Invited article

**Cryptosporidium cf. avium** in an inland-bearded dragon (*Pogona vitticeps*) – A case report and review of the literature

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**ABSTRACT**

Here, we report the first case of *Cryptosporidium cf. avium* from an inland bearded dragon (*Pogona vitticeps*) from a wildlife sanctuary in Victoria, Australia. Molecular characterisation was conducted by PCR-coupled sequencing of regions in the small subunit of nuclear RNA (SSU), *actin* and large subunit of nuclear RNA (LSU) genes. The sequences obtained grouped with those of *C. ornithophilus* and other *C. avium* genotypes/variants originating from reptiles or birds. We discuss this case in relation to the current state of knowledge of *C. avium* of birds and reptiles, considering provenance and environment (agricultural, pet industry, wildlife, zoo or wildlife park) as well as clinical context, and pathological changes associated with cryptosporidiosis in these host animals.

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1. **Introduction**

*Cryptosporidium* sp. are apicomplexan gregarine parasites (Ryan et al., 2016) that typically infect epithelial cells of the gastrointestinal tracts of vertebrates (Chalmers and Davies, 2010). Currently, 41 species and ≥70 genotypes (Holubová et al., 2019) have been recorded in a wide range of host species (Zahedi et al., 2016). The commonest agents causing cryptosporidiosis in reptiles are *C. serpentis* (type A in snakes, type B in lizards), *C. varanii* (syn. *C. saurophilum*) in lizards as well as *C. ducismarci* and *C. testudines* in tortoises and alligators (Xiao et al., 2004; Pavlasek and Ryan, 2008; Ježková et al., 2016; Bogan, 2019; Huang et al., 2020).

Lizards can also harbour *C. avium*-related *Cryptosporidium* taxa (Latney and Wellehan, 2020) of the “*C. avium* clade” (Kubota et al., 2020), comprising *C. avium*, *C. cf. avium* and *C. ornithophilus* (formerly *C. avium* genotype II; Holubová et al., 2020). To date, there have been three reported cases of cryptosporidiosis in lizards caused by *C. avium* genotype V – now known as *C. avium* (see Holubová et al., 2016) – recorded in green iguanas (*Iguana*) with colitis and cystitis (Kik et al., 2011); *C. cf. avium* from spiny-tailed lizards (*Uromastyx* sp.) with catarrhal enteritis (Kubota et al., 2020); or *C. avium* from an inland bearded dragon (*Pogona vitticeps*) in Scotland, presenting with refractory conjunctivitis (Lewis et al., 2020).

Molecular detection or identification of *Cryptosporidium* using PCR-coupled tools is the most effective means of diagnosis, as microscopy is often insufficiently sensitive, and cannot identify or delineate species (Jex et al., 2008; Ryan et al., 2014). Genetic markers in the small subunit of nuclear RNA (SSU), *actin*, 70 kDa heat shock protein (hsp70) and, recently, in the large subunit of nuclear RNA (LSU) genes have been used in these tools to identify and characterise *Cryptosporidium* taxa (Morgan et al., 2001; Ryan et al., 2003; Ng et al., 2006; Koehler et al., 2017).

In the present study, we employed a molecular approach to discover and characterise a member of the *C. avium* clade in an inland bearded dragon, native to central Australia (cf. Cogger, 2014), using PCR-coupled sequencing approach. This is the fourth record of a taxon of the *C. avium* clade from a reptile. The present case is discussed in relation to current state of knowledge of *C. avium* in birds and reptiles as well as clinical and pathological aspects.

2. **Materials and methods**

2.1. **Case report**

In August 2015, some reptiles in a mixed-species exhibit of centralian blue-tongues (*Tiliqua multifasciata*), spiny-tailed monitors (*Varanus acanthurus*) and inland-bearded dragons (*Pogona vitticeps*), at the Healesville Sanctuary (Victoria, Australia), had non-specific clinical signs, including lethargy and inappetence, and some animals died with no prominent signs of illness. A *post mortem* examination of a deceased centralian blue tongue revealed histological evidence of *Cryptosporidium*...
infection in the gastrointestinal tract, but the necrotic tissues taken were formalin-fixed and proved unsuitable for DNA-based testing. Faeces from the live spiny-tailed monitor and the inland-bearded dragon were collected for DNA analysis. Subsequently, the bearded dragon was euthanised due to a diagnosis of adenovirus infection and continued deterioration of this animal.

2.2. DNA extraction, PCR and sequencing

Genomic DNA was extracted from 0.25 g of faeces from the inland bearded dragon, the spiny-tailed monitor and a portion of the centralian blue-tongue’s formalin-fixed gastrointestinal tract using the PowerSoil DNA Isolation Kit (MoBio, USA), according to the manufacturer’s protocol. This DNA was subjected to PCR, targeting (individually) four distinct loci of nuclear DNA: SSU, actin, hsp70 and LSU. Each PCR was conducted in a volume of 50 μl containing GoTaq Flexi buffer (Promega, USA), 3.0 mM of MgCl2, 200 μM of each dNTP, 50 pmol of each primer, 1 U of GoTaq DNA polymerase (Promega, USA) and 2 μl of the genomic DNA sample. Known test-positive, test-negative and no-template controls were included in each step of each PCR run.

An SSU gene region (800 bp) was amplified by nested PCR, first using primers 18SICF2 (forward: 5′-GAC ATA TCA TTC AAG TTT CTG ACC-3′) and 18SIRC2 (reverse: 5′-CTG AAG GAG TAA GGA ACA ACC-3′), and then employing primers 18SICF1 (forward: 5′-CTT ATC AGC TTA AGA CGG TAG G-3′) and 18SIRC1 (reverse: 5′-TCT AAG AAT TCC TCT GAC TG-3′) (Ryan et al., 2003); for both PCR steps, cycling conditions were: 94 °C for 5 min (initial denaturation), followed by 45 cycles of 94 °C for 30 s (denaturation), 58 °C for 30 s (annealing) and 72 °C for 30 s (extension), and a final extension of 72 °C for 10 min.

