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Research Article

The influence of landfill foraging: enteric helminths and bacteria in a population of White Stork (*Ciconia ciconia*) from central Spain

Miguel Garces-Herrero[‡,§], Cristina Verdu-Exposito[‡], Adanys Sanz-Miranda[§], Jorge Pérez-Serrano[‡]

‡ University of Alcalá, ALCALA DE HENARES, Spain
§ GREFA, Majadahonda, Spain

Corresponding author: Miguel Garces-Herrero (m.garces@uah.es)

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Abstract

Anthropogenic food subsidies, such as municipal solid waste landfills, profoundly alter wildlife ecology and host–pathogen dynamics. Under a One Health framework, highly mobile synanthropic species exploiting these polluted sites act as biological vectors, effectively bridging human waste reservoirs with urban environments. In this study, we investigated how reliance on refuse shapes the gastrointestinal parasitome and enteropathogenic bacteria of an urban-breeding White Stork (*Ciconia ciconia*) population in central Spain (Alcalá de Henares) that recently adapted to local landfill closures by commuting to distant active sites. Gastrointestinal samples from 44 individuals were collected between 2022 and 2023. We specifically hypothesised that: (1) overall gastrointestinal parasite prevalence would be low due to reduced natural foraging; (2) the parasite community would be dominated by species with direct biological cycles, as bypassing natural prey interrupts indirect cycles; and (3) storks feeding on anthropogenic waste act as important biological vectors for zoonotic bacterial and parasitic pathogens. Our findings demonstrate how anthropogenic refuse drives epidemiological shifts in synanthropic birds and assess the associated public health risks for surrounding urban communities. Ultimately, this work underscores the far-reaching health implications of

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waste management policies, offering a valuable case study at the interface of urban wildlife ecology and public health.

Keywords

Ecosystem, enteropathogen, foraging, landfill, parasite, white stork

Introduction

Host–pathogen and host–parasite interactions are central to understanding infectious disease dynamics and wildlife health (Poulin 2011, Loker and Hofkin 2022). Across multi-host systems, pathogens frequently cross species barriers within shared habitats, driving the spillover of zoonotic agents — including anthropozoonoses, zooanthroponoses and amphixenoses (Acha and Szyfres 2001, Cable et al. 2017). Under the One Health framework, human, animal and ecosystem health are recognised as intrinsically interconnected (Jenkins et al. 2015).

Within these multi-ecosystem networks, highly mobile wildlife species act as key biological vectors, facilitating the long-distance dissemination of pathogens across diverse geographical scales (Becker et al. 2018). In urban and peri-urban environments, synanthropic and migratory birds possess a high capacity for pathogen dispersal, bridging outer-urban ecosystems with human settlements (Jourdain et al. 2007, Viana et al. 2016, González-Barrio 2022). This dispersal capacity is drastically amplified when birds habitually forage at highly polluted anthropogenic sites, such as municipal solid waste landfills (Malekian et al. 2021). A prominent example is the White Stork (*Ciconia ciconia*), a migratory bird that heavily relies on landfills both as stopover sites during migration and as primary foraging grounds during the breeding season (Gilbert et al. 2016, Arizaga et al. 2018, Cardona-Cabrera et al. 2025). The exploitation of these predictable and abundant food sources fundamentally alters the spatial behaviour and foraging ecology of these birds (Pineda-Pampliega et al. 2021), creating massive aggregation hotspots where high faecal shedding turns landfills into critical contagion hubs (Shen et al. 2025).

Crucially, foraging at landfills restructures the presence, distribution and abundance of gastrointestinal pathogens in the White Stork, affecting bacteria and parasites through distinct mechanisms. On one hand, landfills serve as environmental reservoirs for human-derived enteropathogens and antimicrobial resistance elements; consequently, birds feeding on anthropogenic waste are exposed to a high diversity of opportunistic bacteria (Bonnedahl and Järhult 2014, Wu et al. 2017), leading to a high prevalence of resistant bacterial pathogens in their digestive tracts (Szczepańska et al. 2015, Camacho et al. 2016). On the other hand, the consumption of refuse shifts dietary intake away from natural prey, deeply altering helminth parasite communities according to their biological life cycles. Parasites with indirect life cycles — which require specific intermediate hosts (e.g. insects, earthworms or small vertebrates) — often exhibit reduced prevalence

because storks bypass their natural prey (Blanco 1996, Lafferty and Kuris 2005). Conversely, the unnaturally high density of individuals congregating at landfills promotes the faecal–oral transmission of parasites with direct life cycles (Lafferty and Kuris 2005). Consequently, White Storks serve as hosts and potential vectors for various pathogens, including helminths, such as *Capillaria* spp. (Fuehrer et al. 2011, Rocha et al. 2015, Sitko and Heneberg 2015), protozoans like *Giardia* spp. (Franssen et al. 2000, Ryan and Cacciò 2013, Reboredo-Fernández et al. 2015, Dixon 2021, Huang et al. 2023) and diverse enteropathogenic bacteria.

To evaluate these ecological dynamics, we investigated the gastrointestinal parasites and enteric bacteria of a long-monitored White Stork population in central Spain (Alcalá de Henares, Madrid). Breeding on historical urban buildings in close proximity to human activity, this population expanded dramatically following the opening of a nearby open-sky landfill in 1984 — recovering from ~ 15 pairs in the 1970s to over 130 pairs in 2017 (Bernis 1981, Martí and Del Moral 2003, Molina and del Moral 2004). However, the closure of this local landfill in 2021 in compliance with European waste management directives (Consejo Europeo and Parlamento Europeo 1975, Jefatura de Estado 2020) imposed a severe ecological shift, forcing the population to travel daily to more distant active landfills. Between 2022 and 2023, we sampled 44 individuals from this population to characterise their gastrointestinal parasitome and enteropathogenic bacteria in this post-closure context.

In this study, we addressed the ecological and public health implications of landfill reliance by testing three hypotheses:

- **Low Parasite Prevalence**: We hypothesised that overall gastrointestinal parasite prevalence in this population would be low, predicting that the reduced use of natural foraging habitats minimises exposure to prey-borne infective stages;
- **Dominance of Direct Life-Cycle Parasites**: We hypothesised that the parasite community would be dominated by species with direct biological cycles, predicting a significant reduction or absence of indirect-cycle parasites due to the interruption of intermediate host consumption;
- **Zoonotic Vector Potential**: Given their highly synanthropic habits and intensive reliance on refuse, we hypothesised that White Storks act as critical biological vectors for pathogen transmission, predicting a high prevalence and co-occurrence of zoonotic bacteria and parasites that pose potential public health risks to urban human populations within a One Health framework.

Materials and Methods

Study Population and Sampling Area

The target White Stork (*Ciconia ciconia*) population in Alcalá de Henares (Madrid, central Spain) has been systematically monitored since 2009 via remote identification of alphanumeric PVC rings. Field observations confirmed high site fidelity to urban nesting

sites (historical buildings, churches and municipal buildings) and verified that foraging individuals belonged to this local breeding population.

