



Invited review

Manifold habitat effects on the prevalence and diversity of avian blood parasites



Ravinder N.M. Sehgal

Dept. of Biology, San Francisco State University, 1600 Holloway Ave., San Francisco, CA, 94132, USA

ARTICLE INFO

Article history:

Received 1 July 2015

Received in revised form

30 August 2015

Accepted 5 September 2015

Keywords:

Avian hematozoa

Haemosporidia

Plasmodium

Anthropogenic change

Deforestation

Habitat effects

ABSTRACT

Habitats are rapidly changing across the planet and the consequences will have major and long-lasting effects on wildlife and their parasites. Birds harbor many types of blood parasites, but because of their relatively high prevalence and ease of diagnosis, it is the haemosporidians – *Plasmodium*, *Haemoproteus*, and *Leucocytozoon* – that are the best studied in terms of ecology and evolution. For parasite transmission to occur, environmental conditions must be permissive, and given the many constraints on the competency of parasites, vectors and hosts, it is rather remarkable that these parasites are so prevalent and successful. Over the last decade, a rapidly growing body of literature has begun to clarify how environmental factors affect birds and the insects that vector their hematozoan parasites. Moreover, several studies have modeled how anthropogenic effects such as global climate change, deforestation and urbanization will impact the dynamics of parasite transmission. This review highlights recent research that impacts our understanding of how habitat and environmental changes can affect the distribution, diversity, prevalence and parasitemia of these avian blood parasites. Given the importance of environmental factors on transmission, it remains essential that researchers studying avian hematozoa document abiotic factors such as temperature, moisture and landscape elements. Ultimately, this continued research has the potential to inform conservation policies and help avert the loss of bird species and threatened habitats.

© 2015 The Author. Published by Elsevier Ltd on behalf of Australian Society for Parasitology. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Contents

1. Introduction	422
2. Habitat effects on avian hematozoa in the hosts	422
2.1. Habitat effects on avian hematozoa: birds	422
2.1.1. Habitat: prevalence and parasitemia	422
2.1.2. Habitat: distribution and diversity	424
2.1.3. Habitat: parasite evolution	424
2.2. Habitat effects on avian hematozoa: insect vectors	424
3. Migration, habitat and blood parasites	425
4. Habitat and host specificity	425
5. Anthropogenic changes and avian blood parasites	426
5.1. Global climate change	426
5.2. Deforestation	426
5.3. Urbanization	427
6. Conclusion	427
Conflict of interest	427
Acknowledgments	427
References	427

E-mail address: sehgal@sfsu.edu.

<http://dx.doi.org/10.1016/j.ijppaw.2015.09.001>

2213-2244/© 2015 The Author. Published by Elsevier Ltd on behalf of Australian Society for Parasitology. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

1. Introduction

The habitat of a living organism can broadly be defined as the ecological and environmental space that supports its existence. What constitutes a habitat depends on the species in question, but all the external biotic and abiotic factors that influence the life of the organism can be considered as components of habitat. Presently, climate change, deforestation, urbanization, desertification, invasive species and the expanding human population are leading to irrevocable effects on the habitats of wildlife and their pathogens. The field of wildlife disease ecology examines how these rapid changes will affect populations of animals worldwide. In particular, there has been much recent research centered on the effects of parasitic diseases on avian populations, in part because they harbor a tremendous diversity of parasites, and because they are relatively easy to study. However despite much progress, it is now becoming clear that the systems are exceedingly complex. This review sets out to highlight recent research that is making a major impact on our understanding of how birds, and the insect vectors that transmit their blood parasites are affected by the environments they inhabit.

Of the avian blood parasites, the haemosporidians are the most commonly studied in regards to ecology and evolution; this review will accordingly focus on this group. The highly diverse order Haemosporidia includes the genera *Plasmodium*, *Haemoproteus*, and *Leucocytozoon* (Atkinson et al., 2009). Another genus in the order, *Fallisia*, is much more rare, and in fact there are no recent published accounts of this parasite in birds (Valkiūnas, 2005). The genus *Plasmodium*, as in mammals, is the cause of the disease malaria in birds. *Plasmodium* is transmitted by many species of mosquitoes (Culicidae) (for a review of insect vectors that transmit haemosporidian parasites see Santiago-Alarcón et al., 2012). *Haemoproteus* differs in that it is transmitted by hippoboscids and ceratopogonid flies. *Leucocytozoon* is vectored by simuliid blackflies, or for the subgenus *Akiba*, ceratopogonids. Trypanosomes, unrelated to the haemosporidians, are also widely encountered in avian blood and can be transmitted by several insect species, most typically through the ingestion of the vector (Svobodová et al., 2015). Nematode microfilariae are also common in bird blood (Sehgal et al., 2001; Silveira et al., 2010). Other vector-borne blood parasites of birds include other sporozoan parasites of the genera *Hepatozoon*, *Babesia* and *Atoxoplasma* (Valkiūnas, 2005). Many of the parasites that infect birds have their counterparts in humans but since birds are not affected by socioeconomic factors, they provide an unbiased model system for how habitats can affect the transmission of parasitic diseases.

