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MOLECULAR SYSTEMATICS OF THE AVIAN SCHISTOSOME GENUS *TRICHOBILHARZIA* (TREMATODA: SCHISTOSOMATIDAE) IN NORTH AMERICA

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Abstract

Trichobilharzia is a genus of thread-like schistosomes with a cosmopolitan distribution in birds. Species of Trichobilharzia achieve notoriety as major etiological agents of cercarial dermatitis, or swimmer's itch. There are 40 species described in the literature, for which the majority lacks molecular sequence information. To better understand the phylogenetic relationships, diversity, species boundaries, host use, and geographic distribution of this genus, we surveyed 378 birds and over 10,000 snails from North America. The phylogenetic analysis was based on nuclear 18S, 28S rDNA, internal transcribed spacer region and mitochondrial cytochrome oxidase I sequence data. Specimens were recovered that could be related to 6 of the 14 described species of *Trichobilharzia* from North America (T. physellae, T. querquedulae, T. szidati, T. stagnicolae, T. franki, and T. brantae). An additional 5 lineages were found that could not be related directly to previously described species. Trichobilharzia brantae, transmitted by Gyraulus parvus, grouped outside the clade containing the recognized species of Trichobilharzia. A subgroup of the Trichobilharzia clade designated Clade Q was comprised of closely related species whose adults and eggs are similar, yet the European species use lymnaeids whereas the North American species use physids as snail hosts. This molecular phylogeny provides a useful framework to: 1) facilitate identification of worms, including those involved in dermatitis outbreaks; 2) test hypotheses about the evolution, diversification, host-parasite interactions and character evolution of *Trichobilharzia*; and 3) guide future taxonomic revision of *Trichobilharzia*.

> TrichobilharziaSkrjabin and Zakharov, 1920 is the most speciose genus within the Schistosomatidae Weinland 1858. The genus is comprised of 40 described species worldwide (Blair and Islam, 1983; Horák et al., 2002), of which 14 (Table I) have been described from North America. Members of this genus are reported to infect 5 orders of aquatic birds and 4 families of freshwater snails (Horák et al., 2002). Adult worms occur in the mesenteric or nasal veins of their definitive hosts, usually ducks, except in Africa where they also have been reported from other groups of aquatic birds such as grebes and ibises (Fain, 1956; Blair and Islam, 1983) and in Japan, from passerine birds (Oda, 1973). Blair and Islam (1983) and Horák et al. (2002) present the most recent reviews of this genus. The known snail intermediate hosts for most of the species are members of the basommatophoran families Lymnaeidae Rafinesque, 1815 and Physidae Fitzinger, 1833. Some species of Trichobilharzia also infect snails of Planorbidae Rafinesque, 1815, another basommatophoran family (Basch, 1966; Nassi, 1987; Rind, 1991), and the Pleuroceridae Fischer, 1885, a caenogastropod family (Ito, 1960a, b). The 14 described North American species of Trichobilharzia (Table I) are transmitted by physid snails (T. physellae, T. querquedulae, T. adamsi, T. cameroni, and T. oregonensis) or lymnaeid snails (T. stagnicolae, T. elvae, T. alaskensis, and T. ocellata) snails. The snail hosts of T.

waubesensis, *T. kegonsensis*, *T. burnetti*, and *T. horiconensis*, and *T. brantae* (until this study) are unknown. All of the North American species occur in anatid ducks (Anatinae, Aythyinae, Merginae), except *T. brantae*, which infects geese (Anserinae).

Cercariae of species of *Trichobilharzia* were the first to be implicated in causing cercarial dermatitis or swimmer's itch (Cort, 1928), an underappreciated and underreported condition occurring worldwide except in Antarctica (Cort, 1950; Lindblade, 1998; Larsen et al., 2004). Contemporary swimmer's itch cases are most frequently caused by *Trichobilharzia* cercariae (Loken et al., 1995; Kolářová et al., 1997; Farahnak and Essalat, 2003; Voronin and Beer, 2002; Bouree and Caumes, 2004; Sheng et al., 2004; Żbikowska, 2004; Coady et al., 2006), although several other genera of avian schistosomes can also cause swimmer's itch (Buckley, 1938; Cort, 1950; Stunkard and Hinchliffe, 1952; Chu, 1958; Tang and Tang, 1976).

Avian schistosomes, including Trichobilharzia, are a challenging group to identify and fully characterize due to the difficulties in obtaining intact adult specimens, the paucity of informative adult characters, the short duration of infection in birds and the difficulty of experimentally completing life cycles thereby relating the adult worms in birds to their larval stages, including cercaria, from snails. Moreover, changes over the last several decades in land use and water management have altered habitats for birds and snails, leaving no guarantee that transmission dynamics and species composition reported in the original species descriptions remain the same. Compounding this problem, morphological and behavioral features of the worms may vary depending on their age, season, age and size of the host, and whether or not worms have been collected from a primary or minor host (McMullen and Beaver, 1945; Wu, 1953; Farr and Blankemeyer, 1956; Stunkard, 1959; Combes, 1967; Bayssade-Dufour et al., 2006). In an understandable effort to identify dermatitis-causing schistosomes, some species were named based on only cercariae or on variable or difficult to locate adult morphological features (e.g. length, testes arrangement, position of the cecal reunion). The lack of clearly distinguishable features to identify Trichobilharzia and other avian schistosomes, including their cercariae, has impeded our understanding of the etiology and epidemiology of swimmer's itch.

The application of molecular systematics methods to this group of worms offers great promise as an initial step in resolving many of these difficulties. Molecular markers have expanded our understanding of schistosome parasites by permitting much less ambiguous identification of species or distinct genetic lineages (Morgan et al., 2003; Vilas et al., 2005; Brant and Loker, 2005; Brant et al., 2006; Štefka et al., 2009). The solid reference points provided by DNA sequence data permit differentiation of morphologically similar parasites and the linking of different life cycle stages that may have been collected decades apart (Vilas et al., 2005; Brant et al., 2006). These DNA sequences can be used to augment taxonomy and species delimitation, as corroborating evidence for existing hypotheses, or for falsifying systematic hypotheses (DeSalle et al., 2005).

Throughout this paper, we focus on a clade of schistosomes found in birds, herein designated as the BTGD clade (*sensu* Brant et al., 2006). Carmichael (1984) using morphological characters was the first to propose the phylogenetic relationships within Schistosomatidae and placed the genus *Trichobilharzia* within the BTGD clade. To date molecular phylogenetic analyses undertaken for *Trichobilharzia* include only 3 species (*T. franki*Müller and Kimmig, 1994, *T. szidati* Neuhaus, 1952, and *T. regenti* Horák et al., 1998), all believed to be primarily European in distribution (Picard and Jousson 2001; Dvořák et al., 2002; Ferté et al., 2005; Rudolfová et al., 2005, 2007; Jouet et al., 2008; Aldhoun et al., 2009). This leaves the remaining 37 putative species virtually unknown with respect to molecular markers. To expand our knowledge of the systematics of

Trichobilharzia, we surveyed North American birds and freshwater snails and incorporated these data into a molecular phylogenetic analysis. These results will be valuable for future taxonomic revisions of the genus and this framework will shed new light on understanding the origins, radiation, evolution and patterns of host usage of this diverse group of blood flukes. They will also assist investigators seeking more precise identification of the cercariae involved in dermatitis outbreaks, and will contribute to the eventual unraveling of this complex etiology of this common affliction.

MATERIALS AND METHODS

Specimen collection and examination

Birds were obtained from a variety of sources: our own hunting/collecting; hunters; or frozen carcasses provided by the State of New Mexico Department of Game and Fish or the Museum of Southwestern Biology, Division of Ornithology. The viscera and nasal tissues of freshly killed birds were examined in saline for schistosomes between 30 min to 12 hr postmortem. Frozen birds were thawed and examined immediately. The intestine was divided into thirds and scrapings were made to look for eggs. Worms were teased out and either relaxed and killed in hot water or put immediately into 95% ethanol for subsequent DNA analysis. Young of the year birds, targeted and collected by us before their flight feathers had developed, were collected in Churchill, Manitoba and Douglas Lake, Michigan as a way to guarantee that their parasites were acquired from their natal habitats.

Snails were collected by hand or wire mesh scoop and kept cool and moist until returned to the lab. Each snail was isolated individually in a 24-well tissue culture plate in artificial spring water and placed in natural light to induce cercarial shedding. If conditions allowed, snails that did not shed the first day were placed in aerated containers with lettuce and screened again 2 to 7 days later. In most cases, snails shed cercariae within 30 min after being placed in natural light. All schistosome cercariae were saved in 95% ethanol.

Adult worms were stained in Semichon's acetocarmine and mounted in Canada balsam on slides for measurements and morphological observation (Pritchard and Kruse, 1982). Specimens collected from this study were identified both by morphology (when possible) and by DNA sequence. Morphological determinations were made by comparison with the original species descriptions, and if available, with voucher specimens from the U.S. National Parasite Collection: *Trichobilharzia kegonsensis* (USNPC 044865), *Trichobilharzia horiconensis* (USNPC 044866), *Trichobilharzia burnetti* (USNPC 044867), *Trichobilharzia waubesensis* (USNPC 044868), *Trichobilharzia querquedulae* (USNPC 079068), *Trichobilharzia physellae* (USNPC 079636, 083314), and *Trichobilharzia brantae* (USNPC 047609). Voucher specimens for adults and cercariae from this study were deposited in the Division of Parasitology, Museum of Southwestern Biology, University of New Mexico, Albuquerque, New Mexico (Accession numbers: *T. brantae* male and cercariae MSB Para176, 182, 184; *T. physellae* males and cercariae MSB Para177–178; *T. stagnicolae* cercariae MSB Para179; *T. querquedulae* males and cercariae MSB Para180, 181, 183).

Life cycle investigations

Host verification—In an attempt to verify host use, snails or domestic ducks were exposed experimentally to species of *Trichobilharzia*. Miracidia were hatched from eggs by rinsing and then diluting the feces of the avian host in artificial spring water in an Erlenmeyer flask. All but the neck of the flask was covered with aluminum foil, leaving just the top exposed to light, to concentrate miracidia (McMullen and Beaver, 1945). Flasks were placed in natural light and miracidia were collected within 30 min. Snails were isolated

individually in a tissue culture well plate with artificial spring water and were exposed each to 3 miracidia. The wells were examined after 1 hr to ensure no miracidia remained. Snails were screened for cercarial shedding 3–6 wk post-infection (PI). To verify that adult worms and miracidia derived from the same bird were the same species (in cases where both were collected), cox1 and ITS were sequenced for both. Any worms collected from experimental infections were also sequenced for cox1 and ITS and compared to the initial life cycle stage used in the experiment to verify it was the same species. This was done both to confirm that adults and cercariae were the same species and that all worms collected from experimental infections were identical.

Trichobilharzia querquedulae—In April 2004, at Bitter Lake National Wildlife Refuge, lab-reared strains of *Physa acuta* Draparnaund, 1805 n=30, and *Stagnicola elodes* (Say, 1821) n=30 and pre-screened and trematode-negative wild-caught found not to be shedding cercariae over a 3-day period *Gyraulus parvus* (Say, 1817) n=10 were exposed to miracidia. Half the snails of each species were exposed to miracidia from cinnamon teal, *Anas cyanoptera* Vieillot, 1816, and the other half to miracidia from blue winged teal, *Anas discors* L.