Historically, this population experienced a dramatic expansion until 2017, heavily supported by the open-sky municipal landfill that served as its primary foraging ground. Following the mandatory closure of the local landfill in 2021 in compliance with European waste management regulations (Consejo Europeo and Parlamento Europeo 1975, Jefatura de Estado 2020), long-term tracking revealed an ecological shift: although storks partially incorporated natural habitats (wetlands and croplands) into their foraging routines, they continued to rely predominantly on anthropogenic refuse as their primary food source by commuting daily to more distant active landfills.

Capture, Handling, Demographics and Biosafety

A total of 44 adult White Storks were captured at their foraging sites using nylon nest traps across four distinct sampling sessions:

- **Pre-breeding period**: 1 March 2022 (n = 17) and 15 February 2023 (n = 8).
- **Post-breeding period**: 19 July 2023 (n = 13) and 29 November 2022 (n = 6).

Upon capture, unringed individuals were fitted with standard metallic identification rings and alphanumeric PVC rings for long-distance resighting. All sampled individuals were fully feathered adults, although their exact chronological ages could not be determined. To evaluate body condition, body mass (kg) and wing chord length (cm) were recorded for each bird. Individual body condition was calculated using the Scaled Mass Index (SMI) following the protocol of Peig and Green (2010) and all captured individuals exhibited from "fit" to "excellent" physical condition (Table 2). As White Storks lack external sexual dimorphism, molecular sexing via PCR could not be performed due to budgetary constraints and sex was not incorporated as a variable in the analyses.

Table 1.

Parasitic burden, parasites information and individuals ID information; helminth eggs size average, standard deviation of size average, standard error of the mean are given in [L/W] (length x wide) (µm).

ID individual		Parasite species	Egg size average [L/W]	Standard Deviation (SD) [L/W]	Standard error of the mean (SEM) [L/W]	No. of parasites	Life stage
PVC code	Official ring code						
W[0/73R]	9002093	*Chaunocephalus* sp.	101 x 62	1.41 / 3.54	1.00 / 2.50	2	**Egg (empty)**
W[0/73R]	9002093	*Chaunocephalus* sp.	103 x 60	0.00 / 0.00	0.00 / 0.00	1	**Egg**
W[0/73R]	9002093	*Choanotaenia* sp.	35 x 31	0.00 / 2.89	0.00 / 1.67	3	**Egg**
W[0/742]	9002095	*Chaunocephalus* sp.	105 x 65	4.08 / 4.08	2.04 / 2.04	4	**Egg (empty)**

ID individual		Parasite species	Egg size average [L/W]	Standard Deviation (SD) [L/W]	Standard error of the mean (SEM) [L/W]	No. of parasites	Life stage
PVC code	**Official ring code**						
W[0/73T]	9002094	*Raillietina* sp.	40 x 35	0.00 / 4.24	0.00 / 3.00	2	**Egg**
W[0/722]	9002099	*Chaunocephalus* sp.	90 x 55	0.00 / 7.07	0.00 / 5.00	2	**Egg**
W[0/722]	9002099	*Chaunocephalus* sp.	92 x 60	3.54 / 0.00	2.50 / 0.00	2	**Egg (empty)**
W[AC66]	9059309	*Syngamus trachea*	86 x 42	5.77 / 2.31	3.33 / 1.33	3	**Egg**
W[0/73J]	9002091	*Raillietina* sp.	45 x 42	0.00 / 3.54	0.00 / 2.50	2	**Egg**
WL[0/73J]	9002091	*Chaunocephalus* sp.	95 x 60	0.00 / 0.00	0.00 / 0.00	1	**Egg (empty)**
W[0/741]	9002097	*Contracaecum* sp.	50 x 45	5.00 / 5.00	2.89 / 2.89	4	**Egg**
W[C130]	9065802	*Chaunocephalus* sp.	90 x 52	0.00 / 0.00	0.00 / 0.00	1	**Egg (empty)**
W[CPA]	9002256	*Chaunocephalus* sp.	95 x 55	7.07 / 7.07	5.00 / 5.00	2	**Egg**
W[CPA]	9002256	*Chaunocephalus* sp.	100 x 60	0.00 / 0.00	0.00 / 0.00	1	**Egg (empty)**
W[0/CL7]	9002152	*Chaunocephalus* sp.	95 x 55	6.36 / 0.00	4.50 / 0.00	2	**Egg**
W[0/CL7]	9002152	*Chaunocephalus* sp.	104 x 62	6.93 / 7.64	4.00 / 4.41	3	**Egg (empty)**

Table 2.

Individual morphometric measurements, Scaled Mass Index (SMI) and qualitative body condition estimates for adult White Storks (*Ciconia ciconia*) sampled in Alcalá de Henares (Madrid, Spain) between 2022 and 2023. (**PVC code**: alphanumeric ring for long-distance field identification; **OR code**: official metallic ring ID; **Weight**: body mass in kg; **DFW**: dorsal folded wing in cm).

Date	PVC code	OR code	Weight (kg)	DFW (cm)	SMI	Estimate
feb-23	W[0/73R]	9002093	3,545	58	3,98	Good
mar-22	W[0/722]	9002099	4	61	3,86	Good
mar-22	W[0/73J]	9002091	4,375	61	4,22	Very good
mar-22	W[0/73R]	9002093	4	58	4,49	Excellent
mar-22	W[0/73T]	9002094	3,69	58,2	4,1	Very good
mar-22	W[0/741]	9002097	4,13	62	3,79	Good
mar-22	W[0/742]	9002095	4,28	61,2	4,09	Very good
jul-23	W[0/CL7]	9002152	3,16	56,3	3,88	Good

Date	PVC code	OR code	Weight (kg)	DFW (cm)	SMI	Estimate
mar-22	W[AC66]	9059309	3,63	57,5	4,18	Very good
nov-22	W[C130]	9065802	3,36	61	3,24	Fair
feb-23	W[C130]	9065802	3,53	61	3,4	Fair
jul-23	W[C130]	9065802	3,47	61	3,35	Fair
feb-23	W[CPA]	9002256	3,58	56,8	4,28	Excellent
mar-22	W[0/73J]	9002091	4,375	61	4,22	Very good

Table 3.

Temporal distribution of detected pathogens across four sampling events (March 2022 - November 2022- February 2023- July 2023) and global comparison using Fisher's exact test (*p*-values indicate differences across capture dates (two-sided Fisher's exact test; significance level $p < 0.05$)).

Pathogen	Period	Positives	Negatives	Total	p-value
Salmonella spp.	mar-22	1	16	17	0.7664
Salmonella spp.	nov-22	0	6	6	
Salmonella spp.	feb-23	1	7	8	
Salmonella spp.	jul-23	0	13	13	
Campylobacter spp.	mar-22	2	15	17	0.5328
Campylobacter spp.	nov-22	0	6	6	
Campylobacter spp.	feb-23	1	7	8	
Campylobacter spp.	jul-23	0	13	13	
Escherichia coli	mar-22	17	0	17	1
Escherichia coli	nov-22	6	0	6	
Escherichia coli	feb-23	8	0	8	
Escherichia coli	jul-23	13	0	13	
Syngamus trachea	mar-22	1	14	15	1
Syngamus trachea	nov-22	0	6	6	
Syngamus trachea	feb-23	0	8	8	
Syngamus trachea	jul-23	0	11	11	
Chaunocephalus ferox	mar-22	4	11	15	0.7938
Chaunocephalus ferox	nov-22	1	5	6	
Chaunocephalus ferox	feb-23	1	7	8	

Pathogen	Period	Positives	Negatives	Total	p-value
Chaunocephalus ferox	jul-23	1	10	11	
Choanotaenia infundibulum	mar-22	1	14	15	1
Choanotaenia infundibulum	nov-22	0	6	6	
Choanotaenia infundibulum	feb-23	0	8	8	
Choanotaenia infundibulum	jul-23	0	11	11	
Contracaecum spp.	mar-22	1	14	15	1
Contracaecum spp.	nov-22	0	6	6	
Contracaecum spp.	feb-23	0	8	8	
Contracaecum spp.	jul-23	0	11	11	
Raillietina spp.	mar-22	2	13	15	0.6346
Raillietina spp.	nov-22	0	6	6	
Raillietina spp.	feb-23	0	8	8	
Raillietina spp.	jul-23	0	11	11	

Table 4.

