




## Genetic variation of *Plasmodium* and *Haemoproteus* parasites in birds of Iran

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### ABSTRACT

**Background:** *Plasmodium* and *Haemoproteus* are common parasites transferred to birds by Culicidae, Ceratopogonidae, and Hippoboscidae vectors. These parasites are of particular concern to healthcare researchers and veterinarians due to their impact on avian malaria, association with other animals and humans, and phylogenetic link with human *Plasmodium* species.

**Methods:** This bibliographic review article was designed to deliver a report on the avian malaria infections of *Plasmodium* spp. and *Haemoproteus* spp. in birds in Iran. Published reports in Google Scholar, PubMed, and Science Direct were used for this revision until April 2023.

**Results:** The highest number of recorded infections with *Haemoproteus* spp. and *Plasmodium* spp. was found in Passeridae, as revealed by genetic analysis of *Cytb* DNA sequences. In this revision, following preceding investigations, the overall prevalence of *Haemoproteus* spp. was greater than that of *Plasmodium* spp. discovered by molecular techniques in Iran. Besides, the frequency of published genetic variants (lineages) of *Haemoproteus* is higher than that of *Plasmodium*. Our result indicated that the frequency of novel genetic variants *Haemoproteus* and *Plasmodium* in published reports was 38% and 12.5% of diagnosed lineages, respectively.

**Conclusion:** The region needs more studies to detect parasites in unexplored hosts and vectors, as there is a lack of research. Understanding the prevalence, epidemiology, transmission approach, and vectors of avian blood parasites is crucial for pet health care, zoos, parks, aviaries, and rehabilitation facilities.

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## 1. Introduction

Birds host haemosporidian parasites, and a widespread collection of mosquitoes can harbor these protozoa (1-3). Numerous arthropods encompassing vectors of Culicidae, Ceratopogonidae, and Hippoboscidae are considered the foremost source of infection transmitted to birds (1). *Plasmodium* spp. and *Haemoproteus* spp. have been reported as malaria and malaria-like parasites with substantial ecological and evolutionary effects on their bird hosts, resulting in mortality and extinction of populations (1, 2, 4, 5). These protozoan parasites are also of exceptional concern to healthcare researchers and veterinarians because of the influence of avian malaria on their fitness and their phylogenetic association with human *Plasmodium* species. More than 55 species of *Plasmodium* and 150 species of *Haemoproteus* can infect an extensive range of avian families (6–12).

Numerous studies have tried to discover different characteristics of avian blood parasite infection in passerine and non-passerine birds by microscopic inspection (13–17), molecular-based techniques (18s RNA and *Cytb* genes) (13, 18–22), and histological analysis (23-26) around the world. MalAvi (27), an online database for molecular lineages of avian hemospordian parasites, can be used for comparative analysis of novel sequences. Various elements are accompanied by avian blood parasite prevalence in their hosts and vectors; ecological and biological factors such as geographical regions and sampling time; the availability of competent vectors (mosquitoes); host immunity strength; and other factors related to host-parasite-vector interactions (19, 28–35).

A significant number of passerine and non-passerine bird species (more than 548 species) inhabited Iran (36, 37). Despite having a great diversity of bird species here and being focused on the detection of genetic variants of blood parasites and their hematophagous vectors in many parts of the world, the west part of Asia has been insufficiently studied. However, recently, various investigations focused on studying the prevalence and epidemiology of malaria and malaria-like

parasites in diverse avian hosts by morphological and molecular approaches in Iran (7, 18–22, 38–50).

## 2. Materials and Methods

In this regard, the bibliographic review article was designed to deliver a collection of the avian hosts infected by *Plasmodium* spp. and *Haemoproteus* spp. in birds of Iran. Furthermore, the composition of genetically unique and published lineages was reviewed in published reports in PubMed, Google Scholar, and Science Direct until April 2023.

## 3. Results and discussion

Birds are the most dispersed animals due to their journey throughout the breeding season and migration, which enable them to transfer hematozoan parasites to new geographical areas and intermediate hosts (51, 52). Various investigations were performed for the detection of *Plasmodium* spp. and related parasite species by microscopic inspection of gametocytes in thin blood smears (18, 38, 39, 41, 44, 47-50, 53, 54), while the other studies accomplished the molecular screening of haemosporidian parasites using amplification of the *Cytb* gene and DNA sequencing (18-22, 40, 42, 44, 46). In the molecular (Table 1 and Figure 1) and morphological studies (Table 2), the highest frequency of examined species belonged to the Accipitridae and Phasianidae families, respectively.

