Chapter 5
Avian Disease Ecology in the Neotropics

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5.1 Introduction

Globally, birds are the best studied taxonomic group of vertebrates. Over 10,000 bird species have radiated and spread across the Earth's biomes (Avibase; avibase.bsc-eoc.org), and ornithologists have mapped and dated the diversification of all extant bird species worldwide (Jetz et al. 2012). Through ecological studies, ornithologists have uncovered the high taxonomic and functional diversity of birds, their biogeographical patterns and the drivers of these patterns across different regions and scales (Rahbek and Graves 2001; Herzog et al. 2005; Moura et al. 2016; Matuoka et al. 2020; Sol et al. 2020). However, parasite species affecting bird populations and communities have received fewer research efforts, hindering our capacity to manage and conserve bird species. Bird species play a critical role as hosts of a large array of parasite species that affect animal and human health (Dobson et al.

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2008; Nabi et al. 2021). Birds have been reported to harbor as many zoonoses as those found in flying mammals, such as in bats (Order Chiroptera; Mollentze and Streicker 2020). Moreover, birds latitudinal and altitudinal migration movements between wintering and breeding areas are implicated in the geographical spread of major parasitic species (e.g., influenza viruses, West Nile virus; Feare 2010; Winker and Gibson 2010; Lee et al. 2015; Morin et al. 2018; Mine et al. 2019). For example, Avian Influenza viruses (AIVs) are known to successfully complete reassortment processes (i.e., the processes in which gene segments are exchanged between different influenza viruses) in geographical hotspots for viral transport and mixing, where breeding areas are shared between North American and Asian migrant bird species (Morin et al. 2018). In the Beringia region, phylogeographic analyses have shown that viral reassortment has likely occurred between highly pathogenic influenza strains originating in China (e.g., Asian H5N8) and North American influenza lineages that have ultimately spread across the continental United States (Saito et al. 2015).

Avian parasites can have negative effects on their host populations and ecosystems (Møller 2005). Parasites can significantly affect host fitness by changing their behavior and sexual selection and can regulate avian populations by negatively impacting host reproduction (i.e., affecting the fecundity or survival of individuals) (May and Anderson 1978; Møller 2005). Parasites can also mediate intraspecific competition, predator–prey interactions, and food web stability and determine host community structure (Møller and Erritzøe 2000; Navarro 2004; Lafferty et al. 2006; Wood et al. 2007). Moreover, they can exert evolutionary pressures on their hosts' immune systems, promoting greater investment in immune function that produces fitter and more viable host populations (Møller and Erritzøe 2002). For example, avian malaria (genus *Plasmodium*) has produced epizootic die-offs in immunologically naive Hawaiian insular avifauna (LaPointe et al. 2012), causing population declines and significant altitudinal shifts in the distribution of susceptible forest birds (e.g., Hawaii amakihi; *Hemignathus virens*) (Samuel et al. 2011). While such population declines are commonly associated with acute malaria infections that result in increased predation or starvation of avian hosts, chronic infections in continental avifauna produce long-term subclinical effects that can indirectly impair reproductive success (e.g., *Plasmodium*-infected male songbirds have been observed to reduce song frequency, potentially impacting sexual selection) (Gilman et al. 2007; Meza-Montes et al. 2023).

Although parasitic species such as avian malaria and related haemosporidians are constrained to affect avian populations, others have had critical effects on both avian and human populations. Such is the case for the neurotropic and zoonotic West Nile virus (WNV), which has produced massive bird die-offs in highly susceptible hosts (e.g., American crows; *Corvus brachyrhynchos*), and neurological outbreaks of disease in humans across Europe and the United States (LaDeau et al. 2011; George et al. 2015; Hadfield et al. 2019). WNV is capable of infecting over 608 species of birds (Tolsá et al. 2018); however, not all bird species are amplifying hosts for maintaining and transmitting the infection (Komar et al. 2003). Similarly, not all infected avian species are affected by neurologic illness and death (Steele

et al. 2000). The effects of WNV on birds have affected only a few susceptible host species (Kilpatrick and Wheeler 2019), but WNV-associated declines of avian populations have had indirect ecological and health effects on other species. For instance, abundance variation in susceptible WNV species such as American robins promoted shifts in mosquito feeding preferences to humans and other avian species, increasing the prevalence of human disease (Kilpatrick et al. 2006).

Avian hosts can also produce important effects on parasite populations and communities. For example, when infected by vector-borne viruses, bird species can exert selection pressures over parasite genetic populations, removing variants of lower fitness and affecting intrahost viral diversity (Jerzak et al. 2005). This regulation has been observed for WNV, where strong processes of purifying selection can evolutionarily constrain its genetic diversity in bird hosts (Jerzak et al. 2008). On a much broader scale, avian host ecological traits (e.g., body mass, geographic range size, and relative abundance) can influence a parasite's colonization success, reproduction, and contact with susceptible hosts, affecting parasite diversity and community composition (Poulin and Valtonen 2001; Dáttilo et al. 2020). Moreover, the phylogenetic relatedness of hosts can drive the phylogenetic diversity of parasites across spatial scales (Clark and Clegg 2017).

Few study systems are well understood in relation to the effects of the ecology of avian parasites on the ecology of avian host populations (and vice versa). Additionally, the potential for bird parasites to produce spillover events and emerge as novel zoonoses remains unclear. This stems from the fact that, in general, very little is known about the global parasitic faunas of birds. Most studies on the ecology of birds and their parasites have been performed in temperate regions (i.e., Nearctic and Palearctic) (Titley et al. 2017). Accordingly, a gap in knowledge on avian disease ecology remains for other biogeographical regions, such as the Neotropics. This scenario is worrying, as the Neotropical region is home to approximately 30% of the global avifauna and a high number of endemic species (Reboreda et al. 2019). The high diversity of Neotropical bird species provides a diverse set of ecological niches for parasites (Hudson et al. 2006; Poulin 2014). Furthermore, host species diversity has been shown to be a positive driver of parasite species diversity (Dobson et al. 2008; Poulin 2014; Kamiya et al. 2014). Consequently, the Neotropical region is predicted to harbor not only a great proportion of the world's avifauna but also an extraordinary amount of parasite species (Dobson et al. 2008; Santiago-Alarcon and Rojas Soto 2021).

In the context of global change, parasites are most likely to jump across species and disproportionately affect endangered and naïve native avian populations (e.g., Ortega-Guzmán et al. 2022). Yet, some parasite species are also predicted to decline in abundance and geographical range size due to climate change and habitat destruction (Dobson et al. 2008). This will be contingent on the complexity of a parasites' life cycle, their dependence on host population density, their type of transmission, their host specificity, and the geographical range size of their hosts, among other factors (Dobson et al. 2008). Unfortunately, Neotropical species tend to have smaller range sizes than those inhabiting temperate or polar regions (Jetz and Rahbek 2002); hence, it is likely that their population declines will lead to the decline of their

parasitic faunas (Dobson et al. 2008). This is predicted to impact several ecosystem services that parasite species provide, including regulation of host abundance, increase in food web connectance, concentration and removal of pollutants from their hosts, among others (Sures 2004; Møller 2005; Lafferty et al. 2006). Because parasites represent fundamental components of biodiversity, understanding their ecological and evolutionary interactions with their host species will aid to maintain animal, human, and ecosystem health.

In this chapter, we conducted an extensive search in the Web of Science Core Collection for current information regarding parasite ecology in birds across the Neotropical region from 2000 to 2021. The Web of Science Core Collection is a selective and balanced database that uses relevant information from multiple sources (Birkle et al. 2020). Our first search aimed to retrieve studies focused on parasite groups (i.e., virus, bacteria, protozoa, fungi, and disease), birds (i.e., birds, avian, aves, and avifauna), and the Neotropical region (i.e., Neotropic, South America, and Latin America). We excluded all scientific papers that reported avian parasites in captive bird species, review papers, laboratory/experimental studies, and museum collection studies.

Our second search aimed to retrieve studies that show how anthropogenic (i.e., fragmentation, land use, landscape, urban, and habitat perturbation) and ecological (i.e., temperature, latitude, altitude, precipitation, humidity, and climate change) factors can be associated with the prevalence and diversity of each parasite group. According to prior knowledge, anthropogenic and ecological keywords were chosen regarding fundamental factors that influence the prevalence and diversity of parasite species in their hosts, environment, and space. Last, we conducted a third search seeking to retrieve studies that explicitly assessed the relation between anthropogenic/ecological factors and the prevalence, diversity and/or richness of specific parasite genera or species within each parasite group. We selected one parasite species (or genus) per parasite group (i.e., the parasite species or genus that had the highest number of observations in our first search). An avian parasite record was considered to be an independent observation of a parasite genus or species in a particular Neotropical country, locality, and year. Boolean codes for all three searches can be found in Appendix Table 5.4.

5.2   Results

In our first search, we retrieved and assessed 3064 studies. Only papers that contained parasite group and/or species, avian order and/or species and country were selected, leaving a total of 1338 studies. Only 11 of 26 were conducted in Neotropical countries (i.e., Brazil, Peru, Argentina, Colombia, Chile, Ecuador, Mexico, Venezuela, Costa Rica, Dominican Republic, French Guiana, Panama, Guatemala, Bolivia, and Uruguay), and 15 Neotropical countries were not represented (i.e., Belize, El Salvador, Honduras, Nicaragua, Paraguay, Guyana, Suriname, Cuba, Jamaica, Haiti, and Puerto Rico). We found that Brazil is the Neotropical country

that contains the highest number of avian parasite records (553 observations), followed by Colombia (268 observations), Peru (252 observations), Argentina (86 observations), Chile (53 observations), Mexico (28 observations), and Ecuador (27 observations) (Fig. 5.1). In terms of groups of parasites, Brazil and Mexico were the only countries that had parasite records of all five groups considered in this chapter: Virus, Bacteria, Fungi, Protista, and Animalia (i.e., parasitic insects, worms, cestodes, and rotifers) (Fig. 5.1). Brazil mainly had records of parasitic insects (i.e., Arthropoda, Fig. 5.2), but it also had a significant number of protozoa of the phylum Mizozoa (subphylum Apicomplexa) (e.g., avian haemosporidian parasites) (Fig. 5.3) and of viral families such as Orthomyxoviridae, Coronaviridae, and Bornaviridae (e.g., avian coronaviruses, avian influenza, and avian bornaviruses) (Fig. 5.4). Mexico mainly contained records of viral families such as Flaviviridae (e.g., West Nile virus) (Fig. 5.4), platyhelminthes and rotifers (Fig. 5.2), and Apicomplexa protozoa (i.e., avian haemosporidians) (Fig. 5.3).

Chile followed Brazil and Mexico in number of groups of parasites, showing records of parasitic arthropods, nematodes, and platyhelminthes (Fig. 5.2) but also containing records of Apicomplexa protozoa (Fig. 5.3), and of Orthomyxoviridae and Poxviridae viral families (e.g., Avian Pox and Influenza viruses) (Fig. 5.4). Argentina mainly contained records of parasitic platyhelminthes (Fig. 5.2) and of the Orthomyxoviridae, Adenoviridae, Coronaviridae, Paramyxoviridae, and Bunyaviridae families (e.g., avian influenza virus, avian adenovirus, avian infectious bronchitis virus, and avian paramyxovirus) (Fig. 5.4). After Brazil, Colombia contained the most records of parasitic arthropods (Fig. 5.2) and an important number of records of parasitic protozoa (i.e., both Mizozoa and Euglenozoa phyla) (Fig. 5.3). Following Colombia, Peru also contained an important number of records of parasitic arthropods (Fig. 5.2) and showed records of viral families such as Orthomyxoviridae and Adenoviridae (e.g., avian influenza, Siadenoviruses, and Mastadenoviruses) (Fig. 5.4). Brazil and Argentina contained most studies focusing on avian bacteria (Fig. 5.1), mainly the phyla Proteobacteria (e.g., *Escherichia coli*, *Vibrio cholerae*, *Salmonella* spp), Firmicutes (e.g., *Bacillus* spp., *Clostridium* spp.), and Chlamydiota (e.g., *Chlamydia psittaci*) (Fig. 5.5).

