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Occurrence of Blood Parasites in Illinois Game Birds

Avian blood parasites are found where there is suitable habitat for their vectors (i.e., mosquitos, black flies, and biting midges). They can cause mortality in both wild and captive bird populations and are known to cause lesions on the visceral tissue they invade and rupture from. While inside the host's blood cells (intracellular stage), they can induce anemia, anorexia, lethargy, depression, and death.

Infection starts with the sporozoite, a stage of the parasite found in the insect's saliva. Once the insect feeds on a bird, the sporozoites are transmitted to the host where they travel to various tissues such as liver, lung, muscle, and spleen where they replicate for several generations.

After a period of adaptation to the avian host, the parasites rupture from the tissue and enter the blood stream, invading red or white blood cells, where they grow until sexual maturity. When a biting insect takes a blood meal from an infected bird, the

parasite enters the insect and mates in its gastrointestinal tract. Sporozoites are produced and later travel to the insect's salivary glands where the cycle starts again.

Our objective was to obtain preliminary data on the current prevalence and intensity of hematozoa in wild birds from Illinois. The last research in this area was conducted in 1957 in Illinois. We sampled birds that cover a wide range of habitat types, are ubiquitous throughout the state, and have economic importance to Illinois: Mourning Doves, Wild Turkeys, Wood Ducks, and Canada Geese.



Kendall Annetti about to take a blood sample from a Mourning Dove. Photo by Samantha Carpenter, INHS

Avian blood samples were collected through collaborations with the Illinois Department of Natural Resources, researchers at the University of Illinois Champaign-Urbana, and hunters throughout the state. Blood smears were created and analyzed under a light microscope until 10,000 red blood cells had been observed. Parasites were classified to genus; *Plasmodium*, *Leucocytozoon*, or *Haemoproteus* (Table 1, Fig. 1). Prevalence was

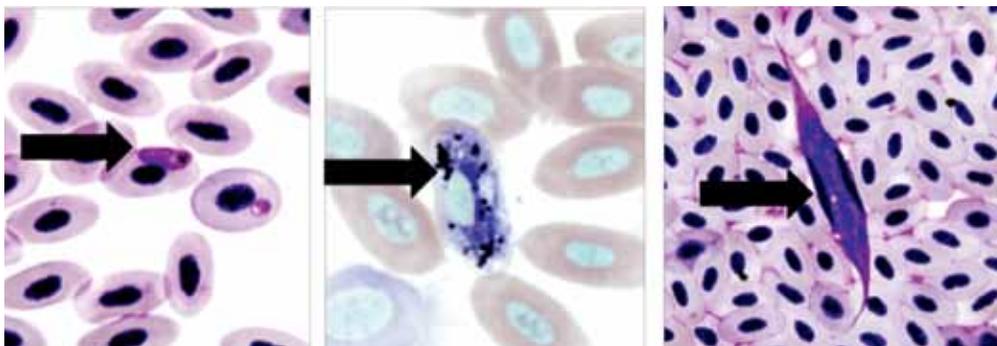


Figure 1. Three different parasite genera, from left to right: *Plasmodium* spp., *Haemoproteus* spp., and *Leucocytozoon* spp. Photomicrographs by Kendall Annetti, UIUC

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Understanding the Effects of Asian Carp on Native Fishes

Bighead and silver carp, together known as Asian carp, are large-bodied, invasive fish species native to Asia that have become established throughout much of the Mississippi River basin. Because Asian carp are planktivores, there is great concern about their effects on native fishes. For instance, large-bodied native planktivores such as bigmouth buffalo, paddlefish, and gizzard shad have lower body condition since Asian carp became established. Understanding the influences of Asian carp on native fishes and food webs is therefore an important step towards devising effective management and control strategies, and forecasting their potential impacts in novel habitats such as the Great Lakes.

An electric barrier currently operates on the Chicago Sanitary and Ship Canal to prevent upstream migration of Asian carp from the Illinois River into Lake Michigan, and although a single bighead carp was captured in Lake Calumet (approximately three miles from Lake Michigan) in 2010 and several bighead carp were captured in Lake Erie between 1995 and 2000, there is no evidence that they have yet become established in the Great Lakes. However, if they were to successfully invade, there is concern that they could devastate the Great Lakes

ecosystem and impact the associated multi-billion dollar commercial and sport-fishing industries.

