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Lectures

ANTONELLI, Alexandre et al.
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The co-evolution of mountains and biodiversity

Mountains are key features of the Earth's surface and contain a substantial proportion of the world's biodiversity. In this talk I will present our current efforts to understand how mountain building may have contributed to generate and maintain diversity on global and regional scales, focusing on the relationship between current diversity and abiotic variables, and how the relative roles of climate change, surface uplift and biotic processes on diversification may be analytically disentangled.

ARUP, Ulf
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Are there more species of lichens to be found in Sweden?

Compared to most countries in the world the lichen flora in Sweden is well known. However, already at the start of my project in 2003 I knew there were undescribed species in the country in my favorite genus *Caloplaca*. During the project, funded by the Swedish Information Centre, I have both split excisting species of *Caloplaca* and discovered completley new ones. When I started there were 85 species kown from Sweden and now there are 105, most of them descovered by me or through collaboration between me and other scientists. Over the last years I have devoted my time mainly to the genus *Lecanora* and found species new to science. You may think that we now should know all species in these genera from Sweden, but this seems not to be true, I keep finding new species, even undescribed ones, and I cannot see the end of it despite more than 12 years of investigation, admittedly on half time.

BIRKEDAL, Linda
Projekt Trollsländor i Skåne; linda.birkedal@naturskyddsforeningen.se

A survey of the dragonfly fauna in Scania

This atlas project represents the first ever survey of the dragonfly fauna in Scania (Skåne), the southernmost province of Sweden. The region was surveyed 2009–2014 by volunteers in a citizen science project. Responsible for the project was the Entomology Society of Lund and the Society for Nature Conservation in Lund and Skåne.

HANSSON, Christer
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Integrative alphataxonomy of parasitic wasps

Integrative taxonomy, alphataxonomy if applied on species-level, involves the analysis of different kinds of data for classification, or for species delimitation. These data are usually from gene(s) and from the morphology. Other data used for this purpose are e.g. biological data. Results from two projects, one ongoing and one finished, where this approach has been used are presented. The ongoing project is with Swedish material of genus *Tetrastichus,* and the finished project with Costa Rican material of genus *Euplectrus*. Both genera include parasitic wasps that develop on other insects, and both belong in family Eulophidae. The analyses comprise barcode data (CO1, a mitochondrial gene) and data from the external morphology, and in *Euplectrus* also complete biological data. Both genera include species that are very similar to one another and which thus are difficult to separate, but with an integrative approach this differentiation has been enhanced. These investigations have revealed several cryptic species.

HEDRÉN, Mikael
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Molecular systematics of the orchid genus *Nigritella*

The small, intensely-coloured and vanilla-scented members of the orchid genus *Nigritella* are well-known to everyone interested in the European mountain flora. The genus has attained increased attention during recent decades, and several new taxa have been proposed based on differences in size and proportions, colour shade and chromosome number.

We have analyzed a representative material of *Nigritella* for differentiation in nuclear and plastid microsatellites. In agreement with predictions from embryological studies, diploid members of *Nigritella* are sexual and mostly out-crossing, whereas triploid, tetraploid and pentaploid members are obligate apomicts with restricted variation at the investigated marker loci.

The polyploids aggregate into three discrete groups, (1) the *N. nigra* group with dark-coloured triploids and tetraploids and including the narrow-endemic *Gymnigritella runei* from Scandinavia, (2) the *N. widderi* group including the tetraploids *N. widderi* and *N. archiducis-joannis* and the pentaploid *N. buschmanniae*, and (3) the *N. miniata* group, comprising red to pinkish-coloured tetraploids and including *N. stiriaca*, *N. miniata* and several recently described segregates of the latter.

The origins of two of the polyploids can be described quite exactly, and in each case the polyploid has arisen from the fusion of an un-reduced egg cell from an already existing polyploid with a sperm cell from a sexual diploid. Thus, *N. buschmanniae* originated by the fusion of a tetraploid egg cell from *N. widderi* with a haploid sperm cell from, possibly, *N. rhellicani*, and *Gymnigritella runei* originated by the fusion of a triploid egg cell from *N. nigra* subsp. *nigra* with a haploid sperm cell from the diploid *Gymnadenia conopsea*.

