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## Abstracts malakozoologischer Abschlussarbeiten

zusammengestellt von IRA RICHLING

An dieser Stelle werden in loser Folge universitäre Abschlussarbeiten mit malakozoologischen Themen in Form der Zusammenfassungen einem breiteren Publikum vorgestellt oder zumindest so überhaupt veröffentlicht.

### Reevaluation of *Ouagapia* and *Ptychorhytida* (Gastropoda: Rhytididae) from New Caledonia based on a redescription of their type species

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2015 – 48 S., Diplomarbeit am Zoologischen Museum der Universität Hamburg; betreut durch Prof. Dr. BERNHARD HAUSDORF.

Publikation in Arbeit.

This study presents redescrptions of the type species of *Ouagapia* CROSSE 1895 and *Ptychorhytida* MOELLEN-DORFF 1903 (Gastropoda: Rhytididae) from New Caledonia as a basis for a reevaluation of the delimitation of these nominal genus group taxa. Furthermore, it presents a comparison of these species with their sibling species and a description of a newly discovered species of these species groups. The genitalia, especially the inner structure of the penis, the pallial complex and the radula of the type species of *Ouagapia* and *Ptychorhytida*, *Ouagapia raynali* (GASSIES 1863) respectively *Ptychorhytida bisulcata* (PFEIFFER 1854) (of which *Helix beraudi* GASSIES 1858 is a synonym) were compared.

*Ptychorhytida* differs from *Ouagapia* especially in the run of the primary ureter, a character hardly variable in other stylommatophoran families. Whereas the primary ureter of *O. raynali* forms a simple bend at the anterior end of the kidney, the primary ureter of *P. bisulcata* forms a convolution at the anterior end of the kidney. Such a convolution has also been found in *Nata* WATSON 1934 from southern Africa whereas most sigmurethran Stylommatophora show a simple bend at the anterior end of the kidney.

It is still unclear whether the convolution of the primary ureter evolved only once in the Rhytididae, which would imply that *Ouagapia* and *Ptychorhytida* do not form a monophylum and that these groups colonized New Caledonia independently, or whether the convolution of the primary ureter evolved convergently in different groups of the Rhytididae.

The *Ouagapia raynali* group includes three species, *O. raynali*, *O. virescens* (DAUTZENBERG 1923) and *Ouagapia* n. sp., which cannot be reliably distinguished by shell characters, but only by the inner structures of the penis. The sibling species of *P. bisulcata*, *P. subsidialis* (CROSSE 1870) differs from *P. bisulcata* in the inner structures of the penis, but also in some shell characters. Within these species groups, the species are allopatric.

## Phylogenetic analysis of the *Alopi* taxa (Gastropoda: Clausiliidae) of the Bucegi mountains in Romania and evolutionary effects of left-right reversal

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2014 – 37 S., Masterarbeit am Zoologischen Museum der Universität Hamburg; betreut durch Prof. Dr. BERNHARD HAUSDORF.

Publikation in Arbeit.

*Alopi*, a land snail genus endemic to the Carpathians, is exceptional in consisting of comparable proportions of dextral (clockwise coiled) and sinistral (counterclockwise coiled) species, whereas the majority of gastropod genera or even families are fixed for one morph. Some species constitute mirror images (enantiomorph pairs) that only differ in coiling direction. A change in chirality was discussed as a possible mechanism for speciation because dextral and sinistral individuals have difficulty in mating. Phylogenetic analyses of mitochondrial cytochrome c oxidase subunit I (COI) sequences as well as amplified fragments length polymorphism (AFLP) were used to study the relationships between the different *Alopi* taxa and to investigate the consequences of a changed chirality. Using a genomic cline analysis patterns of introgression in two contact zones between dextral and sinistral species were compared. The results show extensive gene flow between enantiomorph species pairs. A remarkable concordance of the hybrid zones is the increased introgression of alleles of the sinistral species, whereas nearly all negatively selected loci arise from the dextral species. Sinistral is the more common morph because the corresponding allele is dominant. The increased introgression of sinistral alleles may indicate that intra-chiral mating is favoured resulting in an advantage for the more common morph because of frequency dependent selection. Although a change in chirality does not cause strict reproductive isolation it may contribute to it.

