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**DEPARTMENTAL SEMINAR
INTEGRATIVE ZOOLOGY
Summer Term 2019**

Programme and Abstracts

Tuesdays, 10-11:30 hrs

SR 3, UZA1, Althanstraße 14, 1090 Wien



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Programme

March 19: Rich Mooi

Deep time and deep seas: Enigmatic echinoderms and what bizarre animals can tell us about life on Earth (p.4)

March 26: Paul Wolf

Phylogeny of the Eurasian Jay *Garrulus glandarius* based on mitochondrial marker sequences (p.5)

Margarita Hartlieb

Does yawn duration predicts neurological measures in birds and mammals? (p.6)

April 2: Torben Stemme

Neuroanatomy of Chelicerata – current progress and future directions (p.7)

April 9: Peter Zulka

How to quantify biodiversity impacts? Need for a unified measure and universally applicable protocol (p.8)

April 30: Nikolaus Helmer

Molecular Phylogenetics of Scaphopoda (p.10)

May 7: Kenneth Kuba

Transport and foraging mechanism in social wasps (Vespidae) (p.11)

May 14: Kostya Kornev

What happens with the blood when the insect gets wounded (p.12)

Martina Grabner

Influence of androgens on the gestural signals of the foot-flagging frogs *Staurois parvus* (p.13)

- May 21: Stefan Fischer**
Three-dimensional investigation of miniaturized insect visual systems (p.13)
- May 28: Jakob Prömer**
The nervous system of cheilostome bryozoans (p.14)
- June 4: Julian Bibermaier**
The embryonic development of the fresh-water bryozoan *Plumatella casmiana* (p.15)
- Attila Sachslehner**
Expression of mesodermal genes in the polyplacophoran mollusc *Acanthochitona crinite* (p.16)
- Stephan Schulreich**
Mesoderm & muscle formation in the quagga mussel, *Dreissena rostriformis* (p.17)
- Margret Eckhard**
A characterisation of the defense secretion of centipedes (p.18)
- June 18: Simone Jaritz:**
Biologische Phänomene in den Marchauen - Freilanddidaktische Informationstafeln (p.19)

Deep time and deep seas: Enigmatic echinoderms and what bizarre animals can tell us about life on Earth

Rich Mooi

*Curator of Invertebrate Zoology & Geology
California Academy of Sciences, San Francisco, USA*

Dr. Rich Mooi is Curator of Invertebrate Zoology & Geology at the California Academy of Sciences, San Francisco. He studies the origin and evolution of echinoderms (starfish, sea urchins, sea lilies, and related forms), and will provide a tour of their odd body forms and habits, focusing on enigmatic fossils that go back over half a billion years. How did echinoderms come by their 5-part, radial strangeness, and how do they exploit such traits to inhabit nearly every oceanic biome, including the greatest depths of the sea? The answers lie in understanding unique developmental pathways, as well as the unusual interactions these animals have had with their environment over their long geologic history. These include fossils of animals that would not look out of place in any Star Wars pub scene.



Phylogeny of the genus *Garrulus* (Corvidae, Aves) based on mitochondrial marker sequences

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MSc Thesis

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The genus *Garrulus* (Brisson, 1760) belonging to the family Corvidae is by most authorities considered to comprise three species. The best-known member of the genus, the Eurasian Jay *Garrulus glandarius* (Linnaeus, 1758) exhibits a complex geographic pattern of morphological variation over its wide old-world distribution area. The major checklists currently recognise between 34 and 40 different subspecies that are variably arranged in five to eight groups. Some of these groups have even been proposed to be treated as full species. In the present study the phylogeny of the genus was investigated based on tissue samples as well as foot pad samples from museum specimens of 91 birds, covering the proposed eight subspecies groups of the *Garrulus glandarius* complex, as well as the two other species in the genus, *Garrulus lanceolatus* and *Garrulus lidthi*. Phylogenetic trees constructed with 1300 bp sequences of the mitochondrial control region revealed a division into at least four main lineages within the *G. glandarius* complex: (1) “*japonicus* group”, (2) “*brandtii* group”, a (3) Southeast Asian clade and a (4) western clade. The two last lineages turned out to be further subdivided into subclades mostly corresponding to the morphologically determined subspecies groups. Additionally, two insular subspecies *taivanus* from Taiwan and *glaszneri* from Cyprus proved to be very distinct mitochondrial lineages. Furthermore, the results provide indication for hybridisation between representatives of subspecies groups.