An actin gene region (830 bp) was amplified by nested PCR, first using primers All F1 (forward: 5′-ATG CCG GGW ATG GTD GGT AGT-3′) and Act6R (reverse: 5′-GGD GCA ACR AYR TTR ATC TTC-3′), and using primers All F2 (forward: 5′-GAY GAR CCH CAR TCV AAR AGR GGT AT-3′) and All R1 (reverse: 5′-TDD ATY TTC ATD GTH GAG GGW GC-3′) (Ng et al., 2006); for both PCR steps, the cycling conditions were: one cycle of 94 °C for 120 s (denaturation), 60 °C for 60 s (annealing) and 72 °C for 120 s (extension), followed by 50 cycles of 94 °C for 30 s (denaturation), 58 °C for 20 s (annealing) and 72 °C for 40 s (extension), and a final extension of 72 °C for 7 min.

Amplification of the hsp70 gene region (450 bp) was attempted using primers HSPF4 (forward: 5′-GGT GGT GGT ACT TTT GAT GTA TC-3′) and HSPR4 (reverse: 5′-GCC TGA ACC TTT GGA ATG CG-3′) (Morgan et al., 2001). The cycling conditions were: cycling conditions were: 94 °C for 5 min (initial denaturation), followed by 35 cycles of 94 °C for 30 s (denaturation), 55 °C for 30 s (annealing) and 72 °C for 30 s (extension), and a final extension of 72 °C for 5 min. In addition, a portion of the LSU gene (~500 bp) was amplified previously (Koehler et al., 2017) using primer pairs LSU2040F/LSU3020R and LSU2065F/LSU2557R.

The intensity and size of amplicons were assessed by electrophoresis (7 V/cm) in 1.5% agarose gels. Following electrophoresis, gels were stained with ethidium bromide and their size estimated by comparison to ΦX174-HaeIII (Promega, USA) markers. Aliquots (5 μl) of individual amplicons were treated with ExoSAP-IT (Affymetrix, USA), according to the manufacturer’s instructions, and then subjected to direct, automated sequencing (BigDye Terminator v.3.1 chemistry, Applied Biosystems, USA) in both directions using the same primers as employed for the second PCR step. Sequences were deposited in GenBank under accession nos. KY882314 (SSU), MT744605 (actin) and KY882339 (LSU).

2.3. Sequences alignments

Sequences of the SSU and actin gene regions were trimmed and aligned (over consensus lengths of 661 bp and 804 bp, respectively) with those of representative Cryptosporidium taxa and outgroups using the program Mesquite v.3.61 (Maddison and Maddison, 2015). The percentages of pairwise differences in the SSU and actin sequences between selected Cryptosporidium taxa were calculated using Geneious Prime 2020.0.5 (www.geneious.com) (Table 1).

A shorter alignment (Fig. 1) of partial SSU (400 bp) was also performed, in order to compare the 124 bp sequence (GenBank accession no. HM069184) from the green iguana (Kik et al., 2011) with other sequences in the C. avium group. Originally, this sequence from the iguana represented C. sp. avian genotype V, but given its length, it could not be included in the larger phylogenetic analysis of SSU data. This alignment (over 400 bp) was also used to illustrate the minor differences between the C. avium-like genotype and others in the C. avium group (Fig. 1). A comparison of the LSU sequence obtained (accession no. KY882339) with the very limited number of LSU sequences available in the GenBank database was not informative.

2.4. Phylogenetic analyses

Separate phylogenetic analyses of the aligned SSU (661 bp), actin (804 bp) or the concatenated SSU + actin (1465 bp) sequence data sets were conducted using the neighbour-joining (NJ) distance method (Saitou and Nei, 1987) in the program MEGA X v.10.1.8 (Stecher et al., 2020). Evolutionary distances were computed using the ‘number of differences’ method (Nei and Kumar, 2000), including ‘transitions and transversions’ for the nucleotide data. Rates of evolution among sites were considered uniform, and gaps were treated using pairwise deletion. A total of 10,000 bootstrap replicates were performed and were recorded as bootstrap support percentages (bs). The outgroup used in the analyses was C. andersoni.

2.5. Literature survey of the C. avium clade

To adequately compare our findings with the current state of knowledge in the area, we reviewed the literature to provide up-to-date information on C. cf. avium. We reviewed all reports of C. avium, C. cf. avium, C. avian genotype V and C. ornithophilus; nucleic acid sequence data in the key public repository (GenBank) and salient information, including molecular markers used, host origin, clinical and environmental context (agricultural, pet industry, wildlife, zoo or wildlife park) and country (Table 2).

3. Results

3.1. Sequence comparisons

While cryptosporial SSU could not be PCR-amplified from faecal DNA from either the spiny-tailed monitor or the centralian blue-tongue, amplicons were produced from genomic DNA from faeces from the inland bearded dragon, and sequences obtained were compared with data in the NCBI database using BLASTn. The SSU sequence obtained (747 bp) was identical to that representing C. avium (GenBank accession no. LC310795; over 735 bp) from a brown wood owl (Strix leptogrammica) in Japan (Makino et al., 2018), to that of C. avium (GenBank accession no. LC14646; over 401 bp) from an Arabian blue mastigure (Uromastyx ornata philibii) from Japan (Kubota et al., 2020). The LSU sequence also matched (99% identity over 725 bp) several other C. avium sequences, with an insertion of a thymine in relation to the C. avium reference sequence KU058875. The actin gene sequence obtained (804 bp) was 99% identical to that representing C. cf. avium (GenBank accession no. LC14645; 2 bp differences over 804 bp) from the mastigure (Kubota et al., 2020) and to C. cf. avium (GenBank accession no. LC310796; 4 bp differences over 804 bp) from the brown wood owl (Makino et al., 2018).

Pairwise identities, based on the 401 bp (SSU) and 770 bp (actin) alignments, were calculated (Table 1). For this SSU region, all C. cf.
avium sequences were identical, while the pairwise nucleotide sequence identities between the novel C. cf. avium and C. avium and C. ornithophilus were 99.75% and 99.50%, respectively (Table 1). For the actin gene region, the pairwise nucleotide sequence identities between the novel C. cf. avium and the sequence from the mastigure, brown wood owl, C. ornithophilus and C. avium were 99.75%, 99.50%, 98.38% and 98.13%, respectively (Table 1).

We compared the short SSU sequence (124 bp) publicly available for C. cf. avium of the green iguana (GenBank accession no. HM069184; Kik et al., 2011) with those available for select members of the C. avium clade and C. baileyi, to identify genetic differences. The alignment (Fig. 1) shows that the thymine deletion for this SSU region can be used to differentiate C. cf. avium from C. avium. Further differences that distinguish C. cf. avium from C. avium, C. ornithophilus, C. baileyi genotype I as well as C. baileyi (comparator) are also indicated.

