

SSS-Day 2018 – Program

Friday 9 Nov. 2018 – Naturhistorisches Museum Bern, Bernastr. 15

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- 09.30 Registration. Coffee & Croissants
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- 10.00 Welcome – Alice Cibois, President of the SSS
- 10.05 Invited lecture – Peter Linder (University of Zurich):
Why is the Cape flora so rich?
- 11.00 Ezgi Ogutcen (University of Geneva):
Evolution of Floral Colour in the New World Gesneriaceae
- 11.10 Practical Systematics - Donat Agosti (Plazi):
**Building the European Virtual Natural History Collections Infrastructure
Arcadia Grant: Discovering known biodiversity**
- 11.30 General Assembly, including the vote for the *New Species of the Year*
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- 12.15 Lunch at Restaurant Kirchenfeld
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- 14.00 Invited Lecture – Loïc Coster (Natural History Museum Basel):
Using the inner ear in systematics
- 14.55 Jeremias N. Brand (University of Basel):
**Transcriptome based phylogenomics reveal convergent evolution of
hypodermic insemination in *Macrostomum* flatworms**
- 15.05 Tamara Spasojevic (University of Bern): **Influence of taxon sampling on
age estimates in the first total evidence dating analysis of pimpliform
parasitoid wasps (Hymenoptera, Ichneumonidae)**
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- 15.20 Coffee break
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- 16.00 Master prize presentation – Maud Oïhénart (University of Geneva):
**Lichens and bryophytes from the canton of Geneva's old stonewalls - a
floristic and ecological study**
- 16.15 Morgan Guening (University of Neuchâtel):
**Evaluating NGS methods for routine monitoring of wild bees:
metabarcoding, mitogenomics or massive parallel sequencing**
- 16.25 Clément Duckert (University of Neuchâtel)
**Taxonomic revision of *Nebela militaris*, based on morphology,
molecules... and history!**
- 16.35 Raphaella Garbin (University of Fribourg):
**The collections of the National Museum of Brazil and its importance to
systematics**
- 17.00 End of the meeting

Abstracts

[abstracts are sorted alphabetically according to the authors' last names]

Donat Agosti (Plazi)

Building the European Virtual Natural History Collections Infrastructure

There is an unprecedented constellation of grants from the EU (DiSSCo, ICEDIG, COST MOBILISE, Synthesys), the capacity of handling big biodiversity data at GBIF and smaller, but nevertheless important developments opening up a chance to build a shared open biodiversity collections infrastructure that will make our data much more widely accessible. There is space to collaborate. This lecture will provide a brief introduction as well as a view from Plazi's involvement.

Donat Agosti (Plazi)

Arcadia Grant: Discovering known biodiversity

The UK Arcadia Fund awarded in June the Swiss NGO Plazi with a grant to expand its activities to provide access to the data in scholarly taxonomic publications, and continue building the Biodiversity Literature Repository Website. The goal of this award is to demonstrate the value of access to taxonomic data beyond having open access to individual articles, which is not a given in our community. This will be achieved by developing necessary infrastructures, creating, with access to data of over 50% of the new described species, a game changing approach, and for data by setting up conversion workflows leading from publications to findable, open accessible, interoperable and reusable data that in fact is being used by third parties like GBIF or in the future DiSSCo. Together with Zenodo at CERN, partners in ICEDIG, and Pensoft, novel ways are developed to make taxonomic treatments and published scientific illustrations, alongside of digital objects of specimens and scholarly articles citable, using persistent digital object identifiers. The Arcadia funds allow to collaborate with interested parties to include journals or articles covering taxonomic groups in this workflow. Together, this will speed up this process we consider making taxonomic data first class citizens in a digital world, and with this a first step to discover known biodiversity, not just titles of articles at best.