Does yawn duration predicts neurological measures in birds and mammals?

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Yawning is a basic mechanism, ubiquitous among vertebrate species. Yet, its function remains a hotly debated topic. It has been suggested that yawning serves a cooling function for the brain. In line with that hypothesis, previous studies on mammals found a positive correlation of interspecific variation in the mean yawn duration and the neural anatomy, with yawn duration indeed being a robust predictor of brain weight and cortical neuron number. Here, we aim to investigate whether these results can be generalized across animal classes, and we enquired the yawn duration of different avian, as well as more mammal species. Thus, we coded over 600 bird yawns from more than 200 individuals across 40 bird species, as well as an additional 200 yawns of 114 individuals of 13 mammal species (and more to come) and linked the duration of this action pattern to previously published brain measures of these species. Preliminary analyses on only a subset of the bird yawns showed that the mean yawn duration of also birds is a significant positive predictor of total neuron number, and that, in contrast, there was no significant relationship between yawn duration and body weight. So far, our results thus suggest further support for the brain-cooling hypothesis, as the number of neurons seems directly proportional to the yawn duration necessary for cooling the brain, and that therefore, yawn duration can be used as a marker of interspecific differences in brain measures across vertebrates.

Neuroanatomy of Chelicerata – current progress and future directions

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Within the last two decades, morphological investigations have regained considerable attention within the framework of evo-devo, especially concerning phylogenetic relationships of Arthropoda. Often contradicting results based on traditional external morphology and modern sequence information ask for independent data to evaluate these hypotheses and to supplement our knowledge of arthropod evolution. One promising approach, fuelled by the rapid methodological advancements of imaging techniques, deals with the anatomy and development of the nervous system. Research has been focussed on insect and crustacean species, whereas myriapods and chelicerates have largely been ignored. Information on these taxa is thus of particular interest to assess existing neuroanatomical data and identify apomorphic versus plesiomorphic characters as well as presumptive evolutionary transformations. In this talk, I will focus on two aspects, a) the morphology of individually identifiable neurons and b) the neuroanatomical features of chemosensory organs in Chelicerata.

The distribution and projection patterns of individually identifiable neurons has gained considerable attention in the context of arthropod neurophylogeny. Especially serotonin- and histamine-immunoreactive neurons are well suited for phylogenetic comparisons because of small cell numbers and large amounts of data available for several arthropod taxa. Data on chelicerates are nonetheless extremely limited, but crucial for meaningful conclusions.

Analyses of chemosensory processing in Chelicerata are scarce, not least since Chelicerata do not possess antennae, as do Mandibulata, but evolved dedicated chemosensory organs in several other body regions. The conspicuous pectines in scorpions as well as the raquet organs of camel spiders are prominent examples here. Comparisons of these two structures and with the antennae of Mandibulata show widespread similarities as well as conspicuous differences. Thus, a systematic comparative approach of

neuroanatomical characters can reveal functional prerequisites for chemosensory systems on the one hand and taxon-specific adaptations on the other.

The presentation will provide insights into the evolutionary morphology of individually identifiable neurons and chemosensory organs in Chelicerata with detailed comparisons to Mandibulata, and it will address future directions in this field of research.

How to quantify biodiversity impacts? Need for a unified measure and universally applicable protocol

Klaus Peter Zulka

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Life cycle assessment (LCA) of products – accounting for the environmental effects of products and processes from cradle to grave – has developed into indispensable tool in the transition towards a sustainable lifestyle and planetary wellbeing. However, parameter evaluation has often been limited to greenhouse gas emissions and energy, whereas biodiversity effects are typically excluded. This may lead to perverse incentives and exacerbation of the biodiversity crisis.

