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SHORT COMMUNICATIONS

First report of *Giardia duodenalis* assemblages A and B in wild hornbills

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ABSTRACT

The Kinabatangan Wildlife Sanctuary is internationally known for its biodiversity and is recognized as one of an Important Bird Area (IBA). There are eight species of hornbills that persist in the fragmented landscape of Kinabatangan, Sabah. While the lack of nesting sites, food resources and hunting threats have been well described, little is known about the health status of these birds in the wild. Accordingly, the present study aimed to determine the occurrence of *Cryptosporidium* and *Giardia* genotypes in the wild populations of hornbills in Sabah, East Malaysia as it may have implications to current conservation strategies. Understanding the distribution of parasites in wildlife is a crucial area of study, as parasites can have a substantial impact on the health and viability of wild animals, as well as zoonotic consequences. At the time of writing, the occurrence of *Cryptosporidium* and *Giardia* protozoa in wildlife has been understudied and poorly documented in Southeast Asia. This study provides the first molecular evidence of zoonotic *Giardia duodenalis* assemblages A and B in hornbills. These findings are important to assess the health of wild populations of endangered hornbills. In addition, to emphasize the importance of monitoring the distribution of assemblages of *G. duodenalis* with a broad host distribution as top priority for the development of appropriate public health policies to reduce the potential transmission of this enteric protozoan.

Keywords: *Cryptosporidium*; *Giardia duodenalis*; Bornean hornbill; Malaysia; hornbill conservation.

INTRODUCTION

There are eight species of hornbills that persist in the fragmented landscape of Kinabatangan, Sabah and they are listed in the Red List as critically endangered Helmeted hornbill (*Rhinoplax vigil*), endangered Wrinkled hornbill (*Rhabdotorrhinus corrugatus*) and White-crowned hornbill (*Berenicornis comatus*), three vulnerable species, i.e., Rhinoceros hornbill (*Buceros rhinoceros*), Black hornbill (*Anthracoceros malayanus*) and Wreathed hornbill (*Rhyticeros undulatus*), near threatened Bushy-crested hornbill (*Anorrhinus galeritus*), and least concern Oriental Pied hornbill (*Anthracoceros albirostris*). From the eight species, the Helmeted hornbill, Wreathed hornbill and White-crowned hornbill have become increasingly rare along the Kinabatangan (Kaur, 2020). Limiting factors for any hornbill population include availability of natural tree cavities (Poonswad, 1993, 1995; Datta & Rawat, 2004), food resources and presence of suitable roosting sites. Logging activities diminish available nesting cavities because hornbills nest in valuable timber trees i.e. Dipterocarp trees (Jinamoy *et al*., 2014). The scarcity of nesting opportunities for large-bodied hornbills is also made apparent by the continued utilization of artificial nest-boxes in Kinabatangan (Kaur *et al*., 2020: Vercoe *et al*., 2021)

While the lack of nesting sites, food resources and hunting threats have been well described, little is known about the health status of these birds in the wild. It is important to investigate the types of parasites these birds may be harboring, and to identify potential threats these endangered birds may be facing in the wild. This is especially important for the Helmeted hornbill, a critically endangered bird with a highly specific diet and nesting requirement (Kaur *et al*., 2018). The objectives in this study are also aligned with objective 3.1 of the Helmeted hornbill Action Plan (2017) which identifies 'disease screening' as a high priority research and conservation action for the species (Jain *et al*., 2018).

Cryptosporidium and *Giardia* are enteric protozoa which can be transmitted through ingestion of contaminated food and water sources to humans and animals, including birds. It can affect the upper intestinal tract in humans (Dixon, 2021) causing symptoms such as foul smelling, watery diarrhea. Notably, birds are the known primary host to a few species of *Cryptosporidium* (i.e., *Cryptosporidium ornithophilus*, *Cryptosporidium proventriculi*, *Cryptosporidium galli*, *Cryptosporidium baileyi* and *Cryptosporidium meleagridis*) and several genotypes of *Giardia ardeae* (reviewed in Ryan *et al*., 2021). In the past decade, there have been numerous reports on the human infective *Cryptosporidium* species in wild

