

Abstract Book



9th International Workshop for Cestode Systematics and Phylogeny

Session plan: Saturday 5th of August 2017

SCIENTIFIC ORGANIZATION

Prof. Dr. rer. nat. habil. Harry W. Palm

Dr. rer. nat. Sonja Kleinertz

M. Sc. Berit Wasenitz

TIME	SESSION TITLE	AUTHORS	TALK/POSTER TITEL
08:30-08:45		H. Palm	Welcome speech and organisation
	A	TAPEWORMS OF ELASMOBRANCHS	
09:00-09:20	1	M. Haseli ¹ , M.Z. Bazghalee ¹ , H.W. Palm ²	GENETIC IDENTITY OF EUTETRARHYNCHIDS FROM THE PERSIAN GULF: ARE THERE LIMITS TO MATCH MORPHOLOGICAL AND MOLECULAR IDENTIFICATION?
09:20-09:40	2	B.C. Schaeffner ¹	INTEGRATIVE TAXONOMY UNRAVELS THE SPECIES DIVERSITY OF TRYPANORHYNCH CESTODES FROM BOTH SIDES OF THE PANAMANIAN ISTHMUS
09:40-10:00	3	V. A. Ivanov ^{1,2} , A. Menoret ¹	MARINE CESTODES FROM TELEOSTS AND ELASMOBRANCHS OFF ARGENTINA: DONE, DOING, TO DO
10:00-10:30			COFFEE BREAK / POSTERSESSION
	B	TAPEWORMS OF TELEOSTS	
10:30-10:50	4	A. Menoret ¹ , V. A. Ivanov ^{1,2}	LACISTORHYNCHOID TRYPANORHYNCHS FROM THE ARGENTINE SEA: SPECIFICITY AND TRANSMISSION PATHWAYS
10:50-11:10	5	C. Ben Saad ¹ , N. Ghanmi ¹ , L. Gargouri ¹	DIVERSITY OF TAPEWORM LARVAE IN SOME TELEOST FISHES FROM KALAAT EL ANDALOUS (NORTH OF TUNISIA)
11:10-11:30	6	D. Barčák ¹ , M. Oros ¹ , V. Hanzelová ¹ , T. Scholz ²	CURRENT PROBLEMS IN THE TAXONOMY AND SYSTEMATICS OF CARYOPHYLLIDEAN TAPEWORMS
11:30-11:50	7	P.V. Alves ^{1,4} , A. de Chambrier ² , J.L. Luque ³ , T. Scholz ⁴	TOWARDS A ROBUST SYSTEMATIC BASELINE OF TAPEWORMS (CESTODA: PROTOCEPHALIDAE) OF NEOTROPICAL CATFISHES: A MORPHOLOGICAL REAPPRAISAL OF THREE OLD GENERA
11:50-12:10	8	R. Kuchta ¹ , A. Waeschenbach ² , J. Brabec ¹ , T. Scholz ¹ , D. T. J. Littlewood ²	NEW SYSTEMATICS AND PHYLOGENY OF DIPHYLLOBOTHRIDEAN TAPEWORMS
12:10-12:30	9	T. Scholz ¹ , R. Kuchta ¹	A DIGEST OF FISH TAPEWORMS
12:30-13:40			PHOTOS AND LUNCH BREAK
	C	CYCLOPHYLLIDEANS	
13:40-14:00	10	R. Binkienė ¹ , S. Kornienko ²	REVIEW OF THE CESTODES OF THE TRIBE DITESTOLEPIDINI SPASSKY, 1954 (CYCLOPHYLLIDEA, HYMENOLEPIDIDAE)
14:00-14:20	11	S. Kornienko ¹ , V. Tkach ² , N. Dokuchaev ³	MORPHOLOGICAL AND MOLECULAR DIFFERENTIATION OF THE GENUS <i>NEOSKRJABINOLEPIS</i> (CESTODA, HYMENOLEPIDIDAE) FROM THE SHREW SOREX
14:20-14:40	12	A.A. Makarikov ¹ , V.V. Tkach ² , T.A. Makarikova ¹	ON PHYLOGENETIC RELATIONSHIPS AND PROBLEMS OF TAXONOMY OF HYMENOLEPIDID CESTODES IN THE "RODENTOLEPIS – CLADE"
14:40-15:00	13	D. Ebi ¹	NEW INSIGHTS INTO THE GENETIC DIVERSITY OF <i>ECHINOCOCCUS GRANULOSUS</i> SENSU STRICTO
15:00-15:20			COFFEE BREAK / POSTERSESSION
	D	GENERAL TAPEWORM RESEARCH	
15:20-15:40	14	K.A. Gallagher ¹ , J.N. Caira ¹ , J. Wegrzyn ¹	EXAMINING MORPHOLOGICAL NOVELTY IN AN ENIGMATIC TAPEWORM: A COMPARATIVE GENOMIC AND TRANSCRIPTOMIC APPROACH
15:40-16:00	15	V.M. Bueno ¹ , J.N. Caira ¹	LOST (AND FOUND!) IN A SEA NOVELTY
16:00-16:20	16	M.C.N. Justo ¹ , B.M.M. Fernandes ¹ , M. Knoff ² , M.Q. Cárdenas ¹ , S.C. Cohen ¹	CHECKLIST OF BRAZILIAN CESTODA
16:20-16:40	17	D.A. Lopes ¹ , A. Mainenti ¹ , M. Sanches ¹ , D.C. Gomes ¹ , M. Knoff ¹	TYPE MATERIAL OF CESTODA HOUSED IN THE HELMINTHOLOGICAL COLLECTION OF THE OSWALDO CRUZ INSTITUTE/ FIOCRUZ (CHIOC) FROM 1979 TO 2016
16:40-17:00	18	S. Kleinertz ¹	PARASITE SAMPLES FROM FREE-LIVING MARINE ANIMALS USING NON-INVASIVE METHODS
			POSTER PRESENTATIONS
10:10-10:30	19 P	K. Herzog ¹ , K. Jensen ¹	THE TAPEWORM FAUNA OF THE GIANT DEVILRAY (<i>MOBULA MOBULAR</i> [BONNATERRE]): A TRANS-PACIFIC DISTRIBUTION
15:10-15:20	20 P	M. Oros ¹ , D. Barčák ¹ , R. Kuchta ²	SCANNING ELECTRON MICROSCOPIC OBSERVATION OF <i>DIPHYLLOBOTHRIMUM LATUM</i> (CESTODA)
	21 P	A. Menoret ¹ , V. A. Ivanov ^{1,2}	TRYPANORHYNCHS FROM ELASMOBRANCHS IN THE WARM TEMPERATE SOUTHWESTERN ATLANTIC AND MAGELLANIC PROVINCES
	22 P	S. Franzese ¹ , V. A. Ivanov ^{1,2}	A NEW GENUS OF RHINEBOTHRIDEA FROM SPECIES OF <i>PSAMMOBATIS</i> (RAJIFORMES, ARHYNCHOBATIDAE) OFF ARGENTINA

Session A:

TAPEWORMS OF ELASMOBRANCHS

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GENETIC IDENTITY OF EUTETRARHYNCHIDS FROM THE PERSIAN GULF: ARE THERE LIMITS TO MATCH MORPHOLOGICAL AND MOLECULAR IDENTIFICATION?

