Medical Parasitology Taxonomy Update: January 2012 to December 2015

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ABSTRACT Parasites of medical importance have long been classified taxonomically by morphological characteristics. However, molecular-based techniques have been increasingly used and relied on to determine evolutionary distances for the basis of rational hierarchical classifications. This has resulted in several different classification schemes for parasites and changes in parasite taxonomy. The purpose of this Minireview is to provide a single reference for diagnostic laboratories that summarizes new and revised clinically relevant parasite taxonomy from January 2012 through December 2015.

KEYWORDS taxonomy, parasitology, parasite, clinical

Parasites of medical importance can be divided into the following two broad categories: the single-celled protozoa and the multicellular metazoa (also known as the helminthic worms). To date, approximately 80 protozoan and 200 metazoan human pathogens have been described (1). They have long been classified taxonomically by morphological characteristics and, for the most part, remain so for diagnostic identification of these organisms. However, as with all microbes, molecular-based techniques have been increasingly used and relied on to determine evolutionary distances for the basis of rational hierarchical classifications. This has resulted in several different classification schemes for parasites (1–7). Currently, all classification schemes should be viewed as interim working schemes, as there is no consensus as to which method produces the most scientifically sound and acceptable classification of parasites. Moreover, with rapid and dramatic advances in sequencing and microbiome discoveries, the current classification schemes are likely to evolve further in the coming years. Recently, Cox reviewed this topic in chapter 132 of the 11th edition of the *Manual of Clinical Microbiology* and nicely summarized the classification of medical parasites based on the scheme devised by Cavalier-Smith (1, 3–6). Furthermore, the International Society of Protistologists recently released a revised classification of eukaryotes based on molecular data that is increasingly being recognized as the accepted classification scheme for human parasites and has been adopted by the Centers for Disease Control and Prevention (CDC) DPDx website (<http://www.cdc.gov/dpdx/>) (2). The purpose of this manuscript is to provide a single reference for diagnostic laboratories that summarizes new and revised clinically relevant parasite taxonomy from January 2012 through December 2015.

METHODS

To accomplish this goal, new and revised taxa were updated by using a combination of reference materials. The reference materials included the *Manual of Clinical Microbiology*, 11th ed, section VIII: Parasitology, the Centers for Disease Control and Prevention DPDx website (<http://www.cdc.gov/dpdx/>), and PubMed searches of peer-reviewed journals from January 2012 to December 2015. To identify studies describing new parasite species of medical importance, we conducted a systematic literature search of the PubMed database (<http://www.ncbi.nlm.nih.gov/pubmed>) using “nov. sp.”

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TABLE 1 List of revised parasite taxa from January 2012 through December 2015

Category	Current name	Synonyms	Clinical disease	Rationale for taxonomic change	Clinical relevance	Reference(s)
Intestinal protozoa	<i>Giardia duodenalis</i>	<i>G. lamblia</i> , <i>G. intestinalis</i>	Giardiasis	The changes in <i>Giardia</i> nomenclature relate to (i) the understanding that a single species of <i>Giardia</i> causes giardiasis in most mammals (including humans) and (ii) differences in the interpretation of the complex International Code of Zoological Nomenclature.	This taxonomic change has no clinical impact.	1, 8
Blood/tissue protozoa	<i>Plasmodium ovale wallikeri</i> (variant strain)	<i>P. ovale</i>	<i>P. ovale</i> malaria	Recent molecular studies indicate that <i>Plasmodium ovale</i> malaria is caused by two distinct, closely related species of protozoan parasites: <i>P. ovale wallikeri</i> (variant strain) and <i>P. ovale curtisi</i> (classic strain).	The latency period may be longer in <i>P. ovale curtisi</i> than <i>P. ovale wallikeri</i> (15).	16
	<i>Plasmodium ovale curtisi</i> (classic strain)	<i>P. ovale</i>	<i>P. ovale</i> malaria	Recent molecular studies indicate that <i>Plasmodium ovale</i> malaria is caused by two distinct, closely related species of protozoan parasites: <i>P. ovale wallikeri</i> (variant strain) and <i>P. ovale curtisi</i> (classic strain).	The latency period may be longer in <i>P. ovale curtisi</i> than <i>P. ovale wallikeri</i> (15).	16

as the search term. Only parasites or molecular detection of parasites recovered from human specimens were included. All names are taxonomically recognized if not otherwise indicated. These tables are not meant to be exhaustive and are reflective of the most clinically relevant organisms to be encountered in the diagnostic laboratory.

