A global review of *Cryptosporidium* spp. in pigeons in the context of the One-Health concept

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Pigeons, *Cryptosporidium*, zoonoses, One Health approach, epidemiology, public health

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Summary

Background: The pigeon (*Columba livia*) is a domesticated bird species that frequently comes into contact with humans. Pigeons harbour and disseminate numerous zoonotic pathogens, including apicomplexan parasites from the genus *Cryptosporidium,* a common protist parasite of vertebrates. Pigeon populations have increased in urban and peri-urban areas in recent years, which may pose a public health risk. ***Aim***: A systematic review was conducted to examine the presence and prevalence of *Cryptosporidium* in pigeons worldwide. ***Methods***: The PubMed database was screened for relevant articles between the 1st January and the 1st August 2024. A total of 38 publications were included in this review. ***Results****:* *Cryptosporidium* infection in pigeons was first reported in Turkey in 1994, with clinical symptoms including depression, emaciation, inactivity, diarrhoea and feather ruffling. Histological examination revealed the presence of *Cryptosporidium* in the intestinal epithelium. Subsequent studies have confirmed the prevalence of *Cryptosporidium* worldwide. Traditional diagnostic methods revealed an average prevalence of 14.8%, while molecular tools indicated a higher prevalence (28.4%). The highest rates were observed in Iraq, where captive pigeons were found to be more commonly infected than wild birds. Molecular data, though limited, suggest that domestic pigeons also harbour more diverse *Cryptosporidium* spp. than wild pigeons. *C. meleagridis*, *C. parvum* and *C. hominis* were the main zoonotic species identified in pigeons globally. Microscopic analysis showed variation in infection intensity, with oocyst counts ranging from 3,000 to 36,000 per gram of faeces. Many genotypes of *Cryptosporidium* spp. are considered zoonotic, with known cases of human infection in pigeon handlers. Therefore, it has public health implications. ***Conclusions***: Further studies are needed to clarify the pathogenicity and transmission routes of *Cryptosporidium* spp. in pigeons. Prevention and control of this zoonosis in pigeons should be a public health priority, particularly in regions with large pigeon populations, such as urban areas where they live in close contact with humans and other animals.

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■ INTRODUCTION

The common pigeon (*Columba livia*) is a wild species with a worldwide distribution. Pigeons were domesticated 5000 years ago for use as food and messengers. More recently, they have also been bred for their aesthetic appeal and racing. Today, the species includes the domesticated captive population, as well as feral and wild populations (Schoonheere & Zoller, 2024; Stern & Dickinson, 2019).

Pigeons are highly adaptable to urban environments given their simple dietary requirements and docility. Thus, they are frequently brought into close contact with humans and other urban animals. They can carry pathogens capable of zoonotic transmission, including *Cryptosporidium* spp., a protozoan parasite causing cryptosporidiosis in humans and animals. Therefore, pigeon flocks could pose a public health risk with regard to this transmissible intestinal disease (Méndez-Mancera & Alejandro, 2023). The *Cryptosporidium* parasite commonly infects the digestive and respiratory tracts of a wide range of birds. In humans, infections may be asymptomatic or cause symptoms, such as diarrhoea, vomiting, abdominal pain, fever and, in some cases, more severe outcomes like colon cancer, cognitive deficiencies or growth impairments (Ryan, Feng, *et al*., 2021).

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Currently, 44 valid species and over 120 genotypes of *Cryptosporidium* have been described. In birds, the most common species are *C. galli*, *C. meleagridis*, *C. baileyi*, *C. avium*, *C. ornithophilus* and *C. proventriculi*. In humans, 19 species and 4 genotypes have been identified, of which *C. parvum*, *C. hominis* and *C. meleagridis* are the most common (Ryan, Feng, *et al*., 2021). Cryptosporidiosis is transmitted through the ingestion of food or water contaminated with *Cryptosporidium* spp. oocysts. Wild animals play a significant role in introducing zoonotic *Cryptosporidium* oocysts into water sources, which increases the risk of transmission (Ryan, Feng, *et al*., 2021; Widmer *et al*., 2020). While carrier animals may excrete large numbers of oocysts in their faeces, very few oocysts are needed to cause infection. *Cryptosporidium* exhibits low host specificity (Sréter & Varga, 2000) and is resistant to traditional disinfection methods. It can withstand chlorination and conventional water treatment processes (Widmer *et al*., 2020), which means that *Cryptosporidium* oocysts can persist even in treated drinking water.

Since *Cryptosporidium* spp. was first identified in pigeons in 1994 (Özkul & Aydin, 1994), few studies have addressed its prevalence in pigeons and their role in the epidemiology of cryptosporidiosis. Molecular studies have been conducted on *Cryptosporidium* spp. in a wide range of animal species, but seldom pigeons. Given the increasing number of pigeons living in densely populated cities worldwide (Domyan & Shapiro, 2017), it is essential to identify and better understand this potential pathogen source in order to implement the most appropriate disease prevention and control measures. The aim of this review is to describe the prevalence, species and genotype diversity, as well as the zoonotic potential of this protozoan in pigeons globally.

■ MATERIAL AND METHODS

The PubMed database was used to access published articles over the last 30 years (from 1st January to 1st August 2024). Using the keywords "*Cryptosporidium*" and "pigeon", we identified 22 potentially relevant publications. Two of these were excluded because pigeons were only mentioned in the discussion and were not the primary focus of the studies. A full-text review was conducted for the 20 most relevant articles. Additionally, 18 other relevant articles were identified through references cited in the articles found on PubMed. In total, 38 publications were identified and included in this review.

■ RESULTS

First evidence of Cryptosporidium *and the associated symptoms and lesions of cryptosporidiosis in pigeons.*

The first report of *Cryptosporidium* in pigeons was in a 10-day-old dead pigeon in Turkey in 1994. Symptoms included depression, emaciation, inactivity, cachexia, ruffled feathers and diarrhoea. The infection was localised to the small intestine, with atrophic and deformed villi. Further microscopic investigation identified *Cryptosporidium* sp. on enterocyte apical surfaces and inflammatory cell infiltration was observed in the lamina propria and crypts. Co-infection with *E. coli* was also reported, which may explain why the authors recommended further studies to assess the pathogenicity of *Cryptosporidium* in pigeons (Özkul & Aydin, 1994). Three years later, a case series report described similar signs of clinical infection, especially in younger pigeons, including yellowish diarrhoea, dehydration, weight loss and frailty, with a low mortality rate (5%). The infection was found not only in the small intestine but also extended to the caecum, colon, cloaca and bursa of Fabricius (Rodríguez *et al*., 1997). In another study, haemorrhages were observed in the mucosa, accompanied by necrotic epithelial zones. However, the pigeons in this study were co-infected with *Cryptosporidium* spp. and other parasites, including *Raillietina echinobothrida*, *Syngamus trachea*, *Capillaria columbae*, *Ascaridia columbae*, *Haemoproteus columbae*, *Trichomonas gallinae* and *Eimeria* sp. (Bahrami *et al*., 2012). A more recent study highlighted the species-specific localisation of *Cryptosporidium* spp. in birds, with *C. meleagridis* affecting the intestines, *C. baileyi* the respiratory tract, *C. avium* the large intestine, *C. proventriculi* the ventriculus and proventriculus, and *C. galli* the proventriculus (Altamimi, 2020).

Worldwide prevalence of Cryptosporidium

To date, 33 studies have been published on *Cryptosporidium* spp. in pigeons (Table I).

Comparison of traditional and molecular diagnostic methods for detecting Cryptosporidium *in pigeons: global prevalence trends and regional variations*

Most studies used traditional detection methods based on microscopic examination (27/33) for *Cryptosporidium* diagnosis, rather than molecular tools (18/33). The majority of studies (19/33) were conducted in countries in Asia, specifically Iran, Iraq, Turkey, Thailand, Nepal and China (Adhikari *et al*., 2022; Altamimi, 2020; Badparva *et al*., 2015; Bahrami *et al*., 2012; Dakheel Kremsh Alasadiy *et al*., 2022; Dong *et al*., 2021; Faraj, 2014; Hashim & Al-Zubaidi, 2023, 2024; Jasim & Marhoon, 2015; Kabir *et al*., 2020; Koompapong *et al*., 2014; J. Li *et al*., 2015; Q. Li *et al*., 2016; Liao *et al*., 2021; Mirzaghavami *et al*., 2016, 2023; Qi *et al*., 2011; Radfar *et al*., 2012). Fewer studies were conducted in other continents and included countries, such as Spain, Italy, Poland, Egypt, Venezuela and Brazil (Abou Elez *et al*., 2023; Abreu-Acosta *et al*., 2009; Cazorla Perfetti & Morales Moreno, 2019; Costa & Bomfim, 2016; dos Santos *et al*., 2020a; Holubová *et al*., 2024; Khalifa *et al*., 2020; Oliveira *et al*., 2017; Reboredo-Fernández *et al*., 2015).