Mohammad Haseli¹, Monireh Zare Bazghalee¹, Harry W. Palm²

Following the morphological identification of eutetrarhynchids from the Persian Gulf, their conspecificity with the allopatric specimens was evaluated using sequencing the partial 28S rDNA, calculating genetic distances and a phylogeny resulted also in discovering a cryptic species of *Dollfusiella spinulifera* (Beveridge et Jones, 2000). For *Pr. clarkeae* Beveridge, 1990, the genetic divergence between the Gulf of Carpentaria and the Persian Gulf was the lowest (0.22%). The genetic distance between the Australian specimens of *Parachristianella indonesiensis* Palm, 2004 as well as *Pa. monomegacantha* Kruse, 1959, both from the Arafura Sea and their conspecifics in the Persian Gulf differed. While the sequence length between the conspecifics in *Pa. indonesiensis* was twice in relation to *Pa. monomegacantha*, the genetic distance between the conspecifics of the latter was 2.27 times more. This difference, considering the sequenced fragment of the Iranian *Pa. monomegacantha*, was 5.53 times higher. The genetic divergence between the allopatric conspecifics of *Pa. indonesiensis* was lower between the conspecifics from Northern Australia vs the Persian Gulf, compared with the Arafura Sea vs Celebes Sea, indicating that ecological barriers must be different.

INTEGRATIVE TAXONOMY UNRAVELS THE SPECIES DIVERSITY OF TRYPANORHYNCH CESTODES FROM BOTH SIDES OF THE PANAMANIAN ISTHMUS

B.C. Schaeffner¹

The tropical east Pacific and tropical northwestern Atlantic represent two marine provinces, which have been separated by the formation of the Panamanian isthmus and closure of the interconnected waterway for approximately 3.2 Ma. This paleogeographical event affected many ancestral populations that occupied the interconnected waters of the tropical Central American belt. After the uplift of the Panamanian isthmus, these populations were separated on either side of the Panamanian land bridge and, due to the interruption of gene flow, diverged in which are now two segregated biogeographical regions. This biogeographical scenario led to a diversification of host lineages, such as the batoid sister species *Styracura pacifica* and *S. schmardae*. The vicariance events affecting host species could, in turn, impose patterns of co-divergence in their parasite lineages. A recent study on the diversity of cestodes of the order Trypanorhyncha infecting stingrays from coastal waters in Panama revealed sibling species, confined to either side of the Panamanian isthmus. Biogeographical and molecular evidence support the recognition of independent species, although the few morphological differences could have been interpreted as intraspecific variation. Traditionally, trypanorhynchs with similar tentacular armature patterns were considered conspecific, even when minor morphological discrepancies and biogeographical distribution might have suggested otherwise. The current findings of trans-isthmian sibling species of trypanorhynch cestodes illustrates that the emphasis given to tentacular armature for the recognition and allocation of species might not be sufficient to identify hidden lineages. Integrative approaches to systematics incorporating molecular, morphological and paleogeographical information from a larger sample size and a focus on different localities might therefore represent a solution to better understand morphological variability in order to provide more robust species hypotheses.

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MARINE CESTODES FROM TELEOSTS AND ELASMOBRANCHS OFF ARGENTINA: DONE, DOING, TO DO

V.A. Ivanov^{1,2}, A. Menoret¹

During the last decade extensive field work in search for marine cestodes has been carried out along the coast of Argentina, from shallow waters to deep sea (15-1,500 m depth). More than 80 species of teleosts, and 40 species of elasmobranchs (Rajiformes, Torpediniformes, Myliobatiformes, Carcharhiniformes, Hexanchiformes, Squaliformes and Squatiniformes). Among them, 20 species of elasmobranchs had not been previously examined for cestodes, and 15 are endemic to the Southwestern Atlantic. So far 68 species of tapeworms have been identified, including 23 species recently described and 36 putative new species. They represent 28 genera (at least 3 are new genera) in Bothriocephalidea, Cathetocephalidea, Diphyllidea, Lecanicephalidea, Onchoproteocephalidea, Phyllobothriidea, Rhinebothriidea, Tetraphyllidea and Trypanorhyncha. Also transmission pathways have been described, in part, for 4 species of trypanorhynchs, and interesting biogeographic patterns in hosts and parasites distribution have been observed. Besides documenting and describing host and parasite diversity, we also explore other aspects of this system. Recently, ultrastructural investigations using transmission electron microscopy and histochemistry have been done on selected taxa, in search of a better understanding of the internal morphology of the different types of microtriches and structures related to the scolex. This information might be useful for the recognition of morphological synapomorphies to support the tapeworm orders recently proposed. The purpose of this presentation is to show some preliminary results and future work in our lab.

Session B:
TAPEWORMS OF TELEOSTS

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LACISTORHYNCHOID TRYPANORHYNCHS FROM THE ARGENTINE SEA: SPECIFICITY AND TRANSMISSION PATHWAYS

A. Menoret¹, V. A. Ivanov^{1, 2}

Lacistorhynchoids are parasites of marine elasmobranchs, and also infect a wide range of teleosts as intermediate hosts. A parasitological survey along the coast of Argentina included the examination of 80 species of teleosts and 36 elasmobranchs. Seven species of lacistorhynchoids have been reported from this region, however, the identity of only 4 species has been confirmed, i.e., *Callitetrarhynchus gracilis*, *Dasyrhynchus pacificus*, *Grillotia carvajalregorum* and *Grillotia patagonica*. *Callitetrarhynchus gracilis* has only been recovered as plerocerci from perciform teleosts (Sciaenidae and Serranidae). Plerocerci of *D. pacificus*, *G. carvajalregorum* and *G. patagonica* have been found in a wide array of teleosts, while the adults are more specific for their elasmobranch hosts. The transmission pathways of *D. pacificus* include at least 2 species of teleosts (Perciformes and Gadiformes) and the shark *Carcharhinus brachyurus*. *Grillotia carvajalregorum* infects *Squatina guggenheim* through a wide array of teleosts (18 species of Batrachoidiformes, Gadiformes, Ophidiiformes, Perciformes, Pleuronectiformes, and Scorpaeniformes). *Grillotia patagonica* has a lower specificity for its definitive hosts, being recovered from 3 species in 3 different genera of rajiforms (*Bathyraja*, *Psammobatis* and *Zearaja*). Plerocerci of *G. patagonica* were found in 7 species of teleosts (Perciformes and Gadiformes). In this study, *D. pacificus* and *G. carvajalregorum* were found in hosts from temperate waters of the Warm Temperature Southwestern Atlantic Province, whereas *G. patagonica* seems to be restricted to colder waters in the Patagonian shelf (Magellanic Province).

