRNA and *recA* gene sequence analysis all of these isolates belong to the genus *Burkholderia*. Among these we identified 25 lineages, one of which was apparently conspecific to *B. tuberum* (the rhizobial symbiont of *Aspalathus carnosus* and *Cyclopia* spp. from which respectively rooibos and honeybush teas are prepared), while the remainder were novel. We also included analyses of the symbiotic loci encoding genes involved in nodulation and nitrogen-fixation. Analyses of these genes will shed light on the evolution of this symbiosis within the genus *Burkholderia*. In addition to increasing our knowledge of the rhizobia associated with the targeted legumes, the results of this study suggests that indigenous legumes are likely to be associated with a vast diversity of rhizobial symbionts.

Systematics, taxonomy and biogeography of South African barnacles

A. Biccard* & C.L. Griffiths

Marine Biology Research Centre, Department of Zoology, University of Cape Town, Rondebosch, South Africa

* Corresponding author: aiden.biccard@gmail.com

The last systematic and taxonomic review of the Cirripedia in South Africa was that of K. H. Barnard (1924). He added 48 new species to the previously known 26 species documented by Stubbings (1910). To date, this study has added five new species to the list, including an entire family - the *Pyrgomatidae*. Most of the species introduced to South Africa were found to be well known fouling species.

The existing key, produced by Barnard, is unclear and largely unusable, lacking illustrations and images for almost all species. Extensive revision of the taxonomy and biogeography for each species has been undertaken and a new illustrated dichotomous key compiled. Distribution ranges for several species have been extended, the most notable of which is a 300 km southerly extension of *Tetraclita squamosa rufotincta* into the Natal Bioregion¹.

High morphological plasticity is noted in species belonging to the *Lepas* genus - in particular *Lepas testudinata*. Phylogenetic analyses using two mitochondrial loci (COI and 16S) and one nuclear locus (18S) are currently being conducted in order to resolve whether new species may be present or not.

¹As defined by Lombard et al. (2004)

Pleistocene fragmentation shapes contemporary genetic structure in a forest endemic, the giant golden mole

J.M. Bishop^{1,*}, C. O'Ryan² & G.N. Bronner¹

¹Department of Zoology, University of Cape Town, Private Bag, Rondebosch 7700, South Africa

²Department of Molecular and Cell Biology, University of Cape Town, Private Bag, Rondebosch 7700, South Africa

*Corresponding author: jacqueline.bishop@uct.ac.za

Analysis of historic and contemporary genetic structure is a powerful tool for detecting the history of events that influence present-day patterns of biodiversity. In this study we describe the historical demography of an endangered forest endemic, the giant golden mole *Chrysospalax trevelyani* (Chrysochloridae), in forest fragments of the Eastern Cape region of South Africa. Extant forest distribution patterns in southern Africa are largely thought to be the result of repeated range adjustments in response to climatic cycles during the Quaternary; giant golden moles have a markedly disjunct distribution within these naturally fragmented forest habitats. To investigate the effects of past biogeographic change and current declining forest cover on the long-term persistence of the species, we sequenced the mitochondrial control region for 65 individuals collected over the last ~100 years. We found 36 haplotypes, of which only four were shared among the different forest types in which giant golden moles occur. Haplotypes did not segregate into monophyletic lineages associated with any of the four forest types in which the species is found. Instead, our analyses suggest repeated dispersal from forest refugia and colonisation of new forest habitats following cycles of climate amelioration prior to the Last Glacial Maxima. Our findings also suggest mild erosion of genetic diversity and historic expansion signals; the most important factor contributing to the decline of this species is the continued loss and degradation of its forest habitat and we discuss our findings within the context of preserving forest biodiversity in South Africa.

Variables, variance, variation and variants: speciation in the Cape Fold Mountains

M.N. Britton* & G.A. Verboom

Department of Botany, University of Cape Town, Rondebosch 7700, South Africa

*Corresponding author: matthewnbritton@gmail.com

Analysis of molecular and morphological variation in the widespread montane *Tetralia triangularis* species complex, indicate that it is comprised of a number of distinct cryptic species. The ranges of these cryptic species are reminiscent of the phylogeographic regions of endemism within the CFR. Although the origin of these species is thought to be allopatric in nature, three of these species exist in sympatry in the area of the Hawequas mountains. Populations of each of these species are arranged in distinct niches along an elevation gradient, such that the largest species occurs in the wet lowlands, the intermediate sized species on mid-slopes and the smallest species on the drier rocky open slopes on the tops of peaks. A comparison of plant traits between species growing in allopatry and sympatry suggest that there is character displacement where plants grow in sympatry. Considerable variation in leaf traits is found between populations across species geographical ranges. The relationships between this plant size variation and climatic variables is explored, to see if climate variability best explains the pattern observed. In the context of this morphological variation, we test whether variation in $\delta^{13}\text{C}$ as a proxy for water use efficiency is best explained by species identity or prevalent climatic conditions.

Mozambique's centres of endemism, with special reference to the Rovuma Centre of Endemism of NE Mozambique and SE Tanzania

J. Burrows^{1,*} & J. Timberlake²

¹ Buffelskloof Herbarium, P.O. Box 710, Lydenburg 1120, South Africa

² Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AB, United Kingdom

*Corresponding author: botart@mweb.co.za

The southeastern African country of Mozambique extends for over 2 100 km, stretching from South Africa in the south to Tanzania in the north. Mozambique has three main centres of endemism although all three are shared with adjacent countries. The Maputaland Centre of Endemism is shared with northern KwaZulu-Natal of South Africa and the Chimanimani-Nyanga Centre of Endemism extends into neighbouring Zimbabwe. The third centre straddles the Rovuma River that forms the border between Mozambique and Tanzania. This centre of endemism, until recently thought to be restricted to SE Tanzania, was previously termed the Lindi Centre of Endemism. However, botanical exploration of northeastern Mozambique over the last 10 years has revealed that the so-called Lindi Centre of Endemism extends south of the Rovuma River through coastal Cabo Delgado Province and, to a lesser extent, Nampula Province. The newly-termed Rovuma Centre of Endemism is here briefly described and a first list of plants endemic to the centre is presented.

The Drakensberg Alpine Centre of Plant Endemism, Southern Africa

C. Carbutt^{1,*} & G. Cron²

¹Scientific Services, Ezemvelo KZN Wildlife, PO Box 13053, Cascades 3202, South Africa

²School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, Private Bag 3, Wits 2050, South Africa

*Corresponding author: carbuttc@kznwildlife.com

The Drakensberg Alpine Centre (DAC) comprises the 40 000 km² high-altitude range of hills, mountain peaks and escarpment plateau located within the eastern interior of southern Africa, and is southern Africa's only alpine region. The DAC supports some 2520 angiosperms, of which some 334 are endemic and 595 are near-endemic, meaning that almost 37% of its angiosperm flora is confined to a core region south of the Limpopo River. Strict angiosperm endemism at the species level is *c.* 13%, slightly lower than the 16% endemism for KwaZulu-Natal, and substantially lower than endemism in the Cape Floristic Region (*c.* 69%). Most endemic and near-endemic species belong to the Asteraceae, Scrophulariaceae and Iridaceae, which are the largest, fourth largest and seventh largest angiosperm families in the DAC respectively. *Helichrysum* and *Senecio* contribute the most endemics and near-endemics. Some of the endemic species are rare, poorly known and highly localized due to their very specific habitat preferences. Five genera are endemic, and six genera are near-endemic to the DAC; the speciation patterns and processes for a number of these genera are currently being investigated. This paper also discusses some key principles and lessons learnt in the treatment of a centre of endemism within a floristic framework.

Phylogeography of *Amblyomma hebraeum* and *Hyalomma rufipes* (Acari: Ixodidae) in southern Africa

N. Cangi^{1,*}, I. Horak², L. Neves³ & C. Matthee¹

¹Department of Botany and Zoology-Evolutionary Genomics Group, University of Stellenbosch, Stellenbosch, South Africa

² Department of Veterinary Tropical Diseases, University of Pretoria, Pretoria 0002, South Africa

³ Faculdade de Veterinária, Universidade Eduardo Mondlane, Maputo, Mozambique

*Corresponding author: ncangi@sun.ac.za

In southern Africa, the ticks *Amblyomma hebraeum* and *Hyalomma rufipes* are the main vectors of animal Heartwater and human Crimean Congo Haemorrhagic Fever, respectively. In order to investigate the phylogeographic structure of these ectoparasites, population genetic studies were conducted throughout South Africa and Mozambique. Knowing the levels of genetic diversity in its native range may be useful for implementing control measures (cross country borders for example), evaluate the potential for drug resistance in introduced locations as well as for elucidating its vectorial capacity in the region. Mitochondrial Cytochrome Oxidase I (COI) sequences were obtained from a total of 230 individuals from eleven sampled localities. In general, the haplotype network, the molecular diversity values and unimodal mismatch distribution showed a significant genetic structure between all the populations for both species and suggest recent population expansions following a bottleneck. A Mantel Regression Analysis also revealed isolation by distance for both species. Comparing the two species, *H. rufipes* showed much stronger signals of geographic genetic population structure in relation to *A. hebraeum*. This difference may be explained by the number of hosts required to complete the life cycle (two and three hosts, respectively), type of host species (domestic and wild animals; small and big mammals, birds) and its availability, and host species overlap.

Vicariance or dispersal: does the distribution of genetic diversity in *Galaxias* ‘nebula’ conform to previous biogeographic hypotheses?

A. Chakona^{1,2,*}, E. Swartz², G. Gouws² & P. Bloomer³

¹ Department of Ichthyology and Fisheries Science, Rhodes University, Grahamstown 6140, South Africa

² South African Institute for Aquatic Biodiversity, Grahamstown 6140, South Africa

³ Department of Genetics, University of Pretoria, Pretoria 0002, South Africa

*Corresponding author: achakona@yahoo.com

Cenozoic tectonic events and Pleistocene climatic fluctuations have often been proposed as the principle factors that influenced the distribution patterns of flora and fauna in the Cape Floristic Region (CFR) of South Africa. The present study explicitly evaluated these hypotheses by comparing divergence times among populations of the widely distributed freshwater fish (*Galaxias* ‘nebula’) with known geological and climatic events. In particular, we compared the predicted effects of uplift of the Cape Fold Mountains (CFMs), river capture events, coalescence of rivers during lower sea levels (palaeorivers) and chance movements (via episodic freshwater connections) on levels of genetic variation in *G.* ‘nebula’. Two mitochondrial genes (COI and *cyt b*) were sequenced for 167 individuals collected from 95 streams spanning the species’ entire geographic range. Divergence times were inferred using MDIV and a variable molecular clock calibrated using sequence divergences from *Galaxias* populations with known geological histories in New Zealand. *Galaxias* ‘nebula’ is subdivided into three lineages corresponding to the Olifants, Berg and southern draining river systems. These lineages diverged in the Pleistocene, well after the establishment of the contemporary regional landscape. We therefore reject the hypotheses that Cenozoic uplift of the CFMs and river capture events played a dominant role in influencing the phylogeographic pattern of *G.* ‘nebula’. While large Φ_{ST} values and the restricted geographic distribution of most of the haplotypes imply absence of contemporary gene flow, low sequence divergence values and the phylogeographic structure of this species suggest recent dispersal across drainage divides. Palaeoriver systems during the last glacial maximum about 18 000 years ago do not adequately explain the evolutionary history of this species, because more recent dispersal occurred between such basins. Inter-basin dispersal via episodic freshwater connections during moister periods, possibly augmented by other earlier opportunities as described above, seems to be the most credible explanation for the extensive distribution and the patterns of genetic diversity of *G.* ‘nebula’.

Not all green jewels are the same: cryptic species of African reedfrogs

A. Channing^{1,*}, A. Hillers², S. Lötters³, M-O. Rödel², S. Schick³, V. Mercurio⁴ & D. Rödder³

¹

Biodiversity and Conservation Biology Department, University of the Western Cape, Private Bag X17, Bellville 7535, South Africa

²

Museum für Naturkunde Berlin, Herpetology, Invalidenstr. 43, 10115 Berlin, Germany

³

University of Trier, Biogeography, Am Wissenschaftspark 25-27, 54295 Trier, Germany

⁴

Gneisenaustrasse 57, 10961 Berlin, Germany

* Corresponding author: achanning@uwc.ac.za

The green reedfrogs in the *Hyperolius nasutus* group are morphologically very similar, with very brief advertisement calls, and were previously placed in a single taxon. An earlier study of advertisement calls suggested that at least three species were present. In this study we use 16S and 12S rRNA sequences to delineate species. Material was collected from Angola, Central African Republic, Democratic Republic of Congo, Congo-Brazzaville, Gabon, Ghana, Guinea, Ivory Coast, Kenya, Malawi, Mozambique, Namibia, Nigeria, Sierra Leone, Tanzania, Zambia and Zimbabwe. The analysis was run using direct optimisation as implemented in Poy 4.1.2, and maximum likelihood in MrBayes 3.2, after testing for the appropriate model using JModelTest 0.1.1. Both analyses produced a similar tree topology, although the DO tree was not fully resolved. The tree shows 10 species in what was "*Hyperolius nasutus*", as well as a monophyletic *H. lamottei*, (previously suggested to be a member of the *nasutus* clade). The 16S sequence differences between the 10 species has a mean of 6.1%. The individuals within a species are clustered geographically, and show local substructure. The distributions of the species as represented here are presented.

On-ramps and off-ramps: the phytogeography of the southern Great Escarpment, South Africa

V.R. Clark^{1,*}, N.P. Barker¹ & L. Mucina²

¹Department of Botany, Great Escarpment Biodiversity Programme, Rhodes University, Grahamstown, 6140, South Africa

²Department of Environmental and Aquatic Sciences, Curtin University of Technology, GPO Box U1987, Perth, WA 6845, Australia

*Corresponding author: vincentralph.clark@gmail.com

The Great Escarpment in southern Africa is a 5 000 km-long mountain system stretching from Angola south through Namibia into South Africa, Lesotho and Swaziland and north to Zimbabwe. The Escarpment is rich in biodiversity and endemism, hosting over half of southern Africa's centres of floristic endemism. Despite this richness, the Escarpment has been poorly studied. Here we report on floristic research on the southern Escarpment (the Sneeuwberg, Nuweveldberge and Roggeveldberge), which is 1 000 km long, forms one fifth of the total Escarpment, and has a highest point of 2 504 m. A four-year survey involving extensive fieldwork and literature review was implemented to sample all key habitats and in particular areas that may represent refugia. A database of some 12 000 taxa was created in order to use phenetic methods and Parsimony Analysis of Endemicity to analyse the floristic relationships between the southern Escarpment, the Cape Floristic Region (CFR) and the Drakensberg Alpine Centre (DAC). The southern Escarpment is shown to be rich in endemics (with one new centre of floristic endemism), to be a palaeo-corridor between the western and eastern Escarpment, and to support both palaeo- and recent connections with the CFR. Connectivity along the southern Escarpment is shown to have been broken by the aridification of the Nuweveldberge since the Last Glacial Maximum. The south-eastern connection with the CFR (first purported by Weimarck, 1941) is shown to be the primary conduit of Afromontane connectivity between CFR and the eastern Escarpment in southern Africa.

(Poster 1) Producing a taxonomic key for the South African Sarcophaginae: a tool for forensic science and medicine

*C-L. Clitheroe** & M.H. Villet

Department of Zoology and Entomology, Rhodes University, Grahamstown 6140, South Africa

*Corresponding author: larvalanobium@gmail.com

The flesh flies (family Sarcophagidae) comprise three subfamilies Sarcophaginae, Miltograminae and Paramacronychiinae. Species of the Sarcophaginae commonly complete their larval development on live or dead animals and humans, but the group has a widely varied biology. *Sarcophaga* is a cosmopolitan genus that breeds in carrion, dung and the wounds of living animals. The subfamily is sufficiently important to man that, despite its relatively large size, it was taxonomically reviewed at an African level as early as 1972. It has since received global taxonomic attention in Pape's 1996 catalogue. Its importance comes from the involvement of its members in human and animal diseases (comprehensively reviewed for the Old World by Zumpt (1965)) and in forensic entomology. Several species are synanthropic and distributed beyond Africa, so that the family is of interest internationally as well as continentally. The identification of species within this family is most reliably based on examination of the characters of the male genitalia, although small external differences often occur, namely in the degree of white hairs on the head and in features of the thorax, legs, wing veins and abdomen. Females are essentially unidentifiable unless associated with males. Identifying flesh flies is generally recognised as a challenge because the group is rather uniform in its external morphology. There is an ordinary dichotomous text key by Zumpt (1972), but it is difficult to use because of its terminology and the constraints imposed by having to start at the beginning of the couplets. It is also taxonomically outdated. For these reasons, a clearly illustrated, modern key would be invaluable. Making this available in a matrix-based, random access software package would make it even more accessible to users who are non-experts, like doctors and forensic scientists who need to identify flesh flies. No other comprehensive keys are available for Africa. The final product of this project will be a taxonomic key for the Sarcophaginae based on previous experience using IDENTIFLY, an INTKEY-based key to forensically important South African blow flies that has served as a prototype.

Species diversity within the *Ganoderma lucidum* species complex in southern Africa

M. P.A. Coetzee*, M.J. Wingfield & B.D. Wingfield

Department of Genetics, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa

*Corresponding author: martin.coetzee@fabi.up.ac.za

The bracket forming fungus *Ganoderma lucidum* is well-known in countries outside of South Africa where it causes Ganoderma root rot on various woody hosts. Previous taxonomic studies have established that *G. lucidum* represents a species complex. Little attention, however, has been afforded to determine the species diversity of this complex in South Africa. Therefore, where basidiocarps resembling this species are collected, they are still referred to as representing *G. lucidum*. The aim of this study was to increase our knowledge regarding the species comprising the *G. lucidum* complex in South Africa. Basidiocarps resembling those of *G. lucidum* were collected from various localities in South Africa on infected trees. Isolations were made to obtain pure fungal cultures for storage, DNA extraction and PCR. DNA sequences were obtained for the ITS1, 5.8S gene and ITS-4 regions of the ribosomal RNA operon. DNA sequences were compared to those of *Ganoderma* species available on GenBank. Phylogenetic trees were generated based on parsimony, Bayesian and Maximum Likelihood analyses. Preliminary results from the DNA sequence comparisons and phylogenetic analyses grouped the isolates from basidiocarps resembling *G. lucidum* in five groups. One of the groups belonged to *G. lucidum sensu stricto* while the remainder of the groups could not be identified based on DNA sequence comparisons. The latter groups either represent species for which DNA sequences are not available on GenBank or species that have yet to be described. Future studies will focus on elucidating the identity of these groups.

A platform for biodiversity information is a platform for biodiversity science

*W. Coetzer** & O. Gon

South African Institute for Aquatic Biodiversity, Grahamstown 6140, South Africa

[*Corresponding author: W.Coetzer@saiab.ac.za](mailto:W.Coetzer@saiab.ac.za)

Evidence suggests that the principles of design and management in the earliest South African museum specimen databases were not always continued in later implementations from the 1990s onwards. The Microsoft Access graphical user interface, released in 1992, allowed the importation of data from a well designed relational or hierarchical database into a 'flat' spreadsheet, at once dispensing with database cardinality (relating one thing to many things) and data quality control, thereby compromising the quality and integrity of existing and future data. As a result, the taxon name field became a simple text field, containing any number of variations of a given name, rather than a link to a curated taxon table. In one severe case 39 000 specimen records were captured without ever being assigned catalogue numbers, a situation that would have been prevented by making the field mandatory. Because field data types were not properly defined in these Microsoft Access files, attenuation of text fields was common, and whole fields have been lost. We envisage a national intervention to stem the tide of erosion of South African biodiversity information. A pilot project involving collections from four large South African natural history museums is near completion. Cleaning and migration of specimen records to Specify6 databases at three museums was followed by training workshops. Users were enthusiastic about the new software, which is easy to use, is being actively developed, and incorporates advances in collections management and biodiversity informatics (e.g. label barcodes, DNA barcodes and globally unique identifiers). Specify6 is the latest, comprehensive relational database schema and application, custom designed (for all kinds of natural history specimens) and developed at Kansas University, USA, since 1987. In the information age we can no longer avoid employing skilled information professionals in South African natural history museums. We must develop the skills needed to maximize the benefit from our biodiversity information and not sacrifice our future at the altar of the lowest common denominator.

***Chondrocyclus* - small, forest-dwelling land snails**

*M. Cole**

East London Museum, East London 5213, South Africa

*Corresponding author: maryburse@elmuseum.za.org

Land snails of genus *Chondrocyclus* (Mollusca: Cyclophoridae) have small shells with a well developed periostracum in the form of axial pleats, drawn out into hairs or flange-like bristles. The operculum is horny with a characteristic spirally coiled fringe of fused bristles. Cyclophoridae contains approximately 300 species in over 35 genera and has a tropical distribution. Little is known about their ecology and none of the genera appear to have been revised. *Chondrocyclus* contains nine described species and three potentially new species. The genus is nearly endemic to southern Africa with ten species in South Africa, one in eastern Zimbabwe and one in Malawi. They occur exclusively in leaf litter of forests and are limited to forests south and east of the Great Escarpment, extending down the coast to Cape Town. Several species are narrow-range endemics, but may be locally abundant. Morphology of shell, including periostracal ornamentation, operculum, radula and penis of each species, is illustrated. Shell proportions, number and shape of periostracal lamellae and opercular structure are useful for distinguishing species in most cases, but variation and overlap of features sometimes occurs. Radular morphology divides species into two main groups, with minor differences between species within each group. Genetic studies would assist in resolution of relationships among species. Patterns of distribution have potential to contribute to knowledge of evolutionary biogeography of South Africa's low-vagility forest fauna.