Some studies did not identify *Cryptosporidium* in pigeons (da Cunha *et al*., 2017; Marenzoni *et al*., 2016; Morganti *et al*., 2016; Sari *et al*., 2008). When identified, prevalence rates varied (Figure 1). Traditional methods reported a global average prevalence of 16.4%. The highest prevalence was reported in an urban region in Iraq (55%) (Hashim & Al-Zubaidi, 2023) and the lowest in a rural region in China (0.82%) (J. Li *et al*., 2015). In comparison, the global average prevalence determined with molecular tools was 22.2%. The highest molecular prevalence was also reported in an urban region in Iraq (86%) (Hashim & Al-Zubaidi, 2023) and the lowest in an urban region in Iran (2%) (Mirzaghavami *et al*., 2023).

Only six studies used two different methods to determine the prevalence of *Cryptosporidium* in pigeons (Altamimi, 2020; Costa & Bomfim, 2016; Hashim & Al-Zubaidi, 2023; Holubová *et al*., 2024; Kabir *et al*., 2020; Oliveira *et al*., 2017). In these studies, the global average prevalence was generally numerically higher when using molecular tools (7%, 11%, 86% and 2.8%, respectively), compared to traditional methods (4%, 6%, 55% and 1%, respectively) (Altamimi, 2020; Hashim & Al-Zubaidi, 2023; Holubová *et al*., 2024; Oliveira *et al*., 2017). However, the differences observed between the two methods for detecting *Cryptosporidium* were not statistically significant.

Cryptosporidium *excretion level*

Few studies have reported the *Cryptosporidium* oocyst excretion level in pigeons. Four studies detected low oocyst numbers in faecal samples (dos Santos *et al*., 2020b; Kabir *et al*., 2020; Mirzaghavami *et al*., 2016; Reboredo-Fernández *et al*., 2015). In a further study, the *Cryptosporidium* oocyst excretion level ranged from 7,000 to 36,000 oocysts per gram for *C. Baileyi* and from 3,000 to 36,000 oocysts per gram for *C. meleagridis* (Holubová *et al*., 2024). These findings highlight the considerable variability in the intensity of *Cryptosporidium* spp. infection in pigeons. This variability has been explored in several studies that compare factors, such as health status, age, gender, breed and season to assess their impact on *Cryptosporidium* infection. The different factors will be discussed in greater detail below.

Contradictory findings on age-related Cryptosporidium *infection rate*

In three studies (Abou Elez *et al.*, 2023; Hashim & Al-Zubaidi, 2024; Khalifa *et al.*, 2020), young pigeons exhibited higher *Cryptosporidium* sp. infection rates (40%, 33.3% and 78.3%, respectively) compared to older pigeons (6.7%, 10% and 69%, respectively). Conversely, another report stated that overall parasite prevalence was more frequent among nestlings, while older pigeons showed higher *Cryptosporidium* sp. infection rates than younger birds (Bahrami *et al.*, 2012). In other studies that compared pigeon age groups, the differences in prevalence between young and adult pigeons were not statistically significant. This suggests that age does not significantly influence the risk of *Cryptosporidium* infection (dos Santos *et al.*, 2020a; Faraj, 2014; Oliveira *et al.*, 2017; Radfar *et al.*, 2012).

Gender differences in Cryptosporidium *prevalence among pigeons*

Four studies compared the rates of *Cryptosporidium* spp. infection in male and female pigeons (Abou Elez *et al.*, 2023; Altamimi, 2020; Hashim & Al-Zubaidi, 2024; Oliveira *et al.*, 2017). In the latter three studies, females appeared to have a numerically higher infection rate than males. Conversely, Altamimi (2020) reports that males were more frequently infected than females, and Abou Elez et al. (2023) also noted that the prevalence of *Cryptosporidium* spp. was higher in diseased pigeons. However, these studies did not reveal a statistically significant difference in infection rates between males and females. Overall, pigeon gender does not appear to influence the incidence of *Cryptosporidium* spp. infection (Faraj, 2014).

Seasonal variation in Cryptosporidium *infection rates*

Only two studies compared *Cryptosporidium* sp. infection rates in pigeons across different months and seasons (Faraj, 2014; Hashim & Al-Zubaidi, 2024). In the study conducted in Iraq, the highest infection rates were observed in February (95%), January (85%), and March (80%), corresponding to the winter season. The lowest infection rate was recorded in December, with 35% of pigeons infected (Hashim & Al-Zubaidi, 2024). Similarly, the study conducted in Baghdad also reported higher infection rates in the winter (Faraj, 2014).

Higher prevalence rate of Cryptosporidium *in domestic pigeons than in feral pigeons*

Domestic pigeons have been reported to have higher *Cryptosporidium* sp. infection rates than wild pigeons (Dakheel Kremsh Alasadiy *et al.*, 2022; Holubová *et al.*, 2024). Three studies compared the prevalence of *Cryptosporidium* sp. infection in domestic and feral pigeons (Adhikari *et al.*, 2022; Dakheel Kremsh Alasadiy *et al.*, 2022; Holubová *et al.*, 2024). Two of these studies showed that domestic pigeons had higher infection rates (15.8% and 3%, respectively) compared to feral pigeons (8.8% and 2.7%, respectively) (Dakheel Kremsh Alasadiy *et al.*, 2022; Holubová *et al.*, 2024). In the study conducted in Central Nepal, the prevalence of *Cryptosporidium* sp. was higher in temple pigeons than in household pigeons (Adhikari *et al.*, 2022). Furthermore, more diverse *Cryptosporidium* species were observed in captive pigeons than in feral pigeons (Holubová *et al.*, 2024).

Limited global molecular data on Cryptosporidium *species in pigeons*

To date, there is only limited molecular data available on *Cryptosporidium* species in pigeons worldwide. In fact, only a few studies (n=17) have used the genus-specific *18SrDNA* gene to classify species. Eight *Cryptosporidium* species have been reported in pigeons (Figure 2). These include *C. parvum* (n=32) (Abou Elez *et al.*, 2023; Altamimi, 2020; Dong *et al.*, 2021; Hashim & Al-Zubaidi, 2023; Holubová *et al.*, 2024; Jasim & Marhoon, 2015; Mirzaghavami *et al.*, 2023; Oliveira *et al.*, 2017), *C. baileyi* (n=19) (Altamimi, 2020; Faraj, 2014; Holubová *et al.*, 2024; Jasim & Marhoon, 2015; Kabir *et al.*, 2020; J. Li *et al.*, 2015; Q. Li *et al.*, 2016), *C. meleagridis* (n=14) (Faraj, 2014; Holubová *et al.*, 2024; Kabir *et al.*, 2020; Koompapong *et al.*, 2014; J. Li *et al.*, 2015; Qi *et al.*, 2011), *C. muris* (n=3) (Holubová *et al.*, 2024; Liao *et al.*, 2021), *C. hominis* (n=2) (Abreu-Acosta *et al.*, 2009), *C. andersoni* (n=2) (Holubová *et al.*, 2024), *C. ornithophilus* (n=2) (Holubová *et al.*, 2024), and *C. galli* (n=2) (Faraj, 2014; Holubová *et al.*, 2024). Only three of these *Cryptosporidium* species (*C. baileyi*, *C. parvum* and *C. hominis*) have been found in feral pigeons, while