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DIVERSITY OF TAPEWORM LARVAE IN SOME TELEOST FISHES FROM KALAAT EL ANDALOUS (NORTH OF TUNISIA)

C. Ben Saad¹, N. Ghanmi¹, L. Gargouri¹

Research on cestodes is limited in Tunisia and mainly concerns the adult stage harvested from chondrichthyan fishes. No work has been published on the larvae of cestodes from teleost fish, hence the interest of this work. From January 2015 to February 2017, we examined a total of 918 fishes, from Kalaat El Andalous, belonging to 4 families Mullidae (*Mullus surmuletus* and *Mullus barbatus*); Carangidae (*Trachurus trachurus*); Merluccidae (*Merluccius merluccius*); Scombridae (*Scomber japonicus*) and Scorpaenidae (*Scorpaena porcus*). Cestode larvae, taken from the digestive tract of fishes, are examined in vivo for determination. Our investigations allowed us to identify 3 species: *Progrillotia dasyatidis* (Beveridge Neifear and Euzet, 2004); *Lacistorhynchus tenuis* (V. Beneden, 1858); *Nybelinia africana* (Dollfus, 1960); while 2 other Larvae still unidentified: *Tetrarhynchidae* genus *Trypanorhyncha* (Diesing, 1863) and *Tetraphyllidea* (Carus, 1863). The study of parasitic infra-communities revealed that 61.07% of the fishes are hosting a single parasite species, while 29.53% hosts two species of cestode larvae. Therefore, parasitic infra-communities are considered as poor ones. The study of the distribution of cestoda revealed that those helminths can meet in two or more parts of the digestive tract of their host; so they are considered generalists. The overall dynamic of parasitism showed that *Tetraphyllidea* larvae, is the most frequent species (P = 19.85%) in *M. merluccius*. The diversity of Cestode larvae of fishes in Kalaat El Andalous is compared with the results available in other localities.

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CURRENT PROBLEMS IN THE TAXONOMY AND SYSTEMATICS OF CARYOPHYLLIDEAN TAPEWORMS

D. Barčák¹, M. Oros¹, V. Hanzelová¹, T.Scholz²

Recently, an extensive material of tapeworms of the order Caryophyllidea was studied as a part of an international research project on their taxonomy and phylogeny. Newly collected tapeworms were analysed using multidisciplinary approach combining morphological and molecular methods. In some taxa, cryptic species diversity was detected, whereas extraordinary phenotypic plasticity was observed in others. Cryptic species diversity was detected within the genus *Paracaryophyllaeus* Kulakovskaya, 1961. Three independent, well supported clades were discovered based on molecular data; two of them represented morphologically indistinguishable individuals from East Asia. Specimens of the third clade found in an endemic loach (Cobitidae) in Turkey bore unique combination of morphological traits, and were described as a new species, *P. vladkae*. In contrast, phenotypic plasticity (intraspecific morphological variability) of the two most widespread species of *Caryophyllaeus* Gmelin, 1790, namely *C. laticeps* and *C. brachycollis*, was revealed, and several morphotypes of both species typical for different fish hosts were characterised. Additionally, new taxonomic arrangements were proposed and a new species, *C. chondrostomi*, was described. Species-specific traits were identified in the posterior part of the body (morphology of vas deferens and the cirrus sac), whereas the anterior part of the body seemed to bear highly variable characters (morphology of scolex and localization of most anterior testis and most anterior vitelline follicle). Considering these taxonomic problems, modern tools of integrative taxonomy can unravel the actual species diversity and host specificity of caryophyllidean tapeworms.

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TOWARDS A ROBUST SYSTEMATIC BASELINE OF TAPEWORMS (CESTODA: PROTEOCEPHALIDAE) OF NEOTROPICAL CATFISHES: A MORPHOLOGICAL REAPPRAISAL OF THREE OLD GENERA

P.V. Alves^{1,4}, A. de Chambrier², J.L. Luque³, T. Scholz⁴

The extraordinary diversity of tapeworms of the order Onchoproteocephalidea Caira et al., 2014 from South American pimelodids and other catfishes (Siluriformes) has been documented since the mid-19th century. Three of these old taxa, namely *Ephedrocephalus* Diesing, 1850, *Goezeella* Fuhrmann, 1916 and *Zygobothrium* Diesing, 1850, are reviewed on the basis of taxonomic evaluation of type and newly collected material from catfishes in the Amazon River basin, South America, and their type-species are redescribed. *Ephedrocephalus microcephalus* Diesing, 1850 (Ephedrocephalinae) and *Zygobothrium megacephalum* (Zygobothriinae), both parasites of the redbtail catfish *Phractocephalus hemiliopterus* (Bloch & Schneider), are characterized by the distribution of vitelline follicles in one ventral field, occupying almost entire cortex of proglottids, and the morphology of scolex, which is large, massive, bearing four uniloculate suckers that open externally by two orifices, respectively. *Goezeella siluri* Fuhrmann, 1916 (Monticelliinae) is typified by the exclusively ventral position of the vitelline follicles, the inner longitudinal musculature formed by dense individual muscle fibres, a well-developed metascolex and biloculate suckers. *Goezeella* is also unusual among other Neotropical proteocephalids by its occurrence in catfishes of as many as four different families, i.e. Auchenipteridae, Cetopsidae, Heptapteridae and Pimelodidae. This study sheds light on the morphology of three earlier established genera of proteocephalids and their type species, and highlights the importance of depositing type material in internationally recognized collections.

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NEW SYSTEMATICS AND PHYLOGENY OF DIPHYLLOBOTHRIDEAN TAPEWORMS

R. Kuchta¹, A. Waeschenbach², J. Brabec¹, T. Scholz¹, D. T. J. Littlewood²

Broad tapeworms (Cestoda: Diphyllbothriidea) are the principal agents of widespread food-borne cestodoses. Diphyllbothriosis and diplogonoporosis, caused by members of the genera *Diphyllbothrium*, *Diplogonoporus* and *Adenocephalus*, are the most common fish cestodoses, and has seen recent (re)emergences in Europe due to the increasing popularity of eating raw or undercooked fish. Sparganosis is a debilitating and potentially lethal disease caused by the larvae of the genus *Spirometra*, which occurs throughout much of the (sub)tropics and is caused by the consumption of raw snakes and frogs and water contaminated with infected copepods. Both diseases are caused by several species, however, the frequency by which the transition to humans has occurred has never been studied. Using a phylogenetic framework of 30 species based on large and small nuclear ribosomal RNA subunits (*ssrDNA*, *lsrDNA*), large subunit mitochondrial ribosomal RNA (*rrnL*) and cytochrome *c* oxidase subunit I (*cox1*), we assess that humans have been acquired as accidental hosts four times across the tree of life of diphyllbothriids. However, polytomies prevent an unambiguous reconstruction of the evolution of intermediate and definitive host use. The broad host spectrum and the ease with which switching between major host groups appears to have occurred, may hold the answer as to why accidental human infection occurred multiple times across the phylogeny of diphyllbothriideans. We recommend to synonymize the genus *Diplogonoporus* with *Diphyllbothrium* and to divide the latter polyphyletic genus into (i) the resurrected genus *Dibothriocephalus* to include freshwater and terrestrial species including *Dib. dendriticus*, *Dib. latus* and *Dib. nihonkaiensis* as most common parasites of humans, (ii) the genus *Diphyllbothrium* to accommodate parasites from cetaceans including type species *D. stemmacephalum* and *D. balaenopterae* known also from man, and (iii) the non-monophyletic aggregate of marine species from seals provisionally considered as *incertae sedis*.