Trichobilharzia physellae—In March 2005, at Bitter Lake National Wildlife Refuge, New Mexico, lab-reared *Physa gyrina* (Say, 1821) n=30, and *S. elodes* n=30 were exposed to miracidia from either the lesser scaup, *Aythya affinis* (Eyton, 1838), or the bufflehead, *Bucephalus albeola* L. At Douglas Lake, Michigan, in August 2005, wild-caught *Stagnicola emarginata* Say, 1821 (n=10) and *Physa parkeri* Currier, 1868 (n=10), determined not to be shedding cercariae over a 3-day period, were exposed to miracidia of *T. physellae* hatched from the feces of *Mergus merganser* L. collected from the lake.

Trichobilharzia stagnicolae—In August 2005, individuals of the type host species, *S. emarginata*, were collected from the type locality for *T. stagnicolae* at Douglas Lake, University of Michigan Biological Station (McMullen and Beaver, 1945). Morphology of the cercariae collected was consistent with the original descriptions by Talbot (1936) and McMullen and Beaver (1945). Six domestic mallards and 6 peking ducks, all 10-days-old, were exposed to about 100 cercariae each for up to 30 min. The birds' feet were checked for cercarial dermatitis to determine if penetration had occurred. Feces were examined every other day from 1–4 wk PI. The birds were killed at either 2 and 4 wk PI and examined for worms. Ten specimens each of wild-caught *S. emarginata* (n=10) and *P. parkeri* (n=10) from Douglas Lake determined not to be shedding cercariae over a 3-day period were exposed to miracidia of *T. stagnicolae* from of the common merganser, *M. merganser*, collected from the same lake.

Sequencing data and phylogenetic analysis

DNA was extracted from fresh or alcohol preserved worms with the DNeasy Tissue Kit (Qiagen, Valencia, California) according to manufacturer's guidelines or HotShot Lysis (Truett et al., 2000). In a few cases, multiple worms from a single host were extracted. DNA was amplified by polymerase chain reaction (Takara Ex Taq kit, Takara Biomedicals, Otsu, Japan) and sequenced using previously published primers. For 18S–28S, we used primers listed in Brant et al. (2006). For ITS we used its4, its5 (Dvořák et al., 2002), 3S (Bowles et al., 1995), and 4S (Bowles and McManus, 1993). We designed primers for *cox*1: CO1F15: 5'-TTT NTY TCT TTR GAT CAT AAG C-3' and CO1R15: 5'-TGA GCW AYH ACA AAY CAH GTA TC-3' and an internal sequencing primer CO1RH3R: 5'-TAA ACC TCA GGA TGC CCA AAA AA-3'. PCR products were purified with Montage Microcon columns (Millipore, Billerica, Maryland). Sequencing reactions were performed with Applied

Biosystems BigDye direct sequencing kit, version 3.1 (Applied Biosystems, Foster City, California).

Phylogenetic analyses were performed on 6 different datasets. The first dataset was comprised of combined 18S–28S sequence data to place the samples collected for this study within the larger context of the family Schistosomatidae (Snyder, 2004; Brant et al., 2006). The second dataset comprised a combined matrix of 18S–28S-partial ITS (ITS1-5.8S-ITS2)-cox1 regions to reconstruct the relationships within the genus with existing isolates of *Trichobilharzia* from GenBank and included a greater sampling of individuals from more localities and hosts from our collections. The third and fourth datasets included separate analyses to look at congruence between nuclear DNA (ITS1-58S-ITS2) and mtDNA (cox1). The ITS1-5.8S-ITS2 region was used because it was the only region that was conserved enough to align unambiguously all available schistosomes. The fifth dataset was ITS1, and included *T. franki* samples as well as samples of *Trichobilharzia* that were designated as unidentified from Europe from the studies of Picard and Jousson (2001) and Rudolfová et al., (2007). The sixth dataset was ITS2 that included *T. franki* samples from Jouet et al., (2008). The last 2 analyses were to assess the positions of all available European taxa in GenBank relative to the North American taxa.

Phylogenetic analyses using maximum parsimony (MP), maximum likelihood (ML), and Minimum evolution (ME) were carried out using PAUP* ver 4.0b10 (Swofford, 2002) and Bayesian inference (BI) using MrBayes (Huelsenbeck and Ronquist, 2001; Ronquist and Huelsenbeck, 2003). jModeltest (Posada, 2008) was used to determine the best nucleotide substitution model for ML and ME analyses. In cases where the Bayesian Information Criteria (B.I.C) or Akaike Information Criteria (A.I.C) criteria selected different models, both were used in analyses and in all cases, the tree topologies were the same. The combined 18S-28S-ITS-cox1 was rooted with members of SchistosomaWeinland, 1858 since ITS sequences were available only for Schistosoma.

The model, GTR+I+G, from jModeltest was used for both combined datasets, as well as for the ITS1 dataset. For cox1, ITS2, and ITS1-5.8S-ITS2, the model TVM+I+G was selected for ML and ME analyses. For BI, a mixed model approach was implemented to account for the potential differences in evolutionary model parameters between data partitions (both genes and codon positions). Parsimony trees were reconstructed using heuristic searches, random taxon-input order and tree-bisection and reconnection (TBR) branch swapping. Optimal ME and ML trees were determined from heuristic searches (50 replicates for ME, 5 replicates for ML), random taxon-input order, and TBR. Nodal support was estimated by bootstrap (100 replicates) and was determined for the MP and ME trees using heuristic searches, each with random taxon-input order. In all BI that included cox1, the dataset was partitioned by codon positions. For the BI of the 18S-28S-ITS-cox1 dataset, there were 4 partitions defined by first 18S, 28S (Nst=6 rates=gamma ngammacat=4), second cox1 codon1, third cox1 codon2, and fourth cox1 codon3 (Nst=6 rates-invgamma ngammacat=4). All parameters were unlinked between partitions. For all the analyses, 4 chains were run simultaneously for 5×10^5 generations, trees sampled every 100 cycles, the first 5,000 trees with preasymptotic likelihood scores were discarded as burnin, and the retained trees were used to generate 50% majority-rule consensus trees and posterior probabilities.

RESULTS

Specimen collections

Results of the survey for species of *Trichobilharzia* in North American birds and snails are reported in Table II and Figure 1. Ten lineages of *Trichobilharzia* were collected and the collection localities of specimens used in the phylogenetic analyses are listed in Table III. A

total of 378 birds of 46 species were necropsied (Fig. 1, Table II), of which 92 birds were infected with Trichobilharzia (overall prevalence 24.5%). Nine of the 10 lineages reported were collected as adults and/or miracidia. Approximately 10,000 snails representing 4 families and 21 species were examined, of which 20 snails were infected with a species of Trichobilharzia, representing 7 of the 10 species (Table II). In most cases, prevalence of Trichobilharzia infections in snails was around 1%. However, at Glen Lake in Michigan, the prevalence of T. stagnicolae in Stagnicola emarginata was 30%. No nasal schistosomes were found in birds nor were any cercariae from snails genetically similar to the avian nasal schistosome, T. regenti. Three species of Trichobilharzia (T. physellae, T. querquedulae, and T. brantae) were identified whose adult morphology corresponded to the original species descriptions (Tables IV, V). One species collected was from cercariae with sequence data that matched GenBank sequences attributed to T. szidati (Table III). Adult worms in the lineage identified as T. querquedulae could be differentiated from T. physellae and T. franki by the position of the cecal reunion and the number of testes (Table IV). Also, adults of the lineage identified as T. physellae are consistently smaller and have a shorter gynaecophoric canal as compared to *T. querquedulae* (Table IV).

A fifth schistosome we identified provisionally as T. stagnicolae (Talbot, 1936; McMullen and Beaver, 1945) was collected as miracidia from mergansers. McMullen and Beaver (1945) described T. stagnicolae from an experimental infection in canaries; their study is the only description and record of T. stagnicolae adults. Subsequent reports of presumptive T. stagnicolae in the literature have been as cercariae from S. emarginata (Swales, 1936; McLeod, 1940; Elliott, 1942; Zischke and Zischke, 1968; Keas and Blankespoor, 1997; Leighton et al., 2000; Blankespoor et al., 2001; Coady et al., 2006). In our study, we collected miracidia from mergansers, Mergus merganser, from the type locality, Douglas Lake, but were unable to locate adult worms or eggs. Our assignment of the name *T*. stagnicolae to the samples we collected was justified based on the following: 1) our samples were collected from the type locality and the type snail; 2) we infected successfully the type snail with miracidia collected from the type locality; 3) our cercarial measurements were the same as those reported by Talbot (1936) and McMullen and Beaver (1945); 4) previous fecal examinations of *M. merganser* on Douglas Lake revealed eggs of *T. stagnicolae* (Blankespoor et al., 2001); and 5) our collections of cercariae from S. emarginata from several lakes in northern Michigan, in northern Minnesota, and New Mexico (Table III), all genetically matched what we collected at Douglas Lake, the type locality (0%-1.2% for cox1). The finding of a distinct genetic lineage with widespread representation strongly suggests our samples are T. stagnicolae.

The common morphological features used to differentiate the above mentioned 5 species from other avian schistosomes are provided in Tables IV and V. The infections we observed in mergansers with both *T. physellae* and *T. stagnicolae* may occur more frequently than commonly recognized. Not only can double infections be easily overlooked because of difficulties in finding both adult worms and eggs, but care is also required to ensure adults and eggs are both assigned to the correct species.

The 5 remaining lineages sequenced, 4 of which were represented by portions of adult worms recovered from birds, grouped with species of *Trichobilharzia*, but could not be matched definitively to any existing species description or to GenBank sequences associated with a formal species name. To facilitate our discussion of these species, we designated these specimens as *Trichobilharzia* spp. A–E (Table III). *Trichobilharzia* spp. A and B were found only in the American widgeon, *Anas americana* Gmelin, 1789, from 3 widespread U.S. localities along the Pacific flyway. *Trichobilharzia* sp. A was also found in a widgeon from New Mexico. *Trichobilharzia* sp. C was from the hooded merganser, *Lophodytes cucullatus* L., from the eastern U.S. For *Trichobilharzia* spp. A–C, only worm fragments

were collected that did not have informative morphological features. *Trichobilharzia* sp. D is represented by cercariae from a single lymnaeid snail from Manitoba. *Trichobilharzia* sp. E was collected both as a posterior fragment of an immature worm from a pintail duckling, *Anas acuta*, and as cercariae from *Stagnicola* sp., both from Manitoba. Cercariae morphology and measurements of *Trichobilharzia* sp. E are consistent with *T. elvae*, but these data alone are not sufficient for accurate species discrimination. Although sufficient adult worm material for these 5 lineages was not available for a conclusive morphological study to determine if these 5 lineages represent new or previously described species, the sequence and host-use data provided here are valuable reference points for future studies as additional specimens become available (Brant et al., 2006).

Life cycle experiments

For each life cycle experiment (Table VI), cox1 and ITS sequences from experimentally obtained life cycle stages were identical with sequences from the life cycle stage used as starting material for the infection. Miracidia of each schistosome lineage were able to infect snails of only a single gastropod family, similar to results of previous experiments (Wu, 1953). The only successful infections of *T. stagnicolae* were *Stagnicolae* emarginata from miracidia from *M. merganser* (Table VI). None of the domestic duck experiments resulted in adult worms.

Phylogenetic analyses

DNA sequence data was deposited in GenBank, under Accession numbers FJ174450-FJ174576, FJ711767-68 for the 18S (1776 bp), 28S (1299 bp), cox1 (824 bp), and ITS (1227–1395 bp) datasets (Table III). For the phylogenetic analysis of *Trichobilharzia*, 130 new sequences of *Trichobilharzia* were analyzed along with 55 sequences from GenBank. The numbers of individuals of each species sequenced are shown in Table III. Aligned cox1 sequences appeared to be genuine mitochondrial sequence, rather than nuclear copies: sequences contained no stop codons, overlapping fragments contained no conflicts, base compositions were homogeneous across taxa, codon positions contained expected relative divergences (3>2>1), and highly suspect relationships were not evident.