DNA fingerprinting (AFLP's) in *Colophospermum mopane* and *Imbrasia belina*

M. Cooper¹, M. van der Bank¹, M. Powell² & A. Moteetee³

¹African Centre for DNA Barcoding, University of Johannesburg, APK Campus, PO Box 524, Johannesburg 2006, South Africa

²Genomic Laboratory, Imperial College, Silwood Park Campus, Buckhurst Road, Ascot SL5 7PY, London, United Kingdom

Colophospermum mopane (J. Kirk ex Benth.) J. Kirk ex J. Léonard, commonly known as mopane, has five ecotypes: *alba*, *lesliei*, *acuminata*, *laevigatum* and *parvispermum* based on morphology, physiology and habitat. Recognition of these ecotypes, using genetics, is important as the trees provide natural resources e.g. medicines, timber, fibre and edible caterpillars (mopane worms) for rural communities in southern Africa. The tree is host to a saturnid moth larvae *Imbrasia belina* Westwood that is also variable morphologically and genetically. DNA fingerprinting, particularly Amplified Fragment Length Polymorphism (AFLP), and DNA barcoding are proposed to detect genetic variation within and between widespread populations of *C. mopane* and *I. belina*. In a preliminary study twelve *EcoR1-Mse1* primer pairs were tested and four showed polymorphisms and will therefore be used to determine genetic variation in *C. mopane* and *I. belina*. Polymorphisms will be computed on GeneMapper®. The taxonomic position of *C. mopane* is also being evaluated.

Geodynamics and geobiological fingerprints of tectonism. I. Biotic indicators

F.P.D. Cotterill^{1,2,*} & M.J. de Wit¹

¹ AEON - Africa Earth Observatory Network, Department of Geological Sciences, University of Cape Town, Rondebosch 7701, South Africa

² Department of Molecular and Cell Biology, University of Cape Town, Rondebosch 7701, South Africa

*Corresponding author: fcotterill@gmail.com

This paper is an overview of the principles guiding geodynamics research on landscape evolution, with a focus on the Kalahari Plateau. It describes how geobiological signatures in selected biotic indicators reveal complementary details about the tempo and mode of landscape evolution. Phylogeography confers spatio-temporal constraints on episodes of tectonism to reveal synergistic changes to landforms and biota. We interpret these signatures, preserved in the biosphere, to reflect where and when formative events modified landforms; in these Kalahari examples, tight causal links between biotic and palaeo-drainage dynamics reflect synergistic responses to the pulses of tectonics that altered river topology and lacustrine environments. Interspecific phylogeographic evidence tightens spatio-temporal resolution on these events. Analogous applications of biotic indicators in different landscapes are illustrated. These archived signatures of earth history enable us to reconstruct where and when earth systems impacted on earth surface processes.

Geodynamics and geobiotic fingerprints of tectonism. II. Landscape history

F.P.D. Cotterill^{1,2,*} & M.J. de Wit¹

¹ AEON - Africa Earth Observatory Network, Department of Geological Sciences, University of Cape Town, Rondebosch 7701, South Africa

² Department of Molecular and Cell Biology, University of Cape Town, Rondebosch 7701, South Africa

*Corresponding author: fcotterill@gmail.com

Presenting the findings of recent geocodynamics research on the evolution of the Kalahari Plateau, this paper is a synthesis of phylogeographic evidence; tightening spatio-temporal resolution on formative events, it maps where and when geospheric processes impacted on biodiversity. Combined phylogeographic studies of biotic indicators confers both geochronological precision and spatial resolution to quantify geobiotic events as fingerprints of tectonic pulses. This narrative of geobiological history is interpreted to reflect recurrent epeirogeny across the African plate, which has reconfigured the Kalahari Plateau since the Miocene. For geologists, geocodynamics obtains unprecedented spatio-temporal resolution to quantify the southwest spreading propagation of tectonics and so constrain the rate of individuation of the Kalahari subplate. For biologists, the synthesis of abiotic history and biogeographical events provides otherwise hidden causal evidence; this resolution has widespread applications, not least to constrain which landforms contained and facilitated evolutionary events.

***Ploceus* weavers (Aves: Ploceidae) in central Africa: revisiting old taxa may revise diversity**

A. Craig^{1,*}, M. Louette² & M. Hasson³

¹ Department of Zoology and Entomology, Rhodes University, Grahamstown 6140, South Africa

² Royal Museum for Central Africa, B-3080 Tervuren, Belgium

³ Biodiversité au Katanga, 359 avenue Usoke, Quartier industriel, Commune Kampemba Lubumbashi, Democratic Republic of Congo

*Corresponding author: a.craig@ru.ac.za

Recent fieldwork has confirmed that *Ploceus ruweti*, based on the unique type collected in 1960, is a valid species with a more extensive range on the Lufira River (Katanga, DRC) than was known previously. *Ploceus katangae*, originally described as a sub-species of *Ploceus velatus*, appears to be a distinct species, originally thought to be restricted to the Luapula River system on the Katanga-Zambia border where it is sympatric with three other colonial *Ploceus* species, now known to occur west to Lubumbashi. *Ploceus upembae*, also described as a sub-species of *P. velatus*, from the Upemba region of Katanga, may represent another species taxon, apparently limited to the wetlands of the Lualaba River. However, there are no new biological data or specimens for *P. upembae* to date. The origin of these taxa relates to the history of the river systems, for which alternative scenarios have been suggested.

Phylogenetic relationships and evolution of the Strelitziaceae

G. Cron^{1,*}, M. Bartlett² & C. Pirone³

¹School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, South Africa

²Department of Plant and Microbial Biology, University of California, Berkeley, United States of America

³Department of Biological Sciences, Florida International University, Miami, United States of America

*Corresponding author: Glynis.Cron@wits.ac.za

The Strelitziaceae (in the Zingiberales) comprises three genera with a Gondwanan distribution: *Ravenala madagascariensis* in Madagascar, *Phenakospermum guyamense* in South America, and *Strelitzia* (five species) in southern Africa. To investigate phylogenetic relationships and evolutionary trends in the family, sequence data from 11 chloroplast and two nuclear regions were combined, together with a morphological data set. Maximum Parsimony, Bayesian and Maximum Likelihood approaches were used to analyse the data. Relationships within the family remain somewhat equivocal, with two topologies emerging:

- (i) *Phenakospermum* and *Ravenala* in a clade sister to *Strelitzia* (molecular combined, indels included; + morphology), or
- (ii) *Phenakospermum* sister to the rest of the Strelitziaceae (molecular combined, no indels).

Evolutionary trends are associated with changes in habitat and co-evolution with pollinators. Dispersal from a common ancestor in Africa is hypothesised, and current biogeographic patterns in *Strelitzia* are explained using ancestral ecology reconstructions.

Molecular phylogeny of *Haworthia* (Asphodelaceae): evidence from plastid and nuclear DNA sequences

*B.H. Daru*¹, *O. Maurin*¹, *N. Maclean*², *B. Bayer*³ & *M. van der Bank*¹

¹ African Centre for DNA Barcoding, University of Johannesburg, APK Campus, PO Box 524, Johannesburg 2006, South Africa

² School of Biological Sciences, University of Southampton, Highfield, Southampton, Hants, United Kingdom

³ PO Box 960, Kuilsriver 7579, Western Cape, South Africa

Haworthia Duval (Asparagales: Asphodelaceae: Alooideae) is endemic to southern Africa with modifications to withstand relatively waterless or desert environments. There is considerable variation in form between members of the genus and also, to a lesser extent, between populations of the same species. It is likely that cryptic species are yet to be described. Despite their importance in commercial horticulture, little is known about their evolutionary history and their genetic diversity, and the taxonomy remains unresolved. In the current study, generic limits of *Haworthia* were addressed using molecular sequenced data from three plastid (*rbcLa*, *matK* and *trnH-psbA*) and the nuclear ribosomal Internal Transcribed Spacer (ITS1). Representatives of other genera within Alooideae were also included to infer the placement of the three subgenera of *Haworthia* within Alooideae. Preliminary findings will be discussed.

Taxonomy, systematics and biogeography of ‘marsh cisticolas’, *Cisticola* spp.

O.R. Davies¹, T.M. Crowe^{1,*} & R.Bowie²

¹DST/NRF Centre of Excellence at the Percy FitzPatrick Institute, Department of Zoology University of Cape Town, Private Bag X3, Cape Town 7701, South Africa

²Museum of Vertebrate Zoology, Department of Integrative Biology, 3101 Valley Life Science Building, University of California, Berkeley CA 94720-3160, United States of America

*Corresponding author: Timothy.Crowe@uct.ac.za

My research consists of two main parts. The first, which I shall be presenting here, consists of a large scale reappraisal of the taxonomy of the genus *Cisticola*, with particular emphasis on the validity of the nine natural groupings suggested by Lynes and presented in his review published in 1930. Data published in the review shall be coded and analysed using modern statistical techniques that were unavailable in the 1930’s to determine the robustness of Lynes’ conclusions. This data shall then be combined with morphological data collected from museum specimens as well as data presented in all literature since the publication of the review and reanalysed to gain a greater understanding of the structure within the genus. This comprises the morphological component that shall compliment genetic data collected in collaboration with Asst. Prof. Rauri Bowie at the Museum of Vertebrate Zoology, Berkeley. The combined analysis of morphological, genetic and behavioural data (including vocalizations) will provide us with insight to the broad scale evolution of the genus. The second part of the research will include a detailed investigation of one of the proposed groups, namely the ‘marsh cisticola’ group. Due to their strong wetland affinities, their evolutionary history and biogeography will offer a greater understanding of vegetative and hydrological dynamics on the continent, particularly with respect to drainage basin evolution.

References:

Lynes, H. 1930. Review of the genus *Cisticola*. Ibis 6 (12th ser) (supplement): 1-673

Phylogeography of a pollinator from the GCFR: genetic structure and its ecological relevance

M.L. de Jager* & A.G. Ellis

Botany and Zoology Department, Stellenbosch University, Private Bag X1, Matieland 7602, South Africa

*Corresponding author: mdj@sun.ac.za

Megapalpus capensis (Bombyliidae: Diptera) is the predominant pollinator of the sexually deceptive daisy *Gorteria diffusa* which comprises 14 geographically distinct floral morphotypes. Apart from *G. diffusa* this bee fly also pollinates various other daisies in the Succulent Karoo biome and *Pelargonium*'s in the Fynbos biome. We investigated the genetic structure and evolutionary history of this species through the use of mitochondrial markers. 114 individuals from 42 populations throughout the Greater Cape Floristic Region (GCFR) were sequenced for a 632bp fragment of the COI gene. A subset of 31 individuals from 29 populations was also sequenced for the COII gene. Genetic structure revealed that the Fynbos lineages of *M. capensis* are basal and that there are three Succulent Karoo clades that have expanded relatively recently. This pattern concurs with the evolutionary history of various plant taxa that characterise the GCFR and illustrate a general colonisation of older Fynbos lineages into the Succulent Karoo biome during the recent past. To examine the hypothesis that geographically structured variation in pollinator preference has led to floral diversification within *G. diffusa* we reciprocally tested the preferences of male flies from two *M. capensis* evolutionary lineages for the two sexually deceptive floral morphs of *G. diffusa* they are associated with. Naïve flies that have never encountered *G. diffusa* were also subjected to the same test. We found no evidence for local adaptation on the basis of male fly preference. Instead males exhibited a consistent hierarchy of preference for sexually deceptive morphotypes across their range. Experienced male flies also exhibited a significant reduction in mating intensity relative to naïve males. This learned discrimination of inflorescences as female mimics was confirmed in learning experiments and suggests the exciting possibility that a co-evolutionary arms race may have contributed to the floral diversification of sexually deceptive morphs within *G. diffusa*.

Comparative phylogeography of the four-striped mouse, *Rhabdomys pumilio* and its specific parasitic louse, *Polyplax arvicantis*

N. du Toit^{1,*}, B. van Vuuren¹, S. Matthee² & C.A. Matthee¹

¹Department of Botany and Zoology, Stellenbosch University, Stellenbosch, South Africa

²Department of Conservation Ecology and Entomology, Stellenbosch University, Stellenbosch, South Africa

*Corresponding author: ndt@sun.ac.za

Parasite-host interactions may lead to varying levels of congruence between parasite and host geographic genetic structures, ranging from complete incongruence to instances of strict co-speciation. The level of congruence is usually a reflection of the intimacy of the interaction between the host and parasite species, as determined by life history, ecological and demographic traits. In the current study the phylogeographic structures of the four-striped mouse *Rhabdomys pumilio* (Rodentia: Muridae) and its parasitic sucking louse *Polyplax arvicantis* (Phthiraptera: Anoplura) were determined and compared for potential congruence. *Polyplax arvicantis* possess several traits (such as host specificity, no free living phase or intermediate host as well as high levels of prevalence and abundance) that suggest congruent structure with the host. Amplification and sequencing of the mitochondrial gene Cytochrome Oxidase I (COI) was performed for 307 host and 260 parasite individuals from 13 localities across the distribution of *R. pumilio* within South Africa and Namibia. *Rhabdomys pumilio* was found to consist of three well supported clades/species that are geographically structured according to Biomes. The Orange River and Western Great Escarpment seem to act as contemporary gene flow barriers. Within *P. arvicantis* two highly divergent clades were found. The level of divergence is comparable to that between other recognised *Polyplax* species which may indicate that *P. arvicantis* consists of two morphologically cryptic species. Significant geographic differentiation also exists within each of these divergent louse clades. The parasite and host geographic structures are broadly congruent, as predicted by their close biological association.

The genetic diversity and conservation biology of the rare terrestrial snail genus *Prestonella*

J.L. Fearon^{1,*}, N.P. Barker¹ & D.G. Herbert²

¹ Department of Botany, Rhodes University, Grahamstown 6140, South Africa

² Natal Museum, Private Bag 9070, Pietermaritzburg 3200, South Africa

*Corresponding author: g05f0216@campus.ru.ac.za

The genus *Prestonella* is a distinctive component of the southern African terrestrial malacofauna and is restricted to relictual habitats associated with the southern edge of the Great Escarpment in South Africa. This genus represents the only surviving African element of Gondwanan Bulimulidae *s.l.* Three species-level taxa referable to the genus *Prestonella* have been described, *P. bowkeri*, *P. nuptialis* and *P. quadingensis*. Two species (*P. bowkeri* and *P. nuptialis*) appear to have very specific habitat requirements, being found almost exclusively on near-vertical rock faces above water courses and on moist, shaded (south-facing) cliffs. The habitat requirements of *P. quadingensis* remain unknown. The distribution of the genus is highly fragmented due to the evident habitat specificity of the species.

An assessment of the phylogeographic diversity of *Prestonella* using the mitochondrial markers CO1 and 16S revealed that each population is genetically distinct and that there is no gene flow between populations across their distribution range. The range of many terrestrial snails is limited due to specific habitat requirements and poor dispersal capacity, and this in turn may prevent terrestrial snails from escaping changing ecological conditions. Correlations between genetic diversity (haplotype and nucleotide diversity) and climatic variables reveal that genetically depauperate populations are found in dryer areas with less reliable rainfall patterns. This suggests that past climate change has played a crucial role in the genetic structure and integrity of *Prestonella* and has serious implications for the future of *Prestonella* in the face of global warming. Owing to their specialized habitat requirements and fragmented distributions, *Prestonella* species are likely to be adversely affected both by land degradation and by the regional aridification anticipated to result from global warming. This highlights the need for careful monitoring and site-specific conservation action plans.

(Poster 2) Complete mitochondrial genomes for the plant pathogenic fungi *Fusarium circinatum* and *F.verticillioides*

G. Fourie^{1,*}, B.D. Wingfield², M. Bogale³, M.J. Wingfield¹ & E.T. Steenkamp¹

¹Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa

²Department of Genetics, Centre of Excellence in the Tree Health Biotechnology (CTHB), Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa

³Department of Biology, Brandon University, Brandon, Canada

*Corresponding author: Gerda1.fourie@fabi.up.ac.za

Fusarium circinatum and *F. verticillioides* belong to the *Gibberella fujikuroi* complex (GFC), which is a monophyletic group consisting of many economically important plant pathogenic fungi. All previous DNA-based phylogenies divide this complex into three large clades, although the exact relationships among the clades remain unresolved. The objective of this study was to consider the phylogeny of species in the GFC using mitochondrial DNA data. The mitochondrial genomes of *F. circinatum* and *F. verticillioides* were sequenced, assembled and compared. The mitochondrial genomes of these fungi were 67106 and 53782 base pairs in length, respectively. Genome size differences were mostly due to the presence of 14 Group I introns in *F. circinatum* as opposed to three in the *F. verticillioides* genome. Both genomes had 14 protein-coding genes, two ribosomal RNA genes, 27 transfer RNA genes, and two unique open reading frames in identical gene order. These data will be used to obtain the mitochondrial genome sequences for other *Fusarium* species in the GFC. This will make it possible to reconstruct the evolutionary history of this important group of pathogenic fungi.

Molecular systematics of the red seaweed genus *Laurencia* in South Africa

C.M. Francis^{1,*}, J.J. Bolton¹, T. Mandiwana-Neudani¹ & R.J. Anderson^{1,2}

¹Department of Botany, University of Cape Town, Cape Town, South Africa

²Seaweed Unit, Department of Agriculture Forestry and Fisheries, South Africa

*Corresponding author: Caitlyne.Francis@uct.ac.za

Laurencia Lamouroux, one of the five members of the *Laurencia* complex, is an ecologically important genus on the coastlines of South Africa, which has been little studied locally. The genus also contains suites of potentially useful chemical compounds which are under investigation. Correct taxonomy is, thus, essential. The taxonomy of *Laurencia* is poorly constructed and species delimitation is severely hampered by a lack of clearly defined traits for the constituent species of the genus. Little to no phylogenetic information has been produced for the genus in southern Africa and as yet a phylogeny is lacking. This study aims to improve our knowledge of this Rhodomelacean genus in South Africa using information from the last decade's taxonomic endeavours within the *Laurencia* complex using molecules and anatomical data. Using both Parsimony and Bayesian phylogenetic inferences our preliminary results based on chloroplast DNA sequence characters (RuBisCo gene, 1480bp) have shown good support for several well-known South African species e.g. *L. glomerata*, *L. natalensis* (clade support >90% BPs & PPs). In addition, phylogenetic analyses have revealed a number of apparently new entities within the collections, including the first molecular evidence for the presence of the genera *Chondrophyucus* and *Palisada* in South Africa.

Key words: Rhodophyta, Rhodomelacean, *Laurencia* complex, taxonomy, phylogeny, *rbcL* gene

Phylogenetic relationships within subtribe Terminaliinae (Combretaceae)

J. Gere, M. van der Bank & O. Maurin

African Centre for DNA Barcoding, University of Johannesburg, APK Campus, PO Box 524, Johannesburg 2006, South Africa

Subtribe Terminaliinae is a taxonomically and phylogenetic complex group. In a recent molecular study of Combretaceae, *Terminalia*, the largest genus (~150 species) in subtribe Terminaliinae, was found to be polyphyletic. Two main clades were observed within *Terminalia*. Clade one contained representatives mainly of African *Terminalia* species with *Buchenavia*, *Bucida* and *Pteleopsis* embedded within it. The second clade consisted of Asian *Terminalia* taxa with *Anogeissus* included within it. From this study, it was vividly clear that the genus *Terminalia* needed much more attention and that a wider sampling of *Terminalia* is needed to elucidate the phylogeny of *Terminalia*. A progress report of the study will be presented.

Revision of the cardinalfish genus *Siphamia* (Perciformes, Apogonidae): final report

O. Gon^{1,*}, G.R. Allen² & G. Gouws¹

¹ South African Institute for Aquatic Biodiversity, Grahamstown 6140, South Africa

² Department of Aquatic Zoology, Western Australian Museum, Perth, Australia

*Corresponding author: o.gon@saiab.ac.za

The cardinalfish genus *Siphamia* consists of species of small fishes and differs from all other apogonids in having a bacterial bioluminescent system. In a previous presentation (2006) on this project we showed that species of this genus can be divided into two groups and that character evolution in both groups exhibits parallel trends. Few useful, though highly conservative, characters resulted in uncertainty regarding species identification within each species group. Nevertheless, five new species were reported. The ensuing painstaking search for additional characters yielded some interesting results. Examination of scales from all species revealed that most species of this genus have spinoid scales. The exception was two Australian endemics (*S. cephalotes* and *S. cuneiceps*) that, like most other apogonids, have ctenoid scales; they also differ from all other congeners in having a distinctly elongate body. Quantitative analysis of the decrease in the length of the light organ provided a way of separating the highly similar species within each of the two main species groups, leading to four more new species. It also revealed sexual dimorphism in at least one species. A phylogenetic analysis of morphological characters yielded unresolved relationships due to high level of homoplasy. *Siphamia* has only one species, *S. tubifer*, with an Indo-West Pacific distribution, but this is inconsistent with the life style and reproductive strategy of most species of this genus. A preliminary molecular genetic investigation of several samples collected across the range of this species implies that it could be a species complex. At present *Siphamia* has 23 species of which nine are new, but its relationship to other apogonid genera is still unclear.