3.2. Phylogenetic analyses of SSU and actin gene data sets

When the SSU sequence of C. avium from the present inland bearded dragon (GenBank accession no. KT882314) was placed in a phylogenetic context with closely related reference sequences from GenBank, using C. andersonii as the outgroup (Fig. 2), there was a moderately supported (bs: 86%) C. avium clade consisting of four distinct groups: (1) a moderately-supported (bs: 84%) C. avium; (2) a well-supported (bs: 94%) grouping of C. ornithophilus; (3) a well-supported (bs: 94%) group of the C. cf. avium sequences including the one from this study (accession no. KT882314); and (4) a sole distinct sequence (GenBank accession no. MHS53330) from a Brazilian flat-faced fruit-eating bat (Artibeus planirostris). The sister group to C. avium was comprised of two well-supported groups representing C. avium genotype I and C. baileyi, respectively.

The topology of the actin gene tree was similar to the SSU tree, yet with stronger nodal support values (Fig. 3). There was a strongly supported clade consisting of C. sp. avian genotype I and C. baileyi on one branch, and the collective C. avium group on the other. The C. avium clade was represented by three strongly supported groups (bs: 99/100/97%): (1) the C. avium group; (2) the C. ornithophilus group; and (3) the C. cf. avium group (with some variation within the clade). The concatenated tree (Fig. 4) had the same topology as the actin gene tree. The name C. cf. avium will hereby be used to refer to all four samples within the C. cf. avium clade.

3.3. Literature survey of the C. avium clade

In total, 24 studies recorded species/genotypes of Cryptosporidium belonging to the C. avium clade – three from reptiles, one from a bat and all others from birds (Table 2). Most studies involved animals from the pet trade (61%), followed by animals from farms (26%), wildlife (17%) and zoos (9%). Studies were from eight countries, including Brazil (n = 7), China (n = 4), Japan (4), Czechia (n = 3). The commonest genetic marker used was SSU, followed by the actin and hsp70 genes. In cases associated with C. avium or C. cf. avium infection, clinical signs ranged from gastrointestinal symptoms, such as diarrhoea (Makino et al., 2018), renal cryptosporidiosis (Curtiss et al., 2015), conjunctivitis (Lewis et al., 2020) and cloacal prolapse (Santos et al., 2005; Curtiss et al., 2015). For 12 of 24 of the cases, no pathological changes were detected; for 4 of 24 cases, no pathological investigation was mentioned.

4. Discussion

4.1. First characterisation of C. cf. avium from an inland bearded dragon from Australia

This is the fourth report of C. cf. avium. As “C. cf. avium” was coined only recently (Kubota et al., 2020), we suggest that this name be used to classify Cryptosporidium found in mastigures (Makino et al., 2018), owls (Kubota et al., 2020) and the other inland bearded dragon from Scotland (Lewis et al., 2020), which all grouped together in phylogenetic analyses, with strong statistical/nodal support (Fig. 1).

In the commonly-sequenced SSU region, the difference between C. cf. avium and C. avium is a thymine insertion for C. cf. avium (Fig. 1). The sequence difference between C. cf. avium and C. avium in the partial actin gene sequence is much more pronounced (i.e. 1.87%) (Fig. 3; Table 1). As for other Cryptosporidium species, small differences in the SSU sequence can suggest large differences in other loci, such as the actin and 60 kDa glycoprotein (gp60) gene regions (Koehler et al., 2016, 2018). Makino et al. (2018) concluded that the owl, from which they molecularly-characterised Cryptosporidium, had mixed infections of C. avium (they did not detect the thymine indel) and a novel Cryptosporidium genotype, because of nucleotide differences in the actin and hsp70 loci with respect to C. avium. We propose that the SSU, actin and hsp70 sequences obtained by Makino et al. (2018) were derived from the same taxon of C. cf. avium, and were not the result of sequences originating from distinct Cryptosporidium taxa within a mixed infection.

The C. avium clade – first coined by Kubota et al. (2020) – comprises C. avium, C. cf. avium and C. ornithophilus (Figs. 2–4). The first molecularly-characterised member of this clade was C. avium genotype II (now C. ornithophilus) from a study of birds from wildlife parks and zoos in Western Australia (Ng et al., 2006). C. avium genotype V was first recorded in cockatiels from the Japanese pet trade (Abe and Makino, 2010) and was subsequently described as C. avium (see Holubová et al., 2016). The first record of a C. avium clade-member from reptiles was C. sp. avian genotype V from two green iguanas (Kik et al., 2011); however, due to the short length of the sequence 124 bp and the emergence of C. cf. avium, it was necessary to definitively determine to which group this sequence belongs. Here, the alignment (Fig. 1) which includes the

Table 1

| C. cf. avium Inland bearded lizard Australia | C. cf. avium Inland bearded lizard Scotland | C. cf. avium Spiny-tailed lizard | C. cf. avium Brown wood owl | C. ornithophilus Ostrich | C. avium Chicken | C. baileyi Zebra finch |
|--------------------------------------------|------------------------------------------|-------------------------------|--------------------------|----------------------|-------------------|---------------------|
| -                                          | 100                                      | 100                           | 100                      | 99.50                | 99.50             | 97.51               |
| C. cf. avium Inland bearded lizard, Australia | 99.75                                    | NA                            | 98.38                    | 98.13                | 88.31             |                     |
| C. avium Inland bearded lizard, Scotland   | NA                                       | NA                            | 98.63                    | 98.38                | 88.56             |                     |
| C. cf. avium Spiny-tailed lizard           | 99.75                                    | 99.75                         | 99.75                    | 99.75                | 99.75             | 89.43               |
| C. cf. avium Brown wood owl                | 99.50                                    | 99.50                         | 99.50                    | -                    | 98.51             | 89.18               |
| C. ornithophilus Ostrich                   | 99.75                                    | 99.75                         | 99.75                    | 99.75                | -                 | 89.43               |
| C. avium Chicken                          | 97.51                                    | 97.51                         | 97.51                    | 97.01                | 97.26             | -                   |
| C. baileyi Zebra finch                     |                                          |                               |                          |                      |                   |                     |

NA = Not applicable
Table 2
Summary of known case reports from members of the Cryptosporidium avium clade including: C. cf. avium, C. avium, and C. ornithophilus.