The comparative result showed that the number of bird species examined by molecular method (n = 115) was also higher than the morphological report (n = 78), indicating more interest in genetic analysis for precise identification of genetic variation in blood parasites (4, 16). The highest number of recorded infections of *Haemoproteus* spp. and *Plasmodium* spp. was found in Passeridae, as revealed by genetic analysis of *Cytb* sequences (Table 2).

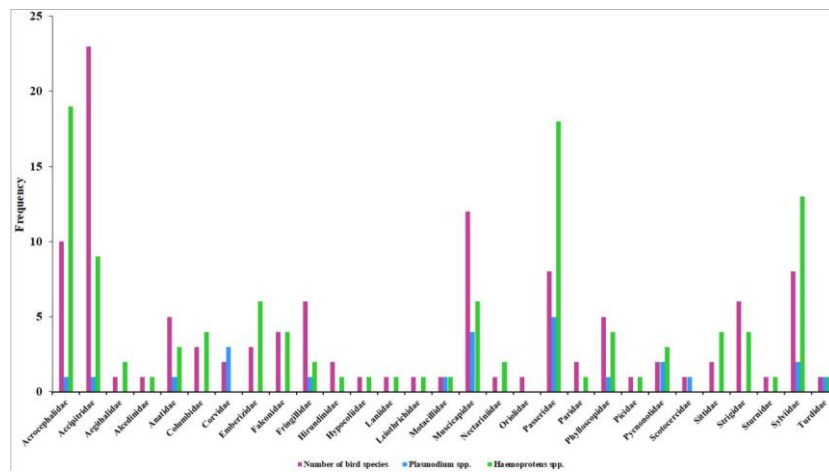


Figure 1. Frequency of detected parasites by molecular approaches in birds of Iran

Table 1. Frequency of detection of malaria and malaria-like parasites by molecular approach in birds of Iran. The number of bird species, the number of Plasmodium spp. and Haemoproteus spp., and their lineages are given. Novel published lineages are in bold format.

Bird Family	Number of bird species <sup>1</sup>	Plasmodium spp. (n) <sup>2</sup>	Plasmodium lineages	Haemoproteus spp. (n) <sup>2</sup>	Haemoproteus lineages	References
Acrocephalidae	5	0	-	12	ACDUM1, ACDUM2, ACDUM3, ARW1, ACSTE1, BRW1, GRW03, HIP2, <b>IDPAL01</b> , HIP4, LULU1, HIICT1	(18)
	5	1	SYBOR10	7	SW4, GRW01, ARW1, MW3, ARW1, MW1, HIP2	(46)
Accipitridae	8	0	-	6	<b>ACCBAD02</b> , <b>BUTBUT04</b> , <b>BUTBUT05</b> , <b>BUTBUT06</b> , <b>CIAE04</b> , <b>MILMIG01</b>	(19)
	14	1	LK05	2	<b>AQCYR01</b> , MILANS02	(22)
	1	0	-	1	BUTBUT15	(43)
Aegithalidae	1	0	-	2	ACDUM2, <b>AEGCAU05</b>	(18)

