

**Coccidia of raptors: morphological and molecular
phylogenetic studies of genus *Eumonospora***

Abstract of Doctoral Thesis

Shyun Chou

Graduate School of Veterinary Medicine and Life Science

Nippon Veterinary and Life Science University

In this study, parasitological fecal examination of raptors imported into Japan was performed. Coccidian oocysts which had characters of single sporocyst with eight sporozoites inside and absence of Stieda body were collected from five genus of Strigiformes and one genus of Falconiformes and these oocysts were all morphologically identified as *Avispora henryae*. However, we resurrected and redescribed genus *Eumonospora* since we found that genus *Avispora* was junior synonym of genus *Eumonospora* during literature review. Genus *Eumonospora* is known as veterinary important parasite for causing diarrhea, blood in feces, and sudden death in raptors, which these clinical symptoms were also observed in those infected individuals and some were recovered after administrated with antiprotozoal, toltrazuril. Although the host specificity of genus *Eumonospora* is regarded as genus-specific, detection of *Eumonospora henryae* from different genera and orders indicates that *E. henryae* might be euryxenous (more than one family of hosts) and the divergent host spectrum between these species. Moreover, the sequence of nuclear 18S rRNA (18S), nuclear 28S rRNA, and mitochondrial cytochrome *c* oxidase subunit 1 amplified from *E. henryae* were used for molecular phylogenetic analyses for resolving the taxonomic position of this genus.

Genus *Eumonospora* clustered in family Sarcocystidae nor than family Eimeriidae with the analyzation of 18S data set of Eimeriorina. Analyzation of data sets including concatenated sequences revealed that genus *Eumonospora* and subfamily Toxoplasmatinae were sister groups with highly supported taxonomic position. On the other hand, phylogenetic topology of genus *Eumonospora* largely corresponded with avian host phylogram might indicated occurrence of cospeciation between parasite and host, while molecular identification of *E. henryae* from different avian orders indicated the possibility of host switching occurred in this species. In the end, the morphological character, single oocyst with eight sporozoites inside, is distinguishable from other subfamilies in family Sarcocystidae. Hence, a new subfamily, Eumonosporinae, was

proposed. Furthermore, defining the family Sarcocystidae based on criteria having oocysts with disporocystic and tetrasporozoic, should be modified.