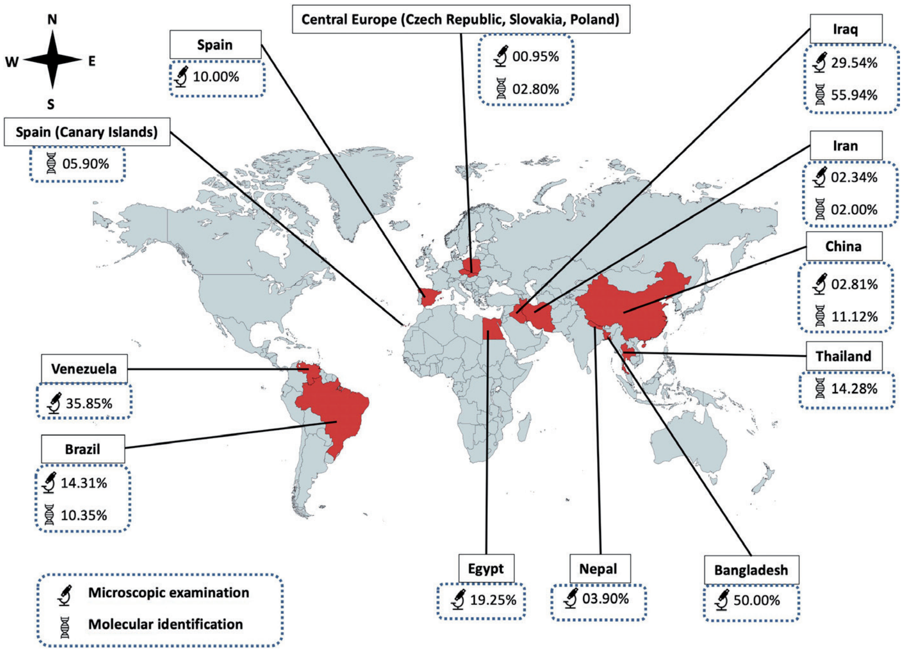

Figure 1: Global map highlighting the prevalence of *Cryptosporidium* spp. in pigeons (1994–2024). The figure also highlights the countries (marked in red) where related studies have been conducted. /// *Carte mondiale mettant en évidence la prévalence de* Cryptosporidium *spp. chez les pigeons (1994-2024). La figure met également en évidence les pays (marqués en rouge) où des études connexes ont été réalisées.*

Sources: (Abou Elez *et al.*, 2023; Abreu-Acosta *et al.*, 2009; Adhikari *et al.*, 2022; Altamimi, 2020; Badparva *et al.*, 2015; Bahrami *et al.*, 2012; Cazorla Perfetti & Morales Moreno, 2019; Costa & Bomfim, 2016; Dakheel Kremsh Alasadiy *et al.*, 2022; Dong *et al.*, 2021; dos Santos *et al.*, 2020b; Faraj, 2014; Hashim & Al-Zubaidi, 2023, 2024; Holubová *et al.*, 2024; Jasim & Marhoon, 2015; Kabir *et al.*, 2020; Khalifa *et al.*, 2020; Koompapong *et al.*, 2014; J. Li *et al.*, 2015; Q. Li *et al.*, 2016; Liao *et al.*, 2021; Mirzaghavami *et al.*, 2016, 2023; Oliveira *et al.*, 2017; Qi *et al.*, 2011; Radfar *et al.*, 2012; Reboredo-Fernández *et al.*, 2015).

Table I: Worldwide occurrence of *Cryptosporidium* spp. in feral and captive pigeons (*Columba livia*) *///Prévalence mondiale de* Cryptosporidium *spp. chez les pigeons sauvages et captifs (*Columba livia*)*

Country (and regions)	Sampling method	Diagnosis techniques	Prevalence % (N positive/N total)	*Cryptosporidium* species/subtypes	Accession number	References
Bangladesh	Intestinal colon samples (n=4)	ME: flotation MI: PCR (*18s rRNA+ gp60*)	50.00 % (002/004)	*C. baileyi (n=1)* *C. meleagridis* (n=1)/ IIIbA21G1R1	MN133968 & MN133966 (*18S rRNA*) (n=2) MN192422 (*gp60*) (n=1)	(Kabir *et al.*, 2020)
Brazil (Rio de Janeiro)**	Fresh faecal samples (n=387)	ME: flotation with sugar MI: PCR (*18s rRNA*)	20.93% (081/387) 13.69 % (053/387)	*Cryptosporidium* spp.	NR	(Costa & Bomfim, 2016)
Brazil (Araçatuba and Formig City)	Faecal samples (n=100)	ME: Malachite green staining MI: PCR (*18s rRNA*)	04.00% (004/100) 7.00 % (007/100)	*C. parvum* (n=6)	KY514062 – KY514066 (n=5)	(Oliveira *et al.*, 2017)
Brazil (Pelotas, Rio Grande do Sul)**	Faecal samples (n=50)	ME: Ritchie technique + modified Kinyoun acid-fast staining	18.00% (09/050)	*Cryptosporidium* spp.	NR	(dos Santos *et al.*, 2020a)
China (Henan Province)	Fresh faecal samples (n=21)	ME: Bright field MI: PCR (*18s rRNA*)	4.80 % (001/021)	*C. meleagridis* (n=1)	HM116382 (n=1)	(Qi *et al.*, 2011)
China (Guangdong Province)	Faecal samples (n=244)	ME: flotation MI: PCR (*18s rRNA*)	0.82 % (002/244)	*C. baileyi* (n=1) *C. meleagridis* (n=1)	KP339977 KP339978 (n=2)	(J. Li *et al.*, 2015)
China (northeast China)	Faecal samples (n=4)	MI: PCR (*18s rRNA*)	25.00 % (001/004)	*C. baileyi* (n=1)	NR	(Q. Li *et al.*, 2016)
China (Henan Province)	Faecal samples (n=21)	MI: PCR (*18s rRNA*)	4.80 % (001/021)	*C. parvum (n=1)*	MN410724 (n=1)	(Dong *et al.*, 2021)
China (Wuhan City, Hubei)	Faecal samples (n=28)	MI: PCR (*18s rRNA*)	3.57 % (001/028)	*C. muris (n=1)*	MW783463 (n=1)	(Liao *et al.*, 2021)
Egypt (Sharkia Governorate)	Fresh faecal samples (n=200)	ME: Sheather's sugar flotation + MZN MI: PCR (*18S rRNA + Actin)*	18.50 % (037/200)	*C. parvum* (n=10)	NR	(Abou Elez *et al.*, 2023)
Egypt (Assiut)	Faecal samples (n=50)	ME: modified Kinyoun acid-fast staining	20.00% (010/050)	*Cryptosporidium* spp.	NR	(Khalifa *et al.*, 2020)
Iran (Tehran)**	Fresh faecal samples (n=40)	ME: MZN	2.50% (001/040)	*Cryptosporidium* spp.	NR	(Mirzaghavami *et al.*, 2016)
Iran (Khorramabad)	Fresh faecal samples (n=37)	ME: MZN	2.70% (001/037)	*Cryptosporidium* spp.	NR	(Badparva *et al.*, 2015)
Iran (Tehran)	Faecal samples (n=100)	MI: PCR (*18s rRNA + gp60)*	2.00 % (002/100)	*C. parvum* (n=2)/ IIdA20G1 + IIdA19G1	KX537652 (*18S rRNA*) (n=1) KX537673-KX537674 (*gp60*) (n=2)	(Mirzaghavami *et al.*, 2023)
Iran (Birjand City, South Khorasan)	Faecal samples (n=102)	ME: sedimentation + MZN	2.94% (003/102)	*Cryptosporidium* spp.	NR	(Radfar *et al.*, 2012)
Iran (Ilam City)	Faecal samples (n=250)	ME: histological study	1.20% (003/250)	*Cryptosporidium* spp.	NR	(Bahrami *et al.*, 2012)

Table I (continued): Worldwide occurrence of *Cryptosporidium* spp. in feral and captive pigeons (*Columba livia*) ///*Prévalence mondiale de* Cryptosporidium *spp. chez les pigeons sauvages et captifs (*Columba livia*)*