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A DIGEST OF FISH TAPEWORMS

T. Scholz¹, R. Kuchta¹

Members of the following seven of a total of 19 cestode orders mature in ray-finned fishes (Actinopterygii): Amphilinidea (mainly in acipenseriforms and osteoglossiforms; 8 species in 6 genera), Bothriocephalidea (in several freshwater and marine fish groups; 129/47), Caryophyllidea (mainly in cyprinids and suckers, also in some catfishes; 117/42), Haplobothriidea (exclusively in bowfin; 2/1), Nippotaeniidea (in osmeriforms and perciforms; 6/1), freshwater Onchoproteocephalidea (mainly in catfishes 194/55), and Spathebothriidea (in several freshwater and marine fish groups; 6/5). Updated information on species diversity, host associations, interrelations and geographical distribution is provided for every group. The existing phylogenetic hypotheses suggest that tapeworms colonized ray-finned fishes several times and form several independent lineages. From a total of 461 fish tapeworms only 92 species are exclusively marine. So, freshwater species dominate the assemblage. No general patterns in host use can be observed at the level of fish definitive hosts because cestodes of fishes occur in not closely related host groups. Nevertheless, only three fish orders host almost three fourth of all tapeworms of fishes, namely Siluriformes (36% of all cestode species), Cypriniformes (22%) and Perciformes (16%). Nearly two thirds (61%) of fish tapeworms have a strict (oioxenous) specificity and one third (33%) is stenoxenous. The highest proportion (8%) of euryxenous species is among the bothriocephalideans, including one of the most opportunistic fish helminth, the invasive Asian fish tapeworm (*Schyzocotyle acheilognathi*), which has been reported from more than 200 fish species and axolotl, snakes and birds. Tapeworms of fishes are more diverse in the temperate zones of the northern hemisphere (Nearctic and Palearctic regions with 26% and 23% of all species) than in the tropics, with the exception of onchoproteocephalideans in South America. However, this may reflect a lower sampling effort in tropical regions and the southern hemisphere.

Session C:
CYCLOPHYLLIDEANS

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REVIEW OF THE CESTODES OF THE TRIBE DITESTOLEPIDINI SPASSKY, 1954 (CYCLOPHYLLIDEA, HYMENOLEPIDIDAE)

R. Binkienė¹, S. Kornienko²

The present study analysed the taxonomic status of the genera of the tribe Ditestolepidini of Holarctic shrews (*Sorex*). The main features of the tribe Ditestolepidini Spassky (1954) considered the serial type of strobilation, confluence of uteri of several proglottides and forming syncapsule. The aim of the present study is to improve diagnosis and to make the key of all genera of this group. Our investigation of cestodes of the tribe Ditestolepidini revealed the complex of morphological features that should be consider during study of these cestodes: type of strobilation (serial homo- or heteronomous, or gradual), number of proglottides in stobila, location of suckers on the scolex, presence of rudimentary rostellum, position and number of testes, position of cirrus-sac relatively to aporal osmoregulatory canals, armament and form of cirrus, absence of internal seminal vesicle, ovary shape, uterus shape and type of it development. After revision of specimens of all genera we concluded that Holarctic shrews (*Sorex*) incorporate seven known genera: *Ditestolepis*, *Spasskylepis*, *Mathevolepis*, *Ecrinolepis*, *Diorchilepis*, *Gulyaevilepis*, *Novobrachylepis*; and one species *Ditestolepis pulchra* does not correspond to the description of the genus *Ditestolepis*. The complex differential features of *D. pulchra* are: serial strobilation, very large scolex with prominent suckers, three testes situating in a straight line, not lobed ovary and spherical uteri; allows to clearly distinguish this species from other known genera. For this species new genus must be created. Research funded by Research Council of Lithuania (grant No. MIP-43/2015) and the Russian Fund for Fundamental Research (Projects No. 14-04-00871, 15-04-03785 and 17-04-00227).

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MORPHOLOGICAL AND MOLECULAR DIFFERENTIATION OF THE GENUS *NEOSKRJABINOLEPIS* (CESTODA, HYMENOLEPIDIDAE) FROM THE SHREW *SOREX*

S. Kornienko¹, V. Tkach², N. Dokuchaev³

Taxonomy and phylogenetic relationships of cestodes of the genus *Neoskrjabinolepis* Spassky, 1947 from long-tailed shrews (*Sorex*) were studied using morphological and DNA sequence data. This genus currently consists of two subgenera separated on the basis of their strobilar development. *Neoskrjabinolepis* (*Neoskrjabinolepis*) (type species *N. schaldybini* Spassky, 1947) is characterized by the gradual maturation of proglottides while members of *Neoskrjabinolepis* (*Neoskrjabinolepidoides*) (type species *N. singularis* (Cholodkowsky, 1912) Spassky, 1954) have strobilae consisting of series of proglottides, each containing segments at the same stage of development. Our study has revealed several morphological characters that can be reliably used for differentiation among *Neoskrjabinolepis* spp., namely the type of strobilation (gradual vs serial), shape and size of rostellar hooks, cirrus length and cirrus armature, size of the cirrus-sac and its position in relation to poral osmoregulatory canals, and number of eggs in gravid proglottides. Currently, the subgenus *Neoskrjabinolepis* includes 5 species and the subgenus *Neoskrjabinolepidoides* includes 10 species while the exact position of one species is uncertain due to the presence of alternating genital pores. Results of sequence comparisons and phylogenetic analysis confirmed the taxonomic utility of morphological characteristics listed above and supported the validity of species described based on morphology alone. Research funded by the Russian Fund for Fundamental Research (Projects No. 15-04-02668 and 17-04-00227).