<b>Alcedinidae</b>	1	0	-	1	<b>ALCATT01</b>	(18)
<b>Anatidae</b>	5	1	SW5	3	<b>ANACRE03, AYTFER01, AYTFER02</b>	(22)
<b>Columbidae</b>	1	0	-	3	COLIV03, COQUI05, HAECOL1	(20)
	2	0	-	1	HAECOL1	(22)
<b>Corvidae</b>	2	3	SGS01, ROFI04, LINN01	0	-	(20)
<b>Emberizidae</b>	3	0	-	6	<b>EMBUC01, GRBRU01, GRBRU02, GRMEL02, GRMEL01, SISKIN01</b>	(18)
<b>Falconidae</b>	2	0	-	3	<b>FALTIN01, LK03, FALSUB02</b>	(19)
	2	0	-	1	LK03	(22)
<b>Fringillidae</b>	5	0	-	2	CCF6, PYERY01	(18)
	1	1	LK05	0	-	(46)
<b>Hirundinidae</b>	2	0	-	1	<b>HIRUS17</b>	(18)
<b>Hypocoliidae</b>	1	0	-	1	PADOM05	(46)
<b>Laniidae</b>	1	0	-	1	RB1	(46)
<b>Leiothrichidae</b>	1	0	-	1	<b>ARGCAU1</b>	(46)
<b>Motacillidae</b>	1	1	<b>MOALB03</b>	1	YWT3	(18)
<b>Muscicapidae</b>	6	0	-	3	<b>FISEM02, FISEM01, OEOEN01</b>	(18)
	6	4	SGS1, <b>LUME4,</b> SYBOR02, LK05	3	PADOM05, SFC1, ROBIN1	(46)
<b>Nectariniidae</b>	1	0	-	2	CCF2, PAHIS2	(46)
<b>Oriolidae</b>	1	0	-	0	-	(46)
<b>Passeridae</b>	3	1	GRW04	6	PADOM05, <b>PADOM32,</b> PAHIS2, PYERY01, <b>PETPET02, PETPET01</b>	(18)
	4	4	SGS1, GRW04, PADOM02, PBPIP1	10	<b>GYMXAN1, GYMXAN2,</b> PAHIS1, PADOM05, PAHIS2, HIP2,	(46)

					<b>PADOM34,</b> <b>PADOM03,</b> <b>CCF2, SW4,</b> <b>PADOM35</b>	
	1	0	-	2	<b>PAHIS1,</b> <b>PADOM41</b>	(42)
<b>Paridae</b>	2	0	-	1	<b>PARUS1</b>	(18)
<b>Phylloscopidae</b>	3	1	ORW1	1	<b>ACDUM1</b>	(18)
	2	0	-	3	<b>PAHIS2,</b> <b>PADOM05,</b> <b>WW1</b>	(46)
<b>Picidae</b>	1	0	-	1	<b>SISKIN01</b>	(18)
<b>Pycnonotidae</b>	2	2	<b>LUME4,</b> <b>GRW04</b>	3	<b>PYCLEU2,</b> <b>CCF2, BUL1</b>	(46)
<b>Scotocercidae</b>	1	1	LK05	0	-	(46)
<b>Sittidae</b>	1	0	-	2	<b>PARUS1,</b> <b>SITTEP01</b>	(18)
	1	0	-	2	<b>SITTEP02,</b> <b>SITTEP03</b>	(46)
<b>Strigidae</b>	3	0	-	3	<b>TYTAL04,</b> <b>LK03,</b> <b>OTSCO07</b>	(19)
	3	0	-	1	<b>STAL06</b>	(22)
<b>Sturnidae</b>	1	0	-	1	<b>LAMPUR01</b>	(18)
<b>Sylviidae</b>	2	0	-	1	<b>CUCUR01</b>	(18)
	6	2	LK05, GRW04	12	<b>SYHOR01,</b> <b>SYLALT01,</b> <b>CURCUR01,</b> LWT1, PAHIS2, SYAT01, SYAT07, SYNIS2, CWT2, CWT3, CWT7, <b>PYCLEU2</b>	(46)
<b>Turdidae</b>	1	1	SYAT5	1	<b>TURDUS2</b>	(18)
<b>Total (n)</b>	<b>115</b>	<b>24 (17.5%)</b>	-	<b>113 (82.4%)</b>	-	-

<sup>1</sup> Number of examined birds' species is given.<sup>2</sup> Number of detected parasites' lineages by molecular technique in each bird family is given.