Many fish and many genes: what are they saying about Western Indian Ocean connectivity and biogeography?

G. Gouws^{1,*}, M. Mwale¹, J. Bourjea², D. Muths², J. Mwaluma³, A. Mwandya⁴ & O. Gon¹

¹ South African Institute for Aquatic Biodiversity, Grahamstown 6140, South Africa

² IFREMER - Delegation de la Réunion, Le Port, Réunion-France

³ Kenya Marine and Fisheries Research Institute, Mombasa, Kenya

⁴ Sokoine University of Agriculture, Morogoro, Tanzania

*Corresponding author: g.gouws@saiab.ac.za

Both dominant biogeographical paradigms - dispersal and vicariance - have been invoked to account for the establishment of the endemic faunas characterising the various regions of the Western Indian Ocean (WIO). However, the extent to which these processes, recognised or proposed biogeographic breaks, and the physical complexity of the WIO have impacted on the contemporary distribution of intraspecific genetic diversity remains largely unexplored. In the present study, we consider and compare coarse phylogeographic structure among a variety of reef-associated fish species, with a view to understanding contemporary and historical connectivity and the relative influence of the above features. Target species - primarily two damselfish (*Abudefduf vaigiensis* and *Dascyllus trimaculatus*) and a parrotfish (*Scarus rubroviolaceus*), but also including representatives of the cardinalfish and triggerfish - were sampled from numerous WIO localities. Sequence data were generated from two mitochondrial gene fragments (cytochrome-*b* and ATPase 6 or NADH dehydrogenase 2) and one nuclear locus (*S7* intron 1) for each taxon. Conventional analyses of population differentiation and phylogeographic structure were performed. Some common and some contrasting patterns emerged from the included species. Most species were characterised by widely distributed haplotypes, indicating a high degree of connectivity among vastly separated localities. Whereas some species (*D. trimaculatus* and the triggerfish *Sufflamen fraenatum*) provided no evidence of geographic structure (despite varying levels of sequence diversity), other species (*A. vaigiensis* and *S. rubroviolaceus*) exhibited greater structure, with a clear distinction of Kenya and Seychelles from the remaining WIO localities. This can perhaps be attributed to the influence of the dominant current patterns and gyre systems in the region. The latter two species also provided some evidence of the existence of historically unique lineages with contemporarily overlapping distributions. These results are discussed in terms of patterns emerging from studies across the Indo-Pacific, and in parallel studies of other WIO reef-fish species. The management and conservation implications of such patterns are also considered.

Assessing the state of knowledge of marine biodiversity in South Africa

C. Griffiths*, T. Robinson & L. Lange

Marine Biology Research Centre, University of Cape Town, Rondebosch 7700, South Africa

*Corresponding author: Charles.Griffiths@uct.ac.za

This presentation aims to document the history and current status of marine biodiversity research in the EEZ of continental South African, which has an area of just over one million square km and extends to a depth of 5700 m. We present historical data on the dates, locations and depth distributions of benthic samples taken in the region. These show an extremely uneven geographic spread and very poor coverage of waters deeper than 1000 m, which comprises some 70% of the EEZ. A total of 12 914 marine species have been recorded from South African waters to date, of which some 32% are endemic. Over 50% of all species belong to three major taxa, the Mollusca (3154), Arthropoda (2451) and Pisces (2000). We estimate the validity of these estimates by comparing relative proportions of various taxa with similar lists for Europe. The results suggest that some 7500 additional species need to be described to bring our state of knowledge up to that in Europe, itself of course incomplete. Taxa with smaller body sizes and from deeper waters are particularly under-reported. The state of knowledge is also influenced by local 'taxonomic impediments' - those groups lacking local taxonomic expertise often being severely under-reported.

Analyses of distributional data show that several taxa, including fish, decapod Crustacea and Gastropoda, increase in diversity towards the east, whereas Amphipoda, Isopoda and Polychaeta, are most species in the south-west. When all taxa are summed, the Atlantic coast emerges much less species rich than the Indian Ocean coast. Rates of endemism vary greatly between taxa and peak in the south and south west. Narrow range restricted endemics peak strongly at the borders between major biogeographic provinces, suggesting that these 'ecotonal' areas are particularly important for conservation. On the positive side enormous opportunities for discovery exist in the region and we conclude by illustrating some remarkable recent finds.

Systematics of the flightless moths (Genus: *Pringleophaga*) on islands in the sub-Antarctic

R. Groenewald^{1,*}, B. van Vuuren^{1,2} & S. Chown^{1,2}

¹ Evolutionary Genomics Group, Department of Botany & Zoology, Stellenbosch University, Stellenbosch, South Africa

² Centre for Invasion Biology, Stellenbosch University, Stellenbosch, South Africa

*Corresponding author: cwg@sun.ac.za

Three flightless tineid species (Lepidoptera) are found exclusively on South Indian Ocean Province (SIP) islands. Speciation in *Pringleophaga* occurred on several islands and the genus currently comprises *Pringleophaga marioni* (Marion Island), *P. kerguelensis* (Prince Edward Island, Îles Crozet and Îles Kerguelen) and *P. crozetensis* (Îles Crozet). Minor morphological differences distinguish *P. kerguelensis* and *P. marioni* while *P. crozetensis* appear more distinct. This study aimed to investigate the phylogenetic relationships among these species, which will provide better insight into their validity as distinct species. Two mitochondrial (COI & COII) and two nuclear (EF1 α & PEPCK) markers were employed to investigate evolutionary relationships, and the results obtained from these were largely congruent. Phylogenetic methods (Parsimony and Bayesian Inference) as well as haplotype networks (constructed in TCS) indicated a close relationship between *P. kerguelensis* and *P. marioni* (these two taxa are separated by ~1.3% uncorrected sequence divergence based on COI) while *P. crozetensis* were more distinct (separated from the other two species by ~5.3% uncorrected sequence divergence based on COI), confirming morphological classifications. If we follow a standard molecular clock approach, the Marion and Prince Edward Islands were colonised soon after their formation some 500,000 years ago, probably from the Kerguelen Islands. These findings hold significant implications for the conservation of *Pringleophaga*, and more broadly for Southern Ocean biogeography.

An assessment of the zoological research collections in South Africa

*M. Hamer**

Biosystematics Division, South African National Biodiversity Institute, Private Bag X101, Pretoria 0001, South Africa

*Corresponding author: M.Hamer@sanbi.org.za

In response to concerns raised by various stakeholders, the South African National Biodiversity Institute (SANBI), in collaboration with the National Research Foundation (NRF), carried out a comprehensive assessment of 70 collections in 22 institutions. The main aims of the assessment were to determine the scale and scope of the collections, to identify the major threats to the collections, to determine use trends, and to make recommendations to address the threats. The assessment took the form of an assessor visiting all the collections and, together with the curator / collection manager, completing a questionnaire comprising 160 questions. In summary, the collections include over 10 million samples, with between 15 and 20 million individual specimens. The largest collections are housed by the Ditsong and the Iziko Museums. Use of the collections varies but is, on average, low in terms of both internal and external researchers. The total number of staff both researching and curating the collections is 115 and the overall curation budget is just over R1 million per annum. Budget for consumables was not a major problem for most collections, but funding for storage cabinets and environmental control is lacking. Over 60% of staff have been employed in their posts for more than 15 years, suggesting that staff retention is not a major problem. One of the main risks is associated with the staffing model, which is generally a single curator and a technician. Loss of one of these staff members through retirement or resignation, results in a 50% decrease in staffing. A lack of transformation of the senior staff could also be considered a risk. The second major risk is associated with governance, with most of the major institutions falling under arts and culture departments, which do not have a mandate for scientific collections or research. The third risk is associated with poor environments, with 77% of collections facing some risk, and 10% at high risk from poor temperature regulation and weak fire and pest management. Finally, the fragmented and isolated nature of operation of the institutions and staff means that there are no common or co-ordinated strategies, policies, procedures or standards, resulting in duplication of collections and effort, as well as highly variable practices and standards for maintenance, scientific curation, databasing and use of the collections. Recommendations for addressing these problems should ideally increase the staffing associated with collections, ensure that budgets are increased for expansion and storage conditions of collections, and provide a mechanism for having professional and unified standards and policies, with a common set of objectives. A major increase in funding for museum collections is probably not realistic and other mechanisms should be considered. These range from the establishment of a network, to consolidation of collections and staffing around research themes which will establish a critical mass of staff and an economy of scale for curation.

The Kamiesberg Centre of Endemism

*N. Helme**

*Corresponding author: botaneek@iafrica.com

The Kamiesberg massif (about 150 000 ha in extent) lies northeast of the town of Garies, some 500 km north of Cape Town, and at its highest point reaches 1706 m, which is also the highest point in Namaqualand. The Kamiesberg, right in the heart of the Succulent Karoo, was first recognised by Marloth in 1908 as being a distinct outlier of the CFR, and this was emphasised by Adamson in 1938, by Weimarck in 1941, and most recently by Van Wyk & Smith in 2001. However, no comprehensive inventory or analysis of the endemic or threatened flora was available until Helme and Desmet undertook this in 2006. This paper presents an analysis of the approximately 57 strict plant endemics and a further 57 near endemics, and touches on the relationships and importance of the area in the context of both the Succulent Karoo and the CFR.

Tracking geobiological linkages between speciation and landscape evolution through space and time - are plants timekeepers of formative events in the geomorphic history of the Cape Fold Belt?

V. Hoffmann^{1,2,*}, F.P.D. Cotterill² & G.A. Verboom³

¹ Department of Botany, University of Cape Town, South Africa

² Africa Earth Observatory Network (AEON), Department of Geosciences, Department of Molecular and Cell Biology, University of Cape Town, South Africa

³ Department of Botany, University of Cape Town, South Africa

*Corresponding author: vera.vhoffmann@gmail.com

The southern tip of the African continent (the Cape Floristic Region) hosts a diverse and highly endemic flora, whose distribution coincides closely with the Cape Fold Belt (CFB) of mountainous terrain. The geomorphological evolution of the CFB is poorly understood, not least because the region awaits low temperature thermochronology studies. Moreover, despite several theories that focus on palaeo-climatic forcing, the causes of “hyper-endemism” of the Cape flora remain enigmatic. Most recently, Cowling et al. (2008) hypothesised that the geomorphological evolution of the CFB could have driven pulses of speciation since the Mid-Cenozoic, such that the origin of new landscapes fostered the origin of local endemics restricted to habitat patches which are characterised by particular lithological/edaphic conditions. Teasing apart these environmental controls will enable us to test the spatial and temporal aspects of ‘substrate-tracking’ by plants through a timescale of geomorphological evolution. This study uses a cross-disciplinary synthesis of time-calibrated plant phylogenies, detailed spatial distribution maps of individual taxa and fine-scale lithology/climate datasets to evaluate geobiological history of selected fynbos clades; our key question asks whether formative events in the geomorphological evolution of the CFB created new opportunities for speciation events and/or range expansions for these Cape plant species. The ability to date these events with a molecular clock on plant phylogenies can not only resolve the turnover of floral habitats, but is expected to provide novel insights into first appearances of particular geomorphological conditions in the CFB.

Assessing changes in the distribution of bottlenose and common dolphins on the South African coast (oral presentation)

G.J. G. Hofmeyr^{1,*}, S.E.E. Plön² & P.A. Pistorius³

¹Port Elizabeth Museum at Bayworld, P.O. Box 13147, Humewood, Port Elizabeth 6013, South Africa

²South African Institute for Aquatic Biodiversity, Private Bag 1015, Grahamstown 6140, South Africa

³Nelson Mandela Metropolitan University, Department of Zoology, PO Box 77000, Port Elizabeth 6031, South Africa

*Corresponding author: greg@bayworld.co.za

The taxonomic status and distribution of two of the most familiar and cosmopolitan genera of dolphins, *Tursiops* and *Delphinus* are subject to much debate. Until relatively recently it was assumed that each genus contained a single species, but currently two species are accepted for each genus. Gaps also exist in knowledge of the distribution of these species. Furthermore, the environments these species inhabit are subject to considerable change leading to possible changes in their distribution. The Port Elizabeth Museum marine mammal collection contains a large number of specimens from both genera, which have been assembled over a number of decades. Since the taxonomic splits within these genera occurred after the inception of the collection, the majority of these specimens have not been identified to species level. Despite this, they are valuable because they are associated with skeletal material, photographs, descriptions and measurements of external morphology and records of geographical location of origin. We are using this material to identify the specimens to species level and determine changes in their distribution over time using a number of methods. This study forms part of an international programme of research into the taxonomic status and distribution of bottlenose dolphins in the Indian Ocean.

The development of an accurate DNA-based identification tool for traded and protected tree species in Africa

R. Kabongo, O. Maurin & M. van der Bank

African Centre for DNA Barcoding, University of Johannesburg, APK Campus, PO Box 524, Johannesburg 2006, South Africa

Timber-producing nations of the developing world are facing an immense problem due to the illegal trade of protected timber species. Currently there is a lack of practical control mechanisms to identify timber and wood products. In South Africa the Department of Water Affairs and Forestry (DWAFF) relies on microscopic identification of wood samples in court cases involving protected trees. The current study aims at building a DNA barcoding library for African traded and protected timber species using the plastid genes *matK* and *rbcLa* agreed upon by the Plant Working Group of the Consortium of the Barcode of Life (CBOL). A list of international and African traded and protected tree species was assembled from various sources and DNA barcodes of these trees species were produced and added to the TreeBOL database. The worldwide accessible database will serve as a backbone to a new control mechanism based on DNA techniques for species identification. Subsequently a test was conducted to assess the practicality of this control mechanism by sampling timber log materials from local and foreign timber exporting entities, then sequencing the standard DNA barcoding regions of the materials and applying a search and match to the database. The outcome of this study will be the ability for customs to rapidly identify species of timber at entry and exit points between countries with simple but accurate DNA techniques.

The Albertine Rift region of Africa: evolution and conservation of small mammals

P. Kaleme^{1,*}, B. van Vuuren^{1,2}, R. Bowie³, J. Bates⁴, E. Solano¹ & C. Born¹

¹ Evolutionary Genomics Group, Department of Botany & Zoology, Stellenbosch University, Stellenbosch, South Africa

² Centre for Invasion Biology, Stellenbosch University, Stellenbosch, South Africa

³ Museum of Vertebrate Zoology & Department of Integrative Biology, University of California, Berkeley, USA

⁴ Department of Zoology, Field Museum of Natural History, Chicago, USA

*Corresponding author: kaleme@sun.ac.za

This study aimed to investigate the effects of historical and human induced fragmentation on the distribution and the taxonomy of *Praomys jacksoni* [complex] in the Albertine Rift. Individuals were sampled from sixteen sites from high- and low- altitudes forests in the Albertine Rift, central-east Africa. We used microsatellites markers, mtDNA (control region and cytochrome b), nuclear markers (7th intron of the Fibrinogen gene) and morphometrics data to investigate phylogeographic relationships. All markers identified the same two main clusters. Within each cluster at least two sub-clusters could be considered as a species. However no clear unique geographic distribution could be attributed to each sub-cluster. Among these four species retrieved, one species has never been reported in the area. Estimation of the divergence times within each species suggests that the separation of the major clades occurred during the Miocene to mid Pleistocene. Our data suggest that past climatic fluctuation and habitat fragmentation created by the lake and river systems in combination with volcanic activity in the Virunga region could have played a key role in the structuring and diversification of species in the region. However this pattern has been partially blurred by possible hybridisation and incomplete lineage sorting.

History and management of black rhino in KwaZulu-Natal: a population genetic approach to assess the past and guide the future

M. Karsten^{1,*}, B. van Vuuren^{1,2}, P. Goodman³ & A. Barnaud^{1,2}

¹ Evolutionary Genomics Group, Department of Botany & Zoology, Stellenbosch University, Stellenbosch, South Africa

² Centre for Invasion Biology, Stellenbosch University, Stellenbosch, South Africa

³ Ezemvelo KZN Wildlife, Cascades, South Africa

*Corresponding author: minnetek@sun.ac.za

The numbers of black rhino (*Diceros bicornis*) in Africa declined dramatically during the last century due to poaching and habitat fragmentation and as such, significant concerns exist with regards to the long-term population viability and the management of these fragmented populations. A considerable proportion of the remaining black rhino (spp. *minor*) are found within South Africa where they fall largely under the protection and management of Ezemvelo KZN Wildlife. Using microsatellite markers, we provide information on the genetic diversity, population differentiation and level of inbreeding among 77 *D. b. minor* individuals sampled in seven protected areas within KZN and a single population from Zimbabwe. We found low levels of differentiation between populations; this result is not unexpected given the history of establishments and translocations between reserves. In fact, we argue that the translocations conducted by Ezemvelo KZN Wildlife have contributed to the acceptable levels of heterozygosity and minimal inbreeding which characterise the majority of protected areas in the province. The information presented here forms the basis of an ongoing monitoring programme aimed at providing vital information which, when taken with ecological and other data, will direct the future management decisions regarding translocations between reserves in South Africa and the exchange of individuals with other countries.

Phylogeography and genetic diversity of the Mountain Beauty butterfly (*Aeropetes tulbaghia*)

G.P. Keevey^{1*}, M.H. Villet² & N.P. Barker¹

¹ Department of Botany, Rhodes University, Grahamstown 6140, South Africa

² Department of Zoology and Entomology, Rhodes University, Grahamstown 6140, South Africa

* Corresponding author: g05k3539@campus.ru.ac.za

Aeropetes tulbaghia has a wide distribution within southern Africa, associated with mountainous regions ranging from the Cape Peninsula, through the Western and Eastern Cape mountains to KwaZulu-Natal. It is also found in the eastern and northeastern escarpments and as well as the southern Transvaal Highveld, and extends its range into the eastern highlands of Zimbabwe and Mozambique. This species is an important pollinator of numerous montane plants and is a strong flyer capable of covering long distances. We used mtDNA sequence data from the Cytochrome Oxidase I gene to assess genetic diversity between samples from sites across the distribution range. The CO1 data shows very little variation between populations across the South African distribution range, but samples found from Mount Gorongoza (Mozambique) were found to be genetically distinct.

Adders and afromontane phylogeography: the Great Escarpment and Cape Fold Mountains as a speciation hot-bed for dwarf *Bitis* (Serpentes: Viperidae)

C.M.R. Kelly^{1*}, W.R. Branch², M.H. Villet³ & N.P. Barker¹

¹ Department of Botany, Rhodes University, Grahamstown 6140, South Africa

² Bayworld, Humewood, Port Elizabeth, South Africa

³ Department of Zoology and Entomology, Rhodes University, Grahamstown 6140, South Africa

* Corresponding author: afrisnake@gmail.com

Stretching more than 5000 km around the perimeter of southern Africa, the Great Escarpment (GE) is the world's third longest mountain range, and to the south the nearby Cape Fold Mountains (CFM) form an integral feature of the Cape Floristic Region global biodiversity hotspot. Several dwarf members of the adder genus *Bitis* are endemic to these mountain systems, distributed widely in the CFM and the eastern and southern GE as a fragmentary series of 'island' populations. We illuminate the contentious systematics of these snakes and investigate their biogeographic history using DNA sequence data from two mitochondrial genes (16S and ND2) and two rapidly-evolving nuclear genes (PRLR and UBN1). Results indicate that montane populations form two non-sister species complexes. The *Bitis atropos* complex (Berg Adders) comprises six basal evolutionary lineages consistent with geographic distribution, diversifying between 5.0 and 0.6 Ma in a northeast to southwest direction. Zimbabwean populations branch first, followed by two Mpumalanga/Limpopo lineages, a Drakensberg/Sneeuberg lineage, and a terminal split between a distinctive Swartberg lineage and populations from the remainder of the Eastern and Western Cape. The *Bitis rubida-inornata-albanica* complex (Red Adders and allies) comprises four basal lineages radiating between 1.0 and 0.4 Ma. The direction of diversification was apparently first southwards (perhaps involving a dispersal event from the GE to the CFR) then west to east, including an altitudinal descent to form the lowland species *B. albanica* in Algoa Bay. Many of the lineages in both complexes represent cryptic species. Flux of montane habitats with tectonic uplift and cooling and aridification in the late Miocene, and with climatic oscillations in the Pleistocene, have probably driven adder speciation by both vicariance and dispersal. We suggest that the GE and CFM have been, and are likely to remain, a speciation hot-bed for dwarf *Bitis* and co-distributed organisms, and should thus be a priority for conservation.

Discovery and investigation of the occurrence of spinoid scales in the cardinalfish family Apogonidae (Pisces: Perciformes)

M. Kraai* & O. Gon

South African Institute for Aquatic Biodiversity, Grahamstown 6140, South Africa

*Corresponding author: m.kraai@saiab.ac.za

Bony fishes have three types of scales, namely cycloid, spinoid and ctenoid, that evolved in this order. The family Apogonidae has been known to have mostly species with ctenoid scales and a few species with cycloid scales, but none with spinoid scales. In a recent revision of the genus *Siphamia* (Perciformes: Apogonidae), spinoid scales were discovered on 20 of 23 species; the remaining three had ctenoid scales. This discovery prompted us to survey the entire family Apogonidae for the occurrence of spinoid scales. Scales taken from adult fish were examined using scanning electron microscopy. While no spinoid scales were found, a number of scales from several genera showed a spinoid pattern, similar to the one observed in *Siphamia*, early in the development of the scales. A comparison of adult and juvenile scales of *Apogon fraenatus* confirmed that scales of this species have a spinoid pattern before ctenii are added to the scale with growth. A second survey ensued but this time the search was for spinoid scales in postlarvae and juveniles of the different genera. The objectives of the project now expanded to include the ontogeny of scales in the Apogonidae and possible implications to the taxonomy of the family.