Country (and regions)	**Sampling method**	**Diagnosis techniques**	**Prevalence % (N positive/N total)**	***Cryptosporidium* species/subtypes**	**Accession number**	**References**
Iraq (Baghdad)**	Faecal samples (n=120)	ME	48.00% (040/120)	*C. meleagridis* *C. baileyi* *C. galli*	NR	(Faraj, 2014)
Iraq (Al-Qadisiya Province)**	Fresh faecal samples (n=30)	ME: MZN MI: PCR (*18s rRNA*)	26.70 % (008/030)	*C. parvum* (n=2) *C. baileyi* (n=2)	NR	(Jasim & Marhoon, 2015)
Iraq (Baghdad)	Fresh faecal samples (n=60)	ME MI: PCR (*18s rRNA*)	55.00% (033/060) 86.00 % (052/060)	*C. parvum* (n=5)	NR	(Hashim & Al-Zubaidi, 2023)
Iraq (Baghdad)	Faecal samples (n=120)	MI: PCR (*18s rRNA*)	70.83 % (085/120)	*Cryptosporidium* spp.	NR	(Hashim & Al-Zubaidi, 2024)
Iraq (Samawah, Al-Muthana Province)**	Faecal samples (n=250)	ME	12.00% (030/250)	*Cryptosporidium* spp.	NR	(Dakheel Kremsh Alasadiy *et al.*, 2022)
Iraq (Babylon Province)**	Faecal samples (n=100)	ME: MZN MI: PCR (*18s rRNA*)	6.00 % (006/100) 11.00 % (011/100)	*C. baileyi* (n=9) *C. parvum* (n=2)	MT308760-MT308770 (n=11)	(Altamimi, 2020)
Central Europe (Czech Republic, Slovakia, Poland)	Faecal samples (n=940)	ME	0.95% (009/940)	*C. meleagridis* (n=10/27)/ IIIaA20G4R1 + IIIlA8G2R1 *C. baileyi* (5/27) *C. parvum* (4/27)/ IIaA16G1R1 + IIaA15G2R1 *C. andersoni* (2/27) *C. muris* (2/27) *C. galli* (2/27) *C. ornithophilus* (2/27)	OR911579-OR911585 (*18s rRNA)* (n=7) OR922804-OR922807 (*gp60*) (n=4)	(Holubová *et al.*, 2024)
Nepal (Central Nepal)**	Fresh faecal samples (n=155)	ME: direct test, formalin ethyl acetate sedimentation + flotation (NaCl) + acid-fast staining	3.90% (005/155)	*Cryptosporidium* spp.	NR	(Adhikari *et al.*, 2022)
Spain (Canary Islands)**	Faecal samples (n=34)	MI: PCR (*18S rRNA*)	5.90 % (002/034)	*C. hominis* (n=2)	EU032319-EU032324 (n=6)	(Abreu-Acosta *et al.*, 2009)
Spain (Galicia)**	Fresh faecal samples (n=10)	ME: FISH MI: PCR	10.00 % (001/010)	spp.	NR	(Reboredo-Fernández *et al.*, 2015)
Thailand (Bangkok)	Fresh faecal samples (n=7*)	MI: PCR (*18s rRNA*)	14.28 % (001/007)	*C. meleagridis* (n=1)	NR	(Koompapong *et al.*, 2014)
Venezuela (Coro, Falcon State)**	Faecal samples (n=516)	ME: direct test + flotation (ClNa, zinc sulphate) + sedimentation + Kinyoun acid-fast staining	35.85% (185/516)	*Cryptosporidium* spp.	NR	(Cazorla Perfetti & Morales Moreno, 2019)

ME: Microscopic Examination; MI: Molecular Identification; MZN: Modified Ziehl-Neelsen staining method; FISH: Fluorescent *in situ* Hybridisation; ND: Not determined; NR: Not reported; *: sets of 10 faecal samples; **: reference concerning feral pigeons only///*ME: Examen microscopique ; MI: Identification moléculaire ; MZN: technique de coloration de Ziehl-Neelsen modifiée ; FISH: Hybridation in situ en fluorescence ; ND : Non déterminé ; NR: Non rapporté ; * ensembles de 10 échantillons fécaux ; ** : Référence concernant les pigeons sauvages*

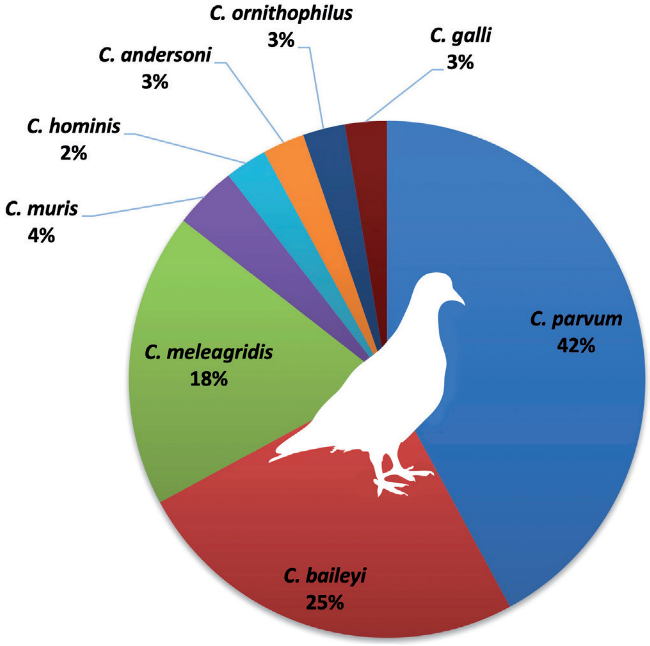

Figure 2: Global prevalence of *Cryptosporidium* species in pigeons: a summary showing the identified species and their percentages. /// *Prévalence mondiale des espèces de* Cryptosporidium *chez les pigeons : un résumé des espèces identifiées et de leurs pourcentages.*
Sources: (Abou Elez *et al*., 2023; Abreu-Acosta *et al*., 2009; Altamimi, 2020; Dong *et al*., 2021; Faraj, 2014; Hashim & Al-Zubaidi, 2023; Holubová *et al*., 2024; Jasim & Marhoon, 2015; Kabir *et al*., 2020; Koompapong *et al*., 2014; J. Li *et al*., 2015; Q. Li *et al*., 2016; Liao *et al*., 2021; Mirzaghavami *et al*., 2023; Oliveira *et al*., 2017; Qi *et al*., 2011).

seven (*C. parvum*, *C. meleagridis*, *C. baileyi*, *C. muris*, *C. galli*, *C. andersoni*, and *C. ornithophilus*) have been identified in domestic pigeons. As mentioned above, reports suggest that captive pigeons harbour a greater diversity of *Cryptosporidium* species than feral pigeons (Holubová *et al*., 2024).

Limited studies using the gp60 gene for Cryptosporidium *subtyping: insights from Bangladesh, Iran, and Central Europe*

Only three studies used the *gp60* gene to identify *Cryptosporidium* subtypes and reveal geographic variation (Holubová *et al*., 2024; Kabir *et al*., 2020; Mirzaghavami *et al*., 2023). The *C. meleagridis* IIIbA21G1R1 subtype was identified in Bangladesh (Kabir *et al*., 2020). The *C. parvum* IIdA20G1 and IIdA19G1 subtypes were reported in another study conducted in Iran (Mirzaghavami *et al*., 2023). In the most recent study, *C. meleagridis* IIIaA20G4R1 and IIIlA8G2R1 subtypes, as well as *C. parvum* IIaA16G1R1 and IIaA15G2R1 subtypes, were identified in Central Europe (Holubová *et al*., 2024). Notably, oocysts of the *C. meleagridis* IIIlA8G2R1 subtype obtained from naturally infected pigeons, were capable of infecting 1-day-old chickens, but were not infectious to adult mice with severe combined immunodeficiency (Holubová *et al*., 2024).

Cryptosporidium *sp. in pigeons, birds and other animal species: prevalence, species diversity and cross-species infections*

Many studies simultaneously investigated the presence of *Cryptosporidium* spp. in pigeons and other bird species. *Cryptosporidium* spp. are among the most common protozoans that infect birds, with an average prevalence of 11.8% (Badparva *et al*., 2015; da Cunha *et al*., 2017; Dong *et al*., 2021; Jasim & Marhoon, 2015; Kabir *et al*., 2020; Q. Li *et al*., 2016; Liao *et al*., 2021; Qi *et al*., 2011; Reboredo-Fernández *et al*., 2015). These studies highlight extensive variation in the prevalence of avian *Cryptosporidium* sp. infection. The highest prevalence of *Cryptosporidium* sp. in wild and domestic birds was 58.1% in Iraq (Jasim & Marhoon, 2015), while the lowest was 2.1% in captive pet birds in China (Dong *et al*., 2021).

