

SSS-Day 2016 – Friday 11 November

Abstracts

10.15 Invited lecture – Jean Mariaux (Natural History Museum of Geneva): **So many tapeworms, so little time... (and the need to think big in systematics)**

The diversity and evolutionary relationships of tapeworms, a class of Platyhelminthes that are enteric parasites of vertebrates, remain poorly known. In this talk I will show how the experts in this group managed to collaborate in order to successfully set-up larger and larger projects, that culminated with a multimillions PBI grant between 2008 and 2014. Significant results of the later will be summarized and the case for larger integrative projects in systematics will be made.

11.00 Luiz Jardim de Queiroz (University of Geneva): **Fish diversification in the Amazon: the contribution of environmental heterogeneities, topographical barriers and geographical distance**

Understanding the processes that drive fish population diversification in the Amazon is challenging due to its immense extension, the many environments and its outstanding biodiversity. We addressed this issue by determining the population genetic structure of the widespread fish *Triportheus albus* across the Amazon Basin and by examining the role played by all the structuring factors suggested to date. We tested for the contribution of isolation-by-distance, isolation-by-barrier with the Teotônio Falls as a physical barrier, and isolation-by-environment using four environmental variables: water pH and transparency, floodplain size, and riparian forest composition. Population genetic analyses based on mitochondrial genes and confirmed by a nuclear marker revealed a strong structuration in this species with three groups: Negro and Tapajós Rivers (black- and clearwaters); Lower Madeira and Central Amazon (whitewaters); and Upper Madeira, upstream of the Teotônio Falls. Using distance-based Redundancy Analysis (dbRDA), we showed for the first time that each of the structuring factors explains a significant fraction of the genetic structure. Our results indicate that multiple factors, either neutral or adaptive, individually proposed as drivers of population divergence, have acted in conjunction on *T. albus*, resulting in an unusually strong genetic structure. Because population structuring processes may ultimately lead to speciation, we suggest that their cumulative action enhance speciation and could account for the high speciation rate characterizing Amazonia.

11.10 Lucie Garnier (Conservatoire et Jardin botaniques de la ville de Genève): **Systematics, species delimitation and conservation in a Madagascar endemic genus of Sapotaceae**

Lucie Garnier^{1,2}, Rhéa Garratt^{1,2}, Yamama Naciri^{1,2}, Laurent Gautier^{1,2}

¹Conservatoire et Jardin botaniques de la Ville de Genève, 1292 Chambésy, Switzerland

²Laboratoire de Systématique végétale et Biodiversité, Université de Genève, 1292 Chambésy, Switzerland

The Convention on biological diversity defines biodiversity at three levels: ecosystems, species and genes. Madagascar is one of the highest hotspots of biodiversity in the world, with 82% of the vascular flora being endemic. As deforestation occurs actively in Madagascar, most of the endemic vascular flora is highly endangered. It is also the case of the Sapotaceae family, and especially the endemic genus *Capurodendron* Aubrév., which trees are currently used for carpentry in Madagascar. Thus the conservation of *Capurodendron* species and the sustainability of natural populations are challenging. In order to define with more accuracy

areas with high conservation priorities, it is necessary to combine phylogenetic diversities and IUCN threat categories. The *Capurodendron* genus is expended on the entire island, in primary forests, today highly fragmented. Twenty three species of these slow-growing trees are presently described, but some doubts remain about the number of species. Actually, they are morphologically very similar from one to another. In a preliminary project, we used DNA sequences to delimitate species in *Capurodendron* Aubrév. The phylogeny, based on herbarium specimens and silica-gel samples, highlighted some issues with the current species taxonomy. A huge arid complex was defined and some new species were observed on the phylogenetic tree. Nevertheless, as only one chloroplast and one nuclear marker were used on 39 individuals, the Multi-Species Coalescent analyses (STACEY software) could not give high posterior supports. This approach will be extended in the frame of a new PhD thesis that aims at improving species delimitation in the genus *Capurodendron* Aubrév. New distribution modelling will be computed using all herbarium specimens at hands, and a field trip will be organized in February-March 2017, to complete the dataset and get rid of the bias sampling of the former analyses. Next Generation Sequencing and gene capture will be used to increase the number of analyses genes. Species delimitation analyses will be conducted and the results matched with morphology, in order to find discriminant characters. Priority areas for conservation will then be defined using the new species circumscriptions. New IUCN threat categories will finally be assigned taking into account the genetic uniqueness of species.

