



SSS Day 2015

Abstracts

November 6, 2015 Natural History Museum Bern Fotos: ©Reto Burri, www.wildlight.ch

Program

09.30	Registration. Coffee and Croissants
10.00	Welcome address
10.10	Invited lecture - Robert Scotland:
	Accelerating the pace of taxonomy
11.00	Practical Systematics session
	Alice Cibois: Nagoya protocol
11.10	Seraina Klopfstein: Biosyst.EU
11.20	Reto Hagmann: SkyIslands Database -
	Effective management of biodiversity data
11.30	Donat Agosti: BioDIP - a proposed infrastructure to link the
	taxonomic to the genomic and other domains
11.50	General Assembly
12.30	Lunch at Restaurant Kirchenfeld
14.00	Invited lecture - Christophe Praz:
	The challenges and future of bee systematics in Europe
14.45	Jean-Luc Gattolliat: When morphology meets genetics: the case of Macaronesian mayflies
15.05	Hannes Baur: Volatile matter, or: how to prolong half-life of morphometric data
15.25	Lukas Schärer: Hypodermic insemination and correlated reproductive trait evolution in a clade of free-living flatworms
15.45	Coffee and cake
16.10	Lucie Cauwet: Morphology, function and evolution of male genitalia (spermatophores and hemispermatophores) in Scorpionoidea
16.30	Anahita Aebli: Recent assembly of the Madagascan biota by replicated adaptive radiation: Case studies in Legumes
16.50	Achim Reisdorf: The Myth - Can Carcasses Explode?
17.10	Manuel Schweizer: Strix owls in the Middle East: un- and re- discovered
17.30	Goodbye

Invited lecture

Robert Scotland

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Accelerating the pace of taxonomy

The talk will illustrate and discuss how new species are discovered in the context of plant taxonomy, and describe an initiative to accelerate the pace of revising and discovering species.

Practical Systematics Session

Alice Cibois

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Nagoya protocol

The Nagoya protocol entered into force on Octobre 2014, and its implementation can impact the working flow of systematists. This talk presents the main elements of this protocol and the relevant documents that should help us to deal with it.

Practical Systematics Session

Seraina Klopfstein

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Biosyst.EU

The Federation of European Biological Systematic Societies, or Biosyst.EU, aims to promote research, teaching and training in all fields of systematic biology. Members are currently the national societies from Austria, France, Germany, Sweden, the UK, and of course the SSS. Biosyst.EU organizes joint meetings every four years. In 2017, the Swedish society will organize the Biosyst.EU conference in Göteborg on August 15-18. All societies are encouraged to propose a half-day or full-day symposium; we are now looking for ideas for the contribution by the SSS.

Practical Systematics Session

Reto Hagmann¹, Michele Menegon², Simon Loader^{1,3}

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Skylslands Database: Effective management of biodiversity data

Tools are increasingly required to manage and access the burgeoning amount and types of biological data being generated. We have developed an integrated data management system for taxonomic data that allows subsequent dissemination of taxonomic knowledge. Our "SkyIslands" database focuses on amphibians found in the Eastern Afromontane Region of Africa an area designated as a biodiversity hotspot, poorly understood with a large undescribed cryptic diversity and highly threatened. Biological data has been obtained from over 20 years of fieldwork and previous historical collections. The database is based on FileMaker, MySQL, and Java. It allows the storage of different types of data including genetic, morphological, distribution records, acoustic, and images. All data can be queried and searched for and subsequently exported in a range of formats. One important aspect is the implementation of BLAST in the database that allows the querying of genetic data against GenBank and other new unpublished genetic data simultaneously (including genetic similarity scores and adjustable cut-off %). This allows rapid and comprehensive barcoding of new and unknown samples including easy data extraction for making phylogenetic trees. The query system we developed provides a best summary of all available genetic data - and therefore species identification and phylogenetic relationships. These user-friendly processes in the "SkyIslands" database lead to rapid identification of samples towards short or long term biodiversity studies in the region. We plan an online platform to be available for various types of users. Overall, the database aims to provide an impetus for increasing knowledge on the biodiversity and its conservation. In addition we want to make this extended BLAST service available to the scientific community: www.graviton.ch/blast

Donat Agosti

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BioDIP - a proposed infrastructure to link the taxonomic to the genomic and other domains

Scientific names are a unique asset in bringing together information on the world's taxa. Though widely used, scientific names are in the digital world essentially disconnected from their published evidence. Not only is a bibliographic reference in most cases not explicitly given, but the taxonomic treatments or even a digital copy of the article are not accessible. We propose to build an infrastructure that provides this access and support the data curation and content mining of those contents. A collaboration of the Swiss Institute of Bioinformatics, Plazi and Zenodo/CERN will lead this effort. We are interested to find partners among the Swiss biodiversity organizations to link services including names (e.g. catalogues, GenBank) with the respective data in publications, especially if the publications are in-house. This will also allow linking digitized specimens with the published record and vice versa.

