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**DEPARTMENTAL SEMINAR
INTEGRATIVE ZOOLOGY
Summer Term 2017**

Programme and Abstracts

Tuesdays, 10-11:30 hrs

SR 3, UZA1, Althanstraße 14, 1090 Wien



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March 14: Christoph Winter

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"We want the world and we want it now!" Flipped Classroom an der Universität Wien - ein hochschuldidaktisches Konzept für zoologische Bestimmungsübungen

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A flipped- or inverted classroom is a new pedagogical method, which removes lectures from the classroom using asynchronous instructional videos. Hence it is about providing time to emphasize active learning and teaching approaches in class, such as collaborative, cooperative or problem-based learning. The purpose of this diploma thesis in Unterrichtsfach Biologie & Umweltkunde is to compare the efficiency of inverted classroom methods with traditional teaching. The study was conducted in two different animal determination courses. The Inverted Classroom Model (ICM) was applied in summer term 2016 and the Inverted Classroom Mastery Model (ICMM) was implemented in winter term 2016/2017. The ICMM is based on mastery learning. Students have to complete online tests to demonstrate mastery of the delivered content. Overall performance was measured using proficiency tests. The information about students' attitudes was gathered via surveys. The ICMM showed best performance, followed by the traditional classroom, whereas the ICM had worst results. These findings suggest that a flipped classroom had positive effects on students performance – as long as mastery learning is applied and as long as the learning process is constantly monitored and supported by trained lecturers.

Cannibalism in female *Allobates femoralis*

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When adult animals are confronted with unrelated young there are three options how they may react: adoption, ignoring, or killing. Adoption could decrease fitness, for example when a bird adopts and feeds a Cuckoo chick. Adoption could also increase fitness in species where females prefer males that already guard another clutch of eggs, as it is the case in many fishes. Killing unrelated young may increase individual fitness relative to others. This behavior is reported in several group living mammals like lions. By killing unrelated young, males may obtain enhanced mating opportunities, increased social status and/or reduce resource competition for their own offspring. By eating unrelated young they can even gain nutrients. Therefore, selective cannibalism of unrelated offspring may lead to significant gain in individual fitness. In the Neotropical poison frog *Allobates femoralis* males are highly territorial and terrestrial clutches are laid inside male territories. After hatching males transport tadpoles to widely dispersed water bodies. Previous experiments have shown that male frogs adopt any clutch inside their own territory, but cannibalize clutches when taking over a new territory, thereby reducing risks and costs of misdirected care. Cannibalistic behavior has previously been observed in other dendrobatid species mainly in females – in both wild and lab. For *A. femoralis* such information was so far absent. In the present study we investigated cannibalism of female *A. femoralis*, and tested under which conditions females prey on unrelated tadpoles under laboratory conditions. The varied parameters were the presence of a male, presence of an own clutch, and the spatial location of the female.

Results show that cannibalism by females was highest when there was no male and no own clutch present. Both the presence of a male and the production of an own clutch reduced cannibalism, indicating that both male presence at a clutch and also hormonal changes due to ovulation may inhibit cannibalistic behavior in the females. These findings are of particular interest when discussing possible adaptive benefits of male territoriality and the evolution of paternal care.

Perils at lunch: Mortality during feeding in macrostomatan snakes and other ectotherm stories

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Snakes are able to immobilize, ingest, transport, and swallow prey of relatively large size as well as dangerous items such as other predators, hard-biting, spiny, or toxic prey. Various incidents have been reported of snakes failing to complete the prey consumption process and being injured or killed during different phases of feeding. Here we provide the first extensive review of such incidents, including 45 publications describing over 68 mortality cases caused by ingestion or attempted consumption of injurious prey. We also report 12 previously unpublished cases from the USA and Bulgaria, including mortality of five juvenile piscivorous snakes (*Natrix tessellata*) from one location. Overall, we identified species representing at least 6 families and 29 genera. We discuss different feeding

scenarios that can lead to negative or even fatal impacts of prey on predatory snakes, and we classify such incidents into four major categories. We discuss a special case of the highly toxic and invasive Cane toad (*Rhinella marina*) in Australia and other locations in which it has been introduced. We perform a meta-analysis of the characteristics of the accumulated data in an attempt to elucidate overarching causes that led to the snakes' mortality. We conclude the review with a set of general conclusions and propose ideas for further research.