C. baileyi was the most prevalent species detected in birds in China (Dong *et al*., 2021; Liao *et al*., 2021; Qi *et al*., 2011), Bangladesh (Kabir *et al*., 2020), Iraq (Jasim & Marhoon, 2015) and Brazil (da Cunha *et al*., 2017). Some studies reported the presence of avian *Cryptosporidium*, with *C. meleagridis* and *C. galli* in eared doves (*Zenaida auriculata*), for example (Seixas *et al*., 2019), or *C. proventriculi* (known as *C. avian* genotype III) and *C. avian* genotype V in cockatiels (*Nymphicus hollandicus*) (Qi *et al*., 2011). In a study conducted in Bangladesh, four subtypes of *C. meleagridis* were found in chickens: IIIbA21G1R1, IIIbA23G1R1, IIIbA21G1R2 and IIIbA20G2R1 (Kabir *et al*., 2020). *C. parvum* was also often identified in turkeys, chickens, ducks and quails in a study investigating both wild and domestic birds in Iraq (Jasim & Marhoon, 2015). The study revealed the presence of IIaA11G2R1 and IIaA13G2R1 subtypes, which have also been identified in many other bird species in China, Bangladesh and Spain (Dong *et al*., 2021; Kabir *et al*., 2020; Reboredo-Fernández *et al*., 2015). In addition to these four species, *C. andersoni* was identified in Henan Province (Dong *et al*., 2021) and *C. proventriculi* in Psittaciformes from the city of Wuhan in China (Liao *et al*., 2021).

Other contemporaneous studies examined the presence of *Cryptosporidium* spp. in pigeons and other animal species (Koompapong *et al*., 2014; Q. Li *et al*., 2016; Mirzaghavami *et al*., 2016, 2023). In Asian studies, mammals were less frequently infected by *Cryptosporidium* spp. than birds (7.7% and 11.1%, respectively), with prevalence rates of 1.3% compared to 15%, respectively (Koompapong *et al*., 2014; Q. Li *et al*., 2016). *C. parvum* was detected in rat, cat, hooded crow (*Corvus cornix*) and carrion crow (*Corvus corone*) samples with a higher infection rate than in pigeons. The *C. parvum* IId20AG1 subtype was detected in all of these animal species, while the *C. parvum* IId19AG1 subtype was only detected in cats and pigeons (Mirzaghavami *et al*., 2016, 2023). In another study from Bangkok, seagulls (*Larus canus*) were infected with *C. proventriculi* (Koompapong *et al*., 2014). Rodents were infected with the *Cryptosporidium* ferret genotype (Q. Li *et al*., 2016).

Cryptosporidium *in the environment: pigeons as a source of contamination?*

Several environmental surveillance studies have reported the presence of *Cryptosporidium* spp. in water (Abou Elez *et al*., 2023; Abreu-Acosta *et al*., 2009; Costa & Bomfim, 2016; dos Santos *et al*., 2020b; Graczyk *et al*., 2008; Koompapong *et al*., 2014; Mahmoudi *et al*., 2011; Mirzaghavami *et al*., 2023). Birds – including pigeons – could play an important role in *Cryptosporidium* spp. dissemination by defecating in or over water, which is a common occurrence (Graczyk *et al*., 2008; Koompapong *et al*., 2014).

Oocysts are highly resistant to environmental stressors. They can preserve their biological characteristics and remain infective for up to a year. Given their small size and low density, they are not damaged by water treatments and chlorination. *Cryptosporidium* spp. have also been identified in drinking and recreational water (Graczyk *et al*., 2008; Mahmoudi *et al*., 2011). *C. parvum* was identified in 6.7% of drinking water samples in Egypt, particularly in surface water (15.4% in surface water compared to 0% in groundwater) (Abou Elez *et al*., 2023). In a study conducted in Thailand, the prevalence of *Cryptosporidium* spp. in sea water samples was 6% compared to 11% in river water samples (Koompapong *et al*., 2014). The parasite is also present in numerous wastewater samples. For example, 100% of wastewater samples from a Canary Islands study were contaminated by *C. hominis* (Abreu-Acosta *et al.*, 2009). While studies confirm the presence of this avian *Cryptosporidium* genotype in water, its virulence in humans is not yet known (Graczyk *et al.*, 2008). The presence of *Cryptosporidium* spp. in the environment is a potential source of contamination and, therefore, dissemination to other animals and humans.

The risk of Cryptosporidium *infection in humans: the role of pigeons*

Human *Cryptosporidium* infections can be transmitted via the environment, especially food and water. However, direct contact with birds, such as pigeons, could also cause infection (Abou Elez *et al.*, 2023; Graczyk *et al.*, 2008; Kabir *et al.*, 2020). The *Cryptosporidium* infection rate among humans varies. Several studies conducted in Iraq report relatively low rates of 14% (14/100) and 29% (32/110) (Al-Robaiee & Al-Farwachi, 2014; Jasm *et al.*, 2011). Further research identified a high prevalence of *Cryptosporidium* infection among domestic pigeon handlers in urban areas in Iraq, with rates of 55% in Baghdad, 58% in Al Najaf and 43.56% in Mosul (Hashim & Al-Zubaidi, 2023; Sayal, 2019; Tawfiq & Omaima, 2012). A study conducted in Baghdad reported a high prevalence of *C. parvum* infection among domestic pigeon handlers in urban areas, with an annual incidence rate of 86% by PCR. This study also revealed a link with the age of handlers and the season: handlers aged 21–40 years old were more frequently infected in January and February (Hashim & Al-Zubaidi, 2023). The prevalence of *Cryptosporidium* spp. in pigeons and humans was compared, revealing that *C. parvum* was detected more frequently in domestic pigeon samples than in pigeon fancier samples (Abou Elez *et al.*, 2023). Direct contact between pigeons and their handlers during breeding may also lead to other complications, such as allergies and itching, probably due to avian ectoparasites transmitted by the birds (Bahrami *et al.*, 2012).

■ DISCUSSION

Determinants of Cryptosporidium *spp. prevalence in pigeons: a global analysis of variability across studies and influencing factors*

The average global prevalence of *Cryptosporidium* spp. in pigeons ranged between 0.82% (Li *et al.*, 2015) and 86.00% (Hashim & Al-Zubaidi, 2023). The observed prevalence variations across different studies on pigeon parasites or diseases can be attributed to a multitude of factors (Abou Elez *et al.*, 2023). Key determinants include sample size, which indicates whether the study is likely to be representative, especially when the prevalence rate is high within a small sample (Toma *et al.*, 2018). Another factor is pigeon age, as susceptibility to infection may differ between younger and older birds.

Pigeon feeding habits, differences in nutrition and the management of nutritional deficiencies also play a critical role in overall pigeon health and resistance to parasites (Dakheel Kremsh Alasadiy *et al.*, 2022). Additionally, both sampling and diagnostic methods can heavily influence study results. For example, the variation and sensitivity of diagnostic methods – such as staining techniques compared to highly sensitive PCR assays – can significantly impact detection rates (Altamimi, 2020; Oliveira *et al.*, 2017; Qi *et al.*, 2011).

Prevalence may vary as a result of geographic location and regional environmental conditions (Dakheel Kremsh Alasadiy *et al.*, 2022). Pigeons may be exposed to unique sets of environmental factors and pathogens in different regions. Furthermore, the duration and season of the sampling period can affect prevalence, as certain parasites may be more active or abundant in specific seasons (dos Santos *et al.*, 2020b; Faraj, 2014). In fact, *Cryptosporidium* infection rates are higher in Iraq during the cooler and wetter season in January and February (Hashim & Al-Zubaidi, 2023). Pigeon housing or living conditions also play a role, as poor hygiene can increase the risk of parasite transmission (Abou Elez *et al.*, 2023). Lastly, host age and gender may have biological implications in terms of bird vulnerability to infection, adding another layer of complexity to the variability reported in different prevalence studies.

Most studies on *Cryptosporidium* spp. in pigeons have been conducted in Asia. In China, in recent years, pigeons have become increasingly bred as a food source, as companion pets or for racing (Li *et al.*, 2016). In India, pigeons could provide an alternative protein source. Pigeons can be raised in relatively simple and affordable breeding systems. They have a short reproductive cycle and lower disease incidence compared to other species that are more expensive to produce. Breeding pigeons may help poor rural communities improve their socio-economic status, especially in Asian countries (Maity *et al.*, 2020). The increase in pigeon farming in Asia may encourage researchers to conduct more studies on pigeons and their zoonotic potential, including their role in the transmission of *Cryptosporidium* spp.

Some studies did not identify *Cryptosporidium* in pigeon faecal samples, which could be due to their small sample sizes. For example, one Brazilian study only investigated two pigeons (da Cunha *et al.*, 2017). Alternatively, sampling methods may be less informative. In another Brazilian study, 25 pigeons were deemed healthy following a sampling method that involved pooling groups of four cloacal swabs (Marenzoni *et al.*, 2016). This method diverges from both classical and molecular *Cryptosporidium* investigation methodologies.