migratory birds (i.e., *Cryptosporidium andersoni*, *C. meleagridis* and *Cryptosporidium parvum*) (Koompapong *et al*., 2014; Reboredo-Fernandez *et al*., 2015; Wang *et al*., 2020; Jian *et al*., 2021), domesticated poultry (i.e., *C. meleagridis* and *C. parvum*) (Bomfim *et al*., 2013; Ayinmode & Falohun, 2018; da Cunha *et al*., 2018; Ferrari *et al*., 2018) and pet birds (i.e., *C. andersoni*, *C. meleagridis*, *Cryptosporidium muris* and *C. parvum*) (Gomes *et al*., 2011; Dong *et al*., 2021; Liao *et al*., 2021) across the continents of Asia, Africa, Europe and South America. On the other hand, *G. duodenalis* has been reported to occur in wild birds in the past ten years, including the human infective assemblages B, D, and E (Reboredo-Fernandez *et al*., 2015; Cano *et al*., 2016; Jian *et al*., 2021). Additionally, *G. duodenalis* assemblages A and E have also been detected in domesticated and pet birds, respectively (da Cunha *et al*., 2017, Dong *et al*., 2021). In a study from Australia, birds such as Budgerigar chicks showed signs of retarded growth, dehydration, and diarrhoea due to *Giardia* infections (Filippich *et al*., 1998).

To the best of our knowledge, there is a lack of studies detecting both *Cryptosporidium* and *Giardia* infections in wild hornbills. Therefore, to provide insights into the health status of hornbill populations and potential zoonotic implication, the present study aimed to investigate the occurrence of *Cryptosporidium* and *Giardia* genotypes in the wild hornbill populations of Sabah, East Malaysia.

METHODOLOGY

Specimen collection

A total of 13 hornbill fecal samples were collected from nesting pairs of Rhinoceros hornbills, Wrinkled hornbills, Helmeted hornbills, Bushy crested hornbills and Wreathed hornbill nesting sites throughout the Kinabatangan Wildlife Sanctuary (Sabah, Malaysia) in 2017 to 2018 (Figure 1). Each fecal sample was collected from the base of the nests and kept in stool container. They were kept in the fridge at 4°C in the nearest village before transported to the main laboratory at Universiti Malaya in Kuala Lumpur.

PCR amplification and sequence analyses

The fecal samples were then subjected to genomic DNA isolation using the NucleoSpin® Soil kit (Macherey-Nagel, Germany). The extracted DNA was subjected to nested polymerase chain reaction (PCR) using MyTaq Red Mix (BioLine, Australia), for amplifications of the 18S rRNA gene of *Cryptosporidium* and triosephosphate isomerase (*tpi*) gene of *G. duodenalis.*

For the detection of *Cryptosporidium*, the first PCR utilized the forward primer 18SiCF2 (5'-GAC ATA TCA TTC AAG TTT CTG ACC-3') and the reverse primer 18SiCR2 (5'-CTG AAG GAG TAA GGA ACA ACC-3'). In the second PCR, a fragment of approximately 580 bp was amplified using 1 µl of the first PCR products by using the forward primer 18SiCF1 (5'-CCT ATC AGC TTT AGA CGG TAG G-3') and the reverse primer 18SiCR1 (5'-TCT AAG AAT TTC ACC TCT GAC TG-3'). Both PCR protocols shared the following steps: initial denaturation at 94°C for 3 minutes, followed by forty-five cycles of PCR (94°C for 30 seconds, 58°C for 30 seconds, 72°C for 30 seconds), and a final extension at 72°C for 10 minutes (Ryan *et al*., 2003).

For the detection of *Giardia*, the first PCR utilized the forward primer AL3543 (5'-AAATIATGCCTGCTCGTCG-3') and the reverse primer AL3546 (5'-CAAACCTTITCCGCAAACC-3'). Subsequently, in the second PCR, a 530 bp fragment was amplified using 2 µl of the first PCR products along with the forward primer AL3544 (5'-CCCTTCATCGGIGGTAACTT-3') and the reverse primer AL3545 (5'-GTGGCCACCACICCCGTGCC-3'). Both PCR protocols for *Giardia* detection involved an initial denaturation at 94°C for 3 minutes, followed by 35 PCR cycles (94°C for 45 seconds, 50°C for 45 seconds, and 72°C for 60 seconds), and a final extension step at 72°C for 10 minutes (Sulaiman *et al*., 2003).

