

SSS-Day 2017 – Program

Friday 10 Nov. 2017 – Pavillon vert Uni Fribourg

- 09.30 Registration. Coffee & Croissants
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- 10.00 Welcome - Peter Wandeler, Director of the Museum
- 10.15 Invited lecture - Walter Joyce (Fribourg):
New insights into the evolution of basal turtles
- 11.00 Practical Systematics - Michelle Price (Geneva):
What is the Distributed System of Scientific Collections (DiSSCo) initiative?
- 11.10 Practical Systematics - Donat Agosti (Bern): **Plazi: Towards Linked Open Taxonomic Data in Switzerland & ICEDIG – Building a European Digitization Infrastructure for specimens in natural history collections**
- 11.30 General Assembly, including the vote for the *New species of the year*
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- 12.15 Lunch at Uni Fr
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- 14.00 Invited Lecture - Gwenaël Jacob (Fribourg): **Population dynamics of small populations - Application for the management of Capercaillie (*Tetrao urogallus*) populations**
- 14.45 Zohar Yanai (Lausanne):
Molecular and morphological analyses reveal a newly described mayfly genus in the Mediterranean Basin (Ephemeroptera: Heptageniidae)
- 15.05 Seraina Klopstein (Bern): **How many genes do we need? - Phylogenomics of pimpliform parasitoid wasps**
- 15.25 Marine Fau (Fribourg): **Comparative anatomy and phylogeny of the Forcipulatacean starfish (Asteroidea, Echinodermata)**
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- 15.45 Coffee break
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- 16.15 Master prize presentation – Clément Duckert (Neuchâtel):
New insights into the molecular and morphological taxonomy of *Euglypha* (testate amoebae)
- 16.35 Erina Balmer (Bern):
The Cinnamon Tree Frog: A Case of Cryptic Diversity
- 16.45 Jean-Luc Gattolliat (Lausanne): **Toward a European reference database of Ephemeroptera DNA barcodes**
- 17.05 End of the meeting



Abstracts

Donat Agosti

Plazi: Towards Linked Open Taxonomic Data in Switzerland

Taxonomic scientific names have been the standard and the glue to tie together data about the world's species and build an enormous corpus of scientific knowledge. In fact, the corpus is so big, that we have no idea how big it is, not even how many species have been described, nor to link changes of names over the centuries. Despite the elegance of the Latin Binomen, lasting for well over 250 years of history and complemented with a taxonomic treatment, the system as such is antiquated in a modern, digital, networked world. It stands a chance to become irrelevant with the increasing amount of daily generated new data in genomics or citizen science networks. However, modern technological approaches provide solutions to convert the biologists' unique naming system as an integral part of a global knowledge graph where data from various areas are seamlessly connected to biodiversity data. A fledgling system based on 155,000 names extracted from literature and developed by Plazi is presented.

ICEDIG – Building a European Digitization Infrastructure for specimens in natural history collections

Modern science requires digital access to data. European collections account for 55% of the natural sciences collections globally, holding more than 1 billion objects, which represent 80% of the world's bio- and geo-diversity. Only around 10% of these have been digitally catalogued and 1-2% imaged, rendering their information underused. The sheer scale and complexity of digitising and providing access to this information requires technological, socio-cultural, and organisational capacity enhancements across the continent. This challenge is being tackled by the new European Strategic Forum on Research Infrastructures (ESFRI) initiative Distributed System of Scientific Collections (DiSSCo). DiSSCo will unify access to collection data in a harmonised and integrated manner across Europe. It will enable critical new insights from integrated digital data to address some of the world's greatest challenges, such as biodiversity loss and impacts of climate change. However, new research and technological innovation will be required to solve the challenges of efficiently digitising and seamlessly accessing the collections. Building on previous project outputs, community and industrial expertise, the ICEDIG project will design all the technical, financial, policy and governance aspects for developing and operating DiSSCo. In this lecture, ICEDIG will be presented.

Erina Balmer

The Cinnamon Tree Frog: A Case of Cryptic Diversity

The Sunda Shelf in Southeast Asia underwent several complex geological and climatological processes in history, which resulted in vicariance and dispersal events for the inhabiting organisms. Today the biogeographical region of Sundaland is a well-recognized global biodiversity hot spot thus making the island of Borneo, located in the very heart of the Sunda Shelf, an attractive study site for evolutionary biology. Despite intense effort over the past 150 years to assess the species richness of Borneo, it still appears to be underestimated. *Nyctixalus pictus* or the “cinnamon tree frog”, first described by Peters 1871 from Kuching, Sarawak, Borneo, has long been considered as widespread on Sundaland. The genetic data of this study suggests for the first time that what today is considered *N. pictus*, is in fact a cryptic species complex consisting of highly diverged clades. In this study, *Nyctixalus pictus* is redescribed and six candidate species are identified.