RESULTS

Tables 1 and 2 summarize the revised and new parasite taxa from January 2012 through December 2015, respectively. Each table includes some information regarding the clinical relevance of the specific species or group. For new parasite taxa, defining laboratory characteristics have also been included (Table 2).

DISCUSSION

Of the revised parasite taxa, the most impactful change relates to *Giardia*, now renamed *Giardia duodenalis* from its previous *Giardia intestinalis* or *Giardia lamblia*. This change is taxonomically recognized, and diagnostic laboratories should be incorporating the updated taxonomy on clinical reports. That being said, *G. intestinalis* and *G. lamblia* should still be considered synonyms of the newly accepted *G. duodenalis*. These taxonomic changes relate to the initial description of a separate species of *Giardia* causing human infections from species that caused infections in animals. However, it is now understood that *Giardia duodenalis* infects most mammals, including humans, their companion animals, and livestock (8). Furthermore, different interpretations of the complex rules of the International Code of Zoological Nomenclature have also contributed to the change in *Giardia* taxonomy. For an in depth description of the rationale of the taxonomic changes of *Giardia*, researchers are encouraged to read the review by Monis et al. (9).

Recent genetic studies have also proven to help consolidate the naming of species within particular genera, where different species were originally thought to have different host specificities when in fact they belonged to the same species. Two examples are *Ascaris lumbricoides* and *Ascaris suum* and *Parastrongylus* (previously *Angiostrongylus*) *cantonensis* and *Parastrongylus mackerrasae*. Both of these examples are still currently being debated among taxonomists. New genetic data support that *A. suum*, originally thought to be a separate species of *Ascaris* in pigs, is genetically similar to and may in fact be considered a synonym to *A. lumbricoides* (10, 11). Similarly, *Parastrongylus* (previously *Angiostrongylus*) *mackerrasae* and *P. cantonensis* share highly similar genetic identities and comparable pathogenesis in murine and guinea pig models (12, 13). Due to the ongoing controversies surrounding these species, they have

TABLE 2 New parasite species recovered from human clinical material reported between January 2012 and December 2015

Scientific name	Family	Source	Defining laboratory characteristics	Clinical relevance	Reference
Intestinal protozoa					
<i>Entamoeba bangladeshi</i> sp. nov.	Amoebidae	Stool	Cysts and trophozoites that resemble <i>E. histolytica</i> . Growth at 25°C and 37°C in axenic culture.	Intestinal amebiasis. Possible cause of diarrheal disease in children.	23
<i>Cryptosporidium viatorum</i> sp. nov.	Cryptosporidiidae	Stool	Morphology and staining characteristics of the oocysts are typical of the genus but do not differentiate it from other <i>Cryptosporidium</i> spp. Cross-reactivity of antibodies incorporated in two immunologically based kits has been demonstrated.	Cryptosporidiosis. Identified among returning travelers from the Indian subcontinent with gastrointestinal symptoms.	24
Free-living amoeba					
<i>Acanthamoeba byersi</i> sp. nov.	Acanthamoebidae	Skin and brain	Grows well on agar plates coated with <i>E. coli</i> at 30°C, 37°C, and 40°C. The life cycle has trophozoite (50–125 µm; single or double nuclei with acanthopodia) and cyst (20–35 µm; round ectocyst and stellate endocyst with five to eight arms or rays at different planes) stages even after suspending in distilled water for 24 h.	Amebic encephalitis. A cause of fatal amoebic encephalitis.	25
Tissue protozoa					
<i>Leishmania (Leishmania) waltoni</i> sp. nov.	Trypanosomatidae	Five cryopreserved strains isolated from human cases of diffuse cutaneous leishmaniasis	Grows well <i>in vitro</i> with a doubling time of 6 h. Promastigote measurements: body length, 7.8 ± 1.7 µm; body width, 1.9 ± 0.4 µm; flagellum length, 5.3 ± 1.6 µm	Leishmaniasis. A cause of human diffuse cutaneous leishmaniasis in the Dominican Republic.	26
<i>Leishmania (Leishmania) martiniquensis</i> Desbois, Pratlong & Dedet sp. nov.	Trypanosomatidae	Tissue biopsy	Difficult to grow <i>in vitro</i> with a doubling time of 24 h. Amastigote measurements: diam, 3.99 ± 0.48 µm. Promastigote measurements: body length, 9.44 ± 3.02 µm; body width, 2.20 ± 0.63 µm; flagellum length, 11.59 ± 3.63 µm.	Leishmaniasis. A cause of human cutaneous leishmaniasis.	27
Nematode					
<i>Mansonella</i> sp. "DEUX" ^a	Onchocercidae	DNA from blood specimens of Gabonese children	Molecular detection. No defining characteristics described.	Filariasis. A potential cause of mansonellosis in humans.	28