The PCR amplified fragments were subsequently sent to a local company (Apical Scientific Sdn Bhd, Kuala Lumpur, Malaysia) for bi-directional sequencing using both forward and reverse primers. Sequences generated from the present study were deposited in the National Center for Biotechnology Information (NCBI) GenBank database under the accession numbers OP729398-OP729399. A maximum likelihood (ML) phylogenetic tree of *Giardia* was plotted using MEGA X (Kumar *et al*., 2018). The ML bootstrap values were estimated using 1,000 replicates with General Time Reversible + Gamma Distributed model. The nucleotide sequences were aligned with known assemblage reference sequences retrieved from the literature. Additional closest sequences displayed in BLAST and other relevant sequences were also included for phylogenetic tree construction. *Giardia muris* (AF069565) was used as an outgroup.

Figure 1. A male *R. vigil* (left) and a male *B. rhinoceros* (right) perched at their respective natural nest cavities (Photo by Sanjitpaal Singh).

RESULTS AND DISCUSSION

Based on the *tpi* gene of *G. duodenalis*, three out of 13 individual hornbills were amplified and successfully sequenced. Phylogenetic analysis revealed the occurrence of zoonotic assemblage AII (OP729398) in one sample of *R. vigil*, and assemblage BIV in two samples of *B. rhinoceros* (OP729399) (Figure 2). None of the samples were positive for *Cryptosporidium.*

In captivity, hornbills are not usually screened for these protozoans, hence it is not clear if infected birds would display any illness. Little attention has been given to *Cryptosporidium* and *Giardia* infections in birds, especially in Malaysia. To date, there have been only two research studies that reported *Cryptosporidium* infection in captive birds. In 2005, Rohela *et al*. reported the occurrence of *Cryptosporidium* oocysts through Ziehl-Neelsen staining technique in 28% (28 of 100) of studied captive birds (i.e., Wrinkled Hornbill, Great Argus Pheasant, Black Swan, Swan Goose, Marabou Stork, and Moluccan Cockatoo) at the Malaysian National Zoo. Subsequent confirmation using immunofluorescence technique revealed that 21.4% (6 of 28) were positive to *Cryptosporidium* (Rohela *et al*., 2005). Two years later, another study was also conducted at the same zoo, in which captive Wreathed hornbill, Great Currasow, Bushy-crested Hornbill and Common Peafowl (4 or 3.4% of 116) were detected positive to *Cryptosporidium* by Ziehl-Neelsen staining (Lim *et al*., 2007). Remarkably, detection of oocysts in a bird handler (12.5% of 8) was also reported in this zoo, suggesting that this zoonotic pathogen was acquired during close contact with the infected animals (Lim *et al*., 2007). However, this postulation remained untested and further molecular tests would be essential to understand how the transmission had occurred.

The present study reported *G. duodenalis* assemblages A and B among studied wild hornbills, though the source of infection is unknown. Nevertheless, these assemblages have been detected in human hosts in Malaysia, including indigenous people (Choy *et al*., 2014), migrant workers (Sahimin *et al*., 2018) and HIV patients (i.e., assemblage A) (Lim *et al*., 2011). In addition, both assemblages have also been reported in domesticated goats (Lim *et al*., 2013), assemblage B in urban rodents (Tan *et al*., 2019) and assemblage A in a recreational lake water (Lim *et al*., 2009) in the country. This study represents the first report of *G. duodenalis* assemblages A and B in hornbills.

The occurrence of *G. duodenalis* in birds has been underreported in Malaysia and in the adjacent countries. However, the human infective *G. duodenalis* assemblages were reported in wild birds in Northern and Northwest Spain, for example, assemblage B in aquatic birds, Common Buzzard, Common Quail and Eurasian Magpie; and assemblage D in Eurasian Jay (Reboredo-Fernandez *et al*., 2015; Cano *et al*., 2016). In addition, *G. duodenalis* assemblage A was

