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Follow-up Report to Missouri Audubon Society

Last year I received a grant from the Missouri Audubon Society to support my graduate research on avian disease ecology. The funding supported lab work on the blood samples I had obtained from mist-netted birds in the Ozarks of southern Missouri and in forests of the St. Louis region and in other parts of eastern North America. Here I will outline my research goals and report on the progress I have made as a direct result of the generous funding from the Missouri Audubon Society.

I started my graduate studies in Bob Ricklefs' lab at the University of Missouri-St. Louis (UMSL) in August of 2010. My research project began to take shape when Bob focused my attention on an important ecological observation: in any given community, most species are rare and few are abundant. Birders know this as well as anyone—how many Red-eyed Vireos do you normally hear on a walk through the woods before you find a Scarlet Tanager, or Northern Parula, or a Black-and-white Warbler? Many ecologists have argued that resource competition between species can explain this pattern (MacArthur 1972, Cody 1974). However, recent analyses of bird communities in eastern North America have failed to support this conclusion (Ricklefs 2011). Given the lack of satisfactory explanations Bob suggested I focus my research on determining the importance of parasites in regulating the commonness and rarity of birds.

There are many reasons to suspect that parasites might control the relative abundance of birds in a community. Like predators, parasites have been shown to cycle in abundance with their hosts, most well-documented in a Scottish Red Grouse (host) nematode (parasite) system (Hudson et al. 1998), and parasites have recently been shown to represent a significant portion of the overall biomass of an entire community (Kuris et al. 2008). Moreover, plant ecologists have recently shown experimentally that soil pathogens can influence the abundance of tropical tree species in a community (Mangan et al. 2010).

Some of the most common parasites of birds are blood parasites in the order Haemosporida (genera *Plasmodium*, *Haemoproteus*, *Leucocytozoon*), commonly referred to as avian malaria. Bob and other members of the Ricklefs Lab in collaboration with the Missouri Ozark Forest Ecosystem Project previously found substantial diversity of avian malaria parasites in the local bird community of the Missouri Ozarks (Ricklefs et al. 2005). For the first part of my dissertation I teamed up with (now graduated) University of Missouri-Columbia graduate student and expert ornithologist Alicia Burke and several undergraduates from UMSL including Melanie Kunkel and Elyse Coffey, to further sample birds in the Missouri Ozarks for avian malaria. Avian malaria can be detected by drawing a small sample of blood from the bird's wing, extracting total DNA and using molecular methods to screen for parasite DNA. Besides molecular screening we made blood smears on glass slides to quantify white blood cell concentrations, an important component of the immune response. One of our first results demonstrated that white blood cell profiles can be used as general indicators of malaria infection. Multivariate analysis indicated that individuals with malaria were shifted into a portion of the overall white blood cell multivariate space that was also occupied by uninfected individuals,

suggesting that these latter individuals might have harbored other pathogens. This is useful because little is known about the natural history of other parasites in these birds.

We also looked into the relationship between local avian abundance in the Ozarks and the prevalence of avian malaria (i.e., the proportion of individuals infected per species). I used abundance data interpolated from the North American Breeding Bird Survey. This analysis showed a strong positive relationship between parasite prevalence and local abundance with the most abundant species having higher parasite prevalence than rarer species (Figure 1). This result suggests a contagion hypothesis wherein the most abundant species have the highest chance of getting infected simply because they are abundant. It also suggests that malaria parasite prevalence may be a consequence of avian abundance patterns, rather than a cause.

An important next step to testing the parasite hypothesis is to look at parasites across several communities. What if an individual species' abundance were negatively related to parasite prevalence? Such a result might suggest that parasites are important in controlling abundance patterns at a bigger scale. I have begun sampling more localities to investigate this possibility, including forested areas of St. Louis in collaboration with Matthew Medeiros, a fellow graduate student in the Ricklefs Lab. I have also been able to sample in many other sites across eastern North America and am in the process of analyzing the samples in the lab.

The research I have outlined makes up a large part of my dissertation and I hope will be relevant to the fields of ecology and conservation biology. I am grateful to the Missouri Audubon Society for recognizing and supporting my research.

Literature Cited

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Figure 1

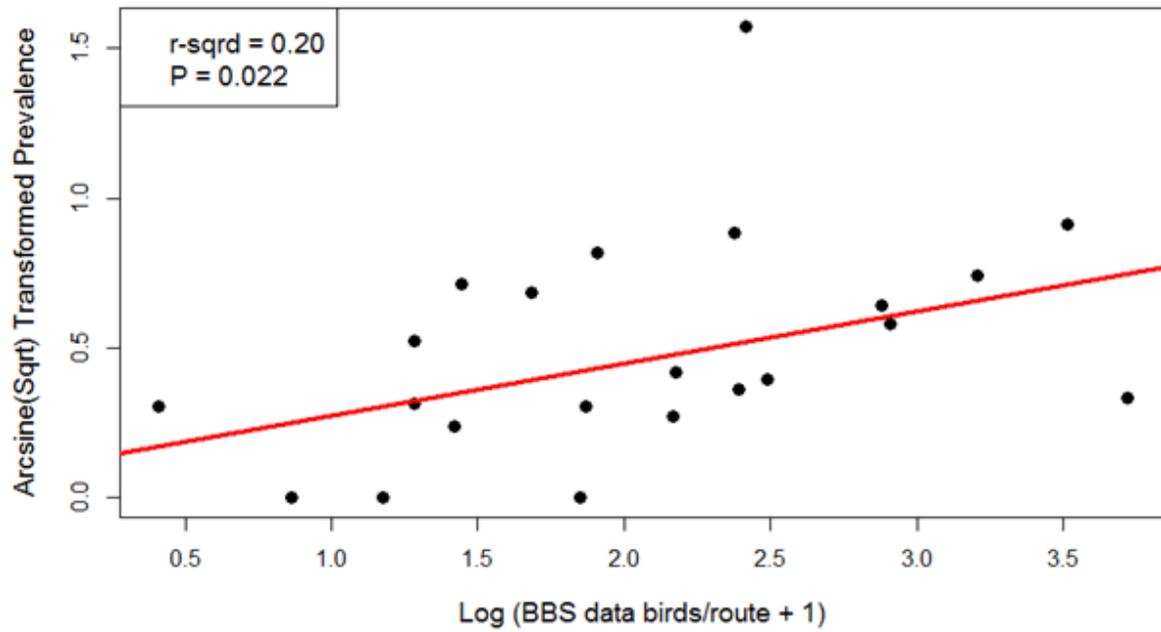


Fig. 1—The relationship between haemosporidian prevalence (acrsine-square-root transformed) and extrapolated log-transformed local abundance of birds in the Ozarks of southern Missouri (Ellis VA, et al. unpublished data). Local abundance was extrapolated from BBS data and is reported as expected number of birds per species per route.