| Species/genotype | Host species | Scientific name(s) | Country | GenBank Accession nos. | Pathology/symptoms | References |
|------------------|--------------|---------------------|---------|------------------------|-------------------|------------|
| C. cf. avium     | Inland-bearded dragon<sup>3</sup> | *Pogona vitticeps* | Australia | KY8882314 | none | none | present study Lewis et al. (2020) |
| C. cf. avium     | Inland-bearded dragon<sup>3</sup> | *Pogona vitticeps* | Scotland | MT074295 | none | none | refractory conjunctivitis Makino et al. (2018) |
| C. cf. avium     | Brown wood owl, Spotted wood owl<sup>3</sup>, Arabian blue mastigure, Sudan mastigure (Spiny-tailed lizards)<sup>3</sup> | *Strix leptogrammica, Strix allopapa, Uromastyx ornata philbyi, Uromastyx dispar flaviscutata* | Japan | LC310795, LC310796, LC310797 | vomiting, diarrhoea | Kubota et al. (2020) |
| C. avium         | Cockatiel<sup>3</sup> | *Nymphicus hollandicus* | Japan | AB471666-1, AB471665, AB581401 | none | none | Abe and Makino (2010) |
| C. avium         | White-eyed parakeet<sup>3</sup>, Cockatiel<sup>3</sup> | *Aratinga leucophthalma* | Brazil | HM126669 | none | none | Sevá et al. (2011) |
| C. avium         | Cockatiel<sup>3</sup> | *Nymphicus hollandicus* | China | AB471647 | none | none | Qi et al. (2011) |
| C. avium         | Green iguana<sup>3</sup> | *Iguana iguana* | Netherlands | HM069184 | none | none | Kik et al. (2011) |
| C. avium         | Blue-fronted parrot<sup>3</sup>, Cockatiel<sup>3</sup> | *Amazona aestiva* | Brazil | KJ487974 | none | none | Nakamura et al. (2014) |
| C. avium         | Major Mitchell Cockatoos<sup>3</sup> | *Lophochora leadbeateri* | USA | KP342400 | none | none | Curtis et al. (2015) |
| C. avium         | Cockatiel<sup>3</sup> | *Nymphicus hollandicus* | Japan | none | none | none | Abe and Matsubara, 2015 |
| C. avium         | Buderigar, Cockatiel<sup>3</sup> | *Melopitucus undulatus* | China | KM267556 | none | none | Zhang et al. (2018) |
| C. avium*        | Red-crowned parakeet, Chicken, Budgerigar<sup>3</sup>, Canary<sup>3</sup> | *Nymphicus hollandicus* | Czechia | KU558875-78, KU558879-82, KU558883-86 | none | none | Holubová et al. (2016) |
| C. avium         | Cockatiel<sup>3</sup>, Chicken<sup>3</sup> | *Gallus gallus* | China | JQ246415, JQ20301, JQ79893 | none | none | Cui et al. (2018) |
| C. avium*        | Mallard, Chicken, Pheasant<sup>3</sup>, Budgerigar<sup>3</sup> | *Anas platyrhynchos, Gallus gallus, Phasianus colchicus* | Czechia | none | none | none | Holubová et al. (2018) |
| C. avium         | Red-crowned parakeet, Budgerigar<sup>3</sup> | *Cyanoramphus novaezealandiae, Gallus gallus, Melopitucus undulatus* | Czechia | MK311139-40, MK311156-57, MK311173-74 | none | none | Holubová et al. (2019) |
| C. ornithophilus | Ostrich<sup>3</sup> | *Struthio camelus* | Brazil | none | none | none | Santos et al. (2005) |
| C. ornithophilus* | Chickens<sup>3</sup> (infected from Ostrich, Santos et al., 2005) | *Gallus gallus* | Brazil | DQ002931, DQ002930, DQ002929 | none | none | Meireles et al. (2006) |
| C. ornithophilus | Major Mitchell cockatoos, Echlectus, Cockatiel, Sun conure, Princess parrot, Galah, Alexandrine<sup>3</sup> | *Lophochora leadbeateri, Echlectus roratus, Nymphicus hollandicus, Aratinga solitaria, Polytelis alexandrae, Eosopha roseicapilla, Psittacula expansa* | Australia | DQ650340, DQ650347, DQ650348 | none | none | Ng et al. (2006) |
| C. ornithophilus | Ostrich<sup>3</sup> | *Struthio camelus* | Brazil | none** | none | none | Nakamura et al. (2009) |
| C. ornithophilus | Ostrich<sup>3</sup> | *Struthio camelus* | Vietnam | AB696811, AB696812, AB696815, AB696816 | none | none | Nguyen et al. (2013) |
| C. ornithophilus | Chicken<sup>3</sup> | *Gallus gallus* | China | JX582921-292 | none | none | Wang et al. (2014) |
| C. ornithophilus* | Ostrich<sup>3</sup>, Chicken<sup>3</sup>, Cockatiel<sup>3</sup>, Goose<sup>3</sup> | *Struthio camelus, Gallus gallus, Nymphicus ornithophilus, Anser anser* | Czechia | MN969957-963, MN969947-953, MN969934-943 | none | none | Holubová et al. (2020) |
| C. avium-like    | Flat-faced fruit-eating bat<sup>3</sup> | *Artibeus planirostris* | Brazil | MH533330 | none | none | Batista et al. (2019) |

A (Agriculture); P (Pet industry); W (Wildlife); Z (Zoo/Wildlife Park); †Also large subunit of ribosomal RNA (LSU) sequence KY882339 from Koehler et al. (2017); *Experimental infection; **Authors claimed there were GenBank sequences but none can be found; ***Listed as C. avian type V on GenBank.
in birds, cryptosporidial infections can be in the respiratory tract (C. baileyi), proventriculus (C. galli), intestines (C. meleagris) and/or the bursa of Fabricius (C. avium genotype III) (Nakamura and Meireles, 2015). In reptiles, infection is typically gastric (C. serpentis) or intestinal (C. varanii) (Bogan, 2019; Latney and Wellehan, 2020). There have been relatively few case reports of members of the C. avium clade, with most studies reporting no clinical signs (n = 14) or no signs recorded (n = 4) (Table 2). The first clinical manifestation of cryptosporidiosis in an ostrich linked to C. ornithophilus in Brazil was a cloacal prolapse (Santos et al., 2005). Previously, a Cryptosporidium sp. had been implicated in cloacal prolapse of ostriches, but had not been molecularly characterised (Penrith et al., 1994). In two green iguanas, recurrent cloacal prolapse and cystitis were indicated in an infection of what turned out to be C. avium (see Kik et al., 2011). C. avium was confirmed by PCR from a Major Mitchell’s cockatoo in the USA, which, like the iguanas and ostriches, presented with cloacal prolapse, but also renal cryptosporidiosis (Curtiss et al., 2015). Cui et al. (2018) suggested that the bursa of Fabricius was the main site of infection for C. avium, which was established via experimental infection of chickens – which showed no clinical signs during infection.