Systematics of the ‘*Apogon unicolor*’ species group (Pisces: Apogonidae: *Apogon*)

M. Kraai* & O. Gon

South African Institute for Aquatic Biodiversity, Grahamstown 6140, South Africa

*Corresponding author: m.kraai@saiab.ac.za

In a 2005 presentation we introduced research on the systematics of the subgenus *Apogon*. Since then this taxon has been elevated to genus level and several new species from the Indo-Pacific region have been described. Review of this group of fishes is currently focusing on the *Apogon unicolor* species group with the objective of elucidating the morphological features characterising the different species in this group, and understanding their phylogenetic relationships and biogeography. Morphological characters such as the number of gill rakers and pectoral fin rays, and the size and shape of the membranous flap making the ventral part of the preopercle have been instrumental in differentiating among species of this group as they were in other species groups of *Apogon*. The preopercular flap is of particular importance because it constitutes evidence for common ancestry between Atlantic and Indo-Pacific species of this genus. Comparison of colour features is also suggestive of a relationship between species of these two biogeographical regions.

(Poster 3) Phylogenetic analyses reveal diverse *Fusarium* species associated with *Syzygium cordatum*

M. Kvas^{1,*}, W.F.O Marasas¹, B.D. Wingfield², M.J. Wingfield¹, C.W. Beukes¹ & E.T. Steenkamp¹

¹ Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa

² Department of Genetics, Centre of Excellence in the Tree Health Biotechnology (CTHB), Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa

*Corresponding author: marija.kvas@fabi.up.ac.za

Fungal diversity in South Africa is predicted to be exceptionally high, although much of our knowledge is restricted to the fungi associated with agricultural crops. The aim of this study was to gain an insight into the actual fungal diversity that might be expected in indigenous ecosystems. For this purpose, we conducted a case study in which the fungi associated with the inflorescences of *Syzygium cordatum* (Myrtaceae) were considered. *Fusarium* species were specifically targeted because they have previously been isolated from this tree. *Fusarium* isolates were obtained from the inflorescences of *S. cordatum* collected from ten sites in South Africa. For each isolate, a portion of the gene encoding Translation Elongation Factor 1-alpha (TEF) was sequenced and compared to those in the *Fusarium* identification database (<http://isolate.fusariumdb.org/index.php>) using BLAST. TEF datasets were aligned and appropriate evolutionary models were determined, after which they were subjected to phylogenetic analyses based on Maximum Likelihood and Bayesian Inference. A total of 185 isolates were obtained and assigned to nine morphological groups. BLAST comparisons of the TEF barcodes with those in the *Fusarium* identification database revealed sequence similarity values ranging from 89% to 100%, with the sequences of only 21% of the isolates being 100% similar to known species. However, phylogenetic analyses made it possible to identify 52 well-supported and mutually exclusive monophyletic groups of isolates. The majority belonged to the *F. incarnatum*/*F. equiseti*, *F. oxysporum* and *Gibberella fujikuroi* species complexes. Of these putative species, only 31% correspond to the known species/lineages of *Fusarium*. TEF-assisted barcoding coupled with phylogenetic analyses is, therefore, a highly efficient approach to generate large-scale *Fusarium* species inventories. The surprisingly large number of species of a single fungal genus on a single native tree emphasises a poorly studied South African fungal biodiversity and the fact that many new species await discovery.

A molecular phylogeny of *Acacia* (Fabaceae)

B. Kyalangalilwa¹, S. Boatwright², O. Maurin¹ & M. van der Bank¹

¹African Centre for DNA Barcoding, University of Johannesburg, APK Campus, PO Box 524, Johannesburg 2006, South Africa

²Compton Herbarium, Kirstenbosch Research Centre, Kirstenbosch Botanical Gardens, SANBI, P/BAG X7, Claremont 7735, South Africa

DNA studies have indicated that the genus *Acacia* Miller *s.l.* is polyphyletic, resulting in the retypification of the genus with *Acacia penninervis* being the new type for *Acacia* and consisting of at least five distinct genera. These genera are: *Vachelia* (formerly *Acacia* subg. *Acacia*), *Senegalia* (formerly subg. *Aculeiferum*), *Acaciella* (formerly sect. *Filicinae*), *Mariosousa* (formerly *Acacia coulteri* group), and *Acacia* (formerly subg. *Phyllodineae*). This new classification has prompted the need to gain further insight into the relationships between the different *Acacia* species in order to determine where the African species fit into the new system. Therefore, a molecular phylogenetic study of the *Acacia* species and close relatives occurring in Africa has been carried out using sequence data from *matK/trnK*, *trnL-F* and *trnH-psbA*. These sequences were combined with relevant sequence data obtained from GenBank (representing all major lineages) to determine the relationships of African *Acacia* species with the other newly formed genera. This study highlights the inevitability of recognising segregate genera from *Acacia s.l.* and new combinations for the genera *Senegalia* and *Vachellia* is presented.

(Poster 4) Using genetic techniques to determine whether *Anthothoe chilensis* should be divided into three separate species

M.C. Laird^{1,*}, C.L. Griffiths¹

¹ Department of Zoology, University of Cape Town, PO Box X3, Rondebosch 7701, South Africa

*Corresponding author: mail.meganl@gmail.com

Many South African marine invertebrate taxa are reasonably well documented; however, the sea anemone fauna have been poorly studied. Three different colour morphs of *Anthothoe chilensis* have been observed around the South African coastline and it is unclear whether a variety of colour morphs exist, or if they are three distinct species. Most genetic work performed on South African sea anemones investigates taxa at family and not species level. This is due to low mtDNA variation.

Formerly, the systematics of South African sea anemones was based on only a few morphological characters with no molecular data. Genetic research performed over the past few decades has resolved several taxonomic problems; however, more molecular work is needed to clarify phylogenies for genera and species. The effectiveness of DNA molecular markers for addressing evolutionary questions in sea anemones has been demonstrated, thus this technique will be applied to *Anthothoe chilensis* to determine whether the different colour morphs are indeed one species or three. This anemone was originally introduced to South Africa from Chile, thus the discovery of two new species might reveal two new alien species. This study aims to enhance the current state of knowledge of sea anemones in South Africa and partially resolve the phylogenetic tree for the order Actiniaria.

Swaziland plant endemism

*L.M. Loffler**

P O Box 764, Mbabane, Swaziland H100.

*Corresponding author: lindad@realnet.co.sz

Swaziland is a landlocked country covering a total area of 17 360 km² and supports a large variety of landscapes, geology, climate and corresponding habitat and biodiversity. Floristically, it falls within the boundaries of two regional phytochoria and boasts a total of 3547 taxa. In the north-west the country borders the Barberton Mountains which forms part of the Barberton Centre of Endemism, a subcentre of the Drakensberg Afromontane Regional System and to the east the Lebombo Mountains an important subcentre of the Maputaland-Pondoland Region. A total of 25 plants (17 confirmed endemics and eight suspected endemics) have been highlighted with the highest concentrations lying within the north western part of the country. Eleven endemics are recorded in the granite-rich Mbabane area and five along the Green stone belt of the Malolotja Nature Reserve making up 64% of the country's endemics. The rhyolites of the Lebombo Mountains in the east harbour five endemics representing 20% of the country's endemic population. The most apparent threats to biodiversity that Swaziland is experiencing include land transformation, alien weed infestation, over-exploitation of natural resources, bush encroachment and outdated and fragmented legislation. In addition Swaziland has no formal institution that acts as refugia for the important plant species. Species that are threatened because of expansion programmes and developments have not been efficiently rescued and propagated and very few species have been monitored effectively. More than 70% of the people in Swaziland live on land typified by subsistence farming and scattered homesteads, making it vulnerable to plant resource utilisation. In addition a small proportion of land is dedicated to parks and wildlife management, with the present system of protected areas covering less than 4% of the country.

Phylogeography of *Marcusenius pongolensis* (Mormyridae: Teleostei) in South Africa

P.A. Maake^{1,2,*}, E. Swartz², B. Kramer³ & O. Gon²

¹ Department of Ichthyology and Fisheries Science, Rhodes University, Grahamstown 6140, South Africa

² South African Institute for Aquatic Biodiversity, Private Bag 1015, Grahamstown 6140, South Africa

³ University of Regensburg, Zoology Institute, Germany, Universitätsstrabe 31, D-93040 Regensburg, Germany

*Corresponding author: p.maake@saiab.ac.za

Marcusenius Gill, 1862 is the largest genus of the fish family Mormyridae, currently comprising 37 species distributed throughout tropical central, western, eastern, and north-eastern Africa (Nile System), reaching south into subtropical South Africa. This family is unique in producing Electric Organ Discharges (EODs) used for mating, communication and object location. The EODs are species-specific and have been used as a taxonomic character in systematic studies of this family. In South Africa this genus is represented by *M. pongolensis*, recently resurrected from the synonymy of the widespread *M. macrolepidotus*. It occurs in rivers draining into the western Indian Ocean, from the Incomati in Mpumalanga to the Mhlatuze in KwaZulu-Natal. Previous studies of mormyrids in some of South Africa's river systems indicated that the mormyrids diversity of our systems exhibit a higher level of between, and possibly even within system differentiation, that is indicative of higher diversity than currently recognised. Mitochondrial Cytochrome *b* results indicate that populations of *M. pongolensis* show sequence divergence that is usually unexpected for a single taxa. Southern populations (i.e. Incomati, Mhlatuze and Pongola river systems) seem to group together compared to populations from the Limpopo River system (a major and independent system). Populations are also heterogeneous in morphology and, to some extent, in EOD patterns, suggesting that the observed divergences could lead to recognition of more species. A separation of at least one million years is in agreement with geological data for the divergence of the Limpopo population. According to the scenario considered most likely at present, the Zambezi discharged to the Indian Ocean through the Limpopo valley until about 2 Mya, before captured and diverted by the encroaching Lower and Middle Zambezi to its northern destination. This isolation mechanism could have caused the divergence of the Limpopo population from the same *Marcusenius* stock in the Zambezi system and the other allopatric populations in South Africa.

(Poster 5) Intraspecific variation in the samango monkey (*Cercopithecus mitis/albogularis*) in South Africa

N. Makhasi, K. Wimberger, F. Génin & J. Masters*

African Primate Initiative for Environmental Sustainability, Department of Zoology and Entomology, University of Fort Hare, Alice, South Africa

*Corresponding author: jdthmasters@gmail.com

Taxonomic information is essential for understanding biological processes and assessing the conservation status of organisms. There is much disagreement among taxonomists about how many species or subspecies of animals there are because of a lack of consensus as to how species should be defined. Taxonomy of the guenon monkeys is particularly confused, and the morphology of guenons has led to a multiplicity of described species and systematic arrangements. This study aims to resolve the taxonomy of the South African forms of *Cercopithecus mitis* (alternatively, *C. albogularis*, L. Sineo, pers. comm.) by exploring subspecific differences between the two samango subspecies described for the region, *C.m. erythrarchus* and *C.m. labiatus*. Our project involves a morphological investigation involving skull morphometrics and body measurements taken from all museum specimens available in southern Africa; a genetic investigation measuring mtDNA variation in three, widely dispersed *C. mitis* populations, including one *C.m. erythrarchus* (KZN) and two *C.m. labiatus* populations (Eastern Cape; Mpumalanga); and an ecological investigation of the predominant environmental features characterising the preferred habitats of the two subspecies. Observed morphometric and genetic variation will be compared spatially, and assessed in relation to habitat differences. If *C.m. labiatus* and *C.m. erythrarchus* are demonstrably distinct morphologically, ecologically and/or genetically, this would imply different adaptive and survival capacities, which in turn would have important implications for their conservation.

(Poster 6) The Euteleost Tree of Life Project

T. Mäkinen^{1,*} & J. Andres Lopez²

¹South African Institute for Aquatic Biodiversity, Grahamstown 6140, South Africa

²Museum of the North, University of Alaska, Fairbanks, United States of America

*Corresponding author: temakine@gmail.com

Euteleosts are the crown group of ray-finned fishes, with over 17 000 species. Phylogenetic relationships among many euteleost groups are still unresolved, even though a well-supported phylogeny is essential to understanding the evolution of this extremely diverse group of fishes. I will present an overview of the project “Euteleost Tree of Life” and some recent results. The ETOL project aims to resolve euteleost relationships by collecting a large dataset of single-copy nuclear gene sequences and integrating it with morphological evidence.

DNA barcoding medicinal plants of South Africa

L.T. Mankga, A. Moteetee, O. Maurin & M. van der Bank

African Centre for DNA Barcoding, University of Johannesburg, APK Campus, PO Box 524, Johannesburg 2006, South Africa

More than 700 plant species with medicinal applications are known to be actively traded throughout South Africa and intensive harvesting of wild materials is acknowledged as a serious threat to biodiversity in the region. The market and public demand of plants over the past few decades has been so great that there is a risk of extinction or loss in genetic diversity. Also the substitution of a valuable commodity (medicinal plant) by a cheaper alternative (other plant species), either inadvertently due to misidentification, or deliberately to cheat consumers raises some serious concerns as these adulterants may not be as effective medicinally or may even be toxic and cause harm to consumers. To add to the problem many species are traded as dried leaf, root, bark products or extracts and their identification becomes problematic. DNA barcoding is a taxonomic tool that can be used as an aid for identification, which uses a standard short genomic region that is universally present in target lineages and has sufficient sequence variation to discriminate among species. The current study aims to produce a set of herbarium identified vouchers for medicinal plants, a set of DNA barcodes produced for fast and easy DNA-based species identification, and illustrations on how customs officers could use DNA barcoding to identify plant fragments from species in which trade is controlled by the Convention on International Trade of Endangered Species (CITES). Preliminary results will be discussed.

A new taxonomic arrangement of Ornithogaloideae (Hyacinthaceae) - morphological evidence supports molecular-based clades

M. Martínez-Azorín¹, M.B. Crespo¹, A. Juan¹, M.F. Fay² & N.P. Barker³

¹ CIBIO (Instituto Universitario de la Biodiversidad), Universidad de Alicante, P.O. Box 99, E-03080 Alicante, España

² Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3DS, United Kingdom

³ Department of Botany, Rhodes University, Grahamstown 6140, South Africa

*Corresponding author: mmartinez@ua.es

The taxonomic arrangement of Ornithogaloideae (Hyacinthaceae) has been a matter of controversy in recent decades, with several new treatments based exclusively on plastid DNA sequences, which resulted in classifications which are, to a great extent, contradictory. In the present contribution, plastid and nuclear data are combined and the phylogenetic trees obtained are better resolved than those with any plastid region alone or plastid regions in combination. On the basis of the phylogenetic analyses, three main clades are found, corresponding to three previously recognised tribes in the subfamily: Albuceae, Dipcadiaceae and Ornithogaleae. In them, 19 monophyletic genera are accepted: *Albuca*, *Avonsera*, *Battandiera*, *Cathissa*, *Coilonox*, *Dipcadi*, *Eliokarmos*, *Elsiea*, *Ethesia*, *Galtonia*, *Honorius*, *Loncomelos*, *Melomphis*, *Neopatersonia*, *Nicipe*, *Ornithogalum*, *Pseudogaltonia*, *Stellarioides* and *Trimelopter*. Each of these has a particular syndrome of morphological characters and/or particular biogeographical distribution, which allow easy recognition. Moreover, the obtained results offer new biogeographic insights on the hypothetical floristic migration routes from southern Africa to Eurasia, according to both the ‘arid corridor’ and the ‘high-altitude corridor’ hypotheses.

Seeing the wood for the trees: over-estimation of family-level diversity in Malagasy lemurs

J.Masters^{1,*}, M. DelPero², D. Silvestro^{3,4} & F.Génin¹

¹ African Primate Initiative for Environmental Sustainability, Department of Zoology and Entomology, University of Fort Hare, Alice, South Africa

² Dipartimento di Biologia Animale e dell'Uomo, Università degli Studi di Torino, Torino, Italy

³ Senckenberg Research Institute, and ⁴Biodiversity and Climate Research Centre (BiK-F), Frankfurt am Main, Germany

*Corresponding author: jdmasters@gmail.com

With the growth of molecular technology, the use of morphological data in phylogenies has slipped from favour. However, analysed in combination with molecular data, well-chosen morphological characters can act to strengthen the historical signal in molecular data, particularly at depths where the molecular signal becomes ambiguous. We present the results of a Bayesian analysis of 3543 mtDNA bp and 42 multistate morphological characters to investigate inconsistencies in strepsirhine phylogenetic models. Our analysis provides a well-supported tree, with most branches having 90-100% support. It also gives four Malagasy strepsirhine families, not five. Our use of morphological characters allows us to trace the evolution of key adaptive character suites during the radiation of this group, with a view to reconstructing their ancestral states. Body size, hind limb proportions and basicranial flexion, dietary adaptations and activity rhythms all show reiterative evolution in several strepsirhine lineages, complicating ancestral reconstructions. We present a reconstruction of the clade ancestor using phylogenetically independent contrasts, which contradicts the common perceptions of the model strepsirhine ancestor.

(Poster 7) Phylogeography and genetic diversity of montane populations of *Otomys* in the southern Great Escarpment, South Africa

G. Mataruse, C.M.R. Kelly & N.P. Barker*

Department of Botany, Rhodes University, Grahamstown 6140, South Africa

*Corresponding author: N.barker@ru.ac.za

Mitochondrial DNA sequences of Cytochrome *b* gene (1137-bp) were used to investigate genetic diversity and phylogeographic relationships of *Otomys irroratus* and *Otomys slogetti* (Family Muridae, Subfamily Otomyinae). A total of 22 specimens of these two species were added to data obtained from GenBank. Outgroups from other genera of the Arvicanthine were included. Phylogenetic relationships were obtained using Bayesian analysis, Maximum Likelihood and Maximum Parsimony methods. Our analysis revealed the existence of two unique mitochondrial lineages of *O. slogetti*, the first lineage occurring in the Sneeuberg region and second lineage from the Drakensberg. *Otomys irroratus* formed two distinct sister clades, one for the coastal/ Albany thicket + fynbos and the second for the inland/ highveld, Inyanga+Drakensberg mountain ranges, as found previously. However, within *O. irroratus*, results show three specimens from Mountain Zebra National Park forming a new lineage which is a sister group to the two *O. irroratus* clades and *O. saundersiae karoensis* samples from the Cederberg. Furthermore, 10 samples from two localities formed a second, new lineage which is a sister to *O. angoniensis* from Mkuze and *O. typus typus* from Ethiopia. The basal relationships within *O. slogetti* and *O. irroratus* are underestimated and poorly resolved, suggesting the possibility of a rapid radiation.

Tempo of genetic diversification in southern African rodents: what role does climate really play?

C.A. Matthee^{1,*} & C. Montgelard²

¹Department of Botany and Zoology, Stellenbosch University, Stellenbosch, South Africa

²Biogéographie et Écologie des Vertébrés (EPHE), Centre d'Écologie Fonctionnelle et Évolutive, CNRS, Montpellier, France

*Corresponding author: cam@sun.ac.za

The distributions of the present-day southern African biomes are thought to originate during the Quaternary and were heavily influenced by climatic oscillations during the last 5.3 Myr. Since then, three Plio-Pleistocene peaks of aridification have occurred at approximately 2.8, 1.7 and 1.0 Mya and these peaks were interspersed by humid periods. Numerous phylogeographic studies argued that the genetic patterns observed within taxa are due to these quaternary climatic changes that potentially caused habitat fragmentation. If this holds it can be hypothesised that the timing of periods characterised by intense aridification should correlate with the timing of divergences among clades/lineages within species. Congruent peaks in cladogeneses are thus expected at 2.8, 1.7 and 1.0 Mya. A relaxed Bayesian clock was used to date the cytochrome b mtDNA divergences amongst seven southern African rodent taxa showing disjunct phylogeographic patterns. No correlation was found between climatic changes and speciation as the cumulative number of lineages per million years increased linearly over time. The outcome of our investigation rather suggests that continuous shifts in the precipitation during glacial cycles probably lead to a continuous expansion/regression phenomenon of vegetation types. The latter caused an evolutionary signature of phyletic gradualism and reject the hypothesis of punctuated speciation due to climate change.

(Poster 8) Genetic variation and biogeography of two coral reef fishes (*Thalassoma*. spp) in the Western Indian Ocean

S. Mayekiso^{1,2,*}, M. Mwale² & L. Vumazonke¹

¹Department of Zoology & Entomology, University of Fort Hare, Alice, South Africa

²South African Institute for Aquatic Biodiversity, Grahamstown 6140, South Africa

*Corresponding author: sisandamayekiso@gmail.com

Although the Western Indian Ocean (WIO) is recognised as an area of endemism among fishes, the biogeography of this region is poorly understood. Two competing biogeographic hypotheses on the origin of WIO fauna suggest either dispersal from a centre of origin to the WIO or vicariant separation of biogeographic regions. Thus two widespread *Thalassoma* species (*T. hebraicum* and *T. lunare*) were selected to determine the relationships and evolutionary history among biogeographical areas of the WIO. Specimens of both species were collected from different biogeographic areas including Mascarene WIO islands (Mauritius and Seychelles), the east and southern African mainland (South Africa, Mozambique, Kenya and Tanzania) and Madagascar. A molecular genetic approach was used to generate phylogenetic relationships among the *Thalassoma* species using mitochondrial genes (cytochrome *b* and 16S rRNA) and one nuclear gene (first intron of the nuclear *S7* ribosomal protein gene). Phylogenetic assessment was done using Maximum Parsimony and Maximum Likelihood procedures in PAUP. The results of this study should contribute to the understanding of the origin of WIO species as well as the formulation of management strategies for long term conservation of marine fishes in this region.

