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2. Abstracts of Posters (in alphabetical order of first author's surname)

Chromosome numbers of terrestrial mollusks (Mollusca: Gastropoda) of Georgia

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In the present study chromosome numbers in terrestrial mollusks of Georgia (Caucasus region) were investigated. Chromosome plates (with both haploid as well as diploid chromosome set) were obtained using well established methods for karyological studies of mollusk species were used. Gonads of colchicine treated animals were subjected to hypotonic treatment and the cell suspension was dropped on glass slides and air-dried. For very small mollusks (e.g., *Elia derasa*, *Circassina frutis*) the gonads were squashed between glass slide and cover slip. Mostly meiotic stages were observed in the species investigated, while mitotic chromosomes were rarely observed. Such a finding was reported earlier in the literature on karyotype analysis of mollusks (Park 2007, Awodıran et al. 2012). According to Boato (1986), gonial cells are in mitosis for very short time. Altogether 13 species (representatives of eight families and 12 genera) were analyzed. *Lytopelte* sp. (family Agriolimacidae), *Elia derasa* (family Clausiliidae), *Caucasotachea calligera*, *Helix buchii* and *Helix lucorum* (family Helicidae), *Caucasigena eichwaldi*, *Circassina frutis*, *Fruticocampylaea narzanensis* and *Xeropicta derbentina* (family Hygromiidae), *Gigantomilax lederi* (family Limacidae), *Poiretia mingrelica* (family Oleacinidae), *Oxychilus koutaisanus* (family Oxychilidae) and *Pomatias rivularis* (family Pomatiidae). Except three species (*Pomatias rivularis*, *Helix lucorum* and *Xeropicta derbentina*) all were endemics of Georgia and Caucasus. On average 28 individuals were examined for each species. The following haploid and diploid chromosome numbers were found in the present study: n = 13 (*Pomatias)*, 19 (*Lytopelte*), 23 (*Caucasigena*, *Circassina*, *Fruticocampylaea*), 26 (*Caucasotachea*, *Xeropicta*, *Poiretia*), 27 (*Elia, Helix*), and 27-29 (*Oxychilus*). Diploid chromosome numbers 2n = 46 (*Circassina*), 2n = 54-58 (*Oxychilus*) and 2n = ca. 62 (*Gigantomilax*). Altogether, the majority of species analyzed possessed karyotypes with chromosome numbers in a narrow range (between n = 13 and n = 31).

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Conservation of freshwater pearl mussels (*Margaritifera margaritifera*) in Austria – the project "Vision Flussperlmuschel"

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The freshwater pearl mussel (*Margaritifera margaritifera*) faces a dramatic decline throughout its distribution area, including Austria, where the species is considered critically endangered. As a consequence, the Austrian conservation project "Vision Flussperlmuschel" was initiated in 2011. The aim of this project is the establishment of reproductive populations in selected river systems in Upper Austria. In order to reach this goal, two main strategies are being followed. On the one hand, captive breeding of juvenile mussels is performed in order to increase the total number of specimens. For this purpose, adult mussels are kept in two raceways within a custom-built rearing facility. Each raceway runs into a consecutive tank in which juvenile brown trout (*Salmo trutta fario*), the host fish, are kept. This setup enables a natural infestation of the host fish in the course of the serotinal release of glochidia. The infested brown trout are then held within the tanks until the juvenile mussels start dropping off the gills. At this time, the juvenile mussels are collected in a sieve and then transferred to a laboratory, where they are supplied with fresh water, food and detritus. As soon as all individuals are large enough for surviving in the wild, they are transferred into various rearing systems and placed into selected river sections. The second strategy focuses on restoration measures in the catchment areas. There are hardly any river systems left in Upper Austria that provide suitable conditions for the establishment of pearl mussel populations. Therefore, a detailed mapping of selected rivers was carried out to identify the most promising sites for future resettlement efforts. In these river sections various abiotic and biotic factors with respect to the requirements of *M. margaritifera* are analyzed. On the basis of these results improvement measures – for example the construction of silt traps for reducing the levels of fine sediments within the rivers – are executed.

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Lungworms of dogs and cats in snail intermediate hosts in eastern Austria – a pilot study