11.20 Jon Peder Lindemann (Natural History Museum of Oslo): **Several species in one - An inventory of Norwegian species of *Pteromalus* (Hymenoptera: Pteromalidae) associated with Asteraceae plants**

Frequently, DNA studies on parasitic Hymenoptera have revealed host specific cryptic species from complexes previously thought of as single generalist species. The parasitic Hymenoptera genus, *Pteromalus*, involves members that attack fruit flies (Diptera: Tephritidae) with variable degrees of host specificities, but with one species, *P. albipennis*, particularly standing out as a generalist. Many members of the genus are also very close morphologically, and the status of some of the species has therefore earlier been questioned. These trends indicate a potential presence of cryptic species, or the opposite, that several nominal species exist within the boundaries of a single species. To test these assumptions, species of *Pteromalus* were investigated based on morphological determinations, sequence data and their host fruit fly relations. The insects were hatched from different Asteraceae plants, and sequence analyses of the *Pteromalus* specimens were conducted based on two loci, the mitochondrial COI and nuclear ITS2 regions. Despite large intraspecific genetic variation in the two loci, no clear indication on cryptic species was revealed. This indicates that the observed polymorphism is caused by other factors, such as population size, speciation in reverse, introgressive hybridization or *Wolbachia* infection. In two cases, sequence analyses were not able to distinguish between species of *Pteromalus*, suggesting that what is currently recognized as seven valid species rather exists within the boundaries of two. These results indicate that the two species, *P. intermedius* and *P. albipennis*, not constitute complexes of host specific cryptic species, but possess broader ranges of host fruit fly preferences than previously expected.

11.30 Ivan Löbl (Natural History Museum of Geneva): **Electronic-only papers: the unforeseen side effects**

Many electronic-only publications are not conform with the dispositions of the ICZN and result in unavailable nomenclatural acts. The respective 2012 Amendment of the Code is discussed and a review of conditions requested for available published nomenclatural acts is given.

11.50 Donat Agosti (Bern): **TreatmentBank: a growing service to taxonomic information**

Each species on Earth is based at least on one taxonomic treatment also known as protologue, or original description. Most species have multiple treatments conveying more knowledge, or nomenclatural changes. Despite this obvious huge corpus of data, these treatments are even hardly every properly cited or listed in the bibliographic references of modern taxonomic work. This needs real specialist's work to find the original publication. In today's world where we talk about the Internet of Things, whereby everything is linked, these missing citations are only the pinnacle of a tragedy that taxonomic work is a well-kept silo. In this lecture, Plazi's TreatmentBank is explained. Its potential contribution to open this silo, and to make the data contained within taxonomic treatments widely accessible is outlined.

14.00 Invited lecture – Frederik Ronquist (Stockholm): **Recent progress in dating phylogenies with fossils**

14.45 **Tamara Spasojevic** (UniBE, Natural History Museum Bern): Leave no stone unturned: challenges in Ichneumonidae palaeontology

The importance of an accurate placement of fossils becomes evident in the context of palaeo-ecological and molecular dating studies, where results heavily rely on the correct taxonomic position of the fossils. There are many factors that can bias the identification of fossil specimens. First of all, imperfect fossilisation hinders taxonomic placement in any group of organisms, as body parts that contain synapomorphies might not be preserved. In Ichneumonidae, another factor that impedes correct placement is widespread homoplasy: several groups have often independently acquired identical character states due to a similar life style, e.g., adaptation to the same host. We describe five new fossil species and two new genera of Ichneumonidae from the Green River Formation (~ 50 Ma) including *Mesoclistus? yamataroti* sp.nov, the first record of the subfamily Acaenitinae for the locality. Additionally, we revise the ten previously described ichneumonid fossils from Green River. Generic positions of most of the revised species proved to be unclear and four of the species have been moved from their subfamilies into Ichneumonidae *incertae subfamiliae*. In the light of these outcomes, we discuss the aforementioned challenges and give suggestions for future practise that can reduce mistakes related to erroneous fossil placement.

