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MINIREVIEW

Medical Parasitology Taxonomy Update, January 2018 to May 2020

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ABSTRACT The taxonomy of parasites of medical and public health importance is rapidly evolving. This minireview provides an update of taxonomic revisions and additions in the field of medical parasitology from January 2018 to May 2020. Several established human parasites have been reassigned to different genera over the past 2 years, while a number of novel parasites of humans have been identified. A comprehensive summary of these changes is provided here, and *Taenia suihominis* is proposed as a replacement name for *Taenia asiaticus* Eom et al., which is a homonym of *Taenia asiatica* von Linstow.

KEYWORDS cestodes, parasite, taxonomy, arthropods, nematodes, protozoans

Taxonomic revisions have a significant impact on the practice of the clinical microbiology laboratory. It is important that clinical microbiologists remain abreast of these changes in order to ensure the currency of laboratory reports and to be able to provide relevant education to the clinical team regarding the reported organisms. It is advisable that laboratories adopt the most up-to-date taxonomic names in a timely fashion, although to avoid confusion, they may also wish to note the previous name of an organism on their reports for 2 to 3 years after a revision is enacted.

In recent years, the advances in molecular characterization of parasites have led to the taxonomic reassignment and revision of many medically important parasites. Furthermore, several species of parasites have been identified for the first time as affecting human hosts in the past 2 years. Combined with prior published taxonomic updates (1, 2), this document allows a comprehensive picture of changes in nomenclature applicable to medical parasitology since 2012.

In addition, advances in molecular characterization of parasites have led to the taxonomic reassignment and revision of many medically important parasites. Molecular data, when judiciously considered in conjunction with morphologic and epidemiologic features, may provide valuable new insights into organism relatedness and phylogeny. Furthermore, several species of parasites have been identified for the first time as affecting human hosts in the past 2 years.

METHODS

A systematic review was conducted using several reference materials to identify peer-reviewed studies describing parasite taxonomic changes and newly reported parasites of clinical importance published between January 2018 through May 2020, continuing from the previous two Medical Parasitology Taxonomic Updates (1, 2). Among the sources consulted were the U.S. Centers for Disease Control and Prevention's Division of Parasitic Diseases and Malaria (DPDM) DPDx website (https://www.cdc.gov/dpdx/). A systematic literature search of the PubMed database (U.S. National Library of Medicine, National Institutes of Health; https://www.ncbi.nlm.nih.gov/pubmed), Google

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Scholar (https://scholar.google.com/), and Google (https://www.google.com) was also performed using keyword search phrases such as "nov. sp." and "new parasite X human" (e.g., new cestode human) and "novel parasite humans" to identify newly described taxa. Only parasites reported from human specimens were included.

RESULTS

Revised and new parasite taxa reported from January 2018 through May 2020 that were not included in the previous version of the taxonomy updates (2) are listed in Tables 1 and 2, respectively, along with their clinical relevance. Diagnostic laboratory methods are also provided for the new taxa.

DISCUSSION

Revised taxa. (i) *Leishmania* and *Endotrypanum*. *(a) Leishmania siamensis and L. martiniquensis*. In 2008, *Leishmania siamensis* was described from a patient in Thailand presenting with visceral leishmaniasis (3). Unfortunately, that name was not formally described under the guidelines of the International Code of Zoological Nomenclature (ICZN), and a type specimen was never designated. As such, this name should be regarded as *nomen nudum* (i.e., a "naked name", a designation that resembles a correct scientific name but does not meet required standards to be one) (4, 5). In 2018, Espinosa and colleagues (5) formally placed *L. siamensis* in synonomy with *Leishmania martiniquensis*, and thus the latter name should be used to refer to this organism.

(b) Endotrypanum equatoriensis and E. colombiensis. *Leishmania equatoriensis* was originally described in 1992 from sloths and squirrels in Ecuador (6), with human infection later described from Colombia (7). *Leishmania colombiensis* was described in 2016 from humans, sloths, and sand flies from Panama and Colombia (8). In 2018, Espinosa and colleagues performed a phylogenetic analysis of *Leishmania* and related organisms and proposed a new taxonomy for the *Leishmaniinae* based on molecular analysis of V7V8 small subunit (SSU) rRNA, Hsp70, and glycosomal glyceraldehyde-3-phosphate dehydrogenase (gGAPDH) (5). In their newly proposed taxonomic scheme, *L. equatoriensis* and *L. colombiensis* were transferred to *Endotrypanum*, a genus of kinetoplastid protozoans from South and Central America that primarily parasitizes sloths and other arboreal mammals (5). At this time, *Endotrypanum equatoriensis* and *Endotrypanum colombiensis* are the only two members of this genus that parasitize humans.