Rare plants and serpentine soils

D. McCallum

C.E. Moss Herbarium, University of the Witwatersrand, Private Bag 3, Wits 2050, South Africa

Serpentine soils are unfavourable for plant growth. They may be toxic due to metal content, are often lacking in major nutrients and have a high Mg to Ca ratio. There are often endemic species at serpentine sites which have a tolerance for these soils. A study of two serpentine areas in Swaziland at different altitudes found that in addition to the endemic species there were more rare species collected on the serpentine soils than was the case for non-serpentine soils in the same area. In the same study it was found that plant cover was reduced on the serpentine soils. This suggests that reduced competition may allow space for species that are poor competitors.

(Poster 9) A revision of the South African Amphipoda species list, with new material from Sodwana Bay, KZN

*R.M. Milne** & C.L. Griffiths

Department of Zoology, University of Cape Town, Rondebosch, South Africa

*Corresponding author: rebecca.milne@uct.ac.za

Macrobenthos from seagrass and algal turf habitats was collected in Sodwana Bay, KwaZulu-Natal. A total of 45 samples were collected from six different depths along the rocky shore and coral reefs. These samples contained 66 amphipod species. Nine of these were new distributional records for South Africa, and four are potentially new species, and have been examined and illustrated. Further investigation is required before these are to be confirmed as new species for publication.

The Amphipoda of South Africa last underwent a comprehensive review in 1976. The South African Amphipoda list has since been updated from 341 to 370 species. New records from this study, as well as all relevant literature published since 1976, have been incorporated into the previous list. Twenty-nine percent of the species in the current list have been revised in synonymy, higher taxonomy or distribution since 1976. This list has also been submitted to the South African Tree of Life (SAToL) project.

Phylogeny of the African ball-rolling dung beetle genus *Epirinus* Reiche (Coleoptera: Scarabaeinae): the origin of rolling?

S. Mlambo*

Scarab Research Group, Department of Zoology & Entomology, University of Pretoria, Pretoria 0002, South Africa

*Corresponding author: smlambo@zoology.up.ac.za

The dung beetle genus *Epirinus* has been suggested as the ancestral roller group in recent phylogenetic analyses. In this study we tested species in the genus for rolling behaviour and, using 16 species, constructed a molecular phylogeny based on mitochondrial genes COI and 16S together with nuclear genes 28S and CAD. Monophyly of the genus was recovered. The phylogenetic hypothesis was found to share some well supported lineages with one published earlier, based on morphological data. Moreover a combined molecular/morphology analysis showed congruence between the molecular and morphological datasets. Flight loss in some species and divergence dates within the genus are discussed.

The phylogenetics and biogeography of the parasitic genus *Thesium* L. (Santalaceae *s.l.*), and the role of the edaphic environment in shaping divergence in heterotrophy-associated traits

T.E. Moore*, G.A. Verboom, M.D. Cramer & F. Forest

Department of Botany, University of Cape Town, Private Bag X3, Rondebosch, Cape Town 7701, South Africa

*Corresponding author: TIMOTHY.MOORE@uct.ac.za

Thesium is a large genus of parasitic shrubs belonging to tribe Thesieae of Santalaceae. It has a principally Old World distribution, with the greatest diversity being found in southern Africa. We present a first estimate of species-level phylogenetic relationships in *Thesium* based on Internal Transcribed Spacer (ITS) and *trnL-trnF* sequence data, and use this to explore the biogeographical history of the group. Ancestral range reconstruction and dating analysis suggest a southern African origin for the group, with a crown age of 39.1 ± 11.9 Mya, followed by dispersal into Europe and South America. A large clade of Cape species split in the Miocene from a clade comprising tropical species (25.5 ± 7.3 Mya) with the diversification of extant species beginning at 16.7 ± 6.3 Mya. In addition to its high specific diversity, the genus also shows high morphology diversity. Using a combined experimental and correlative approach, we examine the role the edaphic environment in the Cape Floristic Region (CFR) in the south-west of South Africa plays in determining divergence in heterotrophy-associated traits in *Thesium*. Broadly, we find that *Thesium* species show significant differences in traits associated with carbon acquisition, and that these differences are associated with divergence in nutritional habitat, with more parasitic species occupying sites with lower nutrient availability.

Keywords: Cape Floristic Region, hemiparasite, oligotrophy

Regional genetic differentiation in the Dory Snapper (*Lutjanus fulvivflamma*) in the Western Indian Ocean

M. Morallana^{1,2,*}, G. Gouws¹ & M. Mwale¹

¹ South African Institute for Aquatic Biodiversity, Grahamstown 6140, South Africa

² Department of Ichthyology and Fisheries Science, Rhodes University, P O Box 94, Grahamstown 6140, South Africa

*Corresponding author: m.morallana@saiab.ac.za

The Western Indian Ocean (WIO) represents a good area for studying factors shaping patterns of marine species diversity because of its isolation and its physical complexity, which includes the current systems (the Agulhas, East Madagascar, and the Equatorial Currents) and the large basins (the Arabian, Mozambique, and the Somali Basins) which may act as barriers to some marine species. The WIO is also characterised by regional endemism found in the Red Sea, around oceanic islands (Mauritius and Reunion), and in the south-western Indian Ocean (southern Mozambique, and the subtropical and warm temperate zones of South Africa). These diverse fish faunas are hypothesised to have arisen and dispersed from a centre of origin (bounded by Indonesia, Malaysia and the Philippines), or have been proposed to have arisen *in situ*; there being no agreement on origins of these faunas. The aim of this study is to investigate the phylogeographic structure of the Dory Snapper (*Lutjanus fulvivflamma*) in the WIO and eventually compare these to the wider Indo-Pacific, and to determine the relationships, interactions and evolutionary history among localities and to identify the processes influencing genetic diversity. The key question is whether there is genetic connectivity among localities or if there is regional differentiation. Five to ten samples of the Dory Snapper were included from each of several different localities in the WIO, including South Africa, Mozambique, Tanzania, Kenya, Red Sea and Seychelles. These localities were selected due to the expectations that populations will differ between localities due to biogeographic discontinuities and transition zones. Samples from Australia and Fiji were also included to determine the placement of the WIO in the context of the wider Indo-Pacific. Standard DNA extraction, amplification by PCR and standard cycle sequencing of two mtDNA fragments (*cyt-b* and ND2), and an nDNA (the first intron of the *S7* gene) were performed. The *cyt-b*, ND2 and *S7* data sets included 729, 850 and 600 base pairs, respectively. Analyses included investigations of genetic diversity, genetic differentiation among populations and the examination of phylogenetics relationships among haplotypes. Preliminary results for the *cyt-b* gene fragment showed low genetic structure with a number of haplotypes shared between localities. Greater genetic structure was observed in ND2 gene with fewer haplotypes shared between localities. The *S7* gene showed many unique haplotypes, but without obvious spatial structure. In summary, there is high genetic diversity (number of haplotypes), and high variation (*cyt-b* & *S7* data), coupled with high gene flow and connectivity among localities. Thus, there is little evidence of spatial genetic structure. These results will be discussed in light of patterns emerging from parallel studies on two other snappers (lutjanids) and in terms of published studies encompassing the wider Indo-Pacific.

(Poster 10) DNA barcoding of larval reef fishes of the Western Indian Ocean

M. Mwale^{1,*}, S. Kaehler^{2,3} & M. Potier⁴

¹ South African Institute for Aquatic Biodiversity, Grahamstown 6140, South Africa

² Department of Botany, Rhodes University, Grahamstown 6140, South Africa

³ ASCLME, Grahamstown 6140, South Africa

⁴ IRD: Institut de Recherche pour le Développement, PO BOX 172, Sainte-Clotilde Cedex, LA REUNION

*Corresponding author: m.mwale@saiab.ac.za

The Fish Barcode of Life programme (FISH-BOL) aims to barcode all fishes to facilitate reliable species diagnostics and rapid assessments of biodiversity. In addition to the barcoding of adult fish, recent advances using the barcode data strongly support the contention that mitochondrial DNA Cytochrome Oxidase I sequences may be additionally useful for the identification of fish juveniles/larvae. Presently no regional keys are available to facilitate the reliable identification of juvenile fish or larvae in the WIO. The management of fisheries is dependant on accurate identification to understand the dispersal, recruitment and connectivity of fishes in the region. Similarly, trophic studies of gut content analysis are currently hampered by the difficulty in identifying juvenile/larval prey species. This project presents an important investigation into the feasibility of using DNA barcoding as a technique for linking juveniles and larvae to respective adults at the genus/species level. Preliminary analyses of more than 600 individuals indicated about 99% differentiation among genera and 96% among species using the COI DNA barcode. Although the distribution of species and generic/family genetic distances partially overlapped, the differences among conspecifics were markedly less than those among congeners. Most of the questionable species ID's (4%) were generally due to unknowns and should be easily verified as the BOLD database is populated with expert identified reference specimens. The material used to initiate this study was collected in the Mozambique Channel during the 2008 and 2009 ASCLME/EAF Nansen cruise. The ultimate aim is to develop an illustrated identification key/database of larvae for the WIO region.

A molecular phylogeny and evolution of goby species of *Caffrogobius*

M. Mwale^{1,*}, C. Mavimbela², N. Mjacu³ & O. Gon¹

¹ South African Institute for Aquatic Biodiversity, Grahamstown 6140, South Africa

² Walter Sisulu University, South Africa

³ University of Fort Hare, Alice, South Africa

*Corresponding author: m.mwale@saiab.ac.za

Caffrogobius is a southern African gobiid genus with small, benthic species that generally inhabit shallow water habitats in estuaries and coastal areas. The genus consists of seven nominal Western Indian Ocean fish species, six of which are endemic and occur in the southern African region (from Mozambique to Namibia) with the seventh species, *C. dubius*, being recorded from the Seychelles and only a type specimen. There is a high degree of morphological similarity in this genus, making it difficult to identify species. Phylogenetic analyses of two mitochondrial (Cytochrome Oxidase 1 and Cytochrome *b*) and one nuclear marker (first intron of *S7* ribosomal gene) was done to recover the relationships among *Caffrogobius* species and to test their monophyly. Phylogenetic analyses indicated that the genus *Caffrogobius* is monophyletic and southern African with *C. natalensis* being the basal species. Two sister pairs were recovered from the genus with the relationship between *C. agulhensis* and *C. saldanha* remaining unresolved. The most basal lineage is an estuarine-dependent species, with marine-dwelling species arising independently in the group. Estimation of divergence times suggests that the divergence of *Caffrogobius* started around Pleistocene probably with the changes in sea level between estuaries and coastal areas.

Mitochondrial genomics: developing tools to characterize sibling species in fungi

K. Naidoo*, B.D. Wingfield & M.J. Wingfield

Department of Genetics, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria 0002, South Africa

*Corresponding author: kershney.naidoo@fabi.up.ac.za

Members of the *Ceratocystis fimbriata sensu lato* complex include numerous economically important fungal pathogens. Most of these fungi are morphologically very similar and difficult, if not impossible, to identify using microscopy. Application of phylogenetic inference based on DNA sequence comparisons has consequently made it possible to identify many cryptic species in this group. It has become apparent that the available nuclear gene sequences are not sufficiently variable to allow for the differentiation of some sibling species. Mitochondrial genes are well known to evolve more rapidly than nuclear genes. Therefore, DNA sequences from the mitochondrial genome could potentially provide a greater number of polymorphisms to aid in species identification. However, the diversity in size, gene content, and gene arrangement of mitochondrial genomes makes the design of universal primers for ascomycete genomic analysis difficult. The overarching aim of this study was to identify species-specific markers to allow for the resolution of sibling species in *Ceratocystis*. Using sequence data that we have recently produced by sequencing the complete *Ceratocystis fimbriata* genome and a lower coverage data set of DNA sequence for *C. albifundus*, the mitochondrial genomes for both species were assembled using CLC Bio Genomics Workbench software. Putative gene orders for both *C. fimbriata* and *C. albifundus* mitochondrial genomes were established. The gene order for these *Ceratocystis* species was similar to that previously observed in the *Neurospora crassa* mitochondrial genome. A total of 14 open reading frames were used to identify polymorphic regions. These included the genes for nitrogen dehydrogenase subunits 2, 3 and 1; Cytochrome Oxidase B, as well as the adenosine triphosphatase transporter system. The newly identified polymorphic regions have provided the foundation to develop tools resolve sibling species boundaries in *Ceratocystis*.

Of bats and accents: gene flow and the evolution of local acoustic signatures in bats

L.J. Odendaal*, D.S. Jacobs & J.M. Bishop

Department of Zoology, University of Cape Town, Private Bag X3, Rondebosch 7701, South Africa

*Corresponding author: lizelle.odendaal@uct.ac.za

Geographic variation in animal signals that function in communication or resource use may be of considerable importance in the evolution of population divergence. Divergence can be the result of selection for specific traits in particular environments or come about through neutral genetic drift. In this study we investigate the role of intra-specific gene flow in shaping acoustic variation in echolocation calls among populations of the Cape horseshoe bat *Rhinolophus capensis* (Rhinolophidae). Bats use echolocation, a biological acoustic imaging system, for orientation, prey detection and communication; variation in the long constant frequency calls of horseshoe bats is the result of both genetic and cultural (mother to offspring transmission) factors, and thereby provides an ideal system to tease apart the influences of genetic drift and selection on population divergence. The Cape horseshoe bat is endemic to the coastal regions of the Cape Floristic Region of South Africa and previous research suggests that differences in peak frequency amongst populations may represent the evolution of local acoustic signatures or accents. These acoustic signatures appear uncoupled from the typical predictors of variation in echolocation calls and may have originated via random founder events, enhanced by a) drift and/or b) local selection. Using mitochondrial control region sequences we investigate a role for drift by quantifying matrilineal population structure and levels of gene flow across the species range. Initial results from seven populations across South Africa suggest a role for isolation by distance, together with repeated dispersals to the east and west from the south coast, in shaping both echolocation variation and population structure. We discuss these results in light of recent findings on the 'hearing gene' *Prestin* in bats, a potential candidate for testing the role of selection in population divergence.

New distribution records of Ophiocomid brittle stars (Echinodermata: Ophiuroidea: Ophiocomidae) from KwaZulu-Natal, South Africa

J.M. Olbers¹*, Y. Samyn² & C.L. Griffiths³

1 Ezemvelo KZN Wildlife, Private Bag X3, Congella, Durban 4013, South Africa

2 Belgian Focal Point to the Global Taxonomy Initiative, Royal Belgian Institute of Natural Sciences, Belgium

3 Department of Zoology, University of Cape Town, PO Box X3, Rondebosch 7701, South Africa

* Corresponding author: olbersj@kznwildlife.com

The last major review of the echinoderms of the region, published in 1976, reported 115 species of brittle star (Echinodermata: Ophiuroidea) from southern Africa. By 2010, a total of 152 species have been recorded from South Africa (including the Prince Edward Islands), as a result of 37 new distribution records. Collections between 1999 and 2009 contributed to the majority of these new distribution records, which is a clear indication that the South African coast still remains poorly explored for this group. Data records in the Iziko South African Museum have also proven to be valuable source of new records. The Ophiocomid brittle stars are known to be associated with coral reefs in subtropical and tropical areas. Until now, the number of *Ophiocoma* species recorded in South Africa was four, but as a result of recent collections, this number has increased to eight. The four species previously reported from South Africa are *O. erinaceus* Müller & Troschel, 1842; *O. pica* Müller & Troschel, 1842; *O. scolopendrina* Lamarck, 1816; and *O. valenciae* Müller & Troschel, 1842. The four additional *Ophiocoma* species newly reported are *O. pusilla* Brock, 1888; *O. brevipes* Peters, 1851; *O. dentata* Müller & Troschel, 1842; and *O. doederleini* de Loriol, 1899. The general taxonomic features and global distribution of the genus *Ophiocoma* are discussed, together with the taxonomy, geographic distribution and ecology of the eight species listed above. A brief overview of the biogeography of the *Ophiocoma* species of KZN will also be provided.

A greater Maputaland-Pondoland-Albany region of vertebrate endemism

*S.J. Perera**, D. Ratnayake-Perera & Ş. Procheş

School of Environmental Sciences, University of KwaZulu-Natal, Westville Campus, Private Bag X 54001, Durban 4000, South Africa

*Corresponding author: sandun.perera@gmail.com

The Maputaland-Pondoland-Albany (MPA) biodiversity hotspot was primarily recognised based on its high plant endemism. Here we present a first ever biogeographical study of the entire endemic vertebrate fauna of south-east Africa in an exercise that (a) refines the delimitation of the MPA, (b) illustrates within-hotspot areas of endemism and (c) defines non-overlapping biogeographical units. The study reviews the distribution patterns of 496 vertebrate taxa endemic to south-east Africa, listing 62 vertebrates endemic and 60 near-endemic to the MPA hotspot. Twenty-three Endemic Vertebrate Distributions (EVDs) are recognised, among which the Eastern Escarpment, Kwazulu-Natal, Drakensberg, and Maputaland distributions are the most common. The geographical patterns illustrated by EVDs suggest an expansion of the hotspot to incorporate sections of the Great Escarpment from the Amatola-Sneeuberg Mountains through the Drakensberg to the Soutpansberg. This redefinition gives rise to a Greater Maputaland-Pondoland-Albany (GMPA) region including 137% more endemics with only about 70% surface area added to the MPA hotspot. The GMPA has a more natural boundary in terms of EVDs and vegetation units and we argue that previous studies on plant endemism support it too. The study also highlights 14 areas of endemism (13 within the GMPA), potentially important to conservation planning within the region. Besides conservation, the accurate delimitation of this hotspot would benefit theoretical biogeography and in this context we use EVDs to delimit zoogeographical units for south-east Africa.

The prickly problem of *Berkheya* Ehrh. (Asteraceae)

N. Phaliso^{1,*}, N.P. Barker¹, R.J. McKenzie¹ & P.-O. Karis²

¹Department of Botany, Rhodes University, Grahamstown 6140, South Africa

²Department of Botany, Stockholm University, SE-106 91, Stockholm, Sweden

*Corresponding author: fikzo_p@yahoo.com

Berkheya Ehrh. is a genus of daisies in the tribe Arctotideae, subtribe Gorteriinae. With over 80 species, most of which occur in southern Africa, this genus has centres of diversity associated with the montane regions of South Africa, including the Drakensberg Alpine Centre and Mpumalanga escarpment regions. Previous molecular and morphological studies indicate that *Berkheya* is paraphyletic. We present preliminary phylogenies based on nrDNA (ITS; Internal Transcribed Spacer) as well as some cpDNA (psbA-trn-H) data. These phylogenies are used to assess generic limits and to investigate the biogeographic patterns and life history traits of *Berkheya* and its allies. The nrDNA phylogeny shows six well supported clades of *Berkheya*, the first two of which are summer rainfall region clades. Clades 3 to 6 are all winter rainfall clades. *Cullumia*, *Cuspidia* and *Didelta* are embedded within *Berkheya*, confirming its paraphyly. Preliminary molecular dating shows that the divergence of *Berkheya* clades occurred at the Miocene-Pliocene boundary.

A densely sampled ITS phylogeny of the Cape flagship genus *Erica* L. reveals numerous shifts in floral macro-morphology

M. D. Pirie^{1,*}, E.G.H. Oliver² & D.U. Bellstedt¹

¹Department of Biochemistry, Stellenbosch University, Stellenbosch, South Africa

²Department of Botany and Zoology, Stellenbosch University, Stellenbosch, South Africa

*Corresponding author: mpirie@sun.ac.za

Erica L. is the largest of the ‘Cape’ clades which together comprise around half of the disproportionately high species richness of the Cape Floristic Region (CFR) of South Africa. Around 840 species of *Erica* are currently recognised, 658 of which are found in the CFR, the rest distributed across the rest of southern Africa, the highlands of tropical Africa and Madagascar, and Europe. *Erica* is taxonomically well documented, but very little is known about species-level relationships. We present the first densely sampled phylogenetic analysis of *Erica*, using nuclear ribosomal DNA sequences (internal transcribed spacers; ITS) of c. 45% of the species from across the full geographic range of the genus, both *Calluna* and *Daboecia* (Ericaceae; monotypic genera and putative sister groups of *Erica*), and further Ericoideae outgroups. Our results show both morphological and geographic coherence of some clades, but numerous shifts in floral macro-morphology as represented by variation in individual morphological characters and pollination syndromes. European Ericaceae is a paraphyletic grade subtending a monophyletic African/Malagasy *Erica*. Further clades are identified that will serve as an effective guide for further targeted sampling from multiple linkage groups.