14.55 Jana Flury (NMBE, University of Bern): **The unexpected diversity of the genus *Occidozyga* on Borneo**

Jana Flury, Stefan T. Hertwig, Naturhistorisches Museum der Burgergemeinde Bern, Rafe Brown, University of Kansas, Ulrich Scheidt, Naturkundemuseum Erfurt, Alexander Haas, CENAK, Universität Hamburg, Indraneil Das, IBEC, UNIMAS Kuching.

The biogeographical region Sundaland is a famous biodiversity hotspot. From Borneo, the biggest island of this region, 186 anuran species are currently known, most of them are endemic on this island. However, the number of species will increase significantly, not least due to the application of sophisticated analyzes of molecular data and the resulting identification of so-called cryptic species. In this study we examine the phylogeny of puddle frogs (Dicroglossidae, *Occidozyga*) using maximum likelihood and Bayesian inference analyzes of nuclear and mitochondrial markers of 157 samples from the whole range of this genus. These frogs, which are distributed from mainland Southeast Asia to the Philippines, Sundaland, and the Lesser Sunda Islands, are known for their unique macro-carnivorous tadpoles. Based on external morphology the puddle frogs from Borneo have been assigned to two species: *Occidozyga laevis*, which is also widespread on the Philippines, and *O. baluensis*, endemic on Borneo. In contrast, our results suggest that the range of *O. laevis* is restricted to the Philippines. Following our obtained phylogenetic hypothesis *Limnonectes rhacodus* must be regarded as a species of *Occidozyga*. Furthermore, our analyses show that at least seven separate lineages of

Occidozyga occur on Borneo, that could be considered as valid species. This unexpectedly high diversity is the result of a complex biogeographic history of vicariance and dispersal events followed by allopatric speciation.

15.05 Christophe Randin (Université de Lausanne): **Ecological niche models to help unraveling the evolution of vascular plants since the Last Glacial Maximum**

Despite intensive studies on speciation, the relationship between adaptation to different environmental conditions and species divergence remains poorly understood. In this context, species with disjunct distributions along various geographic gradients are often characterized by marked phylogeographic divisions and include infraspecific lineages that may have diverged since the Last Glacial Maximum (or even earlier). Most of these phylogeographic lineages could substantially differ from each other in the environmental conditions they currently experience but also in their adaptive potential to changing environments. Here we show how ecological niche models can be used as explanatory or predictive tools to (i) detect ecological differentiation between potential distinct taxa, (ii) reconstruct postglacial history for identifying isolation and secondary contact zones and (iii) account for lineage-specific differences when predicting the potential effects of climate change on their future geographic distribution. We illustrate this from the local to the continental scale and by taking polyploid species and the complex *Quercus petraea*-*Q. pubescens*-*Q. robur* as examples.

16.10 Toprak Zeynep (University of Geneva, Conservatoire et Jardin botaniques de la ville de Genève): **Species Delimitation In the age of Genomics: A Case Study of *Silene* Section Siphonomorpha (Caryophyllaceae)**

Zeynep Toprak, Pierre-Emmanuel Du Pasquier, Daniel Jeanmonod, Bengt Oxelman, Yamama Naciri