Brazil also represented the country with the highest parasite species richness ($S = 243$), followed by Argentina ($S = 58$), Colombia ($S = 48$), Peru ($S = 43$), and Chile ($S = 44$) (Fig. 5.6). These five countries contained most of the studies that we were able to retrieve (Fig. 5.6). Additionally, our first search revealed that almost all avian parasites included in our study (over 800 observations out of 1338 total parasite observations) are being recorded and studied in bird species of the order Passeriformes ($n = 72$ studies), followed by birds of the order Columbiformes ($n = 27$ studies), Charadriiformes ($n = 18$ studies), and Psittaciformes ($n = 17$ studies) (Fig. 5.7). Most records observed in the order Passeriformes belong to parasitic insects of the phylum Arthropoda (Fig. 5.8), followed by Apicomplexa protozoa (Fig. 5.9), and by viral species of the Poxviridae, Flaviviridae, and Bunyaviridae families (Fig. 5.10). Studies that focused on avian bacteria were mostly observed in the orders Psittaciformes, Charadriiformes, and Cathartiformes (Fig. 5.11).
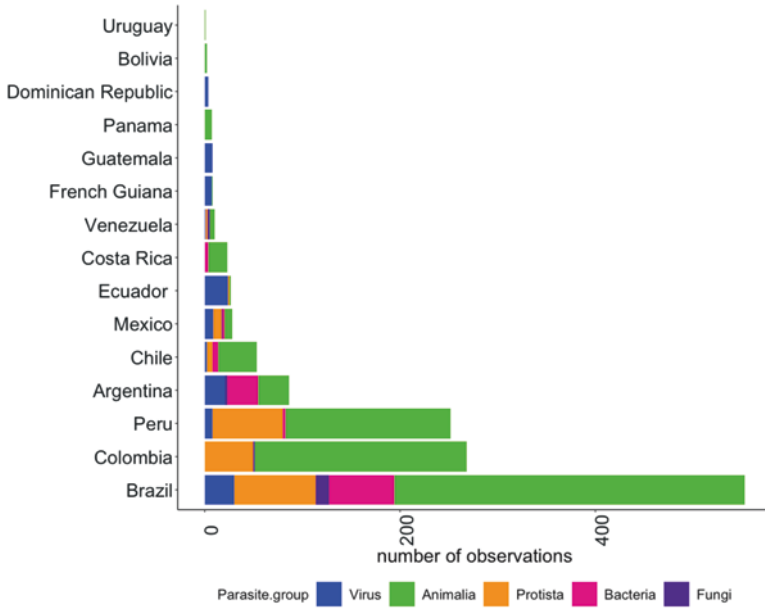
Fig. 5.1 Number of parasite records belonging to the kingdoms Virus, Animalia (i.e., Arthropoda, Nematoda, Platyhelminthes, Rotifera), Protista, Bacteria, and Fungi per studied country in the Neotropical region
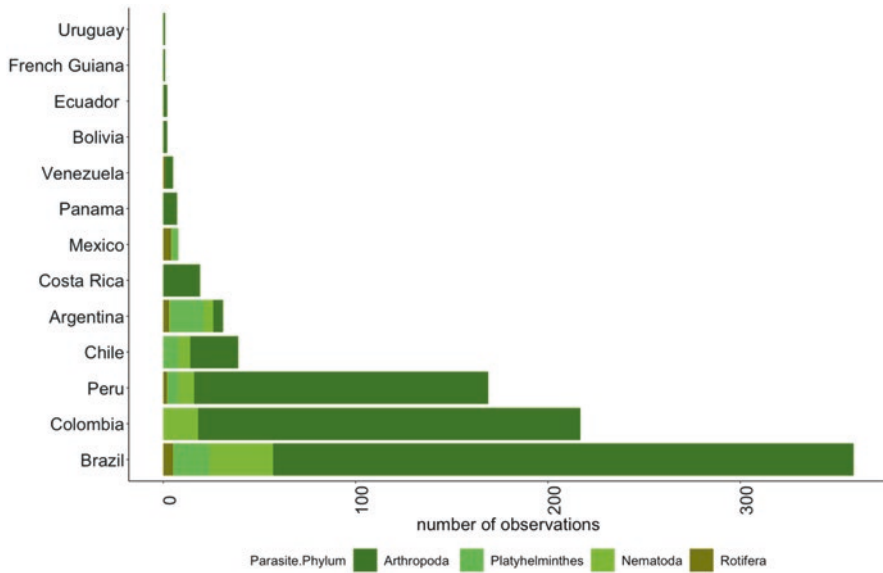

Fig. 5.2 Number of records of avian parasitic arthropods, nematodes, platyhelminthes and rotifers per studied country in the Neotropical region
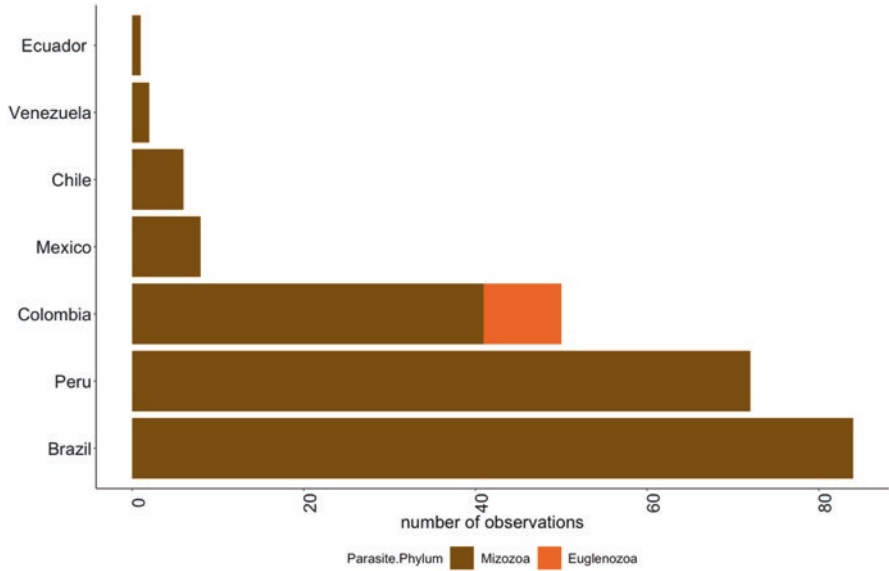
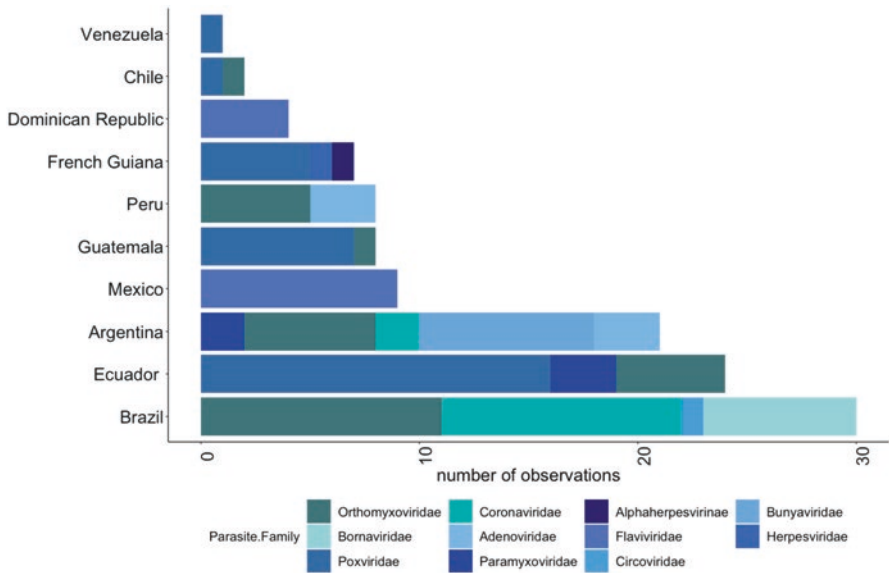**Fig. 5.3** Number of records of avian protozoa per studied country in the Neotropical region

Fig. 5.4 Number of records of viral families per studied country in the Neotropical region
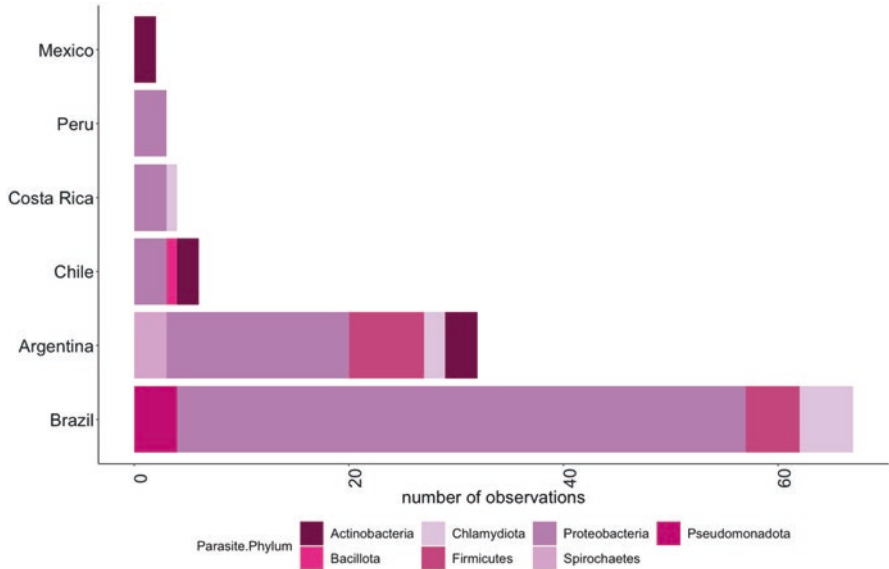
Fig. 5.5 Number of records of bacterial phyla per studied country in the Neotropical region
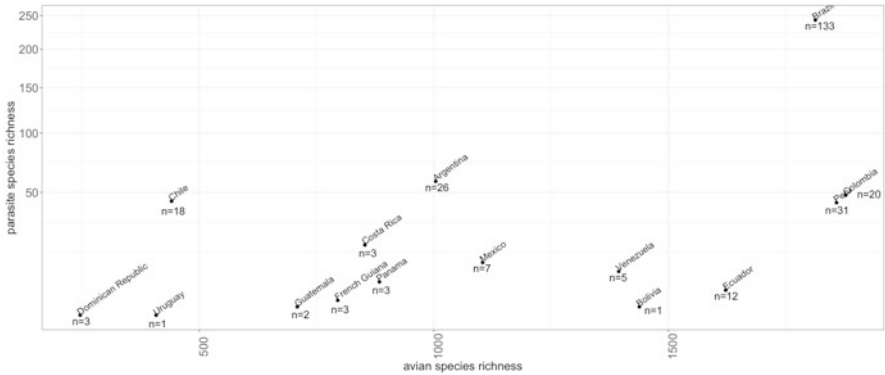

Fig. 5.6 Parasite species richness as a function of avian species richness as analyzed in the Neotropical region. *N* represents the number of studies retrieved from each country. The Y axis was transformed to Sqrt (square root)