MP, ML, ME, and BI methods produced congruent results, except for some differences in the single gene analyses. Topological differences occurred, but no conflicts received high support from bootstrapping or Bayesian posterior probabilities. The 18S-28S tree supported monophyly of the Schistosomatidae and the BTGD clade (as defined in Fig. 2). Representatives of *Trichobilharzia* included in this study did not form a monophyletic group as T. brantae did not group with other North American or European Trichobilharzia, but rather grouped with the morphologically and genetically distinct AllobilharziaKolářová et al. 2006 from swans (Figs. 3-5). The overall relationships among the species of *Trichobilharzia* are shown in Figure 3. There was a basal split, albeit with low node support, between (T. stagnicolae, T. szidati, and Trichobilharzia spp. D and E) and (T. regenti and Clade Q). Here we identify Clade Q that includes species from North American and Europe that are both morphologically (Table IV) and genetically (Table VII) very similar (Fig. 3). Clade Q was recovered in all analyses and is comprised of T. franki, T. querquedulae, T. physellae, and Trichobilharzia spp. A, B, and C (Figs. 3-6, see discussion). Where known, based on our phylogenetic trees, members of Clade Q all have similar sized spindle-shaped eggs and included taxa dependent on either lymnaeid or physid snail hosts. Trichobilharzia regenti, a nasal-inhabiting species, was always recovered basal to Clade Q (Fig. 3).

To further explore the relationships in Clade Q and to fully utilize available sequence data, separate analyses of 4 datasets (*cox*1, ITS1-5.8S-ITS2, ITS1, and ITS2), were completed. Additional individuals of *Trichobilharzia* from our collections (Table III) plus isolates of *T*.

franki from GenBank were used. Many isolates of *T. franki* have been sequenced, however our analyses of these sequences revealed they did not form a monophyletic species group. Several isolates identified as *T. franki* were from either *Radix auricularia* L. snails (Ferté et al., 2005; Rudolfová et al., 2005) or *R. ovata* (Draparnaud, 1805) snails (Picard and Jousson 2001), but based on our analyses, isolates from these two snail species did not appear to be the same species.

In the separate gene analyses, the topologies recovered were generally the same with some exceptions. Only the cox1 tree (Fig. 4) supported Trichobilharzia sp. A as a clade. Unfortunately, there were no additional cox1 samples of T. franki available in GenBank to include in this analysis. In the analysis of the ITS1-5.8S-ITS2 dataset (Fig. 5), T. franki from Radix auricularia was not recovered as monophyletic (see Table III for labels). Furthermore, Trichobilharzia sp. C was identical to several isolates of T. franki (Fig. 5). The ITS1 data set (Fig. 6) included additional samples of T. franki from R. ovata and our analysis indicated that not only did the T. franki from R. ovata not form a clade, but they did not group with any of the T. franki from R. auricularia (Fig. 6). Similarly, the isolates of T. franki from R. auricularia did not group together. Trichobilharzia sp. B grouped with some of the *T. franki* isolates from *R. auricularia* from the two different studies (Table III, Fig. 6) of Picard and Jousson (2001) and Rudolfová et al. (2005). Isolates of T. franki from R. ovata were basal in Clade Q (Fig. 6). Additional samples and gene regions are needed to determine definitively if T. franki as represented by available sequences is actually more than 1 species, and if our *Trichobilharzia* spp. B and C are the same as or distinct from the European samples labeled T. franki. Our data are suggestive that T. franki also occurs in North America. R. auricularia is found in North America, however the snail hosts for Trichobilharzia spp. A-C is not yet known.

The available ITS2 sequences provided yet a different perspective (Fig. 7). In this analysis 3 unidentified species of *Trichobilharzia* (*Trichobilharzia* sp. 3 Pl10, *Trichobilharzia* sp. 3 Pl7, *Trichobilharzia* sp. EAN17) in GenBank for which only ITS2 data were available were added to our dataset (Table III). The positions of *Trichobilharzia* sp. 3 Pl10 and *Trichobilharzia* sp. 3 from *Anas penelope* L. from Poland (Rudolfová et al., 2007), were equivocal, but in the ME analysis they aligned with *Trichobilharzia* sp. D, although without support. The sample *Trichobilharzia* sp. EAN17 from *Radix peregra* (Müller, 1774) from France (Jouet et al., 2008) grouped with *Trichobilharzia* sp. E from Manitoba with strong node support, suggesting they may be conspecific.

To provide a convenient yardstick to measure the extent of sequence difference among species of *Trichobilharzia*, pairwise genetic differences were calculated and compared with values obtained for the relatively well-defined species of *Schistosoma* (Table VII). Based on such comparisons, the lineages of *Trichobilharzia* are as genetically distant from each other as are the named species within both *Trichobilharzia* and *Schistosoma* (Table VII), providing good presumptive evidence that they represent distinct species (Nolan and Cribb, 2005; Vilas et al., 2005). As determined by sequence analysis, 7 of the 10 lineages of *Trichobilharzia* were collected from snails, 4 of which corresponded to sequences that we obtained from *Trichobilharzia* adults (*T. physellae*, *T. querquedulae*, *T. brantae*, and *Trichobilharzia* sp. E). The remaining 3 taxa were from cercariae that grouped with sequence data from miracidia of *T. stagnicolae*, with sequences for *T. szidati* from Europe (Figs. 4, 5; Rudolfová et al., 2005), or that did not group with any species or clade (*Trichobilharzia* sp. D; Figs. 4, 5).

Despite the broad geographic and host sampling for *T. physellae* and *T. querquedulae*, which were both collected from across North America (Fig. 1; Table III), we did not find indications of geographic structuring within either species (Figs. 4, 5). With the genes used

in this study, haplotypes that were identical or that differed in only 1–2 base pairs were found between both eastern and western samples. The *T. stagnicolae* isolates collected from Minnesota, Michigan, Montana, and New Mexico, also show little evidence of geographic differentiation (Fig. 4). The collection of *T. szidati* related isolates from North America was unexpected. Based on the ITS1-5.8S-ITS2 region (Table VII), our samples of *T. szidati*, from Montana (Flathead *Stagnicola* MT) in *Lymnaea stagnalis* L., and Michigan (Blind Sucker *Lymnaea* MI) in *Stagnicola elrodi* (Baker and Henderson, 1933), were genetically very similar (0.4%) to each other, as well as to the European isolates of *T. szidati* (0.36%). These figures are within the range of variation noted for *T. szidati* from Europe based on ITS1-5.8S-ITS2 (0–1.1%). In general, the genetic differences between species pairs within continents were not less than the differences between species pairs from different continents, Europe and North America (Table VII).

DISCUSSION

General observations

This is the first molecular systematics study of species of *Trichobilharzia* collected from a diversity of avian and snail species collected across North America. From North America we collected 5 morphologically identifiable and genetically distinct species of *Trichobilharzia*. These species were *T. brantae*, *T. physellae*, *T. querquedulae*, *T. stagnicolae*, and *T. szidati*, one of which (*T. szidati*) was reported previously from Europe (Rudolfová et al., 2005). We also collected 5 additional genetically distinct lineages that group within *Trichobilharzia* that could not be associated with a named species. These results suggest that at least 10 genetically distinct lineages of *Trichobilharzia* exist in North America. How these latter 5 species relate to the remaining species of *Trichobilharzia* described from North American not found in this study remains to be determined. Nevertheless, the sequence database generated here for North American species of *Trichobilharzia* will contribute to future studies revealing the broader species diversity and the host preferences for each species.

Although an analysis that includes additional specimens of putative *Trichobilharzia* from other continents is necessary to understand the full scope of the genus, our morphology (Table V; Fig. 8) and genetic differences strongly suggests that *T. brantae* should not be included as a member of *Trichobilharzia*. This species from geese and planorbid snails did not group within the *Trichobilharzia* clade, but rather aligned with *Allobilharzia*, a genus of schistosome collected thus far only from swans. *Allobilharzia* is morphologically and genetically distinct from *Trichobilharzia*; egg shape and position of cecal reunion are the two major differences (Table V, Fig. 8; Kolářová et al., 2006;Brant, 2007). Blair and Islam (1983) also suggested that *T. brantae* did not belong in the genus *Trichobilharzia*, but rather *T. brantae* should be transferred to the genus *Jilinobilharzia*Lui and Bai, 1976. However, a morphological comparison does not support inclusion of *T. brantae* in *Jilinobilharzia* or *Allobilharzia*. Table V compares some of the major morphological differences such as; shape of the eggs, position of the seminal vesicle and the start point and length of the gynaecophoric canal.

The *cox*1 genetic difference values obtained for pairs of *Trichobilharzia* taxa outside of Clade Q (9–14%) were comparable to those obtained for congeners of other flatworm groups (Figs. 3, 6), including the confamilial *Schistosoma* (9–21%) in mammals (Vilas et al., 2005). Genetic differences among pairs of taxa within Clade Q were variable but generally low (7–9%), indicative of perhaps a more recent divergence among members of this clade (Table VII). Morphology as well as host use (definitive and intermediate) were considered relative to the molecular phylogenetic results by mapping these features onto the BTGD clade (Fig. 8). Host, morphology and DNA taken together revealed some interesting

patterns discussed below, as well as highlighting the small number of distinguishing morphological features. The molecular and host use data provided here will eventually facilitate assessment of the validity of other species descriptions, assuming the specimens in question belong to a species described previously, and will help delineate new species (Štefka et al., 2009).

Life cycles of species of Trichobilharzia

Sequence markers provide an invaluable tool in connecting life cycle stages from wild hosts that have not been previously integrated into a complete life cycle through experimental infections. Given the challenges in obtaining the necessary approvals for maintenance of vertebrate animals, it may become difficult in the future to resolve life cycles through experimental infections. In our molecular survey, we found 4 sequence matches for cercariae from snails with adult worms from wild birds, thus providing strong direct inferences for the wild hosts involved in those particular life cycles. Such matches were obtained for *T. physellae*, *Trichobilharzia* sp. E, *T. szidati*, and *T. brantae*.

Snail Host Use

Excluding T. brantae, all Trichobilharzia from Europe for which life cycles are known use lymnaeid snails, whereas species from North America use lymnaeids or physids. Members of Lymnaeidae are worldwide in distribution, with their greatest species diversity occurring in North America. Interestingly, Lymnaea stagnalis and Radix auricularia, the former a host of T. szidati and the latter host to T. franki, are not considered endemic to North America (Remigio, 2002). Most of the diversity of *Trichobilharzia* in North America was found in species of Stagnicola (Table III). This is in contrast to studies in Europe where most of the diversity of *Trichobilharzia* was found in species of *Radix* (e.g. Picard and Jousson, 2001; Jouet et al., 2008; Aldhoun et al., 2009). Physidae is mainly a New World family, members of which have spread secondarily to other continents (Taylor, 2003). Thus far, only North America is known to have sequence-verified members of the *Trichobilharzia* clade that use physid snails. Although physid transmitted schistosomes are known from other continents (Ostrowski de Núñez, 1978; Rudolfová and Horák, 2001; Gerard, 2004), they have not been verified as a species of Trichobilharzia and may be representatives of Gigantobilharzia Odhner, 1910, one species of which in North America is also transmitted by physids (Brackett, 1942; Najim, 1956; Daniell, 1978). In no case did we find representatives of a single species of *Trichobilharzia* in snails belonging to more than 1 family, although in some cases we found more than 1 species of a particular snail family could host the same species of Trichobilharzia. For example, we found T. stagnicolae in Stagnicola emarginata and Stagnicola sp. and T. physellae in Physa parkeri and P. gyrina (Table II). In other studies, T. regenti has been collected from both Radix peregra and R. ovata snails (Picard and Jousson, 2001; Dvořák et al., 2002; Rudolfová et al., 2006). There is also an indication that T. franki occurs in more than one species of Radix, excluding those samples of T. franki from Piccard and Jousson (2001) from R. ovata snails (Jouet et al., 2008).