The origin of the *N. miniata* group remains obscure. Whereas the restricted variation at plastid markers points towards a single origin of the group as a whole, the diversity at nuclear microsatellites indicates a long period of diversification and dispersal since its origin. *N. miniata* is often polymorphic and genetically variable within localities. Recently

proposed segregates may be supported within localities by genetic data, but similar morphotypes at different localities are not genetically coherent, and thus not supported at species level.

Among diploids, variation at nuclear microsatellites dismiss the separation of local segregate species from sympatric populations of widespread congeners, such as e.g. *N. cenisia* vs. *N. rhellicani* in the western Alps. However, due to their too high variability, nuclear microsatellites gave restricted information on the proposed species limits between allopatric diploids. Plastid microsatellites gave some support for the separation of the dark-coloured *N. gabasiana* in the Pyrenees from *N. rhellicani* in the Alps, but such a differentiation could alternatively be interpreted as geographic variation within a single species.

HOLLANDER, Johan
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Genital form and evolution by reinforcement in Littorininae

Speciation requires reproductive isolation and biologists have examined multiple different processes of lineage splitting by which it could evolve. Within this range, reinforcement is recognised as having a special position as the only process in which natural selection directly favours an increase in reproductive isolation. Reinforcement is an evolutionary process by which natural selection increases reproductive isolation to avoid maladaptive hybridization. Similarly, a role for genital form influencing copulatory and post-copulatory components of reproductive isolation has long been suspected because, among animals with internal fertilization, male genitalia demonstrate rapid divergent evolution and species-specific forms. However, reinforcement and genital form have virtually always been studied separately. In order to increase our understanding of how genital form may influence the evolution of reinforcement, I will in my presentation try to bring these research directions together.

JONSTRUP, Anneli
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How distinct are the subspecies of the hemi-parasitic herb *Rhinanthus angustifolius*?

The annual hemi-parasitic species of *Rhinanthus* are renowned for their capacity to undergo ecotypic differentiation in flowering time and related characters. The species are generally subdivided into ecotypes that are either treated as subspecies or as varieties. But how distinct are these taxa? There is considerable potential for environmental influence to obscure the differences since the species use a variety of hosts, many with highly specific effects on the phenotype of the parasite. We performed a comprehensive common garden experiment to evaluate the phenotypic distinctness of taxonomically recognized ecotypes in *R. angustifolius* and to study how phenotypic plasticity affects the distinctness of the ecotypes.

LANG, Annick S.[1] & STECH, M.[2,3]
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Species circumscription within the moss genus Dicranum Hedw.

Identification of bryophyte species and in particular polar species is often difficult because morphological characters of the gametophyte can deviate strongly in extreme environmental conditions. Molecular methods, such as barcoding have shown to be useful for the identification of Arctic bryophyte species but the optimal combination of markers, especially for delimiting closely related species, is still under discussion. Lately, many different species delimitation methods have been developed, the generalized mixed yule coalescent (GMYC) approach being the most popular. However, only few studies on land plants have been published so far and GMYC analyses of bryophytes are largely missing. In this presentation, I will discuss the species circumscription and species identification within the moss genus *Dicranum* using six molecular markers (*rps4-trnT* $_{UGU}$, *trnL* $_{UAA}$-*trnF* $_{GAA}$, *trnH* $_{GUG}$-*psbA*, *rps19-rpl2*, *rpoB,* and nrITS1-5.8S-ITS2). Three methods have been employed, phylogenetic reconstruction, barcoding approach and GMYC method. Finally, the delineation capacities of the three methods have been compared with species boundaries inferred the morphological species concept.

NILSSON, Staffan
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Doing the impossible – monitoring bryophytes through citizen science

Usually, citizen science takes advantage of the public´s general knowledge of nature, and uses it to get data on things such as flowering times or bird occurrences. However, in the ongoing project Bryophytes of Skåne, citizen science is taken to a new level by taking on a species group which is virtually unknown to others than devoted specialists. In this talk, the project will be broadly presented, including some of the part time results.