In our second search, we retrieved 1100 and 268 studies where anthropogenic and ecological factors, respectively, were studied concerning the prevalence and diversity of each parasite group. However, only in eight studies, parasite prevalence and/or diversity were explicitly assessed (i.e., using mathematical modeling) in relation to anthropogenic (e.g., land use type, distance to urban sites, forest fragment size, etc.) and ecological (i.e., temperature, precipitation, latitude, etc.) factors (Table 5.1). The parasite groups assessed in these eight studies included Apicomplexa protozoa (i.e., avian haemosporidians), avian viruses (i.e., West Nile virus, St Louis
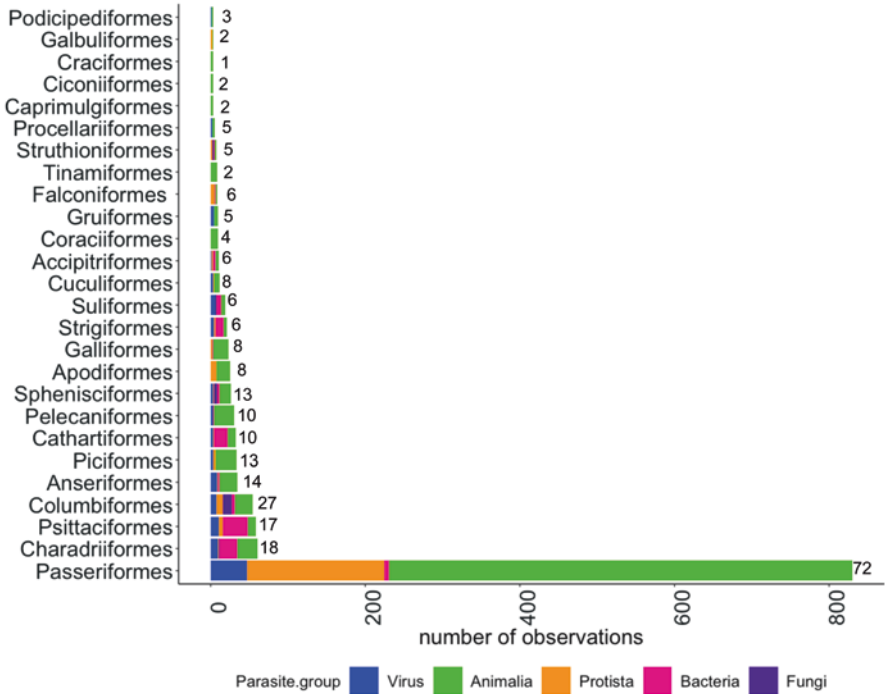
Fig. 5.7 Number of parasite records belonging to the kingdoms Virus, Animalia (i.e., Arthropoda, Nematoda, Platyhelminthes, Rotifera), Protista, Bacteria, and Fungi, per taxonomic bird order. Numbers next to bars represent the number of studies found per bird order
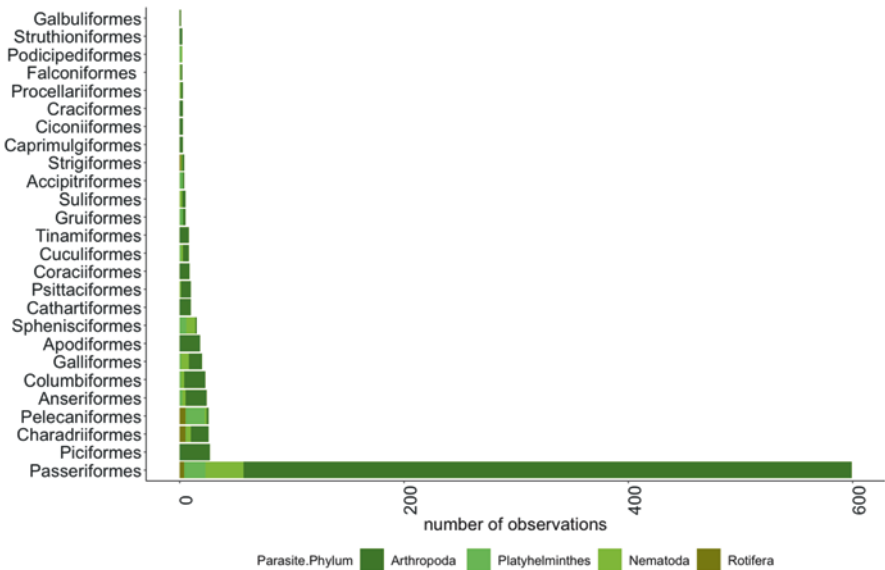
Fig. 5.8 Number of records of avian parasitic arthropods, platyhelminthes, nematodes, and rotifers per taxonomic bird order

Fig. 5.9 Number of records of avian protozoa per taxonomic bird order

Fig. 5.10 Number of records of viral families per taxonomic bird order
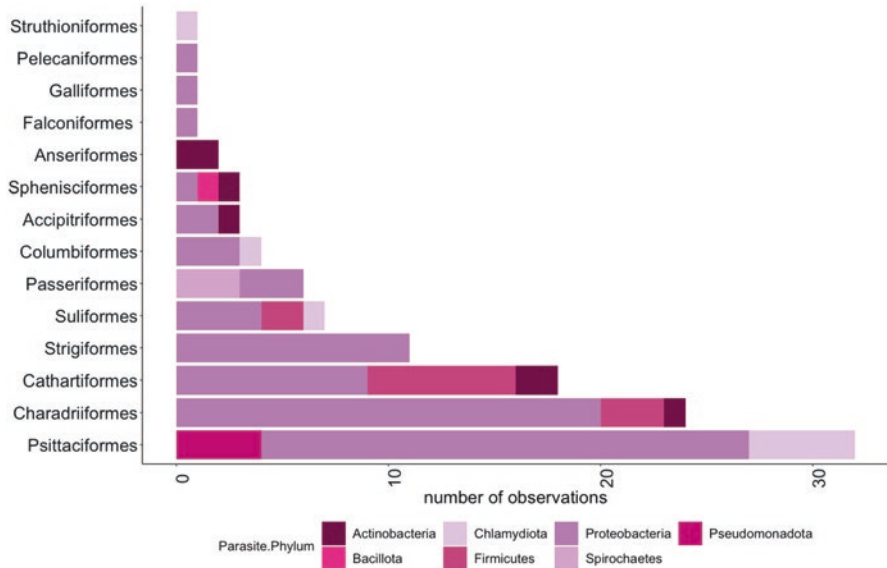
Fig. 5.11 Number of records of bacterial phyla per taxonomic bird order

Encephalitis virus, Avian pox virus), parasitic arthropods (i.e., *Amblyomma* spp.), and helminth communities (Table 5.1).

Finally, our third search retrieved 287 and 62 studies for anthropogenic and ecological factors, respectively. Of these, 12 (Table 5.2) and 17 (Table 5.3) were studies where the prevalence and/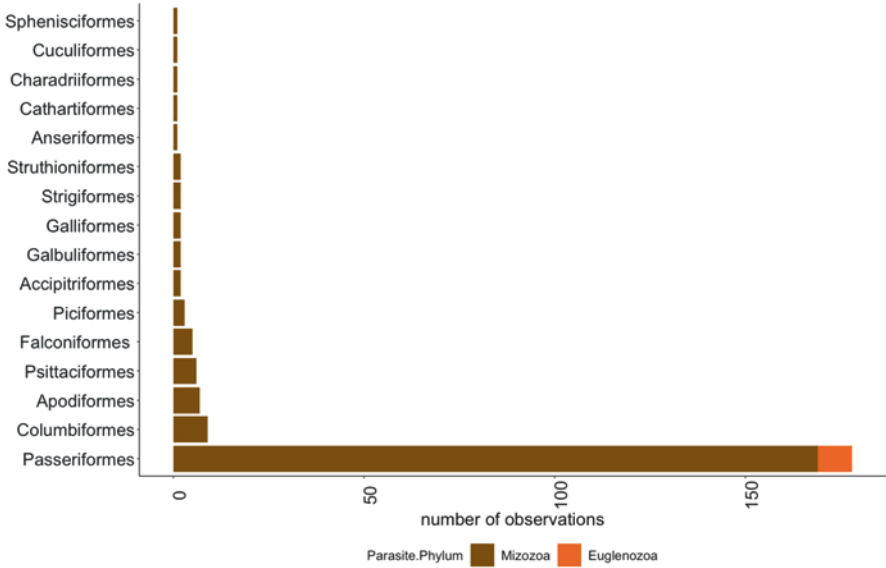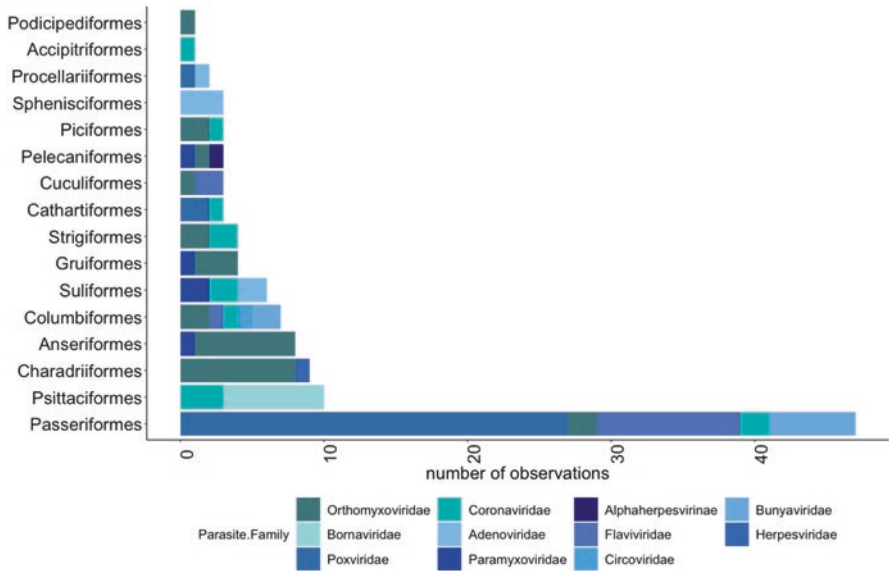or diversity of each parasite genus/species was explicitly assessed for anthropogenic and ecological factors. All studies analyzed avian haemosporidian parasites.

5.3 Discussion

Parasite ecology in birds has gained greater attention in the last two decades. Animal and public health concerns linked to avian disease outbreaks (e.g., highly pathogenic avian flu and West Nile fever) underscore the importance of investigating the ecological and evolutionary relationships between avian parasites, their host communities, and their environments (e.g., Robles-Fernández et al. 2022). Despite this, our research suggests that avian parasite diversity surveys remain rudimentary in most countries of the Neotropical region, and therefore, we have a poor understanding of disease dynamics as a function of ecological and anthropogenic factors.

Our extensive search revealed that within the Neotropics, most avian parasites are being detected in Brazil, Colombia, and Peru. This is not surprising, as these countries represent the three most bird-rich countries in the world (birdlife.org). Several studies have shown that parasite species richness follows host species

Table 5.1 Summary of the selected (second search) studies that explore the association between anthropogenic/ecological factors and parasite prevalence/diversity in Neotropical avifauna

Type of factor	Country	Parasite studied	Avian order	Explanatory variable(s)	Response variable (s)	Effect type	References
Anthropogenic	Brazil	Arthropoda: *Amblyomma* spp.	Passeriformes Columbiformes Coraciiformes	Forest fragment size	Prevalence	Predictive	Ogrzewalska et al. (2011)
	Brazil	Protozoa (Apicomplexa): Haemosporidia (*Plasmodium* sp., *Haemoproteus* sp.)	Passeriformes	Native vegetation cover Distance to urban areas Number of water bodies	Infection probability (molecular prevalence)	Predictive native vegetation increases infection probability	Fecchio et al. (2020)
	Argentina	Virus (Flaviviridae): West Nile virus St. Louis Encephalitis	Passeriformes Piciformes Columbiformes Cuculiformes Accipitriformes	Agricultural area Tree coverage Urban sites Distance to water bodies	Seroprevalence	Predictive	Mansilla et al. (2022)
	Ecuador	Virus (Poxviridae): Avian Pox virus	Passeriformes	Habitat type: Urban Agricultural Undeveloped	Molecular prevalence	Predictive agriculture increases prevalence	Zylberberg et al. (2013)

Ecological		Animalia: (Helminths) Cestoda, Digenea, Nematoda, Acanthocephala	Charadriiformes	Used environments across migratory flyways: Continental Marine	Parasite prevalence, richness and evenness	At component community: predictive At infracommunity: nonpredictive	Capasso et al. (2022)
	Argentina						
	Brazil	Protozoa (Apicomplexa): Haemosporidia (*Plasmodium* sp., *Haemoproteus* sp.)	Passeriformes	Temperature Precipitation	Alpha and beta parasite diversity	Predictive	Lópes et al. (2020)
	Puerto Rico	Protozoa (Apicomplexa): Haemosporidia (*Plasmodium* sp., *Haemoproteus* sp.)	Passeriformes	1- and 10-year time intervals	Lineage composition	1-year interval: predictive negative 10-year interval: predictive positive	Fallon et al. (2004)
	Ecuador	Protozoa (Apicomplexa): Haemosporidia (*Plasmodium* sp., *Haemoproteus* sp.)	Passeriformes	Elevation	Prevalence	Predictive	Escallon et al. (2016)

