[a]*Department of Botany and Plant Biotechnology, APK Campus, University of Johannesburg, PO Box 524, Auckland Park 2006, South Africa*
[b]*Imperial College London, Silwood Park Campus, Buckhurst Road, Ascot SL5 7PY, United Kindgom*
[c]*Royal Botanic Gardens, Kew, Richmond TW9 3DS, United Kingdom*

DNA barcoding is a technique in which species identification is performed using DNA sequences from a small fragment of the genome, with the aim of contributing to a wide range of ecological and conservation studies in which traditional taxonomic identification is not practical. DNA barcoding is well established in animals using the cox1 gene (COI), but there is not yet any proposed universal barcode for plants that has received a broad consensus. We undertook intensive field collections in the renowned Kruger National Park (South Africa), which has its most southern part included in the Maputaland Biodiversity hotspot. Using a selection of trees and shrubs, we compared height potential barcodes: six advised by the plant working group and two from Kress et al. (2007). We applied a battery of metrics to measure intra- and inter-specific genetic divergences, statistical tests, phylogenetic and coalescence analyses. Compared to previous plant studies, we assessed to which extend a 'DNA barcoding gap' is present between intra- and inter-specific variations using multiple accessions per species. We identified a portion of the plastid matK gene as a universal DNA barcodes for flowering plants, which can be used singly or in combination with the trnH-psbA inter-gene for a slight increase in performance. Furthermore, we assessed the accuracy of combining to the previous barcode one of the two newly proposed loci by Ki-Joong Kim (University of Seoul). We further discuss the role that DNA barcoding can play in biodiversity inventories for conservation.

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A synchronous colonization of Madagascar by plants?

R. Lahaye[a], Z. Yang[b], Y. Bouchenak-Khelladi[a], F. Forest[c], J.S. Boatwright[a], J. Klackenberg[d], L. Civeyrel[e], V. Savolainen[f,g]
[a]*Department of Botany and Plant Biotechnology, APK Campus, University of Johannesburg, PO Box 524, Auckland Park 2006, South Africa*
[b]*Department of Biology, University College London, Gower Street, London WC1E 6BT, United Kingdom*
[c]*Royal Botanic Gardens, Kew, Richmond TW9 3DS, United Kingdom*
[d]*Department of Phanerogamic Botany, Swedish Museum of Natural History, S-10405 Stockholm, Sweden*
[e]*Laboratoire d'Ecologie Fonctionnelle, Université Paul Sabatier, 31062 Toulouse cedex 9, France*
[f]*Imperial College London, Silwood Park Campus, Buckhurst Road, Ascot SL5 7PY, United Kingdom*
[g]*Royal Botanic Gardens, Kew, Richmond TW9 3DS, United Kingdom*

Madagascar is renowned for the uniqueness of its fauna and flora with a high endemism. Because Madagascar separated from Africa and India before the diversification of angiosperms, its plant biodiversity is firstly due to colonization events across oceans followed by endemic radiations rather than vicariance. Although the literature can show a tendency in an asynchronous colonization of Madagascar by plants, it is not accurate to rely on such studies because of discrepancies in molecular dating techniques. Here we assess a possible synchronization in plant colonization of Madagascar from Africa by comparing the historical biogeography of 13 groups of plants showing Malagasy endemicity. Representatives from each group are included in a large *rbcL* matrix of 1566 taxa from which phylogenetic trees were inferred using PaupRat. One of the most parsimonious trees was dated by 23 calibrations points using three different dating methods, i.e. PL, NPRS, and a modified version by Ziheng Yang of the source of PAML for using MULTIDIVTIME. The results of this study provide crucial insight into trans-oceanic dispersal mechanism and the factors triggering radiation processes.

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Determining pathogen resistance in Arabidopsis by investigating the interaction between glutathione and non-xpressor of pathogenecity genes (NPR1)

M.E. Makgopa[a], R. Chikwamba[b], K. Kunert[a]
[a]*Department of Botany, University of Pretoria, Pretoria 0002, South Africa*
[b]*Council for Scientific and Industrial Research, PO Box 395, Pretoria 0002, South Africa*

Reactive oxygen species (ROS) control many different processes in plants such as programmed cell death, pathogen defense and systemic signalling thus the steady state level of ROS in cells has to be tightly regulated as accumulation of ROS can be detrimental to the cell. This can be achieved in various ways such as antioxidants, ROS-scavenging enzymes, defense gene expression to name but a few. A key component of the antioxidant process is the thiol glutathione pathway catalysed by the enzyme glutathione reductase and glutathione synthetase. Glutathione has been associated with determining the redox state of the cell and may indirectly activate regulatory proteins such as non-expressor of pathogenicity genes (NPR1) which has been shown to play an important role in the induction of systemic acquired resistance. To date, no direct link has been established between glutathione and the NPR1 therefore the aim of my study is to investigate the interaction between glutathione and the NPR1 gene and what effect they have on pathogen resistance needs to be studied further.