The highest incidence of symptomatic cases has been associated with C. cf. avium group within the C. avium clade (Table 2). The case report of the brown wood owl described ‘vomiting’ and severe diarrhoea; however, another owl from the same pet merchant was PCR test-positive for C. cf. avium, yet asymptomatic (Makino et al., 2018). The case report of the spiny-tailed lizards (mastigures) involved two individual animals: The first, an Arabian blue mastigure, had symptoms of diarrhoea and ‘vomiting’ and then died, with the necropsy revealing catarrhal enteritis; the second, a Sudan mastigure, presented with constipation (Kubota et al., 2020). Finally, conjunctivitis caused by C. cf. avium was reported from an inland bearded dragon which was euthanised; a post mortem examination revealed hepatic fibrosis and biliary hyperplasia, but there was no evidence of Cryptosporidium in the intestines (Lewis et al., 2020).

Multiple case reports have noted the high degree of contagiousness of Cryptosporidium (Kik et al., 2011; Lewis et al., 2020), yet some animals appear to remain asymptomatic; it was reported that the mastigures infected each other (Kubota et al., 2020); at least two owls from the same wholesaler were infected (Makino et al., 2018); and one iguana infected another from the Netherlands case (Kik et al., 2011). Host age and/or immune status could be the reason why some animals display symptoms and others remain asymptomatic, as was thought to be the case for the owls (the one-month-old owllet was sick and the older 3-month-old was asymptomatic) (Makino et al., 2018). In the present case, the inland bearded dragon appeared to be asymptomatic; however, the centralian blue tongue in the same exhibit possibly died from cryptosporidiosis, as it had histological evidence of Cryptosporidium sp. infection in the gastrointestinal tract.

4.3. Cryptosporidium of reptiles

Numerous studies have used PCR to molecularly characterise Cryptosporidium in reptiles (e.g., Xiao et al., 2004; Kuroki et al., 2008; Pedraza-Díaz et al., 2009; Richter et al., 2011; Díaz et al., 2013) and, typically, C. serpentis Type A is the dominant Cryptosporidium taxon in snakes, followed by C. varanii, and C. varanii is dominant in lizards (reviewed in Bogan et al., 2019; Latney and Wellehan, 2020). C. serpentis causes a gastric form of Cryptosporidium, and the major symptoms and pathology are gastritis, regurgitation and midbody oedema, while C. varanii causes an intestinal form of disease, with symptoms of proliferative enteritis and chronic wasting (Bogan et al., 2019; Latney and Wellehan, 2020).

The following cases of Cryptosporidium sp. in reptiles were reported prior to the routine diagnostic use of PCR and, therefore, some of these uncharacterised species might have belonged to the C. avium clade: Gastric cryptosporidiosis from a wild frilled lizard (Chlamydosaurus kingii) from Australia (Öros et al., 1998); oocysts found in the gut epithelium of the starred lizard (Agama steio) in Israel (Ostroska and Paperna, 1990); oocysts in the cloacae of two Madagascar giant day geckos (Phelsuma madagascariensis grandis) from the USA (Upton and Barnard, 1987); proliferative enteritis in leopard geckos (Eublepharis macularius), USA (Terrell, 2003); renal cryptosporidiosis in both an iguana and a Parson’s chameleon (Calumma parsonii), USA (Frye et al., 1999); tympanic cavity of a green iguana, USA (Fitzgerald et al., 1998); and aural-pharyngeal polyps in three green iguanas, USA (Uhl et al., 2001). A survey of 150 pet lizards and snakes in Italy detected Cryptosporidium but the taxa could not be characterised due to a low quality of sequence data obtained using a PCR-based approach (Rinaldi et al., 2012). Some recent studies did not use PCR, such as in the case of eight captive green iguanas in Poland, which were submitted for treatment for cryptosporidiosis after showing signs of diarrhoea (Gałęcki and Sokół, 2018). In our opinion, future studies should use PCR-coupled sequencing of SSU, actin and hsp70 gene regions to allow comparisons with available data sets.

Inland bearded dragons are very popular animals in the pet trade (Doneley, 2006) and are also frequently kept in zoological parks. The first molecularly-characterised case of Cryptosporidium from Pogona vitticeps was C. varanii (syn. C. saurophilum) from the St. Louis Zoo in the
Fig. 2. Relationship of the novel *Cryptosporidium* cf. *avium* taxa (in bold) from the faeces of the inland-bearded dragon with representative *Cryptosporidium* sequences, established based on a phylogenetic analysis of sequence data from a portion of the small subunit of nuclear ribosomal RNA gene (SSU) employing the neighbour-joining distance method. Branch supports are represented by neighbour-joining bootstrap percentages. *C. andersoni* was used as an outgroup.
USA (Xiao et al., 2004). As bearded dragons are common pets, Grosset et al. (2011) attempted to test the effect of paromomycin – an aminoglycoside antimicrobial – on Cryptosporidium. These authors characterised experimental infections of an unknown species of Cryptosporidium (sourced from an adult P. vitticeps) in 10 P. vitticeps individuals (4 months of age), which remained asymptomatic throughout the trial; they noted that the infection was highly contagious (infecting separated, uninfected control animals), and emphasised the point that asymptomatic carriers can quickly spread infection to other species housed nearby, as might be the case in zoos and pet stores Grosset et al. (2011). Other than these aforementioned cases, the present case from a wildlife sanctuary in Australia and a previous case from Scotland (Lewis et al., 2020) are the only records of Cryptosporidium from inland bearded dragons.