River drainage basins channel genetic diversity in the Albany Subtropical Thicket: a comparative phylogeographic study of three plant species

A.J. Potts^{1,*}, T.A. Hedderson¹, R.M. Cowling² & J.H.J. Vlok³

¹ Department of Botany, University of Cape Town, University Private Bag, Rondebosch 7700, South Africa

² Department of Botany, Nelson Mandela Metropolitan University, P.O. Box 77000, Port Elizabeth 6031, South Africa

³ P.O. Box 1512, Oudsthoorn 6620, South Africa

*Corresponding author: potts.a@gmail.com

We test two hypotheses regarding the evolutionary history of the Albany Subtropical Thicket (AST). First, the lowland drainage basins have been identified as unique phytosociological entities of AST. This has been used as the basis for large-scale conservation planning. We utilise comparative phylogeography of three plant species under a multi-locus approach to test whether the patterns of genetic diversity correspond to drainage basins. Second, the distribution of the AST is thought to have been greatly reduced during glacial periods. We utilise two approaches to test this: (1) climate envelope modelling to project the present envelopes of our target species onto global climate models of the Last Glacial Maximum, and (2) we estimate the timing of lineage divergence to determine if lineages diversified before or after the onset of glacial cycles. Our results show that (1) drainage basins are unique evolutionary units of genetic diversity with watersheds as the most likely barriers to gene flow, (2) that AST species experienced a dramatic reduction in range during the LGM, and (3) that lineages diversified after the onset of glacial-interglacial cycles. Glacial periods most likely strengthened the effect of watershed barriers to gene flow, thus acting in synergy to isolate populations within drainage basins.

Who are you? A DNA-based approach to linking the life-cycle stages of Afrotropical Megaloptera

B.W. Price^{1,2,*}, F.C. de Moor^{1,2} & M.H. Villet¹

¹ Department of Zoology and Entomology, Rhodes University, Grahamstown, South Africa

² Department of Freshwater Invertebrates, Albany Museum, Grahamstown, South Africa

* Corresponding author: ben.wills.price@gmail.com

The insect order Megaloptera is especially interesting for its species' long life cycles with a very brief vagile phase, which affects rates of phylogenesis. Comprising the families Corydalidae and Sialidae, it is regarded as one of the most archaic orders of the Holometabola. Both families occur in the Afrotropical Region, four species in Madagascar and seven in South Africa. Megalopteran larvae generally inhabit fast-flowing mountain streams, where they may live for up to five years before pupating on the riverbank. Very few of the slow-flying adults are present in collections because they are only active for brief periods in summer, yet all of the species are described from adult specimens only, resulting in a general lack of knowledge on the group. Previous studies have offered limited insight into the larval morphology of the group and the larvae of only two species are properly defined. Molecular (DNA) data can help to resolve these taxonomic and morphological problems and provide a rapid method to link life stages in organisms which show radical metamorphosis. DNA data, comprising both mitochondrial (COI) and nuclear (28S rRNA) genes, were used to assess phylogenetic diversity within the South African Megaloptera. Samples of adults of all recognised species were sequenced, covering their known geographic range. Larvae from representative localities were then sequenced and the corresponding data used to identify their species. In addition, the degree of divergence between some specimens within recognised species indicated cryptic diversity that was then investigated using morphological data. By uncovering the larval form of each species, a larger suite of morphological characters became available for phylogenetic analysis, and an interactive online key was created to facilitate the identification of both adult and larval specimens. This study has shed light on the diversification of this ancient relict fauna in Africa.

From tree to tree: comparative phylogeography of two forest-dwelling cicada (Hemiptera: Cicadidae) lineages in South Africa

B.W. Price^{1,*}, M.H. Villet¹ & N.P. Barker²

¹ Department of Zoology and Entomology, Rhodes University, Grahamstown 6140, South Africa

² Department of Botany, Rhodes University, Grahamstown 6140, South Africa

*Corresponding author: ben.wills.price@gmail.com

Forests are the smallest, yet second most botanically rich of South Africa's nine biomes. Besides their small area and highly fragmented distribution, forests face many threats including overutilisation, encroachment by alien vegetation, increased fire regimes, and competition with agriculture and silviculture. Thus the forest biome is of high priority for conservation, and understanding the dynamics of forest-associated lineages is crucial in this regard. The population structure of two phylogenetically independent lineages of forest-inhabiting cicadas (the *Platypleura chalybaea* group and *Pycna semiclara*) were examined using mtDNA (COI & COII genes) sequence data. The data was analysed using Likelihood, Parsimony and Bayesian Inference techniques and AMOVA and IBD statistics. Likelihood ratio analyses show that botanically-defined forest types do not correlate with population substructure of these two cicada lineages. In addition the two forest-associated lineages show different patterns of genetic structure in relation to historical forest fragmentation, most likely as a result of a combination of the different ages and dispersal histories of each lineage. However, within each lineage it is clear that within-species diversification is primarily restricted to the Pleistocene, where glaciation cycles have probably repeatedly fragmented the cicada populations. The different phylogeographical pattern observed in two seemingly similar lineages cautions against the extrapolation of data from a single organism to identify population genetic boundaries applicable to a wider range of organisms and suggests that further comparative work is needed to gain a better understanding of the histories of biomes in southern Africa.

The phylogenetic relationships and evolutionary history of the Dirini (Nymphalidae: Satyrinae), a tribe of butterflies endemic to southern Africa

B.W. Price¹, M.H. Villet^{1,*}, S.M. Walton¹ & N.P. Barker²

¹ Department of Zoology and Entomology, Rhodes University, Grahamstown 6140, South Africa

² Department of Botany, Rhodes University, Grahamstown 6140, South Africa

* Corresponding author: M.Villet@ru.ac.za

The first empirically-supported phylogenetic hypothesis of relationships for the southern African endemic butterfly tribe Dirini is presented. Data derived from the morphology and ecology of the adults and immature stages (33 characters), and portions of the mitochondrial gene COI and the nuclear genes EF1- α and wingless (totalling 1734 base pairs) were used to infer the relationships of the in-group genera. An expanded molecular data set, including four genera from the Nymphalini and Satyrini to root the tree, and three genera from the Melanitini to test the monophyly of the tribe, was analysed using Parsimony and Bayesian methods. Estimates of divergence times were calculated using two fossil calibrations under a relaxed molecular clock model. The monophyly of the tribe and of each in-group genus were strongly supported. Key findings are the sister-taxon relationship of *Aeropetes* and *Tarsocera*, the apparent simultaneous or nearly simultaneous radiation of four lineages, the polyphyly of the species within *Torynesis*, and the apparent trans-Atlantic dispersal of the ancestors of *Manataria* about 40 Mya. Estimates of divergence times indicate that the tribe has undergone two major radiations since its origin: the first when they left forest habitats in the mid-late Oligocene, shortly after the radiation of the grasses (Poaceae), and the second in the early-middle Pliocene, coinciding with the aridification of southern Africa and the spread of conditions that favoured C₄ grasses over the C₃ grasses that dirine larvae prefer to eat. The high species diversity within the tribe appears to be partly a taxonomic artefact that may have resulted from the misinterpretation of climate-related phenotypic variation within extant species.

Publication:

Ben W. Price, Martin H. Villet, Shaun M. Walton and Nigel P. Barker (in press) Using molecules and morphology to infer the phylogenetic relationships and evolutionary history of the Dirini (Nymphalidae: Satyrinae), a tribe of butterflies endemic to Southern Africa. *Systematic Entomology*.

(Poster 11) Cryptic variation in an ecological indicator organism: detection of independent lineages in *Baetis harrisoni* (Ephemeroptera: Baetidae) in southern Africa

B.W. Price^{1,2,*}, L.L. Pereira da Conceicao¹, H.M. Barber-James^{1,2}, N.P. Barker³, F. de Moor^{1,2} & M.H. Villet¹

¹

Department of Zoology and Entomology, Rhodes University, Grahamstown 6140, South Africa

²

Department of Freshwater Invertebrates, Albany Museum, Grahamstown 6140, South Africa

³

Department of Botany, Rhodes University, Grahamstown 6140, South Africa

* Corresponding author: ben.wills.price@gmail.com

We present a molecular study of the genetic variation within the mayfly *Baetis harrisoni*, a species regarded as significant in biological monitoring, and which shows signs of comprising cryptic species. Populations from a total of 18 rivers in South Africa and another two rivers from Zambia and Malawi were sampled. Four gene regions were examined (mtDNA: COI & 16S; nDNA: EF-1 α & PEPCK). Gene tree (Bayesian and Parsimony) approaches to phylogeny reconstruction resulted in the recognition of three well supported major lineages. Analysis of the isolation by distance (IBD) between samples as a whole showed a small but significant effect of IBD ($R^2 = 0.084$; $p = 0.001$). Within each individual clade, the contribution of IBD was minimal, suggesting high levels of gene flow. Topologies from the EF-1 α gene were significantly incongruent with both the mitochondrial (COI and 16S) and nuclear (PEPCK) topologies, most likely as a result of incomplete lineage sorting of this gene. The three lineages of *B. harrisoni* found within southern Africa correspond to environmental variation marked by pH-related differences, with two lineages comprising samples from streams that flow over and through acidic Table Mountain Sandstone while the third clade comprised samples from streams of alkaline pH, found within eastern South Africa. The results of this study suggest that *B. harrisoni* as it is currently recognised is not a single species with a wide pH tolerance, but in fact comprises up to three species, each with a limited pH tolerance. The taxonomy and subsequent water quality and biomonitoring sliding score allocated to the *B. harrisoni* species group is thus in need of review.

Plant endemism in the greater Maputaland-Pondoland-Albany Region: ancient lineages, radiations and trait distributions

S. Ramdhani^{1,*}, S. Procheş¹, N. Mahadeo¹ & R.M. Cowling²

¹School of Environmental Sciences, University of KwaZulu Natal Westville, Private Bag X54001, Durban 4000, South Africa

²Department of Botany, Nelson Mandela Metropolitan University, P.O. Box 77000, Port Elizabeth 6031, South Africa

*Corresponding author: syd_za@yahoo.com

The Maputaland-Pondoland-Albany (MPA) Region is one of the three biodiversity hotspots in South Africa, and was primarily identified as such based on its high levels of plant endemism. The region has received substantial collecting and floristic attention. However, the factors that underpin plant diversity patterns in the region are little understood and poorly explored. The concept of a greater MPA was advocated for vertebrates as an extended region cutting across several biomes and vegetation units. The present study is a preliminary exercise applying this concept to plants. It focuses on endemic and near-endemic ancient lineages, radiations, and trait distributions, in an attempt to understand factors responsible for the endemism, diversity and complexity of the greater MPA. We plotted the distribution of selected ancient lineages to determine possible areas of palaeo-endemism. Selected lineages that have undergone radiations (old or recent) centred here were identified and mapped in a search for leads as to what may have driven plant diversification in the region. Lastly, we examined traits in selected endemic lineages to determine how these traits varied across the distribution range of the lineage, and possible factors responsible for this variation. The preliminary results show that patterns are complex, possibly because of the great spatial extent and heterogeneity of the MPA region. Our studies are ongoing, and we discuss several avenues of research needed to better understand the MPA hotspot.

Morphological evidence of hybridisation between *L. capensis* and *L. umbratus* (Cyprinidae)

M. Ramoeljane^{1,2,*}, E. Swartz¹ & O. Weyl¹

¹South African Institute for Aquatic Biodiversity, Grahamstown 6140, South Africa

²Department of Ichthyology and Fisheries Science, Rhodes University, Grahamstown 6140, South Africa

* Corresponding author: m.ramoeljane@saiab.ac.za

Labeo capensis and *L. umbratus* are large cyprinids that are thought to be sister species with several morphological characters that overlap between them. They are thought to hybridise in Hardap and Darlington dams. Previous studies suggested that hybrids could not be identified based on morphology alone. The aim of this study was to assess which characters could be used to reliably identify *L. capensis* and *L. umbratus* and to reassess whether morphology is useful for identifying hybrids. A total of 275 specimens of *L. umbratus* (N = 115) and *L. capensis* (N = 60) from suspected pure populations were analysed to assess differentiation between the two species. Individuals from suspected hybrid populations (N = 100) were then compared to these to assess whether hybrids could be identified. The two species could be differentiated using four morphometric (dorsal fin base, inter-orbital, width head length and eye to operculum distance) and four meristic (scale counts along the lateral line, between the lateral line and origin of the dorsal fin, between the lateral line and origin of the pelvic fin, and around the caudal peduncle) characters. There was differentiation within *L. umbratus*, especially between the southern flowing rivers populations, but this did not affect species determination. In most cases, hybridisation detected with morphology was confirmed by nuclear and mitochondrial DNA analysis. In some cases, however, genetics suggested that individuals were pure, whilst morphology suggested that hybridisation occurred. These could be due to backcrossing or undetected natural variation in the pure species.

Ecotype formation - a stepping stone towards endemism

R A. Reddy¹; T. McLellan² & K. Balkwill¹

¹ C.E. Moss Herbarium, School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, Private Bag 3, Wits 2050, South Africa

² School of Molecular and Cell Biology, University of the Witwatersrand, Private Bag 3, Wits 2050, South Africa

Serpentine soils have high concentrations of heavy metals, especially nickel and often chrome, low concentrations of essential minerals and high magnesium to calcium ratio. These factors make serpentine soils unfavourable and potentially toxic to plants. As a result the vegetation in these areas is often sparse and stunted. A number of plant species are unique (endemic) to serpentine soils and many others are excluded. Some plants, however, appear to be indifferent (*bodenvag*) to these soil conditions, but are they really indifferent, or are they actually genetically different ecotypes? *Indigofera dregeana*, a dwarf shrub in the pea family appeared to be equally common on and off the serpentine soils at the Songimvelo Game Reserve in the Barberton Greenstone Belt area. Leaf samples were collected in silica gel from plants growing on and off serpentine soils. The Amplified Fragment Length Polymorphism (AFLP) technique was used to determine whether the sub-populations on and off serpentine soils were genetically different from each other. It was found that while plants of the sub-populations on and off serpentine soils appeared to be morphologically similar, they were genetically diverse. It is concluded that *I. dregeana* is in the process of differentiating into serpentine tolerant and intolerant ecotypes.

Pleistocene climatic changes and ocean currents influence the phylogeography of the South African barnacle, *Tetraclita serrata* (Thoracica; Cirripedia)

T.V. Reynolds*, S. von der Heyden & C.A. Matthee

Department of Botany and Zoology, Stellenbosch University, Stellenbosch, South Africa

*Corresponding author: 14347210@sun.ac.za

To investigate the phylogeographic pattern in the volcano barnacle, *Tetraclita serrata*, along the South African coastline, 410 individuals from 20 sampling localities were analysed. Restricted gene flow in some geographical areas was hypothesised for this species based on oceanic circulation patterns, known biogeographic regions, and features such as the Agulhas Bank, which has shaped the population genetic structure of several other South African marine organisms. The population genetic structure was investigated using the mitochondrial Cytochrome Oxidase subunit 1 (COI) and nuclear Internal Transcribed Spacer 1 (ITS1) genes. No clear phylogeographic structure was found and the direction of gene flow of *T. serrata* individuals can be linked to the oceanographic features found along the South African coast. Phylogenetic and population genetic analyses of the COI gene revealed two distinct clades but with overlapping distributions and ITS1 data analysis performed on a subset of individuals revealed a single lineage. The pattern observed reflects a significant historical differentiation of the two clades. A historical event may have been responsible for the formation of allopatric lineages that have since come into secondary contact. The haplotype network, mismatch distributions and time since expansion indicate that *T. serrata* survived the Last Glacial Maximum. To date, no South African marine species has revealed such a pattern. Thus, further investigations into the phylogeography of coastal marine species, particularly obligately sessile species such as barnacles, are required to determine whether the pattern observed in *T. serrata* is a rare history or not.

A molecular phylogeny and DNA barcoding of African endemic cycads: preliminary findings

*P. Rousseau*¹, *P. Vorster*² & *M. van der Bank*¹

¹African Centre for DNA Barcoding, University of Johannesburg, APK Campus, PO Box 524, Johannesburg 2006, South Africa

²Department of Botany and Zoology, University of Stellenbosch, Private Bag X1, Matieland 7602, South Africa

Cycads are an ancient grouping of gymnosperms of great significance to all botanical disciplines. They are living fossils providing unprecedented access to higher plant evolution. They are however also highly endangered with over 50% IUCN red listed. Africa, and specifically southern Africa, is a cycad diversity hotspot with ~66 species in two endemic genera, namely *Encephalartos* Lehm. and *Stangeria* T.Moore. To date infrageneric relations are poorly understood, no complete molecular phylogeny has been produced and species concepts are unclear. The genus *Encephalartos* is also in dire need of revision. These preliminary results form part of a project aiming to both DNA barcode and produce a completely resolved molecular phylogeny of all endemic species, possibly serving as the first step to a revision. Specific results include the application of DNA barcoding to African cycads, the viability of the proposed DNA barcoding regions and a preliminary phylogenetic tree of *Encephalartos* compared to current views on relationships based on morpho-geographic data.

Towards DNA barcoding scale insects of economic importance in South Africa

*M.T. Sethusa*¹, I.M. Millar¹ & M. van der Bank²

¹Biosystematics Division, ARC-Plant Protection Research Institute, P/BAG X134, Queenswood, Pretoria, 0121 South Africa

²African Centre for DNA Barcoding, University of Johannesburg, APK Campus, PO Box 524, Johannesburg 2006, South Africa

Scale insects (Hemiptera: Sternorrhyncha: Coccoidea) are a group of sap-sucking plant parasites that are morphologically specialised, with relationships between families and higher classification unresolved. They are small and cryptic in habit and often resemble parts of their host plants. Most of the life stages are sessile and feed on the twigs, leaves and fruit of their host plants; this makes them a major quarantine risk, and one of the most invasive groups of animals. Traditionally, scale insects have been identified and classified into genera and higher taxa on the basis of the morphology of adult females. However, identifying scale insects is notoriously difficult and time consuming, and requires a high level of taxonomic expertise. Immature and damaged specimens intercepted by quarantine agencies are usually impossible to identify. Despite these challenges, accurate and timely identification is critical for pest management and import/export of fresh produce. Recently the use of a standardised short DNA sequence, the DNA barcode, for species identification is the route of choice. In animals, the mitochondrial Cytochrome Oxidase subunit 1 (CO1) is the DNA barcode of choice, however, there often are difficulties using this gene region for scale insects. In this study, we investigated the viability of the nuclear large subunit D2D3 28s gene as an alternative barcode. Our results show that sequences generated group into the correct families and also cluster according to species. We conclude that the D2D3 28s gene may be used as an alternative and/or additional barcode for identification of scale insects.

Solving the Mantispidae puzzle: generating a key to the genera of South Africa

L.P. Snyman*, M.W. Mansell & C.H. Scholtz

University of Pretoria, Pretoria 0002, South Africa

*Corresponding author: lsnyman@zoology.up.ac.za

Mantispidae (Insecta: Neuroptera) are lacewings with a worldwide distribution. They can be recognised by an elongated prothorax, triangular head as well as raptorial forelegs. These morphological traits manifest convergent evolution with Mantodea (praying mantids). Mantispidae are however holometabolous insects with hyaline wings held in a roof-like manner over the abdomen whereas the hemimetabolous praying mantids have tegmina. Mantispidae larvae undergo hypermetamorphic ontogeny and parasitise spider egg-sacs. The Afrotropical Mantispidae have never been fully revised and are in dire need of revision. Five genera comprising 35 species are currently regarded as valid in South Africa. The family is morphologically complex because of intraspecific variation and interspecific similarities of genera and species characters. Furthermore, the large number of synonyms adds to the taxonomic complexity of the family. The descriptions were often published in Latin, German and French and were usually described by entomologists lacking sufficient experience in Neuroptera taxonomy. This resulted in vague descriptions that cannot be correlated with specimens or to valid species. Access to Mantispidae must consequently be provided by generating a morphological key to facilitate future research in genetic, biodiversity and ecological fields. Four genera, *Perlamantispa*, *Mantispa*, *Necyla* and *Pseudoclimaciella* are now recognised as valid genera occurring in the region. *Cercomantispa* is identified as a synonym of *Necyla*. All four valid genera of the region are described and the first morphological key to these genera has been prepared.

Cytogenetic and phylogenetic studies in the genus *Lachenalia*

P. Spies^{1,*}, R. Kleynhans^{1,2} & J.J. Spies¹

¹ Department of Genetics (64), University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa

² Agricultural Research Council (ARC), Roodeplaat Vegetable and Ornamental Plant Institute (VOPI), Private Bag X293, Pretoria 0001, South Africa

*Corresponding author e-mail: spiesp@ufs.ac.za

The genus *Lachenalia* (family Asparagaceae) is endemic to southern Africa and is a horticultural diverse genus, with a widespread distribution range and many species featuring in the red data list of southern Africa. The extensive morphological variation within some species complicates species delimitation and has led to taxonomic confusion.

Chromosome numbers of 89 species have been recorded in literature, with $2n = 10$ to 56 and $n = 5$ to 28. B-chromosomes have been described in some species. Basic chromosome numbers include $x = 5, 6, 7, 8, 9$, (probably 10), 11, (probably 12), 13 and (probably 15). Polyploidy was reported in 19 taxa (23%), and is most common in the $x = 7$ group.

Haplotype and molecular systematic studies of the *trnL-F* chloroplast region were compared with other studies (*ITS* sequencing, molecular cytogenetics, morphology and breeding trials). All these studies indicate that species with the same basic chromosome number are closely related. The one deviation is that it appears as if there are two separate groups in the $x = 7$ group. This is supported by molecular and breeding studies, where the best results are generally obtained from crosses within a group or by closely related groups. This comparative study reveals how different studies obtain similar results and how these results can be used in a practical way by plant breeders.