Physid transmitted species of *Trichobilharzia* were found only in Clade Q (Figs. 3,6) delineated in this study. In fact, so far as is known, *Trichobilharzia* is the only avian schistosome genus to use lymnaeid snails. The planorbid transmitted *T. brantae*, *Dendritobilharzia*Skrjabin, 1920, and *Bilharziella* Looss, 1899 and the physid transmitted *Gigantobilharzia huronensis* Najim, 1950 are basal to *Trichobilharzia* within the BTGD clade, suggesting that in our results, lymnaeids are the basal hosts within species of *Trichobilharzia* (Fig. 8). Members of Clade Q (Fig. 6) are not strongly differentiated from one another on either morphological or genetic characters (Tables VI, VII), yet given that the clade includes 2 known physid transmitted species, *T. physellae* and *T. querquedulae*, it is suggested that at least 2 switches from one snail family to another occurred within Clade

Q. Also, even though the genetic distances between physid and lymnaeid transmitted species in Clade Q (Table VII) are not great, all the available specimens for each physid transmitted species cluster together with unequivocally strong support in all analyses. Taken together, these results suggest that members of Clade Q have diverged relatively recently from one another, and that switches between 2 different snail families have occurred after which the taxa occupying different snail families remained genetically distinct from one another.

Definitive host use

In North America and Europe, all specimens of *Trichobilharzia*, *Allobilharzia*, and *T. brantae* for which there are molecular data, were found in avian hosts of the order Anseriformes (ducks, geese, and swans). *Allobilharzia* is known only from swans (Kolářová et al., 2006; Brant, 2007), and *T. brantae* is known only from geese (Farr and Blankemeyer, 1956; Wojcinski et al., 1987). The remaining species of *Trichobilharzia* collected for this study parasitize ducks of the Anatinae, Aythyinae, and Merginae. Species of *Trichobilharzia* from other continents have been described from other orders of birds, but thus far representatives of these species have not been available for sequencing to determine if they fall within the *Trichobilharzia* clade defined here.

Although there is not a strong pattern of definitive host specificity, some trends were identified (Fig. 8). *Trichobilharzia querquedulae* has been found only in 3 species of dabbling ducks (Table II; *Anas clypeata* L., *A. cyanoptera*, and *A. discors*) that are each other's closest relatives (Johnson and Sorenson, 1999). In contrast, *T. physellae* utilizes mainly diving ducks (Aythyinae, mostly species of *Aythya* Boie, 1822) and mergansers (Merginae) as its major definitive hosts (ecological rather than phylogenetic). While these duck hosts are not each other's closest relative, they are united ecologically by their preferred feeding habitat and style (diving). Although other duck species are also infected, prevalence is very low or there were few worms, most immature (Table II). One of the principal hosts of *T. stagnicolae* is a merganser (Blankespoor and Reimink, 1988;Leighton et al., 2000;Blankespoor et al., 2001;Coady et al., 2006), corroborated by our survey. It is interesting to note that 2 of the 3 unidentified lineages in Clade Q came from *Anas americana*, the American widgeon.

Some biogeographical remarks regarding North American Trichobilharzia

North American species of *Trichobilharzia* that we collected have broad geographic ranges and, at least as suggested by the markers used here, show little evidence of intraspecific genetic structure (Figs. 4–6). This is true for *T. stagnicolae*, which has been collected from Michigan, Minnesota, Montana, and New Mexico (Table III), and for specimens of *T. physellae* and *T. querquedulae* were collected from all the major avian migratory flyways, and from latitudes as distant as Alaska and Manitoba to Louisiana and Florida (Fig. 1; Table III). The latter 2 species have yet to be collected outside of North America.

Using sequence similarity as the criterion to designate species as outlined in Vilas et al. (2005), 4 avian schistosome lineages from North America have presumptive representatives in Europe (Table VII): (1) *T. szidati*, which is considered a European species (Rudolfová et al., 2005), was collected from North American snails (Table III, Fig. 5); (2) *Trichobilharzia* sp. B grouped with the European *T. franki* from *R. auricularia* (Fig. 6); (3) *Trichobilharzia* sp. E was closely aligned with *Trichobilharzia* sp. EAN17 from the snail, *Radix peregra*, collected in France (Fig. 7); and (4) although not the specific subject of this paper, specimens of *Allobilharzia visceralis* collected from the North American swans as part of this survey were indistinguishable from worms collected from swans in Iceland (see Kolářová et al., 2006; Brant, 2007). Thus, the continent of origin by no means represents an

infallible indicator for species designations either for species of *Trichobilharzia* or other genera of avian schistosomes.

Diversification of Trichobilharzia

Incomplete taxon sampling and uncertainty among the basal nodes of the *Trichobilharzia* spp. radiation continue to challenge our understanding of the global diversification of this genus. The 40 named species of *Trichobilharzia* have been described from multiple locations in Europe and North America, Brazil (Leite et al., 1978), Australia (Blair and Islam, 1983; Islam, 1986; Islam and Copeman, 1986), New Zealand (Davis, 2006), China (Pao and Yung, 1957; Tang and Tang, 1976; Lui et al., 1977; Tsai et al., 1979), India (Baugh, 1963; Chauhan et al., 1973), Malaya (Basch, 1966), Japan (Ito, 1960; Yamaguti, 1971), Congo-Rwanda (Fain, 1955, 1956, 1959) and South Africa (Appleton, 1982, 1986). Most of these species were reported from ducks, geese and swans, however a few were reported from passerine birds, kingfishers, grebes and ibises (Fain, 1955, 1956; Ito, 1960; Tsai et al., 1979). Snail hosts where known, with one exception (Ito, 1960), are physid or lymnaeid snails. Reports of species of Trichobilharzia in North America, including this study, were all collected from ducks and/or physid or lymnaeid snails. The exception is T. brantae, which we now know occurs in geese and uses a planorbid snail as an intermediate host. A true global definition of Trichobilharzia awaits inclusion of genetically verified species from South America, Asia, and Africa.

Recent studies have shown that uncovering additional diversity among avian schistosomes is a frequent occurrence, particularly when snails are surveyed and molecular approaches are applied (Larsen et al., 2004; Brant et al., 2006; Rudolfová et al., 2007; Jouet et al., 2008; Skirnisson and Kolářová, 2008; Aldhoun et al., 2009). This suggests there is more diversity to discover with respect to *Trichobilharzia*, already considered the most speciose genus in the family. The second most speciose genus is *Schistosoma*, currently comprised of 22 species.

Perhaps what is more noteworthy is the relatively large number of distinct lineages for a parasite group that colonizes vagile, migratory definitive hosts. This is particularly so considering the overlaps in host species use and spatial and temporal sympatry among host species that regularly occurs on their breeding/wintering grounds and in other wetland habitats. The lack of host isolation coupled with the mobility of their host species would seem to weaken barriers to gene flow among the avian schistosomes. Moreover, lymnaeid and physid snails are both common, occur in large numbers, and are widely distributed, seemingly further reducing opportunities for regional diversification. The extent to which mating behavior/preferences or temporal or spatial separation within definitive hosts may disrupt gene flow and isolate species is not well known for avian schistosomes and will be excellent model systems for future investigations. Also, the acquisition of new molluscan hosts (for example, a switch from lymnaeid to physid snails as seems to have occurred in Clade Q) may also serve as a major isolating mechanism.

The relationships among *T. franki, T. physellae*, and *Trichobilharzia* spp. A, B, and C in Clade Q provide an interesting opportunity to address questions about gene flow, and speciation, and ultimately, diversification. There are several hypotheses, not necessarily mutually exclusive, that might explain the patterns observed in this clade that includes geographically distant, yet closely related North American and European species. It may be that (1) given the genetic and morphological similarities, these taxa are not fully differentiated as species because they have only recently diverged; (2) there may be isolation and incipient diversification among populations or species of *Trichobilharzia* that is diminished by ongoing gene flow that is maintained by the mobility of their hosts; (3) even though they are found in hosts considered mobile and that migrate long distances, the

different taxa of Clade Q actually have subtle patterns of host use, or different geographical preferences that are not yet differentiated or require more sensitive genetic markers (like microsatellites) to reveal cryptic variation (Štefka et al., 2009); (4) hybridization may have occurred (Morgan et al., 2003; Fan and Lin, 2005; Steinauer et al., 2008); (5) the equivocal positions, or low branch support of individuals like *Trichobilharzia* spp. A, B, and C might imply that there remains undiscovered diversity (missing taxa) that, if available, would clarify relationships in this clade. Future work to increase the sample size within Clade Q and selection of alternative, faster evolving, markers to estimate gene flow will help address which of these processes have been important to shaping the diversity we find. We also need to accumulate more morphological data and understand how it correlates with genetic variation, to better define the status of species such as *T. szidati* and *T. franki* in North America.

Medical significance including cercarial dermatitis

None of the North American adult worms was found in host nasal turbinates, a location inhabited by some *Trichobilharzia* species in Europe (*T. regenti*), Australia (*T. australis*Blair and Islam, 1983, *T. arcuata* Islam, 1986), and Africa (*T. spinulata* Fain, 1955, *T. rodhaini* Fain, 1955, *T. nasicola* Fain, 1955, *T. aureliani* Fain, 1956, *T. duboisi*, Fain, 1959). This is of note from a public health perspective because the nasal-dwelling *T. regenti* migrates via both peripheral nerves and the central nervous system to reach its preferred site of infection. This species has been shown to cause anomalous behavior in both experimentally infected birds and mammals (Horák et al., 1999; Hrádková and Horák, 2002; Kouřilová et al., 2004) and has the potential to present similar consequences in humans.

Although most North American outbreaks of cercarial dermatitis are ascribed to *T. physellae* or *T. stagnicolae* (Swales, 1936; Cort, 1950; McMullen and Brackett, 1941; McLeod, 1940; Hunter, 1960; Zischke and Zischke, 1968; Leighton et al., 2000; Blankespoor et al., 2001; Coady et al., 2006), such identifications typically reflect whether the cercariae were shed from a physid or lymnaeid snail, respectively. The framework incorporating molecular markers developed here will be of immediate use in making more precise determinations. For example, although *T. physellae* was the taxon we most frequently collected from snails, at least 3 additional avian schistosome taxa from physid snails were collected, including representatives of other genera; accordingly, caution is required in ascribing physid transmitted outbreaks of dermatitis to *T. physellae* (S. Brant pers. obs.). The extent to which each of the 10 different taxa of *Trichobilharzia* noted here is actually involved in causing cercarial dermatitis in North America is an important priority for future study.

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FIGURE 1.