A bioinformatician walks into a molecular biology lab

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The molecular laboratory is a daunting place for bioinformaticians: PCR workstations, thermal cyclers, micro tubes, centrifuges, wide range of pipettes, and some nasty solutions that could kill a man thousand times. Recently, I abandoned the safe Viennese Linux space present in my life, and ventured myself into the wild environment of the molecular lab. In this talk, I would like to share my experiences on the molecular workbench with anyone interested, and emphasize how important this enterprise was in my ongoing formation as a scientist.

The polyclad flatworm perspective of spiral quartet cleavage

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The Lophotrochozoans (or Spiralian) are an evolutionary interesting clade in which the majority of today's animal body plans is found. Despite their diverse appearance these mostly marine animals often share fundamental similarities such as free-swimming, planktonic larval stages and most iconically a stereotypic developmental pattern, commonly known as spiral cleavage. This striking similarity during the early development opens the door for comparative studies allowing us to better understand the evolution of these vastly different body plans found in the Lophotrochozoa. We focus on the comparative developmental biology of the marine flatworm *Maritigrella crozieri* by studying in detail its early development. We followed the development of *Maritigrella* from a fertilized egg into an advanced stage of the embryo consisting of hundreds of cells using 4d light-sheet microscopy. Based on our live-imaging data, we created a cell lineage of the early development, which contains information about the relative rate of blastomere divisions, as well as spindle position information during embryogenesis and were used for a comparison with other polyclad flatworms and spiralian taxa. Our results address some fundamental mechanisms of the spiral cleavage mode found in early cleavage of many Lophotrochozoans studied so far, namely equal versus unequal cleavers, the specification of the D-quadrant and the break from a radial into a bilateral symmetric embryo, initiated by micromere 4d that takes a key role in endomesoderm formation of many spiral cleaving embryos, including polyclad flatworms. Our study of the development of the polyclad flatworm *Maritigrella crozieri* could resolve conflicting evidence of the cleavage of the mesentoblast in

polyclad flatworms, provides a new insight into the fundamental mechanisms of the early spiral cleavage form a polyclad flatworm perspective and provides comparative data that show both distinct and shared patterns with other Lophotrochozoan members and bring both polyclad suborders, based on shared similarities into a close relationship.

Skeletogenesis and regeneration in the brittle star *Amphiura filiformis*

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One of the most pertinent questions in regenerative biology concerns the extent to which it re-capitulates embryonic development. We use the brittle star *Amphiura filiformis*, a member of the echinoderm phylum of marine invertebrate deuterostomes, as a model to compare skeletogenesis during adult regeneration and embryonic development. We first characterized the cellular and morphogenetic aspects of arm regeneration and skeletogenesis in this species. Next, we carried out a large-scale spatio-temporal expression analysis to characterize genes involved in adult arm regeneration. Finally we perturbed FGF signalling using the SU5402 inhibitor and found that this treatment interferes with skeleton formation during both embryonic development and adult regeneration of the brittle star. Consistently with this phenotype, a cohort of skeletogenic genes was specifically downregulated by SU5402 treatment both in the embryo and adult regenerating arm. In conclusion, we found vast similarities between skeleton development during regeneration and embryogenesis in terms of morphology and its underlying molecular network.