Pathogen occurrence across phenological periods (pre-breeding vs. post-breeding) in White Storks, including Fisher's exact test p-values, Odds Ratios (OR) and 95% confidence intervals (95% CI) (p-values were determined via two-sided Fisher's exact tests (α = 0.05). + ∞ indicates undefined odds ratios or confidence limits resulting from zero cell frequencies.

Pathogen	Phenological Period	Positives	Negatives	Total	p-value	Odds ratio	IC 95%
Salmonella spp.	pre-breeding	2	23	25	0.4979	+ ∞	0.1428852, + ∞
	post-breeding	0	19	19			
Campylobacter spp.	pre-breeding	3	22	25	0.2468	+ ∞	0.3190373,
	post-breeding	0	19	19			
Escherichia coli	pre-breeding	25	0	25	1	0	0, + ∞
	post-breeding	19	0	19			
Syngamus trachea	pre-breeding	1	22	23	1	+ ∞	0.01896739, + ∞
	post-breeding	0	17	17			
Chaunocephalus ferox	pre-breeding	5	18	23	0.677	2.04713	0.282946, 24.449191
	post-breeding	2	15	17			
Choanotaenia infundibulum	pre-breeding	1	22	23	1	+ ∞	0.01896739, + ∞

Pathogen	Phenological Period	Positives	Negatives	Total	p-value	Odds ratio	IC 95%
	post-breeding	0	17	17			
Contracaecum spp.	pre-breeding	1	22	23	1	+ ∞	0.01896739, + ∞
	post-breeding	0	17	17			
Raillietina spp.	pre-breeding	2	21	23	1	+ ∞	0.1388757, + ∞
	post-breeding	0	17	17			

To minimise cross-contamination and health risks during field handling, biosafety protocols were strictly implemented: field operators wore nitrile gloves (changed between individual birds) and all measuring instruments and sampling devices were sanitised prior to each handling event.

Sample Collection and Parasitological Analysis

Fresh faeces were collected directly during bird handling from 40 of the 44 captured individuals (World Health Organisation 1992) using sterile Mini Parasep® faecal parasite concentrators, while cloacal swabs were collected from all 44 individuals using sterile transport swabs.

To standardise parasitological processing across individuals, sample mass was fixed to 3.5 g per faecal sample, constrained by the minimum mass obtained amongst all collected samples. Samples were processed using Mini Parasep® and concentration solutions with Bailenger and ethyl acetate solutions (Bailenger 1979, World Health Organisation 2003). Following the manufacturer's guidelines for Mini Parasep®, the samples were centrifuged at 400 × g for 2 minutes.

For microscopic examination, three separate glass slide preparations (wet mounts/ smears) were examined per sample under optical microscopy at 100/times and 400/times magnifications. To assess egg viability and structural integrity, eggs were systematically inspected optical-microscopically to distinguish between filled (intact internal embryo/ vitelline contents) and empty (degraded or ruptured shell without cellular contents) propagules. Helminth taxa were identified, based on diagnostic morphometric parameters described in standard literature (Khalil et al. 1994, Gibson et al. 2005, Foreyt 2013, Centers for Disease Control and Prevention 2019, World Health Organization 2019).

Microbiological Screening of Enteric Bacteria

Cloacal swabs were processed to screen for three target zoonotic enteropathogens: *Salmonella* spp., *Campylobacter* spp. and *Escherichia coli*. Due to methodological

limitations, bacterial identification relied on standard culture-based and phenotypic screening protocols (Jorgensen et al. 2015):

- **Sample Pre-enrichment**: Swabs were incubated in buffered peptone water (Ref. 02-277-500, Scharlab®) at 37ºC for 24 hours (Gray et al. 2008);
- ***Salmonella* spp. Screening**: Aliquots were inoculated into Muller-Kauffmann selective enrichment broth (Ref. 02-335-500, Scharlab®) and incubated at 37ºC for 24 hours (Muller 1923, Kauffmann 1930). Selective subcultures were subsequently plated on Hektoen Enteric Agar (HEA; Ref. 01-216-500, Scharlab®) and Xylose Lysine Deoxycholate Agar (XLD; Ref. 64PA0034LL, Scharlab®) at 37ºC for 24 hours, following ISO 6579 recommendations (International Organization for Standardization. 2002);
- ***Campylobacter* spp. Screening**: Samples were plated on modified Charcoal Cefoperazone Deoxycholate Agar (mCCDA; Ref. 01-685-500, Scharlab®) and incubated at 42ºC for 48 hours under micro-aerophilic conditions using a candle jar system, in accordance with ISO 10272 standards (Bolton et al. 1984, International Organization for Standardization 2017);
- ***Escherichia coli* Screening**: Samples were inoculated on MacConkey Agar (Ref. 01-118-500, Scharlab®) and incubated at 37ºC for 24 hours (MacConkey 1905).

All isolates were classified as presumptive, based on characteristic colony morphology and selective growth media properties.

Morphometric and Statistical Analyses

Morphometric characterisation of recovered parasitic eggs was conducted by measuring maximum length and width (µm) for each identified taxon. Mean, minimum, maximum, standard deviation (SD) and standard error of the mean (SEM) were calculated to evaluate phenotypic variability and dimensional stability across taxa.

Individual body condition was evaluated using the Scaled Mass Index (SMI) (Table 2), calculated according to the methodology of Peig and Green (2010) using the following formula:

$$SMIi = Mi(L0/Li)^{b_{SMA}}$$

where M_i and L_i represent the observed body mass (kg) and structural body size (dorsal folded wing, DFW, in cm) of individual *i*, respectively. L_0 is the arithmetic mean of L for the studied population (L_0 = 60.27cm) and b_{SMA} is the scaling exponent estimated via standardised major axis (SMA) regression of ln *M* on ln *L* (b_{SMA} = 3.00).

To evaluate scientific robustness and test for temporal differences in pathogen occurrence, inferential statistical analyses were performed:

- **Prevalence and Confidence Intervals**: Parasite and bacterial prevalences were calculated as the proportion of positive individuals relative to the total sampled

(n). Exact 95% Confidence Intervals (95% CI) were estimated using the Wilson score method (Fisher 1922, Zar 1999);

- **Comparative Analyses**: Fisher's exact test was used to compare prevalence rates across sampling dates (March 2022, February 2023, July 2023, November 2022) and between key functional phenological periods (**pre-breeding period**: March 2022 + February 2023 vs. **post-breeding period**: July 2023 + November 2022) (Wilson 1927, Brown et al. 2001).