## Räumliche Verteilung abundanter Schneckenarten in einem Xerothermrassen

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2013 – 37 S., Bachelorarbeit an der Biologisch-Pharmazeutischen Fakultät, Friedrich-Schiller-Universität Jena; betreut durch Dr. WINFRIED VOIGT.

In kalkreichen mitteleuropäischen Halbtrocken- und Trockenrasen gehören Landschnecken zu den typischen Faunenelementen. In dieser Bachelorarbeit wurde mit der Frequenzanalyse – einer Methode aus der Vegetationsökologie zur Klärung räumlicher Verbreitung von Pflanzengesellschaften – die kleinräumliche Verteilung der drei Arten *Euomphalia strigella*, *Granaria frumentum* und *Helicella itala* in einem Xerothermrassen untersucht. Dazu wurde eine 100 m<sup>2</sup> große zusammenhängende Fläche in 10.000 Einzelquadrate unterteilt. Es konnte gezeigt werden, dass Inklination, Vegetationsdichte und die unterschiedlichen Bearbeiter bei der Bodenlese der Schneckengehäuse kaum Variation in der Verteilung der Schneckenarten erklären, d. h. diese drei Variablen spielen offenbar keine Rolle für die kleinräumliche Verteilung der Arten, sowohl bei Leergehäusen als auch bei lebenden Tieren. Die Analyse mittels der Erzeugung von Konturplots der Lebendindividuen (basierend auf generalisierten linearen Modellen) lässt vermuten, dass interspezifische Konkurrenz zwischen den untersuchten Arten auszuschließen ist. Angewandte Clusteranalysen ergaben, dass *G. frumentum* und *H. itala* ähnliche Umweltansprüche stellen, jedoch weisen sie im kleinräumlichen Maßstab Unterschiede bezüglich ihrer Verteilung auf. *E. strigella* als Art lichter Gebüsch- und Wälder hingegen korreliert nicht mit den Umweltansprüchen der anderen hier betrachteten Arten. Es gibt Anzeichen für eine agglomerierte Verteilung bei den vorgefundenen Individuen aller drei Arten, insbesondere bei den Lebendindividuen von *G. frumentum* und *H. itala*. Sie weisen zudem deutliche Gradienten in ihrer Abundanz auf. Insgesamt gestaltet sich die Frequenzanalyse als probates und kostengünstiges Mittel zur Untersuchung der relativ immobilen Gehäuseschnecken. Zudem hat sie den großen Vorteil, individuelle Suchfehler der Bearbeiter zu reduzieren (erklärte Variation durch die Bearbeiter = 2,4 %). Es ist anzunehmen, dass heterogen lokale Maxima der Abundanz aufgrund der Verteilung der Nahrungsressourcen (nicht im Detail bekannt) auftreten. Dafür spricht, dass in dieser Arbeit keine interspezifische Konkurrenz zwischen den untersuchten Arten belegt werden konnte. Eine andere Erklärung könnten sich ändernde mikroklimatische Bedingungen im Zuge des sukzessionsbedingten Wandels des offenen Xerothermrassens hin zu Gehölzbeständen darstellen.

**Phylogenetic and phylogeographic studies on selected Palaearctic land snails (Gastropoda: Stylommatophora), with a special focus on the Caucasus region**

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2016 – IX + 310 S., Dissertation am Zoologischen Museum der Universität Hamburg; betreut durch Prof. Dr. BERNHARD HAUSDORF.

Bisherige Publikationen:

NEIBER, M. T. & HAUSDORF, B. (2015): Phylogeography of the land snail genus *Circassina* (Gastropoda: Hygromiidae) implies multiple Pleistocene refugia in the western Caucasus region. — *Molecular Phylogenetics and Evolution*, **93**: 129-142, San Diego.