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ON PHYLOGENETIC RELATIONSHIPS AND PROBLEMS OF TAXONOMY OF HYMENOLEPIDID CESTODES IN THE “*RODENTOLEPIS* – CLADE”

A.A. Makarikov¹, V.V. Tkach², T.A. Makarikova¹

Available morphological and molecular evidence strongly suggests that many hymenolepidids belonging to the “*Rodentolepis* - clade” which occur in small mammals represent composite and non-monophyletic taxa. This study addresses some existing problems of systematic and taxonomy of this group of cestodes. Our analysis has demonstrated several distinct genus-level lineages among species traditionally attributed to the *Rodentolepis* complex from rodents. One of these lineages represents *Rodentolepis* (sensu stricto) and includes the type species and several congeners, while two other groups were recently separated into genera *Pararodentolepis* and *Nomadolepis* based on morphological characteristics and molecular phylogenetic evidence. In addition, we discovered new morphological distinctive characters typical for the genera *Armadolepis* (sensu stricto) from dormice and *Vampirolepis* (sensu stricto) from bats. A new genus of hymenolepidids from bats was described. We established complex of the most useful morphological characters for classification of cestodes from the “*Rodentolepis* - clade” at generic level. Our phylogenetic analysis based on nuclear ribosomal 28S DNA gene fully corroborates the results of morphological study and supports the status of genera *Armadolepis*, *Nomadolepis* and *Pararodentolepis* as valid taxa. Denser taxon sampling for molecular phylogenetic analyses, including type species of nominal genera, is essential in order to further clarify the phylogenetic relationships, systematics and taxonomy of this diverse group of hymenolepidids. Ultimately, its revision should be based on a combination of morphological analysis and molecular phylogenetic data.

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NEW INSIGHTS INTO THE GENETIC DIVERSITY OF *ECHINOCOCCUS GRANULOSUS* SENSU STRICTO

Dennis Ebi¹

Echinococcus granulosus sensu stricto (s.s.) is a taeniid cestode with worldwide distribution. It is primarily transmitted in domestic lifecycles involving dogs and livestock, with which it has been distributed globally. It is particularly well adapted to sheep as hosts, but has a sufficiently low intermediate host specificity to allow the involvement of numerous other hosts (including wildlife) in the transmission, and has even been able to establish secondary wildlife cycles (e.g. in Australia). Concerning the origin of the parasite, the Middle East and western Asia are candidate regions where the switch from its (putative) ancestral transmission between wolves and wild sheep may have occurred. Among other indicators, this hypothesis is based on the analysis of mitochondrial sequence diversity, which has become increasingly useful to re-trace the global expansion of this important zoonosis, including translocations by human activity.

To establish baseline data for biogeographical studies, a total of 1085 isolates from different regions of the world were analyzed for microdiversity of a 1609 bp fragment of the mitochondrial *cox1* gene. A total of 386 haplotypes were found in these set of samples. In addition with 71 haplotypes from public databases diversity and similarity of populations were visualized with haplotype networks, and diversity indices were calculated. Results give convincing support to a hypothetical origin of this parasite in western Asia and provide indications for an early spread into the Mediterranean region and - later - into sub-Saharan Africa and to other continents.

Session D:
GENERAL TAPEWORM RESEARCH

¹Ecology and Evolutionary Biology, University of Connecticut, USA

EXAMINING MORPHOLOGICAL NOVELTY IN AN ENIGMATIC TAPEWORM: A COMPARATIVE GENOMIC AND TRANSCRIPTOMIC APPROACH

K.A. Gallagher¹, J.N. Caira¹, J. Wegrzyn¹

This study examines factors underlying the evolution of the morphology of *Litobothrium aenigmaticum*, a bizarre tapeworm that parasitizes pelagic thresher sharks in Taiwan and Mexico. Although phylogenetically nesting robustly within the genus *Litobothrium*, this species does not resemble its congeners. This study will use comparative genomics and transcriptomics to investigate gene sequence, expression, and/or regulation differences that might account for this novel morphology. Living specimens of *L. aenigmaticum*, *Litobothrium daileyi*, and *Litobothrium amplifica* were collected from 2 pelagic thresher sharks in Taiwan. Subsets of each species were preserved in 95% ethanol for genomics and in RNAlater for transcriptomics. Several specimens of *L. daileyi* were also preserved for cytogenetic work. Small insert (i.e. 350 and 550 bp in length) libraries were generated for genomic sequencing of all 3 species. Mate-pair libraries, 2 and 7 kb in length, were also prepared for *L. aenigmaticum*. Rough estimates of genome sizes obtained using the program *Jellyfish*, were 350 Mb for *L. aenigmaticum*, 360 for *L. daileyi*, and 390 Mb for *L. amplifica*. Following removal of low quality and/or short reads, using *Sickle* for the small insert libraries and *Trimmomatic* for the mate-pair libraries, reads were assembled using *SOAPdenovo*, *ABYSS2*, *SPAdes*, and *MaSURCA*. Assembly quality was evaluated using *QUAST*. Genome scaffolding was done using *SSPACE* and quality again evaluated using *QUAST*. These assemblies yielded refined genome size estimates of 302–317 Mb for *L. aenigmaticum*, 280–345 Mb for *L. daileyi*, and 304–384 Mb for *L. amplifica*. RNA extraction and library preparation are currently underway. Preliminary RNA yields indicate that transcriptome libraries can be generated from single specimens of *L. aenigmaticum* and *L. nickoli*. However, as result of their small size, specimens of *L. daileyi* and *L. amplifica* will need to be pooled for transcriptome library preparation. Once sequenced, the RNAseq libraries will be mapped back to the assembled genomes for differential gene expression analyses. Cytogenic work using *L. daileyi* will be completed in the near future to determine number and

arrangement of chromosomes in this species. Our results indicate that the genomes of litobothriideans are smaller than those of diphyllbothriidans, but larger than those of cyclophyllideans.

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LOST (AND FOUND!) IN A SEA OF NOVELTY

V.M. Bueno¹, J.N. Caira¹

Historically, tapeworm species parasitizing skates have commonly been reported from multiple host species, resulting in an apparent pattern of low species diversity, low host specificity, and broad geographic distribution of these tapeworms. For example, *Echeneibothrium variable*, has been reported from 8 skate species in 13 distinct localities across Europe and the USA. Furthermore, although skates represent a highly diverse group of elasmobranchs, their superficial morphological homogeneity has led to approximately half of the several hundred species being assigned to the single genus *Raja*. This may have reinforced the notion that skate tapeworms exhibit low species diversity and are able to parasitize several species of hosts, because their hosts were considered to be closely related. Advances in the systematics and taxonomy of skates over the past 25 years have included the generation of a robust elasmobranch phylogeny based on molecular data, which has greatly contributed to the revision and stability of the current status of skate taxonomy. The majority of the species once placed in *Raja* has now been assigned to one of the 35 other skate genera currently recognized. This revised systematic framework has led to questions about the apparent low species diversity, and therefore low host specificity, observed in their tapeworms. Necropsy of 24 skate species—19 for the first time—allowed us to examine questions of low diversity and host specificity in tapeworms, by focusing on, but not limited to, species of *Echeneibothrium*. In total, 15 of these species of skates hosted *Echeneibothrium* species. Contrary to previous work, 43 distinct morphotypes of *Echeneibothrium*, 34 of which are potentially new to science, were found. Sequencing of a subset of the morphotypes revealed that at least some *Echeneibothrium* species seem to track host phylogeny and are, in fact, highly host specific and restricted in distribution. A more accurate understanding of the taxonomy and systematics of skates and their tapeworms has allowed us to revise the patterns of host associations in this system, directing our efforts for more meaningful future research questions.