**Table 2.** Occurrence of malaria and malaria-like parasites by morphological inspection in birds of Iran.

<b>Bird Family</b>	<b>Number of bird species *</b>	<b><i>Plasmodium</i> infection</b>	<b><i>Haemoproteus</i> infection</b>	<b>References</b>
<b>Accipitridae</b>	8	-	+	(41)
<b>Acrocephalidae</b>	3	-	+	(39)
	2	-	+	(38)
<b>Acrocephalidae</b>	3	-	+	(39)
	2	-	+	(38)
<b>Anatidae</b>	9	+	+	(50)
	NA	+	-	(54)
	NA	+	-	(44)
<b>Columbidae</b>	1	+	+	(49)
	1	-	+	(48)
	1	+	-	(54)
	1	-	+	(44)
<b>Emberizidae</b>	1	-	+	(39)
	2	-	+	(38)
<b>Falconidae</b>	2	-	+	(41)
<b>Fringillidae</b>	4	-	+	(39)
	2	-	+	(38)
<b>Hirundinidae</b>	2	-	+	(39)
<b>Laniidae</b>	1	-	-	(38)
<b>Motacillidae</b>	1	-	+	(39)
<b>Muscicapidae</b>	2	-	+	(39)
	3	-	-	(38)
<b>Paridae</b>	1	-	-	(39)
	1	-	-	(38)
<b>Passeridae</b>	2	-	+	(39)
	2	-	+	(38)
	1	+	-	(47)
<b>Phasianidae</b>	1	+	-	(53)
	4	+	+	(49)
	4	+	+	(48)
	2	+	-	(54)
<b>Phylloscopidae</b>	3	-	-	(39)
<b>Sittidae</b>	1	-	+	(38)

<b>Strigidae</b>	3	-	+	(41)
<b>Turdidae</b>	1	-	-	(39)
	1	-	+	(38)
<b>Total (n)</b>	<b>78</b>			

\* Number of examined birds' species is given. The positive and negative specimens by morphological inspection are highlighted with (+) and (-) symbols. NA: not applicable.

In this revision, following preceding investigations in different geographical regions, the number of detected lineages of *Haemoproteus* spp. (n = 113, 82.4%) was greater than *Plasmodium* spp. (n = 24, 17.5%) discovered by molecular techniques in Iran (18, 22, 46). The result, summarized in Table 1, indicated that the frequency of novel genetic lineages of *Haemoproteus* and *Plasmodium* in published reports was 38% and 12.5% of diagnosed lineages, respectively. The *Haemoproteus* lineages of IDPAL01, ACCBAD02, BUTBUT04, BUTBUT05, BUTBUT06, CIAE04, MILMIG01, AQUCYR01, AEGCAU05, ALCATT01, ANACRE03, AYTFER01, AYTFER02, EMBUC01, GRBRU01, GRBRU02, GRMEL02, GRMEL01, FALTIN01, FALSUB02, HIRUS17, ARGCAU1, FISEM02, FISEM01, OEOEN01, PADOM32, PETPET02, PETPET01, GYMXAN1, GYMXAN2, PADOM34, PADOM35, PADOM41, PYCLEU2, SITTEP01, SITTEP02, SITTEP03, OTSCO07, STAL06, SYLALT01, PYCLEU2, and CUCUR01, and *Plasmodium* lineages of LUME4 and MOALB03 were novel and first records for Iranian birds' hosts, whereas the rest of detected lineages have been reported in preceding studies around the world (Table 1).

The *Plasmodium* lineages of LK05 and GRW04 were repeated and common genetic variants discovered in birds of Iran, which were inconsistent with global records as they were introduced as generalist infections in birds (7). The submitted gene sequences of *Plasmodium* and *Haemoproteus* lineages have 479 base pairs (bp) in length and are accessible in NCBI with the following IDs: MG976505-MG976576 (18), MK929542-MK929552 & MN224223-MN224224 (22), MN224217-MN224231 & MW209702-

MW209713 (19), MT802174-MT802190 (20), MG428417 (43), KY885015 and KY885016 (42), and MT925798-MT925931 (46).

Though the overall prevalence of *Haemoproteus* spp. was higher than other genera in more reports (18, 19), in some morphological research, no infection with *Plasmodium* was detected in any host (38, 39, 41). Furthermore, novel lineages of blood parasites that have not been previously detected around the world were identified in several investigations diagnosed by genetic analysis of DNA sequences (18–20, 22, 46). Although the microscopic method is introduced as the gold standard for the identification of malarial blood parasites (16), the more accurate and sensitive potency of molecular approaches should be used in parallel (21, 22). Haemosporidian parasite infections affect the population structure by causing short-term or continuing reductions in their richness and extinction (55). So, due to the undesirable influence of parasites, detection and surveillance of parasites in domesticated, free-living, wild birds, and captive birds or pets are essential to protecting birds like raptors that are crucial for keeping balance in trophic levels of the food web (56, 57). Captive birds, especially raptors (Accipitridae, Falconidae, and Strigidae), are susceptible to infectious diseases. Thus, the higher prevalence of captive raptors to hemosporean parasites might be associated with stressful conditions like captivity, which diminish immune system function to clear infections from their bloodstream (19, 41).