As LCA typically deals with inputs and outputs, accounting for biodiversity effects within the framework has shown to be notoriously difficult.

At EAA, a new and universally applicable method for biodiversity accounting in LCAs has been developed, mainly based on zoological species information. The biodiversity effect measure BE quantifies the change in extinction risk of all species in an assemblage as a result of a land use change or some other kind of external influence impinging on the species, summed across the assemblage. It consists of four components, impact overlap IO_i , population impact PI_i , national and international Red List risk categories ($PE_{nat, i}$; $PE_{int, i}$), and a concentration measure C_i . Impact overlap IO_i quantifies the spatial relationship between impact area and species range. Population impact PI_i specifies the degree and direction of the land use change consequences for a population of the species i within

the impact area. The use of national and international Red List categories is based on the consideration that extinction risk change owing to land use change intervention depends on extinction risk in the first place – the first derivative of an exponential function is also an exponential function. Finally, the effect on a particular species depends on the concentration of populations C_i in the impact area; the more a species is restricted to the impact habitat and impact area, the higher the quantitative weight of the species within the assemblage. The measure BE, accounting for biodiversity effects in a standardized area, is then obtained by summing up the values obtained for single species. To obtain universally comparable values, the quantification method is currently restricted to mammals, birds, amphibians and reptiles, organism groups for which Red List categorizations are largely complete and ecological information is in most cases easily accessible.

The method can be applied both to subtle local changes in land use intensity and to large-scale or global product comparisons, as three application examples show. The first example quantifies the biodiversity effects of setting aside field margins as flower strips in Central Europe. The second example compares the biodiversity effects of conventionally grown potatoes and potatoes from organic agriculture. The third example quantifies the biodiversity effects of soybeans cultivated in Austria with those cultivated in Brazil based on several land use change scenarios.

Reduction of the equations developed for the most general case – biodiversity accounting in LCAs – makes the method applicable to special cases, for example biodiversity accounting in monitoring or Environmental Impact Assessment.

Molecular Phylogenetics of Scaphopoda

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MSc Student

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Technical Advisor: Christian Baranyi

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Despite the global marine distribution, the taxon of Scaphopoda is notoriously understudied. The evolutionary position of this infaunal group within the molluscs is as disputed as the internal systematics. Due to the uncertain assignment of earlier fossils to the Scaphopoda, this taxon is listed as the youngest major group of molluscs (~360 mya). The greatest diversity of scaphopod species is recorded from depths below 200 m and tropical shallow water habitats. Diagnoses of the 576 recent species are mostly based on shell characters. Only in some cases the description is supplemented by radula features. Scaphopod systematics was investigated in several morphological studies based on softbody characters. Although the major subtaxa are well defined, the validity of many family and genus-rank taxa remains unresolved. Two molecular phylogenetic studies suffered from limited taxon sampling and agreed with the morphological studies on a robust support for the subtaxa Dentaliida and Gadilida only. The present study is mostly based on Indo-Pacific dentaliid specimens from the National Museum of Natural History, Paris. Nuclear and mitochondrial markers (18S and 28S rDNA, ITS, 16S rDNA, CO1) are used to add new taxa to molecular phylogenetic analyses. We hope to improve our knowledge on the phylogenetic signal of these markers and to test the monophyly of some of the doubtful genus-level taxa and the questionable shell characters they are based on.

Feeding, foraging and food transport in social wasps (Vespidae)

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Vespiniae and Polistinae are sister taxa within the Vespidae which both are eusocial. They construct paper nests, exploit several forms of carbohydrate sources, hunt and scavenge actively to provision the colony offspring with meat. Before feeding meat, social wasps malaxate it to form a small meatball. However previous studies are discordant if this is performed inside or outside of the nest. In the late thirties the gnathal pouch, a hypopharyngeal invagination close to the mouth opening, was described in Vespiniae. This organ is described to store dirt, dust and detritus. However first preliminary tests showed possible other materials in the gnathal pouch. The oral pecten, a row of comb like setae, right in front of the mouth opening leads solid particles into the gnathal pouch. The morphology and function of the whole organ system is not completely understood, as for example the mechanism to empty it could not be found. Furthermore no behaviour related to this organ in social wasps can be found in previous studies. This study focuses on the morphology and function of the gnathal pouch using LM, SEM and μ CT data. These data will be analysed comparatively between several genera of central european Vespiniae and Polisitinae. Additional aims are to assign behaviour to this organ and to test if the malaxation site is depending on the size of prey.