X-Ray Computed Tomography: a tool to quantify plant reproductive phenotypes

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The 3D shape of flowers has, until the advent of modern 3D dataset acquisition techniques, remained as elusive as it was thought to be crucially important for pollination. We present here patterns of 3D flower shape variation gained in the study of two systems: the sexually deceptive orchid *Ophrys* and the heterostylous *Primula*. In *Ophrys*, we show that floral shape is more tightly correlated to the shape of the male bee (pollinator) than it is to the shape of the female bee (object of mimicry). We show that the parts involved in pollen transfer belong to well-supported shape modules, both in the bee and the flower. In *Primula*, we present a novel, multidimensional approach to quantify and analyse heterostyly. The best-supported shape module for flowers of both morphs together involves the apex of the stamens and the corolla mouth, both of which restrict the access of pollinators to the floral tube in one morph. Taken together, our analyses of the modularity of flower shape, in two unrelated systems, challenge the established paradigm of a division of flowers into modules of “attraction” vs. “reproduction”, and support a division into a module of parts that are directly in contact with pollinators vs. a module of parts that are not. Our results emphasise the relevance of modularity in flower shape and provide new perspectives into a rapidly expanding field.

Out- of- School experience "Biology of alpine organisms": a concept for a week- long field excursion for secondary School"

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In cooperation with the Naturpark Kaunergrat a program and a handbook for a week-long fieldtrip for students of secondary school has been designed. It is a modular program which includes flora, fauna and ecological topics concerning the alpine region. There is no central- European habitat which displays the geological and ecological relations as well as high- altitude mountain. In the program the students get to know adaptations of animals and plants to the alpine environment and learn how species survive even in the nival zone. They learn about the characteristic species and typical plant communities of the high mountain region. In addition, the students get familiar with general ecological concepts. The method of enquiry- based learning is applied, so that the students are introduced in scientific research methods. They learn to use simple methods of collecting and evaluating data, such as measuring climate data measurements to understand the hypsometric changes, plant mapping by using advanced field guides, working with pit-fall traps for the epigaic species or using the transect methods to analyze the biodiversity in birds, butterflies and bumblebees. Working outside in the field and practicing scientific methods are memorable experiences and the learned contents have a higher significance for the students.

The handbook is provided for the employees of the Naturpark Kaunergrat and enables them to use different modules in an independent way and in different constellations.

Population genetics of groundwater copepod *Diacyclops cohabitatus*

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Diacyclops is one of the largest copepod taxa and occurs in a great variability of habitats around the world. Next to freshwater habitats like temporary pools and moss, several species inhabit alluvial groundwater. One of them, *Diacyclops cohabitatus*, is described from groundwater near Vienna, especially in the Lobau wetland. Although copepods are well studied, there is hardly anything known about their life below surface. Until now the distribution of *Diacyclops cohabitatus* in the groundwater near the Danube was never studied. It is not known if this species forms separate populations or if it is evenly distributed by underground water flows. *Diacyclops cohabitatus* was found in benthos of freshwater pools too. Since life in groundwater puts some constraints on organisms, it can be assumed that *Diacyclops cohabitatus* shows some adaptations. They might differ between populations from groundwater and from surface water bodies. To test those assumptions, samples are taken from groundwater and benthos at the riverside of the Danube and at the Lobau wetland. To see whether the individuals differ genetically, DNA sequences of the 18s and CO1 gene regions will be compared. A non destructive DNA extraction method is used to preserve the cuticle for further species determination. Additionally the morphology of the copepods will be studied under the microscope to detect any differences between individuals from groundwater and surface water. As a result this study might give some insight in the distribution of groundwater

populations of *Diacyclops cohabitatus* and their relationship with surface water.

Bacterial symbionts in aquatic colonial invertebrates: example of the phylum Bryozoa

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Many secondary metabolites isolated from invertebrates have been shown to be synthesized by mutualistic microorganisms living in association with the host. These symbiont-produced natural products play an important role in the survival of the host by either satisfying nutritional requirements or defending the host against pathogens, parasites, and predators. Else, the substances with biological activities produced by microbial symbionts are of particular interest as a possible source of new therapeutic agents for medicine, veterinary, agri- or aquaculture.