Another study found that suburban pigeons were in better health than pigeons in the city centre. Highly urban pigeons are predisposed to *Cryptosporidium* spp. infection (Weber *et al.*, 1994) due to greater pigeon densities and proximity to contaminated waste or other hosts. Indeed, health conditions play a major role in pigeon *Cryptosporidium* spp. infection. Poor health status increases pigeon susceptibility to infection (Abou Elez *et al.*, 2023). In the same way, more *Cryptosporidium* spp. are found in domestic pigeon droppings than in feral pigeon droppings (Adhikari *et al.*, 2022; Dakheel Kremsh Alasadiy *et al.*, 2022; Holubová *et al.*, 2024). Similar results have also been observed in rodents, with a higher *Cryptosporidium* spp. infection rate in pet rodents than in wild rodents (Lv *et al.*, 2009). This difference in prevalence may be due to overcrowding, which is common on pigeon farms.

Variable hygiene practices could also explain the different prevalence rates observed in captive pigeons. As stated earlier, poor hygiene increases the risk of *Cryptosporidium* spp. infection in pigeons (Abou Elez *et al.*, 2023), Indeed, several studies did not identify *Cryptosporidium* spp. at any of the bird markets in a single region (Kabir *et al.*, 2020), which may reflect good hygiene practices in that area.

The higher prevalence of parasites – including *Cryptosporidium* – in domestic pigeons compared to wild pigeons may be attributed to diet and increased parasite transmission due to greater flock densities and/or poor farm hygiene. In contrast, the lower infection rate in wild pigeons may be linked to their tendency to travel long distances in search of food, which may limit their exposure to pathogens (Dakheel Kremsh Alasadiy *et al.*, 2022). There are obviously exceptions. One study conducted in central Nepal reports that household pigeons were less frequently infected by parasites (75.4%) than temple pigeons (95.6%) (Adhikari *et al.*, 2022). This could be explained by the higher flock densities in temples than in houses.

Several studies comparing young and adult pigeon *Cryptosporidium* spp. infection rates reported that younger pigeons are more frequently infected than older birds (Hashim & Al-Zubaidi, 2024; Khalifa *et al.*, 2020). Immunologic status could play a role, where the underdeveloped immune systems of young pigeons are less resistant to parasitic challenges. In contrast, some studies have not found a link between infection prevalence and pigeon age (dos Santos *et al.*, 2020b; Oliveira *et al.*, 2017; Radfar *et al.*, 2012). Further investigation into age as a risk factor for *Cryptosporidium* spp. infection in pigeons is needed to improve our understanding of the impact of age on infection dynamics.

Diversity of Cryptosporidium *species and subtypes in pigeons*

To date, only four species of *Cryptosporidium* have been proven to infect birds: *C. baileyi, C. galli, C. meleagridis* and *C. avium* (da Cunha *et al.*, 2017; J. Li *et al.*, 2015; Oliveira *et al.*, 2017; Radfar *et al.*, 2012; Reboredo-Fernández *et al.*, 2015; Seixas *et al.*, 2019).

C. baileyi is the most prevalent *Cryptosporidium* species identified in birds (Altamimi, 2020; Jasim & Marhoon, 2015; Ryan, 2010). It was first described in a domestic chicken from the USA in 1986 (Šlapeta, 2013). Pigeons are one of the most important avian hosts infected by *C. baileyi*. High morbidity and mortality, characterised by severe tracheitis or air sacculitis, are associated with *C. baileyi* infections (J. Li *et al.*, 2015; Ryan, 2010). This species was also detected more frequently in domestic pigeons than in wild pigeons (Holubová *et al.*, 2024). In 1991 in the Czech Republic, *C. baileyi* was detected for the first time in an immunodeficient person (Ditrich *et al.*, 1991). In this case report, experimental infection was unsuccessful in suckling mice, but became well established in the chicken model, affecting both respiratory and digestive tracts. The prepatent period was reported to be 12 days (Ditrich *et al.*, 1991). Pigeons may serve as reservoirs for *C. baileyi*, potentially contributing to its spread among other bird species. Pigeon breeding operations could play a significant role in human transmission.

Pavlàsek reported the first occurrence of *C. galli* in hens (Pavlasek, 1999; Ryan *et al.*, 2003). *C. galli* is preferentially localised in the proventriculus of a variety of exotic and wild birds (Order *Passeriformes*, *Phasianidae*, *Fringillidae* and *Icteridae*), causing high mortality in the rare cases where clinical signs are reported (Faraj, 2014; Holubová *et al.*, 2024; Ryan, 2010). This species does not infect the respiratory tract and has been experimentally transmitted to chickens (Ryan *et al.*, 2003).

C. proventriculi infects the proventriculus and ventriculus of psittacine birds, but is not infectious to budgerigars, chickens or mice (Holubova *et al.*, 2019).

C. galli has only been detected in feral pigeons, while *C. proventriculi* was only found in domestic pigeons (Holubová *et al.*, 2024). As yet, no study has investigated whether these species are truly capable of infecting pigeons or whether these findings are accidental, due to contact with wild birds. In addition, no studies report *C. galli* or *C. proventriculi* infection in humans, which may indicate that the infection rate in humans is very low or that this *Cryptosporidium* species is not zoonotic.

C. meleagridis was first described in birds (turkeys) in 1955 (Slavin, 1955), and found in domestic pigeons for the first time in China, in 2011 (Qi *et al.*, 2011). This *Cryptosporidium* species could be pathogenic and causes digestive disorders, such as diarrhoea. In addition to avian species, it has the ability to infect a variety of mammals including calves, pigs, rabbits, mice and humans. Phylogenetic analyses suggest a potential mammalian origin (Ryan, 2010). This species is the third most common zoonotic *Cryptosporidium* reported in humans after *C. hominis* and *C. parvum*, both of which are more frequently transmitted by cattle (Ryan, Zahedi, *et al.*, 2021).

C. parvum is the most commonly identified species in pigeons. It is present in a large host range, including livestock, wild birds and humans. Pigeons could be contaminated by interacting with other birds, through contact with other animals or the environment, before disseminating *C. parvum* throughout pigeon lofts (Altamimi, 2020). As with *C. muris* and *C. andersoni*, there is no proof that *C. parvum* is infectious in pigeons. The presence of these *Cryptosporidium* species in pigeon droppings may be due to environmental contamination by cattle or rodent faeces (Holubová *et al.*, 2024). These three non-avian-specific *Cryptosporidium* species have a broad host range. They are more frequently identified in domestic pigeons than in wild pigeons (Holubová *et al.*, 2024). This could be explained by the presence of domestic pigeons in cities and their proximity to human or animal waste. Furthermore, Li did not identify *C. parvum* in their study in China (Q. Li *et al.*, 2016). This may be because the study was conducted with caged birds, which prevented contact with other animals.

C. hominis was first described in pigeons in Spain, in 2009 (Abreu-Acosta *et al.*, 2009). To date, only a few studies have reported non-human *C. hominis* infections and only mammals were infected. Pigeons could potentially act as mechanical vectors for *C. hominis*, after being contaminated by eating and drinking in unhygienic places near human activities (Abreu-Acosta *et al.*, 2009).

Although *Cryptosporidium* spp. infection levels appear to be similar between domestic and feral pigeons, more diverse *Cryptosporidium* species were found in captive pigeons (Holubová *et al.*, 2024). This difference in prevalence could be due to overcrowding in pigeon breeding units, which facilitates pathogen transmission. New *Cryptosporidium* species could be introduced into breeding units when captive pigeons and rodents come into contact with wild species. Some *Cryptosporidium* spp. may actually be present in wild pigeons, but remain undetected due to their low prevalence. Thus, further research on pigeon breeding units may help identify which *Cryptosporidium* species are actually present in wild pigeons and rodents.

Few studies reported the infectivity of *Cryptosporidium* species. In the first reported incidence of this parasite in pigeons, *Cryptosporidium* spp. infectivity was demonstrated, but the species involved were not identified (Özkul & Aydin, 1994). The infectivity of *Cryptosporidium* species has been more intensively studied in other bird species. For example, *C. meleagridis* was reported as infective in a chicken, but not in a mouse model (Holubová *et al.*, 2024). Multiple species have been identified in pigeons using molecular biology. It is possible that some of the species detected may be in transit through the pigeon's digestive tract without causing a true infection. This demonstrates the impact of the environment and breeding management on the prevalence of different *Cryptosporidium* species. Pigeons can shed a wide variety of *Cryptosporidium* species and subtypes without necessarily displaying any clinical signs. Therefore, their faeces could be a potential source of infection for both livestock and humans. Future studies to collect sufficient molecular and epidemiological data could help determine which other *Cryptosporidium* species exist in domestic pigeons and whether they are infectious. This would contribute useful information for evaluating the disease risk potential of *Cryptosporidium*. Improving our understanding of pigeon geographical location is crucial for identifying risk factors. These include their proximity to other animal species, such as ruminants or rats, as well as environmental factors, like temperature. For example, when exposed to heat stress conditions, pigeons may be more susceptible to infection. Further studies to quantify the *Cryptosporidium* spp. load in pigeon faeces would also contribute to evaluating the risk of transmission to other hosts, including humans.