What happens with the blood when the insect gets wounded

Kostya Kornev

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The insect blood, hemolymph, plays a vital role in processes that range in scale from macroscopic – such as primary wound healing – to microscopic – such as flowing through vessels to deliver nutrients – to nanoscopic – such as fending off bacteria and viruses. When studying insect biomechanics, it is therefore crucial to understand hemolymph mechanical properties at different scales. Hemolymph is a suspension of adherent and non-adherent micron-sized cells, hemocytes, in plasma. Even though at a macro-scale the suspension seems to behave as a single-phase liquid, it has been a long standing challenge to measure its mechanical properties at the micro and nano-scales where the effects of hemocytes are crucial.

Here, we present the findings of a multi-scale study of hemolymph using a combination of traditional and novel characterization techniques. To probe micro- and nano-rheology, we suspend magnetic micro- and nano-wires, respectively, in a droplet of hemolymph in a controlled inert atmosphere and perform Magnetic Rotational Spectroscopy. We find that as we go down in scale, the effect of hemocytes on rheology of hemolymph becomes increasingly dominant and drastically changes the mechanical response of the hemolymph.

BIO: Dr. Kostya Kornev is Dean's Distinguished Professor in the Department of Materials Science & Engineering at Clemson University, SC. His Micro and Nanofluidics Systems Lab is actively working on fiber-based nanofluidics and insect biomechanics. Dr. Kornev graduated with a PhD degree in Physics & Mathematics from Kazan State University (KSU) in Russia in 1988. In 2000, he joined the Textile Research Institute in Princeton, NJ and then the faculty at Clemson University in 2006. He is recipient of the 2013 Award for the Outstanding Faculty Achievements in Science of the College of Engineering & Science of Clemson University, 2017 Theodore Von Karman Fellowship of RWTH Aachen University in Germany, and 2018 Founder's Award of the Fiber Society.

Influence of androgens on the gestural signals of the foot-flagging frogs *Staurois parvus*

Influence of androgens on the gestural signals of the foot-flagging frogs *Staurois parvus*

Martina Grabner

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The project aims to test how the actions of androgenic hormones modify visual foot-flagging signals in male *Staurois parvus*. Prior data show that the emergence of foot flagging – a signal that is produced by conspicuously waving the hind limb – is marked by a 10-fold increase in androgen receptors (ARs) within the skeletal muscles that control this movement, compared to frogs that do not foot flag. Testosterone increases the frequency of foot-flags. We hypothesize that activation of AR also influences the kinematics of the signal and increased Testosterone during advertising likely enables precise control of foot flagging. We present and discuss results of experimental tests and slow-motion analysis of foot-flagging displays.

Three-dimensional investigation of miniaturized insect visual systems

Stefan Fischer

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In spite of the numerous studies on insect compound eyes within the last 100 years, the number of investigations specifically dealing with the eyes of species of smallest body size is scarce. Based on theoretical optical examinations and considerations about spatial constraints, it had been predicted that an unlimited reduction in the size of a compound eye is not

possible; a suggestion that begged the question as to how tiniest insects might then deal with the postulated restrictions. The seminar talk will present a series of morphological studies (2D & 3D) on compound eyes and the visual neuropils of tiniest insects of body sizes down to 0.2 - 0.5 mm, discussing adaptations to functional and spatial constraints, as well as limits of miniaturization.

