phylogenomic studies strongly suggest that many of the traditional higher taxa (order to genus) are poly- or paraphyletic. Our new morphological approach showed that many of the characters traditionally used to delimit and organize ophiuroid taxa are not suitable for phylogenetic analyses because of previously unrecognized homeoplasies. These are often caused by paedomorphosis, a factor that was until recently hardly studied in ophiuroids. We also discovered many new characters that had never been considered before. This was achieved by large scale SEM examination of skeletal elements, of both recent and extinct species. The discovery of new characters and the identification of key structures unlock the fossil record which consists mainly of disassociated skeletal elements. The inclusion of fossils proved crucial for the analysis. The resulting tree, constructed by Bayesian inference, supports the phylogenomic analysis. The advantages of morphology are 1. support of clades with phenotypic data, 2. providing identification tools for non-specialists, 3. inclusion of fossil data, vital for filling in gaps in a group with long history. Future plans include the use of x-ray micro-ct, geometric morphometrics, and the application of more advanced probabilistic models of morphological evolution.

11.30 – 12.00
Keynote:
Lars Vogt[1]:
Morphology goes digital: How semantic techniques are about to revolutionize morphology
[1]University of Bonn.

High-throughput technologies enable us to produce more data than we could manage. Because in many cases adequately analyzing and interpreting these data require the collection of relevant metadata, the amount of information that has to be recorded and subsequently managed is even larger. As a consequence, new technologies and applications for knowledge management have been developed, all of which considerably changed the way we do research, ultimately leading to what we call eScience today. Storing and making data openly accessible has become an established standard in many scientific communities and is required by many funding agencies as well. By now, many communities have their own data repositories and developed new data and metadata standards that enable their data to be represented in a semantically transparent and computer-parsable form, both of which are necessary prerequisites for easy retrievability of data and effective data mining and data exploration.   How is morphology doing in eScience, what could its role be, and what challenges must it face? I will argue that especially bio-ontologies, which take a central role in the newly emerging technologies and applications for knowledge management, have the potential to solve some of morphology's basic conceptual problems and help open morphology to other scientific communities. I will start with some simple examples of applications of bio-ontologies that already exist today, before I will briefly talk about some ongoing projects that utilize bio-ontologies and knowledge management techniques in the field of morphology and taxonomy. Then I will introduce the concept of instance anatomy and argue that with the application of semantic techniques, instance anatomies, together with a semantic machinery, have the potential to provide a framework for measuring and quantifying morphological similarity. This would have far-reaching implications not only in terms of developing new applications and morphological analytical approaches, but also for the theoretical foundations of morphology. I will discuss some of these implications, involving the idea of comparative homology, semi-automatic identification of morphological structures, dynamic multi-entry keys, detection of character dependencies and a new approach for numerical tree inference in phylogenetics. Finally, I will briefly report from an ongoing project in which we develop a new module for Morph·D·Base with which instance anatomies can be entered, documented and stored.

Posters:

Alexander Ordynets[1], David Scherf[1], Felix Pansegrau[1], Jonathan Denecke[1], Karl-Henrik Larsson[2], Ewald Langer[1]**:**
Morphology complements molecular data for the delimitation of species in peculiar fungal genus (Subulicystidium, Agaricomycetes, Basidiomycota).
[1] Department of Ecology, FB 10 Mathematics and Natural Sciences, University of Kassel, Heinrich-Plett-Str. 40, 34132 Kassel, Germany.; [2] Natural History Museum, University of Oslo, P.O. Box 1172 Blindern, 0318 Oslo, Norway.

Molecular information plays an increasingly big role in the identification of fungi. The internal transcribed spacer (ITS) of the nuclear ribosomal DNA is the first choice for identification and phylogenetic inferences in fungi since more than two decades. It has become the official DNA barcode for fungi after showing best performance on a large spectrum of fungal lineages. Nevertheless, cases when ITS sequences from different species are highly similar or identical have also been reported. In such cases species borders must be evaluated using additional criteria.

Generally, for morphology-based fungal taxonomy, the features of the disseminated propagules, the spores, is of highest priority among phenotypic characters. The value of the spore morphology is especially high in groups that possess few macroscopical characters, such as corticioid fungi, i.e. Agaricomycetes with effused fruiting bodies. The genus Subulicystidium has been largely neglected in taxonomical and molecular studies during the last decades. We studied 56 collections of Subulicystidium from Paleo- and Neotropics. After morphological examination and comparison with the relevant literature, we assigned our collections to ten provisionally new species and four known species. About 3000 spores were measured from the set of specimens, and parameters of