Furthermore, the transmission of parasites will be facilitated by migratory birds in charge of the intercontinental spreading of avian infections on different continents and the reversal track back to their home (44, 58–60). In this regard, shared-

structure populations such as Anatidae have a great chance of harboring infections (58, 61). The surveillance of contagion pathogens in domestic birds (e.g., Phasianidae) and pets is vital due to their potential effects on the meat and egg production of chickens, turkeys, and fowl and their direct exposure to other animals and humans (22, 48, 62, 63). While some domestic species of Phasianidae and other pet families (20, 22) in some studies were not infected with blood parasites, further surveys have to be designed to detect infections in other parts of the country.

#### 4. Conclusion

Due to the limited number of studies in this region, designing further investigations for the detection of parasites in numerous unstudied hosts and vectors will provide valuable data. More understanding of the prevalence and epidemiology of avian blood parasites, transmission approaches, and vectors is compulsory for pet healthcare centers, zoos, parks, and rehabilitation facilities to protect these treasured bird species.

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#### Reference

1. Atkinson CT, Thomas NJ, Hunter DB. Parasitic diseases of wild birds: John Wiley & Sons; 2009.
2. Atkinson CT, van Riper III C. Pathogenicity and epizootiology of avian haematozoa: *Plasmodium*, *Leucocytozoon*, and *Haemoproteus*. Bird-parasite interactions. 1991:19-48.
3. Ferraguti M, Martínez-de la Puente J, Muñoz J, Roiz D, Ruiz S, Soriguer R, et al. Avian *Plasmodium* in *Culex* and *Ochlerotatus* mosquitoes from southern Spain: effects of season and host-feeding source on parasite dynamics. PloS One. 2013;8(6):e66237.
4. Bensch S, Stjernman M, Hasselquist D, Örjan Ö, Hansson B, Westerdahl H, et al. Host specificity in avian blood parasites: a study of *Plasmodium* and *Haemoproteus* mitochondrial DNA amplified from birds. Proc Royal Soc B. 2000;267(1452):1583-9.
5. Palinauskas V, Iezhova TA, Križanauskienė A, Markovets MY, Bensch S, Valkiūnas G. Molecular characterization and distribution of *Haemoproteus minutus* (Haemosporida, Haemoproteidae): a pathogenic avian parasite. Parasitol Int. 2013;62(4):358-63.
6. Valkiūnas G, Iezhova TA, Brooks DR, Hanelt B, Brant SV, Sutherlin ME, et al. Additional observations on blood parasites of birds in Costa Rica. J Wildl Dis. 2004;40(3):555-61.
7. Nourani L, Zakeri S, Dinparast Djadid N. Dynamics of prevalence and distribution pattern of avian *Plasmodium* species and its vectors in diverse zoogeographical areas-A review. Infect Genet Evol. 2020;81:104244.
8. Oakgrove KS, Harrigan RJ, Loiseau C, Guers S, Seppi B, Sehgal RN. Distribution, diversity and drivers of blood-borne parasite co-infections in Alaskan bird populations. Int J Parasitol. 2014;44(10):717-27.
9. Synek P, Albrecht T, Vinkler M, Schnitzer J, Votýpka J, Munclinger P. Haemosporidian parasites of a European passerine wintering in South Asia: diversity, mixed infections and effect on host condition. Parasitol Res. 2013;112(4):1667-77.
10. Bensch S, Waldenström J, Jonzén N, Westerdahl H, Hansson B, Sejberg D, et al. Temporal dynamics and diversity of avian malaria parasites in a single host species. J Anim Ecol. 2007;76(1):112-22.
11. Zehntindjiev P, Ilieva M, Westerdahl H, Hansson B, Valkiūnas G, Bensch S. Dynamics of parasitemia of malaria parasites in a naturally and experimentally infected migratory songbird, the great reed warbler *Acrocephalus arundinaceus*. Exp Parasitol. 2008;119(1):99-110.
12. Zélé F, Vézilier J, L'Ambert G, Nicot A, Gandon S, Rivero A, et al. Dynamics of prevalence and diversity of avian malaria infections in wild *Culex pipiens* mosquitoes: the effects of *Wolbachia*, filarial nematodes and insecticide resistance. Parasit Vector. 2014;7(1):437.
13. Belo N, Passos L, Júnior L, Goulart C, Sherlock T, Braga E. Avian malaria in captive psittacine birds: Detection by microscopy and 18S rRNA gene amplification. Prevent Vet Med. 2009;88(3):220-4.
14. Ciloglu A, Yildirim A, Duzlu O, Onder Z, Dogan Z, Inci A. Investigation of avian haemosporidian parasites from raptor birds in Turkey, with molecular characterisation and microscopic confirmation. Folia Parasitol. 2016;63.
15. Tostes R, Vashist U, Scopel KK, Massard CL, Daemon E, D'Agosto M. *Plasmodium* spp. and