PAUN, Ovidiu
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Genomic approaches to evolution in non-models

In the recent years powerful tools have become available to understand why and how organisms diversify. In my talk I will exemplify the use of "omics" in natural populations, giving insights into three different studies. What are the processes shaping the adaptive radiation of 24 species of *Diospyros* (Ebanaceae) on New Caledonia after a single long-distance dispersal event? What is the importance of recurrent allopolyploidization in *Dactylorhiza* (Orchidaceae) and what mechanisms allow sibling polyploids to adapt to divergent environments? How reproducible is parallel evolution of distinct ecotypes in *Heliosperma* (Caryophyllaceae)? By investigating the links between the genetic constitution of individuals, their epigenetic regulatory landscape and their native environmental conditions we obtain surprising insights on the way evolution proceeds. Evolutionary biology is more exciting than ever!

PETTERSSON, Lars
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Svensk Dagfjärilsövervakning: de första fem åren

Svensk Dagfjärilsövervakning är ett nationellt miljöövervakningsprogram som koordineras av Lunds universitet på uppdrag av Naturvårdsverket sedan 2010. Svensk Dagfjärilsövervakning är ett samarbete mellan Sveriges Entomologiska Förening, Naturvårdsverket, Lunds universitet, Sveriges lantbruksuniversitet och Länsstyrelserna. Verksamheten möjliggörs av frivilliga landet runt som mellan den 1 april och 30 september räknar fjärilar. Räkningen sker med en gemensam, systematisk metodik och fördelas på 3-7 inventeringstillfällen under säsongen. Det finns två olika sätt att övervaka, dels punktlokaler som är områden med 25 m radie som bevakas i 15 min per besök, dels slingor som är 0,5-3 km långa rutter som man inventerar i lugn promenadtakt. Genom att övervakningen upprepas inom säsongen och över flera år är det möjligt att skatta hur fjärilsfaunan förändras i antal och i artsammansättning. Slingorna och punkterna är spridda över hela landet, från Beddingestrand i söder till Vuollerim i norr. Data används bland annat till trendskattningar för enskilada arter men även till sammanvägda miljöindikatorer. Två av våra fjärilsindikatorer finns från och med i år med på den svenska miljömålsmålsportalen. På europeisk nivå är vi med och skattar trender för fjärilar i samarbete med 21 andra nationella fjärilsövervakningsprogram.

SUNDIN, Rikard & LILJEBLAD, Johan
ArtDatabanken; rikard.sundin@slu.se

The talk will be held in Swedish, but the abstract and the slide show is in English, to make it easier to follow for those participants who are not fluent in Swedish.

Aktuellt från Svenska artprojektet och ArtDatabanken

In 2001, ArtDatabanken at SLU (Sveriges lantbruksuniversitet) was appointed by the Swedish Parliament and Government to perform *The Swedish Taxonomy Initiative (STI)*, which started in 2002. The goal was to chart and describe the multicellular Swedish fauna, funga and flora (>50,000 species).

Since then about 10 000 of the most poorly known species have been treated taxonomically, c. 3 000 new species to Sweden have been found (about a third of them are new to science) and c. 2 500 species have been thoroughly presented to the public in the book series *Nationalnyckeln till Sveriges Flora och fauna*.

In 2013 STI's budget was reduced by 10 million SEK. However, the current Swedish Government has now proposed that STI's budget should be increased with 15 million SEK from 2016. The final decision will be taken by the Swedish Parliament in December.

Preliminary the new 15 million SEK will be used for: 1)Taxonomic research and inventories (+ c. 2 million SEK), 2) Support to biological collections of importance for the STI (+ c. 6 million SEK and last but not least, 3) Species information (+ c. 7 million SEK).

ArtDatabanken's taxonomic database, *Dyntaxa*, serves as a taxonomic standard for Sweden's conservation authorities as well as a taxonomic backbone for all databases run by ArtDatabanken (e.g. Artportalen, Artfakta etc.). During 2016 high priority will be given to the "filling-in" of the biggest "gaps" in the database, which means that after next year we should have a more or less complete estimation and taxonomic overview of the Swedish multicellular species.