Bryozoans are aquatic colonial invertebrates–filter-feeders constituting an important part of bottom communities. As well as other sessile organisms they constantly face with the impact of foulers, both pro- and eukaryotes. During last decades a wide range of substances (depsipeptides, amides, isoprenoids, ethylenes, polyketides, etc.) with broad spectrum of possible biological activities, including antifouling, antimicrobial and antitumor activities, was isolated from the tissues of different bryozoan species. It is not much known, however, about their symbionts as well as their role in the life of the host. A seminar talk aims to make a general picture of these relationships based on the latest data obtained.

Hox and ParaHox gene expression in the zebra mussel, *Dreissena polymorpha*

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Mollusca constitutes the second most speciose animal group after Arthropoda. The great diversity of its representatives is reflected not only in species number, but, more importantly, in the wide range of morphological plasticity they exhibit. This plasticity of homologous structures (e.g., radula, shell, foot, neuromuscular systems) raises questions concerning the molecular basis that underlies morphological variation in molluscan representatives. Hox and ParaHox genes are commonly recognized as key players in establishing the anterior-posterior body axis of bilaterian animals. In many bilaterian animals, Hox genes show an orchestrated expression that is temporally and spatially correlated with the arrangement of the individual genes on the genome (collinear mode of expression). In mollusks, Hox genes show such a mode of expression in polyplacophorans, while in representatives of the conchiferan clades Gastropoda and Cephalopoda this collinearity has been lost, whereby the Hox genes most likely evolved lineage-specific novel functions. However, a broad comparison throughout the conchiferans is yet hampered by the lack of Hox expression data on crucial clades including Scaphopoda, Monoplacophora, and Bivalvia. To partially fill this gap and to contribute to the question concerning the putative role of Hox genes in molluscan body plan diversification, Hox gene expression will be analysed in the bivalve *Dreissena polymorpha*. To this end, an initial characterization of gene expression domains by in-situ hybridization will be performed for the expected 11 Hox and 3

ParaHox genes that are commonly known in mollusks. This will help to reconstruct scenarios of morphological evolution based on molluscan phylogeny and at the same time will provide insights into putative novel and conserved functions of Hox and ParaHox genes in this diverse lophotrochozoan phylum.

Shedding light on the evolution and maintenance of colour polymorphism in Black Sparrowhawks

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Animals often display striking variation with respect to their phenotype. Intraspecific and interspecific variation in body colour represents one of the most well studied forms of phenotypic variation. For decades evolutionary biologists have been fascinated by the mechanisms that maintain colour variation in species and traditional explanations for this diversity of colour in nature often invoke an interaction between selection for conspicuous signals and natural selection for crypsis. Colour polymorphic species have frequently been used to explore the evolutionary processes that lead to colour variation in species. Geographic variation in colour morph ratios also occurs frequently in polymorphic species and is often considered an ideal model system to examine the interplay of gene flow and local adaptation in populations. In this talk I will explore the role and maintenance of plumage colour polymorphism in a raptor, the Black Sparrowhawk (*Accipiter melanoleucus*) in South Africa.

Genomics and transcriptomics in the invasive Zebra mussel: insights in to molluscan genome architecture and regulatory evolution

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PostDoc

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Molluscs are a morphologically diverse and speciose phyla. Recent progress has begun to elucidate the developmental and genetic innovations that underpin these phenomena and with the increasing power of phylogenetic approaches, we are gaining an ever clearer understanding of the history of molluscan evolution. Despite these successes, the relationship between evolutionary innovation in molluscs and changes to the gene regulatory environment remain largely unexplored. In this talk I will discuss ideas about how we might investigate whether changes to genome architecture could have influenced gene regulation and evolution in molluscs. I will outline my work on building the genome and several transcriptomes of the invasive bivalve, the Zebra mussel *Dreissena polymorpha*, and I will present the wnt pathway as a specific example of how we will use these tools to investigate individual gene regulatory systems. This talk will provide an update of my work to date and will lay out a plan for future studies.