Jeremias N. Brand (University of Basel)

Transcriptome based phylogenomics reveal convergent evolution of hypodermic insemination in *Macrostomum* flatworms

Hypodermic insemination is a type of mating during which the sperm donor injects sperm through the epidermis of the mating partner using an intromittent organ. Sperm subsequently move through the tissues to the site of fertilization. In metazoans it has evolved independently multiple times and is prevalent in some invertebrate taxa (e.g. Arachnida and Hirundinae). Additionally, this mating system is overrepresented in hermaphrodites, possibly because positive effects on male fitness can compensate for female fitness costs. Since we lack adequate molecular data for most clades with hypodermic insemination, it is not clear how readily animals shift to this mating system. We investigate this question within a clade of simultaneous hermaphrodites, the free-living flatworm genus *Macrostomum*. To date, two independent origins of hypodermic insemination have been described within the genus. We here present results from our recent fieldwork aimed at improving both taxon sampling and geographical coverage. Based on a phylogenomic analysis of 107 species (75 new to science), from *de novo* assembled transcriptomes, we conclude that *Macrostomum* flatworms have transitioned to hypodermic insemination at least seven times. We present comparative analysis of changes in female genital morphology that are evolutionarily correlated with hypodermic insemination. Furthermore, we describe novel sperm morphologies that expand our understanding of sperm design in this clade.

Clément Duckert (University of Neuchâtel)

Taxonomic revision of *Nebela militaris*, based on morphology, molecules... and history!

Molecular data have considerably contributed to building the taxonomy of protists. Recently, the systematics of Hyalospheniidae (Amoebozoa; Tubulinea; Arcellinida) has been widely revised, with implications extending to ecological, biogeographical and evolutionary investigations. Certain taxa, however, still have an uncertain phylogenetic position, including the common and conspicuous species *Nebela militaris*. A phylogenetic reconstruction of the Hyalospheniidae using partial sequences of the mitochondrial Cytochrome Oxidase Subunit 1 (COI) shows that *N. militaris* does not belong to the genus *Nebela*, but should be placed in its own genus. The morphological singularities (strongly curved pseudostome and a marked notch in lateral view) and phylogenetic placement of our isolates motivated the creation of a new genus: *Alabasta* gen. nov. Based on an extensive search of the literature, we also show that old descriptions must be interpreted with caution and discuss why historical work is an important part of taxonomic revisions.

Raphaella Garbin (University of Fribourg)

The collections of the National Museum of Brazil and its importance to systematics

The National Museum of Brazil (Museu Nacional, MNRJ) is a 200-year-old institution founded during Brazil's colonial epoch. Since then the museum has received numerous important artifacts and specimens from around the world to aggregate its collections of zoology, botany, paleontology, geology, egyptology, ethnography, biological anthropology and others. By 2018 the museum's collection houses more than 20 million items, making the Museu Nacional the largest scientific institution in Brazil. As any natural history museum of this magnitude, the MNRJ is a reference collection for deposition of new material, especially those collected in Brazil's diverse tropical forests, counting with more than 15.000 type specimens of plants and vertebrates. Traditionally, Brazilian zoologists and botanists have been working on systematics based on morphology since 1980s and their work relied mostly on material from large museum collections, as the one from MNRJ. The tragic fire that destroyed the main building of the National Museum of Brazil and 70% of the museum's collection on September 2nd is not only a tragic lost for Brazilian culture and history, but for natural sciences and systematics particularly. With this talk I wish to show the different uses of the Museu Nacional collections in systematic studies, and promote discussions on collection preservation and fire prevention.

Morgan Guening (University of Neuchâtel)

Evaluating NGS methods for routine monitoring of wild bees: metabarcoding, mitogenomics or massive parallel sequencing

Implementing cost-effective monitoring programs for wild bees remains challenging due to high costs of sampling and specimen identification. To reduce costs, next generation sequencing (NGS)-based methods have lately been suggested as alternatives to morphology-based identifications. Nevertheless, with the ever increasing number of molecular identification methods, it is currently unclear which method is most suitable for routine monitoring programs, especially because only few studies have thoroughly compared identification accuracy, cost and workload. To bridge this knowledge gap, we assessed and compared three NGS approaches likely to be among the most suitable to be implemented in routine monitoring programs, namely metabarcoding, mitogenomics, and massive parallel sequencing.