Collection localities. Refer to Table III for more details. Localities are as follows: 1 Canada: Manitoba, Churchill 58.7541 N; 93.8066 W, July/August 2007; 2 Colorado: El Paso Co. 38.827 N; 104.804 W, June 2007; 3 New Mexico: Bernalillo Co. 35.1305 N; 106.6822 W, July 2002; 4 New Mexico: Sandoval Co. 35.8485 N; 106.4907 W, July 2006; 5 Pennsylvania: Erie Co. 42.1703 N; 80.0868 W, November 2004; 6 New Mexico: Chavez Co. 33.45 N; 104.4 W, April 2005, March 2006; 7 Alaska: North Slope Borough 68.9820 N; 148.8318 W, June 2005; 8 Nevada: Churchill Co. 39.9 N; 118.817W, November 2005; 9 Michigan: Cheboygan Co. 45.581 N; 84.697 W, July, 1999, August 2005; 10 Florida; 11 Louisiana, Cameron Parish 26.661 N; 92.688 W, November 2003; 12 California: Imperial Co. 33.2988 N; 115.5875 W, November 2004; 13 New Mexico: Socorro Co. 33.7131 N 106.9579 W, April 2004; 14 Alaska: Yukon-Koyukuk Borough 65.665 N; 149.098 W, May 2005; 15 Nebraska: Nemaha Co. 40.467 N; 95.7 W, November 2004; 16 Montana: Big Fork Lake Co. 47.483 N; 114.217 W, 1999; 17 New Mexico: Taos Co. 36.8467 N; 105.3794 W, June 2004; 18 Minnesota: Itasca Co. 47.510 N; 94.185 W, July 2008; 19 Michigan: Luce

Co. 46.667 N; 85.733 W, July 1999; **20** New Mexico: Sierra Co. 32.9071 N; 107.3116 W, February 2005; **21** Pennsylvania: Crawford Co. 41.575 N; 80.212 W, November 2004.

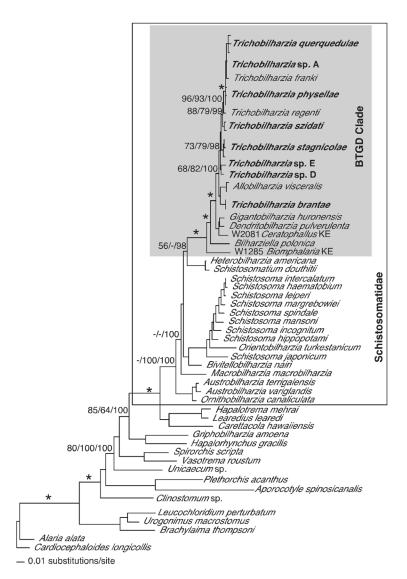


FIGURE 2.

Maximum likelihood tree based on 18S–28S sequences. The schistosomatids are enclosed in the box, and the BTGD clade delimited by shading. Samples in bold are those collected from this study. Within the BTGD clade, individual specimens of *Trichobilharzia* were collapsed and are labeled only by the taxon name. Node support is indicated by MP and ME bootstrap values and Bayesian posterior probabilities (PP), respectively. The "*" indicates MP and ME bootstrap values of >90 and PP of 100. The '-' indicates no significant node support. Branch support is designated only for the major clades.

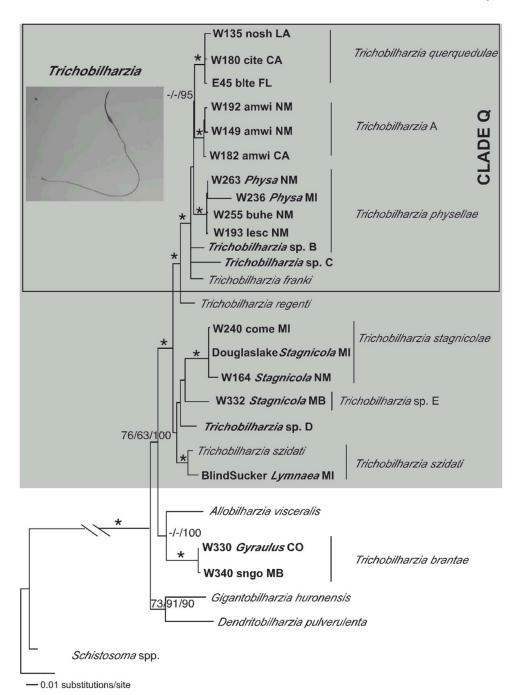


FIGURE 3.

Maximum likelihood tree based on 18S-28S-*cox*1-ITS sequences. *Trichobilharzia* is highlighted. Samples in bold are those collected from this study. Node support is indicated by MP and ME bootstrap values and Bayesian PP, respectively. The '*'indicates MP and ME bootstrap values of >90 and PP of 100. The '-' indicates no significant node support. Image is of *Trichobilharzia physellae* (USNPC# 079636).

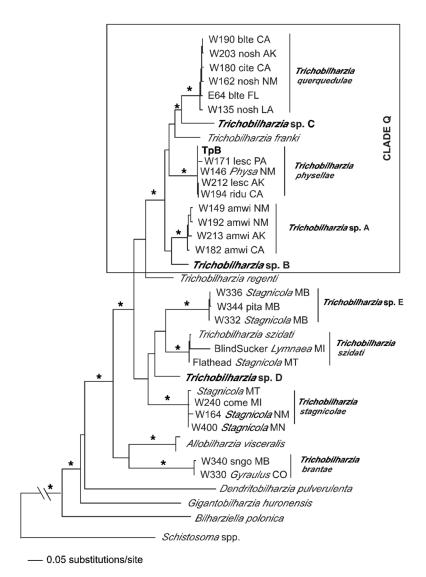


FIGURE 4.

Maximum likelihood tree based on *cox*1 sequences. For the *Trichobilharzia querquedulae* clade only some of the worms sequenced are represented as many differed by only one base pair. The "*" indicates node support of >95% bootstrap for MP and ME and >98 Bayesian PP. The '-' indicates no significant node support. Outgroup species of *Schistosoma* were collapsed. For convenience, the following taxa were trimmed from the tree, but were fully supported in the clade: W137blteLA, W156blteNM, W148.1citeNM, W148.2citeNM, W155.3citeNM, W158noshNM, W162noshNM, W183noshCA, SDS1006noshNE, E45blteFL (Table III). The same was done for *T. physellae*, except in one case there were identical haplotypes: **TpB** = W171lescPA, W193lescNM, W255buheNM, W263*Physa*NM. Otherwise, the following with only 1–2 bp differences were removed W211olsqAK, W193lescNM, W236*Physa*MI, W230.1comeMI, and W256lescNM.

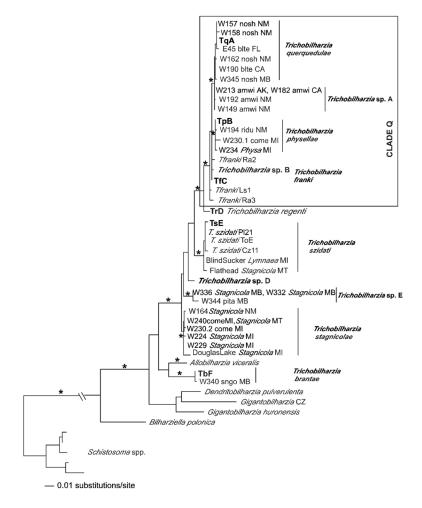


FIGURE 5.

Maximum likelihood tree based on ITS sequences. The following labels apply to samples with identical haplotypes: *Trichobilharzia querquedulae* **TqA**= W135blteLA, W137blteLA, W156blteNM, W148.1citeNM, W155.3citeNM, W180citeCA, W203noshAK, W183noshCA, SDS1006noshNE. *Trichobilharzia physellae* **TpB** = W146*Physa*NM, W263*Physa*NM, W171lescPA, W212lescAK, W249cabaNV, W255buheNM. *Trichobilharzia franki* **TfC** = *Trichobilharzia* sp. C, *T. franki* Ra1, and *T. franki* RSFO1. All haplotypes of *T. regenti* downloaded from GenBank were identical; **TrD** = *T. regenti* Cz79, *T. regenti* Cz31, *T. regenti* Pl27, *T. regenti* Pl20, *T. regenti* Pl17, *T. regenti* Pl14. *Trichobilharzia szidati* **TsE** = *T. szidati* Tsz, *T. szidati* Ls5, *T. szidati* ToA. *Trichobilharzia brantae* **TbF** = W346*Gyraulus*MB, W331*Gyraulus*CO, W330*Gyraulus*CO. Isolates of *T. franki* are from *R. ovata* (ov) and *R. auricularia* (Ra) snails (one sample is from *Lymnaea stagnalis* = Ls). The "*" indicates node support of >95% bootstrap for MP and ME and >98 Bayesian PP. The '-' indicates no significant node support.

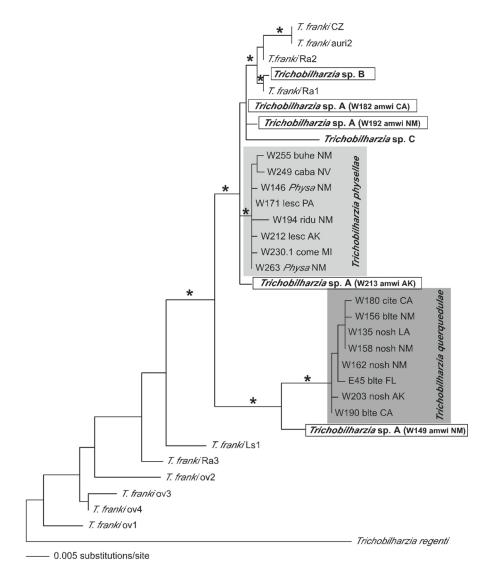
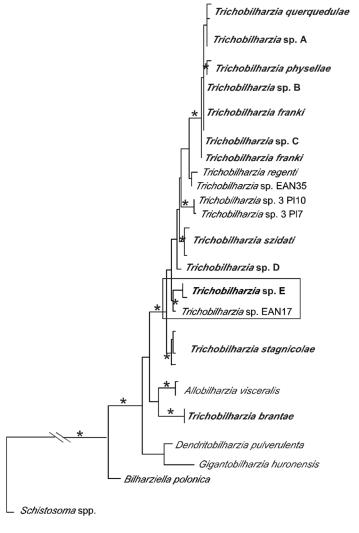


FIGURE 6.

Maximum likelihood tree based on ITS1 sequences of an expanded Clade Q. *Trichobilharzia* A is boxed to show its variable position in the tree and paraphyly of *T. franki*. Isolates of *T. franki* are from *R. ovata* (ov) and *R. auricularia* (Ra) snails (one sample is from *Lymnaea stagnalis* = Ls). See Table III for label descriptions. The "*" indicates node support of >95% bootstrap for MP and ME and >98 Bayesian PP. The '-' indicates no significant node support.



- 0.01 substitutions/site

FIGURE 7.

Maximum likelihood tree based on ITS2 sequences showing the positions of the unidentified avian schistosome isolates from GenBank. The boxed clade highlights the relationship between the samples from North America and France. Bolded samples indicate those from this study. See Table III for label descriptions. The "*" indicates node support of >95% bootstrap for MP and ME and >98 Bayesian PP. The '-' indicates no significant node support.

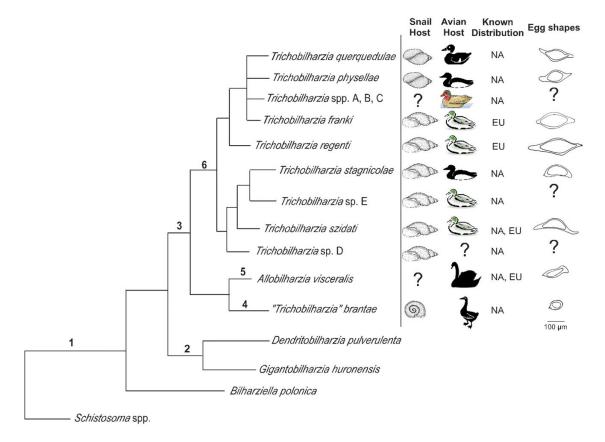


FIGURE 8.