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CHECKLIST OF BRAZILIAN CESTODA

M.C.N. Justo¹, B.M.M. Fernandes¹, M. Knoff², M.Q. Cárdenas¹, S.C. Cohen¹

Several studies have been published over the years concerning the cestode parasites of different Brazilian host groups, comprising the vertebrates and invertebrates. Several authors have been studying this group of helminths since that preliminary considerations on Brazilian cestodes were published by Travassos (1965), describing and reporting on new and known species from wild, domestic and human hosts. The aim of the present study is to bring a surveyed checklist of species of Cestoda that have been described and/or reported in Brazil. In this study the order, family, genus and parasite species are presented in alphabetical order. For each parasite species listed, the following information is provided: current scientific name, including author(s) and date(s), followed by updated scientific name of host species, with original host record name in parentheses (when changed), site and locality (when available), records and remarks. Species described or reported with different names are noted in the remarks. It resulted in information on 432 species of Cestoda, distributed across 15 orders and 36 families. Fifty species were unidentified and nine considered *species inquirenda*. Among fish, *Zungaro zungaro* was the most parasitized host (with 18 species of cestodes); on amphibians, it was *Rhinella icterica*, with 3 species; on reptiles, it was *Bothrops jararaca*, with seven species; on birds, *Gallus gallus* presented the largest association with cestodes, with 13 species reported; considering mammals, *Homo sapiens*, presented 13 different species; and from invertebrates were reported few cestode species. The small number of parasitic helminths described is probably due to undersampling of potential hosts, along with the small number of helminth taxonomists.

¹Helminthological Collection of the Oswaldo Cruz Institute, Fiocruz, Rio de Janeiro, RJ, Brazil

TYPE MATERIAL OF CESTODA HOUSED IN THE HELMINTHOLOGICAL COLLECTION OF THE OSWALDO CRUZ INSTITUTE/ FIOCRUZ (CHIOC) FROM 1979 TO 2016

D.A. Lopes¹, A. Mainenti¹, M. Sanches¹, D.C. Gomes¹, M. Knoff¹

The century-old Helminthological Collection of the Oswaldo Cruz Institute/Fiocruz (CHIOC) contains helminths that form part of the fauna of Brazil and other countries, from a wide range of hosts that were caught in different biomes. Nowadays, the CHIOC holds around 38.400 samples of helminth parasites. They are holotypes, paratypes and representative specimens of Platyhelminthes, Acanthocephala, Nematoda and other non-helminth phyla. The first catalogue of the type material held in this Collection was published by Rego et al., in 1979. The authors recorded 719 types (only holotypes or type series) of helminths, including 408 nematodes, 216 digenetic trematodes, 11 monogenoids, 52 acanthocephalans, 28 cestodes and four pentastomids. Subsequent to this publication, the collection has grown substantially and the number of types has increased significantly as well. Recently, Lopes et al. (2016) published another catalogue listing 203 type species of Monogenoidea. The present study aims present a catalog of type species held in this collection, including platyhelminths of the classes Cestoda that have been deposited in CHIOC since 1979, up to 1 December 2016, arranged taxonomically as orders, families, genera and species, under the original spelling and combinations. It has now added 130 primary types of Cestoda, represented by 44 species distributed across 28 genera and 10 families. It was observed that the species of parasites were deposited from 37 different hosts caught in seven Brazilian states, and more three countries of American continent (Paraguay, Ecuador and Costa Rica). Most of these deposits were made by Brazilian researchers, but foreigners also had the significant contribution, expanding and diversifying its parasitological heritage.

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PARASITE SAMPLES FROM FREE-LIVING MARINE ANIMALS USING NON-INVASIVE METHODS

S. Kleinertz¹

First reports on the gastrointestinal parasite fauna infecting free-living marine mammals and seabirds, such as Indo-Pacific bottlenose dolphins (*Tursiops aduncus*) from the Red Sea in Egypt, large whales (Baleen whales: *Balaenoptera musculus*, *B. physalus*, *B. borealis* and Sperm whales: *Physeter macrocephalus*) from the Azores as well as protected Emperor penguins (*Aptenodytes forsteri*) from Atka-Bay, Antarctica, revealed the presence of cestode parasites amongst others. Using classical veterinarian parasitological techniques, such as SAF-method, carbol-fuchsin stained faecal smears, coproantigen-ELISA, PCR and macroscopical analyses were applied. The studies revealed infections with a variety of different parasite species belonging to the protozoans and metazoans (e.g. trematodes, cestodes, nematodes) with some of them bearing zoonotic and pathogenic potential. Cestodes identified during these studies were especially eggs of *Diphyllobothrium* spp. (*Tursiops aduncus* and *B. physalus*) and *Tetrabothrius* spp. (*A. forsteri*) as well as proglottids of *Parorchites zederi* (*A. forsteri*). These studies demonstrate that non-invasive methods are a useful tool for future monitoring studies, targeting the impact of environmental change in marine mammals, seabirds and possibly elasmobranchs.

POSTER PRESENTATIONS

¹Department of Ecology & Evolutionary Biology and Biodiversity Institute, University of Kansas

THE TAPEWORM FAUNA OF THE GIANT DEVILRAY (*MOBULA MOBULAR* [BONNATERRE]): A TRANS-PACIFIC DISTRIBUTION

K.S. Herzog¹, K. Jensen¹

Over two decades ago, specimens of the giant devilray, *Mobula mobular* (Bonnaterre), were collected from the Gulf of California and examined for tapeworms for the first time. Since then, six tapeworm species representing four genera have been described from this enigmatic host as new. These included three species in the order Lecanicephalidea (*Healyum harenamica* Jensen 2001, *Healyum pulvis* Jensen 2001, and *Quadcuspibothrium francisi* Jensen 2001) and three species in the order Trypanorhyncha (*Fellicocestus mobulae* Campbell & Beveridge 2006, *Hemionchos major* Campbell & Beveridge 2006, and *Hemionchos mobulae* Campbell & Beveridge 2006). Though *M. mobular* is known to possess a circumglobal distribution, to date, these tapeworm species have only been reported from host specimens collected from localities in the eastern Pacific Ocean. Recent elasmobranch collection efforts off the island of Taiwan allowed for the examination of tapeworms from *M. mobular* from localities in the western Pacific Ocean. The two host specimens from the island of Taiwan were parasitized by all four genera and five of the six species originally described from the Gulf of California. This newly collected material allowed for generation of the first molecular sequence data for representatives of these four genera, ultimately informing their phylogenetic placement within their respective orders. This material also allowed for generation of the first data on microthrix patterns for trypanorhynchs from *M. mobular*. The expanded ranges of these tapeworms suggest that they possess a trans-Pacific distribution; whether these tapeworm distributions mirror the circumglobal distribution of their host species remains to be determined.