(ii) *Balantioides*. During the last Medical Parasitology Update (2), *Neobalantidium* was proposed as the new genus for the species historically known as *Balantidium coli*, based on work by Pomajbiková et al. (9). Unfortunately, Pomajbiková and colleagues were not aware of *Balantioides*, a name proposed by Alexeieff in 1931 to accommodate *B. coli*, at the time that they proposed *Neobalantidium* as a new genus (10). In 2018, the authors revisited this issue and acknowledged that *Balantioides* was the valid genus for this parasite (11). On the basis of these works, Mathison and Pritt (12) corrected their earlier taxonomic update and provided a taxonomic history of this species. For clinical reporting, the currently accepted name of this species is *Balantioides coli* and the clinical disease is balantiosis.

(iii) *Cryptosporidium*. *Cryptosporidium* genotype *C. parvum* VF383, a parasite of rats and domestic ruminants, has for many years been known to cause zoonotic disease in humans. The genotype has also been referred to as *Cryptosporidium suis*-like due to its morphologic similarities and phylogenetic relationship to *C. suis*. Molecular phylogenetic analysis of the 18S rRNA, actin, and HSP70 gene sequences, in conjunction with morphologic and biological data, demonstrated that *C. parvum* VF383 was a distinct species from *C. suis* and related species. A new name, *Cryptosporidium occultus*, was therefore proposed for *C. parvum* VF383 (13).

(iv) *Taenia*. *Taenia asiatica* was described by Eom and Rim in 1993 based on morphologic and biologic differences from *T. saginata* and *T. solium* (14), and at times has been considered a subspecies of *T. saginata* (15), However, the name *T. asiatica* was preoccupied by *T. asiatica* von Linstow, 1901 (now in *Raillietina*), making the names

TABLE 1 Changes in parasite taxa from January 2018 to May 2020

Category	Current scientific name	Previous scientific name(s)	Clinical disease	Reason for taxonomic change	Reporting suggestion	Reference(s)
Tissue protozoa	*Leishmania martiniquensis*	*Leishmania siamensis*	Cutaneous and visceral leishmaniasis	The species was never formally described, and no type specimen was designated (*nomen nudum*). Later found to be synonymous with *L. martiniquensis*	*Leishmania martiniquensis*	4, 5
	Endotrypanum equatoriensis	*Leishmania equatoriensis*	Cutaneous leishmaniasis	Reclassification of *Leishmaniinae*based on molecular analyses	*Endotrypanum equatoriensis*	5
	Endotrypanum colombiensis	*Leishmania colombiensis*	Cutaneous leishmanisis	Reclassification of *Leishmaniinae* based on molecular analyses	*Endotrypanum colombiensis*	5
Intestinal protozoa	*Balantioides coli*	*Neobalantidium coli*, *Balantidium coli*	Balantiosis	Rediscovery of literature giving precedence to *Balantioides*, based on morphologic characteristics	*Balantioides coli*	11, 12
	Cryptosporidium occultus	*Cryptosporidium parvum* VF383	Intestinal cryptosporidosis	Phylogenetic analysis of 18S rRNA, actin, and HSP70 genes	*Cryptosporidium occultus* where molecular testing allows for species-level identification	13
Intestinal helminths	*Taenia suihominis*	*Taenia asiaticus*	Intestinal taeniasis	*Taenia asiaticus* Eom et al., 2020 is a primary homonym of *T. asiatica* von Linstow, 1901	*Taenia suihominis*	This study

TABLE 2 Parasite taxa newly described or reported from humans from January 2018 through May 2020