Fisher's exact tests were performed as two-sided tests to evaluate prevalence differences across sampling dates and phenological periods, with statistical significance set at $\alpha = 0.05$. All statistical analyses and graphical renders were executed in R Core Team 2024 using packages "binom" (Dorai-Raj 2022) and "stats" (R Core Team 2024).

Prevalence estimates are presented alongside their 95% confidence intervals (95% CI) calculated using the Wilson score method, which is highly recommended for small sample sizes and extreme proportions near 0 or 1 (Wilson 1927, Brown et al. 2001). Differences in pathogen occurrence between phenological periods and capture dates were evaluated using the Fisher's exact test (Fisher 1922). This exact non-parametric method was chosen over Pearson's χ^2 test due to the small sample sizes and the presence of expected cell frequencies below 5 in the contingency tables (Zar 1999).

Results

Parasitology analysis

The stool samples were analysed and helminth eggs were determined by 100x and 400x magnification using morphometric information established in literature (Levine 1968, Georgi and Mcculloch 1988, Khalil et al. 1994, Hugot et al. 2000, Georgi and Georgi 2003, Gibson et al. 2005, Anderson et al. 2009, Foreyt 2013, Centers for Disease Control and Prevention 2019, World Health Organization 2019). We did not find evidence of the presence of enteroparasitic protozoa.

The helminth parasite species detected after the microscopic analysis of faecal samples were *Chaunocephalus ferox*, *Choanotaenia infundibulum*, *Raillietina* spp., *Contracaecum* spp. (identified as *C. microcephalum*) and *Syngamus trachea* (Fig. 1). Overall parasite prevalences were generally low (Table 5). *C. ferox* was the most frequently detected helminth, exhibiting an overall prevalence of 15.9% (95% CI: 7.9–29.4%, Wilson score method). The remaining taxa were detected at lower frequencies: *Raillietina* spp. showed a prevalence of 4.5% (95% CI: 1.3–15.1%), while *Choanotaenia infundibulum*, *Contracaecum* spp. and *Syngamus trachea* each presented a prevalence of 2.3% (95% CI: 0.4–11.8%; Table 5).

Table 1 indicates the species (or genus), the number of parasites in each collected faecal sample, the individual from which the sample was taken and the average size of each species per sample. For samples where n=1, the standard deviation cannot be determined because a single measurement does not allow for the calculation of variance.

In light of these results, it should be noted that qualitative morphological characteristics are of paramount importance and should take precedence over dimensions, as the latter may frequently fall outside the established ranges in scientific literature.

Table 5.

Overall prevalence estimates and Wilson score 95% confidence intervals for detected bacterial and parasitic taxa in White Storks (n = *44*) (*mean* represents overall prevalence as a proportion; *lower* and *upper* denote the 95% confidence limits calculated via the Wilson score method).

Pathogen	positives	n	mean	lower	upper
Salmonella spp.	2	44	0.04545455	0.01255511	0.15135
Campylobacter spp.	3	44	0.06818182	0.0234594	0.1822504
Escherichia coli	44	44	1	0.9197044	1
Chaunocephalus ferox	7	44	0.1590909	0.07926677	0.2936621
Choanotaenia infundibulum	1	44	0.02272727	0.004023252	0.1180771
Raillietina spp.	2	44	0.04545455	0.01255511	0.15135
Syngamus trachea	1	44	0.02272727	0.004023252	0.1180771
Contracaecum spp.	1	44	0.02272727	0.004023252	0.1180771

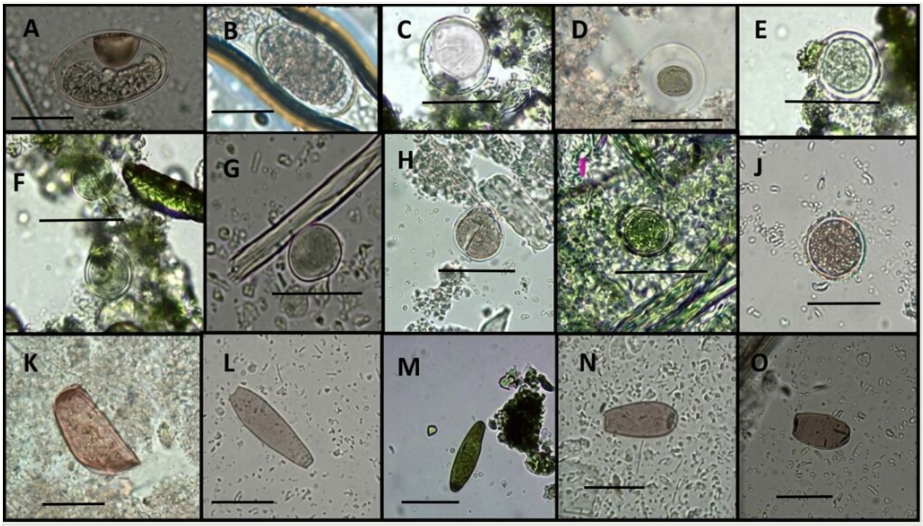

Figure 1.

The images show helminth eggs found in the samples from White Stork in this study; **A, B)** *Syngamus trachea*; **C, D)** *Raillietina* sp.; **E, F)** *Choanotaenia infundibulum*; **G-J)** *Contracaecum microcephalum*; **K-O)** empty eggs (except for **M)**, of *Chaunocephalus ferox*. Scale bars in all panels represent 50 µm.

Further inferential statistical analyses revealed that helminth prevalences remained stable across the studied timeframe. Comparisons between phenological periods (pre-breeding vs. post-breeding) showed no statistically significant differences for any parasitic taxon (Fisher's exact test, two-sided; all $p \geq 0.677$; Table 3). For instance, the prevalence of *C. ferox* did not differ significantly between the pre-breeding (21.7%, 5/23) and post-breeding (11.8%, 2/17) periods ($p = 0.677$; OR = 2.05, 95% CI: 0.28–24.45; Table 3). Similarly, temporal analyses across the four specific sampling capture dates yielded no significant variations for any helminth species (Fisher's exact test; all $p \geq 0.635$, Table 4).

Enterobacteriaceae analysis

Conversely, the results for enteropathogenic bacteria are all presumptive due to identification exclusively through selective culture. Positive identification of *Escherichia coli*, *Salmonella* spp. and *Campylobacter* spp. was based on the growth and appearance of colonies in the corresponding selective and differential media (Fig. 2).

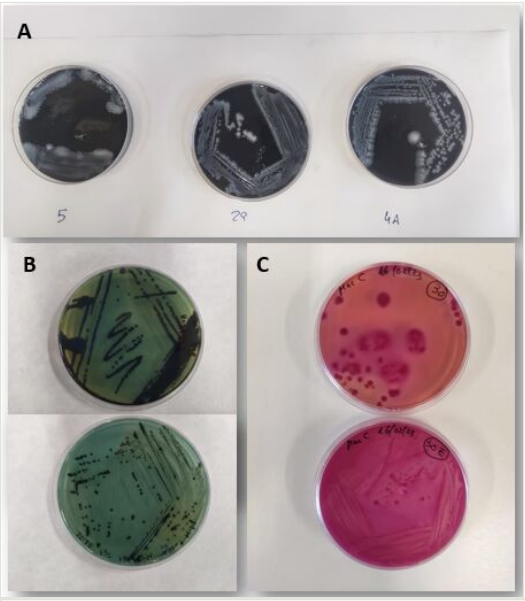

Figure 2.