To determine the effects of Asian carp on native fishes, we used controlled competition trials and field-based examination of changes in food web structure over time. In one controlled competition trial, we varied the densities of both bighead carp and native bluegill sunfish in experimental tanks to investigate the effects of both inter- and intra-specific competition. We also recorded changes in zooplankton density, macroinvertebrate density, chlorophyll-a concentration (a measure of phytoplankton abundance), and phosphorus concentration to better understand how these fish influence the entire aquatic community.

Our results were surprising. Whereas bluegill appear to exhibit density-dependent competition, the bighead carp grew larger and were in better condition when they occurred with bluegill. Bluegill rely on larger zooplankton than bighead carp; they selectively remove large zooplankters from the water column, which allowed populations of small zooplankton to increase. The increases in small zooplankton populations seemed to

benefit the bighead carp, as they can filter these smaller zooplankters out of the water column. Once the large-bodied zooplankters were removed, they were unable to recover due to the filtering capabilities of the bighead carp, which resulted in a shift to smaller-bodied zooplankton populations. Unlike some species, bluegill are omnivorous and can switch to prey sources other than zooplankton; however, it is unclear if decreased zooplankton prey resources will be detrimental.

Because the biochemical compositions of different food sources vary, and these differences are passed on to consumers such as invertebrates and fish, we can use a technique called stable isotope analysis to look at changes in the ratios of different isotopes of carbon (^{12}C and ^{13}C) and nitrogen (^{14}N and ^{15}N). Together, these reveal whether a fish has been deriving nutrients from benthic or planktonic sources and where in the food chain (at what trophic level) it has been feeding. Furthermore, these stable isotope “signatures” are conserved in fishes, which have been preserved in museums for decades. Using a grant from Illinois-Indiana SeaGrant, we examined changes in stable isotope signatures of fishes from before Asian carp invaded the Illinois River (~1960 – 1980), and compared them with modern post-invasion samples (2011) to look at changes in food web structure.

The stable isotope analysis revealed that there is high overlap between Asian carp and many native species such as gizzard shad and bluegill. We also found lower observed trophic levels of most native species since Asian carp invaded. This suggests that Asian carp are altering the zooplankton community and outcompeting native fishes.



Silver carp jumping out of the water near Havana, IL. Photo by Jonathan Freedman, INHS

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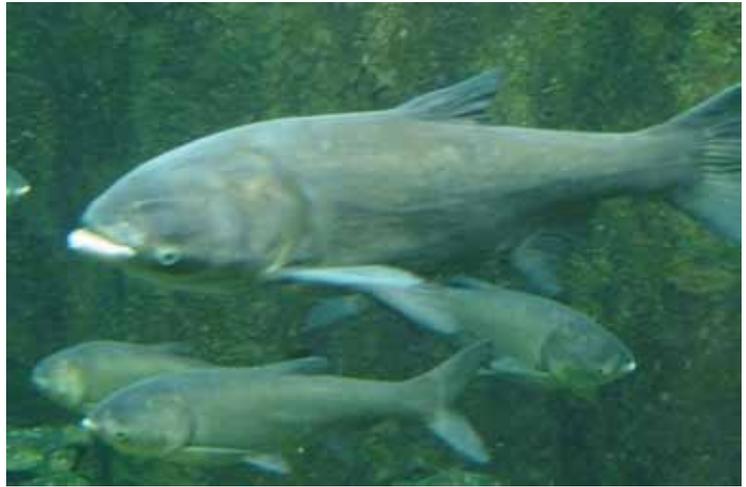
Asian carp

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Smaller zooplankton are less energy efficient prey for fishes, and consuming them may thus impact not only large native planktivores, but also small minnows that provide food for sportfish such as largemouth bass. Juveniles of most fish species also feed on plankton, so recruitment and condition of all native fish species may be affected by Asian carp.

By using controlled experiments and observational field data, we found that Asian carp compete directly with native and established species and decrease their growth rates and condition. By shifting the Illinois River plankton community to a smaller size structure, Asian carp are reducing food resources for native fishes. Plankton densities are significantly lower in the Great Lakes than in the Illinois River; if Asian carp become established in the Great Lakes, competition for plankton resources may be greater and therefore have an even larger impact on native fishes than what we observed in the Illinois River. Asian carp, with their high abundance in the Illinois River and potential threat to the Great Lakes, highlight the unique problems that invasive species can pose, both to ecosystems as well as the people that depend on those systems.