Table 5.2 Summary of the selected (third search) studies that explore the association between anthropogenic factors and parasite prevalence/diversity in Neotropical avifauna

Country	Avian order	Explanatory variables	Response variables	Effect type	References
Ecuador	NA	Forest fragment size	Prevalence (*Plasmodium*)	Nonpredictive	Sebaio et al. (2010)
		Forest fragment size	Prevalence (*Haemoproteus*)	Nonpredictive	
		Forest dependence	Prevalence (*Plasmodium*)	Predictive	
		Forest dependence	Prevalence (*Haemoproteus*)	Nonpredictive	
Ecuador	Passeriformes	Fragment area	Infection status (Haemosporidian)	Nonpredictive	Rivero de Aguilar et al. (2018)
		Forest quality	Infection status (Haemosporidian)	Nonpredictive	
		Tree cover around fragments	Infection status (Haemosporidian)	Nonpredictive	
		Mist-net location (edge or interior)	Infection status (Haemosporidian)	Nonpredictive	
		Date	Infection status (*Plasmodium*)	Predictive	
		Cover	Infection status (*Haemoproteus*)	Predictive	
Brazil	Passeriformes	Proportion of native vegetation	Probability of infection (Haemosporidian)	Predictive	Fecchio et al. (2021)
		Distance to urban regions	Probability of infection (Haemosporidian)	Nonpredictive	
Brazil	NA	Habitat type (disturbed and undisturbed)	prevalence (Haemosporidian)	Predictive	Fecchio et al. (2021)
		Habitat type (disturbed and undisturbed)	prevalence (*Haemoproteus*)	Predictive	
		Habitat type (disturbed and undisturbed)	Prevalence (*Plasmodium*)	Predictive	
		Habitat type (disturbed and undisturbed)	Diversity (*Plasmodium*)	Predictive	
		Habitat type (disturbed and undisturbed)	Diversity (Haemosporidian)	Predictive	

Table 5.2 (continued)

Country	Avian order	Explanatory variables	Response variables	Effect type	References
México	Passeriformes	Land use types	Lineage richness (Haemosporidian)	Predictive	Hernandez-Lara et al. (2020)
		Land use types	Prevalence (Haemosporidian)	Predictive	
		Land use types	Parasitemia (Haemosporidian)	Nonpredictive	
		Land use types	Aggregation (*Plasmodium*)	Nonpredictive	
Brazil	Passeriformes	Habitat type qué tipos?	Prevalence (Haemosporidian)	Predictive	Belo et al. (2011)
			Diversity (Haemosporidian)	Predictive	
Argentina, Uruguay, Bolivia, Mexico, Brazil, Peru, and Guatemala	Passeriformes	Host species diversity	Prevalence (*Haemoproteus*)	Predictive	Doussang et al. (2021)
Argentina, Uruguay, Bolivia, Mexico, Brazil, Peru, and Guatemala	Passeriformes	Host species diversity	Prevalence (*Plasmodium*)	Predictive	
Guadeloupe and Martinique	Passeriformes	Habitat loss	Prevalence (Haemosporidian)	Predictive	Perez-Rodriguez et al. (2018)
		Habitat fragmentation	Prevalence (Haemosporidian)	Predictive	

Table 5.2 (continued)

Country	Avian order	Explanatory variables	Response variables	Effect type	References
Brazil	NA	Proportion native forest	Prevalence (*Haemoproteus*)	Nonpredictive	Fecchio et al. (2021)
			Taxonomic diversity (*Haemoproteus*)	Nonpredictive	
			Phylogenetic diversity (*Haemoproteus*)	Nonpredictive	
		Host functional diversity	Prevalence (*Haemoproteus*)	Nonpredictive	
			Taxonomic diversity (*Haemoproteus*)	Nonpredictive	
			Phylogenetic diversity (*Haemoproteus*)	Nonpredictive	
		Host phylogenetic diversity	Prevalence (*Haemoproteus*)	Nonpredictive	
			Taxonomic diversity (*Haemoproteus*)	Nonpredictive	
			Phylogenetic diversity (*Haemoproteus*)	Nonpredictive	
		Host taxonomic diversity	Prevalence (*Haemoproteus*)	Nonpredictive	
			Taxonomic diversity (*Haemoproteus*)	Predictive	
			Phylogenetic diversity (*Haemoproteus*)	Nonpredictive	
		Proportion native forest	Prevalence (*Plasmodium*)	Predictive	
			Taxonomic diversity (*Plasmodium*)	Nonpredictive	
			Phylogenetic diversity (*Plasmodium*)	Nonpredictive	

Table 5.2 (continued)

Country	Avian order	Explanatory variables	Response variables	Effect type	References
		Host functional diversity	Prevalence (*Plasmodium*)	Predictive	
			Taxonomic diversity (*Plasmodium*)	Predictive	
			Phylogenetic diversity (*Plasmodium*)	Nonpredictive	
		Host phylogenetic diversity	Prevalence (*Plasmodium*)	Nonpredictive	
			Taxonomic diversity (*Plasmodium*)	Nonpredictive	
			Phylogenetic diversity (*Plasmodium*)	Nonpredictive	
		Host taxonomic diversity	Prevalence (*Plasmodium*)	Nonpredictive	
			Taxonomic diversity (*Plasmodium*)	Predictive	
			Phylogenetic diversity (*Plasmodium*)	Predictive	
		Null model (without any predictor variables)	Prevalence (*Haemoproteus*)	Nonpredictive	
		Null model (without any predictor variables)	Taxonomic diversity (*Haemoproteus*)	Nonpredictive	
		Null model (without any predictor variables)	Phylogenetic diversity (*Haemoproteus*)	Nonpredictive	
Mexico	Passeriformes	Land use types	Prevalence (Haemosporidian)	Predictive	Hernandez-Lara et al. (2017)
		Land use types	Parasitaemia (Haemosporidian)	Predictive	
		Land use types	Aggregation (Haemosporidian)	Nonpredictive	
Brazil	Passeriformes and Columbiformes	Succession stage	Prevalence (Haemosporidian)	Predictive	Ferreira et al. (2017)
			Diversity (Haemosporidian)	Predictive	

Table 5.3 Summary of the selected (third search) studies that explore the association between ecological factors and parasite prevalence/diversity in Neotropical avifauna

Country	Avian order	Explanatory variables	Response variables	Effect type	References
Chile, Costa Rica, Bolivia, Peru, and Argentina	Passeriformes	Altitude	Prevalence (*Haemoproteus*)	Predictive	Doussang. et al. (2021)
			Prevalence (*Plasmodium*)	Predictive	
			Genetic diversity (*Haemoproteus*)	Nonpredictive	
			Genetic diversity (*Plasmodium*)	Nonpredictive	
		Latitude	Prevalence (*Haemoproteus*)	Predictive	
			Prevalence (*Plasmodium*)	Predictive	
			Genetic diversity (*Haemoproteus*)	Nonpredictive	
			Genetic diversity (*Plasmodium*)	Nonpredictive	
Brazil	Apodiformes, Passeriformes, Columbiformes, Accipitriformes, Galbuliformes, Psittaciformes	Humidity	Infection (Haemosporidian)	Predictive	Ferreira de Souza et al. (2020)
Peru	Passeriformes	Altitude	Prevalence (*Plasmodium*)	Predictive	Jones et al. (2013)
Chile	Passeriformes	Latitude	Prevalence (*Plasmodium*)	Predictive	Cuevas et al. (2020)
			Diversity (*Plasmodium*)	Predictive	
			Prevalence (*Leucocytozoon*)	Predictive	
			Diversity (*Leucocytozoon*)	Predictive	
			Prevalence (*Haemoproteus*)	Predictive	
			Diversity (*Haemoproteus*)	Nonpredictive	

(continued)

Table 5.3 (continued)

Country	Avian order	Explanatory variables	Response variables	Effect type	References
Chile	NA	Latitude	Prevalence (*Leucocytozoon*)	Predictive	Merino et al. (2008)
			Prevalence (*Plasmodium*)	Predictive	
			Prevalence (*Haemoproteus*)	Predictive	
			Prevalence (*Haemosporidian*)	Predictive	
			Parasite richness (*Leucocytozoon*)	Nonpredictive	
			Parasite richness (*Plasmodium*)	Nonpredictive	
			Parasite richness (*Haemoproteus*)	Nonpredictive	
			Parasite richness (Haemosporidian)	Nonpredictive	
Ecuador	Passeriformes	Precipitation	Prevalence (Haemosporidian)	Predictive	Cadena-Ortiz et al. (2019)
		Site	Parasitemia (Haemosporidian)	Predictive	
Colombia	Passeriformes	Precipitation	Prevalence (Haemosporidian) *Eucometis penicillata*	Predictive	Pulgarin-R et al. (2018)
			Prevalence (Haemosporidian) *Manacus manacus*	Predictive	
			Diversity (Haemosporidian)	Nonpredictive	
Brazil	Passeriformes and Columbiformes	Temperature	Prevalence (*Plasmodium*)	Predictive	Rodriguez et al. (2021)
			Prevalence (*Haemoproteus*)	Nonpredictive	
		Rainfall	Prevalence (*Plasmodium*)	Nonpredictive	
			Prevalence (*Haemoproteus*)	Nonpredictive	

Table 5.3 (continued)

Country	Avian order	Explanatory variables	Response variables	Effect type	References
Peru	Passeriformes, Caprimulgiformes, Apodiformes, Strigiformes, Cuculiformes, Galbuliformes, Piciformes, Tinamiformes, Trogoniformes, and Columbiformes	Precipitation	Parasite turnover (Haemosporidian)	Predictive	McNew et al. (2021)
		Temperature	Parasite turnover (Haemosporidian)	Nonpredictive	
		Elevation	Parasite turnover (Haemosporidian)	Predictive	
		Net primary production	Parasite turnover (Haemosporidian)	Predictive	
		Host turnover	Parasite turnover (Haemosporidian)	Predictive	
		Precipitation	Taxonomic diversity	Nonpredictive	
		Temperature	Taxonomic diversity	Nonpredictive	
		Elevation	Taxonomic diversity	Predictive	
		Net primary production	Taxonomic diversity	Predictive	
		Host turnover	Taxonomic diversity	Predictive	
Mexico	Columbiformes, Cuculiformes, Apodiformes, Strigiformes, Coraciiformes, Piciformes, Passeriformes	Elevation	Prevalence (*Plasmodium*)	Predictive	Rodríguez-Hernandez et al. (2021)
			Prevalence (*Haemoproteus*)	Predictive	
			Prevalence (*Leucocytozoon*)	Predictive	
			Parasitemia (*Plasmodium*)	Predictive	
			Parasitemia (*Haemoproteus*)	Predictive	
			Parasitemia (*Leucocytozoon*)	Predictive	
			Aggregation (*Plasmodium*)	Predictive	
			Aggregation (*Haemoproteus*)	Predictive	
			Aggregation (*Plasmodium*)	Predictive	
			Prevalence (Haemosporidia)	Predictive	
			Parasitemia (Haemosporidia)	Predictive	
			Aggregation (Haemosporidia)	Predictive	

(continued)

Table 5.3 (continued)