The role of pigeons, ruminants and migratory birds in the spread of Cryptosporidium *spp.*

Several authors have highlighted the role of eared doves (*Zenaida auriculata*) and other small animals in the long distance transmission of *Cryptosporidium* spp. to animals and humans (Seixas *et al.*, 2019). Similar to rodents, pigeons are a potential reservoir of many pathogens, including *Cryptosporidium* spp. (Hancke & Suárez, 2022).

C. meleagridis subtypes IIIbA21G1R1, IIIaA20G4R1 and IIIlA8G2R1 (Holubová *et al.*, 2024; Kabir *et al.*, 2020), common subtypes of *C. parvum,* IIaA16G1R1, IIaA15G2R1 (Holubová *et al.*, 2024), IIdA20G1 and IId19AG1 (Mirzaghavami *et al.*, 2023), *C. muris* and *C. andersoni* have been identified in free-ranging animals, including pigeons. Therefore, these animals could play a significant role in the transmission of cryptosporidiosis.

C. parvum and *C. andersoni* are frequently found in cattle, along with *C. bovis* and *C. ryanae* (Thomson *et al.*, 2017). *Cryptosporidium* spp. prevalence in cattle varies from 6.25 to 39.65% (Gattan *et al.*, 2023). For example, 8.4% of healthy adult cows were infected on 48% of the farms in Galicia in Spain (Castro-Hermida *et al.*, 2007). Several studies have shown that small ruminants can also be infected. For example, infection prevalence varies from 2 to 85% in lambs (Paraud & Chartier, 2011); 72% of goats and 67% of sheep were reported to be infected in Mexico (Romero-Salas *et al.*, 2016); 19% of goats and sheep were infected in Spain (Castro-Hermida *et al.*, 2007). Cryptosporidiosis causes higher mortality in younger animals, with neonatal diarrhoea in lambs, goat kids, and calves (Romero-Salas *et al.*, 2016). This may lead to severe economic losses (Gattan *et al.*, 2023). Adults are less impacted by cryptosporidiosis than calves and lambs (Keomoungkhoun *et al.*, 2024), due to their more mature immune systems. This could explain why there is a higher cryptosporidiosis prevalence in spring, with calving and lambing (Thomson *et al.*, 2017). Similar to pigeons, numerous risk factors impact *Cryptosporidium* infection rates in ruminants. The agro-ecosystem where ruminants are raised has a significant influence on infection levels. Poor hygiene, shared water with other farms or contact with other animal species all contribute to increasing the risk of *Cryptosporidium* infection (Gattan *et al.*, 2023). *C. parvum* IIa subtypes – the most common subtype in bovine calves – were also identified in pigeons in Central Europe (Holubová *et al.*, 2024). This suggests that ruminants could be a breeding ground for several *Cryptosporidium* species, especially *C. parvum* and *C. hominis*. Furthermore, calves excrete a vast number of oocysts, which can contaminate the environment very effectively, particularly surface water during intense precipitation events (Brankston *et al.*, 2018). Cohabitation with other animal species, such as pigeons, rodents or other migratory birds could lead to inter-species contamination, thus facilitating further dissemination of *Cryptosporidium*. Several authors report a seasonal difference in infection rates. Infection peaks of bovine *Cryptosporidium* were observed in winter and spring in Canada (Brankston *et al.*, 2018). The same phenomenon was reported in pigeons in Iraq (Hashim & Al-Zubaidi, 2024).

Although farms and agricultural environments are a likely source of surface water *Cryptosporidium* contamination, it is difficult to say which species is responsible for pathogen transmission. Farm-based pigeons and rodents could contaminate stock feed, causing livestock infection. Similarly, migratory birds fly long distances and could also contaminate new environments and hosts.

Cryptosporidium *in water: tracking the hidden threat from birds to humans*

Cryptosporidium is frequently found in water (Castro-Hermida *et al.*, 2009; Gallas-Lindemann *et al.*, 2013; Graczyk *et al.*, 2008; Ligda *et al.*, 2020). Its presence could be attributed to pigeons or wild birds. Oocysts appear to be preferentially found in surface water (lakes, rivers) (Abou Elez *et al.*, 2023; Gallas-Lindemann *et al.*, 2013), which could impact *Cryptosporidium* transmission. Oocysts are notably more frequent in drinking and recreational water supplies in the spring and summer (Graczyk *et al.*, 2008; Koompapong *et al.*, 2014; Mahmoudi *et al.*, 2011). This coincides with the pigeon laying peak in Europe from May to October and corresponds to the dry period when there are more young pigeons. Furthermore, people generally take part in recreational activities in rivers and lakes in the summer, which increases the risk of accidently ingesting water and becoming infected. These combined factors justify the increased monitoring of surface water during spring and summer, as has been recommended in Spain (Ligda *et al.*, 2020).

The presence of *Cryptosporidium* in surface water could also be due to the release of effluent water into the environment. For example, agricultural practices, such as liquid manure spreading, could be a source of contamination (Gallas-Lindemann *et al.*, 2013). The environmental impacts of human activity could easily cause greater *Cryptosporidium* spp. infection rates in pigeons. Indeed, when pigeons drink from wastewater in public parks and gardens or forage in unhygienic places, they are exposed to a higher risk of parasitic contamination (Abreu-Acosta *et al.*, 2009).

Current water treatments and/or chlorination methods are not sufficient to eliminate *Cryptosporidium* in water. Additionally, the retention time for water in wastewater treatment plants may increase the likelihood of contamination due to bird faeces because different species, including pigeons, frequent these sites (Castro-Hermida *et al.*, 2009; Gallas-Lindemann *et al.*, 2013). Reports of *Cryptosporidium* spp. in drinking water highlight the risk of waterborne transmission to humans, especially given the parasite's low infectious dose. Therefore, the presence of *Cryptosporidium* spp. oocysts in water should be investigated using molecular tools to identify which species are involved. This will improve our understanding of transmission routes, especially zoonotic transmission. It is important to note that large numbers of oocysts indicate that *Cryptosporidium* is actively regenerated by a source host. Another approach is to predict the risk of drinking water contamination by developing machine-learning models that include biological, physiochemical and meteorological factors (Ligda *et al.*, 2020, 2024). Establishing recommendations for water quality in relation to pathogen monitoring could help reduce *Cryptosporidium* spp. transmission to humans.

Cryptosporidium *spp. and pigeons: unravelling the zoonotic link to the human health risk*

C. parvum and *C. meleagridis* are the two most frequently identified species in pigeons. Both species have previously been detected in human faeces. *Cryptosporidium parvum* is one of the most common species infecting humans, along with *Cryptosporidium hominis* (Akiyoshi *et al.*, 2003; Hao *et al.*, 2024; Marie & Petri, 2024).

The variation in *Cryptosporidium* spp. infection prevalence among humans can be influenced by a combination of several factors. These include the studied region, environmental conditions, as well as hygiene practices (Hashim & Al-Zubaidi, 2023). For example, the risk of infection is higher among elderly people and children due to their weaker immune status and close contact with birds in public parks and gardens (Haro *et al.*, 2005). In Europe, a higher infection rate was observed in children aged 0–4 years (European Centre for Disease Prevention and Control, 2019). To date, the majority of studies on *Cryptosporidium* in humans focus on young children. We do not know whether people who work with birds are more frequently infected by *Cryptosporidium* spp. In addition, as has been shown for calves and pigeons (Hashim & Al-Zubaidi, 2024;

Majeed *et al*., 2022), humans may be more frequently infected by *Cryptosporidium* spp. during the winter season in Iraq (Hashim & Al-Zubaidi, 2023). There may be a potential link between *Cryptosporidium* spp. infection rates in humans and animals, including pigeons. Further research is needed to identify risk factors for zoonotic transmission and to develop effective control strategies.