4.4. Current state of knowledge about C. cf. avium and associated cryptosporidiosis

In order to adequately discuss our findings in relation to the current state of knowledge in the area, we elected to review the literature to provide up-to-date information on C. cf. avium. Table 2 reveals some biases in the studies of members of the C. avium clade. Two thirds of the studies related to animals associated with the pet trade and/or zoos (66%; 16/24) (Table 2). Clearly, domestic pets are more likely to be treated and subsequently reported by clinicians as cases vs-à-vis wildlife cases. The species diversity in Table 2 is likely limited, because the types of pets examined would typically include exotic animals, such as Psittaciformes, and commonly-kept reptiles, such as iguanas and bearded dragons. Ostriches were also well-sampled (66.6%; four of six C. ornithophilus reports) due to ostrich farming being relatively common (Santos et al., 2005; Meireles et al., 2006; Nakamura et al., 2009;...
There is also a bias in the countries (including Australia, Brazil, China, Czech Republic and Japan), from which studies were published, as these are countries in which there is an active research focus on Cryptosporidium. There were limited samples directly from wild-caught animals (n = 4) (Sevá et al., 2011; Nakamura et al., 2014; Holubová et al., 2018; Batista et al., 2019). We believe that investigating such animals is critical when attempting to discover a possible endemic origin for C. avium cases, vis-à-vis those from pet shops, zoos and agriculture.

Nguyen et al., 2013; Holubová et al., 2020). There is also a bias in the countries (including Australia, Brazil, China, Czech Republic and Japan), from which studies were published, as these are countries in which there is an active research focus on Cryptosporidium. There were limited samples directly from wild-caught animals (n = 4) (Sevá et al., 2011; Nakamura et al., 2014; Holubová et al., 2018; Batista et al., 2019). We believe that investigating such animals is critical when attempting to discover a possible endemic origin for C. avium cases, vis-à-vis those from pet shops, zoos and agriculture.

4.5. Possible sources of infection

Fig. 4. Relationship of the novel Cryptosporidium cf. avium taxa (in bold) from the faeces of the inland-bearded dragon with representative Cryptosporidium sequences, established based on a phylogenetic analysis of sequence data from concatenated SSU and actin genes employing the neighbour-joining distance method. Branch supports are represented by neighbour-joining bootstrap percentages. C. andersoni was used as an outgroup.
allow for reliable source-tracking. Two of the cases originated from wild-caught animals (present case and mastigures – Kubota et al., 2020), and the others were either reared in captivity (owls; Makino et al., 2018) or of unknown origin (the Scottish inland bearded dragon was abandoned at a pet shop; Lewis et al., 2020).

Food sources were mentioned in some case reports: owls were fed defrosted quail, and mastigures were fed commercial tortoise pellets, commercial bird seed and vegetable matter (Makino et al., 2018; Kubota et al., 2020). Both the mastigure and owl cases originated from or near Tokyo, although the pet stores were not located in the same suburbs. As C. cf avium has now been seen in Australia, Japan and Scotland, it is probably circulating throughout the pet trade. Sampling more wildlife and identifying Cryptosporidium species/genotypes should assist in identifying sources of infection and reservoir hosts. Processes such as ecological fitting, where chance contact (increased globalisation of pet trade) between novel hosts and novel pathogens results in an adequate environment for the pathogen to persist (Araujo et al., 2015), could be the answer. Or, C. cf avium could potentially be a host-switching relict, from when birds split from reptiles prior to the Cretaceous-Tertiary extinction event (Cracraft, 2001). Other pristian parasites share a close relationship between their closely-related bird and lizard hosts (e.g., malaria; cf. Perkins and Schall, 2002; Hayakawa et al., 2008; Martinsen et al., 2008).

4.6. Conclusions

Clearly, members of the C. cf. avium clade are capable of infecting avian and reptilian hosts, causing morbidity and mortality. Precautions involving biosecurity and quarantine procedures should be implemented in pet stores, zoological enclosures harbouring both birds and reptiles. When infections are discovered, it is important that PCR-coupled sequencing analysis be performed, ideally with SSU, actin and hp70 gene markers wherever possible. As evidenced here, Cryptosporidium is not limited to the gastrointestinal tracts of reptiles; multiple organs should be examined for disease when performing a necropsy. Future work should include defining a panel of single-copy gene markers in the nuclear genome, including gp60, which would aid in the refining the genetic characterisation of members of this genus. Continued wildlife surveys will assist in filling knowledge gaps surrounding the systematics, epidemiology and population genetics of Cryptosporidium, including members of the C. cf. avium clade, and associated cryptosporidiosis.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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References