Category	Scientific name	Source(s)	Diagnostic laboratory methods	Clinical relevance	Reference(s)
Intestinal protozoa	*Cryptosporidium ditrichi*	Stool	Molecular analysis of the SSU rRNA, actin, and COWP genes	Cause of intestinal cryptosporidiosis	18
Blood protozoa	*Babesia crassa*-like	Blood	Molecular analysis of 18S rRNA gene	Cause of babesiosis	20, 21
Tissue protozoa	*Leishmania orientalis*	Skin nodule	Molecular analysis of rRNA ITS1, RPL23a, RNA PolII, and HSP70	Cause of cutaneous leishmaniasis	4
	Crithidia spp.	Skin nodules	Molecular analysis of GAPDH, SSU RNA, and rRNA ITS1	Cause of cutaneous leishmaniasis-like illness	22, 23
	Acanthamoeba genotype T8	Corneal epithelium	PCR followed by sequencing of 5′-NTR and VP1 gene sequences	Cause of *Acanthamoeba* keratitis	26
	Allovahlkampfia spelaea	Corneal scrapings	Morphology; sequencing of 18S rRNA; animal inoculation studies	Cause of amebic keratitis	28
Tissue helminths	*Oxyspirura* sp.	Skin	Morphologic analysis of larvae and molecular analysis of 18S rDNA	Cause of cutaneous larval migrans	31
Arthropods	*Ixodes pararicinus*	Skin	Morphologic identification of the tick	Ectoparasitism	33
	Cosmoglyphus sp.	Ear	Morphologic identification of mites	Otoacariasis	34
	Lasioderma serricore	Stool	Morphologic identification of beetle larvae	Canthariasis	36, 37

primary homonyms. As such, the newer of the two names is considered invalid. Eon and colleagues tried to rectify the situation by changing the name to *Taenia asiaticus* (16). Unfortunately, changing the gender in itself does not solve the problem of homonymy, and according to Article 31.2 of the ICZN, the gender of the species-group name must agree with the generic name with which at any time it is combined (https://code.iczn.org/formation-and-treatment-of-names/article-31-species-group-names/?frame=1#art-31-2). We therefore propose *Taenia suihominis* as a replacement name for *T. asiaticus*. The etymology of the new name combines *sui-* (from the Latin, *sus*, pig), in recognition of the parasite's intermediate host, and *-hominis* (from the Latin, *hominum*, human), in recognition of the parasite's definitive host.

New taxa. (i) *Cryptosporidium*. In 2018, *Cryptosporidium ditrichi* was described from field mice in the genus *Apodemus* from Europe based on sequencing analysis of SSU rRNA, *Cryptosporidium* oocyst wall protein (COWP), and actin genes (17). In 2020, *C. ditrichi* was isolated for the first time in humans from three patients in Sweden presenting with clinical symptoms consistent with intestinal cryptosporidiosis (18).

(ii) *Babesia*. *Babesia crassa* was originally described from sheep in Iran (19) and has since been detected in goats and ticks in Turkey and ticks in Hungary (20). Several reports in recent years have documented the presence of *Babesia crassa*-like organisms in human patients in China (21) and Slovenia (20). The similarities of the human isolates to *B. crassa* are based on molecular analysis of the 18S rRNA genes (20). It is still uncertain whether this represents human infection with true *B. crassa* or evidence of a new, cryptic species related to *B. crassa*.

(iii) *Leishmania*. *Leishmania orientalis* was described in 2018 from a patient from Nan Province, Thailand, presenting with cutaneous leishmaniasis. The isolate was described based on molecular analysis of rRNA ITS1, RPL23a, RNA polymerase II (PolII), and HSP70 genes (4). Phylogenetic analysis suggests that it is a sister species to *L. enriettii*, a parasite of guinea pigs in South America, and closely related to the human parasite *L. martiniquensis* (4).

(iv) *Crithidia*. *Crithidia* is a genus of protozoan parasites of arthropods related to *Trypanosoma* (22). Recently, reports of human infection with *Crithidia* have been documented in Iran (22) and Brazil (23). In Iran, 12 patients presenting clinically with cutaneous leishmaniasis were found to be infected with *Crithidia*, eight of which had coinfection with *Leishmania major*. The genus-level identification was made based on molecular analysis of the glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene in combination with morphologic and biologic analysis, including mammalian macrophage infection studies (22). The vector of *Crithidia* in Iran is not known, but it is suspected as being *Phlebotomus* sand flies (22). In the case from Brazil, *Crithidia* was isolated from skin and bone marrow from a patient with a fatal visceral leishmaniasis-like illness. The diagnosis was made based on molecular analysis of SSU rRNA, ITS1, and GAPDH genes. The vector of human *Crithidia* in Brazil is also not known. *Crithidia fasciculata* is known to be transmitted by anopheline and culicine mosquitoes and has recently also been detected in the sand fly *Nyssomyia whitmani* in Brazil (23). *Crithidia* should be in the differential of patients presenting with leishmaniasis-like illness that are positive morphologically but are not molecularly consistent with known human *Leishmania* species.