The former Swedish Government, in February 2013, gave instructions to the STI to focus on digital presentation of species information, and to narrow down the "target audience" mainly to researchers and professional conservationists. These instructions, combined with the reduced budget, more or less forced ArtDatabanken to stop producing the book series *Nationalnyckeln* and to start constructing a digital system for species information, currently called *Artfakta*. The first version, focussing on redlisted species, was launched 28 April 2015. The system will be further developed, and will eventually also include digital "determination keys".

STI invited all active researchers and "inventory makers" within the project to a *forskarträf*f (researcher's meeting) in October. The aim was to update our researchers on what's going on within the STI, to get a good picture of how researchers supported by the STI are working and how they collect, treat and store the data assembled within their projects, and, last but not least, to get valuable input from the researchers on what the STI should do in the future.

Early next year (preliminary in February) the next application round for the support grants for biological collections in Sweden will be launched.

Last but not least, we hope to be able to present, to Systematikdagarna's audience, the new research/inventory projects that will receive support from the STI from January, 2016.

THELL, Arne
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Betony (*Betonica officinalis*) in Stehag – a piece of living plant history

Betony, *Betonica officinalis* L., is one of the rarest plants in Scandinavia, and has the longest documented history. It was reported from the parish of Stehag in Skåne, southernmost Sweden, by the Danish humanist and publisher Christiern Pedersen as early as 1534, one of the world's oldest records where a species is tied to a specific locality. Literature and collections testify that Betony was commoner in the past, when meadows were a significant part of the landscape. A recent survey shows that only about 150 individuals remain at five spots in western Central Skåne, a northwestern outpost of its Eurasian distribution. Betony is reviewed here through 500 years of documentation in Scandinavian literature and collections.

TYLER, Torbjörn
Lund University, Department of Biology, Biological Museum; torbjorn.tyler@biol.lu.se

Invasive plant species in the Swedish flora: Developing criteria and definitions, and assessing the invasiveness of individual taxa

In a north European context, identifying invasive species is far from trivial since the vegetation has been influenced by human activities for thousands of years. New species have immigrated continuously since the end of the last glaciation, both spontaneously and through the direct or indirect help by man. Still, newly immigrated species may be problematic in a nature conservation context and may harm biodiversity, and cause changes in ecosystem services. In our study, all 721 presently established vascular plant and bryophyte taxa known to have been introduced to, or to have immigrated to, Sweden since the year 1700 were assessed for their invasive potential. The assessment was based on six components considered relevant for their invasiveness: 1) ability to compete in natural vegetation, 2) ability to form dense populations, 3) realized dispersal ability, 4) gene flow to native relatives, 5) time since immigration and 6) distance to their native range. Although the relative importance of these components is context dependent, we proposed a compound general Index of invasive concern. The Index of invasive concern was validated by comparing it to assessments by a Bayesian Belief Network in which the influences of the same six components were assigned by expert opinions. In addition, rough estimates of the present-day abundance of each taxon in Sweden was presented. The origin, biology and possible impact of the 150 taxa with the highest index values were discussed. Based on the Index of invasive concern, we identified *Campylopus introflexus*, *Epilobium adenocaulon*, *E. ciliatum*, *Rosa rugosa*, *Lamiastrum galeobdolon* subsp. *argentatum*, *Orthodontium lineare*, *Solidago canadensis*, *Calystegia sepium* subsp. *spectabilis*, *Rubus armeniacus* and *Prunus serotina* as the ten most problematic alien vascular plant and bryophyte taxa in Sweden.

VAJDA, Vivi
Swedish Museum of Natural History; vivi.vajda@nrm.se

The significance of a new Osmunda from Jurassic volcanic deposits of Skåne

During the Jurassic (ca. 180 million year ago) volcanic activity was a common feature in what is today southern Sweden, Skåne. These volcanoes are still present in central Skåne, as so called volcanic necks hidden in the landscape. Volcanoes may also serve as "super-fossilizers" entombing plants in calcite or silica, sometimes preserving anatomy down to cellular structure for millions of years. In this contribution, the fossilized vegetation (macroplants and pollen) from Jurassic ash deposits at Korsaröd, Skåne will be presented, especially focusing on an exceptionally preserved fern belonging to Osmundaceae (Royal Ferns). The specimen is a three dimensionally preserved rhizome in which even the cell walls, membranes and some of the cell nuclei are preserved. Such spectacular preservation opens up new avenues for future research on fossil fauna and flora.