Abe, N., Makino, J., 2010. Multilocus genotypic analysis of Cryptosporidium isolates from cockatiels. Japan. Parasitol. Res. 106, 1491–1497.
Abe, N., Matsubara, K., 2015. Molecular identification of Cryptosporidium isolates from exotic pet animals in Japan. Vet. Parasitol. 209, 254–257.
Araujo, S.B., Braga, M.P., Brooks, D.R., Agosta, S.J., Hoberg, E.P., von Hardtlen, F.W., Boeger, W.A., 2015. Understanding host-switching by ecological fitting. PloS One 10, e0139225.
Batista, J.M.N., de Carvalho, C., Pedro, W.A., Santana, B.N., Camargo, V.S., Ferrari, E.D., Nascimento, L.G., Meireles, M.V., 2019. Identification of Cryptosporidium bat genotypes XVI-XVIII in bats from Brazil. Parasitol. Res. 118, 2183–2191.
Bogan, J.E., 2019. Gastric cryptosporidiosis in snakes, a review. J. Herpetol. Med. Surg. 29, 71–86.
Camargo, V.d.S., Santana, B.N., Ferrari, E.D., Nakamura, A.A., Nagata, W.B., Nardi, A.R.M., Meireles, M.V., 2018. Detection and molecular characterization of Cryptosporidium spp. in captive reptiles (Sauria variabilis) using different diagnostic methods. Rev. Bras. Parasitol. Vet. 27, 60–65.
Chalmers, R.M., Davies, A.P., 2010. Minireview: clinical cryptosporidiosis. Exp. Parasitol. 124, 138–146.
Cogger, H., 2014. Reptiles and Amphibians of Australia. CSIRO Publishing, Collingwood, p. 1064.
Cracraft, J., 2001. Avian evolution, Gondwana biogeography and the Cretaceous-Tertiary mass extinction event. Proc. Biol. Sci. 268, 459–469.
Cui, Z., Song, D., Qi, M., Zhang, S., Wang, R., Jian, F., Ning, C., Zhang, L., 2018. Revisiting the infectivity and pathogenicity of Cryptosporidium avium provides new information on parasitic sites within the host. Parasites Vectors 11, 514.
Crunch, E.B., Abe, N., Zikmundov a, V., Limpouchov a, M., Hl akov c, M., 2019. Host specificity and age-dependent resistance to Cryptosporidium avium in chickens, ducks and pheasants. Exp. Pathol. 191, 62–65.
Crunch, E.B., Abe, N., Horcickov a, M., Hl akov c, M., Kvetov tov a, D., Menchaca, S., McEvoy, J., Kv c, M., 2016. Cryptosporidium avium n. sp. (Apicomplexa: cryptosporididae) in birds. Parasitol. Res. 115, 2243–2251.
Crunch, E.B., Kubota, R., Tokiwa, T., Matsubara, K., Okamoto, M., Ike, K., 2020. Detection and molecular characterization of Cryptosporidium avium n. sp. (Apicomplexa: cryptosporididae) in farmed ostriches. Parasites Vectors 13, 1–17.
Crunch, E.B., Zikmundova, V., Limpouchova, Z., Sak, B., Hajebov a, A., Konecny, R., Hl akov c, M., Rajsky, D., Kopeck, Z., McEvoy, J., Kv c, M., 2020. Description of Cryptosporidium ornithophilus n. sp. (Apicomplexa: cryptosporididae) in Psittaciformes birds. Eur. J. Protistol. 69, 70–87.
Huang, J.M., Chen, H.L., Zhou, Y.K., Wang, S., Ren, Q., Fang, Z., Li, H.H., Zheng, K.L., Liu, X.C., Gu, Y.F., Li, W.C., 2020. The first report of Cryptosporidium testudinis in Chinese alligators (Alligator sinensis) in China. Parasitol. Res. 119, 2359–2362.
Jex, A.R., Smith, H.V., Monis, P.T., Campbell, B.E., Gasser, R.B., 2008. Cryptosporidium - biotechnological advances in the detection, diagnosis and analysis of genetic variation. Biotechnol. Adv. 26, 304–317.
Jezkova, J., Horcickova, M., Hlaskova, L., Sak, B., Kvetotova, D., Novak, V., Hofmannova, L., McEvoy, J., Kv c, M., 2016. Cryptosporidium ducimarti Traversa, 2010 and Cryptosporidium tortoise genotype III (Apicomplexa: cryptosporididae) in tortoises. Folia Parasitol. (Praha). 63 (10), 14411.
Kg, M.J., van Asten, A.J., Lenstra, J.A., Kirpenstein, J., 2011. Cloaca prolapse and cystitis in green iguana (Iguana iguana) caused by a novel Cryptosporidium species. Vet. Parasitol. 175, 165–167.
Koehler, A.V., Haydon, S.R., Jex, A.R., Gasser, R.B., 2016. Is Cryptosporidium from the common wombat (Vombatus uruinau) a new species and distinct from Cryptosporidium ubiquitum? Infect. Genet. Evol. 44, 28–33.
Koehler, A.V., Korhonen, P.K., Hall, R.S., Young, N.D., Wang, T., Haydon, S.R., Gasser, R.B., 2017. Use of a bioinformatic-assisted primer design strategy to establish a new nested PCR-based method for Cryptosporidium. Parasites Vectors 10, 509.
Koehler, A.V., Wang, T., Haydon, S.R., Gasser, R.B., 2018. Cryptosporidium viannia from the native Australian swamp rat Rattus lutreolus – an emerging zoonotic pathogen? Int. J. Parasitol. Parasites Wildl. 7, 18–26.
Kubota, R., Tokiwa, T., Matsubara, K., Okamoto, M., Ike, K., 2020. Detection and molecular characterization of Cryptosporidium species in wild-caught pet spiny-tailed lizards. Int. J. Parasitol. Parasites Wildl. 11, 83–87.
Kuroki, T., Izumiya, S., Yagita, K., Une, Y., Hayashidani, H., Kuro-o, M., Mori, A., Moriguchi, H., Toriba, M., Ishibashi, T., 2008. Occurrence of Cryptosporidium sp. in experimental animals. J. Parasitol. Res. 103, 861–865.
Lateney, L.T.W., Wellehan, J.F., 2010. Selected emerging infectious diseases of Squamata: an update. Vet. Clin. Exotic Animal Practice 23, 553–571.
Lewis, M., Bartley, P., Katz, F., Morrison, L., Philbee, R., Denslow, K., Walker, D., 2020. Conjunctival Cryptosporidium avium infection in a captive inland bearded dragon (Pogona vitticeps). J. Exot. Pet. Med. 35, 23–26. https://doi.org/10.1053/j. jepm.2020.05.014.
Maddison, W.P., Maddison, D.R., 2015. Mesquite; a Modular System for Evolutionary Analysis, 3.04.
Makino, I., Inumaru, M., Abe, N., Sato, Y., 2018. A new avian Cryptosporidium genotype in a 1-month-old caged brown wood owl (Strix leptogrammica) with severe dehydration and diarrhea. Parasit. Res. 117, 3003–3008.

Martinsen, E.S., Perkins, S.L., Schall, J.J., 2008. A three-genome phylogeny of malaria parasites (Plasmodium and closely related genera) reveals life-history traits and host switches. Mol. Phylogenet. Evol. 47, 261–273.

Meireles, M.V., Soares, R.M., Marcaia Mereces Aparecida Bianchi dos, S., Gennari, S.M., 2006. Biological studies and molecular characterization of a Cryptosporidium isolate from ostriches (Struthio camelus). J. Parasitol. 92, 623–626.

Morgan, U.M., Monis, P.T., Xiao, L., Limor, J., Sulaiman, I., Raidal, S., O’Donoghue, P., Gasser, R., Murray, A., Fayer, R., Blagburn, B.L., Lal, A.A., Thompson, R.C.A., 2001. Molecular and phylogenetic characterisation of Cryptosporidium from birds. Int. J. Parasitol. 31, 289–296.

Nakamura, A.A., Homem, C.G., da Silva, A.M., Meireles, M.V., 2014. Diagnosis of gastric cryptosporidiosis in birds using a duplex real-time PCR assay. Vet. Parasitol. 205, 7–13.

Nakamura, A.A., Meireles, M.V., 2015. Cryptosporidium infections in birds - a review. Rev. Bras. Parasitol. Vet. 24, 253–267.