Jonathan Freedman, Kirsten Nelson, Steven Butler, Matthew Diana, and David Wahl, INHS



Bighead carp at the Shedd Aquarium, Chicago, IL. Photo by Jonathan Freedman, INHS



Experimental tanks at Sam Parr Biological Station used for determining competition between Asian carp and native fishes. Photo by Kirsten Nelson, INHS

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Does Larval Environment Influence the Microbial Communities in Mosquito Midguts?

Microorganisms are an indispensable component of our ecosystem. They play a primary role in regulating the biological, geological, and chemical systems in all environments. However, a small fraction of these microorganisms impact negatively on human, veterinary, and wildlife health by causing debilitating and sometimes life threatening diseases or by promoting the growth and survival of arthropod vectors. Mosquitoes are among the most important vectors that have an obligate relationship with microorganisms. Microbial communities associated with decaying organic matter serve as food for mosquito larvae, stimulate egg hatching, and provide chemical cues that enable gravid females to select oviposition sites that would promote larval growth and survival. Some of the microbes ingested by mosquito larvae colonize the mosquito midguts and provide important physiological functions including blood digestion, stimulation of the immune system, and protection against pathogens including arboviruses. Clearly, microbial communities are critical determinants of mosquito population dynamics and reproductive success and can directly influence the risk of mosquito-borne pathogen transmission. A better understanding of mosquito-microbe interactions could open new avenues for vector-borne disease management through manipulation of microbial communities. Currently, our knowledge of the composition, diversity, and abundance of microbial

communities in mosquito larval habitats and midguts is limited.

One of our current research goals is to generate knowledge that will enhance our understanding of mosquito-microbe interactions. Some of the research objectives we are addressing include: 1) identifying the microbial communities in different types of detritus and how they influence mosquito performance and the outcome of interspecific competition, 2) identifying the specific bacterial species that are utilized as food by mosquito larvae, and 3) elucidating how conditions of the larval environment influences microbial community assembly in mosquito larval habitats and midguts and associated impact on vector ability to transmit pathogens such as dengue and La Crosse viruses.

In efforts towards this endeavor, we conducted studies to elucidate how the larval environment influences the relative abundance of seven bacterial phyla/subphyla in the larval habitats and in mosquito midguts. Water samples and mosquito larvae and pupae were collected from waste tire habitats (Fig. 1) located at two study sites: Trelease Woods and South Farm in Urbana, IL. The pupae were allowed to eclose and larval and adult mosquito midguts were dissected under sterile conditions. Genomic DNA was extracted from the water samples and mosquito midguts and the relative abundance of the seven bacterial taxa was determined by rDNA quantitative polymerase chain reaction (qPCR). At both study sites, the relative abundances of different bacterial taxa were

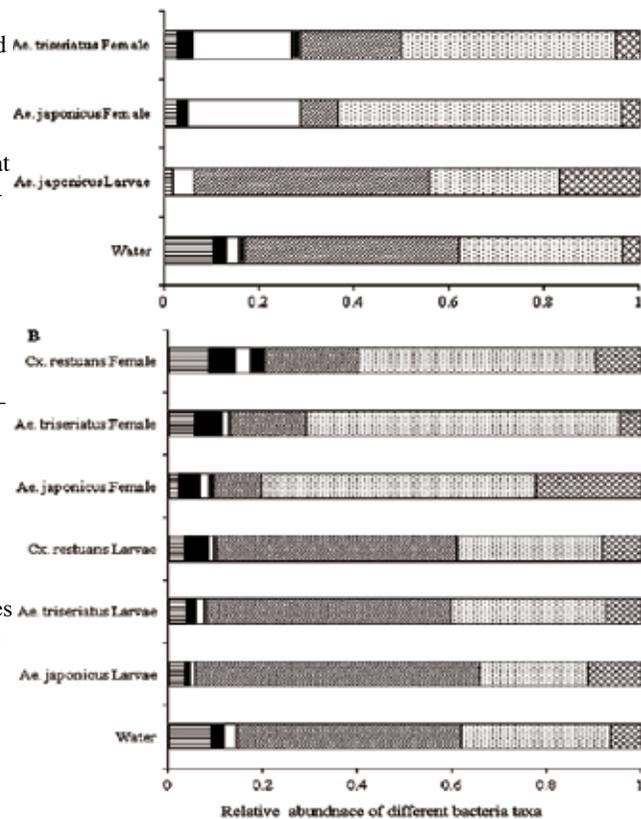


Figure 2. Relative abundance of bacterial taxa in water and mosquito samples from waste tires at A) Trelease Woods and B) U of I South Farms.