The nervous system of cheilostome bryozoans

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Bryozoans are sessile aquatic suspension feeders in mainly marine, but also freshwater habitats. They form colonies composed of numerous individuals called zooids. The majority of extant species is present in the taxon Cheilostomata that, among other characters, have a calcified body wall. The nervous system of this clade is very little investigated, particularly with more recent morphological tools. Consequently, the main focus of this study lies in the analysis and characterization of the cheilostome nervous system employing a range of complementary traditional and modern techniques. In order to gain a clearer reconstruction of the ground pattern of the cheilostome nervous system, a range of different species of various clades are studied. First results show that the brain/cerebral ganglion is located at the base of the lophophore, wherefrom neurite bundles innervate the tentacle crown and peripheral areas such as the digestive tract and towards the body wall via the tentacle sheath. Preliminary observations show that the cheilostome nervous system is similar to other myolaemate bryozoans, in particular ctenostome ones.

The embryonic development of the fresh-water bryozoan *Plumatella casmiana*

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Phylactolaemates are a small group of bryozoans occurring exclusively in freshwater. Little information is available on the reproduction, in particular its sexual reproduction. All examined taxa to date show embryos being brooded in internal embryo sacs. These form from an invagination of the body wall close to the ovary and where fertilized oocytes are transferred into. The only profound studies that examined phylactolaemate development was on a fredericellid and plumatellid, and date back to the 19th and beginning of the 20th century. Consequently, there are several gaps in our understanding of the developmental processes in this clade. The present study focuses on the embryonic development of *Plumatella casmiana* by analysing reproductive zooids and different developmental stages via sectioning methods and 3D-reconstruction. In sum, there are several unanswered questions the current study tries to address. These include how the oocyte is transferred to the embryo sac and how and when is it fertilised, how embryos develop and how are they nourished. Increase of embryonic size indicates that phylactolaemates are matrotrophic and are partly placental brooders. Distinct ultrastructural evidence of this nutrition is wanting, and the current study aims to analyse these placental-cells to prove that these provide nutrient supply to the embryo. This study is thus the first to reconstruct the complete embryonic development by more modern methods and the first to analyse ultrastructure of phylactolaemate reproduction.

Expression of mesodermal marker genes in the polyplacophoran mollusc *Acanthochitona crinita*

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The mesoderm is argued to be the youngest of the three germ-layers. It may either form by cells that immigrate from the blastopore margin into the blastocoel as in many protostomes or by detachment from the archenteron wall (in deuterostomes and some protostomes). Although its morphogenesis is well studied for numerous metazoans, the molecular components underlying this process remain largely unresolved. Gene expression studies in the mesoderm-lacking cnidarians showed that genes that contribute to mesoderm formation in bilaterians are expressed both in the cnidarian ectoderm and endoderm. This leads to the assumption that these genes were co-opted into mesoderm development in bilaterians. Mesodermal gene expression has yet to be studied in many protostomes, particularly in molluscs, where little is known about key genes involved in mesoderm formation. In our ongoing study, expression of common mesodermal marker genes belonging to the hairy and enhancer of split (HES) and Mox family are studied in the polyplacophoran mollusk *Acanthochitona crinita*. One copy of *AcMox* was found in the *A. crinita* transcriptome, while seven putative *AcHES* genes were found. HES genes are fast evolving genes, which may lead to many species-specific duplications. Our findings support the monophyly of HES genes but it remains unclear how the individual HES genes of different species are related to each other. *AcMox* groups well with orthologs of other metazoans. Based on comparative data of other lophotrochozoans, expression of *AcMox* is expected to start early in larval development. This is in accordance with *Mox* expression of other lophotrochozoans such as *Terebratalia transversa* (brachiopod), *Alitta virens* (annelid) or *Haliotis asinina* (gastropod). HES genes are involved in many developmental processes such as partitioning of morphological territories or neurogenesis. Expression patterns of genes of this family differ in various bilaterians, currently hampering a clear hypothesis concerning its functions during early molluscan development.