Country	Avian order	Explanatory variables	Response variables	Effect type	References
Mexico	Columbiformes, Cuculiformes, Apodiformes, Strigiformes, Coraciiformes, Piciformes, Passeriformes	Temperature	Lineage community composition	Predictive	Alvarez-Medizabal et al. (2021)
		Precipitation	Lineage community composition	Predictive	
Brazil	Passeriformes	Number of water bodies	Probability of infection (Haemosporidian)	Nonpredictive	Fecchio et al. (2021)
		Precipitation	Probability of infection (Haemosporidian)	Predictive	
		Temperature	Probability of infection (Haemosporidian)	Predictive	
Mexico	Passeriformes	Seasonality	Prevalence (Haemosporidia)	Predictive	Hernandez-Lara et al. (2020)
			Prevalence (*Haemoproteus*)	Predictive	
			Prevalence (*Plasmodium*)	Predictive	
			Parasitemia (Haemosporidia)	Predictive	
			Aggregation (Haemosporidia)	Predictive	
Brazil	NA	Temperature	Prevalence (*Plasmodium*)	Nonpredictive	Fecchio et al. (2021)
			Taxonomic diversity (*Plasmodium*)	Nonpredictive	
			Phylogenetic diversity (*Plasmodium*)	Nonpredictive	
			Prevalence (*Haemoproteus*)	Nonpredictive	
			Taxonomic diversity (*Haemoproteus*)	Nonpredictive	
			Phylogenetic diversity (*Haemoproteus*)	Nonpredictive	
Mexico	Passeriformes	Seasonality	Prevalence	Predictive	Hernandez-Lara et al. (2017)
			Parasitaemia	Predictive	
			Aggregation	Nonpredictive	

Table 5.3 (continued)

Country	Avian order	Explanatory variables	Response variables	Effect type	References
Brazil	Passeriformes and Columbiformes	Seasonality	Prevalence	Nonpredictive	Ferrerira et al. (2017)
Ecuador	Passeriformes	Seasonality	Infection status (*Plasmodium*)	Nonpredictive	Rivero de Aguilar et al. (2018)

richness (Dobson et al. 2008; Poulin 2014; Kamiya et al. 2014). Consequently, these three bird-rich countries offer a high diversity of hosts for parasites to occupy, increasing the likelihood of parasite detection. Most observations for Brazil, Colombia, and Peru are of parasitic Arthropoda, which are mainly represented by chewing lice of the genus *Myrsidea* sp. Avian chewing lice are ubiquitous and highly diverse ectoparasites of birds in Neotropical regions (Soto-Madrid et al. 2020). Apart from being studied for their relevance as members of Neotropical communities, arthropods such as chewing lice are methodologically more straightforward to detect than other groups of parasites (e.g., viruses). We suggest that their vast diversity, direct detection, and usefulness as parasite models to understand ecological interactions explains the high number of arthropod records observed in Brazil, Colombia, and Peru.

Following arthropod insects, avian protozoa comprised the next best-studied parasite group in the Neotropics. Brazil, Peru, Colombia, Mexico, and Chile contained most avian protozoa records. Phylum Mizozoa (subphylum Apicomplexa) represented most of the observations, mainly including avian haemosporidian parasites (*Plasmodium* sp., *Haemoproteus* sp., and *Leucocytozoon* sp.). Apicomplexan parasites such as avian haemosporidians have become a model system for ecological and evolutionary studies of bird–parasite interactions (e.g., see chapters in Santiago-Alarcon and Marzal 2020b). Their importance for avian conservation, worldwide distribution, and high probability of detection in blood smears and PCR molecular samples has contributed to more scientists dedicating their research to this highly diverse parasite system (Valkiūnas and Atkinson 2020; Bensch and Hellgren 2020). Although much effort to detect and understand avian haemosporidian diversity in tropical settings has taken place in the last decade, most of their studies have been performed in temperate regions (Santiago-Alarcon and Marzal 2020a; Chapa-Vargas et al. 2020). Moreover, haemosporidian haplotype sequence divergence has suggested that haemosporidian genetic richness could match worldwide avian species richness (i.e., 10,000 bird species) (Bensch et al. 2004; Bensch and Hellgren 2020). Consequently, detection of avian haemosporidian diversity will help to understand complex antagonistic interactions – particularly of vector-borne parasites – and should be prioritized within Neotropical settings considered hotspots for host and parasite biodiversity (Santiago-Alarcon and Rojas Soto 2021).

After avian protozoa, avian viruses were the next best-studied group. In particular, we found that the Poxviridae, Orthomyxoviridae, Flaviviridae, and Coronaviridae families have been the most studied avian viruses in Neotropical countries. Ecuador, French Guiana, Guatemala, Chile, and Venezuela contained all studies focusing on avian pox virus. Avian pox viruses have been observed in over 350 species of birds (Williams et al. 2021). Because their incidence has increased over the last 10 years, avian pox has been considered an emerging viral disease (Alehegn et al. 2014), mainly affecting songbirds, birds of prey, marine birds, and poultry within tropical regions. A high prevalence of the disease has been observed in remote populations (e.g., Galapagos Islands), suggesting a threat to naive endemic insular avifauna in the Neotropical region (Williams et al. 2021). In wild continental birds, pox prevalence has been highly variable, and information regarding host specificity, strain virulence, and strain diversity remains elusive (Williams et al. 2021). In addition to finding many observations on avian pox viruses, our results showed avian influenza viruses (AIV) as the second most studied avian viruses in Neotropical countries. Brazil, Argentina, Peru, Ecuador, Chile, and Guatemala contained most AIV observations. Research efforts have been conducted worldwide to better understand the ecology of AIVs in wild birds (Wille and Barr 2022). Today, we know that highly pathogenic AIVs (HPAIVs) circulate on all continents except Australia and Antarctica (Willie and Barr 2022). Moreover, HPAIVs have caused recent outbreaks in South America, killing over 22,000 wild birds, mainly Peruvian pelicans (*Pelecanus thagusI*) and boobies (*Sula variegata*) (Gamarra-Toledo et al. 2023). Apart from these species, HPAIV has affected the near-threatened Guanay cormorant (*Leucocarbo bougainvillii*) across the coastline of Peru and has been suggested to be a potential threat to scavenger species such as the Andean condor (*Vultur gryphus*) (Gamarra-Toledo et al. 2023). Researchers are calling for epidemiological surveillance to better understand the extent to which such outbreaks could progress.

Following avian influenza, West Nile virus was the third most studied avian virus in the Neotropical region. Mexico and the Dominican Republic contained all of the records. WNV belongs to the Flavivirus genus, and its transmission cycle involves mosquitoes as vectors and wild birds as their vertebrate hosts. For more than 20 years, this virus has represented a threat to bird populations with persistent impacts on some wild bird species in North America (Passeriformes comprises the order with more susceptible avian species for this virus) and on human populations producing outbreaks of neurological disease (LaDeau et al. 2007; George et al. 2015). However, despite its importance for bird conservation, human health, and evidence suggesting migratory birds are important carriers of this virus, WNV is poorly known in the Neotropical region. A worldwide study showed that Mexico, Guatemala, and Argentina are countries with serological and molecular evidence in wild birds (Tolsá et al. 2018). However, WNV has already been classified as a neglected tropical disease because funding and research efforts have declined over time (Ronca et al. 2021).

Regarding bacteria, we found few records, even though birds are recognized as hosts of many bacterial species relevant to avian and human health (Reed 2002; Benskin et al. 2009). *Escherichia coli* was the best-represented bacterial species in

our search and was studied in Brazil, Chile, Costa Rica, and Argentina mainly in Charadriiformes, Psittaciformes, and Sphenisciformes hosts. In the Neotropics, the study of *E. coli* should be a priority because it has been associated with mass die-offs of various wild bird species, which are suggested to act as carriers of multidrug-resistant *E. coli* (Reed 2002; Smith et al. 2020). The genus *Salmonella* was the second most studied bacteria in the Neotropics, mainly in Peru and Argentina in the Charadriiformes and Passeriformes. Various studies have shown that this genus, specifically *Salmonella typhimurium,* is commonly isolated in intestinal samples of wild birds and has been associated with mass mortality events (Smith et al. 2020).

Fungi was the least studied parasite group in the Neotropics (*n* = 19). The best-represented species were *Cryptococcus neoformans* and *Aspergillus* spp. *Cryptococcus neoformans* was identified infecting the order Columbiformes (pigeons and doves) in Brazil, Venezuela, and Colombia. *Cryptococcus* spp. have been found in avian orders such as Passeriformes, Anseriformes, Accipitriformes, Apterygiformes, Psittaciformes, and Columbiformes, with wide variability in susceptibility between bird species (Johnston et al. 2016). Additionally, *Aspergillus* spp. were identified in samples of Sphenisciformes, Suliformes, and Charadriiformes in Brazil, Argentina, and Mexico, respectively. At the parasite species level, we also recorded *Aspergillus fumigatus*, a common parasite among wild and domestic birds, with a prevalence of approximately 95% (Arné et al. 2021).

5.3.1 Parasite Dynamics as a Function of Anthropogenic and Ecological Factors

Understanding parasite infection patterns, their diversity and distribution in relation to environmental, spatial, and anthropogenic factors remains a challenge for infectious disease ecology. Our synthesis found that the main anthropogenic variables associated to prevalence and diversity of avian parasites are land-use or habitat type, habitat fragmentation or loss, the proportion of native vegetation, and habitat-associated host diversity in its taxonomic, phylogenetic, and functional forms. These variables often relate differently to each parasite system, sometimes producing opposing trends even within the same parasite taxa. For example, the prevalence of avian pox viruses has increased with agricultural intensification (Zylberberg et al. 2013). In contrast, the probability of haemosporidian parasite infection has increased with higher proportion of native vegetation cover (Fecchio et al. 2020) or decrease with advanced stages of forest succession (Ferreira Junior et al. 2017). In the case of avian haemosporidians, parasite genera can produce these contrasting results because each Haemosporidian genus is transmitted by different Diptera families and species whose reproduction and development depend on different microclimatic conditions (Rodríguez-Hernández et al. 2021). For instance, the *Plasmodium* genus might be favored by anthropogenic transformation, while the *Haemoproteus* genus might be more prevalent in preserved forests (Hernández-Lara et al. 2020).

This shows how the response of parasites to anthropogenic drivers of prevalence varies spatially and may be contingent on the host–parasite system.

Habitat-associated host diversity has also been related to contrasting infection patterns and parasite diversity in systems such as avian haemosporidians. Increased host functional diversity in preserved remnants of the Brazilian Atlantic Forest decreased *Plasmodium* lineage diversity (Fecchio et al. 2021). However, high host taxonomic diversity within the same locations increased *Plasmodium* taxonomic lineage diversity but decreased *Plasmodium* phylogenetic lineage diversity (i.e., more diverse avian communities in preserved remnants harbored more taxonomically diverse but phylogenetically clustered parasite assemblages). Apparently, different facets of avian host diversity (e.g., functional, taxonomic, and phylogenetic) can produce differential effects over the taxonomic and phylogenetic components of haemosporidian parasite diversity, underscoring the complexity and relevance of assessing the spatial patterns of host diversity in all of its facets as drivers of parasite diversity and distribution.

Beyond the diverse effects of anthropogenic factors, the prevalence and diversity of avian parasites can be driven by ecological factors (i.e., environmental and spatial factors). We found that latitude, altitude, temperature, precipitation, humidity, and seasonality are the most studied ecological drivers of parasite prevalence and diversity in the Neotropics. For instance, the inverse relationship between altitude and temperature has been associated with the differential distribution of avian haemosporidian genera across elevational gradients in different settings (Zamora-Vilchis et al. 2012; van Rooyen et al. 2013; Álvarez-Mendizábal et al. 2021). Similarly, an inverse latitudinal diversity gradient has explained the infection probability and phylogenetic diversity of *Leucocytozoon* parasites in New World birds (Fecchio et al. 2019). Moreover, within Neotropical countries such as Mexico and Brazil, haemosporidian parasite prevalence, diversity, and community composition have been explained by temperature, precipitation, humidity, and seasonality (Hernández-Lara et al. 2017; Hernández-Lara et al. 2020; Ferreira de Souza et al. 2020). In the Caatinga of Brazil, there was a high frequency of hemoparasites in birds due to high levels of humidity and rainfall (Ferreira de Souza et al. 2020). Similarly, contrasting patterns in prevalence among bird species were reported in Colombia (e.g., gray-headed tanagers, *Eucometis penicillata*, exhibited higher prevalence rates in locations with less precipitation, while white-bearded manakins, *Manacus manacus,* showed higher prevalence in locations with high precipitation) (Pulgarín-R et al. 2018). In Mexico, increased infection rates have been associated with wet seasons, where there is an increase in the abundance of mosquito vectors, and coincide with avian host breeding seasons, where reproduction generates a trade-off between immune function and reproductive output (Hernández-Lara et al. 2020).