Invited lecture

Christophe Praz

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The challenges and future of bee systematics in Europe

Despite 200 years of taxonomy, the systematics of wild bees in Europe is still insufficiently known. This talk will address current issues and present opportunities for obtaining a better understanding of these important pollinators.

Regular talk

Iean-Luc Gattolliat

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When morphology meets genetics : the case of Macaronesian mayflies

Recent genetic studies using a general mixed Yule-coalescent (GMYC) model revealed the presence of 12 putative species of Baetidae (Ephemeroptera) in the Canary Islands and Madeira. Pronounced island endemism contradicts previous taxonomic work, which reported a depauperate fauna that included several mainland species. With a set of morphological characters already applied to continental cryptic species within the genera *Baetis* and Cloeon, we wanted to test the extent to which morphology supports the genetic results. For most putative species, we were able to find morphological characters to reinforce the validity of the species status. Each cryptic species seems to be endemic to a distinct island except Baetis atlanticus, which occurs both on Madeira and Continental Europe. These results have important conservation implications; because of their small population size and extensive habitat alteration, most species must be considered as highly endangered.

Hannes Baur

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Volatile matter, or: how to prolong half-life of morphometric data

In morphometric studies, raw data files are usually not published. The lack of original data often causes problems, in particular when new studies contradict earlier findings, as it is then impossible to check the old data for errors, e.g., in precision or accuracy. It also prevents accumulation of larger data sets, because the compilation of hundreds or thousands of measurements is normally a rather time consuming task. Hence, researchers usually have to work with relatively small data established from scratch. In principal, similar problems would exist in the case of molecular studies, but here authors are forced to deposit their DNA sequences in GenBank or BOLD, otherwise publication is prohibited. Hence, raw sequences are naturally available for future tests and analysis. Here, we present a protocol for making morphometric data publicly available in a sustainable manner. The most important points are as follows: (1) individual documentation of each measurement using a digital photographic tool (if possible, see below); (2) establishment of measurement error for a set of critical or (practically or conceptually) difficult characters; establishment of data and training images (or objects) for setting the gold standard, which can be used in subsequent studies for checking accuracy of measurements using the Bland-Altman graph, a well-known tool used in countless medical studies; (4) deposition of raw data, images, and other relevant documents in

an open repository, such as DRYAD. The protocol is exemplified with data of various groups of invertebrates (spiders, insects, snail shells), vertebrates (fish, frogs, birds, archaeozoological bones of sheep and goats, skulls of badgers), and flowering plants (possibly also fungi). One set of data is generated using a standard, non-documentable measurement tool (caliper, eyepiece micrometer of a stereomicroscope, microscribe) and compared with results from a documentable photographic tool (single focus images taken with a digital microscope or system camera, measured with Image]). Measurement error is shown to be at least comparable, but mostly also much lower in the case of the digital tool. We also discuss the situation where documentation is not possible, for instance in the case of measurement of living birds. Special measures are presented that should provide accuracy and precision of data from different surveyors. A similar case concerns the use of the microscribe, which is often used for establishing 3D landmark data, but of course cannot be dismissed. Although most examples concern distance measurements, most parts of the protocol apply also for the data used in geometric morphometrics. It is important to notice that the infrastructure for the spread of morphometric data of all kind already exists in the form of data repositories like DRYAD. Therefore, morphometric data cannot only be made available and sustainable very easily, but we can also start right now.

Regular talk

Lukas Schärer

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Hypodermic insemination and correlated reproductive trait evolution in a clade of free-living flatworms

Hypodermic insemination is a form of traumatic mating where sperm cells are transferred to the mating partner through the epidermis, rather than being deposited into a female genital system via a female genital opening. In my talk I explore the idea that hypodermic insemination evolves due to sexual conflicts over the fate of received ejaculate components between a sperm donor and a sperm recipient. Specifically, I present evidence that hypodermic insemination has evolved several times independently, not only among the taxon Macrostomorpha as whole, but also within a single genus, *Macrostomum*, and suggest that this can go along with drastic changes in a number of reproductive traits, including sperm morphology, male copulatory organ morphology, female genital morphology, and the mode of sexual reproduction.