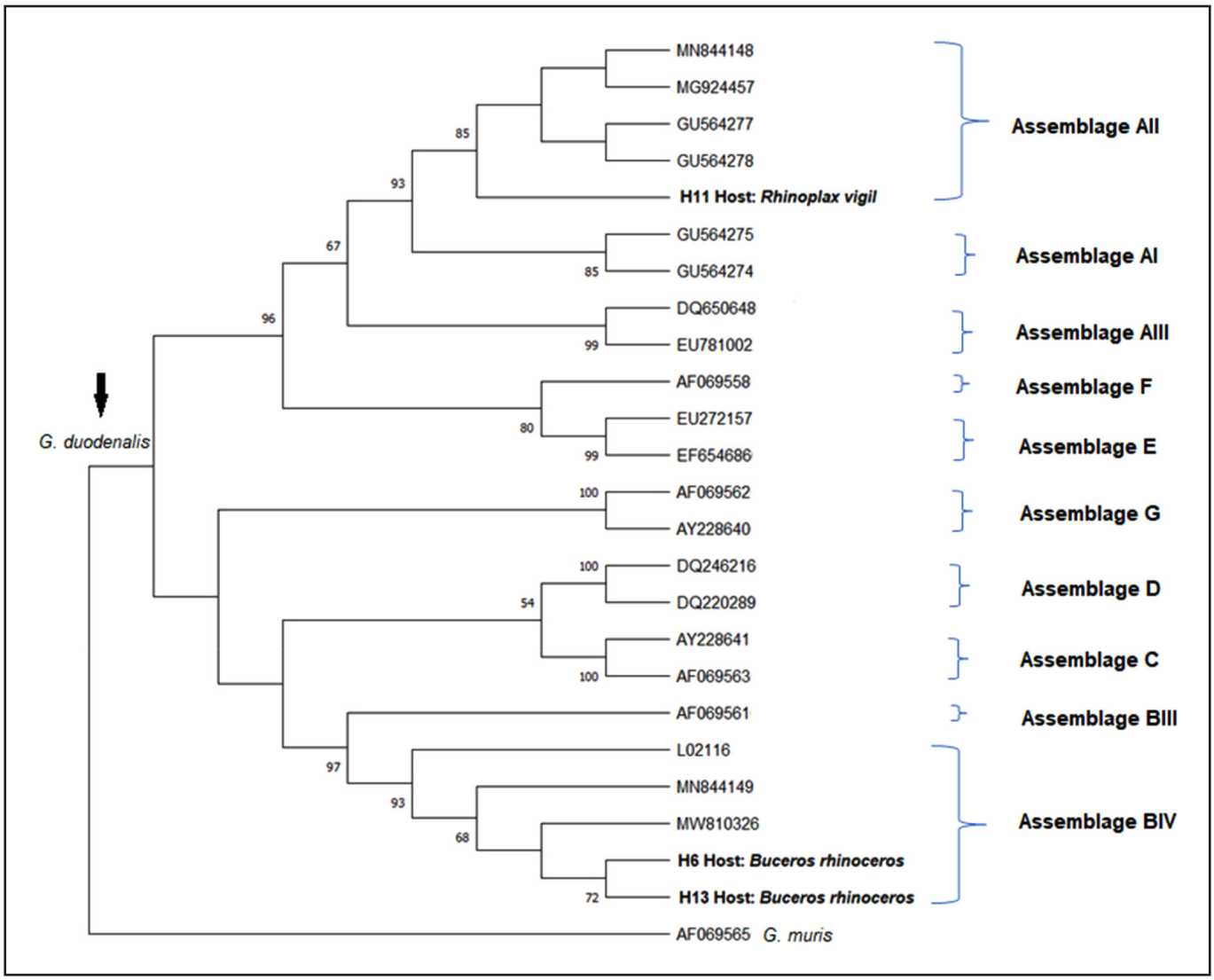

Figure 2. Maximum likelihood phylogenetic tree of *Giardia duodenalis* assemblages based on *tpi* gene sequences. Sequences generated in the present study are in bold.

also reported in captive Toco Toucan from aviary in Brazil (da Cunha *et al*., 2017). In Asia, *G. duodenalis* ruminant assemblage or E was detected in 33 out of 1005 (3.3%) captive pet birds from trading places in Henan Province, China (Dong *et al*., 2021). Additionally, low prevalence (3.3%/23 of 679) of assemblages B and E in wild-birds was also reported in Qinghai Lake, Qinghai-Tibetan Plateau (Jian *et al*., 2021).

In conclusion, this study represents the first molecular evidence of zoonotic *Giardia duodenalis* assemblages A and B in hornbills. Though their potential as a source of infection should not be disregarded, direct contact between humans and wild hornbills are rare, resulting in low risk for zoonosis. In situations where direct contact is anticipated, (i.e. captive zoological setting, confiscation of live birds, etc), transmission can be controlled and minimized through improved hygiene and sanitation (Dixon, 2021). Available evidence suggests that wild birds play a limited role in transmitting infectious diseases in humans (Tsiodras *et al*., 2008).

