Transmission Dynamics of *Cryptosporidium* Infection in a Natural Population of Non-Human Primates at Polonnaruwa, Sri Lanka

Dilrukshi K. Ekanayake, David Mark Welch, Rudo Kieft, Stephen Hajduk, and Wolfgang P. J. Dittus*

Department of Biochemistry and Molecular Biology, University of Georgia, Athens, Georgia; Josephine Bay Paul Center, Marine Biological Laboratory, Woods Hole, Massachusetts; Global Infectious Disease Program, Marine Biological Laboratory, Woods Hole, Massachusetts; Department of Biochemistry and Molecular Biology, University of Georgia, Athens, Georgia; Association for the Conservation of Primate Diversity, Kandy, Sri Lanka; Institute of Fundamental Studies, Sri Lanka; Department of Conservation Biology, Smithsonian National Zoological Park, Washington, District of Columbia

Abstract. Infections from *Cryptosporidium parvum* are of interest not only to public health, but also to wildlife conservation, particularly when humans and livestock encroach on nature and thereby increase the risk of cross-species transmissions. To clarify this risk, we used polymerase chain reaction to examine the hypervariable region of the *C. parvum* 18S rRNA gene in feces from three monkey species. Samples were isolated from regions where disease transmission between monkeys, livestock, and humans was likely (soiled habitat) or unlikely (clean habitat). Monkey individuals, their social groups, and different species shared multiple genotypes/isolates of *C. parvum*. Ecological and molecular analyses suggested that *Cryptosporidium* infection among Toque macaques in soiled habitats was mainly the bovine genotype *C. parvum*. Monkeys inhabiting clean habitat, particularly gray and purple-faced langurs, lacked *Cryptosporidium* species/types associated with bovines. Livestock apparently was a main source of infection for wild primates.