Lucie Cauwet

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Morphology, function and evolution of male genitalia (spermatophores and hemispermatophores) in Scorpionoidea

Insemination in scorpions occurs via the use of a sclerotized structure, deposited on the substrate by the male, called spermatophore. It is composed of two halves that are mirror images of each other, the hemispermatophores. Spermatophores and hemispermatophores come in a great variety of shapes and structures and provide informative, reliable characters for systematics, at diverse taxonomic levels. However, because they are not easily obtained and because most previous authors did not compare them across the different families, there are thus far no satisfying hypothesis of homology and therefore no consensus nomenclature for those structures in the order Scorpiones. For my Master thesis, I proposed to review the extant literature on scorpions spermatophores and hemispermatophores. I illustrated scorpion taxa for those structures, with emphasis on the superfamily Scorpionoidea, in which they happen to be the more complex. I also explored structural homologies among the order and proposed a revised nomenclature for scorpions spermatophores and hemispermatophores. Additionally, I used a maximum parsimony reconstruction of their evolution by mapping characters on the extant phylogeny, which allowed me to retrieve synapomorphies for taxa of different phylogenetic levels.

Anahita Aebli

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Recent assembly of the Madagascan biota by replicated adaptive radiation: Case studies in Legumes

Despite the fact that Madagascar has been an island for more than 80Myr, there is evidence to suggest that recent adaptive radiations, akin to those on younger oceanic islands, have played a prominent role in the evolutionary diversification of the Madagascan flora. To test this idea, we investigated geotemporal trajectories of diversification in Madagascan mimosoid legumes via a comparative study of two species-rich Madagascan clades, the informal Dichrostachys group and Mimosa. Robust and densely sampled phylogenies for these two clades were reconstructed using genome-wide RADseq data. Species occurrence data were used to assess whether these globally niche-conserved dry-adapted lineages have been able to shift into other biomes within Madagascar as well as their modes of speciation, based on geographic and ecological data to test for a signal of allopatry using sister species comparisons. For both study groups, contemporaneous late Miocene colonization of Madagasacar followed by an early burst of diversification were inferred.

Regular talk

Achim Reisdorf

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The Myth: Can Carcasses Explode?

In the palaeontological and archaeological literature of the past almost four decades, we encounter a non-uniformitarian taphonomic scenario not recognized by veterinary and human medicine, that of the "exploding carcass", an explosive bursting of a body in an advanced state of decomposition (postulated for a great taxonomic variety of vertebrates). We are convinced that the hypothesis of subaquatic carcass explosion is not tenable: The maximal values of intra-abdominal pressure measured on recent vertebrates filled with putrefaction gases is lower by several orders of magnitude than the hydrostatic pressures that according to bathymetric calculations were assumed to have prevailed at the depositional sites of the fossils (e.g., fossil sites at Holzmaden, Messel, Solnhofen, and Monte San Giorgio). In the calculated bathymetries of the depositional sites in question, the main components of the putrefaction gases (CO2, N2, O2 [sic!]) would be dissolved in the bodily fluids and putrefaction fluids of the carcass. The potential transport mechanisms for skeletal elements in low-energy and life-hostile aquatic depositional environments are: bottom currents (induced, e.g., by storms or internal waves); turbidites; disarticulation and gravitational settling within an intact yet putrefaction-fluid-filled body cavity; current-induced transport by the discharge of putrefaction fluids from an ruptured integument.

Manuel Schweizer

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Strix owls in the Middle East: un- and re-discovered

Genetic and morphological analyses revealed that the type specimen of Hume's Owl Strix butleri, the geographical provenance of which is open to doubt but was supposed to be in Southern Pakistan, differs significantly from all other specimens from the Middle East previously ascribed to this species. Despite the absence of vocal data definitively linked to the same population as the type specimen, we considered that two species-level taxa were involved, principally because the degree of molecular differentiation is close to that seen in other taxa of Strix traditionally recognised as species. We consequently described other populations heretofore ascribed to S. butleri as a new species. Partially complicating this otherwise straightforward issue was the recent description of the Omani Owl S. omanensis from northern Oman based solely on photographs and sound-recordings. However, we considered it as likely that omanensis is a synonym of butleri. A recent study by the original authors of *S. omanensis* revealed that a bird from the type locality of the latter is genetically identical to the type of S. butleri and that omanensis is indeed a synonym of butleri.