Ezgi Ogutcen (University of Geneva)

Evolution of Floral Colour in the New World Gesneriaceae

Changes in floral pigmentation can have a dramatic effect on angiosperm evolution by making flowers either attractive or inconspicuous to different types of pollinators. The recurrent convergence in floral colour evolution has been largely interpreted as a response to pollinator-mediated selection. However, constraints imposed by the genetic architecture and the molecular pathways of floral pigment biosynthesis could also shape the course of phenotypic evolution. To explore the relative importance of these factors, we will integrate comparative analyses of flower colour, anthocyanins composition and molecular evolution in the Gesnerioideae (ca. 1200 spp.), a Neotropical lineage that exhibits an outstanding floral diversity associated with repeated adaptations to different pollinators such as hummingbird, bees, and bats.

For this project, we will collect pollinator and floral reflectance data for over 200 Gesnerioideae species to establish how flowers with various reflectance profiles are discriminated by different pollinators. We will also identify and quantify floral anthocyanins using high performance liquid chromatography and mass spectrometry. This dataset will help us to determine whether the utilization of different branches of the anthocyanin pathway impose different pollinator-mediated selection on floral colour evolution in Gesnerioideae. Finally, we are currently developing a sequence capture method targeting the structural and regulatory genes of the anthocyanin pathway in Gesnerioideae to identify candidate genes involved in floral colour transitions and to determine the genetic basis of convergent evolution of pollination syndromes.

The outcome of this research will allow us to elucidate the genetic patterns underlying the floral colour evolution and to understand how alternative branches of the anthocyanin pathway can constrain or promote pollinator-mediated diversification in angiosperms.

Maud Oihénart (University of Geneva)

Lichens and bryophytes from the canton of Geneva's old stonewalls - a floristic and ecological study

Apart from the works carried by Segal (1969) and Darlington (1981), the biodiversity of stonewalls has not been studied much, even less so when cryptogamic organisms are considered. In Great Britain, the Churchyard project (Chester 1991) has allowed for a better knowledge of the lichen flora colonizing anthropogenic substrates. This project has led the way to similar studies in various European countries (for example Dobson 2013, Malysheva 1995, Aptroot et al. 1994). In Geneva, an inventory of the lichens of the canton's cemeteries was carried out in 2013 (Vust et al. 2013) and demonstrated the importance of

anthropogenic substrates for lichens in this region. Indeed, there is no natural rocky outcrop in the canton of Geneva, so that stonewalls constitute the only available substrate for saxicolous cryptogamic species. Recent research projects on urban biodiversity in the city of Geneva (Habashi & Clerc 2013, Mombrial et al. 2013, Hinden 2015) and the Red Lists on bryophytes (Burgisser & Cailliau 2012) and lichens from the canton of Geneva (Vust et al. 2015) laid the foundation for the introduction in September 2016 of a master project on the cryptogamic biodiversity of stonewalls in the canton of Geneva. This short talk will present the results and findings of this work.

Tamara Spasojevic (Natural History Museum Bern)

Influence of taxon sampling on age estimates in the first total evidence dating analysis of pimpliform parasitoid wasps (Hymenoptera, Ichneumonidae)

Ichneumon wasps are parasitoids of insects and spiders and belong to one of the most species-rich families, the Ichneumonidae (Insecta: Hymenoptera). The group shows remarkable morphological, behavioural and host diversity, but most of it is still unknown, with the estimated number of species almost three times as high as the number of described species. Reconstruction of the phylogenetic relationships of ichneumonids is thus very challenging and still an open question. In this work, we are performing an integrative Bayesian phylogenetic analysis of Pimpliformes, a monophyletic group of nine ichneumonid subfamilies. The analysis is based on an extensive data set composed of 222 morphological characters and ten protein coding genes for almost 200 recent taxa. Furthermore, we include more than 50 ichneumonid fossils—many of them revised or newly described for this study—in the morphological matrix in order to perform total-evidence dating of the pimpliform tree. We present the first molecular-based age estimates for the major ichneumonid subfamilies and answer the question whether the ichneumonid radiation occurred before or after the Cretaceous-Paleogene boundary. In addition, we demonstrate a negative influence of poor outgroup sampling on the age estimates, and provide best practice for sampling in total evidence dating analyses.