Summary tree based on 28S depicting comparative features (hosts, distribution, and egg morphology) for North American and European avian schistosomes. Morphological features listed for well-supported nodes. 1– reduced sexual dimorphism, males and females flattened or thread-like, gynaecophoric canal absent or weakly developed or short (not extending to posterior), testes numerous; 2 – Absence of ventral sucker, absent or weakly developed oral sucker, uterus with numerous eggs, eggs ovoid; 3 – Well developed oral and ventral suckers, uterus usually with single egg, seminal vesicle between gynaecophoric canal and ventral sucker; 4 – cecal reunion at or anterior to seminal vesicle, >400 testes, gynaecophoric canal terminates well anterior to first testes; 5 – cecal reunion posterior to gynaecophoric canal, >400 testes, gynaecophoric canal terminates well anterior to first testes; 6 – Position of the cecal reunion overlaps the position of the seminal vesicle, gynaecophoric canal terminates at first testes, cercariae large with eyespots.

Physidae,
 Lymnaeidae,
 Planorbidae,
 teal,
 diving ducks,
 Anas americana
 most ducks,
 swans,
 geese. Eggs scaled to relative sizes.

Table I

List of the North American species of *Trichobilharzia* and their definitive and/or intermediate hosts from the type descriptions.

Species		Intermediate host	Definitive host	Type Locality
Trichobilharzia adamsi	Edwards & Jansch, 1955	Physa gyrina [†]	* Exp: peking duck	Canada
Trichobilharzia alaskensis	Harkema, 1960	Lymnaea stagnalis †	Exp: peking duck	Alaska
Trichobilharzia brantae	Farr & Blankemeyer, 1956	unknown	Branta canadensis †	Virginia
Trichobilharzia burnetti	Brackett, 1942	unknown	Aythya collaris †	Wisconsin
Trichobilharzia cameroni	Wu, 1953	Physa gyrina [†]	Exp: canary, pigeon, domestic duck	Canada
Trichobilharzia elvae	(Miller, 1923) Talbot, 1936	Lymnaea stagnalis †	Exp: peking & black duck	Michigan
Trichobilharzia horiconensis	Brackett, 1942	unknown	Anas americana †	Wisconsin
Trichobilharzia kegonsensis	Brackett, 1942	unknown	Aythya valisinera †	Wisconsin
Trichobilharzia ocellata	(La Valette, 1855) Brumpt, 1931	Lymnaea stagnalis [†]	Exp: domestic duck	Germany
Trichobilharzia oregonensis	MacFarlane & Macy 1946	Physa gyrina †	Exp: peking duck	Oregon
Trichobilharzia physellae	(Talbot, 1936) McMullen & Beaver, 1945	Physa parkeri [†]	Exp: domestic duck	Michigan
Trichobilharzia querquedulae	McLeod, 1937		Anas discors †	Canada
Trichobilharzia stagnicolae	(Talbot, 1936) McMullen & Beaver, 1945	Stagnicola emarginata †	Exp: canary	Michigan
Trichobilharzia waubesensis	Brackett, 1942	unknown	Anas americana †	Wisconsin

^{*}Exp=experimental exposure;

 $^{^{\}dagger}$ Type host.

Table II

List of the hosts examined harboring species of *Trichobilharzia*. Localities are labeled with the U.S. state abbreviation, except for Manitoba, Canada (MB). Schistosomes were found in hosts and localities in bold. See text for further description.

North America Avian Host	Number examined	Viscera positive	Nasals examined	Species of Trichobilharzia	Locality
Larus delawarensis	5	0	0		LA, CA
Larus delawarensis	10	0	0		CA
Larus californicus	1	0	0		CA
Larus fuscus	-	0	0		LA
Sterna maxima	1	0	0		LA
Anhinga anhinga	10	0	0		FL, LA
Phalacrocorax auritus	2	0	0		LA
Pluvialis dominicus	1	0	0		LA
Egretta tricolor	1	0	0/1		LA
Egretta thula	-	0	0/1		LA
Plegadis chihi	9	0	0		LA
Eudocimus albus	12	0	6/2		LA
Aramus guarauna	-	0	0		FL
Podilymbus podiceps	2	0	0		NM
Gavia immer	-	0	0		NM
Xanthocephalus xanthocephalus	-	0	0		NM
Aythya affinis	28	11	L/0	T. physellae	AK, CA, LA, NM, PA
Aythya americana	4	0	0		CA, LA, NM
Aythya collaris	5	1	0	T. physellae	CA, LA, NM
Aythya marila	6	0	0		AK, PA, MB
Aythya valisineria	5	1	0/3	T. physellae	NM, NV
Anas acuta	23	-	0/1	Trichobilharzia sp. E	AK, CA, LA, NV, NM, MB
Anas americana	23	&	0/1	Trichobilharzia spp. A and B	AK, CA, NM
Anas carolinensis	41	4	<i>L</i> /0	Trichobilharzia physellae	AK, CA, LA, NM, PA
Anas clypeata	22	20	0/13	T. querquedulae	AK, CA, LA, NE, NM, MB
Anas cyanoptera	12	111	0/2	T. querquedulae	CA, NM
Anas discors	20	20	0/4	T. querquedulae	CA, FL, LA, NM, PA
Anas fulvieula	5	0	0/3		LA

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North America Avian Host	Number examined	Viscera positive	Nasals examined	Species of Trichobilharzia	Locality
Anas platyrhynchos	12	2	0/3	T. physellae	AK, LA, MI, PA ,
Anas rubripes	3	0	0		PA
Anas strepera	27	1	6/2	T. physellae	LA, NM, PA
Aix sponsa	4	П	0/1	T. physellae	LA, NM, PA
Bucephala albeola	∞	1	0	T. physellae	NM, NV, PA
Bucephala clangula	3	0	0	1	CA, NM
Clangula hyemalis	6	П	0	T. physellae	AK
Histrionicus histrionicus	1	0	0		AK
Lophodytes cucullatus	'n	1	0	Trichobilharzia sp. C	LA, PA
Mergus merganser	9	8	0/1	$T.\ stagnicolae+T.\ physellae$	MI
Mergus serrator	3	0	0		CA, NM
Oxyura jamaicensis	9	0	0/2	1	CA, NM, NV
Melanitta fusca	ĸ	0	0		AK, MB
Melanitta perspicillata	33	0	0		AK
Somateria mollissima	1	0	0/1		MB
Cygnus columbianus	13	0	9/2	*	NV, NM
Chen caerulescens	6	2	L/0	Trichobilharzia brantae	LA, NM, MB
Branta canadensis	7	33	5/0	T. brantae	NM, NV, MB
Snail Hosts					
Physidae					
Physa gyrina				T. physellae	CA, MT, MN, NE, NM, NV, MB
Physa acuta				T. querquedulae	experimental in NM
Physa parkeri				T. physellae	MI, MN
Aplexa sp.				1	MB
Lymnaeidae					
Stagnicola emarginata				$T.\ stagnicolae$	MI, MN
Stagnicola elrodi				T. szidati	MT, MN, MB
Stagnicola elodes					MN, NM
Stagnicola sp.				Trichobilharzia sp. D	MB
Stagnicola sp.				Trichobilharzia sp. E	MB
Radix auricularia					NM

North America Avian Host	Number examined	Viscera positive	Nasals examined	Number examined Viscera positive Nasals examined Species of Trichobilharzia Locality	Locality
Fossaria sp.					NM
Lymnaea stagnalis				T. szidati	AK, MI, MT, MN, MB
Bulimnaea megasoma					MN
Planorbidae					
Gyraulus parvus				T. brantae	CO, MT, MN, MB
Planorbula armigera				1	MN
Promenetus exacuous					MIN
Pecosorbis kansasensis					NM
Helisoma trivolvus					LA, NM, MI, MN
Helisoma anceps					MI, MN

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* This host had Allobilharzia visceralis reported in Brant, 2007. The '+' indicates co-infection in all three hosts examined.

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Table III

The host and locality origin of the specimens used in this study. Numbered localities were collected for this study and relate to Fig. 1.

			GenBank Accession numbers	ion numbers				
Schistosome Taxa	Host	Life cycle stage	Locality	18S	28S	SLI	C01	Reference
Trichobilharzia brantae								
W340 sngo MB	Chen caerulescens	*	1 Canada	FJ174451	FJ174467	FJ174533	FJ174482	This paper
W346 Gyraulus MB	Gyraulus parvus	C	1 Canada			FJ174534		This paper
W330 Gyraulus CO	Gyraulus parvus	C	2 Colorado	FJ174450	FJ174466	FJ174532	FJ174484	This paper
W331 Gyraulus CO	Gyraulus parvus	C	2 Colorado			FJ174531		This paper
								This paper
Trichobilharzia franki	Radix sp.	C	Germany	FJ711767	FJ711768		FJ174530	This paper
T. franki Cz	Radix auricularia	C	Czech Republic			AF356845		Dvořák et al., 2002
T. franki Ral	Radix auricularia	C	Czech Republic			AY713969		Rudolfová et al., 2005
T. franki Ra2	Radix auricularia	C	Poland			AY713964		Rudolfová et al., 2005
T. franki Ra3	Radix auricularia	C	Poland			AY713966		Rudolfová et al., 2005
T. franki RSFO1	Radix auricularia	C	France			AY795572		Ferte et al., 2005
T. franki Ls1	Lymnaea stagnalis	C	Czech Republic			AY713973		Rudolfová et al., 2007
T. franki auril	Radix auricularia	C	Switzerland			AJ312041		Picard & Jousson, 2001
T. franki auri2	Radix auricularia	C	Switzerland			AJ312042		Picard & Jousson, 2001
T. franki ov 1	Radix ovata	C	Switzerland			AJ312043		Picard & Jousson, 2001
T. franki ov2	Radix ovata	C	Switzerland			AJ312044		Picard & Jousson, 2001
T. franki ov3	Radix ovata	C	Switzerland			AJ312045		Picard & Jousson, 2001
T. franki ov4	Radix ovata	C	Switzerland			AJ312046		Picard & Jousson, 2001
Trichobilharzia physellae								
W146 Physa NM	Physa gyrina	C	3 New Mexico			FJ174568	FJ174513	This paper
W263PhysaNM	Physa gyrina	C	4 New Mexico			FJ174562	FJ174523	This paper
W171 lesc PA	Aythya affinis	Ą	5 Pennsylvania			FJ174564	FJ174515	This paper
W193 lesc NM	Aythya affinis	A	6 New Mexico	FJ174457	FJ174473		FJ174518	This paper
W212 lesc AK	Aythya affinis	Ą	7 Alaska			FJ174563	FJ174512	This paper
W256 lesc NM	Aythya affinis	A	6 New Mexico			FJ174575	FJ174522	This paper
W194 ridu NM	Aythya collaris	Ą	6 New Mexico			FJ174566	FJ174517	This paper