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Various lungworm species of the genera *Crenosoma*, *Aeluorstrongylus*, *Angiostrongylus* and *Troglostrongylus* are important parasites of veterinary concern. They are causative agents of respiratory/pulmonary diseases in cats, dogs and several other mammals. The adult female worm deposits its eggs into the host's alveoli (or in case of *Angiostrongylus*, into the pulmonary blood vessels from which they penetrate into the alveoli). The eggs and developing first-stage larvae are coughed up, swallowed, and excreted with the feces. Snails ingest these larvae while feeding on faecal matter. Within the permissive intermediate snail host, larvae develop to infective third-stage larvae (L3) in the snail's body. The life cycle is completed with the ingestion of L3 by carnivore hosts (e.g. dogs) and subsequent development in the mammalian (final) host to fertile adult worms. The distribution of lungworms is closely associated to those of their intermediate hosts – slugs and snails. In recent years, lungworms were documented in new geographic distribution areas and hosts, but there is virtually no information for Austria. Therefore, slugs and snails are sampled at various locations in Eastern Austria (Vienna, Lower Austria, Burgenland and Styria), determined to genus/species (using the novel Schneckenatlas), and analysed for the presence of lungworm larvae. Lungworms itself will be specified to species level using morphological and molecular tools. This project will give a first insight into the presence, distribution and host association of canine and feline lungworm species in Austria. It is a collaboration between the Vetmeduni Vienna (Brauchart Thomas, Bleicher Julian, Hering Tatjana, Reinelt Simon, Lerchner Sigrun, Eisschiel Nicole, Edler Mirjam) the Natural History Museum Vienna and the Veterinary Faculty of the University of Teramo, Italy (Prof. Traversa, Dr. di Cesare).

Monacha cantiana s.l. (Montagu, 1803) (Gastropoda: Hygromiidae) – mitochondrial lineage occurring in Austria

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In Austria, *Monacha cantiana* s.l. (Montagu, 1803) was first discovered in 1995 in Horner Becken (Waldviertel, NÖ). New populations were found not far from Vienna recently. Analyses of mitochondrial *COI* and *16SrRNA* gene fragments showed that Viennese populations represent a mitochondrial lineage (CAN-3) different to populations of *M. cantiana* s.str. occurring in UK and Italy (Latium region) (CAN-1). However, haplotypes similar to Austrian CAN-3 were found in two north Italian localities – one near Bologna (Emilia Romagna), another in Passo di Monte (Friuli-Venezia Giulia). K2P distances for *COI* nucleotide sequences between CAN-3 lineage and other Italian *Monacha cantiana* lineages (CAN-1, also CAN-5 and CAN-6) were rather high (13.1-19.5%). On the other hand, K2P distances were smaller (4.2-7.2%) between *M. cantiana* CAN-3 and CAN-4 lineages. The latter, occurring in South France (Sainte Thecle near Nice), corresponds to *M. cemenelea* (Risso, 1826). Moreover, the shells of CAN-3 and CAN-4 are similar, while the differences in the structure of the genitalia of CAN-3 and CAN-4 remains to be better investigated. No differences in genital tract anatomy and shell features were observed between CAN-1 and CAN-3 lineages. Our results suggest that there are closer relationships between Austrian CAN-3 and French CAN-4 populations. However, species delimitation appears complicated and molecular genetic data alone should not be used to distinguish species and to make decisions on taxonomy or nomenclature. Ideally they should be supported by morphological features (of shells and/or genital anatomy), analysed in a broad geographic sample specifically including CAN-4.

Integrative taxonomy of the genus *Siciliaria* Vest, 1867 from northwestern Sicily with insights into related genera

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Siciliaria Vest, 1867 is a clausiliid genus that has its core of distribution along the limestone area of northwestern Sicily. Currently 17 taxa (12 species and 5 subspecies), are considered as valid and the systematics is completely based upon shell characters. While the genitalia of a few *Siciliaria* taxa were depicted in Reitano et al. (2007), a comprehensive analysis of the genital anatomy in *Siciliaria* has not been performed so far. In the present study, almost all *Siciliaria* taxa were investigated anatomically. Moreover, taxonomically undetermined specimens of a few populations were also included in the anatomical and molecular genetic investigations. At least three specimens of every locality were thoroughly dissected, depicting both the outer and inner features of the genital apparatus. In the present molecular genetic study, we analyzed the *mitochondrial cytochrome c oxidase subunit 1* (*COI*) gene in specimens from 35 populations of *Siciliaria* sensu stricto from northwestern Sicily. In order to understand the position of *Siciliaria* among the morphologically similar and biogeographically close genera, we included also representatives of *Stigmatica*, *Gibbularia*, *Charpentieria* and *Papillifera*. In the *COI* tree the *Siciliaria* species from northwestern Sicily clearly split into two separate main clades (A and B). Clade A includes the species that inhabit the eastern part of the distribution area plus the ubiquitary *Siciliaria calcarae* ssp., which is present along the whole territory, whereas clade B comprises the western species. Our results confirm that *Siciliaria* and *Charpentieria* should be considered as separate genera. The genera *Gibbularia* and *Papillifera* also fall into separate clades. Nevertheless, still dealing with low support values, further molecular systematic investigations are necessary to elucidate the relationships between the genera *Siciliaria*, *Stigmatica*, *Charpentieria, and Papillifera*.

