Abstract

*Cyclospora cayetanensis* is a diarrhea-causing, intracellular, intestinal parasite of humans. It completes its life cycle in individual hosts, but many aspects of its biology are not well understood, including its infectious dose and its virulence and/or pathogenicity. The drug of choice is trimethoprim-sulfamethoxazole and immune reconstitution using HAART and secondary trimethoprim-sulfamethoxazole prophylaxis should be considered in HIV-infected individuals.

Both foodborne and waterborne outbreaks have been documented. Foodborne clusters have affected large numbers of individuals in North America, with cases occurring most commonly in springtime and early summer. Increased global sourcing and rapid transport of soft fruit, salad vegetables, and seafood can enhance both the likelihood of oocyst contamination and the oocyst survival. Standardized methods for detecting oocysts on foods must be maximized as, unlike pre-enrichment methods that increase organism numbers for prokaryotic pathogens and indicators, there is no method to augment parasite numbers prior to detection. Oocyst contamination of food can be on the surface of, or in, the food matrix and products at greatest risk of transmitting infection to man include those that receive no, or minimal, heat treatment after they become contaminated. Temperature elevation kills oocysts and disinfectants and other treatment processes used in the food industry may be detrimental to oocyst survival or lethal, but further research in this important area is required.

Key Words: *Cyclospora*; oocysts; occurrence; detection; outbreaks; foodborne; environment.

1. CLASSIFICATION AND IDENTIFICATION

1.1. Classification

1.1.1. Historical

In 1979, Ashford (1) reported the finding of unsporulated, *Isospora*-like oocysts in routine stool samples from three individuals from Papua New Guinea and described them as undistinctive, uniformly sized, and easily confused with fungal spores. From 1985 onwards, 8–10 μm oocysts of an unknown *Cryptosporidium muris*-like parasite were reported from expatriates and native Peruvians suffering from extended bouts of chronic diarrhea, weight loss, and fatigue (2,3). Further reports from the USA (4) and Kathmandu (5) identified the local occurrence of this parasite and confirmed its broad geographical distribution. Since that time, these “*Isospora*-like” oocysts, also known as “Big Crypto” or “Crypto Grande”, have been described as a flagellate (2), a blue-green alga (6), cyanobacterium-like body (7), coccidian-like body, coccidian-like organism or *cyclospora*-like body (8), and identified as a cause of prolonged diarrhea in both the immunocompetent and the immunocompromised. Finally classified in 1994 (9),
C. cayetanensis oocysts have been described in the stools of residents in, and travelers returning from, developing nations, and in association with diarrheal illness in individuals from north, central, and south America, the Caribbean, Africa, the Indian sub-continent, southeast Asia, Australia, and Europe. C. cayetanensis was named after the location of the authors’ principal studies, Cayetano Heredia University in Lima, Peru.

1.1.2. Current Classification

Originally described in the intestines of moles by Eimer in 1870, Cyclospora is related taxonomically to other coccidian parasites, including Eimeria and the human pathogens Cryptosporidium and Toxoplasma. Cyclospora is a member of the subphylum Apicomplexa, class Sporozoasida, subclass Coccidiasina, and family Eimeriidae. Organisms of the genus Cyclospora have an oocyst with two sporocysts, each of which contains two sporozoites (10). Seventeen species have been described: C. cayetanensis (from humans) (9), C. cercopitheci (from Cercopticus aethopis, African green or vervet monkey), C. colobi (from Colobus guereza, colobus monkey), C. papionis (from Papio anubis, olive baboon), C. angimurinensis (from Chaetodipus hispidus hispudus), C. ashtabulensis (from Parascalops breweri), C. babaulti (from Vipera berus), C. caryolytica (from Talpea europea, Talpea micrura coreana and possibly P. brevii), C. glomerica, (from Glomeris species), C. megacephali (from Scalopus aquaticus), C. ninae (from Ninia s. sebac), C. parascalopi (from P. brevii), C. scinc (from Scincus officinalis), C. talpea (from Talpea europaeae), C. mopidonori (from Natrix natrix and Natrix stolata), C. viperae (from Vipera aspis and possibly Coluber scalaris, Coronella australis and Natrix viperinus) and C. zamenis (from Coluber v. viridiflavus) (11). Four species infect primates, namely C. cayetanensis (9), and based on morphological and molecular analyses, three further species from non-human primates (Cyclospora cercopitheci sp.n., C. colobi sp.n., and C. papionis sp.n. (12).

Oocyst size and shape, sporulation characteristics, life cycle, host range, and anatomical site(s) of infection are the important criteria for classifying coccidia; however, reliance on phenotypic characteristics for classifying Cyclospora has identified certain limitations resulting in misclassification (2–8,13). Molecular methods have advanced our understanding of the phylogenetic relationships among closely related organisms and have helped us to resolve some previous limitations. Comparative 18S rRNA phylogenetic analysis reveals that C. cayetanensis is most closely related to the genus Eimeria (14). The 18S rRNA sequence data suggest that the relationship between C. cayetanensis and Eimeria is as close as that between some Eimeria species and have prompted speculation that nonhuman reservoirs of C. cayetanensis may exist (11) and that Cyclospora might be an Eimeria species (15). Taxonomic revisions such as these are difficult to reconcile completely because the sporulation characteristics for each genus are quite distinct: Eimeria oocysts have four sporocysts, each containing two sporozoites; while Cyclospora oocysts have two sporocysts, each containing two sporozoites. Eimeria are host-species specific, nonhuman pathogens whose oocysts sporulate outside the host and complete their asexual and sexual developmental life cycles within one host. The close molecular phylogenetic relationship between Eimeria and Cyclospora predicts that they may share similar phenotypic characteristics beyond sporogony outside the host (16,17) and a monoxenous life cycle (18). Variability in nucleotide sequences in the first internal-transcribed spacer (ITS1) region