(1909) respectively. A.A. Bullock did some work in the genus on the tropical African taxa in 1952–1963. In 1984 F. Kupicha partly revised the genus and split it into *Schizoglossum s.s.*, *Miraglossum* and *Aspidoglossum*. Despite this revision many taxa remained unresolved in *Schizoglossum s.l.* These 59 residual names left in *Schizoglossum* were merely informally assigned to prospective groups which are *Glossostelma* (7 taxa), *Pachycarpus* (19 taxa), *Stensotelma* (8 taxa), one group allied to *Aspidoglossum* but not congeneric to that genus (14 taxa) and the remaining 11 taxa with uncertain/unknown affinity. Except for the recent work by D. Goyder on the tropical taxa effectively this group of residual names have not received any taxonomic attention since Brown's work. More than half of these are restricted to southern Africa. In this presentation an overview of and outline for the proposed revision of the split-tongues (*Aspidoglossum, Miraglossum* and *Schizoglossum s.s.*) and their cousins (*Aspidonepsis, Cordylogyne, Periglossum* and *Stenostelma*) is given. Historically the flower and corona-structure are the most important diagnostic characters used in the generic and specific circumscriptions of these groups. However, global studies in the Asclepiadoideae have now show many previously used coronal-structures are not homologous and due to convergent evolution rather than ancestry. In this talk, these previously used diagnostic morphological characters are compared and illustrated. In the final formal revision of the group we aim to determine whether these characters and the DNA-data of their species are correlated. If this is the case then both sources of evidence will be used towards producing a concordant phylogeny and classification for this recently evolved complex of taxa.

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Phylogenetic and evolutionary studies of the family Thymelaeaceae in southern Africa

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The family Thymelaeaceae comprises about 800 species distributed across 45 genera that occur in many parts of the tropics and Neotropics and display a wide range of diagnostic features. Several of the genera occur in Africa (*Craterosiphon*, *Dais*, *Dicranolepis*, *Englerodaphne*, *Gnidia, Lachnaea*, *Lasiosiphon, Octolepis, Peddiea, Struthiola, Synandrodaphne,* and *Synaptolepis*) and many are in need of revision and phylogenetic study due to unsatisfactory or uncertain generic circumscription. The main problems in the classification are within the subfamily Thymelaeoideae and revolve around the unplaced species of the dismembered genus *Arthrosolen,* the recently reinstated genus *Lasiosiphon* and the polyphyly of *Gnidia,* which impacts on the genera *Lachnaea, Passerina,* and *Struthiola.* In this study, we present the current state of knowledge, the taxonomic issues and phylogenetic relationships of the southern African Thymelaeaceae based on DNA sequences from both plastid (*matK, rbcL, trnH-psbA*) and nuclear (ITS) data sets as well as morphological data. The study aims to sample the remaining poorly studied genera or species and to propose a revised classification. The options available to achieve this will be discussed.

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Counterintuitive performance of core DNA barcodes within clades of southern African Combretaceae

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Recent studies indicate that the core DNA barcodes for land plants may have been overrated because its performance has arguably been tested using only few closely related species. In this study, we examined species discrimination within southern African Combretaceae using the core barcodes but also the combination core + supplementary barcodes. First, we tested the discriminatory power of single and gene combinations within the family as a whole. As expected, we found that the core barcode performed poorly compared to core + *trnH-psbA* or core + nrITS. Due to some limitations found for nrITS, we suggest that the core + *trnH-psbA* have greater barcode potential for the family. Second, based on the most recent and largest phylogeny available for the family, we identified major clades, and tested the efficacy of both core and core + *trnH-psbA* in discriminating species within five subsections (Angustimarginata, Ciliatipetala, Conniventia, Hypocrateropsis, Macrostigmatea) and the two subgenera (*Combretum* and *Cacoucia*) of the largest genus *Combretum*. In general, our results validate the lower performance of the core barcodes. Surprisingly however, we found that, in subsection Macrostigmatea, the performance of core barcodes surpasses by far not only its own performance (compared to the rest of the subsections tested), but more interestingly, the core barcodes outperform even the core + *trnH-psbA*. Our results indicate that the success of DNA barcode in discriminating closely related species may be contingent upon the evolutionary and possibly the biogeographic histories of the taxonomic group tested.

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Phylogeny of African Bruchids and their host plant *Acacia* species

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Seed beetles, (Chrysomelidae: Bruchinae) are globally distributed and include approximately 60 genera and 1700 species. Many bruchine beetles are found on host plants from a narrow selection of species in the legume family (Leguminosae / Fabaceae). Bruchine larval stages develop exclusively inside the seeds of these plants. Studies of host-parasite co-evolution at the species level can therefore be explored within this group of beetles. Co-evolutionary studies of bruchines have been restricted to crop plant parasitism, and studies focussing on African bruchines are non-existent. We present results of a phylogeographic and co-evolutionary exploration of the South African bruchines that complete their life cycle on host plant genus Acacia. Mitochondrial DNA sequences from collected samples within the South African distribution range of the beetles were aligned with existing GenBank data, and paired phylogenies of beetles and host plants were generated. The comparison of host and parasite phylogeographic patterns, contrasted with previous studies of host-parasite interactions in other groups of bruchines assessed the co-evolutionary dynamics of this host-parasite relationship.

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