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SCANNING ELECTRON MICROSCOPIC OBSERVATION OF *DIPHYLLOBOTHRIMUM LATUM* (CESTODA)

M. Oros¹, D. Barčák¹, R. Kuchta²

A comparative study of the plerocercoids of *Diphyllobothrium latum* was carried out using scanning electron microscopy. Three-dimensional micrographs of *Diphyllobothrium latum* from the musculature of perch (*Perca fluviatilis*) collected in Como Lake, Italy in April 2017 were documented. The main aim of the present study was to present comparative data on the scolex morphology, bothrium and the body of these cestodes based on the material processed by the different method of fixation, with hot 4% formaldehyde solution (= formalin) and cold 96% ethanol fixation of specimens collected from the same host in same locality. Specimens used for SEM observations were dehydrated through a graded ethanol series, followed by acetone series, dried by HMDS (hexamethyldisilazane), sputter-coated with 20–25 nm of gold and examined with a JEOL JSM 6510LA microscope. The whole body (10 mm maximum length) of studied plerocercoid fixed by hot fixative (formalin) is lanceolate that is widest in the anterior third and tapered posteriorly. Deep, transvers grooves were observed regularly along the body surface. The scolex with very shallow bothria extends anteriorly. In contrast, plerocercoid of *D. latum* fixed by cold ethanol is more contracted (3 mm maximum length), with less developed grooves, only lightly wrinkled, and the scolex is drawn inside. Since morphology and morphometrics of the plerocercoids are consistently influenced by different fixation technique, it is likely that inadequate preparation technique may introduced several errors in the taxonomic and ecological literature of *Diphyllobothrium*.

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TRYPANORHYNCHS FROM ELASMOBRANCHS IN THE WARM TEMPERATE SOUTHWESTERN ATLANTIC AND MAGELLANIC PROVINCES

A. Menoret¹, V. A. Ivanov^{1, 2}

Trypanorhynchs are well represented in the Temperate South America Realm, with a total of 29 species described from adults in 17 genera, recovered from sharks and batoids along the Warm Temperature Southwestern Atlantic Province (WTSWA) and the Magellanic Province (MA). Most species (14) are cosmopolitan or have a wide distribution, and infect hosts with oceanic or circumglobal distribution. Five species are restricted to the WTSWA (i.e., *Heteronybelinia mattisi*, *Dollfusiella acuta*, *Dollfusiella taminii*, *Grillotia carvajalregorum* and *Parachristianella damiani*), and 4 species were only found in the MA (i.e., *Prochristianella heteroacantha*, *Dollfusiella musteli*, *Mecistobothrium oblongum* and *Grillotia patagonica*). *Dollfusiella vooremi* was found in both regions. In general, all the species follow the range of distribution of their respective hosts. Exceptions to this pattern are *G. patagonica*, *P. damiani* and *M. oblongum*, which are restricted to a particular biogeographic province, regardless their respective hosts have a wider distribution. *Grillotia patagonica* is only found in the Patagonian shelf (MA), while its host, *Psammobatis rudis*, has a wider distribution up to warmer waters. Despite the wide distribution of *Myliobatis goodei* along the western Atlantic, the specimens show locally distinctive cestode faunas, which are correlated with well-defined biogeographic regions (i.e., *P. damiani* in WTSWA and *M. oblongum* in MA). A similar pattern has been observed in the same host and lecanicephalidean cestodes.

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A NEW GENUS OF RHINEBOTHRIIDEA FROM SPECIES OF *PSAMMOBATIS* (RAJIFORMES, ARHYNCHOBATIDAE) OFF ARGENTINA

S. Franzese¹, V.A. Ivanov^{1,2}

Rhinebothriideans are parasites of a wide array of batoids (i.e., Myliobatiformes, Rajiformes, Rhinopristiformes and Torpediniformes). The order is cosmopolitan in distribution, with a great diversity in tropical and subtropical regions, having some genera a particular affinity for cooler waters. During a parasitological survey along the coast of Argentina, 4 species of the arrhynchobatid genus *Psammobatis* were caught in different locations: *P. normani* and *P. extenta* off Buenos Aires Province, and *P. rudis* and *P. bergi* off Tierra del Fuego Province. *Psammobatis normani* and *P. rudis* harbored a particular species of a new genus of Rhinebothriidae. Specimens of the new genus can be identified by having a unique pattern of septa and loculi on the distal bothridial surface, including a central region with semicircular septa. It can also be distinguished from all other described genera in Rhinebothriidea by a combination of several morphological features. The species collected from *P. normani* and *P. rudis* can be differentiated from one another by features including the number of bothridial loculi, the shape of the cirrus sac and by slight differences in the microthrix pattern. Only a few specimens of *P. bergi* and *P. extenta* have been examined so far. We expect to find more representatives of the new genus as the sample size of the different species of *Psammobatis* increase.

Workshop plan



9th International Workshop for Cestode Systematics and
Phylogeny

Monday 7th – 10th of August 2017

SCIENTIFIC ORGANIZATION

Prof. Dr. rer. nat. habil. Harry W. Palm

Dr. rer. nat. Sonja Kleinertz

M. Sc. Berit Wasenitz

Monday, 7.8.17		AUTHORS	TALK	Room
08:30-08:45		Mohr	Welcome speech of the Dean of the AUF Faculty	SR 2
08:45-10:15	23	Caira, Jensen	Presentation of the synopsis PBI	SR 2
10:15-10:45	COFFEE BREAK			
10:45-11:45	24	Caira, Scholz	Future of the cestode database	SR 2
11:45-12:15		All participants/Discussion	Cestode Identification Keys/Examples and format	SR 2
12:15-13:00	LUNCH BREAK			
13:00-13:20	25	Waeschenbach, Briscoe, Hocking, Foster, Georgiev, Mariaux, Tkach, Caira, Jensen, Nakao, Wan-Zhong Jia, Littlewood	A mitogenome phylogeny of the Cestoda	SR 2
13:20-17:00		Working groups 1-7	WORKSHOP: Generic level Keys I	SR 1, 2, 3, 4, 18, OKI, Hörsaal (JLAG)
Workshop groups	Working group 1	Cestodaria (and smaller taxa) e.g.: Bray, <i>Stolz</i>		SR 1
	Working group 2	Diphyllidea Ivanov, <i>Wasenitz</i>		SR 2
	Working group 3	Tetraphyllidea Caira, Jensen, <i>Unger</i>		SR 3
	Working group 4	Trypanorhyncha <i>Palm</i> , Hasseli, Schaeffner		OKI
	Working group 5	Diphyllbothriidea, Botriocephalidea Scholz, Kuchta, <i>Kleinertz</i>		SR 18 (LAG)
	Working group 6	Proteocephalidea Knoff, Rego, <i>Theisen</i>		SR 4
	Working group 7	Cyclophillidea Makarikov, Kornienko, Binkienė, Ebi, <i>Pikalov</i>		Hörsaal (JLAG)