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Survey on Spring Snails (Hydrobiidae) in the Kalkalpen National Park

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The Kalkalpen National Park, situated in Upper Austria and comprising about 210 km^2, is home to several thousand different animal and plant species. The international importance of this park is, from the perspective of nature conservation directives, highly significant (Natura 2000 area, recognized wetland of the Ramsar convention). For the protection of the local endemics, which exist exclusively in the national park and its close surroundings, the national park bears absolute responsibility. So far, almost ten species of local endemics are known, all of them are found in the small alpine region of the Sengsengebirge, some in cave systems including the outlets of springs. Two of them are molluscs of the family Hydrobiidae, which were described based on morphological and anatomical examination as new species: *Belgrandiella aulaei* and *Bythiospeum nocki* Haase et al., 2000. Otherwise the knowledge of the Hydrobiidae in the national park is incomplete, but preliminary investigations indicate a high diversity of spring snails. Different morphotypes of the genera *Bythinella* Moquin-Tandon, 1856, and *Hauffenia* Pollonera, 1899 were found (Weigand 2012). In the current study, the spring snails of the Kalkalpen National Park will be investigated in more detail. Snails will be collected from more than 50 springs and examined by morphological determination, photographic documentation and genetic analysis through DNA barcodes. The data will be compared with hydrobiid sequences from the ABOL Mollusca project. Because of the importance of hydrobiids in the assessment of the water quality of springs, their investigation is especially desirable. Due to their limited habitat, numerous Hydrobiidae are highly endangered. When spring areas are influenced or even destroyed, for example through construction works for drinking water production, it can lead to the extinction of these unique species. This exemplifies the need of a better knowledge of the species distribution, which will be facilitated using DNA barcoding.

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The land snail fauna of the Gesäuse National Park. Ecology of Alpine land snails, with a special focus on endemic species

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The Gesäuse National Park is located in the Eastern Alps in the north of Styria (Austria). It covers an area of about 110 km² and was established in 2002. It is characterized by high limestone mountains, crossed by the Enns-River in east-west-direction. Situated at the easternmost border of the glaciations during the last ice age, the Gesäuse National Park is home to a high number of land snails, featuring also several endemic species. As many studies have been conducted in this area in the last century, the first part of this thesis summarizes our knowledge concerning the land snail fauna of the Gesäuse National Park (Volkmer 2017). In the main part, data gained by fieldwork in the summer of 2014 concerning habitat preferences of the alpine land snail fauna are presented. 54 sites (18 covered by bare limestone, 18 by alpine grasslands and 18 transition habitats) with a size of 25 m² each were investigated. Additionally, small square samples (0.16 m²) in each location were collected, sieved and surveyed for snails. Land snail communities in limestone rock and calcareous meadows are described. Data analysis shows that several species are restricted to distinct elevations and habitats. The total number of species decreases with increasing elevation. The mean number of species and the mean "biodiversity" (measured by the Shannon Index) increases with ascending elevation and decreases only above at 1900 m a.s.l. The mean number of individuals increases significantly with higher altitude.

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Molecular characterization of gelatinous egg masses in the lucinid *Loripes orbiculatus* argues for an acquisition of bacterial symbionts from the environment

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Lucinidae, one of the most species-rich taxa in the ocean, are associated with sulfur-oxidizing bacterial symbionts, which live inside the host's gill cells. Despite their worldwide distribution, little is known about their life cycle in the wild. They are all assumed to initially lack symbionts and take these up from the environment during development. In one species, broadcast spawning has been induced in the laboratory while another reproduces differently by forming gelatinous egg masses, a rare strategy in marine bivalves. In corals, reproductive mode is thought to be linked to symbiont transmission strategy, with brooders passing symbionts directly to the offspring, and broadcast spawners more likely to take up symbionts from the environment later in development. Our lab focuses on the lucinid species *Loripes orbiculatus*, which is distributed along the English coast, throughout the Mediterranean and Atlantic coasts, to West Africa. In Mauritania, this species forms gelatinous egg masses. We sampled reproductive stages in two consecutive years to investigate the potential for vertical transmission of symbionts via the egg masses. If symbionts can be detected in the egg masses, and are passed vertically from parent to offspring, this would challenge current assumptions about this widespread symbiosis. We identified the host and symbiont on the molecular level using Sanger sequencing of host and symbiont marker genes. We used amplicon sequencing to comprehensively fingerprint the bacterial communities in the egg masses. These results were confirmed by imaging with fluorescence in situ hybridization. Both methods support the dominance of alphaproteobacteria, gammaproteobacteria and bacteroidetes but although we analyzed 215000 sequences, none matched the symbiont of the adult *L. orbiculatus* at this site. Transmission electron microscopy revealed that the gills were still free of symbionts in freshly hatched, 10- and 54-days old juveniles. These results suggest that although this species produces egg masses, this unusual reproductive mode is not linked to its conspicuous gill symbiosis.

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