Different plates after the corresponding incubation periods (24 or 48 hours); **A)** positive cultures for *Campylobacter* sp. in Agar modified Charcoal Cefoperazone Deoxycholate medium (mCCD); **B)** positive cultures for *Salmonella* sp. in Hektoen Enteric Agar (HEA); **C)** positive cultures for *Escherichia coli* in Agar-MacConkey medium.

All samples were positive for *Escherichia coli*, resulting in a 100% overall prevalence (44/44; 95% CI: 92.0–100%; Table 5). However, only three samples were positive for *Campylobacter* spp. (6.8%; 95% CI: 2.3–18.2%) and two samples for *Salmonella* spp. (4.5%; 95% CI: 1.3–15.1%, Table 5). Notably, one of the *Campylobacter* spp. positive

samples was also positive for presumptive *Shigella* spp., which was determined by its appearance on XLD and HEA plates.

Consistent with the parasitological findings, the occurrence of enteropathogenic bacteria did not fluctuate significantly over time. No statistically significant differences in prevalence were detected between the pre-breeding and post-breeding periods for *Salmonella* spp. (8.7% vs. 0.0%; Fisher's exact test, p = 0.498) or *Campylobacter* spp. (12.0% vs. 0.0%; p = 0.247; Table 3). Likewise, no significant temporal variations were observed when comparing the four independent capture dates for *Salmonella* spp. (p = 0.766) or *Campylobacter* spp. (p = 0.533; Table 4).

Longitudinal Consistency in Recaptures

Two individuals (W[0/73R] and W[C130]) were recaptured once and twice, respectively. In both cases, no parasites were detected in samples from the recaptures and the results for culturing enteropathogenic bacteria remained consistent across all captures.

Discussion

The structural composition of helminth communities in the White Stork is fundamentally governed by the transmission dynamics of parasites with direct and indirect life cycles. The nematode *Syngamus trachea*, for instance, utilises a flexible strategy, employing either a direct faecal-oral route or paratenic hosts such as terrestrial snails and earthworms (Anderson 2000). In contrast, several taxa depend strictly on the consumption of specific intermediate hosts. The cestodes *Choanotaenia infundibulum* and *Raillietina* spp. require the ingestion of arthropods; *C. infundibulum* is well-documented for utilising the housefly (*Musca domestica*) and various beetles as intermediate hosts (Mizikar 2018), while *Raillietina* species typically depend on ants or coleopterans (Atkinson et al. 2008).

More complex multi-host dynamics are observed in the trematode *Chaunocephalus ferox* which involves a primary developmental stage in Planorbidae snails followed by encystment in fish or amphibians (Sitko and Heneberg 2015). Similarly, the nematode *Contracaecum microcephalum* follows a cycle involving aquatic copepods as first intermediate hosts and fish as second intermediate hosts (Moravec 1994). As these heteroxenous parasites rely on trophic transmission, their distribution and prevalence are intrinsically linked to the consumption of specific natural prey acting as intermediate hosts. Although direct dietary data and local intermediate host abundances were not measured in this study, we hypothesise that a behavioural shift towards foraging on anthropogenic refuse in landfills could logically interrupt or weaken these indirect life cycles. By substituting natural prey (such as aquatic snails, fish or terrestrial invertebrates) with human organic waste, White Storks may experience a reduced exposure rate to the infective stages (e.g. metacercariae or cysticercoids) required to complete these parasitic life cycles (Blanco 1996, Sitko and Heneberg 2015). This proposed mechanism provides a plausible explanation for the remarkably low

prevalences recorded in our population for *Chaunocephalus ferox* (15.9%), *Choanotaenia infundibulum* (2.3%) and *Raillietina* spp. (4.5%), as well as the complete temporal stability of these low infection rates across phenological periods (Fisher's exact test, $p \geq 0.677$; Table 3).

Our overall findings strongly support this ecological shift. The species identified in our samples align with previous research on the White Stork (Girisgin et al. 2017, Michalczyk et al. 2020, Meister et al. 2022); however, our estimated prevalences were remarkably low. For instance, we recorded a 15.9% overall prevalence (95% CI: 7.9–29.4%, Wilson score; Table 5) for *C. ferox*, which is drastically lower than the 77.7% reported in necropsy studies by Girisgin et al. (2017). Similarly, our reported prevalence for *S. trachea* (2.3%; 95% CI: 0.4–11.8%; Table 5) is lower than the 5.26% published by Michalczyk et al. (2020). It is important to note that Michalczyk et al. (2020) focused on both nestlings and adults and previous research suggests that prevalence in adults decreases with maturity due to the development of natural resistance (Atkinson et al. 2008). Other studies showing higher prevalences, such as 20.83% (Meister et al. 2022), were based on dead nestlings, further corroborating the hypothesis that acquired immunity in adult individuals — like those comprising our sample — plays a key role in infection rates (Atkinson et al. 2008).

Regarding cestodes, the detection of *C. infundibulum* (2.3%) represents a rare finding, with very few cases reported in White Storks and none previously in Spain, although it agrees with the generally low prevalence of this taxon noted by Michalczyk et al. (2020). A similar scenario was observed for *Raillietina* spp. (4.5%; 95% CI: 1.3–15.1%), which was markedly lower than the 23.07% prevalence reported in other populations (Michalczyk et al. 2020). Crucially, our inferential statistical analyses (Fisher's exact tests) revealed that the low occurrence of all detected helminths remained statistically stable across different capture dates ($p \geq 0.635$; Table 4) and phenological periods ($p \geq 0.677$; Table 3). This lack of temporal and seasonal variation strongly suggests that the reduced exposure to natural intermediate hosts is a constant, year-round phenomenon in this population.

We suggest that any remaining discrepancies with other studies may be attributed to specific geographical distributions or differences in foraging strategies, as the compared populations often exhibit a hybrid foraging behaviour (landfills combined with natural wetlands or croplands).

From a methodological perspective, detailed morphometric analysis initially aimed to establish taxon-specific dimensional ranges. However, due to the low infection intensities recorded (1-4 parasites per infested individual), calculating dimensional variance (Standard Deviation and Standard Error of the Mean) became mathematically impossible or ecologically uninformative for samples where only a single egg was recovered ($n = 1$). Consequently, we emphasise that qualitative morphological characteristics are of paramount importance and must take precedence over strict morphometric dimensions, which frequently display phenotypic plasticity and fall outside established literature ranges. Additionally, a subset of *C. ferox* eggs was found to be empty. While atypical for

fresh faecal samples, prolonged exposure to reagents in the Mini Parasep® system likely induced significant osmotic or chemical stress, triggering premature dehiscence of the operculum — a process previously documented in digenetic trematodes subjected to fixatives or pH variations (Ash and Orihel 2007, Garcia and Procop 2016). The centrifugation steps inherent to such concentrators can also compromise the structural integrity of operculated eggs (Zeeshan et al. 2011).