The phylogeny and historical biogeography of the Caucasian land snail genus *Circassina* was reconstructed using multilocus amplified fragment length polymorphism (AFLP) data and mitochondrial DNA sequences. Diversification within the group started with a divergence of populations from the western Lesser Caucasus from those of the Greater Caucasus during the late Miocene. Distinct AFLP clusters and major mitochondrial clades separated by long internal branches lend evidence to the hypothesis of separate glacial refuges in the Lesser and Greater Caucasus during the Pleistocene. High genetic distances across low geographic distances and admixture analysis revealed a phylogeographic boundary running through the Colchis lowlands, which may have been established and maintained in part by repeated transgressions of the Black Sea during the Pleistocene and Holocene. Localities in Ciscaucasia were probably colonised through long-distance dispersal across the main ridge of the Greater Caucasus. The phylogeny implies multiple independent losses of accessory genital organs, i. e. dart sac and mucus glands, within *Circassina*. None of the anatomically defined (sub-) species distinguished so far is monophyletic and there is gene flow between the two main population groups across the Colchis lowlands. Thus, we propose to classify these population groups as subspecies of a single species.

NEIBER, M. T. & HAUSDORF, B. (2015): Molecular phylogeny reveals the polyphyly of the snail genus *Cepaea* (Gastropoda: Helicidae). — *Molecular Phylogenetics and Evolution*, **93**: 143-149, San Diego.

Snails in the genus *Cepaea* are important model organisms in ecogenetic studies because of their colour and banding polymorphism. The monophyly of this group has been almost unanimously assumed based on superficial similarities in shell form and colouration. However, molecular phylogenetic analyses based on mitochondrial and nuclear sequences of 20 genera of Helicidae unequivocally demonstrated that *Cepaea* as currently understood is a polyphyletic assemblage. Only *C. nemoralis* and *C. hortensis* are retained in *Cepaea*, whereas *C. vindobonensis* is referred to *Caucasotachea* and *C. sylvatica* to *Macularia* based on our molecular phylogeny. *Cepaea* and *Macularia* belong to the western clade of the Helicinae, whereas *Caucasotachea* is nested in the eastern clade which probably diverged in the late Eocene. Because of the large phylogenetic distances between *Cepaea*, *Macularia* and *Caucasotachea*, it has to be shown whether the genetic mechanism underlying the simpler banding polymorphism in *C. vindobonensis* and *M. sylvatica* is a simpler version of the supergene that determines the polymorphism in *Cepaea* in the strict sense. This case illustrates the importance of sound phylogenetic analyses as a basis for any predictions in comparative biology.

NEIBER, M. T., SAGORNY, C. & HAUSDORF, B. (2016): Increasing the number of molecular markers resolves the phylogenetic relationship of '*Cepaea*' *vindobonensis* (PFEIFFER, 1828) with *Caucasotachea* BOETTGER, 1909 (Gastropoda: Pulmonata: Helicidae). — *Journal of Zoological Systematics and Evolutionary Research*, **54** (1): 40-45, Berlin.

'*Cepaea*' *vindobonensis* has been shown to be closely related to *Caucasotachea* in recent molecular studies. The phylogenetic relationships within this clade and especially the phylogenetic position of '*Cepaea*' *vindobonensis* were, however, not well resolved. Our phylogenetic analyses on the basis of an increased number of molecular genetic loci from the mitochondrial and nuclear genomes unambiguously demonstrate that '*Cepaea*' *vindobonensis* represents the sister group of the *Caucasotachea* taxa, with *C. leucoranea* from the Caspian region of Azerbaijan and Iran being the sister species of the remaining Caucasian and eastern Pontic *Caucasotachea* species. We argue for the inclusion of '*Cepaea*' *vindobonensis* in *Caucasotachea* rather than for a re-erection of a monotypic genus *Austrotachea* for the species because of the overall low degree of morphological differentiation and the low number of species in the group.

KOCH, E., NEIBER, M. T., WALTHER, F. & HAUSDORF, B. (2016): Presumable incipient hybrid speciation of door snails in previously glaciated altitudes in the Caucasus. — *Molecular Phylogenetics and Evolution*, **97**: 120-128, San Diego.