WAHLBERG, Niklas [1,2], PEÑA, Carlos[1] & WHEAT, Chris[3]
[1]Lund University, Department of Biology, University of Turku, Finland, [2]Department of Biology, Lund University, Sweden; niklas.wahlberg@biol.lu.se, [3]Department of Zoology, Stockholm University, Sweden

Cornucopia or Pandora's Box? Phylogenomics comes of age, data are no longer limiting

In the past couple of years it has become routine to generate transcriptomic or genomic data to e.g. resolve the relationships of taxa. The field of phylogenomics is based on using a large number of molecular markers in phylogenetics, anywhere from tens to hundreds or thousands of genes. It appears that data are no longer limiting. But still, different phylogenomic datasets produce different phylogenetic hypotheses, despite huge numbers of genes. Phylogenomic datasets have in effect become black boxes where we have no idea what genes are being analyzed. We use transcriptomes of Lepidoptera from 144 species to search for a panel of protein coding genes that are widely expressed in lepidopteran tissues of any origin and assess their phlogenetic utility. We found 333 genes that are widely expressed and easy to align by eye at the amino acid level. A phylogenetic hypothesis is presented based on these genes and and their use in various subclades of Lepidoptera is discussed.

Posters

DIOGO, Ivan
University of Gothenburg, Biology and Environmental Sciences; ivanjsdiogo@bioenv.gu.se

Ecotonal areas in Northeastern Brazil

We aimed to investigate the floristic influence of Amazonian, Caatinga and Atlantic forests on the mountain forests of northeastern Brazil. We prepared an abundance matrix of woody plants for the different domains. We made a Venn diagram, a similarity analysis by UPGMA, a MRPP and a nMDS. Amazon and Atlantic Forest have a particular flora since they show 34.8% and 26.9% of unique species, respectively. We sampled 367 species for mountain forests, 81.2% are common to other areas. The areas have heterogeneity of species (A = 0.53). It is evident the formation of two groups: a group consists of dry formations, which contains Caatinga areas and two mountain forests. The other one is formed by humid formations, Amazonian, Atlantic and five mountain forests. We observed a gradient Amazon - mountain forests - Atlantic (S = 0.1356). The high similarity and the gradient formation show that mountain forests are historically representative. The shared species between the domains indicate that might have had environmental conditions during the Holocene and late Pleistocene to allow exchanges between flora and to generate ecotonal environments.

FREITAS, Fernanda S., PELSER, Pieter, TELES, Aristônio Magalhães, ANTONELLI, Alexandre & BATISTA, João A. N.
University of Gothenburg, Biology and Environmental Sciences; freitas.fernandasantos@bioenv.gu.se

A re-evaluation of Brazilian Senecio sections Adamantina and Paranaia (Senecioneae: Asteraceae) based on molecular data

Senecio L. is a recognized polyphyletic genus. Since the genus posses more than 1.000 species, the best approach to understand the relations inside it is treating by sections. *Senecio* sect. *Adamantina* and *Paranaia* are small sections endemic to Brazil that emerged in previous studies as a monophyletic group. This study investigated the phylogenetic relations of this sections using nuclear DNA (ITS and ETS) and plastids (trnH-psbA and trnL-F) sequences. Results show that *Senecio* sects. *Adamantina* and *Paranaia* are polyphyletic and closely related to some sympatric *Dendrophorbium* species restricted to campos rupestres and campos de altitude of southeastern and southern Brazil. This group is here designated *Tomentecio* due to the conspicuous, white indument present in most of the species. Further work with morphological approaches will provide more insights into their the relations between *Senecio* sects. *Adamantina*, and *Paranaia*, and *Dendrophorbium*, and on the evolution of this group.