Clément Duckert

New insights into the molecular and morphological taxonomy of *Euglypha* (testate amoebae)

The genus *Euglypha* is composed of testate amoebae that can be found in a broad variety of soil and freshwater environments. They strengthen their tests with small ornamented self-secreted silica scales whose shape, dimensions and arrangement are taxonomically informative. However, because of their small size, species identification can be reliably achieved only based on good quality light or scanning electron microscopy. For this reason, the taxonomy of these organisms is still incomplete or even controversial. As a consequence, many forms with diverging taxonomic positions (and, most probably, ecologies) are pooled together in ecological studies. In this study, we characterized 16 isolates by documenting their morphology with scanning electron microscopy and obtaining partial 18S rRNA sequences, constructed a phylogenetic tree of previously and newly barcoded species, and calibrated a time-scale phylogenetic tree based on previously established fossil records to evaluate the evolution within genus *Euglypha*. Firstly, it appears that several isolates can be described as new species. We demonstrated that the species *Euglypha rotunda* (the most common and widespread member of the genus) is not monophyletic based on morphology as well as molecular data. Several traits seem to be synapomorphic for some lineages, allowing us to infer the position of the different fossils within the phylogenetic tree of the Euglyphidae. Our molecular clock analysis shows that the genus *Euglypha* appeared during the Jurassic and that some of these species have diverged very recently.

Marine Fau

Comparative anatomy and phylogeny of the Forcipulatacean starfish (Asteroidea, Echinodermata)

Among echinoderm groups, the use of both molecular and morphological data favoured the emergence of a comprehensive and operational systematics in Echinoidea and Ophiuroidea. Unfortunately we are far from reaching such a consensus in the Asteroidea, despite a background of 30 years of modern phylogenetic analyses. Debates on starfish phylogeny still oppose various hypotheses, each supported by both molecular data and morphological characters. Recent researches demonstrate that a large set of morphological characters can be defined from comparative anatomy of skeletal elements (ossicles) for phylogenetic purposes, describing ossicle shapes, articulations among ossicles, marks of soft tissues on the skeleton (e.g. tube feet or muscle insertions). Both extant and extinct taxa can be analysed conjointly in phylogenetic studies of ossicle characters, which may help with tree rooting and consideration of fossils. The superorder Forcipulatacea is one of the major monophyletic groups with about 400 extant species, morphologically well-delimited, and for which a few phylogenetic hypotheses are available for its internal relationships. We explored the diversity of morphological features expressed in the group, considering 30 extant species and at least 5 fossil forms. The anatomy was investigated from progressive dissection of specimens from the zoological collections of the Muséum National d'Histoire Naturelle, Paris and the Yale Peabody Museum. The comparative work allowed definition of about 130 characters, a majority being new or reconsidering previous homology hypothesis. Four distinct taxon of each major clade of living forms (Velatida, Valvatida, Paxillosida and Spinulosida) were tested as outgroup for rooting.

Jean-Luc Gattolliat

Toward a European reference database of Ephemeroptera DNA barcodes

DNA barcoding has been applied very successfully for many fields, including species delimitation, discovery of cryptic species, association of different stages, tracking invasive species, conservation, and community ecology. Previous barcode assessment of European mayflies so far rather focused on restricted geographic areas such as northern Norway, Central Italy, Corsica, or Bavaria. The present study covers the whole Europe from Portugal to Russia and Georgia. If the main objectives are to develop a comprehensive DNA barcode library for European mayflies, and to test whether mayflies can be reliably identified with DNA barcodes, this study will also have a large impact on the systematic of the Europe mayflies by revealing cryptic species and regions with unsuspected high degree of endemism (i.e. Balkan, Iberian Peninsula). These taxonomic riddles need to solve before the database can be commonly used (applied ecology, assessment of water quality, etc).

Seraina Klopstein

How many genes do we need? - Phylogenomics of pimpliform parasitoid wasps

Next-generation sequencing technologies allow us to assemble increasingly larger molecular datasets even for non-model organisms. Unfortunately, even with hundreds or thousands of genes being sequenced, numerous studies recover conflicting phylogenies. With a group of parasitoid wasps as an example, we investigate how many genes we need to recover a stable phylogeny, and how this number is influenced by careful choice of the genes to analyze.

Michelle Price

What is the Distributed System of Scientific Collections (DiSSCo) initiative?

DiSSCo is a new pan-European Research Infrastructure initiative of 21 European countries that aims to position European natural science collections at the centre of data-driven scientific excellence and innovation in environmental research, climate change, food security, one health and the bioeconomy. Of relevance to the scientific community at large as well as to Swiss natural history collection holders and users, the initiative will be introduced and steps towards Swiss integration outlined.

Zohar Yanai

Molecular and morphological analyses reveal a newly described mayfly genus in the Mediterranean Basin (Ephemeroptera: Heptageniidae)

Heptageniidae is a species-rich mayfly family (Ephemeroptera), whose systematics has been largely based on traditional morphological studies, resulting in vague generic concepts and unresolved phylogenetic relationships. We recently combined thorough morphological and molecular phylogenetic analyses to resolve the generic concept of two species within this family, which have been continuously transferred between the big genera *Afronorus* and *Electrogena* but did not fit in either. Our results supported the assignment of these species to the newly described genus *Anapos*, currently known from the Mediterranean Basin and readily diagnosed based on morphological characters.