^a*Mansonella* sp. "DEUX" is not taxonomically recognized.

not been included in Table 1 but are important to mention, as their taxonomy may be revised in the near future as more information is generated.

Recently, it was discovered through multilocus genetic analysis that *Plasmodium ovale* malaria may be caused by two distinct but closely related strains—the classic strain *Plasmodium ovale wallikeri* and the variant strain *Plasmodium ovale curtisi*. The two strains tend to coexist in the same geographic areas without interbreeding (14). Currently, the Centers for Disease Control and Prevention (CDC) has not fully acknowledged the two distinct strains of *P. ovale* as causes of human malaria (<http://www.cdc.gov/dpdx/malaria/index.html>). They are described as being indistinguishable by microscopy but may differ clinically in their duration of latency (15). PCR-based methods for the detection of *P. ovale* may be designed to either detect both strains simultaneously or further differentiate the two strains (16). Readers are directed to an excellent review on the subject by Fuehrer and Noedl (16). However, until further information on the differences in clinical presentation and management of the two strains is elucidated, clinical laboratories should continue to report *P. ovale* to the species level unless further differentiation based on molecular methods has been performed to identify the individual strains.

Although *Plasmodium knowlesi* was first described as causing malaria in humans in 2004 and is excluded from Tables 1 and 2 (limited to new/revised taxa from 2012 to

2015), it is worthwhile to note that the simian malaria parasite has increasingly been recognized as a cause of malaria in humans in most of the countries in Southeast Asia (17–21). It is still considered a zoonotic malaria species by the CDC and the World Health Organization, as it has not been determined if *P. knowlesi* can be transmitted from human to human via mosquitos of the *Anopheles* spp. without macaque monkeys (genus *Macaca*) as the natural intermediate host (<http://www.cdc.gov/dpdx/malaria/index.html>). Microscopically, early trophozoites of *P. knowlesi* may resemble *Plasmodium falciparum* with rings less than or equal to one-third of the diameter of erythrocytes with the presence of double chromatin dots and occasional appliqué forms. However, the presence of all parasite stages—mature trophozoites in the shape of band forms, schizonts with 10 to 12 merozoites (10 to 16 merozoites can occur with *P. knowlesi* and overlap the 6 to 12 merozoites seen in *Plasmodium malariae*), and round/oval gametocytes filling the erythrocyte—may cause *P. knowlesi* to be misidentified as *P. malariae*. Thus, identification of *P. malariae* in patients with a travel history to Southeast Asia should raise the possibility of *P. knowlesi* infection due to the morphological similarities described. In this situation, severe clinical disease and high parasite burden would be consistent with *P. knowlesi*. PCR-based methods are available for identification of the *Plasmodium* species and can be applied to further differentiate *P. malariae* from *P. knowlesi* (22).

Overall, the new parasite species described in Table 2 have been described using molecular methods. These new taxa are generally indistinguishable microscopically from other currently known parasitic pathogens (i.e., *Entamoeba bangladeshi* sp. nov. is indistinguishable from *Entamoeba histolytica*). The identification of most of these new species further confuses traditional microscope-based methods for detecting and reporting these pathogens in the clinical laboratory. For example, should we now consider adding *E. bangladeshi* to our reporting of organisms that resemble *E. histolytica* by microscopy, where the organism reported would be *Entamoeba histolytica/dispar/bangladeshi*? It may also demonstrate that the roles of molecular-based techniques are likely to become more and more important, not only for taxonomic purposes but for use in clinical labs for differentiation and identification of parasitic pathogens, especially among morphologically similar parasites with distinct clinical diseases.

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