Future studies with a larger sample size from wild hornbills are warranted to gain a better understanding of the epidemiology of these parasites in the region, especially when asymptomatic infections are common in both humans and animals (Dixon, 2021). Obtaining this information would enhance the knowledge on potential reservoir for these parasites. This in turn allow the establishment of public health policy to prevent zoonotic transmission while ensuring appropriate conservation strategies are put in place to preserve the biodiversity in the region.

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Conflict of interests

The authors declare no competing interests or financial conflicts of interest.

REFERENCES

Ayinmode, A.B. & Falohun, O.O. (2018). Molecular detection of *Cryptosporidium* species in domestic ducks sold for food in Nigerian live bird markets. *Folia Veteri*naria **64**: 74-49. https://doi.org/10.2478/fv-2018-0040

Bomfim, T.C.B., Gomes, R.S., Huber, F. & Couto, M.C.M. (2013). The importance of poultry in environmental dissemination of *Cryptosporidium* spp. *The Open Veterinary Science Journal* **7**: 12-17. https://doi.org/10.2174/1874318801307010012

Cano, L., de Lucio, A., Bailo, B., Cardona, G.A., Muadica, A.S.O., Lobo, L. & Carmena, D. (2016). Identification and genotyping of *Giardia* spp. and *Cryptosporidium* spp. isolates in aquatic birds in the Salburua wetlands, Alava, Northern Spain. *Veterinary Parasitology* **221**: 144-148. https://doi.org/10.1016/j.vetpar.2016.03.026

Choy, S.H., Al-Mekhlafi, H.M., Mahdy, M.A.K., Nasr, N.N., Sulaiman, M., Lim, Y.A.L. & Surin, J. (2014). Prevalence and associated risk factors of *Giardia* infection among indigenous communities in rural Malaysia. *Scientific Reports* **4**: 6909. https://doi.org/10.1038/srep06909

da Cunha, M.J.R., Cury, M.C. & Santin, M. (2018). Molecular characterization of *Cryptosporidium* spp. in poultry from Brazil. *Research in Veterinary Science* **118**: 331-335. https://doi.org/10.1016/j.rvsc.2018.03.010

da Cunha, M.J.R., Cury, M.C. & Santin, M. (2017). Molecular identification of *Enterocytozoon bieneusi*, *Cryptospotidium*, and *Giardia* in Brazilian captive birds. *Parasitology Research* **116**: 487-493. https://doi.org/10.1007/s00436-016-5309-6

Datta, A. & Rawat, G.S. (2004). Nest-site selection and nesting success of three hornbill species in Arunachal Pradesh, north-east India Great Hornbill *Buceros bicornis*, wreathed hornbill *Aceros undulates* and Oriental pied hornbill *Anthracoceros albirostris*. *Bird Conservation International* **14**: 39-52. https://doi.org/10.1017/S0959270905000213

Dixon, B.R. (2021). *Giardia duodenalis* in humans and animals – Transmission and disease. Research in Veterinary Science **135**: 283-289. https://doi.org/10.1016/j.rvsc.2020.09.034

Dong, H., Cheng, R., Li, X., Li, J., Chen, Y., Ban, C., Zhang, X., Liu, F. & Zhang, L. (2021). Molecular identification of *Cryptosporidium* spp., *Enterocytozoon bieneusi*, and *Giardia duodenalis* in Captive Pet Birds in Henan Province, Central China. *Journal of Eukaryotic Microbiology* **68**: e12839. https://doi.org/10.1111/jeu.12839

Ferrari, E.D., Nakamura, A.A., Nardi, A.R.M., Santana, B.N., da Silva Camargo, V., Nagata, W.B., Bresciani, K.D.S. & Meireles, M.V. (2018). *Cryptosporidium* spp. in caged exotic psittacines from Brazil: Evaluation of diagnostic methods and molecular characterization. *Experimental Parasitology* **184**: 109-114. https://doi.org/10.1016/j.exppara.2017.12.004

Filippich, l., Mcdonnell, P., Munoz, E. & Upcroft, J. (1998). *Giardia* infection in budgerigars. *Australian Veterinary Journal* **76**: 246-249. https://doi.org/10.1111/j.1751-0813.1998.tb10148.x