People living in developing countries are more frequently infected by *Cryptosporidium* spp. than people living in developed countries. Poor hygiene and environments shared with animals increase the risks of contamination. Similarly, lack of knowledge about disease transmission and the role of clean drinking water may also have an impact (Abou Elez *et al*., 2023; Hashim & Al-Zubaidi, 2023). Furthermore, the high density of pigeon populations in urban areas may increase the risk of human exposure to *Cryptosporidium* spp. The higher infestation rate in domestic pigeons compared to wild pigeons could increase the risk of zoonotic transmission, especially for pigeon handlers. Zoonotic transmission may involve direct or indirect contact with pigeon faeces, which means bird owners are particularly at risk. Feral pigeons are becoming better adapted to the urban environment, to the point of being dependent on the people who feed them. In big cities, pigeons have developed special strategies to be fed. They can recognise the people who feed them and are attracted by the rustle of a plastic or paper bag (Weber *et al*., 1994). This more frequent direct or indirect contact with humans is likely to increase the risk of pathogen transmission. The relationship between humans and pigeons is a multidisciplinary issue that warrants thorough investigation (Burt *et al*., 2021). Further studies should be conducted on the role of pigeons in the spread of zoonotic agents, such as *Cryptosporidium* spp. parasites. With the current body of research, it is difficult to confirm whether *Cryptosporidium* spp. are transmitted preferentially from pigeons to humans or from humans to pigeons. Given the prevalence of *C. parvum* in humans, domestic bird owners who frequently interact with their birds could potentially transmit the infection to their pets. Conversely, bird owners could risk becoming infected through contact with oocysts shed by their birds. In-depth epidemiological studies could improve our understanding of the impact of *Cryptosporidium* spp. in household pigeons and its implications for public health.

■ CONCLUSION

To date, few publications have studied the prevalence and molecular characterisation of *Cryptosporidium* in pigeons. However, current data suggest that pigeons are principally infected with zoonotic *Cryptosporidium* species, such as *C. parvum* and *C. meleagridis*, and that prevalence is higher among domestic pigeons than in wild or feral pigeons. Therefore, domestic birds may play a key role in spreading *Cryptosporidium* spp. parasites. Given the global popularity of pigeons, it is important to implement preventive measures to control this disease, including proper hygiene in pigeon roosts, lofts and cages.

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Conflict of interest

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Author contributions

BP, MM: conception and design of the review. AD, MM: data analysis. Writing - Original Draft: all authors (AD, BP, MM) critically reviewed the manuscript.

Ethics approval

Approval from an ethics committee regarding the use of animals was not necessary for this study because data were collected from previously published sources.

Data availability

The data were not deposited in an official repository. The data that support the study findings are available from the authors upon request.

Declaration of Generative AI in the writing process

The authors did not use any artificial intelligence-assisted technologies in the writing process.

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Résumé

Devulder A., Polack B., Mammeri M. Une revue mondiale sur *Cryptosporidium* spp. chez les pigeons avec un accent sur le concept « Une seule santé »

Contexte : Le pigeon (*Columba livia*) est une espèce d'oiseau domestique qui entre fréquemment en contact avec les humains. Les pigeons hébergent et disséminent de nombreux pathogènes zoonotiques, notamment des parasites apicomplexes du genre *Cryptosporidium*, un parasite protiste commun des vertébrés. Ces dernières années, les populations de pigeons ont augmenté dans les zones urbaines et périurbaines, ce qui peut constituer un risque pour la santé publique. ***Objectif*** : Une revue systématique a été réalisée pour examiner la présence et la prévalence de *Cryptosporidium* chez les pigeons à l'échelle mondiale. ***Méthodes*** : Les articles publiés ont été obtenus dans la base de données PubMed, couvrant la période du 1er janvier 1994 au 1er août 2024. Au total, 38 publications ont été incluses dans cette revue. ***Résultats*** : L'infection à *Cryptosporidium* chez les pigeons a été signalée pour la première fois en Turquie en 1994, avec des symptômes cliniques comprenant la dépression, l'inactivité, la diarrhée et le plumage piqué. L'examen histologique a révélé la présence de *Cryptosporidium* dans l'épithélium intestinal. Des études ultérieures ont confirmé la prévalence de *Cryptosporidium* à l'échelle mondiale, avec des méthodes de diagnostic traditionnelles révélant une prévalence moyenne de 14,8 %, tandis que les outils moléculaires ont montré une prévalence plus élevée (28,4 %). Les taux les plus élevés ont été observés en Irak, les pigeons captifs étant plus fréquemment infectés que les pigeons sauvages. Les données moléculaires, bien que limitées, suggèrent une plus grande diversité chez les pigeons domestiques que chez les pigeons sauvages. *C. meleagridis*, *C. parvum* et *C. hominis* étaient les principales espèces zoonotiques identifiées chez les pigeons à l'échelle mondiale. L'analyse microscopique a montré des variations dans l'intensité de l'infection, avec un taux d'oocystes allant de 3 000 à 36 000 par gramme de fèces. De nombreux génotypes de *Cryptosporidium* spp. sont considérés comme zoonotiques, avec des cas connus d'infection humaine chez des personnes manipulant des pigeons, soulignant sa pertinence pour la santé publique. ***Conclusions*** : Des études supplémentaires sont nécessaires pour clarifier la pathogénicité et les voies de transmission de *Cryptosporidium* spp. chez les pigeons. La prévention et le contrôle de cette zoonose chez les pigeons devraient constituer une priorité de santé publique, en particulier dans les régions où les populations de pigeons sont importantes, telles que les zones urbaines où ils vivent en contact étroit avec les humains et d'autres animaux.

Mots-clés : Pigeon, *Cryptosporidium*, zoonose, approche Une seule santé, épidémiologie, santé publique

Resumen

Devulder A., Polack B., Mammeri M. Revisión a escala mundial de la presencia de *Cryptosporidium* spp. en palomas centrada en el concepto «Una sola salud»

Contexto: La paloma (*Columba livia*) es una especie de ave doméstica que entra frecuentemente en contacto con los humanos. Las palomas albergan y diseminan numerosos patógenos zoonóticos, especialmente parásitos apicomplejos del género *Cryptosporidium*, un parásito protista común en los vertebrados. Estos últimos años, las poblaciones de palomas han aumentado en las zonas urbanas y periurbanas, lo que puede constituir un riesgo para la salud pública. ***Objetivo***: Se realizó una revisión sistemática para examinar la presencia y la prevalencia de *Cryptosporidium* en las palomas a escala mundial. ***Métodos***: Los artículos publicados se obtuvieron en la base de datos PubMed, que cubre el período del 1 de enero de 1994 al 1 de agosto de 2024. En total, se incluyeron 38 publicaciones en esta revisión. ***Resultados***: La infección de *Cryptosporidium* en las palomas se señaló por primera vez en Turquía el 1994, con síntomas clínicos que comprendían depresión, inactividad, diarrea y plumaje picado. El examen histológico reveló la presencia de *Cryptosporidium* en el epitelio intestinal. Estudios posteriores confirmaron la prevalencia de *Cryptosporidium* a escala mundial, con métodos de diagnóstico tradicionales que revelaron una prevalencia media del 14,8 %, mientras que las herramientas moleculares mostraron una prevalencia más elevada (28,4 %). Las tasas más elevadas se observaron en Irak, donde las palomas cautivas estaban infectadas con más frecuencia que las palomas salvajes. Los datos moleculares, aunque limitados, sugieren una mayor diversidad en las palomas domésticas que en las palomas salvajes. *C. meleagridis*, *C. parvum* y *C. hominis* son las principales especies zoonóticas identificadas en las palomas a escala mundial. El análisis microscópico mostró variaciones en la intensidad de la infección, con una tasa de oocistos que va de 3 000 a 36 000 por gramo de heces. Numerosos genotipos de *Cryptosporidium* spp. se consideran zoonóticos, con casos conocidos de infección humana en personas que manipulan palomas, lo que muestra su pertinencia para la salud pública. ***Conclusiones***: Se necesitan estudios suplementarios para clarificar la patogenicidad y las vías de transmisión de *Cryptosporidium* spp. en las palomas. La prevención y el control de esta zoonosis en las palomas debería constituir una prioridad de salud pública, en particular, en las regiones donde las poblaciones de palomas son importantes, como las zonas urbanas donde viven en estrecho contacto con los humanos y otros animales.

Palabras clave : Paloma, *Cryptosporidium*, zoonosis, Enfoque Una salud, epidemiología, salud pública