Since the turn of the 21st century, new methods have emerged to study how blood parasites are affected by their environment. First and foremost, the use of the polymerase chain reaction (PCR) and DNA sequencing has transformed how researchers detect, and classify these eukaryotic organisms. It is becoming clear that avian blood parasites, including the haemosporidians, trypanosomes and microfilariae are surprisingly diverse (Bensch et al., 2009; Svobodova et al., 2015; Sehgal et al., 2005b). Among the haemosporidian genera, the cytochrome *b* gene has most commonly been used as a “bar code” (Bensch et al., 2000). However recently, with the advent of high throughput DNA sequencing, it is apparent that the diversity of the avian haemosporidian order is even higher than previously thought. For example, presently it is known that the malaria genes *trap*, *msp-1*, *ama-1* and *chitinase* are more highly variable than cytochrome *b* when used for detecting haemosporidian diversity (Jarvi et al., 2008; Hellgren et al., 2013a; Lauron et al., 2014; García-Longoria et al., 2014). The publication of new hematozoan genomes and transcriptomes will eventually help clarify the confounding species concepts for these parasites

(Outlaw and Ricklefs, 2014; Perkins, 2014). Nevertheless, a synthesis of both microscopy and molecular approaches is the safest means to confirm infections of blood parasites from both avian and insect hosts. This is because PCR has been shown to selectively amplify certain lineages in mixed infections (Zehindjiev et al., 2012), and it cannot distinguish among the various life stages of the parasite (Valkiūnas et al., 2009). This can lead to misleading diagnoses because a positive PCR product from either avian blood or an insect does not necessarily mean that the parasite completes development in that particular host (Valkiūnas et al., 2009, 2014). On the other hand, it is also clear that some parasites can be cryptic and indistinguishable using solely microscopy (Sehgal et al., 2006; Valkiūnas et al., 2010; Palinauskas et al., 2015). In addition, there have been some efforts to use immunological methods for the detection of avian haemosporidians (Jarvi et al., 2002; Ito and Gotanda, 2005; Palmer et al., 2013), but the development of specific antibodies to avian blood parasite proteins would be a major asset for immunohistochemistry and cell sorting approaches.

Advances have also been made in how scientists measure and model environmental effects on disease transmission. With human infectious diseases, mathematical modeling has been useful for predicting and controlling epidemics (for a review see Heesterbeek et al., 2015). In addition, climate and habitats can be monitored at the microclimate scale with data loggers (da Cunha, 2015; Paaijmans et al., 2010), at the global scale with remote sensing and satellites (Hay et al., 2013), and more recently at the landscape level with drones (Fornace et al., 2014) and mobile phones (Wesolowski et al., 2012). As these methods and technologies develop, they will become increasingly useful to scientists studying the epizootiology of avian blood parasites. Some initial studies using these approaches with avian hematozoa are described below.

2. Habitat effects on avian hematozoa in the hosts

2.1. Habitat effects on avian hematozoa: birds

For parasite transmission to occur, the parasite must be in the correct life stage, the bird must be susceptible to the parasite, the vector must be present and competent, and the environment must be permissive (Fig. 1). Since birds are warm blooded, they serve as a constant and relatively safe environment for the blood parasites that have evolved to evade the host's immune system. On the other hand, during their life stages in their ectothermic insect vectors, parasites are subject to changes in temperature that can affect their development (Paaijmans et al., 2010, 2013). Thus when studying habitat effects on parasites, it is primarily the insect stages that will influence the prevalence and distribution. However, since scientists have traditionally focused on sampling birds, most of the data concerning the occurrence of avian blood parasites has been from wild-caught birds. This can lead to potential problems regarding the true patterns of distribution, since birds can fly long distances, and thus obscure the precise location of parasite transmission. In addition, methods and timing of bird capture can also greatly influence the observed prevalence and parasitemia of blood parasites (Valkiūnas, 1998; Holmstad et al., 2003; Valkiūnas, 2005). However, given these caveats, much has been learned from blood samples about how habitat can affect the prevalence, parasitemia, distribution, diversity and evolution of avian blood parasites.

2.1.1. Habitat: prevalence and parasitemia

Avian haemosporidians have been detected and studied on all the continents besides Antarctica, and prevalence can vary widely depending on the habitat and the bird species (Valkiūnas, 2005). Although numerous factors can affect the prevalence and parasitemia of blood parasites in birds, the habitat of the birds plays an

Download English Version:

<https://daneshyari.com/en/article/2055203>

Download Persian Version:

<https://daneshyari.com/article/2055203>

[Daneshyari.com](https://daneshyari.com)