Gomes, R.S., Huber, F., da Silva, S. & do Bomfim, T.C.B. (2011). *Cryptosporidium* spp. parasitize exotic birds that are commercialized in markets, commercial aviaries, and pet shops. *Parasitology Research* **110**: 1363-1370. https://doi.org/10.1007/s00436-011-2636-5

Jain, A., Lee, J.G.H., Chao, N., Lees, C., Orenstein, R., Strange, B.C., Chng, S.C.L., Marthy, W., Yeap, C.A. & Rao, M. (2018). Helmeted Hornbill (*Rhinoplax vigil*): Status Review, Range-wide Conservation Strategy and Action Plan (2018-2027). IUCN SSC Hornbill Specialist Group, pp. 54.

Jian, Y., Zhang, X., Li, X., Schou, Chad, Charalambidou, I., Ma, L. & Karanis, P. (2021). Occurrence of *Cryptosporidium* and *Giardia* in wild birds from Qinghai Lake on the Qinghai-Tibetan Plateau, China. *Parasitology Research* **120**: 615-628. https://doi.org/10.1007/s00436-020-06993-w

Jinamoy, S., Trisurat, Y., Pattanavibool, A., Pisdamkham, C., Thongsikem, S., Veerasamphan, V., Poonswad, P. & Kemp, A. (2014). Predictive distribution modelling for Rufous-necked Hornbill *Aceros nipalensis* (Hodgson, 1829) in the core area of the Western Forest Complex, Thailand. *Raffles Bulletin Zoology* **62**: 12-20.

Kaur, R. (2020). Dissertation: Breeding and conservation ecolo gy of Asian hornbills (Aves: Bucerotidae) in Kinabatangan, Sabah. Universiti Malaya.

Kaur, R., Ramli, R., Ancrenaz, M., Hassan, H., Ahmad, E., Ratag, M., Elahan, B., Sinyor, H. & Rajak, A. (2020). Estimating the availability of potential hornbill nest trees in a secondary forest patch in Kinabatangan, Sabah. *Forktail* **36**: 56-62.

Kaur, R., Singh, S., Ramli, R., Hassan, H., Majinun, A., Ancrenaz, M., Ratag, M., Rauf, H.A., Jamal, J., Rauf, A.S.A. *et al*. (2018). Observations at a nest of Helmeted Hornbill *Rhinoplax vigil* in Borneo, Malaysia. *Forktail* **34**: 68-73.

Koompapong, K., Mori, H., Thammasonthijarern, N., Prasertbun, R., Pintong, A., Popruk, S., Rojektitikhun, W., Chaisiri, K., Sukthana, Y. & Mahittikorn, A. (2014). Molecular identification of *Cryptosporidium* spp. in seagulls, pigeons, dogs, and cats in Thailand. *Parasite* **21**: 52. https://doi.org/10.1051/parasite/2014053

Kumar, S., Stecher, G., Li, M., Knyaz, C. & Tamura, K., 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. *Molecular Biology Evolution* **35**: 1547-1549. https://doi.org/10.1093/molbev/msy096

Liao, C., Wang, T., Koehler, A.V., Hu, M. & Gasser, R.B. (2021). *Cryptosporidium* of birds in pet markets in Wuhan city, Hubei, China. *Current Research in Parasitology & Vector-Borne Diseases* **1**: 100025. https://doi.org/10.1016/j.crpvbd.2021.100025

Lim, Y.A.L., Iqbal, A., Surin, J., Sim, B.L.H., Jex, A.R., Nolan, M.J., Smith, H.V. & Gasser, R.B. (2011). First genetic classification of Cryptosporidium and Giardia from HIV/AIDA patients in Malaysia. *Infection, Genetics and Evolution* **11**: 968-974. https://doi.org/10.1016/j.meegid.2011.03.007

Lim, Y.A.L., Mahdy, M.A.K., Tan, T.K., Goh, X.T., Jex, A.R., Nola, M.J., Sharma, R.S.K. & Gasser, R.B. (2013). First molecular characterization of Giardia duodenalis from goats in Malaysia. *Molecular and Cellular Probes* **27**: 28-31. https://doi.org/10.1016/j.mcp.2012.08.006

Lim, Y.A.L., Ramasame, S.D., Mahdy, M.A.K., Sulaiman, W.Y.W. & Smith, H.V. (2009). Detection and molecular characterization of *Giardia* isolated from recreational lake water in Malaysia. *Parasitology Research* **106**: 289-291. https://doi.org/10.1007/s00436-009-1602-y

Lim, Y.A.L., Rohela, M. & Muhamat Shukri, M. (2007). Cryptosporidiosis among birds and bird handlers at Zoo Negara, Malaysia. *Southeast Asian Journal of Tropical Medicine and Public Health* **38**(Suppl): 19-26.