Despite being one of the central themes in systematics, species delimitation is a rather challenging issue. With the advances in tools, availability of genetic data, and introduction of the Multispecies Coalescent (MSC) model, great improvements have been made in the accuracy of identifying species limits although some model limitations remain. The use of the MSC will be illustrated with an example on the section Siphonomorpha sensu lato. This section comprises a number of Mediterranean species, showing differing life forms, a wide range of habitats, and, various shapes in their distribution pattern. The delimitation of the group has long remained controversial, with three entities described as groups or sections by different authors. In this study, we used sequence data to estimate the relationships and species delimitation in the section Siphonomorpha sensu lato based on the MSC model, using the recent method STACEY that eliminates the need of assigning individual to the species in priori. Preliminary results indicate that Siphonomorpha sensu lato is paraphyletic and four sections could be recognized and delimited: Italicae, Paradoxae, Giganteae and Siphonomorpha sensu stricto. We furthermore showed that species delimitation within the Italicae section, is easier with Eastern Mediterranean species than Western ones. This might be due to larger population sizes in the Western species compared to the Eastern ones.

16.20 Master prize presentation – Lea Waser (Naturhistorisches Museum Bern): **From a lost world: phylogeny of the genus *Ansonia* Stoliczka, 1870 (Lissamphibia: Anura: Bufonidae) and the description of a new species including its morphometric discrimination**

While the island of Borneo is considered a global biodiversity hotspot, the species richness in many groups remains unknown and appears underestimated. During herpetological surveys carried out in the interior of Sarawak, East Malaysia, several individuals of a small species of the genus *Ansonia* Stoliczka 1870 were collected on the Usun Apau plateau and in the Gunung Hose mountain range (*Ansonia* sp. Usun Apau). An integrative taxonomic approach comprising phylogenetic (2.4 kb mitochondrial rDNA fragment, Bayesian

Inference and Maximum Likelihood, >5.1 % to its closest relative) and morphometric analyses (25 measurements, multivariate ratio analysis and linear discriminant analysis), as well as morphological comparisons support the status of this operational taxonomic unit as a separate taxon at species level. The obtained phylogenetic hypothesis corroborates the two major clades within *Ansonia* found in previous studies. Within Clade One *Ansonia* sp. Usun Apau and the enigmatic *Ansonia torrentis* are part of a monophyletic group of the Bornean species *Ansonia hanitschi*, *Ansonia minuta*, *Ansonia platysoma*, *Ansonia spinulifer*, *Ansonia vidua*, and two additional undescribed taxa. This subclade must be considered as the result of an on-island radiation in the complex evolution of *Ansonia*. The new species is formally described including the identification of diagnostic morphometric traits. *Ansonia* sp. Usun Apau is endemic to two isolated mountain ridges in central Sarawak and must be considered as a new element of the unique diversity of the Bornean amphibian fauna that is potentially threatened by habitat loss at least in parts of its range.

16.40 Clément Duckert (Laboratory of Soil Biodiversity, University of Neuchâtel): **Morphological and molecular taxonomy of *Euglypha* - Towards a calibration of the molecular clock**

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 10 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, we described five new species from that genus. 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.

16.50 Alice Gerlach (Conservatoire et Jardin botaniques de la ville de Genève): **The corticolous, shrubby, apotheciate species of *Usnea* Adans. (lichenized Ascomycetes, Parmeliaceae) of Brazil: an integrative taxonomy approach**

Alice Gerlach & Philippe Clerc

Usnea is a highly supported monophyletic and megadiverse cosmopolitan genus. The taxonomy of this group is considered exceptionally difficult due to the extensive morphological and chemical variability within species and a molecular approach is needed to evaluate species delimitation. Shrubby –apotheciate species are characterized by the erect-bushy thallus, the usually numerous apothecia and the absence of vegetative propagules. For the first time, we provide systematics of shrubby –apotheciate corticolous species occurring on Brazil based on integrative approach i. e. morpho-anatomical, chemical and molecular features. Newly collected and herbarium material were analysed with standard methods used in *Usnea* systematics. Seventeen corticolous shrubby apotheciate *Usnea* species are reported from southern Brazil, including five species that are new to science. For the molecular analyses we sequenced ITS rDNA, Mcm7 and RPB1 markers. A concatenated dataset with 55 specimens from 25 *Usnea* species were analysed with maximum likelihood and Bayesian inferences. The four new species based on traditional characters were supported by the molecular analyses.