The eFLOWER initiative: A framework for understanding the evolution and diversification of extant and fossil flowers

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Flowers are central to the biology and evolution of angiosperms (flowering plants). eFLOWER focuses on the history of floral diversification through deep evolutionary time. A comprehensive understanding of global patterns of floral evolution has been prevented so far by the lack of an adequate morphological data set spanning all major angiosperm lineages. Using a new flexible and innovative approach, centered on a multi-user database (PROTEUS), we have built such a data set. Unlike most earlier studies of character evolution at the scale of angiosperms, we have recorded exemplar species instead of higher taxa such as genera or families. This approach allows for explicit reconstructions without assumptions about ancestral states or monophyly of supraspecific taxa, although we acknowledge that it also entails the risk of undersampling morphological variation. Importantly, the exemplar approach allows a direct match with the species sampled in molecular phylogenetic trees, providing the possibility to take branch lengths into account and to explore character evolution with probabilistic models. We report results from a data set of floral traits for 792 species representing all orders and 367 families (87%) of angiosperms, sampled from a recently published timetree calibrated with 136 fossil age constraints. Using this data set and tree, we reconstruct ancestral states for 27 key floral traits using parsimony, maximum likelihood, and Bayesian approaches. These results shed new light

on long-standing questions on floral evolution across angiosperms, with important implications for a wide range of disciplines including Evo-Devo, pollination biology, and paleobotany.

Feeding patterns and 3D-reconstruction of the keeled box turtle *Cuora mouhotii* (Gray 1862)

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Geoemydids, especially the genus *Cuora* with its 12 species, comprise aquatic, semiaquatic and terrestrial species. One of those terrestrial species is *Cuora mouhotii*. It is listed in the IUCN red list for threatened species, because of trade (pets, traditional chinese medicine) and destruction of its habitat. It occurs in south China up to central Vietnam and in north east India. Its habitats are subtropical broadleaf forests with a thick undergrowth where they can hide. The existing knowledge lacks information about its ecology in the wild. This study examines the feeding mechanism of terrestrial food ingestion and manipulation with hard (snail) and soft (fruit) food. Differences in the manipulation phase, because of the snail shell, are expected. Furthermore, the feeding patterns in water are examined. It is likely, that the secondarily terrestrial species is able to feed underwater with a form of suction feeding, carried out by the hyoid complex. Additionally, a micro CT-scan of the head region will be scanned by the Vetmed, which is reconstructed afterwards by using the program AMIRA. The data will be compared with other *Cuora* species and could give conclusions if the head shows any adaptations for manipulating hard food. For the investigation, the Zoo

Schönbrunn kindly provides 4 individuals for highspeed kinematography. The animal for the micro CT-scan is provided by the Naturhistorische Museum.

Breeding Carnolian bees on different comb cell sizes and analyzing the effect of the different cell sizes on the *Varroa* infestation rates. (Small breeding cells in honeybee - An experimental approach)

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Worldwide on *Apis mellifera* the “new” ectoparasite *Varroa destructor* is considered as a major cause of bee colony-looses.

In 1997, after the arrival of the *Varroa* mite (*Varroa destructor* Anderson & Trueman, 2000) in Arizona, Ed and Dee Lusby observed a better survival rate of their colonies on honey combs with a small cell size (5,08 mm). Nowadays the western honeybees are commonly kept at the cell size 5,4mm to 5,6 mm. In this study, I analyzed whether small cells (4,9 mm) have a negative effect on the population development of varroa mite compared to the standard cell size (5,5 mm).

First I had to search in my Carnolian (*Apis mellifera carnica* Pollmann, 1879) closed breeding population for colonies who could built small cells. Then I created 2 groups of test colonies consisting of young sister queens and 1,5 kg *Varroa*-infested bees on small cell size (4,9 mm) and large cell size (5,5 mm) respectively. To prevent any contamination with residues from miticides new hives and organic-certified foundation were used.

The bottom boards were equipped with mesh-protected drawers to collect the natural mite mortality.

The data of 3 years, analyzing 494 test-colonies, have shown a positive result: the colonies on small cells had a slower *Varroa*-mite population development.