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Colophospermum mopane wood utilisation in the Lowveld, Limpopo Province

R.A. Makhado[a], M.J. Potgieter[b], D.C.J. Wessels[c]
[a]*Natural Resources and the Environment, CSIR, PO Box 395, Pretoria 0001, South Africa*
[b]*Department of Biodiversity, University of Limpopo, Private Bag X1106, Sovenga, South Africa*
[c]*Research Development and Administration, University of Limpopo, Private Bag X1106, Sovenga, South Africa*

The wood and non-wood products from mopane woodland were quantified from six villages in the Lowveld, Limpopo Province, South Africa. One hundred and eighty individuals were interviewed from the selected villages. Three villages were located in the depleted woodlands and the remaining three at abundant woodlands. Traditional governance structures within the selected villages and relevant conservation department officials were also interviewed. *Colophospermum mopane* is an essential source of fuelwood and provide poles used for construction of traditional structures. Each family uses 6.8±0.1 kg of *C. mopane* fuelwood for cooking/day in the woodland depleted villages, while 8.2±0.2 kg is used at the woodland abundant villages. The average volume of wood consumed to construct an adult's hut is 0.24 m^3 in the woodland depleted villages and 0.33 m^3 in the woodland abundant villages. The role played by mopane worms to the wellbeing of the rural people was also assessed and options to promote efficient use of woodland resources were suggested.

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Clarification of generic delimitation in *Justicia* and *Siphonoglossa* (Acanthaceae)

T.M. Makholela[a], K. Balkwill[b], J.C. Manning[c]
[a]*Pretoria National Herbarium, South African National Biodiversity Institute, Private Bag X101, Pretoria 0001, South Africa*
[b]*School of Animal, Plant and Environmental Sciences, University of the Witswatersrand, Private Bag 3, Wits 2050, Johannesburg, South Africa*
[c]*The Compton Herbarium, Kirstenbosch Research Centre, Private Bag X7, Claremont 7735, Cape Town, South Africa*

Siphonoglossa has been regarded as an artificial genus and treated as a clade within *Justicia* in New World Species based on morphological, chromosome and phytochemical data. This might be the same with the Old World Species. The genus *Siphonoglossa* has three described species in southern Africa, one with two varieties and there are 23 species in *Justicia*. *Siphonoglossa* is distinguished from *Justicia* by the long corolla tube (which in *S. leptantha subs. late-ovata* approaches the length and proportions of *Justicia protracta*), two or three areoles on the pollen instead of one or two rows, and the fact that the anthers do not reflex as the flowers age. This study reports the use of stylar cells as taxonomically important characters for the first time. Stylar cells closer to the stigma and stylar cells away from the stigma were studied in all *Justicia* and *Siphonoglossa* species using Herbarium specimens and Scanning Electron Microscope techniques. *Justicia* had short cells closer to the stigma and long elongate cells away from the stigma. *Siphonoglossa* only had long elongate cells except *S. linifolia*. Thecae form and corolla tube length which were previously used to justify the placement of *S. linifolia* were analysed and were observed not to be good characters. Stylar cells were found to be extremely useful in distinguishing between *Siphonoglossa* and *Justicia* and suggest that *S. linifolia* must be treated within *Justicia*. Further studies must focus on inclusion of New World species.

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Contribution of South African plants to medicinal plant biotechnology

N.P. Makunga[a], A.K. Jäger[b], J. Van Staden[c]
[a]*Department of Botany and Zoology, Stellenbosch University, Private Bag X1, Matieland 7602, South Africa*
[b]*Department of Medicinal Chemistry, Faculty of Pharmaceutical Sciences, University of Copenhagen, Universitetsparken 2, DK-2100 Copenhagen, Denmark*
[c]*Research Centre for Plant Growth and Development, School of Biological and Conservation Sciences, University of KwaZulu-Natal Pietermaritzburg, Scottsville 3209, South Africa*

Plants are able to produce a wide array of secondary metabolites through intricate metabolic pathways. The ability of plants to manufacture secondary metabolites has been widely exploited by man. Reliance of human communities on plant-based remedies has a long-standing history and remains a vibrant culture interfacing with modern healthcare. Plant biotechnology can make important contributions to the natural products sector. Even so, use of this technology in Africa is limited. The potential of biotechnological applications of South African flora is discussed and several species serve to highlight the benefits of this approach. Several culture systems established in our laboratories, with particular reference to the Genus *Salvia*, are proving valuable as models to study pharmacologically-active compounds and investigate the complexities of secondary metabolism using a metabolomics approach. We have been using a multidirectional strategy in order to understand biochemical and genetic changes resulting from genetic transformation and/or plant tissue culture. Our findings on the possibilities of influencing the productivity of secondary metabolism in various culture systems are discussed.