identical between the water samples and mosquito larval midguts, and completely different from adult female mosquito midguts (Fig. 2). In particular, *actinobacteria* were more abundant in water and larval midguts while *Bacteroidetes* were more abundant in adult female midguts. These findings appear to support previous findings that bacterial communities in mosquito midguts are acquired from the larval environment and that a significant proportion of these bacteria are lost during metamorphosis from pupae to adult. We are currently in the process of identifying these bacterial communities to species level, which will provide a more refined picture of the relationship between the larval environment and mosquito midgut microbial communities.

Ephantus J. Muturi and Chang-Hyun Kim, INHS

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Figure 1. Waste tire piles at the U of I South Farm study site, Urbana, IL. Photo by Ephantus Muturi,

INHS

Time Flies on Ancient Wings: Insect Fossils and Their Importance

After more than 3.5 billion years of biotic evolution on our planet, one group of organisms—the insects—has surpassed all others in terms of its biodiversity. Indeed, insects are unrivalled in terms of their numbers (both of species and individuals), their morphological and ecological diversity, and their great antiquity. The earliest insects appeared over 400 million years ago during the Early Devonian and were among the first animals to conquer life on land. Since then, they have undergone numerous explosive evolutionary radiations, culminating in their truly remarkable contemporary diversity. Understanding the origins of this diversity and reconstructing evolutionary history through the study of the insect fossil record is the primary focus of paleoentomology. In fact, the study of fossil insects is essential if we are ever to understand the big picture of insect evolution, and it can shed important light on questions concerning the relationships of modern insect groups as well as provide insight into the nature of the evolutionary process itself and the effects of global environmental change.

On the whole, insects have rather low preservation potential with their chitinous exoskeletons easily broken down by microbes *post mortem*. Disintegration of insect cuticle can take place alarmingly fast and transportation of remains in water can further reduce insect bodies to a jumble of disarticulated fragments long before they



A dragonfly (Odonata: Anisoptera) from the Early Cretaceous (~110 million years ago) Crato Formation limestone of northeast Brazil. Scale bar = 10 mm.

Photo by author

reach the site of deposition. Once in a suitable body of water where incorporation into the sedimentary record can take place, the remains must first penetrate the surface tension boundary in order to sink—no mean feat for something so small—and once buried in the sediment below, survive the microbial and chemical onslaught that can rapidly decompose and obliterate their fragile bodies. Despite these seemingly insurmountable obstacles, the insects have a rich and temporally extensive fossil record reaching back over 400 million years. This record, though incomplete, serves as an archives of insect biological history—a testament to their astonishing evolutionary success and one that we have only recently started to explore.

The oldest fossil insects are tiny fragments preserved in 410 million-year-old chert from Rhynie, Scotland. We know little about the biology of these oldest insects, but we do know that they were well adapted to life on land and probably already possessed the wings that would lead to their future ascendancy. The insects were the first animals to evolve powered flight and did so at least 100 million years before pterosaurs (extinct flying reptiles that first evolved during the Triassic), 220 million years before birds (the earliest undisputed flying birds appeared during the Cretaceous), and 300 million years before bats (which first took to the wing during the Eocene). Moreover, insects are the only invertebrates known to have evolved flight, an adaptation that has undoubtedly contributed to their remarkable success.