- Haemoproteus* spp. infection in birds of the Brazilian Atlantic Forest detected by microscopy and polymerase chain reaction. *Pesq Vet Bras*. 2015;35(1):67-74.
16. Valkiunas G, Iezhova TA, Krizanauskiene A, Palinauskas V, Sehgal RN, Bensch S. A comparative analysis of microscopy and PCR-based detection methods for blood parasites. *J Parasitol*. 2008;94(6):1395-401.
  17. Zehtindjiev P, Krizanauskiene A, Bensch S, Palinauskas V, Asghar M, Dimitrov D, et al. A new morphologically distinct avian malaria parasite that fails detection by established polymerase chain reaction-based protocols for amplification of the cytochrome B gene. *J Parasitol*. 2012;98(3):657-65.
  18. Nourani L, Aliabadian M, Mirshamsi O, Dinparast Djadid N. Molecular detection and genetic diversity of avian haemosporidian parasites in Iran. *PloS One*. 2018;13(11):e0206638.
  19. Nourani L, Aliabadian M, Mirshamsi O, Dinparast Djadid N. Prevalence of co-infection and genetic diversity of avian haemosporidian parasites in two rehabilitation facilities in Iran: implications for the conservation of captive raptors. *BMC Ecol Evol*. 2022;22(1):114.
  20. Nourani L, Baghkheirati AA, Zargar M, Karimi V, Djadid ND. Haemoproteosis and avian malaria in Columbidae and Corvidae from Iran. *Vet Med Sci*. 2021;7(5):2043-50.
  21. Nourani L, Dinparast Djadid N, editors. Molecular identification of avian malaria in wild birds from Iran. 2nd International Congress of Climate Change & vector borne Diseases and 4th National Congress of Medical; 2019.
  22. Nourani L, Djadid ND, Rabiee K, Mezerji MS, Shakiba M, Bakhshi H, et al. Detection of haemosporidian parasites in wild and domestic birds in northern and central provinces of Iran: Introduction of new lineages and hosts. *Int J Parasitol: Parasit and Wildl*. 2020;13:203-12.
  23. Bobeva A, Ilieva M, Dimitrov D, Zehtindjiev P. Degree of associations among vectors of the genus *Culicoides* (Diptera: Ceratopogonidae) and host bird species with respect to haemosporidian parasites in NE Bulgaria. *Parasitol Res*. 2014;113(12):4505-11.
  24. Dinhopl N, Mostegl MM, Richter B, Nedorost N, Maderner A, Fragner K, et al. Application of in-situ hybridization for the detection and identification of avian malaria parasites in paraffin wax-embedded tissues from captive penguins. *Avian Pathol*. 2011;40(3):315-20.
  25. Scaglione FE, Cannizzo FT, Pregel P, Perez Rodriguez AD, Bollo E. Blood parasites in hooded crows (*Corvus corone cornix*) in Northwest Italy. *Vet Itali*. 2016;52(2):111-6.
  26. Shurulinkov P, Chakarov N, Daskalova G. Blood parasites, body condition, and wing length in two subspecies of yellow wagtail (*Motacilla flava*) during migration. *Parasitol Res*. 2012;110(5):2043-51.
  27. Bensch S, Hellgren O, Pérez-Tris J. MalAvi: a public database of malaria parasites and related haemosporidians in avian hosts based on mitochondrial cytochrome b lineages. *Mol Ecol Res*. 2009;9(5):1353-8.
  28. Krone O, Priemer J, Streich J, Sommer P, Langgemach T, Lessow O. Haemosporida of birds of prey and owls from Germany. *Acta Protozool*. 2001;40(4):281-90.
  29. Krone O, Waldenström J, Valkiūnas G, Lessow O, Müller K, Iezhova T, et al. Haemosporidian blood parasites in European birds of prey and owls. *J Parasitol*. 2008;94(3):709-15.
  30. Chasar A, Loiseau C, Valkiūnas G, Iezhova T, Smith TB, Sehgal RN. Prevalence and diversity patterns of avian blood parasites in degraded African rainforest habitats. *Mol Ecol*. 2009;18(19):4121-33.
  31. Drovetski SV, Aghayan SA, Mata VA, Lopes RJ, Mode NA, Harvey JA, et al. Does the niche breadth or trade-off hypothesis explain the abundance–occupancy relationship in avian Haemosporidia? *Mol Ecol*. 2014;23(13):3322-9.
  32. Hellgren O, Waldenström J, Peréz-Tris J, Szöll E, Si Ö, Hasselquist D, et al. Detecting shifts of transmission areas in avian blood parasites—a phylogenetic approach. *Mol Ecol*. 2007;16(6):1281-90.
  33. Kim K, Tsuda Y. Seasonal changes in the feeding pattern of *Culex pipiens pallens* govern the transmission dynamics of multiple lineages of avian malaria parasites in Japanese wild bird community. *Mol Ecol*. 2010;19(24):5545-54.
  34. Kim K, Tsuda Y. Avian Plasmodium lineages found in spot surveys of mosquitoes from 2007 to 2010 at Sakata wetland, Japan: do dominant lineages persist for multiple years? *Mol Ecol*. 2012;21(21):5374-85.
  35. Scordato ES, Kardish MR. Prevalence and beta diversity in avian malaria communities: host species is a better predictor than geography. *J Anim Ecol*. 2014;83(6):1387-97.