Environmental and spatial heterogeneity can structure the distribution and diversity of avian parasites and their hosts and vectors. However, a wide variation in responses to the heterogeneity in ecological factors can be observed for most host–parasite systems. The relative importance of environmental versus spatial drivers of parasite infection and diversity can also depend on the scale of the study (e.g.,

microclimatic variables can explain parasite distribution patterns at local-landscape scales, while geographic barriers or latitude could be more important drivers at regional and global scales). Consequently, it is fundamental to continue studying avian host–parasite systems in regions that provide this type of environmental heterogeneity (i.e., tropical and subtropical) at different spatiotemporal scales to better understand the relative importance of such drivers for specific parasite systems.

5.4   Conclusions and Synthesis

Our study showed that arthropod insects, protozoa, and viruses are the main parasite groups being studied in birds across the Neotropical region. Although bacteria and fungi have been less studied, the potential for these parasites to produce diseases in avian populations should not be overlooked. Most of the published information regarding parasite ecology in Neotropical birds has been directed to the order Passeriformes, mainly because of its high number of species and because there is a sampling bias for passerine birds when using understory mist nets. This has allowed in-depth knowledge of parasite dynamics within some passerine populations (e.g., West Nile virus infecting American robins); however, the diversity and distribution of avian parasites among nonpasserine birds remains scarce, and it is an area of opportunity to advance the field. Our data showed that parasite species richness was higher in Brazil, Argentina, Colombia, Peru, and Chile than in the other analyzed Neotropical countries. This was certainly associated with the high bird species richness that these countries harbor, and it should also be associated with the high number of studies that we retrieved for those countries. The low parasite and bird species richness that was observed for countries, such as the Dominican Republic, Guatemala, Bolivia, and Uruguay, is likely explained by the few studies that we found, suggesting that parasite surveillance and scientific publication in these countries is insufficient. The lack of studies focusing on avian disease ecology in Neotropical islands (e.g., Cuba, Jamaica, Haiti, Puerto Rico; but see (Parker 2018) for synthesis of disease ecology research in the Galápagos Islands) underscores the need to focus our scientific research on parasite dynamics of endemic insular avifauna.

   We identified several anthropogenic and ecological factors affecting parasite prevalence and diversity across space. However, our synthesis did not include all relevant factors that could potentially drive parasite diversity and distribution (e.g., host-associated factors such as life-history traits). Although we showed that the diversity and distribution of some Neotropical avian parasites have been thoroughly assessed concerning anthropogenic and ecological drivers (e.g., avian haemosporidians), most parasite systems remain understudied in the Neotropical region (i.e., their presence in avian hosts is not assessed as a function of relevant drivers of disease), and their diversity is yet to be uncovered (Fernandez Correa et al. 2019). We underscore the large knowledge gap when considering the temporal aspect of

disease ecology (e.g., Rubio et al. 2017). Future research efforts should focus on determining how the temporal component (e.g., variation across the day and across seasons or months) (Castro-Arellano et al. 2010) affects the ecological dynamics of host-parasite systems.

Appendix A: Supplementary Data

Table 5.4 Boolean codes used for our first, second, and third searches

First search	
General overview of parasite groups	((virus* OR bacteria* OR protozoa* OR *parasite* OR fungi* OR disease*) AND (birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) NOT (review* OR laboratory OR experiment*) NOT (zoos OR captivity OR domestic OR poultry))
Second search	
Anthropogenic factors/ parasite groups	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (fragmentation OR land use OR landscape OR urban*OR habitat perturbation) NOT (review* OR laboratory OR experiment*) NOT (zoos OR captivity OR domestic OR poultry) AND (**virus***)
	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (fragmentation OR land use OR landscape OR urban*OR habitat perturbation) NOT (review* OR laboratory OR experiment*) NOT (zoos OR captivity OR domestic OR poultry) AND (**bacteria***)
	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (fragmentation OR land use OR landscape OR urban*OR habitat perturbation) NOT (review* OR laboratory OR experiment*) NOT (zoos OR captivity OR domestic OR poultry) AND (**fungi*** OR **fungus**)
	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (fragmentation OR land use OR landscape OR urban*OR habitat perturbation) NOT (review* OR laboratory OR experiment*) NOT (zoos OR captivity OR domestic OR poultry) AND (**protista** OR **protozoa***)
	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (fragmentation OR land use OR landscape OR urban*OR habitat perturbation) NOT (review* OR laboratory OR experiment*) NOT (zoos OR captivity OR domestic OR poultry) AND (**Arthropoda** OR **Platyhelminthes** OR **Nematoda** OR **Rotifera**)

(continued)

Table 5.4 (continued)

Ecological factors/ parasite groups	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (temperature OR latitude OR altitude OR precipitation OR humidity OR climate change) NOT (review* OR laboratory OR experiment*) NOT (zoos OR captivity OR domestic OR poultry) AND (**virus***)
	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (temperature OR latitude OR altitude OR precipitation OR humidity OR climate change) NOT (review* OR laboratory OR experiment*) NOT (zoos OR captivity OR domestic OR poultry) AND (**bacteria***)
	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (temperature OR latitude OR altitude OR precipitation OR humidity OR climate change) NOT (review* OR laboratory OR experiment*) NOT (zoos OR captivity OR domestic OR poultry) AND (**fungi*** OR **fungus**)
	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (temperature OR latitude OR altitude OR precipitation OR humidity OR climate change) NOT (review* OR laboratory OR experiment*) NOT (zoos OR captivity OR domestic OR poultry) AND (**protista** OR **protozoa***)
	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (temperature OR latitude OR altitude OR precipitation OR humidity OR climate change) NOT (review* OR laboratory OR experiment*) NOT (zoos OR captivity OR domestic OR poultry) AND (**Arthropoda** OR **Platyhelminthes** OR **Nematoda** OR **Rotifera**)
Third search	
Anthropogenic factors/ prevalence and diversity/ parasite genus or species	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (fragmentation OR land use OR landscape OR urban*OR habitat perturbation) AND (**presence** OR **prevalence** OR **diversity** OR **richness**) AND (**Avian pox virus**)
	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (fragmentation OR land use OR landscape OR urban*OR habitat perturbation) AND (**presence** OR **prevalence** OR **diversity** OR **richness**) AND (**Escherichia coli**)
	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (fragmentation OR land use OR landscape OR urban*OR habitat perturbation) AND (**presence** OR **prevalence** OR **diversity** OR **richness**) AND (**Cryptococcus neoformans**)
	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (fragmentation OR land use OR landscape OR urban*OR habitat perturbation) AND (presence OR prevalence OR diversity OR richness) AND (**Plasmodium sp**)
	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (fragmentation OR land use OR landscape OR urban*OR habitat perturbation) AND (presence OR prevalence OR diversity OR richness) AND (**Myrsidea sp**)

(continued)

Table 5.4 (continued)

Ecological factors/ prevalence and diversity/ parasite genus or species	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (temperature OR latitude OR altitude OR precipitation OR humidity OR climate change) AND (presence OR prevalence OR diversity OR richness) AND (**Avian pox virus**)
	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (temperature OR latitude OR altitude OR precipitation OR humidity OR climate change) AND (presence OR prevalence OR diversity OR richness) AND (**Escherichia coli**)
	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (temperature OR latitude OR altitude OR precipitation OR humidity OR climate change) AND (presence OR prevalence OR diversity OR richness) AND (**Cryptococcus neoformans**)
	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (temperature OR latitude OR altitude OR precipitation OR humidity OR climate change) AND (presence OR prevalence OR diversity OR richness) AND (**Plasmodium sp**)
	(birds OR avian OR aves OR avifauna) AND (neotropic* OR South America OR Latin America) AND (temperature OR latitude OR altitude OR precipitation OR humidity OR climate change) AND (presence OR prevalence OR diversity OR richness) AND (**Myrsidea sp**)

References

Alehegn E, Mersha C, Mengesha D (2014) A systematic review of serological and clinicopathological features and associated risk factors of avian pox. Br J Poult Sci 3(3):78–87. https://doi.org/10.20372/NADRE:1547201106.08

Álvarez-Mendizábal P, Villalobos F, Rodríguez-Hernández K, Hernández-Lara C, Rico-Chávez O, Suzán G, Chapa-Vargas L, Santiago-Alarcon D (2021) Metacommunity structure reveals that temperature affects the landscape compositional patterns of avian malaria and related haemosporidian parasites across elevations. Acta Oecol 113(November):103789. https://doi.org/10.1016/j.actao.2021.103789

Arné P, Risco-Castillo V, Jouvion G, Le Barzic C, Guillot J (2021) Aspergillosis in Wild Birds. J Fungi (Basel). 7(3):241. https://doi.org/10.3390/jof7030241. PMID: 33807065; PMCID: PMC8004873.

Belo NO, Pinheiro RT, Reis ES, Ricklefs RE, Braga ÉM (2011) Correction: Prevalence and lineage diversity of avian haemosporidians from three distinct cerrado habitats in Brazil. PLoS ONE 6(4). https://doi.org/10.1371/annotation/993592b8-5719-45b1-814e-2052318532e7

Bensch S, Hellgren O (2020) The use of molecular methods in studies of avian haemosporidians. In: Santiago-Alarcon D, Marzal A (eds) Avian malaria and related parasites in the tropics. Springer, Cham, pp 113–135. https://doi.org/10.1007/978-3-030-51633-8_4

Bensch S, Péarez-Tris J, Waldenström J, Hellgren O (2004) Linkage between nuclear and mitochondrial dna sequences in avian malaria parasites: multiple cases of cryptic speciation? Evolution 58(7):1617–1621. https://doi.org/10.1111/j.0014-3820.2004.tb01742.x

Benskin CM, Wilson K, Jones K, Hartley IR (2009) Bacterial pathogens in wild birds: a review of the frequency and effects of infection. Biol Rev Camb Philos Soc 84(3):349–373. https://doi.org/10.1111/j.1469-185X.2008.00076.x. Epub Apr 29. PMID: 19438430.

Birkle C, Pendlebury DA, Schnell J, Adams J (2020) Web of science as a data source for research on scientific and scholarly activity. Quant Sci Stud 1(1):363–376. https://doi.org/10.1162/qss_a_00018

Cadena-Ortiz H, Mantilla JS, de Aguilar JR, Flores D, Bahamonde D, Matta NE, Bonaccorso E (2019) Avian haemosporidian infections in rufous-collared sparrows in an Andean dry forest: diversity and factors related to prevalence and parasitaemia. Parasitology. 146(6):765–773. https://doi.org/10.1017/S0031182018002081. Epub 2018 Dec 26. Erratum in: Parasitology. 2022 Sep;149(11):1521–1522. PMID: 30585147.