A molecular genetic approach to consider regional connectivity and differentiation of three goatfishes (*Parupeneus spp.*) in the Western Indian Ocean

N. Springbok^{1,2,*}, M. Mwale², G. Gouws² & O. Gon²

¹ Department of Zoology, University of Fort Hare, Alice, South Africa

² South African Institute for Aquatic Biodiversity, Grahamstown 6140, South Africa

*Corresponding author: n.springbok@saiab.ac.za

Goatfishes inhabit inshore reef and coral areas and are commercially important throughout their areas of distribution in the Western Indian Ocean (WIO). However, the biogeography of these species has not been explored. A phylogenetic approach using molecular markers can provide an understanding of the origins of regional fauna and relationships among biogeographic regions. It may be predicted that species differ in genetic structure or show different patterns in response to their life history strategies or physical factors of the environment. This study will assess the genetic diversity, connectivity, patterns of differentiation and origins of the three goatfish species of the genus *Parupeneus* (*P. barberinus*, *P. macronemus* and *P. rubescens*) in the WIO. Analysed samples were collected from east and southern African continental coastlines, island regions and the Mascarene plateau and around Madagascar. Mitochondrial DNA (NADH Dehydrogenase Subunit 2, Cytochrome *b* and 16S ribosomal RNA) and nuclear DNA (ribosomal protein S7 gene) markers were amplified. Diversity and variance measures of sequences within species among regions will be analysed to see if species differ between localities. In addition, phylogenetic analyses using Parsimony, Bayesian Inference and Maximum Likelihood will be performed to determine relationships. This study should provide clarity on the connectivity, origins and the processes that have influenced the distribution of the selected goatfishes in the WIO.

Phylogeny of the family Trogidae (Coleoptera: Scarabaeoidea)

W.P. Strümpher^{1,2,*}, D. Downie¹, C.L. Sole² & C.H. Scholtz²

¹

Department of Zoology and Entomology, Rhodes University, Grahamstown 6140, South Africa

²

Scarab Research Group, Department of Zoology and Entomology, University of Pretoria, Pretoria 0002, South Africa

*Corresponding author: wstrumpher@zoology.up.ac.za

Trogidae constitute a unique family within the Scarabaeoidea being the only keratinophagous (keratin digesting) beetles in the superfamily. The adults and larvae of all known species are associated with animal remains where they may be found feeding on various sources of keratinous matter. The monophyletic status of Trogidae is well-defined and is considered as one of the most primitive families within the Scarabaeoidea. The family comprises three genera, *Trox* Fabricius, 1775; *Omorgus* Erichson, 1847; and *Polynoncus* Burmeister, 1876. The well defined genus *Polynoncus* is endemic to South America. The genus *Omorgus* has a wide distribution throughout the arid regions of the southern continents, being absent from the Palaearctic region, while the genus *Trox* is found in all the major biomes of the Holarctic as well as the tropical and semi-tropical regions of Africa. The only attempt at resolving the phylogenetic relationships within the Trogidae was based on shared derived morphological characters and current distribution patterns. The current hypothesis for the evolution of trogids proposes that this ancient family evolved in central Pangaea, prior to the breakup of the supercontinent that formed Laurasia and Gondwana and that the ancestral *Omorgus* and *Polynoncus* lineages radiated on the Gondwana continents. Furthermore, a Laurasian origin is proposed for the *Trox*-lineage, with one sub-lineage radiating into the Holarctic and another derived lineage spreading into Africa. Here we present the first comprehensive molecular phylogeny of the family Trogidae based on four gene regions: CO1, 16S, 18S and 28S domain 2. Bayesian analysis resolved four well supported lineages *Polynoncus*, *Omorgus*, Holarctic *Trox* (*Trox* s.str.) and African *Trox* (*Phoberus*). The results strongly support the monophyly of the African *Trox* lineage, and that the promotion of *Phoberus* to full generic status may be justified.

(Poster 12) Towards the phylogeny of *Boerhavia* L. and *Commicarpus* Standl. in southern Africa

M. Struwig^{1,*}, N.A. Douglas², S.J. Siebert¹ & A. Jordaan³

¹ A.P. Goossens Herbarium, School of Environmental Sciences and Development, North-West University, Potchefstroom, South Africa

² Department of Plant Biology, North Carolina State University, Raleigh, United States of America

³ School of Environmental Sciences and Development, North-West University, Potchefstroom, South Africa

*Corresponding author: madeleen.struwig@nwu.ac.za

Within the Caryophyllales, the Nyctaginaceae is a family of trees, shrubs and herbs classified into 30 genera and 400 species. The first phylogenetic analysis of the Nyctaginaceae was done in 2000 on three genera (*i.e. Ascleisanthos*, *Selinocarpus* and *Mirabilis*), but limited sampling and poor backbone resolution hindered meaningful results. This was followed in 2007 by a broad analysis of nearly all the currently accepted genera and the results suggested that the then tribal classification was incongruent with the evolutionary relationships among the genera as demonstrated by molecular evidence, leading to a revised tribal classification published in 2010.

In southern Africa, 5 genera and 20 species of the Nyctaginaceae (*i.e. Boerhavia*, *Commicarpus*, *Mirabilis*, *Phaeoptilum* and *Pisonia*) occur, of which *Boerhavia* and *Commicarpus* is the most species rich; totaling sixteen species, with six species endemic to the region. The phylogenetic relationship amongst southern African *Boerhavia* and *Commicarpus* species has not previously been studied. Since the family's phylogeny is currently receiving attention worldwide, this proposed study to fill the gap in southern Africa is therefore relevant. Chloroplast and mitochondrial genes will be used to analyse the phylogenetic relationship within these two genera and the resulting cladogram will be translated into a classification for the southern African *Boerhavia* and *Commicarpus* species.

How does African *Galaxias* diversity compare with global patterns?

E. Swartz^{1,*} & R. McDowall²

¹ South African Institute for Aquatic Biodiversity, Grahamstown 6140, South Africa

² National Institute of Water and Atmospheric Research, Christchurch, New Zealand

* Corresponding author: e.swartz@sajab.ac.za

Until recently, Africa was a “backwater” of Galaxiidae diversity with only one recognised species. There has been recognition, however, that *Galaxias zebratus* represents a species complex. This has been confirmed by ad hoc genetic studies, but how many species are we dealing with and what does it mean for fish diversity and conservation studies in the Cape Floristic Region? Recent morphological, genetic and ecological investigations are revealing more than 10 distinct species with different life histories. Some of these species even occur in sympatry. Many of them will be classified in highly threatened IUCN categories, which raises the question whether we have already lost some species. These studies are also putting the Cape Floristic Region “on the map” of Galaxiidae diversity per area, possibly equalling the diversity found in New Zealand (thought to have the highest species diversity per area in the world). It unfortunately also puts South Africa on the map as a potential global hotspot for threatened *Galaxias* species, due to the invasion of alien fishes and habitat destruction. In a region of Africa known for its poor fish species diversity, this new knowledge has dramatic implications for how we view the biogeography of the Cape Floristic Region.

Beetle relicts of the Western Cape: evaluating species delineation within *Colophon* (Coleoptera: Scarabaeoidea: Lucanidae)

A.K. Switala*, C.H. Scholtz & C.L. Sole

Department Zoology and Entomology, University of Pretoria, Pretoria 0002, South Africa

*Corresponding author: akswitala@zoology.up.ac.za

The Cape high-mountain stag beetle genus *Colophon* Gray is endemic to South Africa and classified in the family Lucanidae. All 17 flightless species are geographically isolated to high altitudes in the Western Cape mountains and show a strict association with the fynbos biome. Even though very little is known about their biology and behaviour the genus was given a CITES III listing. Studies based on COI data identified a species complex between the sympatric *Colophon haughtoni* and *C. kawaii*. It was also noted that *C. cameroni* is morphologically similar to *C. kawaii*. The aim of this study is to re-evaluate the species delineation of *C. haughtoni*, *C. kawaii* and *C. cameroni* by analysing three gene regions COI, ITS2 and *wingless*. Additional landmark-based geometric morphometric analyses are also included to analyse their morphology.

Cryptic species of horseshoe bats in the *Rhinolophus hildebrandtii* complex: a taxonomic jigsaw puzzle

P.J. Taylor^{1,6,*}, S. Stoffberg², A. Monadjem³, M.C. Schoeman⁴ & F.P.D. Cotterill⁵

¹ Durban Natural Science Museum, P. O Box 4085, Durban 4000, South Africa

² Evolutionary Genomics Group, Department of Botany and Zoology, University of Stellenbosch, Private Bag X1, Matieland, South Africa

³ All Out Africa Research Unit, Department of Biological Sciences, University of Swaziland, Private Bag 4, Kwaluseni, Swaziland

⁴ School of Biological and Conservation Sciences, University of KwaZulu-Natal, Durban 4000, South Africa

⁵ Evolutionary Genomics Group, Department of Botany and Zoology, University of Stellenbosch, Private Bag X1, Matieland, South Africa

⁶ Department of Ecology & Resource Management, University of Venda, P/Bag X5050, Thohoyandou 0950, South Africa

*Corresponding author: Peter.Taylor@univen.ac.za

Hildebrandt's horseshoe bat (*Rhinolophus hildebrandtii* Peters, 1878), one of three species in the *fumigatus*-group, is endemic to the Afrotropical region. These large bats are easily distinguished from most sub-Saharan horseshoe bats on body size, dental and noseleaf characters. This study used genetic, acoustic (echolocation peak frequency: PF) and morphological (of the skull, noseleaf and baculum) characters to characterise cryptic diversity in what we now recognise as the *R. hildebrandtii* species complex. Mitochondrial DNA sequence analyses demonstrated parapatry among southern African specimens previously identified as *R. hildebrandtii*. We characterised eight morphologically, sonotypically and/or genetically distinct populations which grouped into two major clades associated with montane and savanna habitats and separated by cytochrome-b genetic distances (uncorrected) of 9%. Based on comparisons with GenBank sequences from east Africa, these two clades can be taxonomically associated with the species *hildebrandtii* and *eloquens* respectively. Populations within the montane (*hildebrandtii*) clade also exhibited cranial shape and echolocation frequency differences between them that concur with shallow genetic divergences. Sonotype differences distinguish Mpumalanga animals (PF=33) from those from the northern Kruger (PF=40 kHz) and lowland Mozambique (PF=35-38 kHz). Furthermore, additional sonotypes (PF of 38 and 46 kHz) occur sympatrically at Lutope in northern Zimbabwe. We proposed that fragmentation of populations occupying the South African escarpment during the Last Glacial Maximum (LGM) can account for the modern distribution of acoustically and cranially distinctive lineages within the montane clade whereas the savanna clade probably expanded into southern Africa following the LGM.

(Poster 13) *Agathosma* (Diosmeae, Rutaceae): Lumping or splitting, whitherto lies the destiny of the Cape's biggest sister to citrus?

T.H. Trinder-Smith* & G.A. Verboom

Bolus Herbarium, Department of Botany, University of Cape Town, Private Bag X3, Rondebosch, Cape Town 7701, South Africa

*Corresponding author: Terry.Trinder-Smith@uct.ac.za

Agathosma is the largest genus in the tribe Diosmeae (Rutaceae) and is the third largest genus in the Cape flora, thus making it an important component of the CFR landscape. The generic limits of this genus has hitherto been somewhat fluid. Presently the genus includes a previously recognised genus *Barosma* that held some 25 species. A previous study by the authors in which three chloroplast gene regions (*psbA-trnH*, *atpB-rbcL* and *rpl16*) were used, showed a number of genera in the tribe and also, in particular, the genus *Agathosma* to be polyphyletic. The polyphyletic clades of the previous study however did not correspond to the once accepted *Agathosma/Baroma* circumscriptions based on morphology. In this study a phylogeny is sought using the highly variable *rpl32-trnL* intergeneric spacer region. A nuclear marker showing high inter-specific divergence, which is to be combined with the chloroplast data for improved clade resolution, is being sought concurrently. The ITS2 region shows promise in this regard. Once the major clades are established, the aim is to reconcile these with a suite of morphological characters pertaining to the leaf, fruit and floral structures to best explain the evolution of these traits in one of the large Cape clades.

Relationships and evolution in the Drakensberg near-endemic genus, *Craterocapsa* (Campanulaceae)

*E. Uys**

Animal, Plant and Environmental Sciences Department (APES Department), University of the Witwatersrand, Johannesburg, South Africa

*Corresponding author: else.uys@gmail.com

Craterocapsa (Campanulaceae) was first circumscribed in 1973 by Hilliard and Burt and constituted four species, *C. congesta*, *C. insizwae*, *C. montana* and *C. tarsodes*. The genus is centred around the Drakensberg with the distribution of *C. tarsodes* being the widest and extending from the southern Drakensberg to Mount Inyangani in Zimbabwe; *C. montana* is disjunct occurring north and south of Lesotho, whilst *C. congesta* is centred in Lesotho and the Drakensberg. The remaining species occur in and around the Mount Ayliff district in KwaZulu-Natal and the Eastern Cape. Hong (2002) described a new species, *Craterocapsa alfredica*. The phylogenetic relationships within the genus were not resolved prior to this study and there was some doubt surrounding the inclusion of *C. alfredica* in the genus as well as its validity as a species. Molecular and morphological phylogenetic studies were undertaken using the nuclear ribosomal ITS region and the chloroplast trnL-trnF region to verify the generic status of *Craterocapsa* and to elucidate possible evolutionary trends within the genus. Results from the study verified the generic circumscription of *Craterocapsa*, however a partition homogeneity test showed that the morphological and molecular evidence are not congruent. The two DNA regions were compatible and a combined analysis was done. The results from the analysis included the morphologically dissimilar species, *C. congesta* and *C. montana* being sister species. *Craterocapsa insizwae* and *C. alfredica* were both part of the very well supported genus with bootstrap support of 100%, but their possible conspecificity was not resolved. The relationship of *C. tarsodes* at the base of the *Craterocapsa* clade in the cladograms was not resolved for any of the molecular regions.

(Poster 14) The relationships between the Namibian *Zygophyllum stapffii* and the Angolan *Zygophyllum orbiculatum* as revealed by a molecular systematic analysis of the genus *Zygophyllum*

P.D.W. van der Merwe, P. Craven, M. Pirie & D.U. Bellstedt*

Department of Biochemistry, University of Stellenbosch, Private Bag X1, Stellenbosch 7602, South Africa

*Corresponding author: dub@sun.ac.za

The recent SANBI biodiversity expedition (January 2009) to Angola has allowed the collection of *Zygophyllum orbiculatum* Welw. ex Oliver from the northern Namib / Koakoveld region, and this was compared to *Zygophyllum stapffii* Schinz from the southern Namib / Kaakoveld region. Morphological comparisons showed that other than unifoliate leaves in *Zygophyllum orbiculatum* as opposed to bifoliate leaves in *Zygophyllum stapffii*, they were identical. A comparison of the nuclear ITS and the chloroplast *trnL* intron, *trnLF* spacer and *rbcL* sequences of a number of collections of these taxa in Angola and Namibia showed them to be identical at the level of variation that these markers exhibited.

When the sequences of these taxa were compared with *Zygophyllum* species occurring in the other paleotropical arid areas of the world and a phylogeny was constructed using Parsimony and Bayesian statistics this revealed that *Zygophyllum stapffii/orbiculatum* was sister to the monotypic genus *Augea capensis*. These results indicated that *Zygophyllum stapffii* and *Zygophyllum orbiculatum* should not only be combined into a single species but into a new genus as well.

The phylogeny also gives important insights into the biogeography of the genus across the African continent, south-eastern and central Asia, Madagascar and Australia. These findings and their implications will be presented.

Keywords: *Zygophyllum*, molecular phylogeny, ITS, *trnLF*, *rbcL*, African arid corridor

The vicariance biogeography of terrestrial gamebirds (Galliformes)

*V.C. van der Merwe**

Percy FitzPatrick Institute, University of Cape Town, Rondebosch 7701, South Africa

*Corresponding author: vnctvdm@yahoo.com

One of the major goals of conservation biology is to identify and prioritise areas for conservation. Ever since the hotspot concept was proposed by Myers, various statistical methods have been formulated to identify areas with exceptional biological richness. Whilst this approach may conserve a large proportion of current biodiversity, it fails to take into consideration the reality of evolutionary potential. In order to preserve the ability for species to evolve, a concerted effort should be made to identify areas that have, on numerous occasions, been responsible for the radiation of large numbers of taxa. Biogeographic analyses to identify these centres of vicariance. Quantification in historical biogeography has traditionally been based on the search for a single branching relationship amongst areas of endemism (cladistic biogeography). This method aims to identify the influence of geographic history of a particular area on the phylogenetic history of the species inhabiting that area. However, there exist numerous problems with using taxa in biogeographical analyses as characters are used in phylogenetic analyses. A new method of biogeographical history proposed by Hovenkamp states that reconstruction of biogeographical history should only be concerned only with the observed disjunctions in the distribution of taxa. Vicariance biogeography aims to identify centres of vicariance that have caused multiple speciation events to occur simultaneously. The Galliformes (gamebirds) are one the most cosmopolitan and specious orders of birds. They have been comprehensively studied and there exist up to date distribution maps for virtually all terminal taxa of gamebirds. Additionally, the phylogenetic tree for gamebirds is now almost fully resolved. I hope to determine the extent to which this information can be used to identify centres of vicariance that have been important in the evolution of gamebirds.

Population structure in *Mungotictis decemlineata*, a mysterious Malagasy mongoose

B. van Vuuren^{1,2,*} & S. Goodman^{3,4}

¹ Centre for Invasion Biology, Stellenbosch University, Stellenbosch, South Africa

² Evolutionary Genomics Group, Department of Botany & Zoology, Stellenbosch University, Stellenbosch, South Africa

³ Department of Zoology, Field Museum of Natural History, Chicago, USA

⁴ Vahatra, Antananarivo, Madagascar

*Corresponding author: bjvv@sun.ac.za

The narrow-striped mongoose, *Mungotictis decemlineata*, is one of the more enigmatic taxa belonging to the unique Malagasy carnivore family Eupleridae. This species has a restricted distribution in western and southwestern Madagascar. Two subspecies are recognised; *M. d. decemlineata* which occupies the more northern sections of the species' range and *M. d. lineata* to the south. Until recently, the latter was known only from the holotype and is likely to occur at much lower densities *cf.* the former which is considered locally common. The habitat of the species, namely dry deciduous forests, is increasingly fragmented leading to the narrow-striped mongoose being considered as vulnerable by the IUCN given continued habitat loss, fragmentation and restricted range. We set out to determine the genetic structure and levels of genetic variation across the distribution range. One nuclear and two mitochondrial fragments were sequenced for 50 specimens collected from four sites across the distribution. Acceptable levels of genetic diversity characterise the species. Overall, little to no geographic partitioning of genetic variation was detected across the range. These findings hold implications for the conservation of the species as a whole.

Morphology as an arbiter of gene tree incongruence: phylogenetic relationships and biome history in the African flowering plant genus *Jamesbrittenia* (Scrophulariaceae: Limoselleae)

G.A. Verboom*, M.L. Herron & J.A. Slingsby

Department of Botany, University of Cape Town, Rondebosch 7701, South Africa

*Corresponding author: tony.verboom@uct.ac.za

The recognition that gene tree incongruence has a real, biological basis, rather than being a mere analytical or sampling artifact, casts doubt on the validity of analysing multiple, contradictory gene loci in a single combined analysis (“total evidence”), especially where conflict is strong and spans deep nodes. Combining data in spite of conflict may compromise both topology and branch length estimation, with consequences for the quality of molecular age estimates. In this paper we employ a novel approach to resolving gene tree conflict which involves: identifying the set of taxa responsible for incongruence; splitting each of these into entities representing each locus; running a combined analysis to identify alternative placements of each ‘conflict taxon’ according to each locus; and identifying which placement, in each case, is most consistent with morphology. We justify the use of morphology as an arbiter of gene tree conflict on the grounds that it represents an integrated genotypic signal, based on multiple loci sampled from across the genome. Application of the approach to *Jamesbrittenia* (Scrophulariaceae), an African-endemic genus of flowering plants, shows morphology to be capable of resolving decisively the positions of several conflict taxa, even with a small number of characters. Comparison with other methods (concatenation, consensus and concordance) identifies our method as superior in terms of supported resolution, character consistency and taxon stability. Accuracy is difficult to assess, but is likely to be limited by morphological character quality and, as with other methods, taxon and gene tree sampling. A molecular dating analysis and reconstruction of historical biome shifts in *Jamesbrittenia* indicates a mid-Miocene origin in arid scrubby vegetation, probably along the margins of the Namib Desert. This supports an earlier interpretation of the Namib as a relatively ancient centre of origin for the southern African flora. The subsequent (Miocene-Pliocene) radiation of *Jamesbrittenia* into a suite of vegetation types associated with the central Escarpment (Grassland and Nama Karoo) and the southern margin of southern Africa (Albany Thicket and Limestone Fynbos), may reflect the relative youth of these systems, their origins being tied to a major continental uplift during the Pliocene.

Phytogeographic affiliation of the flora of the Klein Karoo - a unique pattern or a model of regional phytogeographic assemblage?

*J.H.J Vlok**

Regalis Environmental Services, PO Box 1512, Oudtshoorn 6620, South Africa.