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The response of selected C_3 and C_4 grass species to fire: Proposed experimentation and preliminary results

T. Martin, B. Ripley
Botany Department, Rhodes University, PO Box 94, Grahamstown 6140, South Africa

C_4 grasses showed a global expansion during the late Miocene, twenty five million years after they were thought to have first appeared. Many studies have focused on what caused this global phenomenon in an attempt to understand the impact anthropogenic changes in climate might have on tropical agriculture and grassland ecosystems, both of which are of huge economic importance in Africa. It has recently been proposed that fire might have played a critical role in the observed expansion of the C_4 grasslands. C_3 and C_4 grasses occur in disturbance (fire) prone environments with C_4 grasses frequently being dominant. The aim of this study is (i) to investigate whether plant response to fire is a result of C_4 physiology or whether there is a phylogenetic component to the response and (ii) whether C_4 plants have evolved fire related characteristics that are advantageous under conditions of disturbance. Twelve grass species, six C_3 and six C_4 species, will be grown in pots and burned at the end of winter, after the frosts. The plants will be destructively harvested at three time intervals and their reallocation patterns and relative growth rates compared between species and photosynthetic type. Photosynthetic spot measurements will also be done to determine whether burning has an affect on the rate of photosynthesis. Additionally, the growth response of these species subsequent to natural fire is being monitored and preliminary results show that fire does have a differential affect on C_3 and C_4 species.

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Proteinase activity in soybean nodules

L.A. Mashamba, U. Schlüter, K. Kunert
Department of Plant Science, University of Pretoria, Pretoria 0002, South Africa

The symbiotic association between the roots of leguminous plant and soil fixing nitrogen bacteria results in a development of specific organ called nodules, whose primary function is nitrogen fixation from atmosphere into an accessible form for plants (Ammonia). The product of symbiotic nitrogen-fixation is exported from nodules to the rest of plant, where they are incorporated into essential macromolecules that drive plant growth and development. Aging of nodules is called nodule senescence. External environmental factors e.g. (light limitation and drought) can trigger premature nodule senescence causing a decrease in quality of seeds. Senescence process is correlated with up-regulated of proteinases gene expression. Development of soybean nodules was investigated and proteinase activity was measured in nodules of different age.

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nrDNA inheritance in the African genus *Streptocarpus* and the phylogenetic implications

M. Möller[a], K. Jong[a], G. Kokubugata[b]
[a]*Royal Botanic Garden Edinburgh, 20A Inverleith Row, Edinburgh EH3 5LR, United Kingdom*
[b]*Tsukuba Botanical Garden, 4 Amakubo, Tsukuba, Ibaraki, National Science Museum, Tokyo, 4 Amakubo, Tsukuba, Ibaraki 305-0005, Japan*

As part of a phylogenetic study of *Streptocarpus* (Cape Primrose, Gesneriaceae), the pattern of variation in the position, location of the 45S nuclear ribosomal DNA (nrDNA) and its evolutionary significance have been examined. The nrDNA sites were detected by fluorescent in situ hybridisation (FISH) and these mapped onto simplified phylogenies. The data indicated that nrDNA site duplications occurred several times independently, and recently in evolutionary terms. The findings in *Streptocarpus* are compared to results obtained from several other Gesneriaceae genera, *Aeschynanthus* and *Agalmyla*. Species of *Agalmyla* analysed were uniformly diploid and possess one 45S-nrDNA locus per genome, and *Aeschynanthus* species are either diploid or tetraploid, possessing either one or two loci per genome. In contrast to *Streptocarpus*, *Aeschynanthus* nrDNA locus changes involved duplications by polyploidisation as well as intragenomic changes. Unlike in *Streptocarpus* the latter appears to have occurred early in the diversification of the genus. The relevance of this investigation to the study of evolution of nrDNA loci and to issues relating to the reconstruction of phylogenies using multicopy nrDNA gene sequences and the rate of nrDNA evolution is discussed.

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