In terms of protozoa, no parasitic species were detected, aligning with prior studies demonstrating that zoonotic enteroparasitic protozoa, such as *Giardia intestinalis*, are highly uncommon in White Storks (Franssen et al. 2000).

Conversely, our enteric bacterial analysis highlighted a high burden of bacterial exposure. All samples were positive for presumptive *Escherichia coli* (100% prevalence; 95% CI: 92.0–100%; Table 5). Meanwhile, presumptive *Campylobacter* spp. and presumptive *Salmonella* spp. were detected at overall prevalences of 6.8% (95% CI: 2.3–18.2%) and 4.5% (95% CI: 1.3–15.1%), respectively (Table 5). Again, Fisher's exact tests confirmed that the shedding of these enteropathogens did not fluctuate significantly across phenological periods ($p \geq 0.247$; Table 3) or capture dates ($p \geq 0.533$; Table 4), pointing to a chronic and continuous exposure source.

These findings agree with previous research documenting *E. coli* prevalences of 90.9% (Ivan et al. 2025), 85.6% (Camacho et al. 2016) and 100% (Uslu et al. 2024), as well as a 4.4% prevalence for *Salmonella* spp. (Camacho et al. 2016). Studies reporting higher *Salmonella* spp. rates, such as 18.2% (Ivan et al. 2025) and 22% (Martín-Maldonado et al. 2020), were conducted on storks foraging exclusively in landfills. Our lower *Salmonella* prevalence mirrors populations that maintain a mixed foraging strategy. The White Storks in Alcalá de Henares utilise natural ecosystems (wetlands, croplands) alongside landfills, which may dilute the overall exposure to human waste. Regarding *Campylobacter* spp., the higher prevalence (7.6%) reported by Szczepańska et al. (2015) can be explained by their sampling of nestlings; differences in age and immunological maturity likely account for this minor discrepancy compared to our adult cohort.

In summary, it is evident that the utilisation of anthropogenic food sources, particularly landfills, has significantly altered the health profiles of wild bird populations (Pineda-Pampliega et al. 2021). Current research indicates a clear divergence in health status between individuals maintaining natural foraging strategies and those increasingly dependent on municipal waste deposits (Blanco 1996). One of the most critical impacts of landfill foraging is the marked increase in the acquisition of zoonotic bacterial pathogens (Szczepańska et al. 2015, Camacho et al. 2016). The consumption of decaying organic matter facilitates infection by pathogenic bacteria (Bonnedahl and Järhult 2014) and landfills serve as environmental reservoirs for multi-drug-resistant bacteria, exposing wildlife to clinical waste and antibiotic residues (Wu et al. 2017).

Simultaneously, this dietary transition plausibly triggers a complex shift in host-parasite dynamics. We suggest that the substitution of natural prey with municipal waste may act as a functional barrier in the trophic transmission chains of heteroxenous helminths

(Lafferty and Kuris 2005). While this remains a theoretical framework that requires future verification through combined dietary and prey-availability studies, the observed pattern — characterised by a low burden of complex-cycle parasites alongside a high and continuous exposure to enteric bacteria — points towards a significant ecological trade-off. Landfills may offer an abundant caloric influx that relaxes natural foraging constraints, but potentially at the expense of altered parasite assembly rules and increased exposure to anthropogenic pathogens. Ultimately, foraging in landfills represents a profound sanitary trade-off. While it offers short-term caloric abundance that facilitates population growth, it functions as an ecological trap that compromises the long-term physiological integrity and evolutionary fitness of avian populations, underscoring the multifaceted health risks associated with wildlife adaptation to human-modified landscapes.

Conflicts of interest

The authors declare no conflicts of interest. The funders had no role in the design of the study; in the collection, analysis or interpretation of data; in the writing of the manuscript; or in the decision to publish the results.

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This study was approved by Ethics Committee providing us a PROEX code 090.1/22 and the capturing, handling, ring-marking (specific licence for White Stork, code: 530541) and sampling permission from Biodiversity Department of the Regional Government of Madrid allowing us to capture up to 50 White Storks.

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Ethics and security

The project was approved by an Ethics Committee, which authorised the use of animals under code PROEX 090.1/22. Likewise, it was endorsed by the competent authorities of the Autonomous Community of Madrid (Spanish Government), which granted the permits for the capture, marking and sampling of wild animals for subsequent analysis (ring marking licence code: 530541).

Conflicts of interest

The authors have declared that no competing interests exist.

References

- Acha PN, Szyfres B (2001) Zoonosis y enfermedades transmisibles comunes al hombre y a los animales. Vols 1-3, 3rd ed.. Pan American Health Org (PAHO)., Washington, D.C. [ISBN 92-75-31993-6]
- Anderson RC (2000) Nematode parasites of vertebrates: their development and transmission. 2nd ed. CABI Publishing.
- Anderson RC, Chabaud AG, Willmott S (Eds) (2009) Keys to the Nematode Parasites of Vertebrates. Archival volume. CABI Publishing.
- Arizaga J, Resano-Mayor J, Villanúa D, Alonso D, Barbarin J, Herrero A, Lekuona J, Rodríguez R (2018) Importance of artificial stopover sites through avian migration flyways: a landfill-based assessment with the White Stork *Ciconia ciconia*. Ibis 160 (3): 542-553. https://doi.org/10.1111/ibi.12566
- Ash L, Orihel TC (2007) Atlas of Human Parasitology. 5th Ed. American Society for Clinical Pathology Press, Chicago.
- Atkinson C, Thomas N, Hunter DB (Eds) (2008) Parasitic diseases of wild birds. 1st Ed. Wiley-Blackwell.
- Bailenger J (1979) Mechanisms of parasitical concentration in coprology and their practical consequences. American Journal of Medical Technology 41: 65-71.
- Becker DJ, Snedden CE, Altizer S, Hall RJ (2018) Host Dispersal Responses to Resource Supplementation Determine Pathogen Spread in Wildlife Metapopulations. The american naturalist 192 (4). https://doi.org/10.5061/dryad.44dr859
- Bernis F (1981) La población de las cigüeñas españolas: Estudios y tablas de censos, período 1948-1974. Universidad Complutense de Madrid, Cátedra de Zoología de Vertebrados.