36. Dickinson E, Remsen Jr J. The Howard and Moore Complete Checklist of the Birds of the World. 1 Non-passerines. Aves Press, Eastbourne, UK I; 2013.
37. Scott DA, Adhami A. An updated checklist of the birds of Iran. *Podoces*. 2006;1(1/2):1-16.
38. Nourani L, Aliabadian M, Dinparast-Djadid N, Mirshamsi O. New Host Records for *Haemoproteus* spp. (Apicomplexa: Haemosporidiasina) in Passeriformes from North-West of Iran. *J arthropod-born Dis*. 2017;11(2):236.
39. Nourani L, Aliabadian M, Djadid Nd, Mirshamsi O. Occurrence of *Haemoproteus* spp. (Haemosporida: Haemoproteidae) in New Host Records of Passerine Birds from the East of Iran. *Iran J Parasitol*. 2018;13(2):267-74.
40. Nourani L, Aliabadian M, Mirshamsi O, Djadid ND, editors. Detection of the avian blood parasites from northeast of Iran. 1st International Congress on Vector-Borne Diseases and Climate Change; 2017.
41. Nourani L, Aliabadian M, Amini H, Mirshamsi O. Prevalence of haemosporidian parasite infections in raptors of Iran. *J Rapt Res*. 2020;54(4):455-62.
42. Rahmati M, Norouzian H, Nayebzadeh H, Shokrani H. Molecular Detection and Phylogenetic Analysis of Avian Haemosporidian Parasites in House Sparrows (*Passer domesticus*) of Western Iran. *J Wildl Dis*. 2023.
43. Shokrani H, Norouzian H, Dezfoulian O. Exo-erythrocytic stages of *Haemoproteus* sp. in common buzzard (*Buteo buteo*): A histopathological and molecular study. *Int J Parasitol: Parasit and Wildl*. 2021;16:64-9.
44. Amrei SFE, Haghi AM, Nateghpour M, Mohebbali M, Youssefi MR, Raiesi O, et al. Detection of Malaria Parasites and Other Haemosporidia in Migratory and Native Birds in Mazandaran and Golestan Provinces, Iran. *J Arthropod-Born Dis*. 2022;16(1):26–33-26–33.
45. Fakhar M, Kalani H, Rahimi-Esboei B, Armat S. Hemoprotozoa in free-ranging birds from rural areas of Mazandaran Province, northern Iran. *Comp Clin Path*. 2013;22(3):509-12.
46. Ghaemitalab V, Mirshamsi O, Valkiūnas G, Aliabadian M. Prevalence and Genetic Diversity of Avian Haemosporidian Parasites in Southern Iran. *Pathogens*. 2021;10(6):645.
47. Gorji SF, Shemshadi B, Habibi H, Jalali S, Davary M, Sepehri M. Survey on parasites in sparrows of Amol (Mazandaran Province, Iran). *J Life Sci*. 2012;6(7):783.
48. Mirzaei F, Siyadatpanah A, Norouzi R, Pournasir S, Nissapatorn V, Pereira MdL. Blood parasites in domestic birds in Central Iran. *Vet Sci*. 2020;7(3):126.