(v) *Acanthamoeba*. It is becoming more commonplace to report *Acanthamoeba* isolates by their genotypes rather than traditional binomial Latin names (24). The *Acanthamoeba* genotype T8 (also known as *A. tubiashi*) was originally isolated from freshwater (25) and until only recently had not been implicated in human disease. In 2018, *Acanthamoeba* genotype T8 was isolated from a corneal epithelial abrasion from a 27-year-old soft contact lens wearer in Hungary. The identity of the isolate was confirmed by PCR followed by sequencing of 5′ N-terminal repeat (5′-NTR) and VP1 gene sequences (26).

(vi) *Allovahlkampfia*. *Allovahlkampfia spelaea* was described in 2009 from carbonate precipitating habitats in karst caves in Slovenia (27). In 2018, *A. spelaea* was isolated

from corneal scrapings in an Egyptian patient presenting with keratitis (28). The identification of *A. spelaea* was made based on morphology of trophozoites and cysts that grew on nonnutritive agar seeded with *Escherichia coli* and then confirmed by sequencing analysis of the entire 18S rRNA subunit. Additional animal inoculation studies were performed on rabbits to simulate clinical keratitis (28). *Allovahlkampfia spelaea* should be in the differential of patients presenting with amebic keratitis.

(vii) *Oxyspirura*. *Oxyspirura* is a large genus of parasitic nematodes. Most species in the genus are ocular parasites of birds, but two species have been reported from nonhuman primates (29, 30). In 2020, *Oxyspirura* (Spirurida: Thelaziidae) was reported as a cause of pruritic cutaneous larval migrans (CLM) in a patient from Vietnam. Larval worms isolated from the patient's skin were identified by the morphologic features of the nerve ring, buccal canal, alimentary canal, and size. Molecular confirmation was performed by sequencing analysis of partial 18S and 26S rDNA sequences, identifying the larvae as being closely related to *Oxyspirura petrowi* (31). Comparison of photographs and morphometric data from this case with published morphological descriptions of *Oxyspirura petrowi* (32) allowed identification as third stage larvae. *Oxyspirura* spp. are transmitted to the definitive host by ingestion of an infected arthropod intermediate host. In the case from Vietnam, the patient admitted to have eaten grasshoppers and crickets (31). *Oxyspirura* should be in the differential of patients presenting with CLM, especially in those that have a dietary history of eating arthropods. Most cases of CLM are diagnosed clinically, and rarely are specimens collected for morphologic or molecular analysis. It is possible that past CLM infections attributed to zoonotic hookworms may actually have been caused by *Oxyspirura*.

(viii) *Ixodes*. *Ixodes pararicinus* is a hard tick endemic to South America. Immature stages feed primarily on small mammals and birds, while adults parasitize large mammals, including cattle, deer, and peccaries. In 2018, a nymph of *I. pararicinus* was reported feeding on a human in Argentina (33).

(ix) *Cosmoglyphus* sp. *Cosmoglyphus* is a cosmopolitan genus of saprophytic mites. In 2018, the first report of otoacariasis (infection of the ear with mites and ticks) caused by a member of the genus *Cosmoglyphus* was reported from the ear of a female patient in India who worked as a grain dealer. Eggs, larvae, and nymphs of mites were observed in KOH wet mounts of ear discharge, and then again among *Aspergillus niger* colonies that grew in fungal cultures of the discharge (34). The identification to the genus level was confirmed by the morphology of the mite, but a species-level identification was not possible because the appropriate magnification (electron microscopy) was not available to see species-specific features (34).

(x) *Lasioderma serricorne*. *Lasioderma serricorne*, commonly referred to as the tobacco beetle or cigarette beetle, is a cosmopolitan pest of dried organic materials, including tobacco, cereals, dried fruit, and dried animal products (35). In 2016, two reports were published documenting the finding of *L. serricorne* larvae in the stools of infants in Malaysia (36) and China (37) as causes of intestinal cantharisis (infestation with beetles). Given the habits of the beetles and the ages of the patients, these cases probably represent spurious passage of the larvae following consumption of infested foodstuffs. In the absence of described pathology associated with these beetles, readers should remain skeptical on whether they should be considered truly parasitic. One should always remain cautious about these kinds of reports, as they often lead to a perpetuation of misinformation and therefore a misunderstanding on behalf of the reader.

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