*Corresponding author: janvlok@mweb.co.za

About 3 200 angiosperm species occur in the Klein Karoo, of which about 400 are endemic to the region. The area is not a distinct phytogeographic centre, but contains an interesting assembly of species. Most are endemic to the Cape Floristic Region, but many are widespread.

An analysis of the local flora revealed a surprising (and statistically significant) linear correlation between the number of species and how widespread they are (number of phytogeographic areas in which they occur). This analysis seems to be a first of its kind, but it could be a useful tool to develop a new understanding of the collection of species that occurs in a selected region.

Four questions arise from the results of this study.

1. Does this pattern hold for other regional areas?
2. Why is there a linear correlation in the data?
3. Can one predict the number of local endemics in an area from such an analysis?
4. Is there some unknown ecological rule that controls the number of species that can occur in a region?

The challenges of using molecular techniques for identifying *Lucilia* blowflies

K.A. Williams^{1,2,*} & M.H. Villet¹

¹ Department of Zoology and Entomology, Rhodes University, Grahamstown 6140, South Africa

² Entomology Department, Durban Natural Science Museum, Durban, South Africa

*Corresponding author: williamsk@durban.gov.za

Blowflies, such as various species of the genus *Lucilia*, are usually the first insects to arrive at dead bodies and are thus vitally important to forensic entomology in determining post mortem intervals. These flies have to be correctly identified but several species are very difficult to distinguish morphologically as adults, let alone as eggs or larvae. We collected green bottle blowflies that belong to the genus *Lucilia*, from various localities around the world and identified them using published morphological keys. Two nuclear genes (28S and Per; 1376 base pairs in total) and one mitochondrial gene (COI; 576 base pairs) were sequenced. Phylograms produced by Bayesian and maximum parsimony analyses showed incongruence between the nuclear and mitochondrial genes. The use of COI for identification purposes in blowflies was shown to be unreliable and suggests that using COI alone will not provide reliable identifications. This implies that using COI as the universal barcoding gene is not suitable for at least some blowflies. The same conclusion has been reached for the blowfly genera *Calliphora* in Australia and *Protocalliphora* in North America.

Endemism and diversity hotspots within the serpentine outcrops of the Barberton Greenstone Belt, Mpumalanga

SD Williamson & K Balkwill

C.E. Moss Herbarium, School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, Private Bag 3, Wits 2050, South Africa

The Barberton Greenstone Belt in Mpumalanga consists of approximately 30 large ($>1\text{km}^2$) and many smaller serpentine outcrops. Serpentine soils have phytotoxic concentrations of nickel and chromium and very high magnesium to calcium ratios. Serpentine outcrops usually harbour a flora distinct from the surrounding substrates as well as a large number of endemic species. The distributions of 29 serpentine endemics are discussed and used to determine which outcrops have the largest number of endemics. Endemic diversity is then compared to overall species diversity to determine whether endemic hotspots within the Barberton Greenstone Belt are correlated with diversity hotspots. The flora of the serpentine outcrops of the Barberton Greenstone Belt contributes significantly to the Barberton Centre of Endemism and the overall diversity of the province. Threats to the endemics and outcrops with high diversity are highlighted, which contribute to determining conservation priorities for the area.

The relative utility of 20 nuclear markers in assembling the Amphibian Tree of Life

S. Willows-Munro^{1, 2,*}, M.J. Morgan³, J.C. Santos⁴, D.M. Hillis² & D.C. Cannatella²

¹

University of KwaZulu-Natal, South Africa

²

University of Texas at Austin, United States of America

³

CSIRO Ecosystem Sciences, Australia

⁴

NESCent, United States of America

*Corresponding author: willows-munro@ukzn.ac.za

The analysis of large data matrices incorporating multiple independent genetic markers sequenced from large numbers of taxa is now considered routine. Although it is widely accepted that the accuracy of any tree produced by phylogenomic methods is dependent on the quality of data used, few studies specifically examine the contribution of each marker towards the combined tree. The taxonomically diverse frogs (Anura) were used as a case study in the present study. Despite much historical and contemporary work several important associations within the group remain contentious (e.g. Frost et al. 2006 and Roelants et al. 2007). The main aim of this study was to provide resolution and support for the higher-level associations within frogs by the combined analysis of 20 nuclear genes. The independent analysis of genes suggested high levels of topological variation. But when the contribution of each nuclear gene towards the phylogenomic tree was examined using partitioned likelihood support values, most genes generally contributed favourably towards the concatenated topology. Relationships among sets of trees obtained from the independent analysis of the nuclear genes were further explored using a multidimensional scaling method. This visualization tool allowed us to identify clusters of genes with similar topologies and highlights the importance of gene choice in any phylogenomic approach.

Plant survival strategies in a tropical African savanna, Kruger National Park, South Africa

*K. Yessoufou*¹, *V. Savolainen*², *O. Maurin*¹ & *M. van der Bank*¹

¹African Centre for DNA Barcoding, University of Johannesburg, APK Campus, PO Box 524, Johannesburg 2006, South Africa

²Genomic Laboratory, Imperial College, Silwood Park Campus, Buckhurst Road, Ascot SL5 7PY, London, United Kingdom

Processes driving diversity patterns are increasingly occupying the core of conservation strategies. Trade-offs in plant traits are acknowledged as revealing these processes and continuous efforts are still required to uncover them. In this study, we applied Bivariate Trait Correlations (BTC) and Phylogenetic Independent Contrast (PIC) analyses to investigate shifts in six key traits of 216 species occurring in Kruger National Park (KNP), and Principal Component Analysis (PCA) to test for specialisation in trait variations. BTC and PIC yielded congruent results. Leaf dry matter content was shown to be a poor predictor of leaf economics spectrum. We showed that positive correlations are mostly directed to secure nutrients while negative correlations aim to efficient uses of water resources. The first PCA axis was identified as key predictor of leaf economics strategy and the location on PCA axis 2 can be linked to major plant defence strategy dimensions. These findings are key understandings of savanna ecosystem functioning and help predict species reactions to change.

DELEGATES' ADDRESSES

A list of all registered delegates', including those who did not present work.

Barber-James, Helen Albany Museum & Rhodes University Email: h.james@ru.ac.za
Barker, Nigel Rhodes University Email: n.barker@ru.ac.za
Beheregaray, Luciano Flinders University. luciano.beheregaray@flinders.edu.au
Bellstedt, Dirk Stellenbosch University Email: dub@sun.ac.za
Bentley, Joanne University of Cape Town Email: bntjoanne@gmail.com
Bergh, Nicola Compton Herbarium, SANBI Email: n.bergh@sanbi.org.za
Berthouly-Salazar, Cecile Stellenbosch University Email: c.berthouly@gmail.com
Beukes, Chrizelle FABI University Pretoria Email: s22010743@tuks.co.za
Biccard, Aiden University of Cape Town Email: aiden.biccard@gmail.com
Bishop, Jacqueline University of Cape Town Email: jacqueline.bishop@uct.ac.za
Bloomer, Paulette University of Pretoria Email: paulette.bloomer@up.ac.za
Britton, Matthew University of Cape Town Email: matthewbritton@gmail.com
Bytebier, Benny University of Kwazulu Natal Email: bytebier@ukzn.ac.za
Cangi, Nidia Stellenbosch University Email: ncangi@sun.ac.za
Chakona, Albert Rhodes University & SAIAB Email: a.chakona@saiab.ac.za
Channing, Alan University of the Western Cape Email: achanning@uwc.ac.za
Clitheroe, Crystal Rhodes University Email: larvalanobium@gmail.com
Cloete, Elize Walter Sisulu University Email: elizecloete@yahoo.com
Coetzee, Martin FABI University Pretoria Email: martin.coetzee@fabi.up.ac.za
Coetzer, Willem SAIAB Email: w.coetzer@saiab.ac.za
Cole, Mary East London Museum Email: marybursey@elmuseum.za.org
Cooper, Mark University of Johannesburg Email: cybamic@yahoo.com
Cotterill, Woody AEON - University of Cape Town Email: fcotterill@gmail.com
Cozien, Ruth University of Kwazulu Natal Email: vdniet@gmail.com
Craig, Adrian Rhodes University Email: a.craig@ru.ac.za
Cron, Glynis University of Witwatersrand Email: glynis.cron@wits.ac.za
Crous, Kendall Rhodes University Email: k.crous@ru.ac.za
Crowe, Tim University of Cape Town Email: timothy.crowe@uct.ac.za
Daru, Barnabas University of Johannesburg Email: darunabas@yahoo.com
Davies, Owen University of Cape Town Email: owen.davies@uct.ac.za
de Jager, Marinus Stellenbosch University Email: mdj@sun.ac.za
de Moor, Ferdinand Albany Museum, Grahamstown Email: f.demoor@ru.ac.za
de Villiers, Margaret Stellenbosch University Email: margaret@sun.ac.za
du Toit, Nina Stellenbosch University Email: ndt@sun.ac.za
Fearon, Janine Rhodes University Email: janine.fearon@gmail.com
Fourie, Gerda University of Pretoria Email: gerda.l.fourie@fabi.up.ac.za
Francis, Caitlynne University of Cape Town Email: Caitlynne.Francis@uct.ac.za
Furrer, Eliane Rhodes University Email: eliane.furrer@bluewin.ch
Gere, Jephris University of Johannesburg Email: gerejephris@gmail.com

Gon, Ofer SAIAB Email: o.gon@saiab.ac.za
Goodman, Steven Field Museum,USA Email: sgoodman@fieldmuseum.org
Gouws, Gavin SAIAB Email: g.gouws@saiab.ac.za
Griffiths, Charles University of Cape Town Email: charles.griffiths@uct.ac.za
Groenewald, Rina Stellenbosch University Email: cwg@sun.ac.za
Gryzenhout, Marieka University of the Free State Email: gryzenhoutm@ufs.ac.za
Hamer, Michelle SANBI Email: m.hamer@sanbi.org.za
Hoffmann, Vera University of Cape Town Email: vera.vhoffmann@gmail.com
Hofmeyr, Greg Port Elizabeth Museum Email: greg@bayworld.co.za
Kabongo, Ronny University of Johannesburg Email: ronnypremier@gmail.com
Kaleme, Prince Stellenbosch University Email: kaleme@sun.ac.za
Karsten, Minette Stellenbosch University Email: minettek@sun.ac.za
Keevey, Garreth Rhodes University Email: g05k3539@ru.ac.za
Kelly, Chris Rhodes University Email: afrisnake@gmail.com
Koekemoer, Marinda SANBI Email: m.koekemoer@sanbi.org
Kortenhoeven, Cornéll University of Pretoria Email: cornellkortenhoeven@gmail.com
Kraai, Manqhai SAIAB Email: m.kraai@saiab.ac.za
Kruger, Jerraleigh Rhodes University Email: jerraleigh@gmail.com
Kyalangalilwa, Bruce University of Johannesburg Email: cebrussy@yahoo.fr
Laird, Megan PhD Candidate: Marine Biology, UCT Email: mail.meganl@gmail.com
Ligavha-Mbelengwa, Maanda University of Venda Email: ligav@univen.ac.za
Maake, Pholoshi Rhodes University & SAIAB Email: p.maake@saiab.ac.za
Makhasi, Ntuthuzelo University of Fort Hare Email: 200602178@ufh.ac.za
Makinen, Tuuli SAIAB Email: temakine@gmail.com
Mankga, Ledile University of Johannesburg Email: lmankga@yahoo.com
Martinez-Azorin, Mario Univeristy of Alicante Email: mmazorin79@hotmail.com
Masters, Judith University of Fort Hare Email: jdthmasters@gmail.com
Mataruse, Gamuchirai Rhodes University Email: matarutseg@yahoo.com
Mathee, Conrad Stellenbosch University Email: cam@sun.ac.za
Mayekiso, Sisanda SAIAB Email: maye4liwa@yahoo.com
Mazibuko, Frank NRF Email: fmazibuko@nrf.ac.za
Milne, Rebecca University of Cape Town Email: rebecca.milne@uct.ac.za
Mkhize, Awelani Onndwela Department of Environmental Affairs(DEA) Email: amkhize@environment.gov.za
Mlambo, Sukoluhle University of Pretoria Email: smlambo@zoology.up.za
Moore, Timothy University of Cape Town Email: timothy.moore@uct.ac.za
Morallana, Moqebelo Rhodes University & SAIAB Email: m.morallana@saiab.ac.za
Mthinkhulu, Yolanda Department of Environmental Affairs(DEA) Email: ymthinkhulu@environment.gov.za
Mwale, Monica SAIAB Email: m.mwale@saiab.ac.za
Naidoo, Kershney FABI University Pretoria Email: kershney.naidoo@fabi.up.ac.za
Odendaal, Lizelle University of Cape Town Email: lizelle.odendaal@uct.ac.za
Olbers, Jennifer University of Cape Town Email: olbersj@kznwildlife.com
Perera, Sandun University of Kwazulu Natal Email: sandun.perera@gmail.com
Perl, Franziska University of Zurich Email: franziska.perl@hotmail.com
Phaliso, Ntombifikile Rhodes University Email: fikzo_p@yahoo.com

Pirie, Michael Stellenbosch University Email: mpirie@sun.ac.za
Potts, Alastair University of Cape Town Email: pott.a@gmail.com
Price, Ben Rhodes University Email: ben.wills.price@gmail.com
Ramoejane, Mpho Rhodes University & SAIAB Email: m.ramoejane@saiab.ac.za
Reynolds, Terry Stellenbosch University Email: 14347210@sun.ac.za
Rius, Marc University of Cape Town Email: marc.rius@uct.ac.za
Rousseau, Philip University of Johannesburg Email: pr.philiprousseau@gmail.com
Sethusa, Theresa University of Johannesburg Email: sethusaTM@arc.agric.za
Shuttleworth, Adam University of Kwazulu Natal Email: 201504425@ukzn.ac.za
Simoene, Bezeng University of Johannesburg Email: bezengsimmy@yahoo.com
Smith, Gideon SANBI Email: g.smith@sanbi.org.za
Snyman, Louwtjie University of Pretoria Email: ipsnyman@zoology.up.ac.za
Spies, Paula University of Free State Email: spiesp@ufs.ac.za
Springbok, Nosiphiwo SAIAB Email: n.springbok@saiab.ac.za
Stiller, Michael Agricultural Research Council Email: stillerm@arc.agric.za
Stoev, Pavel Pensoft Publishers, Bulgaria Email: pavel.e.stoev@gmail.com
Strumpher, Werner University of Pretoria Email: wstrumpher@zoology.up.ac.za
Struwig, Madeleen North-West University Email: madeleen.struwig@nwu.ac.za
Swartz, Ernst SAIAB Email: e.swartz@saiab.ac.za
Switala, Angelika University of Pretoria Email: akswitala@zoology.up.ac.za
Taylor, Peter John University of Venda Email: peter.taylor@univen.ac.za
Trinder-Smith, Terry Bolus Herbarium, UCT Email: terry.trinder-smith@uct.ac.za
Uys, Else University of Witwatersrand Email: else.uys@gmail.com
van der Merwe, Vincent University of Cape Town Email: vnctvdm@yahoo.com
van der Merwe, De Wet Stellenbosch University Email: pdw@sun.ac.za
van der Niet, Timotheus University of Kwazulu Natal Email: vdniet@gmail.com
van Vuuren, Bettine Stellenbosch University Email: bjvv@sun.ac.za
Venter, Stephanus University of Pretoria Email: fanus.venter@up.ac.za
Verboom, Tony University of Cape Town Email: tony.verboom@uct.ac.za
Villet, Martin Rhodes University Email: m.villet@ru.ac.za
Weston, Peter Royal Botanical Gardens, Sydney Email:
Peter.Weston@rbgsyd.nsw.gov.au
Williams, Kirstin Durban Natural Science Museum Email: williamsk@durban.gov.za
Willows-Munro, Sandi University of Kwazulu Natal Email: willows-munro@ukzn.ac.za
Yessoufou, Kowiyou University of Johannesburg Email: kyessoufou@yahoo.fr

INDEX

A

Allen, 40
Anderson, 38
Andres Lopez, 61

B

Balkwill, 108
Barber-James, 8, 85
Barker, 36, 51, 52, 63,
65, 79, 83, 84, 85
Barker, 9, 22
Barnaud, 50
Bartlett, 31
Bates, 49
Bayer, 32
Beheregaray, 1
Bellstedt, 80, 102
Bentley, 10
Bergh, 10, 11
Berthouly-Salazar, 12
Beukes, 13, 55
Biccard, 14
Bishop, 15, 76
Bloomer, 20
Boatwright, 56
Bogale, 37
Bolton, 38
Born, 49
Bourjea, 41
Bowie, 33, 49
Branch, 52
Britton, 16
Bronner, 15
Burrows, 17

C

Cangi, 19

Cannatella, 109
Carbutt, 18
Chakona, 20
Channing, 21
Chown, 43
Clark, 9, 22
Clitheroe, 23
Coetzee, 24
Coetzer, 25
Coetzer, 5
Cole, 26
Cooper, 27
Cotterill, 28, 29, 46,
99
Cowling, 81, 86
Craig, 30
Cramer, 71
Craven, 102
Crespo, 63
Cron, 18, 31
Crowe, 2, 33

D

Daru, 32
Davies, 33
de Jager, 34
de Moor, 82, 85
de Wit, 28, 29
DelPero, 64
Douglas, 96
Downie, 95
du Toit, 35

E

Ellis, 34
Erwin, 7

F

Fay, 63
Fearon, 36
Forest, 71
Fourie, 37
Francis, 38

G

Génin, 60, 64
Gere, 39
Gon, 25, 40, 41, 53,
54, 59, 74, 94
Goodman P, 50
Goodman S, 3, 104
Gouws, 20, 40, 41, 72,
94
Griffiths, 14, 42, 57,
69, 77
Groenewald, 43

H

Hamer, 6, 44
Hasson, 30
Hedderson, 81
Helme, 45
Herbert, 36
Herron, 105
Hillers, 21
Hillis, 109
Hoffmann, 46
Hofmeyr, 47
Horak, 19
Hui, 12

J

Jacobs, 76
Jordaan, 96
Juan, 63

K

Kabongo, 48
Kaehler, 73
Kaleme, 49
Karis, 79
Karsten, 50
Keevey, 51
Kelly, 52, 65
Kleynhans, 93
Knapp, 7
Kraai, 53, 54
Kramer, 59
Kress, 7
Kvas, 55
Kyalangalilwa, 56

L

Laird, 57
Lange, 42
Law, 13
Le Roux, 12
Loffler, 58
Lötters, 21
Louette, 30

M

Maake, 59
Maclean, 32
Mahadeo, 86
Makhasi, 60
Mäkinen, 61
Mandiwana-Neudani,
38
Mankga, 62
Mansell, 92
Marasas, 55

Martínez-Azorín, 63
Masters, 60, 64
Mataruse, 65
Matthee CA, 19, 35,
66, 89
Matthee S, 35
Maurin, 32, 39, 48, 56,
62, 110
Mavimbela, 74
Mayekiso, 67
McCallum, 68
McDowall, 97
McKenzie, 79
Mercurio, 21
Millar, 91
Milne, 69
Mjacu, 74
Mlambo, 70
Monadjem, 99
Montgelard, 66
Moore, 71
Morallana, 72
Morgan, 109
Moteetee, 27, 62
Mucina, 22
Muths, 41
Mwale, 41, 67, 72, 73,
74, 94
Mwaluma, 41
Mwandya, 41

N

Naidoo, 75
Neves, 19

O

Odendaal, 76
Olbers, 77
Oliver, 80
O’Ryan, 15

P

Penev, 7
Pereira-da-Conceicoa,
85
Perera, 78
Phaliso, 79
Pirie, 80, 102
Pirone, 31
Pistorius, 47
Plön, 47
Potier, 73
Potts, 81
Powell, 27
Price, 82, 83, 84, 85
Procheş, 78, 86

R

Ramdhani, 86
Ramoejane, 87
Ratnayake-Perera, 78
Reynolds, 89
Robinson, 42
Rödder D, 21
Rödel M-O, 21
Rousseau, 90

S

Samyn, 77
Santos, 109
Savolainen, 110
Schick, 21
Schoeman, 99
Scholtz, 92, 95, 98
Sethusa, 91
Siebert, 96
Silvestro, 64
Slingsby, 105
Snyman, 92
Solano, 49
Sole, 95, 98
Spies JJ, 93
Spies P, 93

Springbok, 94
Steenkamp, 13, 37, 55
Stoev, 7
Stoffberg, 99
Strümpher, 95
Struwig, 96
Swartz, 20, 59, 87, 97
Switala, 98

T

Taylor, 99
Timberlake, 17
Trinder-Smith, 100

U

Uys, 101

V

van der Bank, 27, 32,
39, 48, 56, 62, 90,
91, 110
van der Merwe PDW,
102
van der Merwe VC,
103
van Rensburg, 12
van Vuuren, 12, 35,
43, 49, 50, 104
Venter, 13
Verboom, 10, 11, 16,
46, 71, 100, 105
Villet, 23, 51, 52, 82,
83, 84, 85, 107
Vlok, 81
Vlok, 106
von der Heyden, 89
Vorster, 90

Vumazonke, 67

W

Walton, 84
Weston, 4
Weyl, 87
Williams, 107
Williamson, 108
Willows-Munro, 109
Wimberger, 60
Wingfield BD, 24, 37,
55, 75
Wingfield MJ, 24, 37,
55, 75

Y

Yessoufou, 110