- Blanco G (1996) Population Dynamics and Communal Roosting of White Storks Foraging at a Spanish Refuse Dump. Colonial Waterbirds. 19 (2): 273-276.. https://doi.org/10.2307/1521871
- Bolton FJ, Hutchinson DN, Coates D (1984) Blood-Free Selective Medium for Isolation of *Campylobacter jejuni* from Feces. Journal of Clinical Microbiology 19 (2): 169-171. https://doi.org/10.1128/jcm.19.2.169-171.1984
- Bonnedahl J, Järhult J (2014) Antibiotic resistance in wild birds. Upsala Journal of Medical Sciences 119 (2): 113-116. https://doi.org/10.3109/03009734.2014.905663
- Brown L, Cai TT, DasGupta A (2001) Interval Estimation for a Binomial Proportion. Statistical Science 16 (2). https://doi.org/10.1214/ss/1009213286
- Cable J, Barber I, Boag B, Ellison A, Morgan E, Murray K, Pascoe E, Sait S, Wilson A, Booth M (2017) Global change, parasite transmission and disease control: Lessons from ecology. Philosophical Transactions of the Royal Society B: Biological Sciences 372 (1719). https://doi.org/10.1098/rstb.2016.0088
- Camacho MC, Hernández JM, Lima-Barbero JF, Höfle U (2016) Use of wildlife rehabilitation centres in pathogen surveillance: A case study in white storks (*Ciconia ciconia*). Preventive Veterinary Medicine 130: 106-111. https://doi.org/10.1016/j.prevetmed.2016.06.012
- Cardona-Cabrera T, Martínez-Álvarez S, Muela-Trujillo Y, Sánchez-Cano A, Montero JC, Fernández-Gallego JM, Torres C, Höfle U (2025) Sentinel or Disperser? The Role of White Storks (*Ciconia ciconia*) in the Spread of Antibiotic-Resistant Bacteria. Microbiology Research 16 (9). https://doi.org/10.3390/microbiolres16090202
- Centers for Disease Control and Prevention (2019) CDC DPDx — Parasites A–Z / Morphologic comparison & species pages (Ascariasis, Schistosomiasis, etc.). Centers for Disease Control and Prevention (DPDx materials). U.S. Department of Health & Human Services. A review WITHIN URL: https://www.cdc.gov/dpdx/az.html
- Consejo Europeo, Parlamento Europeo (1975) Directiva del Consejo 75/442/CEE. Comisión Europea.
- Dixon B (2021) *Giardia duodenalis* in humans and animals – Transmission and disease. Research in Veterinary Science 135: 283-289. https://doi.org/10.1016/j.rvsc.2020.09.034
- Dorai-Raj S (2022) binom: Binomial Confidence Intervals for Several Parameterizations. R package version 1.1-1.1. URL: https://CRAN.R-project.org/package=binom
- Fisher RA (1922) On the Interpretation of χ 2 from Contingency Tables, and the Calculation of P. Journal of the Royal Statistical Society 85 (1): 87-94. https://doi.org/10.2307/2340521
- Foreyt WJ (2013) Veterinary parasitology reference manual. 5th Ed. Blackwell Publishing, Ames, Iowa, U.S.. [ISBN 978-0-8138-2419-2]
- Franssen FFJ, Hooimeijer J, Blankenstein B, Houwers DJ (2000) Giardiasis in a White Stork in The Netherlands. *The Journal of Wildlife Diseases*, 36(4), 764-76.
- Fuehrer HP, Igel P, Auer H (2011) *Capillaria hepatica* in man-an overview of hepatic capillariosis and spurious infections. Parasitology Research 109 (4): 969-979. https://doi.org/10.1007/s00436-011-2494-1
- Garcia LS, Procop GW (2016) Manual of Commercial Methods in Clinical Microbiology. John Wiley & Sons.. URL: www.wiley.com/go/truant/clinicalmicrobiology
- Georgi JR, Mcculloch CE (1988) Diagnostic Morphometry: Identification of Helminth Eggs by Discriminant Analysis of Morphometric Data. Proceedings of the Helminthological Society of Washington 56 (1): 44-57.

- Georgi JR, Georgi ME (2003) Parasitology for veterinarians. 8th edition. Elsevier, Saunders, New york. [ISBN 978-1-4160-4412-3]
- Gibson D, Jones A, Bray R (2005) Keys to the Trematoda. Vol. 2. CABI and the Natural History Museum (London).
- Gilbert N, Correia R, Silva JP, Pacheco C, Catry I, Atkinson P, Gill J, Aldina A (2016) Are white storks addicted to junk food? Impacts of landfill use on the movement and behaviour of resident white storks (*Ciconia ciconia*) from a partially migratory population. Movement Ecology 4 (1). https://doi.org/10.1186/s40462-016-0070-0
- Girisgin AO, Birlik S, Senlik B, Yildirimhan HS (2017) Intestinal helminths of the white stork (*Ciconia ciconia* Linnaeus 1758) from an inter-route site in Turkey. Acta Veterinaria Hungarica 65 (2): 221-233.
- González-Barrio D (2022) Zoonoses and Wildlife: One Health Approach. Animals 12 (4). https://doi.org/10.3390/ani12040480
- Gray VL, Müller CT, Watkins ID, Lloyd D (2008) Peptones from diverse sources: pivotal determinants of bacterial growth dynamics. Journal of Applied Microbiology 104 (2): 554-565.
- Huang Q, Huang S, Li B, Xiong Y, Kuang W, Xiao S, Yi J, Zhao F, Xiao G (2023) Spatially explicit model of the *Cryptosporidium* and *Giardia* disease burden from surface and ground waters in urban and rural areas of the Three Gorges Reservoir watershed in Chongqing, China. Environmental Science and Pollution Research 30 (13): 37127-37142. https://doi.org/10.1007/s11356-022-24690-2
- Hugot JP, Baujard P, Morand S (2000) Biodiversity in helminths and nematodes as a field of study: an overview. Nematology 3 (3): 199-208.
- International Organization for Standardization (2017) Microbiology of the food chain — Horizontal method for detection and enumeration of *Campylobacter* spp. — Part 1: Detection method (ISO Standard No. 10272-1:2017).
- International Organization for Standardization. (2002) Microbiology of food and animal feeding stuffs — Horizontal method for the detection of Salmonella spp. (ISO Standard No. 6579:2002).
- Ivan AA, Bucur I, Moza AC, Priporeanu-Gritu M, Nichita I, Vizitiu DA, Gros R, Tîrziu E (2025) Isolation and identification of bacterial species in white stork (*Ciconia ciconia*) in Romania. Romanian Journal of Veterinary Sciences 58 (2): 228-236. https://doi.org/10.59463/rjvs.2025.2.05
- Jefatura de Estado (2020) Real Decreto 646/2020, de 7 de julio. Boletín Oficial del Estado 187 URL: https://www.boe.es
- Jenkins E, Simon A, Bachand N, Stephen C (2015) Wildlife parasites in a One Health world. Trends in Parasitology 31 (5): 174-180. https://doi.org/10.1016/j.pt.2015.01.002
- Jorgensen JH, Carroll KC, Funke G, Pfaller MA, Landry ML, Richter SS, Warnock DW (Eds) (2015) Manual of clinical microbiology. 11th Ed. ASM Press, Washington D. C..
- Jourdain E, Gauthier-Clerc M, Bicout DJ, Sabatier† P (2007) Bird Migration Routes and Risk for Pathogen Dispersion into Western Mediterranean Wetlands. Emerging Infectious Diseases 13 (3): 365.
- Kauffmann F (1930) Weitere Erfahrungen mit dem kombinierten Anreicherungsverfahren fiir Salmonellabacillem. Zeitschrift für Hygiene und Infektionskrankheiten 111 (1): 233-246.
- Khalil LF, Jones A, Bray RA (Eds) (1994) Keys to the Cestode Parasites of Vertebrates. CABI, Wallingford, xiii+-751 pp.