NORÉN, Michael
Swedish Museum of Natural History; michael.noren@nrm.se

Genetic characterization of freshwater fishes in Bangladesh using DNA barcodes

The purpose of the present project is to establish a genetic characterisation of Bangladesh's freshwater fish fauna, correlated with a stable taxonomic nomenclature. This entails research expressly aimed at morphological identification of species; using these well-identified specimens to establish a baseline DNA library of standardized mitochondrial COI sequences ("barcodes") with corresponding curated voucher specimens; resolution of common problems such as hybridisation and lack of differentiation between related species; and application of this barcode library in metagenomic (eDNA) studies. The ultimate goal is to have identification tools based on both morphology and genetics for use in fishery, conservation, environmental monitoring, and food industry.

RAUTENBERG, Anja
Länsstyrelsen i Uppsala län, The Rise of Systematic Biology; anja.rautenberg@gmail.com

Systematic biology as World Heritage – possible or not? About the project "The Rise of Systematic Biology"

"The Rise of Systematic Biology" is a Swedish initiative to nominate a selection of historic botanical gardens and excursion areas around the world to the UNESCO World Heritage list, because the sites were important to the development of systematic biology in the 18th century.

The field of science that we today call systematic biology evolved rapidly during the 18th century. This development has resulted in immaterial heritage (knowledge and practices), objects (collections, literature and instruments), locations (buildings, botanical gardens and excursion areas) as well as a biological cultural heritage. This bio-cultural heritage can be populations of plants, animals or other organisms that remain in the areas where they were once collected or studied, and old cultivated specimens in botanical gardens. Today, these organisms are historically interesting, and in some cases even have a scientific value.

SAWANGPROH, Weerachon & CRONBERG, Nils
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Spore germination frequencies in putiative hybrid populations of the mosses *Homalothecium sericeum* and *H. lutescens*.

In this study, we investigated the fertility of putative hybrid and parental populations of two closely related mosses *Homalothecium sericeum* and *H. lutescens*, which collected from various places of southern Öland Island (Sweden). To examine spore viability, we cultivated spores of putative hybrids and parental species on agar media with *Sphagnum* nutrient solution for 7 days at 8 h light, air temperature of 22 °C. The percentage of spore germination was then counted, classified, and tested for homogeneous frequencies. The result showed that there are no statistically significant different germinations among hybrid and parental species ($\chi^2_{14} = 17.886, p > 0.05$). Spore germination failure widely occur both the parental species and the putative hybrid populations, maybe due to different processes, for example inbreeding depression in parental species and genome incompatibility in hybrid population. Molecular analyses will be needed to investigate this.

STÅLSTEDT, Jeanette, WOHLTMANN A, BERGSTEN J. & MĄKOL J.
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Towards resolving the double classification in *Erythraeus* (Acari) using DNA and rearing

Species of velvet mites were mostly described as adults in the early years, but have more commonly been described as larvae in the last decades. This has created a problem of "double classification". One of the most speciose terrestrial parasitengone genera, *Erythraeus* Latreille, 1806 (Acari), comprises over one hundred nominal species. Only two species of these are known from both instars. How many of the names based on larval descriptions that actually represent the same species as a name based on an adult description is anyone's guess. Previously, experimental rearing was the only option to connect all life history forms. An alternative today is to match larvae and adults with DNA, one of the most useful applications of DNA barcoding. Combining morphological, biological and molecular data, five commonly occurring Erythraeus species in Sweden can now be re-described with a list of new junior synonyms and neotype designations.

ZIZKA, Alexander
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Differential diversification of Lepidocaryeae (Clamoideae) between Africa and South America

Despite their similar latitudinal position South America and Africa show a striking difference in plant diversity. Especially the Neotropics are home to an exceptional number of taxa with documented rapid radiations. Palms are an important ecological and evolutionary component of tropical ecosystems worldwide. The tribe Lepidocaryeae (Calamoideae) presents an intriguing pattern with around 40 species in Africa and just seven in South America (Figure 1). Why does this tribe contradict the general pattern and is more diverse in Africa than in South America? In order to understand the evolutionary processes on both continents, we will generate a species level phylogeny of the Lepidocaryeae based on next generation sequencing data. Fossil calibrations in combination with distribution data will be used to infer speciation and extinction rates and reconstruct climatic niche evolution. A comparative analysis between subtribes will allow us to address evolutionary differences between South America and Africa. Here I present the project and an outline of the methodological approaches we will use.