			Gembank Access	GenBank Accession numbers				
Schistosome Taxa	Host	Life cycle stage	Locality	18S	28S	ITS	CO1	Reference
W249 caba NV	Aythya valisineria	А	8 Nevada			FJ174565		This paper
W255 buhe NM	Bucephala albeola	A	6 New Mexico	FJ174458	FJ174474	FJ174561	FJ174514	This paper
W211 olsq AK	Clangula hyemalis	А	7 Alaska				FJ174516	This paper
W230.1 come MI	Mergus merganser	M	9 Michigan			FJ174567	FJ174521	This paper
W234 come MI	Mergus merganser	M	9 Michigan			FJ174569	FJ174519	This paper
W236 Physa MI	Physa parkeri	C	9 Michigan	FJ174459	FJ174475		FJ174520	This paper
Trichobilharzia querquedulae	ae							
E45 blte FL	Anas discors	A	10 Florida	FJ174453	FJ174469	FJ174555	FJ174510	This paper
E64 blte FL	Anas discors	A	10 Florida				FJ174511	This paper
W137 blte LA	Anas discors	A	11 Louisana	FJ174452	FJ174468	FJ174558	FJ174498	This paper
W156 blte NM	Anas discors	A	6 New Mexico			FJ174554	FJ174502	This paper
W190 blte CA	Anas discors	Ą	12 California			FJ174550	FJ174507	This paper
W148.1 cite NM^{\neq}	Anas cyanoptera	Ą	13 New Mexico			FJ174559	FJ174499	This paper
W148.2 cite NM	Anas cyanoptera	A	13 New Mexico				FJ174500	This paper
W155.3 cite NM	Anas cyanoptera	A	13 New Mexico			FJ174553	FJ174501	This paper
W180 cite CA	Anas cyanoptera	Ą	12 California	FJ174454	FJ174470	FJ174556	FJ174505	This paper
W135 nosh LA	Anas clypeata	Ą	11 Louisana			FJ174557	FJ174497	This paper
W203 nosh AK	Anas clypeata	A	14 Alaska			FJ174552	FJ174508	This paper
W158 nosh NM	Anas clypeata	A	6 New Mexico			FJ174549	FJ174503	This paper
W162 nosh NM	Anas clypeata	Ą	6 New Mexico			FJ174551	FJ174504	This paper
W183 nosh CA	Anas clypeata	Ą	12 California			FJ174560	FJ174506	This paper
SDS1006 nosh NE	Anas clypeata	Ą	15 Nebraska			FJ174548		This paper
W345 nosh MB	Anas clypeata	A	1 Canada			FJ174547	FJ174509	This paper
Trichobilharzia regenti	Radix peregra	C	Czech Republic	AY157219	AY157245		AY157190	Lockyer et al., 2003
T. regenti Pl14	Anas clypeata	M	Poland			EF094533		Rudolfová et al., 2006
T. regenti P117	Aythya fuligula	M	Poland			EF094534		Rudolfová et al., 2006
T. regenti P120	Anas platyrhynchus	M	Poland			EF094535		Rudolfová et al., 2006
T. regenti Pl27	Anas platyrhynchus	M	Poland			EF094537		Rudolfová et al., 2006
T. regenti Cz31	Anas platyrhynchus	M	Poland			EF094538		Rudolfová et al., 2006
T. regenti Cz79	Anas clypeata	M	Czech Republic			EF094540		Rudolfová et al., 2006

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			GenBank Accession numbers	ion numbers				
Schistosome Taxa	Host	Life cycle stage	Locality	18S	28S	ITS	C01	Reference
T. regenti ad1	Anas platyrhynchus	Ą	Switzerland			AJ312049		Picard & Jousson, 2001
T. regenti ov1	Radix ovata	C	Switzerland			AJ312047		Picard & Jousson, 2001
T. regenti ov2	Radix ovata	C	Switzerland			AJ312048		Picard & Jousson, 2001
Trichobilharzia stagnicolae								
W240 come MI	Mergus merganser	M	9 Michigan	FJ174462	FJ174478	FJ174544	FJ174490	This paper
W230.2 come MI	Mergus merganser	M	9 Michigan			FJ174545	FJ174493	This paper
Stagnicola MT	Stagnicola sp.	C	16 Montana			FJ174541	FJ174488	This paper
DouglasLake Stagnicola MI	Stagnicola emarginata	C	9 Michigan	FJ174463	FJ174479	FJ174546	FJ174489	This paper
W164 Stagnicola NM	Stagnicola sp.	C	17 New Mexico	FJ174461	FJ174477	FJ174540	FJ174492	This paper
W224 Stagnicola MI	Stagnicola emarginata	C	9 Michigan			FJ174542	FJ174494	This paper
W229 Stagnicola MI	Stagnicola emarginata	C	9 Michigan			FJ174543	FJ174491	This paper
W400 Stagnicola MN	Stagnicola emarginata	C	18 Minnesota					
Trichobilharzia szidati	Lymnaea stagnalis	C	Czech Republic			AF263828	AY157191	Dvořák et al., 2002
				AY157219	AY157245			Lockyer et al., 2003
Blind Sucker Lymnaea MI	Lymnaea stagnalis	C	19 Michigan	FJ174460	FJ174476	FJ174538	FJ174496	This paper
Flathead Stagnicola MT	Stagnicola elrodi	C	16 Montana			FJ174539	FJ174495	This paper
T. szidati Ls5	Lymnaea stagnalis	C	Poland			AY713967		Rudolfová et al., 2006
T. szidati ToA	Lymnaea stagnalis	C	Netherlands			AY713970		Rudolfová et al., 2005
T. szidati ToE	Lymnaea stagnalis	C	Germany			AY713971		Rudolfová et al., 2005
T. szidati Tsz	Lymnaea stagnalis	C	Czech Republic			AY713972		Rudolfová et al., 2005
T. szidati Pl21	Anas platyrhynchos	M	Poland			EF094536		Rudolfová et al., 2006
T. szidati Cz11	Anas platyrhynchos	Ą	Czech Republic			EF094541		Rudolfová et al., 2006
Unspecified species of Trichobilharzia	obilharzia							
Trichobilharzia sp. 3 P110	Anas penelope	M	Poland			EF094531		Aldhoun et al., 2009
Trichobilharzia sp. 3 Pl7	Anas penelope	M	Poland			EF094532		Aldhoun et al., 2009
Trichobilharzia sp. EAN17	Radix peregra	C	France			EU413971		Jouet et al., 2008
Trichobilharzia sp. EAN35	Radix peregra	C	France			EU413974		Jouet et al., 2008
Trichobilharzia sp. A								
W149 amwi NM	Anas americana	A	13 New Mexico	FJ174456	FJ174472	FJ174574	FJ174524	This paper
W182 amwi CA	Anas americana	A	12 California			FJ174573	FJ174525	This paper

Schistosome Taxa	7.1							
	HOST	Life cycle stage	Locality	18S	28S	ITS	CO1	Reference
W192 amwi NM	Anas americana	A	20 New Mexico	FJ174455	FJ174471	FJ174572	FJ174526	This paper
W213 amwi AK	Anas americana	A	7 Alaska			FJ174570	FJ174527	This paper
Trichobilharzia sp. B								
W205 amwi AK	Anas americana	Ą	14 Alaska			FJ174571	FJ174528	This paper
Trichobilharzia sp. C								
W173 home PA	Lophodytes cucullatus	Ą	21 Pennsylvania			FJ174576	FJ174529	This paper
Trichobilharzia sp. D								
W376 Stagnicola MB	Stagnicola sp.	C	1 Canada	FJ174465	FJ174481	FJ174537	FJ174485	This paper
Trichobilharzia sp. E								
W332 Stagnicola MB	Stagnicola sp.	C	1 Canada	FJ174464	FJ174480		FJ174483	This paper
W336 Stagnicola MB	Stagnicola sp.	C	1 Canada			FJ174535	FJ174486	This paper
W344 pita MB	Anas acuta	Ą	1 Canada			FJ174536	FJ174487	This paper
Other schistosomatids								
Ornithobilharzia canaliculata Larus delawarensis	Larus delawarensis	Α	U.S.A.	AY157222	AY157248			Lockyer et al., 2003
Austrobilharzia variglandis	Larus delawarensis	A	U.S.A.	AY157224	AY157250		AY157196	Lockyer et al., 2003
Austrobilharzia terrigalensis	Batillaria australis	C	Australia	AY157223	AY157249		AY157195	Lockyer et al., 2003
Macrobilharzia macrobilharziaAnhinga anhinga	aAnhinga anhinga	Y	U.S.A.	AY829260	AY858885			Brant et al., 2006
Bivitellobilharzia nairi	Elephas maximus	A	Sri Lanka	AY829261	AY858888		AY829249	Brant et al., 2006
Schistosoma japonicum	†Mus musculus	Ą	Tanzania	AY157226	AY157607			Lockyer et al., 2003
Orientobilharzia turkestanicumOvis aries	nOvis aries	A	Iran	AF442499	AY157254			Lockyer et al., 2003
Schistosoma hippopotami	Bulinus truncatus	C	Uganda			AY197343		Morgan et al., 2003
Schistosoma incognitum	Bandicota indica	A	Thailand	AY157229	AY157255			Lockyer et al., 2003
Schistosome spindale	†Mus musculus	Ą	Sri Lanka	Z11979				Johnston et al., 1993
					AY157257			Lockyer et al., 2003
Schistosoma margrebowiei	†Mus musculus	A	Zambia	AY157233	AY157260			Lockyer et al., 2003
Schistosoma leiperi	$^{\dagger}Mesocricetus$ auratus	Ą	South Africa	AY157234	AY157261			Lockyer et al., 2003
Schistosoma haematobium	$^{\dagger}Mesocricetus$ auratus	Ą	Mali	Z11976	AY157263			Lockyer et al., 2003
Schistosoma intercalatum	†Mus musculus	Ą	Sao Tome	AY157235	AY157262			Lockyer et al., 2003

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Schistosome Taxa	Host	Life cycle stage	Locality	18S	28S	ITS	C01	Reference
Heterobilharzia americana	†Mesocricetus auratus	A	U.S.A.	AY157220	AY157246			Lockyer et al., 2003
W1285 Biomphalaria KE	Biomphalaria sudanica	C	Kenya	AY829258	AY858886			Brant et al., 2006
Bilharziella polonica	Anas platyrhynchus	V	Ukraine, Czech Reparkiis 7214	p athi 67214	AY157240	EF094539	AY157186	Lockyer et al., 2003 Rudolfová et al., 2006
W2081 Ceratophallus KE	Ceratophallus sp.	C	Kenya	AY829259	AY858887			Brant et al., 2006
Dendritobilharzia pulverulenta Gallus, Mergus	ı Gallus, Mergus	Α	U.S.A.	AY157215	AY157241		AY157187	Lockyer et al., 2003
						EF071988		Brant, 2007
Gigantobilharzia huronensis	Agelaius phoeniceus	A	U.S.A.	AY157216	AY157242		AY157188	Lockyer et al., 2003
Gigantobilharzia huronensis	Agelaius phoeniceus	Ą	U.S.A.			EF071987		Brant, 2007
Allobilharzia visceralis	Cygnus cygnus	Ą	Iceland			DQ067561		Kolářová et al., 2006
Allobilharzia visceralis	Cygnus columbianus	Ą	U.S.A.	EF114220	EF114222	EF071989	EF114219	Brant, 2007
Allobilharzia visceralis	Cygnus columbianus	A	U.S.A.	EF114221	EF114223	EF071991	EF114224	Brant, 2007
Outgroups								
Cardiocephaloides longicollis Larus ridibundus	Larus ridibundus		Ukraine	AY222089	AY222171			Olson et al., 2003
Alaria alata	Nyctereutes procyonoides	-	Ukraine	AY222091	AF184263			Olson et al., 2003
Brachylaima thompsoni	Blarina brevicauda		U.S.A.	AY222085				Olson et al., 2003
					AF184262			Tkach et al., 2001
Urogonimus macrostomus	Anas platyrhynchus		Ukraine	AY222086	AY222168			Olson et al., 2003
Leucochloridium perturbatum Turdus merula	Turdus merula		Czech Republic	AY222087	AY222169			Olson et al., 2003
Clinostomum sp. USA	Rana catesbeiana		U.S.A.	AY222095	AY222095			Olson et al., 2003
Aporocotyle spinosicanalis	Merluccius merluccius		United Kingdom	AJ287477				Cribb et al., 2001
					AY222177			Olson et al., 2003
Plethorchis acanthus	Mugil cephalus		Australia	AY222096	AY222178			Olson et al., 2003
Unicaecum sp.	Trachemys scripta		U.S.A.	AY604719	AY604711			Snyder, 2004
Vasotrema robustum	Apalone spinifera		U.S.A.	AY829257	AY858883			Brant et al., 2006
Spirorchis scripta	Chrysemys picta marginata	ta	U.S.A.	AY829256	AY858882			Brant et al., 2006
Hapalorhynchus gracilis	Chelydra serpentina		U.S.A.	AY604718	AY604710			Snyder, 2004
Griphobilharzia amoena	Crocodylus johnstoni		Australia	AY899915	AY899914			Brant et al., 2006
Carettacola hawaiiensis	Chelonia mydas		U.S.A.	AY604717	AY604709			Snyder, 2004
Learedius learedi	Chelonia mydas		U.S.A.	AY604715	AY604707			Snyder, 2004
Hapalotrema mehrai	Chelonia mydas		U.S.A.	AY604716	AY604708			Snyder, 2004

* A=adults M=miracidia C=cercariae;

 $^{\tau}_{\text{experimental;}}$

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Table IV

Morphological comparisons useful in diagnosing both adults and cercariae. Measurements in micrometers unless otherwise indicated.