Mesoderm and muscle formation in the quagga mussel, *Dreissena rostriformis*

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Myogenesis involves modification, reduction and de novo formation of muscular tissue and is particularly dynamic in molluscs. Only few studies on myogenesis in bivalves using state-of-the-art methods such as fluorescence labelling and confocal microscopy are currently available, with the most detailed ones stemming from the scallop *Nodipecten nodosus* and the shipworm *Lyrodus pedicellatus*. The quagga mussel *Dreissena rostriformis* is a small, mytiliform freshwater mussel with an indirect life cycle that includes a trochophore and a veliger larva. *Dreissena rostriformis* is an invasive species in Europe and in the USA. Herein, we describe the dynamics of myogenesis and larval myoanatomy in the quagga mussel. The first visible F-actin positive cells are found in the gastrula and in the trochophore larva. In the early veliger larva there are two anterior adductors, a ventral larval retractor, a velum ring musculature and a dorsal and ventral velum retractor. Subsequent muscle development includes a median velum retractor and an accessory velum, foot and mantle retractors. A comparative analysis suggests that the ground pattern of bivalve larvae includes a velum ring, velum retractors, a ventral larval retractor and anterior adductors. Unfortunately, we have so far not been able to produce postmetamorphic quagga mussels in the lab, thus hampering reconstruction of the fate of larval muscles and emergence of the adult muscular bodyplan.

Very little is known about gene expression during mesoderm formation (the germ layer from which the musculature forms) in molluscs. Therefore, we investigate expression patterns of some well-known mesodermal marker genes (e.g., *Hes*, *myosin heavy chain*, *even skipped*, *brachyury*) during *Dreissena rostriformis* development. Preliminary results suggest that a *Hes* gene is expressed during early mesoderm formation at gastrulation. We found *myosin heavy chain* expression from the late gastrula until the veliger stage, where it is colocalized with developing muscle cells.

A characterisation of the defense secretion of centipedes

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Chemical adhesives are used by various organisms including bacteria as well as terrestrial and aquatic metazoans for surface attachment. These chemical adhesives are also used for prey capture or in a defensive strategy. One of the major features of these adhesives are that they have a short curing time, a strong bonding ability and they seem to be non-toxic and biodegradable. Chilopodes, which belong to the group of Myriapoda, are known for their hunting behavior. They capture their prey, like insects, spiders or even small mammals, by using highly lethal venoms. Beside this toxic predation strategy, some centipedes defend themselves through a fast secreting glue. In Geophilomorpha, this glue is produced in so-called sternal glands, which are located on the ventral surface of each sternite. It is not known whether there is a morphological difference in the gland cells between different species of this family. In addition it is not clear how the secretion is squeezed out, either by hydrostatic and/or muscular pressure. Earlier studies assumed that the animal prevents being glued to its own secretion by a glue-repellent which is produced by an epidermal gland that is located between the sternal glands. However, direct evidence for this hypothesis is still lacking.

The current project focuses on the characterization of three centipede species (*Henia vesuviana*, *Haplophilus subterraneus* and *Strigamia maritima*) with the aim to characterize the chemical properties of the glue components. This comparative study provides insights into the diversity of epithelial secretions in centipedes and thus elucidates the process of glue synthesis and secretion in this large arthropod taxon.

Biologische Phänomene in den Marchauen - Freilanddidaktische Informationstafeln

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In meiner Diplomarbeit beschäftige ich mich mit Phänomenen, die in den March-Auen vorkommen. Von den 30 ausgewählten Arten bzw. Phänomenen sind einige endemisch manche nicht, sie kommen aber aufgrund des speziellen Standortes dort sehr häufig vor oder sind nur noch dort zu finden. Einige von diesen Arten stehen bereits auf der Roten Liste. Die Arten sind für Exkursionen mit Schulklassen spannende Vorzeigeobjekte, für welche, im Rahmen dieser Arbeit, Informationstafeln entstehen. Sie dienen der Sensibilisierung von Schülerinnen und Schülern für Artenschutz und der Wissensaneignung.

Auf diesen Tafeln werden Lebenszyklus, Symbiosen und verschiedene ökologische Aspekte beschrieben. Sie sollen phänologische Stadien aufzeigen, die zum Exkursionszeitpunkt nicht ersichtlich sind und Besonderheiten der Species hervorheben. Die Schautafeln helfen bei der Wissensweitergabe und -aneignung. Sie sind fürs Vorzeigen, Lernen und Wiederholen gedacht und überdies auch für den Stationenbetrieb im Freiland als auch in der Klasse gut anwendbar.

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