Capasso S, D'Amico VL, Minardi G et al (2022) The helminth community structure as an indicator of habitat use: the case of the Baird's Sandpiper (Calidris bairdii) and the White-Rumped Sandpiper (Calidris fuscicollis) on their non-breeding grounds in Patagonia. Polar Biol 45, 297–307 https://doi.org/10.1007/s00300-021-02990-6

Castro-Arellano I, Lacher TE, Willig MR, Rangel TF (2010) Assessment of assemblage-wide temporal niche segregation using null models: assemblage-wide temporal niche overlap assessment. Methods Ecol Evol 1(3):311–318. https://doi.org/10.1111/j.2041-210X.2010.00031.x

Chapa-Vargas L, Matta NE, Merino S (2020) Effects of ecological gradients on tropical avian hemoparasites. In: Santiago-Alarcon D, Marzal A (eds) Avian malaria and related parasites in the tropics. Springer, Cham, pp 349–377. https://doi.org/10.1007/978-3-030-51633-8_10

Clark NJ, Clegg SM (2017) Integrating phylogenetic and ecological distances reveals new insights into parasite host specificity. Mol Ecol 26(11):3074–3086. https://doi.org/10.1111/mec.14101

Cuevas E, Vianna JA, Botero-Delgadillo E, Doussang D, González-Acuña D, Barroso O, Rozzi R, Vásquez RA, Quirici V (2020) Latitudinal gradients of haemosporidian parasites: prevalence, diversity and drivers of infection in the Thorn-tailed Rayadito (Aphrastura spinicauda). Int J Parasitol Parasites Wildl. 11:1–1. https://doi.org/10.1016/j.ijppaw.2019.11.002

Dáttilo W, Barrozo-Chávez N, Lira-Noriega A, Guevara R, Villalobos F, Santiago-Alarcon D, Neves FS, Izzo T, Ribeiro SP (2020) Species-level drivers of mammalian ectoparasite faunas. Edited by Jenny Dunn. J Anim Ecol 89(8):1754–1765. https://doi.org/10.1111/1365-2656.13216

de Souza F, Carolina R, Teixeira BLB, Gusmão CLS, Fernandes AM (2020) Humidity effects on avian blood parasites in the Caatinga of Brazil. Ornithol Res 28(2):98–104. https://doi.org/10.1007/s43388-020-00009-y

Dobson A, Lafferty KD, Kuris AM, Hechinger RF, Jetz W (2008) Homage to linnaeus: how many parasites? How many hosts? Proc Natl Acad Sci 105(Supplement 1):11482–11489. https://doi.org/10.1073/pnas.0803232105

Doussang D, Sallaberry-Pincheira N, Cabanne GS, Lijtmaer DA, González-Acuña D, Vianna JA (2021) Specialist versus generalist parasites: the interactions between host diversity, environment and geographic barriers in avian malaria. Int J Parasitol 51(11):899–911. https://doi.org/10.1016/j.ijpara.2021.04.003

Escallón C, Weinstein NM, Tallant JA, Wojtenek W, Rodríguez-Saltos CA, Bonaccorso E, Moore IT (2016) Testosterone and haemosporidian parasites along a tropical elevational gradient in rufous-collared sparrows (Zonotrichia capensis). J Exp Zool 325A:501–510.

Fallon SM, Ricklefs RE, Latta SC, Bermingham E (2004) Temporal stability of insular avian malarial parasite communities. Proc Biol Sci 271(1538):493–500. https://doi.org/10.1098/rspb.2003.2621. PMID: 15129959; PMCID: PMC1691613.

Feare CJ (2010) Role of wild birds in the spread of highly pathogenic avian influenza virus H5N1 and implications for global surveillance. Avian Dis 54(s1):201–212. https://doi.org/10.1637/8766-033109-ResNote.1

Fecchio A, Bell JA, Bosholn M, Vaughan JA, Tkach VV, Lutz HL, Cueto VR et al (2019) An inverse latitudinal gradient in infection probability and phylogenetic diversity for *Leucocytozoon* blood parasites in new world birds. Edited by David Richardson. J Anim Ecol. https://doi.org/10.1111/1365-2656.13117

Fecchio A, Ribeiro RM, Ferreira FC, de Angeli D, Dutra GT-P, Alquezar RD, Khan AU et al (2020) Higher infection probability of haemosporidian parasites in Blue-black Grassquits (*Volatinia Jacarina*) inhabiting native vegetation across Brazil. Parasitol Int 80(February):102204. https://doi.org/10.1016/j.parint.2020.102204

Fecchio A, Lima MR, Bell JA, Schunck F, Corrêa AH, Beco R, Jahn AE et al (2021) Loss of forest cover and host functional diversity increases prevalence of avian malaria parasites in the Atlantic forest. Int J Parasitol 51(9):719–728. https://doi.org/10.1016/j.ijpara.2021.01.001

Ferreira Junior FC, Rodrigues RA, Ellis VA, Leite LO, Borges MAZ, Braga ÉM (2017) Habitat modification and seasonality influence avian haemosporidian parasite distributions in Southeastern Brazil. Edited by Petr Heneberg. PLoS One 12(6):e0178791. https://doi.org/10.1371/journal.pone.0178791

Fernández-Correa I, Truchado DA, Gomez-Lucia E, et al (2019) A novel group of avian astroviruses from Neotropical passerine birds broaden the diversity and host range of Astroviridae. Sci Rep 9:9513. https://doi.org/10.1038/s41598-019-45889-3

Gamarra-Toledo V, Plaza PI, Gutiérrez R, Luyo P, Hernani L, Angulo F, Lambertucci SA (2023) Avian flu threatens neotropical birds. Science 379(6629):246–246. https://doi.org/10.1126/science.adg2271

George TL, Harrigan RJ, LaManna JA, DeSante DF, Saracco JF, Smith TB (2015) Persistent impacts of West Nile virus on North American bird populations. Proc Natl Acad Sci 112(46):14290–14294. https://doi.org/10.1073/pnas.1507747112

Gilman S, Blumstein DT, Foufopoulos J (2007) The effect of hemosporidian infections on white-crowned sparrow singing behavior. Ethology 113(5):437–445. https://doi.org/10.1111/j.1439-0310.2006.01341.x

Hadfield J, Brito AF, Swetnam DM, Vogels CBF, Tokarz RE, Andersen KG, Smith RC, Bedford T, Grubaugh ND (2019) Twenty years of West Nile virus spread and evolution in the Americas visualized by Nextstrain. Edited by Tom C. Hobman. PLoS Pathog 15(10):e1008042. https://doi.org/10.1371/journal.ppat.1008042

Hernández-Lara C, González-García F, Santiago-Alarcon D (2017) Spatial and seasonal variation of avian malaria infections in five different land use types within a neotropical montane forest matrix. Landsc Urban Plan 157(January):151–160. https://doi.org/10.1016/j.landurbplan.2016.05.025

Hernández-Lara C, Carbó-Ramírez P, Santiago-Alarcon D (2020) Effects of land use change (rural-urban) on the diversity and epizootiological parameters of avian haemosporida in a widespread neotropical bird. Acta Trop 209(September):105542. https://doi.org/10.1016/j.actatropica.2020.105542

Herzog SK, Kessler M, Bach K (2005) The elevational gradient in Andean bird species richness at the local scale: a foothill peak and a high-elevation plateau. Ecography 28(2):209–222. https://doi.org/10.1111/j.0906-7590.2005.03935.x

Hudson PJ, Dobson AP, Lafferty KD (2006) Is a healthy ecosystem one that is rich in parasites? Trends Ecol Evol 21(7):381–385. https://doi.org/10.1016/j.tree.2006.04.007

Jerzak G, Bernard KA, Kramer LD, Ebel GD (2005) Genetic variation in West Nile virus from naturally infected mosquitoes and birds suggests quasispecies structure and strong purifying selection. J Gen Virol 86(8):2175–2183. https://doi.org/10.1099/vir.0.81015-0

Jerzak GVS, Brown I, Shi P-Y, Kramer LD, Ebel GD (2008) Genetic diversity and purifying selection in West Nile virus populations are maintained during host switching. Virology 374(2):256–260. https://doi.org/10.1016/j.virol.2008.02.032

Jetz W, Rahbek C (2002) Geographic range size and determinants of avian species richness. Science 297(5586):1548–1551. https://doi.org/10.1126/science.1072779

Jetz GH, Thomas JB, Joy KH, Mooers AO (2012) The global diversity of birds in space and time. Nature 491(7424):444–448. https://doi.org/10.1038/nature11631

Jones MR, Cheviron ZA, Carling MD (2013) Spatial patterns of avian malaria prevalence in Zonotrichia capensis on the western slope of the Peruvian Andes. J Parasitol 99(5):903–905. https://doi.org/10.1645/12-147.1

Johnston SA, Voelz K, May RC (2016) Cryptococcus neoformans Thermotolerance to Avian Body Temperature Is Sufficient For Extracellular Growth But Not Intracellular Survival In Macrophages. Sci Rep 6:20977. https://doi.org/10.1038/srep20977. PMID: 26883088; PMCID: PMC4756366.

Kamiya T, O'Dwyer K, Nakagawa S, Poulin R (2014) Host diversity drives parasite diversity: meta-analytical insights into patterns and causal mechanisms. Ecography 37(7):689–697. https://doi.org/10.1111/j.1600-0587.2013.00571.x

Kilpatrick AM, Wheeler SS (2019) Impact of West Nile virus on bird populations: limited lasting effects, evidence for recovery, and gaps in our understanding of impacts on ecosystems. Edited by William Reisen. J Med Entomol 56(6):1491–1497. https://doi.org/10.1093/jme/tjz149

Kilpatrick AM, Kramer LD, Jones MJ, Marra PP, Daszak P (2006) West Nile virus epidemics in North America are driven by shifts in mosquito feeding behavior. Edited by Rick Ostfeld. PLoS Biol 4(4):e82. https://doi.org/10.1371/journal.pbio.0040082

Komar N, Langevin S, Hinten S, Nemeth N, Edwards E, Hettler D, Davis B, Bowen R, Bunning M (2003) Experimental infection of North American birds with the New York 1999 strain of West Nile virus. Emerg Infect Dis 9(3):311–322

LaDeau S, Kilpatrick A, Marra P (2007) West Nile virus emergence and large-scale declines of North American bird populations. Nature 447:710–713. https://doi.org/10.1038/nature05829

LaDeau SL, Calder CA, Doran PJ, Marra PP (2011) West Nile virus impacts in American crow populations are associated with human land use and climate. Ecol Res 26(5):909–916. https://doi.org/10.1007/s11284-010-0725-z

Lafferty KD, Dobson AP, Kuris AM (2006) Parasites dominate food web links. Proc Natl Acad Sci 103(30):11211–11216. https://doi.org/10.1073/pnas.0604755103

LaPointe DA, Atkinson CT, Samuel MD (2012) Ecology and conservation biology of avian malaria. Ann N Y Acad Sci 1249(1):211–226. https://doi.org/10.1111/j.1749-6632.2011.06431.x

Lee D-H, Torchetti MK, Winker K, Ip HS, Song C-S, Swayne DE (2015) Intercontinental spread of Asian-origin H5N8 to North America through Beringia by migratory birds. Edited by A. García-Sastre. J Virol 89(12):6521–6524. https://doi.org/10.1128/JVI.00728-15

Lopes VL, Costa FV, Rodrigues RA et al (2020) High fidelity defines the temporal consistency of host-parasite interactions in a tropical coastal ecosystem. Sci Rep 10:16839. https://doi.org/10.1038/s41598-020-73563-6

Mansilla AP, Grande JM, Diaz A (2022) Effect of Agroecosystems on Seroprevalence of St. Louis Encephalitis and West Nile Viruses in Birds, La Pampa, Argentina, 2017–2019. Emerg Infect Dis 28(7):1393–1402. https://doi.org/10.3201/eid2807.211485. PMID: 35731160; PMCID: PMC9239869.