For 2 additional years the *Varroa* reproduction parameters were determined.

Four lines with 80 new colonies on large cells and small cells with small sized bees were created. From each colony a comb with older sealed brood was analyzed for reproductive success of *Varroa*.

The following year 2 lines with small cells queens and bees were used for 20 new test-colonies. Each fitted with 4 small cell and 4 large cell drawn combs alternately positioned. The infested brood cells were analyzed again.

The collected data allowed to calculate the VSH parameter (=Varroa Sensitive Hygienic) as the quotient of brood cells with a non-reproductive varroa per total number of infested brood-cells.

Comparing both cell sizes in one colony has shown that there is a higher level of VSH for infested brood-cells on small cells in the selected Carnolian bee population.

The heritable traits “ability to construct small cell size comb” plus “VSH” results in a reduced population growth of *Varroa* in those colonies where worker bees when both traits are present. Smaller cell size combs in combination with breeding for the ‘right genetics’ (cell size and VSH) can be one part of an integrated sustainable treatment concept for *Varroa* control.

It remains unclear what made the VSH-activity on small cell size combs more intensive as compared to the large cell size infested cells in the same colony.

New ultrastructural data on crisiid Cyclostomata

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Our research is focused on ultrastructural details of the sexual reproduction, in particular, embryonic incubation in marine bryozoans. The central group is Cyclostomata, one of the most ancient bryozoan taxa, that is still diverse and abundant in modern seas. Unique combination of their reproductive traits includes intracoelomic incubation of embryos (viviparity), matrotrophic nourishment (via placentation) and polyembryony (multiple clonal development of embryos from a single fertilized egg). Only seven papers have been published on this topic, however, the most recent one being 90 years old. All of them were based on the light-microscopic observations often resulting in unclear, dubious or contradictory statements.

We studied two common boreal species, *Crisia eburnea* and *Crisiella producta* collected at the White Sea. Detailed study of gonozooidal anatomy and embryonic incubation accompanied by matrotrophy provided new interesting data on the embryo and placental ultrastructure. There are still a lot of questions but the information obtained adds greatly to our understanding of cyclostome zooidal structure, functioning of the placental analogue and embryonic development.

These new morphological data are also necessary in the light of current revision of cyclostome phylogeny since many skeletal morphological characters were shown to be homoplasious. Further research will include representatives of some other families. We hope that some of the revealed characters will prove to be phylogenetically significant.

The anatomy of the feeding apparatus of *Calyptocephalella gayi*

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In continuation of Verena Wiesinger's diploma thesis, in which she investigated the feeding mechanism of *Calyptocephalella gayi* through highspeed video analysis, now the focus will be on anatomy of this frog. Depending on their habitat, frogs use different mechanisms to capture their prey. Aquatic feeding mechanisms include suction feeding, ram feeding, jaw prehension and forearm scooping, whereas in a terrestrial environment jaw prehension or three different ways of lingual prehension (mechanical pulling, inertial elongation, hydrostatic elongation) are employed. *Calyptocephalella gayi* is an endangered aquatic frog species from Chile; nevertheless, Wiesinger found that it can also successfully feed on land. While feeding underwater, *Calyptocephalella gayi* uses suction feeding and its hands to prevent its prey from escaping again. When feeding on land, it uses jaw prehension or mechanical pulling with varying degrees of tongue activity. Considering its aquatic lifestyle, it seems somewhat unexpected that *Calyptocephalella gayi* is also well equipped for terrestrial feeding. Therefore, this thesis will now examine the anatomy of its feeding apparatus and compare it to that of *Leptodactylus pentadactylus* – a fully terrestrial species from northern South America that feeds by using lingual prehension; mechanical pulling to be exact. The two species are rather closely related, as they both belong to the family of Leptodactylidae. In order to compare the anatomy of their tongues, hyoid apparatus and jaws, their muscles and the hyoid will be reconstructed from micro CT-scans using AMIRA.

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