- Lafferty KD, Kuris AM (2005) Parasitism and environmental disturbances. In: Thomas F, Renaud F, Guégan J (Eds) Parasitism and ecosystems. Oxford University Press, Oxford, Reino Unido / Nueva York, EE. UU, 113-123 pp.
- Levine ND (1968) Nematode parasites of domestic animals and of man. 2nd Ed. Burgess Publishing Company.
- Loker ES, Hofkin BV (2022) Parasitology: a conceptual approach. CRC Press.
- MacConkey A (1905) Lactose-fermenting bacteria in faeces. Journal of Hygiene 5 (3): 333-379. https://doi.org/10.1017/S002217240000259X
- Malekian M, Shagholian J, Hosseinpour Z (2021) Pathogen Presence in Wild Birds Inhabiting Landfills in Central Iran. EcoHealth 18 (1): 76-83. https://doi.org/10.1007/s10393-021-01516-0
- Martín-Maldonado B, Vega S, Mencía-Gutiérrez A, Lorenzo-Rebenaque L, de Frutos C, González F, Revuelta L, Marin C (2020) Urban birds: An important source of antimicrobial resistant *Salmonella* strains in Central Spain. Comparative Immunology, Microbiology and Infectious Diseases 72 https://doi.org/10.1016/j.cimid.2020.101519
- Martí R, Del Moral JC (2003) Cigüeña blanca, *Ciconia ciconia*. In: Dirección General de Conservacion de la Naturaleza-Sociedad Española de Ornitología. (Ed.) Atlas de las Aves reproductoras de España.
- Meister S, Wenker C, Wyss F, Zühlke I, Berenguer Veiga I, Basso W (2022) Syngamus trachea in free-ranging white stork (*Ciconia ciconia*) nestlings in Switzerland. International Journal for Parasitology: Parasites and Wildlife 18: 76-81. https://doi.org/10.1016/j.ijppaw.2022.04.007
- Michalczyk M, Sokół R, Gesek M, Mączyński M, Będzłowicz D (2020) Internal parasites and associated histopathological changes in deceased white storks from Poland. Belgian Journal of Zoology 150: 71-80. https://doi.org/10.26496/bjz.2020.74
- Mizikar A (2018) Encyclopedia of Parasitology. Springer, Berlin.
- Molina B, del Moral JC (2004) La Cigüeña blanca en España: VI censo internacional. Seguimiento de aves , SEO/Birdlife URL: www.esteller.com
- Moravec F (1994) Parasitic nematodes of freshwater fishes of Europe. 101. Kluwer Academic Publishers, Dordrecht.
- Muller L (1923) Un nouveau milieu d'enrichissement pour la recherche du bacille typhique et des paratyphiques. CR Seances Soc. Biol. Fil 89: 434-437.
- Peig J, Green AJ (2010) The paradigm of body condition: a critical reappraisal of current methods based on mass and length. *Functional Ecology* 24 (6): 1323-1332. [In english]. https://doi.org/10.1111/j.1365-2435.2010.01751.x
- Pineda-Pampliega J, Ramiro Y, Herrera-Dueñas A, Martinez-Haro M, Hernández JM, Aguirre JI, Höfle U (2021) A multidisciplinary approach to the evaluation of the effects of foraging on landfills on white stork nestlings. Science of the Total Environment 775 https://doi.org/10.1016/j.scitotenv.2021.145197
- Poulin R (2011) Evolutionary ecology of parasites. Princeton University Press.
- R Core Team (2024) R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria. URL: https://www.R-project.org/
- Reboredo-Fernández A, Ares-Mazás E, Cacciò S, Gómez-Couso H (2015) Occurrence of *Giardia* and *Cryptosporidium* in wild birds in Galicia (Northwest Spain). Parasitology 142 (7): 917-925. https://doi.org/10.1017/S0031182015000049
- Rocha EJGD, De Almeida Basano S, De Souza MM, Honda ER, De Castro MB, Colodel EM, Silva J, Barros LP, Rodrigues ES, Camargo LMA (2015) Study of the prevalence of

Capillaria hepatica in humans and rodents in an urban area of the city of porto velho, Rondônia, Brazil. Revista do Instituto de Medicina Tropical de Sao Paulo 57 (1): 39-46. https://doi.org/10.1590/S0036-46652015000100006

- Ryan U, Cacciò S (2013) Zoonotic potential of *Giardia*. International Journal for Parasitology 43 (12-13): 943-956. https://doi.org/10.1016/j.ijpara.2013.06.001
- Shen D, Wu X, Hui C, Zhang Y, Long Y (2025) Characterization of pathogen distribution and pathogenicity from landfill site. Journal of Hazardous Materials 484 https://doi.org/10.1016/j.jhazmat.2024.136736
- Sitko J, Heneberg P (2015) Composition, structure and pattern of helminth assemblages associated with central European storks (Ciconiidae). Parasitology International 64 (2): 130-134. https://doi.org/10.1016/j.parint.2014.11.004
- Szczepańska B, Kamiński P, Andrzejewska M, Åšpica D, Kartanas E, Ulrich W, Jerzak L, Kasprzak M, Bocheński M, Klawe J (2015) Prevalence, virulence, and antimicrobial resistance of *Campylobacter jejuni* and *Campylobacter coli* in white stork *Ciconia ciconia* in Poland. Foodborne Pathogens and Disease 12 (1): 24-31. https://doi.org/10.1089/fpd.2014.1793
- Uslu A, Toslak EE, Denizli O, Balevi A, Sayin Z, Erganis O (2024) Microbiological Analysis of Gut Flora and Determination of AntibioticResistance from White Storks (*Ciconia ciconia*) Resting Area during Migration in Türkiye. *Eurasian Journal of Veterinary Sciences*. 40 (3): 107-114. https://doi.org/10.15312/EurasianJVetSci.2024.434
- Viana D, Santamaría L, Figuerola J (2016) Migratory Birds as Global Dispersal Vectors. Trends in Ecology and Evolution 31 (10): 763-775. https://doi.org/10.1016/j.tree.2016.07.005
- Wilson EB (1927) Probable inference, the law of succession, and statistical inference. Journal of the American Statistical Association 22 (158): 209-212. [In english]. URL: https://www.jstor.org/stable/2276774
- World Health Organisation (1992) Métodos básicos de laboratorio en parasitología médica.
- World Health Organisation (2003) Manual de técnicas básicas para un laboratorio de salud.
- World Health Organization (2019) World Health Organization. (2019). Bench aids for the diagnosis of intestinal parasites. 2. World Health Organization.
- Wu D, Huang XH, Sun JZ, Graham D, Xie B (2017) Antibiotic Resistance Genes and Associated Microbial Community Conditions in Aging Landfill Systems. Environmental Science and Technology 51 (21): 12859-12867. https://doi.org/10.1021/acs.est.7b03797
- Zar JH (1999) Biostatistical Analysis. 5. Pearson Education India, Upper Saddle River, New Jersey (USA), 663 pp. [In english]. [ISBN 8177585827, 9788177585827]
- Zeeshan M, Zafar A, Saeed Z, Irfan S, Sobani Z, Shakoor S, Beg MA (2011) Use of "parasep filter fecal concentrator tubes" for the detection of intestinal parasites in stool samples under routine conditions. Indian Journal of Pathology and Microbiology 54 (1): 121-123. https://doi.org/10.4103/0377-4929.77358