Matuoka MA, Benchimol M, de Almeida-Rocha JM, Morante-Filho JC (2020) Effects of anthropogenic disturbances on bird functional diversity: a global meta-analysis. Ecol Indic 116(September):106471. https://doi.org/10.1016/j.ecolind.2020.106471

May RM, Anderson RM (1978) Regulation and stability of host-parasite population interactions: II. destabilizing processes. J Anim Ecol 47(1):249. https://doi.org/10.2307/3934

McNew SM, Barrow LN, Williamson JL, Galen SC, Skeen HR, DuBay SG, Gaffney AM, Johnson AB, Bautista E, Ordoñez P, Schmitt CJ (2021) Contrasting drivers of diversity in hosts and parasites across the tropical Andes. Proceedings of the National Academy of Sciences. 118(12):e2010714118. https://doi.org/10.1073/pnas.2010714118

Merino S, Moreno J, Vasquez RA, Martinez J, Sánchez-Monsávez IN, Estades CF, Ippi S, Sabat P, Rozzi R, Mcgehee S (2008) Haematozoa in forest birds from southern Chile: latitudinal gradients in prevalence and parasite lineage richness. Austral Ecol 33(3):329–340. https://doi.org/10.1111/j.1442-9993.2008.01820.x

Meza-Montes E, Fernández-Gómez RA, Llanes-Quevedo A, Navarro-Sigüenza AG, Santiago-Alarcon D, Roberto Sosa-López J (2023) Vocal behaviour, parasitic infection, chronic stress and body condition in Rufous-naped Wrens (*Campylorhynchus Rufinucha*). Ibis 165(2):676–684. https://doi.org/10.1111/ibi.13130

Mine J, Uchida Y, Sharshov K, Sobolev I, Shestopalov A, Saito T (2019) Phylogeographic evidence for the inter- and intracontinental dissemination of avian influenza viruses via migration flyways. Edited by Charles J. Russell. PLoS One 14(6):e0218506. https://doi.org/10.1371/journal.pone.0218506

Mollentze N, Streicker DG (2020) Viral zoonotic risk is homogenous among taxonomic orders of mammalian and avian reservoir hosts. Proc Natl Acad Sci 117(17):9423–9430. https://doi.org/10.1073/pnas.1919176117

Møller AP (2005) Parasitism and the regulation of host populations. In: Thomas F, Renaud F, Guegan J-F (eds) Parasitism and ecosystems. Oxford University Press, pp 43–53. https://doi.org/10.1093/acprof:oso/9780198529873.003.0004

Møller AP, Erritzøe J (2000) Predation against birds with low immunocompetence. Oecologia 122(4):500–504. https://doi.org/10.1007/s004420050972

Møller AP, Erritzøe J (2002) Coevolution of host immune defence and parasite-induced mortality: relative spleen size and mortality in altricial birds. Oikos 99(1):95–100. https://doi.org/10.1034/j.1600-0706.2002.990110.x

Morin CW, Stoner-Duncan B, Winker K, Scotch M, Hess JJ, Meschke JS, Ebi KL, Rabinowitz PM (2018) Avian influenza virus ecology and evolution through a climatic lens. Environ Int 119(October):241–249. https://doi.org/10.1016/j.envint.2018.06.018

Moura MR, Villalobos F, Costa GC, Garcia PCA (2016) Disentangling the role of climate, topography and vegetation in species richness gradients. Edited by Maura (Gee) Geraldine Chapman. PLoS One 11(3):e0152468. https://doi.org/10.1371/journal.pone.0152468

Nabi G, Wang Y, Lü L, Jiang C, Ahmad S, Yuefeng W, Li D (2021) Bats and birds as viral reservoirs: a physiological and ecological perspective. Sci Total Environ 754(February):142372. https://doi.org/10.1016/j.scitotenv.2020.142372

Navarro C (2004) Predation risk, host immune response, and parasitism. Behav Ecol 15(4):629–635. https://doi.org/10.1093/beheco/arh054

Ogrzewalska M, Uezu A, Jenkins CN, Labruna MB (2011) Effect of forest fragmentation on tick infestations of birds and tick infection rates by rickettsia in the Atlantic forest of Brazil. Ecohealth 8(3):320–331. https://doi.org/10.1007/s10393-011-0726-6. Epub 2011 Dec 16. PMID: 22173291.

Ortega-Guzmán L, Rojas-Soto O, Santiago-Alarcon D, Huber-Sannwald E, Chapa-Vargas L (2022) Climate predictors and climate change projections for avian haemosporidian prevalence in Mexico. Parasitology 149(8):1129–1144. https://doi.org/10.1017/S0031182022000683

Parker PG (ed) (2018) Disease ecology: Galapagos birds and their parasites, Social and ecological interactions in the Galapagos Islands. Springer, Cham. https://doi.org/10.1007/978-3-319-65909-1

Pérez-Rodríguez A, Khimoun A, Ollivier A, Eraud C, Faivre B, Garnier S (2018) Habitat fragmentation, not habitat loss, drives the prevalence of blood parasites in a Caribbean passerine. Ecography, 41:1835–1849. https://doi.org/10.1111/ecog.03189

Poulin R (2014) Parasite biodiversity revisited: frontiers and constraints. Int J Parasitol 44(9):581–589. https://doi.org/10.1016/j.ijpara.2014.02.003

Poulin R, Tellervo Valtonen E (2001) Nested assemblages resulting from host size variation: the case of endoparasite communities in fish hosts. Int J Parasitol 31(11):1194–1204. https://doi.org/10.1016/S0020-7519(01)00262-4

Pulgarín-R PC, Gómez JP, Robinson S, Ricklefs RE, Cadena CD (2018) Host Species, and not environment, predicts variation in blood parasite prevalence, distribution, and diversity along a humidity gradient in Northern South America. Ecol Evol 8(8):3800–3814. https://doi.org/10.1002/ece3.3785

Rahbek C, Graves GR (2001) Multiscale assessment of patterns of avian species richness. Proc Natl Acad Sci 98(8):4534–4539. https://doi.org/10.1073/pnas.071034898

Reboreda, J. C., Fiorini, V. D., Tuero, D. T. (Eds.) (2019). Behavioral Ecology of Neotropical Birds. Springer International Publishing. ISBNs 978-3-03-014279-7. https://doi.org/10.1007/978-3-030-14280-3

Reed KD (2002) Laboratory testing for Lyme disease: possibilities and practicalities. J Clin Microbiol. 40(2):319–324. https://doi.org/10.1128/JCM.40.2.319-324.2002. PMID: 11825936; PMCID: PMC153420.

Rivero de Aguilar J, Castillo F, Moreno A, Peñafiel N, Browne L, Walter ST, Karubian J, Bonaccorso E (2018) Patterns of avian haemosporidian infections vary with time, but not habitat, in a fragmented Neotropical landscape. PLoS One. 13(10):e0206493. https://doi.org/10.1371/journal.pone.0206493. PMID: 30379912; PMCID: PMC6209335.

Robles-Fernández ÁL, Santiago-Alarcon D, Lira-Noriega A (2022) Wildlife susceptibility to infectious diseases at global scales. Proc Natl Acad Sci 119(35):e2122851119. https://doi.org/10.1073/pnas.2122851119

Rodríguez-Hernández K, Álvarez-Mendizábal P, Chapa-Vargas L, Escobar F, González-García F, Santiago-Alarcon D (2021) Haemosporidian prevalence, parasitaemia and aggregation in relation to avian assemblage life history traits at different elevations. Int J Parasitol 51(5):365–378. https://doi.org/10.1016/j.ijpara.2020.10.006

Ronca SE, Ruff JC, Murray KO (2021) A 20-year historical review of West Nile virus since its initial emergence in North America: has West Nile virus become a neglected tropical disease? Edited by Pedro F. C. Vasconcelos. PLoS Negl Trop Dis 15(5):e0009190. https://doi.org/10.1371/journal.pntd.0009190

Rubio AV, Castro-Arellano I, Mills JN, List R, Ávila-Flores R, Suzán G (2017) Is species richness driving intra- and interspecific interactions and temporal activity overlap of a hantavirus host? An experimental test. Edited by W. F. de Boer. PLoS One 12(11):e0188060. https://doi.org/10.1371/journal.pone.0188060

Saito T, Tanikawa T, Uchida Y, Takemae N, Kanehira K, Tsunekuni R (2015) Intracontinental and intercontinental dissemination of Asian H5 highly pathogenic avian influenza virus (Clade 2.3.4.4) in the winter of 2014-2015: dissemination of clade 2.3.4.4 HPAIV in 2014-2015. Rev Med Virol 25(6):388–405. https://doi.org/10.1002/rmv.1857

Samuel MD, Hobbelen PHF, DeCastro F, Ahumada JA, LaPointe DA, Atkinson CT, Woodworth BL, Hart PJ, Duffy DC (2011) The dynamics, transmission, and population impacts of avian malaria in native Hawaiian birds: a modeling approach. Ecol Appl 21(8):2960–2973. https://doi.org/10.1890/10-1311.1

Santiago-Alarcon D, Marzal A (2020a) Research on avian haemosporidian parasites in the tropics before the year 2000. In: Santiago-Alarcon D, Marzal A (eds) Avian malaria and related parasites in the tropics. Springer, Cham, pp 1–44. https://doi.org/10.1007/978-3-030-51633-8_1

Santiago-Alarcon D, Marzal A (2020b) Avian malaria and related parasites in the tropics – ecology, evolution and systematics. Springer

Santiago-Alarcon D, Soto OR (2021) Discovering parasite biodiversity in the tropics: a framework based on multi-host-species ecological niche models. Ecotropicos 33(May):1–9. https://doi.org/10.53157/ecotropicos.33e0016

Sebaio F, Braga É, Branquinho F, Manica L, Marini M (2010) Blood parasites in Brazilian atlantic forest birds: effects of fragment size and habitat dependency. Bird Conserv Int 20(4):432–439. https://doi.org/10.1017/S0959270910000110

Smith OM, Snyder WE, Owen JP (2020) Are we overestimating risk of enteric pathogen spillover from wild birds to humans?. Biol Rev 95(3):652–679. https://doi.org/10.1111/brv.12581

Sol D, Trisos C, Múrria C, Jeliazkov A, González-Lagos C, Pigot AL, Ricotta C, Swan CM, Tobias JA, Pavoine S (2020) The worldwide impact of urbanisation on avian functional diversity. Edited by David Storch. Ecol Lett 23(6):962–972. https://doi.org/10.1111/ele.13495

Soto-Madrid R, Sychra O, Benedick S, Edwards DP, Efeykin BD, Fandrem M, Haugaasen T, Teterina A, Tomassi S, Tolstenkov O (2020) Diversity and host associations of Myrsidea chewing lice (Phthiraptera: Menoponidae) in the tropical rainforest of Malaysian Borneo. Int J Parasitol Parasites Wildl 13(December):231–247. https://doi.org/10.1016/j.ijppaw.2020.10.011

Steele KE, Linn MJ, Schoepp RJ, Komar N, Geisbert TW, Manduca RM, Calle PP et al (2000) Pathology of fatal West Nile virus infections in native and exotic birds during the 1999 outbreak in New York City, New York. Vet Pathol 37(3):208–224. https://doi.org/10.1354/vp.37-3-208

Sures B (2004) Environmental parasitology: relevancy of parasites in monitoring environmental pollution. Trends Parasitol 20(4):170–177. https://doi.org/10.1016/j.pt.2004.01.014

Titley MA, Snaddon JL, Turner EC (2017) Scientific research on animal biodiversity is systematically biased towards vertebrates and temperate regions. Edited by Bernd Schierwater. PLoS One 12(12):e0189577. https://doi.org/10.1371/journal.pone.0189577

Tolsá MJ, García-Peña GE, Rico-Chávez O, Roche B, Suzán G (2018) Macroecology of birds potentially susceptible to West Nile virus. Proc R Soc B Biol Sci 285(1893):20182178. https://doi.org/10.1098/rspb.2018.2178

Valkiūnas G, Atkinson CT (2020) Introduction to life cycles, taxonomy, distribution, and basic research techniques. In: Santiago-Alarcon D, Marzal A (eds) Avian malaria and related parasites in the tropics. Springer, Cham, pp 45–80. https://doi.org/10.1007/978-3-030-51633-8_2

van Rooyen J, Lalubin F, Glaizot O, Christe P (2013) Altitudinal variation in haemosporidian parasite distribution in great tit populations. Parasit Vectors 6(1):139. https://doi.org/10.1186/1756-3305-6-139

Wille M, Barr IG (2022) Resurgence of avian influenza virus. Science 376(6592):459–460. https://doi.org/10.1126/science.abo1232

Williams RAJ, Truchado DA, Benitez L (2021) A review on the prevalence of poxvirus disease in free-living and captive wild birds. Microbiol Res 12(2):403–418. https://doi.org/10.3390/microbiolres12020028

Winker K, Gibson DD (2010) The Asia-to-America influx of avian influenza wild bird hosts is large. Avian Dis 54(s1):477–482. https://doi.org/10.1637/8741-032509-Reg.1

Wood CL, Byers JE, Cottingham KL, Altman I, Donahue MJ, Blakeslee AMH (2007) Parasites alter community structure. Proc Natl Acad Sci 104(22):9335–9339. https://doi.org/10.1073/pnas.0700062104

Zamora-Vilchis I, Williams SE, Johnson CN (2012) Environmental temperature affects prevalence of blood parasites of birds on an elevation gradient: implications for disease in a warming climate. Edited by Justin David Brown. PLoS One 7(6):e39208. https://doi.org/10.1371/journal.pone.0039208

Zylberberg M, Lee KA, Klasing KC, Wikelski M (2013) Variation with land use of immune function and prevalence of avian pox in Galapagos finches: avian pox, immunity, and land use. Conserv Biol 27(1):103–112. https://doi.org/10.1111/j.1523-1739.2012.01944.x