Tuesday 8.8.17		AUTHORS	TALK	Room
08:30-09:45	26	Vandepitte, Decock, Vranken, Dekeyzer, Verfaillie, Vanhoorne	An introduction to Aphia and the World Register of Marine Species (WoRMS)	SR 2
09:45-10:15	COFFEE BREAK			
10:15-11:00		All participants/Discussion	Update of the manual for cestode research according to groups	SR 2
11:00-12:00		Working groups 1-7	Workshop: Generic level Keys II	SR 1, 2, 3, 4, 18, OKI, Hörsaal (JLAG)
12:00-13:00	LUNCH BREAK			
13:00-17:00		Working groups 1-7	Workshop: Species level Keys	SR 1, 2, 3, 4, 18, OKI, Hörsaal (JLAG)

Wednesday 9.8.17	AUTHORS		TALK	Room
08:30-10:00	27	Palm, Hasseli, Schaeffner	Morphological characters of the Trypanorhyncha	SR 2
10:00-10:15	COFFEE BREAK			
10:15-11:45	28	Scholz, Kuchta	Presentation of morphological characters of the Bothriocephalidea and Diphyllbothrioidea	SR 2
11:45-12:30	LUNCH BREAK			
12:30	Field Trip			

Thursday 10.8.17	AUTHORS		TALK	Room
08:30-10:00		All participants/Discussion	Summary of results according to groups	Penta Hotel
10:00-10:15	COFFEE BREAK			
10:15-11:00		All participants/Discussion	Presentation of next Meeting locations and election	Penta Hotel
11:00-12:00		All participants/Discussion	Final discussions and outlook; Closing	Penta Hotel

J.N. Caira, K. Jensen

„Presentation of the synopsis PBI”

REMARKS:

J.N Caira, T. Scholz

„Future of the cestode database”

REMARKS:

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A MITOGENOME PHYLOGENY OF THE CESTODA

Andrea Waeschenbach¹, Andrew G Briscoe², Suzanne Hocking, Peter Foster¹ Boyko Georgiev³, Jean Mariaux⁴, Vasyl Tkach⁵, Janine N Caira⁶, Kirsten Jensen⁷, Minoru Nakao⁸, Wan-Zhong Jia⁹, D Tim J Littlewood¹

Although significant advances have been made in reconstructing the ordinal-level backbone of the Cestoda, the addition of more taxa, specifically the various orphan lineages of the “Tetraphyllidea”, has resulted in a number of polytomies that need resolving (Caira et al., 2014). Furthermore, limited advances have been made in resolving the interrelationships of the major cyclophyllidean lineages, as most sequencing effort has historically been spent on medically important taxa. Here, we capitalize on the vast molecular tissue collection that was accrued during the PBI project and selected key taxa (14 “tetraphyllideans”; 38 cyclophyllideans) for complete or almost complete mitogenome sequencing. In addition, mitogenomes were completed for taxa for which ~4,000 bp of mtDNA had been generated for the Waeschenbach et al. 2012 paper. The methodology involved Illumina sequencing of both long-range PCR amplicons as well as bioinformatic genome-skimming of total genomic DNA reads. These newly generated data were combined with unpublished genomes generated by co-authors Minoru Nakao and Wan-Zhong Jia and all currently available published mitogenomes. In order to maximize phylogenetic resolution, the mitogenome data were combined with nuclear ribosomal RNA gene data (18S and 28S rDNA) wherever possible.

Caira et al. (2014) *Int J Parasitol* 44:55-73

Waeschenbach et al. (2012) *Mol Phylogenet Evol* 63:834-847

A.G. Waeschenbach, A.G. Briscoe, S. Hocking, P. Foster, B. Georgiev, J. Mariaux, V. Tkach,
J.N. Caira, K. Jensen, M. Nakao, Wan-Zhong Jia⁹, D.T.J. Littlewood

„ A mitogenome phylogeny of the Cestoda ”

REMARKS:

AN INTRODUCTION TO APHIA AND THE WORLD REGISTER OF MARINE SPECIES (WORMS)

Leen Vandepitte¹, Wim Decock¹, Sofie Vranken¹, Stefanie Dekeyzer¹, Kevin Verfaille¹, Bart Vanhoorne¹

The Aphia platform is an infrastructure designed to capture taxonomic and related data and information, and includes an online editing environment. The latter allows easy access to experts so they can update the content of the database in a timely fashion. Aphia is the core platform that underpins the World Register of Marine Species (WoRMS) and its more than 80 related global, regional and thematic species database, but it also allows storage of non-marine data. The content of Aphia can be consulted online, either by individual users or machine-to-machine interactions. Although the focus is on taxonomy, Aphia can also capture e.g. distributions and traits information, including the relation between parasites and their hosts.

The content of Aphia is part of the LifeWatch Taxonomic Backbone (LW-TaxBB), an infrastructure that facilitates the standardization of species data and that (virtually) brings together the many distributed biodiversity data repositories and operating facilities. The LW-TaxBB deals with five major components, being taxonomy, biogeography, ecology, genetics and literature.

Over the years, relationships with other existing regional, thematic and global players in the field of biodiversity have been built, for example with the Catalogue of Life (CoL), Encyclopedia of Life (EoL), FishBase and the Ocean Biogeographic Information System (OBIS), and data from Aphia are being used within many biodiversity-related projects. This presentation will provide an overview of Aphia - its structure and content - with a focus on WoRMS and its global, regional and thematic sub-registers, and will highlight the relationships that Aphia has with many other international initiatives, through which it contributes to the availability and accessibility of taxonomy and related information.

L. Vandepitte, W. Decock, S.Vranken, S. Dekeyzer, K. Verfaille, B. Vanhoorne
„An introduction to Aphia and the World Register of Marine Species (WoRMS)”

REMARKS:

HW. Palm, M. Hasseli, B.C. Schaeffner

„Morphological characters of the Trypanorhyncha”

REMARKS:

T. Scholz, R. Kuchta

**„Presentation of morphological characters of the Bothriocephalidea and
Diphyllobothrioidea”**

REMARKS:

- 1 FishGlassHouse (FGH)
- 2 Lecture Hall HSK
- 3 Lecture Hall HSL
- 4 Harry's office **A**
- 5 Justus-von-Liebig-Weg 7
- 6 Justus-von-Liebig-Weg 8
- 7 Main Building
Justus-von-Liebig-Weg 6
- 8 FGH Head House
- 9 Laboratory

- 10 New Building "Animal"
- 11 PC-Laboratories
- 12 Seminar Rooms 1 & 2
- 13 Seminar Rooms 3, 4 & 57a
- 14 OKI
Justus-von-Liebig-Weg 2 **B**

A: LAG: SR 18 + Hörsaal (JLAG)
B: SR 1-4 + OKI



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