	T. querquedulae	T. querquedulae	T. physellae	T. physellae	T. franki
Reference	this paper (average)	McLeod, 1937	this paper (average)	McMullen & Beaver 1945	Müller & Kimmig 1994
Adults	n=3		n=3		
length of males	4.8 mm	3.7 mm	2.6 mm	1.3–7.5 mm	3.2-4.0 mm
VS - OS*	417	274–375	320	160–340	485–530
VS - GC	400	NA^{\neq}	440	NA	495–550(522)
length SV	325	NA	400	NA	
length GC	225	375	186	100–190	212–291(246)
cecal reunion	not seen	between SV & GC	not seen	between VS & SV	between SV & GC
testes size	18–23	NA	25–30	28–32	95–106
number of testes	>200	210–240	>100	96–160	41–64
egg shape	spindle with spine	spindle with spine	spindle with spine	spindle with spine	spindle with spine
eggs in utero	ı	140×30	1	170×65	206×69
eggs in feces	150×35	ı	180×70	1	ı
Cercariae					
snail host	Physa gyrina exp.	P. gyrina	P. gyrina	P. parkeri, P. gyrina	Radix auricularia
	n=5		n=5		
length body	327	1	270	265	307
length tail	410	1	352	374	419
length furcae	221–224	1	188	196	234
ratio: body:furcae	0.68		0.7	0.74	0.76
ratio: body:tail	1.25		1.3	1.41	1.36

^{*} VS=ventral sucker, OS=oral sucker, GC=gynaecophoric canal, SV=seminal vesicle, exp=experimental infection.

 $^{^{\}not \tau} NA = not \ available.$

Table VMorphological comparisons of the key differentiating features among closely related genera of avian schistosomes.

	Trichobliharzia brantae	Allobilharzia	Trichobilharzia	Jilinobilharzia
References	Farr & Blankenmeyer, 1956 This study	Kolářová et al., 2006 Brant, 2007	Skrjabin & Zakharov, 1920 Blair & Islam, 1983	Lui & Bai, 1976
Total length males	33.5 mm	65 mm	2.2–12 mm	3.6–4.6 mm
Cecal reunion	at or anterior to the seminal vesicle	posterior to gynaecophoric canal	variable but within range of the seminal vesicle	middle gynaecophoric canal, posterior to seminal vesicle
Position of the seminal vesicle	between ventral sucker and gynaecophoric canal	between ventral sucker and gynaecophoric canal	between ventral sucker and gynaecophoric canal	in gynaecophoric canal
Start of the gynaecophoric canal	posterior to seminal vesicle	posterior to seminal vesicle	posterior to seminal vesicle	posterior to ventral sucker
End of the gynaecophoric canal	well before start of testes	well before start of testes	at start of testes	at start of testes
Testes	585	>400	57–240	83–132
Average egg shape	ovoid with spine	long nonsymmetrical with spine	spindle with spine	spindle with spine
Cercaria flame cells	5+1	unknown	6+1	unknown

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Table VI

Results of experimental infections of birds and snails with species of *Trichobilharzia*. Hosts from which worms were used for exposures are on the left column; hosts exposed are along the top of the table.

Schistosome Taxa	Stagniola emarginata Stagnicola elodes Physa parkeri Physa gyrina Physa acuta Gyraulus parvus Peking duck Domestic mallard	Stagnicola elodes	Physa parkeri	Physa gyrina	Physa acuta	Gyraulus parvus	Peking duck	Domestic mallard
Trichobilharzia stagnicolae	ø							
ex. Mergus merganser	9/10	1	0/10			1		ı
ex. Stagnicola emarginata	ı	1	,	,	,	1	9/0	9/0
Trichobilharzia physellae								
ex. Aythya affinis	ı	0/15		10/15				ı
ex. Bucephalus albeola	ı	0/15	•	8/15		1	,	ı
ex. Mergus merganser	0/10	1	8/10					
Trichobilharzia querquedulae	lae							
ex. Anas cyanoptera	ı	0/15			12/15	5/0		ı
ex. Anas discors	1	0/15	1		11/15	0/5		

 Table VII

 Genetic differences comparing ITS1, CO1 and ITS1-5.8S-ITS2 among schistosomes.

Taxa	ITS1*	$cox1^*$	ITS1-5.8S-ITS2
Within Schistosoma			
S. japonicum - S. malayensis		16.40%	
S. japonicum - S. mekongi		15.80%	
S. malayensis - S. mekongi	4.60%	9.4%	
S. mansoni - S. rodhaini	1.10%	13.30%	-
S. haematobium - S. mattheei	6.60%	16.20%	1.40%
S. haematobium - S. intercalatum	0	11.60%	0.50%
S. hippopotami - S. edwardiense	4.80%	21.40%	
Avian genera			
Allobilharzia - T. brantae	-	14.30%	2.70%
Trichobilharzia - T. brantae	-	14.50%	6.40%
Allobilharzia - Trichobilharzia	-	14.80%	5.50%
Within Trichobilharzia			
T. stagnicolae - T. physellae	-	13.40%	2.00%
T. stagnicolae - T. regenti	-	12.7%	1.90%
T. stagnicolae - T. querquedulae	-	12.00%	2.00%
T. stagnicolae - T. szidati	-	11.20%	1.80%
T. stagnicolae - Trichobilharzia sp. A	-	11.40%	2.00%
T. stagnicolae - Trichobilharzia sp. B	-	12.50%	1.80%
T. stagnicolae - Trichobilharzia sp. C	-	12.50%	1.80%
T. stagnicolae - Trichobilharzia sp. D	-	10.70%	
T. stagnicolae - Trichobilharzia sp. E	-	11.60%	1.70%
T. szidati -T. physellae	-	11.70%	3.00%
T. szidati -T. regenti	-	11.50%	2.50%
T. szidati - T. querquedulae	-	10.70%	2.00%
T. szidati - Blindsucker Lymnaea MT		4.70%	0.36%
T. szidati - Flathead Stagnicola MI		0.48%	0.40%
T. szidati - Trichobilharzia sp. A	-	11.00%	2.80%
T. szidati - Trichobilharzia sp. B	-	10.60%	2.70%
T. szidati - Trichobilharzia sp. C	-	11.50%	2.70%
T. szidati - Trichobilharzia sp. D	-	9.80%	
T. szidati - Trichobilharzia sp. E	-	10.30%	2.60%
T. regenti -T. querquedulae	-	11.50%	1.80%
T. regenti -T. physellae	-	10.60%	1.70%
T. regenti - Trichobilharzia sp. A	-	10.50%	1.50%
T. regenti - Trichobilharzia sp. B	-	9.10%	1.40%
T. regenti - Trichobilharzia sp. C	-	11.10%	1.20%
T. regenti - Trichobilharzia sp. D	-	10.8%	
T. regenti - Trichobilharzia sp. E	-	12.00%	2.30%

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ITS1* cox1* Taxa ITS1-5.8S-ITS2 Trichobilharzia sp. D -Trichobilharzia sp. A 11.10% Trichobilharzia sp. D - Trichobilharzia sp. C 12.10% Trichobilharzia sp. D - Trichobilharzia sp. E 11.10% Trichobilharzia sp. D - T. querquedulae 11.30% Trichobilharzia sp. D - T. physellae 12.30% Trichobilharzia sp. E - Trichobilharzia sp. A 13.10% 3.20% Trichobilharzia sp. E - Trichobilharzia sp. B 12.30% 2.70% Trichobilharzia sp. E - T. querquedulae 12.10% 3.70% Trichobilharzia sp. E - T. physellae 12.80% 3.50% Within T. stagnicolae 0.70% 0.17% Within T. szidati 3.30% 0.35% Within T. regenti 0.00% Within T. physelllae 0.23% 0.80% 0.22% 0.82% Within T. querquedulae 0.40% 0.18% Within T. franki from R. auricularia 0.70% 0.20% Within T. franki from R. ovata 0.52 - 2.8%0.50% Within Trichobilharzia sp. A 0.41% 0.10% Within Trichobilharzia sp. E 0.50% 0.60% Clade Q T. querquedulae - T. physellae 3.00% 8.60% 0.88% T. querquedulae - Trichobilharzia sp. A 3.10% 9.00% 0.32% T. querquedulae - Trichobilharzia sp. B 3.20% 8.10% 0.70% T. querquedulae - Trichobilharzia sp. C 3.80% 8.50% 0.50% T. querquedulae - T. franki from R. auricularia 3.1 - 3.4%8.10% 0.64% T. querquedulae - T. franki from R. ovata 3.4-5.3% 1.00% T. physellae - Trichobilharzia sp. A 9.30% 0.76% 0.60% T. physellae - Trichobilharzia sp. B 0.95% 8.30% 0.50% T. physellae - Trichobilharzia sp. C 3.00% 9.40% 0.50% T. physellae - T. franki from R. auricularia 0.82-1.3% 9.10% 0.60% T. physellae - T. franki from R. ovata 2.5-3.6% 0.87% 0.70% Trichobilharzia sp. A - Trichobilharzia sp. B 6.80% 0.40% Trichobilharzia sp. A - Trichobilharzia sp. C 1.70% 8.80% 0.30% Trichobilharzia sp. B - Trichobilharzia sp. C 1.80% 8.80% 0.13% Trichobilharzia sp. A - T. franki from R. auricularia 0.60% 8.90% 0.40% Trichobilharzia sp. A - T. franki from R. ovata 3.10% 0.70% Trichobilharzia sp. B - T. franki from R. auricularia 8.30% 0.12-0-36% 0.20% Trichobilharzia sp. B - T. franki from R. ovata 4.00% 0.50% Trichobilharzia sp. C -T. franki from R. auricularia 2.30% 8.60% 0.12% Trichobilharzia sp. C - T. franki from R. ovata 4.60% 0.40%

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^{*} Values for ITS1 and *cox*1 in *Schistosoma* are taken from Vilas et al., 2005.