Nakamura, A.A., Simões, D.C., Antunes, R.G., da Silva, D.C., Meireles, M.V., 2009. Molecular characterization of Cryptosporidium spp. from fecal samples of birds kept in captivity in Brazil. Vet. Parasitol. 166, 47–51.

Nei, M., Kumar, S., 2000. Molecular Evolution and Phylogenetics. Oxford University Press.

Ng, J., Pavlasek, I., Ryan, U.M., 2006. Identification of novel Cryptosporidium genotypes from avian hosts. Appl. Environ. Microbiol. 72, 7548–7553.

Nguyen, S.T., Fukuda, Y., Tada, C., Huynh, V.V., Nguyen, D.T., Nakai, Y., 2013. Prevalence and molecular characterization of Cryptosporidium spp. on a farm in central Vietnam. Exp. Parasitol. 133, 8–12.

Oros, J., Rodrigues, J.J., Patterson-Kane, J., 1998. Gastric cryptosporidiosis in a wild frilled lizard from Australia. J. Wildl. Dis. 34, 807–810.

Ostrovska, K., Paperna, I.K., 1990. Cryptosporidium sp. of the starred lizard Agama stellio ultrastructure and life cycle. Z. Parasitenkd. 76, 712–716.

Pedraza-Díaz, S., Agama stellio, K., Paperna, I.K., 1990. Cryptosporidium sp. of the starred lizard Agama stellio ultrastructure and life cycle. Z. Parasitenkd. 76, 712–720.

Pavlasek, I., Ryan, U.M., 2008. Cryptosporidium urumii takes precedence over C. saurophilum. Exp. Parasitol. 118, 434–437.

Pedraza-Díaz, S., Ortega-Mora, L.M., Carrión, B.A., Navarro, V., Gómez-Bastista, M., 2009. Molecular characterization of Cryptosporidium isolates from pet reptiles. Vet. Parasitol. 160, 204–210.

Perkins, S.L., Benzieuizenhoest, A.J., Burger, W.P., Putterill, J.J., 1994. Evidence for cryptosporidial infection as a cause of prolapse of the phallus and cloaca in ostrich chicks (Struthio camelus). Underst. Pest. Res. 61, 283–289.

Perkins, S.L., Schall, J.J., 2002. A molecular phylogeny of malarial parasites recovered from cytochrome b gene sequences. J. Parasitol. 88, 972–978.

Qi, M., Wang, R., Ning, C., Li, X., Zhang, L., Jian, F., Sun, Y., Xiao, L., 2011. Cryptosporidium spp. in pet birds: genetic diversity and potential public health significance. Exp. Parasitol. 128, 356–360.

Richter, B., Nederost, N., Madenner, A., Weissenbock, H., 2011. Detection of Cryptosporidium species in feces or gastric contents from snakes and lizards as determined by polymerase chain reaction analysis and partial sequencing of the 18S ribosomal RNA gene. J. Vet. Diagn. Invest. 23, 430–435.

Rinaldi, L., Capasso, M., Mihalca, A., Cirillo, R., Cringoli, G., Caccio, S., 2012. Prevalence and molecular identification of Cryptosporidium isolates from pet lizards and snakes in Italy. Parasitol. 139, 437.

Ryan, U., Fayer, R., Xiao, L., 2014. Cryptosporidium species in humans and animals: current understanding and research needs. Parasitology 141, 1667–1685.

Ryan, U., Paparini, A., Monis, P., Hijjawi, N., 2016. It’s official-Cryptosporidium is a gregarine: what are the implications for the water industry? Water Res. 105, 305–313.

Ryan, U.M., Xiao, L., Read, C., Zhou, L., Lal, A.A., Pavlasek, I., 2003. Identification of novel Cryptosporidium genotypes from the Czech republic. Appl. Environ. Microbiol. 69, 4302–4307.

Saitou, N., Nei, M., 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol. Biol. Evol. 4, 406–425.

Santos, M., Peiró, J., Meireles, M., 2005. Cryptosporidium infection in ostriches (Struthio camelus) in Brazil: clinical, morphological and molecular studies. Braz. J. Poultry Sci. 7, 113–117.

Sevá, A.D., Funada, M.R., Richtenthain, L., Guimarães, M.B., de Oliveira Souza, S., Allegretti, L., Sinhorini, J.A., Duarte, V.V., Soares, R.M., 2011. Genotyping of Cryptosporidium spp. from free-living wild birds from Brazil. Vet. Parasitol. 175, 27–32.

Stecher, G., Tamura, K., Kumar, S., 2020. Molecular evolutionary genetics analysis (MEGA) for macOS. Mol. Biol. Evol. 37, 1237–1239.

Terrell, S.P., 2003. Proliferative enteritis in leopard geckos (Crypotosporidium sp.) infection. J. Zoo Wildl. Med. 34, 69–75.

Upton, S., Barnard, S., 1987. Two new species of coccidia (Apicomplexa: eimeriidae) from Madagascar gekkonids. J. Protozool. 34, 452–454.

Uhl, E., Jacobson, E., Bartick, T., Micinilio, J., Schmidt, R., 2001. Aural-parhyangeal polyps associated with Cryptosporidium infection in three iguanas (Iguana iguana). Vet. Pathol. 38, 239–242.

Wang, L., Xue, X., Li, J., Zhou, Q., Yu, Y., Du, A., 2014. Cryptosporidiosis in broiler chickens in Zhejiang Province, China: molecular characterization of oocysts detected in fecal samples. Parasit 21, 36.

Xiao, L., Ryan, U.M., Graczcyk, T.K., Limor, I., Li, L., Komber, M., Junge, R., Sulaiman, I.M., Zhou, L., Arrowood, M.J., 2004. Genetic diversity of Cryptosporidium spp. in captive reptiles. Appl. Environ. Microbiol. 70, 891–899.

Zahedi, A., Paparini, A., Jian, F., Robertson, I., Ryan, U., 2016. Public health significance of zoonotic Cryptosporidium species in wildlife: critical insights into better drinking water management. Int. J. Parasitol. Parasites Wildl. 5, 88–109.

Zhang, X.-X., Zhang, N.-Z., Zhao, G.-H., Zhao, Q., Zhu, X.-Q., 2015. Prevalence and genotyping of Cryptosporidium infection in pet parrots in North China. BioMed Res. Int. 2015, 1–6.
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