49. Mohaghegh MA, Namdar F, Azami M, Ghomashlooyan M, Kalani H, Hejazi SH. The first report of blood parasites in the birds in Fasa district, Southern Iran. *Comp Clin Path*. 2018;27(2):289-93.
50. Shemshadi B, Ranjbar-Bahadori S, Faghihzadeh-Gorgi S. Occurrence of parasitic protozoa in wild waterfowl in southern coastal Caspian sea lagoons. *Iran J Vet Med*. 2015;8(4):261-7.
51. Valkiūnas G. Avian malaria parasites and other haemosporidia: CRC press; 2005.
52. Waldenström J, Bensch S, Kiboi S, Hasselquist D, Ottosson U. Cross-species infection of blood parasites between resident and migratory songbirds in Africa. *Mol Ecol*. 2002;11(8):1545-54.
53. Nazifi S, Razavi S, Yavari F, Rajaifar M, Bazyar E, Esmailnejad Z. Evaluation of hematological values in indigenous chickens infected with *Plasmodium gallinaceum* and *Aegyptianella pullorum*. *Comp Clin Path*. 2008;17(3):145.
54. Kalani H, Faridnia R, Pestechian N, Cheraghpor K. The first report of hematozoa in migratory and native birds in Isfahan Province, Iran. *Comp Clin Path*. 2015;24(1):65-8.
55. Motta ROC, Marques MVR, Junior FCF, de Assis Andery D, Horta RS, Peixoto RB, et al. Does haemosporidian infection affect hematological and biochemical profiles of the endangered Black-fronted piping-guan (*Aburria jacutinga*)? *PeerJ*. 2013;1:e45.
56. Deem SL. The role of veterinarians in the conservation of avian species. *J Avian Med Surg*. 2011;25(3):225-30.
57. Deem SL, Karesh WB, Weisman W. Putting theory into practice: wildlife health in conservation. *Conserv Biol*. 2001;15(5):1224-33.
58. Aghayan S. Migratory birds as a tool to colonize new territories for avian haemosporidians. *ЕСТЕСТВЕННЫЕ НАУКИ*. 2012;1:18.
59. Fallon SM, Fleischer RC, Graves GR. Malarial parasites as geographical markers in migratory birds? *Biol Let*. 2006;2(2):213-6.
60. Gutierrez-Lopez R, Gangoso L, Martinez-de la Puente J, Fric J, Lopez-Lopez P, Maillieux M, et al. Low prevalence of blood parasites in a long-distance migratory raptor: the importance of host habitat. *Parasit Vector*. 2015;8:189.

61. Hubálek Z. An annotated checklist of pathogenic microorganisms associated with migratory birds. J Wildl Dis. 2004;40(4):639-59.
62. Dezfoulian O, Zibaei M, Nayebzadeh H, Haghgoo M, Emami-Razavi A, Kiani K. Leucocytozoonosis in domestic birds in southwestern iran: an ultrastructural study. Iran J Parasitol. 2013;8(1):171.
63. Laird M. *Plasmodium durae* Herman from the introduced common peafowl in northern Nigeria. J Protozool. 1978;25(1):21-4.