Homoploid hybrid speciation, speciation by hybridization without a change in chromosome number, may be the result of an encounter of closely related species in a habitat that is different from that usually occupied by these species. In the northwestern Caucasus the land snail species *Micropontica caucasica* and *M. circassica* form two distinct entities with little admixture at low and intermediate altitudes. However, at higher altitudes in the Lagonaki plateau, which were repeatedly glaciated, *Micropontica* populations with intermediate characters occur. Admixture analyses based on AFLP data demonstrated that the populations from the Lagonaki plateau are homoploid hybrids that now form a cluster separate from the parental species. The Lagonaki populations are characterized by a mtDNA haplotype clade that has been found in the parental species only once. The fixation of this haplotype clade in most hybrid populations suggests that these haplotypes are better adapted to the cooler conditions in high altitude habitats and have replaced the haplotypes of the parental species in a selective sweep. The fixation of a presumably adaptive mitochondrial haplotype clade in the Lagonaki populations is an important step towards speciation under the differential fitness species concept.

WALTHER, F., NEIBER, M. T. & HAUSDORF, B. (2016): Systematic revision and molecular phylogeny of the land snail genus *Fruticocampylaea* (Gastropoda: Hygromiidae) from the Caucasus region. — *Systematics and Biodiversity*, **14** (1): 32-54, Abingdon & Cambridge.

This paper presents a systematic revision and a molecular phylogenetic analysis of the Caucasian land snail genus *Fruticocampylaea*. The genus is newly delimited based on the reduction of the cavities adjoining the seminal duct in the penial papilla. Shell and genitalia of all five species (*F. narzanensis*, *F. kobensis*, *F. tushetica* sp. nov., *F. christophori*, *F. daghestana*) are described and figures provided. All synonyms and all locality records are listed. Maximum likelihood and Bayesian analyses of mitochondrial and nuclear DNA sequences (fragments of *cox1*, 16S rDNA, ITS2 and 28S rDNA) confirm the monophyly of *Fruticocampylaea*. The reduction of the dart apparatus and the conical plug, via which the dart apparatus inserts into the vagina, as well as the molecular phylogenetic analyses, suggest a sister group relationship between *Fruticocampylaea* and *Circassina* (without *Abchasohela*). Furthermore, the molecular phylogenetic analyses indicate that the *Fruticocampylaea* species originated in a rapid radiation. The uplift of the Greater Caucasus in the Late Miocene or Pliocene or climatic changes at the end of the Pliocene or in the early Pleistocene may have caused the radiation of *Fruticocampylaea*. Low intraspecific variability can be explained by population bottlenecks during Pleistocene glacial periods followed by postglacial population increase.

Weitere Kapitel:

NEIBER, M. T., SAGORNY, C., WALTHER, F., SAUER, J. & HAUSDORF, B. (2016): Phylogeographic analyses reveal Transpontic dispersal in the *Caucasotachea atrolabiata* complex (Gastropoda: Helicidae). — In: NEIBER, M. T.: Phylogenetic and phylogeographic studies on selected Palaeartic land snails (Gastropoda: Stylommatophora), with a special focus on the Caucasus region: 67-96. Dissertation, Universität Hamburg (Hamburg).

We investigated the phylogeography and population structure of land snails belonging to the *Caucasotachea atrolabiata* complex in the Caucasus region to obtain a better understanding of diversification processes in this hotspot of biodiversity. So far the complex has been classified into three species, *C. atrolabiata* from the northwestern Caucasus, *C. calligera* from Transcaucasia and *C. intercedens* from the eastern Pontus Mountains. Analyses based on AFLP data showed that the complex consists of two clusters of populations corresponding to *C. atrolabiata* and *C. calligera*. The populations assigned to *C. intercedens* consisted of different proportions of the genomes of *C. atrolabiata* and *C. calligera*. The presence of mitochondrial *C. atrolabiata* haplotypes in northern Turkey can only be explained by passive dispersal across the Black Sea. There is a broad transition zone between *C. atrolabiata* and *C. calligera* in the Pontic Mountains and a second transition zone between these taxa in Abkhazia. Because of the evidence for gene flow between these taxa, we suggest to classify them as subspecies. The distribution of *C. a. atrolabiata* and additional cases of land snails with disjunct Transpontic distribution patterns cannot be ascribed to a common cause, but are results of long-distance dispersal events that occurred at different times.