Poonswad, P. (1993). Current status and distribution of hornbills and their habitats in Thailand. In: Manual to the Conservation of Asian Hornbills, Poonswad, P. & Kemp, A.C. (editors). Bangkok: Sirivatana Interprint Co. Ltd., pp. 436-475.

Poonswad, P. (1995). Nest site characteristics of four sympatric species of hornbills in Khao Yai National Park, Thailand. *Ibis* **137**: 183-191.

Reboredo-Fernandez, A., Ares-Mazas, E., Caccio, S. & Gomez-Couso, H. (2015). Occurrence of *Giardia* and *Crypsotporidium* in wild birds in Galicia (Northwest Spain). *Parasitology* **142**: 917-925. https://doi.org/10.1017/S0031182015000049

Rohela, M., Lim, Y.A.L., Jamaiah, I., Khadijah, P.Y.Y., Laang, S.T., Mohd Nazri, M.H. & Nurulhuda, Z. (2005). Occurrence of *Cryptosporidium* oocysts in Wrinkled Hornbill and other birds in the Kuala Lumpur National Zoo. *Southeast Asian J Trop Med Public Health* **36**(Suppl): 34-40.

Ryan, U., Xiao, L., Read, C., Zhou, L., Lal, A.A. & Pavlasek, I. (2003). Identification of novel *Cryptosporidium* genotypes from the Czech Republic. *Applied and Environmental Microbiology* **69**: 4302-4307. https://doi.org/10.1128/AEM.69.7.4302-4307.2003

Ryan, U.M., Feng, Y., Fayer, R. & Xiao, L. (2021). Taxonomy and molecular epidemiology of *Cryptosporidium* and *Giardia* – a 50-year perspective (1971-2021). *International Journal for Parasitology* **51**: 1099-1119. https://doi.org/10.1016/j.ijpara.2021.08.007

Sahimin, N., Douadi, B., Lim, Y.A.L., Behnke, J.M. & Zain, S.N.M. (2018). Distribution of *Giardia duodenalis* (assemblages A and B) and *Cryptosporidium parvum* amongst migrant workers in Peninsular Malaysia. *Acta Tropica* **182**: 178-184. https://doi.org/10.1016/j.actatropica.2018.02.033

Sulaiman, I.M., Fayer, R., Bern, C., Gilman, R.H., Trout, J.M., Schantz, P.M., Das, P., Lal, A.A. & Xiao, L. (2003). Triosephosphate isomerase gene characterization and potential zoonotic transmission of *Giardia duodenalis*, *Emerging Infectious Diseases* **9**: 1444-1452. https://doi.org/10.3201/eid0911.030084

Tan, T.K., Low, V.L., Ng, W.H., Ibrahim, J., Wang, D., Tan, C.H., Chellappan, S. & Lim, Y.A.L. (2019). Occurrence of zoonotic *Cryptosporidium* and *Giardia duodenalis* species/ genotypes in urban rodents. *Parasitology International* **69**: 110-113. https://doi.org/10.1016/j.parint.2018.12.007

Tsiodras S., Kelesidis T., Kelesidis I., Bauchinger, U. & Falagas, M.E. (2008). Human infections associated with wild birds. *Journal of Infection* **56**: 83-98. https://doi.org/10.1016/j.jinf.2007.11.001

Vercoe, M., Barton, C., Kaur, R., Figueira, R., Macaulay, B., Boyd, M. & Ancrenaz, M. (2021). Artificial nest cavities can sustain populations of hornbills in the degraded forests of Kinabatangan, Borneo. *Oryx* **55**: 330-331. https://doi.org/10.1017/S003060532100020X

Wang, K., Gazizova, A., Wang, Y., Zhang, K., Zhang, Y., Chang, Y., Cui, Y., Zhang, Y., Zhang, S. & Zhang, L. (2020). First detection of *Cryptosporidium* spp. in migratory whooper swans (*Cygnus cygnus*) in China. *Microorganisms* **8**: 6. https://doi.org/10.3390/microorganisms8010006