

P-0621 INTRAGENERIC STATUS OF TWO *BRACHYLAIMA* (TREMATODA) SYMPATRIC SPECIES: MORPHOLOGICAL AND BIOLOGICAL CHARACTERIZATION

González-Moreno O., Gracenea M., Carretero M.A.**

*Lab. Parasitology, Faculty Pharmacy, University Barcelona, Spain and
**Dpto. Animal Biology, Faculty Biology, University Barcelona, Spain.

Two morphometrically different intestinal brachylaimid adults have been detected at the Llobregat Delta (Mediterranean, Spain), parasitizing the gut of the small mammals *Mus spretus* (Rodentia), *Crocidura russula* (Insectivora) (Type 1) and *Rattus rattus*, *R. norvegicus* (Rodentia) (Type 2). Experimental life cycles have been achieved involving the terrestrial helioid snails *Helix (C.) aspersa* as first and second intermediate host for Type 1. *Pseudotachea splendida* and *Otala punctata* act as first intermediate hosts and *H. (C.) aspersa* as second intermediate host for Type 2. Experimental adults have been obtained in *Mus musculus* (Type 1 & 2). To rule out conspecificity with these brachylaimids, available information (biological and morphometric) has been used from: A: *B. ruminae*, *Brachylaima* sp. I, *Brachylaima* sp. II and *Brachylaima* sp. III from a near biotope (Pitiusic Islands, Spain) and B: *Brachylaima* species developed in different geographical areas and in several definitive hosts.

A. Canonical Variate Analysis (CVA) was performed to examine the extent of separation among *B. ruminae* and Llobregat Delta species. The first root accounted for 69.7% of the total variation and separated widely *Brachylaima* Type 1-2 and *B. ruminae*. The second root (accounting for 20.43%) separated the *Brachylaima* Type 2 according to their definitive hosts. UPGMA phenograms of Mahalanobis distances of CVA suggested differences between the three species, *Brachylaima* Type 1 being more similar to *B. ruminae* than to *Brachylaima* Type 2. The arrangement of cercarial papillae (chaetotaxy) was an efficient tool to distinguish between cercariae from different species. UPGMA phenograms and Multidimensional Scaling Analysis (MDS) of chaetotaxic cercarial pattern showed clear differences between *B. ruminae*, *Brachylaima* Type 1 & 2; *Brachylaima* Type 1 chaetotaxy was the most similar to *B. ruminae*. The comparison of Llobregat species with *B. sp I* & *B. sp III* (adults) and *B. sp. I* & *B. sp. II* (chaetotaxy) showed differences among all species except *B. sp. I*, which was similar *Brachylaima* Type 2 using chaetotaxic pattern.

B. Euclidean distances were used to generate UPGMA phenograms and MSD in order to reflect morphometrical similarities. *B. Type 2* was morphometrically different while *B. Type 1* was similar to *B. ruminae* & *B. recurvus* group. *B. Type 1 & 2* were morphometrically different from the remaining species compared (14). Morphometrical convergence between different species described and intraspecific variation within the same species due to the nature of the definitive host have been confirmed.

P-0622

FAUNA OF WATERFOWL HELMINTHS OF LAKE SEVAN, ARMENIA

Nikoghossian M.A., Movsessian S. Q.

Institute of Zoology, Armenian National Academy of Sciences, Yerevan, Armenia

The aim of our investigations was to reveal the infection of all taxonomic groups of waterfowls with helminths in highland conditions of Lake Sevan. Lake Sevan is the unique large highland reservoir in Armenia where diversity of the vertebrate fauna, especially ornithofauna of invertebrates, have been observed. The method of complete helminthological dissection was worked out by Skrjabin (1928). Five hundred waterfowls of 47 species and 6 orders have been studied. Chamber treatment of the material was conducted due to Mathevossian and Movsessian's method. Over 313 birds (or 62,6%) out of 500 were infected with helminths and trematodes (23,3%), cestodes (81%), nematodes (7%), acanthocephala (17%). As a result, 72 helminth species of which 33 - trematodes, 22 - cestodes, 7 - acanthocephala and 10 - nematodes were revealed. In addition, the revealed species were of 10 families of trematodes, 4 - cestodes, 3 - acanthocephala and 5 - nematodes. As to species Echinostomatidae (8 species), Diplostomatidae (7), Strigeidae (5), Hymenolepididae (14), Choanotaeniidae (4), Polymorphidae (4) and Anizakidae (4) were more diverse. The analysis of helminth fauna gives evidence on the results of our investigations. Their species composition became considerably rich thirty - six helminth species were recorded in Armenia 7 of which in Transcaucasus, 3 in CIS.

P-0623

PHYLOGENETIC AND BIOGEOGRAPHIC ANALYSIS OF THE FAMILY PHILOPHTHALMIDAE TRAVASSOS, 1917 (PLATYHELMINTHES, DIGENEA)

Muniz-Pereira, L.C. & Pinto R. M.

Laboratório de Helmintos Parasitos de Vertebrados, Instituto Oswaldo Cruz, FIOCRUZ, Rio de Janeiro, Brasil

The present paper deals with the phylogenetic and biogeographic analysis of Philophthalmidae, parasites from birds with a worldwide geographic distribution. An initial hypothesis on evolutionary relationship, from 10 genera, was constructed using Hennigian argumentation and tested with PAUP (Phylogenetic Analysis Using Parsimony). A total of 42 morphological characters obtained from literature or preserved helminthological material was used in the analysis. Polarization was determined by outgroup comparison. The phylogenetic analysis resulted in a single evolutionary tree with 61 evolutive steps. The analysis presented herein shows clearly two groups (subfamilies) supported by synapomorphies. A new genus and a new species are proposed on this analysis. The Philophthalmidae family shows to be monophyletic, supported by eight synapomorphies. The biogeographic analysis presents typical patterns resulted from the breakup of the supercontinent Pangaea. One family has its distribution restricted to the Laurasic region, and its sister group mainly presents a Gondwanic distribution.

P-0624

GENETIC VARIABILITY IN *TRICHINELLA* GENUS: COMPARISON OF CHINESE *T. SPIRALIS* AND *T. NATIVA* ISOLATES WITH AN EUROPEAN *T. SPIRALIS* STRAIN.

Liu Mingyuan*, Sauzeau C.**, Xu Kecheng*, Trap C.*, Li Chengyao*, Garcia-Reyna P.*, Perret C.*, Soulé C. *, Boireau P.*
*CNEVA Alfort, Parasitology Unit, Maisons Alfort, France,
**University of Agriculture and Animal Sciences, Changchun, China.

The most recent taxonomic revision in *Trichinella* genus included 8 taxa. *Trichinella spiralis* (Ts) is the most thoroughly studied species but most of the isolates come from Europe or American continents. Few informations are available from Chinese country about the *Trichinella* isolates and their diversity. In this report we characterized two isolates from two Chinese provinces corresponding to different epidemiological cycles. *In vitro* prolificity index of these isolates was compared with those of an European strain. Ts and *T. nativa* (Tn) were purified from the mice intestinal tract on day 4, 5 and 6 post infection (pi). The *in vitro* release of new born larvae was determined for the two species. The NBL appeared on day 4 pi with Ts instead of day 5 pi with Tn. So a new parameter was defined to characterize the virulence of *Trichinella* strains. The random PCR was used with the cDNA of the adult/new born larvae stages of these different isolates. Species marker were identified and a low inner-species variability was proved.

This work was supported by the grants AFCRST 96 06Bt and ECOS M96B03.