NEIBER, M. T. & HAUSDORF, B. (2016): Molecular phylogeny reveals multiple parallel losses in the genital system of the land snail genus *Monacha* (Gastropoda: Hygromiidae). — In: NEIBER, M. T.: Phylogenetic and phylogeographic studies on selected Palaearctic land snails (Gastropoda: Stylommatophora), with a special focus on the Caucasus region: 169-191. Dissertation, Universität Hamburg (Hamburg).

*Monacha* is the most species-rich genus in the family Hygromiidae with a centre of diversity in Anatolia. On the basis of the presence or absence of accessory genital appendages, the group was subdivided into three subgenera, *Monacha* s. str., *Paratheba* and *Metatheba*, in the past. We used mitochondrial and nuclear DNA sequences of a representative sample of species 1) to reconstruct the phylogeny of the major lineages of *Monacha*, 2) to reconstruct the evolution of the accessory genital appendages, and 3) to reconstruct the biogeography of the group. Our results show that the accessory genital appendages upon which the classification of *Monacha* into subgenera rested so far, i. e. the appendicula, which is homologous to the dart sac or its accessory sac in other helicoid land snails and the penis retractor muscle, were lost several times independently in different lineages of *Monacha*. Even among sister species these characters were found to be variable. Thus, the typologically defined subgenera are polyphyletic assemblages. The reconstruction of the biogeographical history indicated an origin of *Monacha* in Anatolia and the adjacent Caucasus region which is consistent with the observation that most other genera currently included in the subfamily Monachinae are also endemic to this region. Most major *Monacha* lineages remained restricted to northern Anatolia. Southern Europe was colonized by *Monacha* s. str., the Crimean Peninsula by *Paratheba*, the Levant by *Platytheba* and the Aegean region by an as yet unnamed lineage. On the basis of our phylogenetic analyses and testing of alternative hypotheses, we propose to divide *Monacha* into seven subgenera. We newly delimit the previously proposed subgenera *Monacha* s. str., *Metatheba*, *Paratheba* and *Platytheba*, and describe four new subgenera.

NEIBER, M. T., RAZKIN, O. & HAUSDORF, B. (2016): Molecular phylogeny and biogeography of the land snail family Hygromiidae (Gastropoda: Helicoidea). — In: NEIBER, M. T.: Phylogenetic and phylogeographic studies on selected Palaearctic land snails (Gastropoda: Stylommatophora), with a special focus on the Caucasus region: 193-237. Dissertation, Universität Hamburg (Hamburg).

The family Hygromiidae is a highly diverse group of land snails with a distribution range stretching throughout the Palearctic region from the Macaronesian Islands in the west to the Russian Far East in the east and reaching southwards to the north-eastern Ethiopian region. The classification of the family largely rested on few characters of the dart apparatus of the genitalia so far. We used nuclear and mitochondrial DNA sequences of almost all genera to reconstruct the phylogeny of the Hygromiidae. The molecular phylogenetic trees indicate widespread homoplasies with regard to the characters of the dart apparatus so that many of the currently accepted subdivisions of the family turned out to be polyphyletic. We newly delimit three subfamilies within the family Hygromiidae, Hygromiinae (with three tribes), Leptaxinae (with three tribes) and Trochulinae (with nine tribes), on the basis of our phylogenetic analyses and describe seven new tribes and two new genera. The reconstruction of the biogeographical history of the Hygromiidae indicated an origin of the family in the western Palearctic, from where the Tian Shan and Altai Mountain regions in Central Asia, the Macaronesian Islands, the Caucasus region and sub-Saharan East Africa were colonized.