Fossil insects are preserved in a variety of ways, the most famous of which is undoubtedly as inclusions within amber; the fossilized resin of ancient trees. Insect fossils are also often found as organic compressions or mineral replications in sedimentary rocks, or encapsulated within crystalline mineral deposits, and even entombed within the asphalt of ancient tar seeps. Fossil insects represent an invaluable



The pygmy grasshopper Baeotettix lottiae (Orthoptera: Tetrigidae) in Early Miocene (~18 million years old) amber from the Dominican Republic. Scale bar = 2 mm. Photo by author

source of data concerning not only their own evolutionary history, but also the evolution and ecological dynamics of the ancient biotas they represent. They provide information about ancient continental configurations and the climate of the remote past. Their fossil record helps us understand significant events in the history of life. Events such as the evolution of flowering plants and the origin and spread of grasslands had significant impacts on the insects—a group well known for their sensitivity to environmental change—all of which is documented in their fossil record by changes in the composition of ancient insect faunas and the rates of their origination and extinction through time. A resource as valuable as the insect fossil record will provide unprecedented insight into the evolution of these fascinating animals and—because of the important ecological roles they play—the very nature of terrestrial ecosystems in general. The insects have witnessed the rise and fall of dinosaurs, mammoths, and mastodons, all the while evolving in a complex and inextricable chorus with the other life around them. Their ancient lineage has experienced extreme environmental and climatic changes and survived global mass extinctions time and time again. Yet, we have only just begun to scratch at the surface of this great archives of knowledge and still have much to learn about the evolution of the insects.

Sam W. Heads, INHS

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Species Spotlight

Northern Riffleshell

Jen Mui

Historically, Illinois rivers supported approximately 80 species of freshwater mussels. Scientists estimate that 17 of those species have been extirpated (5 of which are globally extinct), including the northern riffleshell (*Epioblasma rangiana*). Last seen in Illinois over 100 years ago, the riffleshell was listed as federally endangered under the Endangered Species Protection Act in 1994.

Found in the shallow, oxygen-rich riffles of medium and large rivers, northern riffleshells bury themselves fully or partially in the gravel or sand bottom, leaving their “siphons” exposed. A muscular “foot” holds the mussel in place but can also be used to move through the substrate. Water is pumped in through the incurrent or branchial aperture and out through the excurrent or anal aperture. Food particles, including detritus (organic debris formed from the decay of organisms) and plankton (small floating plants and animals) are filtered from the water.

Reproduction

Males release sperm into the water, which is taken in by females downstream. Eggs are fertilized internally and stored in a brood pouch (marsupium) located in the female’s gills. After the eggs develop into the larval glochidia stage, the female northern riffleshell uses a lure to attract a fish to serve as a host, (e.g., darter or sculpin) to complete its life cycle. The female grabs the fish by the head and transfers the larvae into the fish’s mouth. The larvae attach to the gills of the fish where they remain until they grow shells of their own and drop into the sediment.

The first part of the shell formed is the umbo or beak, which is the dorsal margin of the adult shell. The mantle (the soft tissue that surrounds the body) secretes calcium carbonate to form the hard shell throughout its life. Northern riffleshells are small, up to 2 inches in length, yellowish brown or green with two ridges separated by a sulcus (shallow depression). On the posterior end, males have a sulcus from the umbo to the ventral margin, whereas females are broadly rounded. Northern riffleshells have a shorter lifespan than many other mussel species, living approximately 15 to 20 years.

Ecosystem Function

Mussels are often referred to as “the livers of the rivers” because of their ability to filter particles and contaminants from the water. (To see mussel filtering in action, watch our video <http://www.inhs.illinois.edu/outreach/mussels>.) Mussels are also an important part of the food web, consuming detritus, bacteria, and plankton and in turn being eaten by minks, otters, muskrats, raccoons, birds, and fish. Species like the northern riffleshell are sensitive to environmental conditions and serve as a sort of “canary in the coalmine.” As their population declines, this indicates problems with water quality.



Northern riffleshell mussels with PIT (passive integrated transponder) tags. Photo by Jeremy Tiemann, INHS

Problems for Mussels

According to INHS malacologist Kevin Cummings, more than 70% of the 300 freshwater mussel species historically known from North America are threatened, endangered, or in need of conservation. A variety of causes have been identified for declines in freshwater mussel populations. Erosion leads to an increase of silt in rivers, which can suffocate and bury mussels. Chemical pollutants can be taken in and accumulate in tissues, poisoning the mussel. Large numbers of the exotic invasive Zebra mussel (*Dreissena polymorpha*) attach to living native mussels and deprive them of food, thus starving or suffocating them. Dams and other modifications alter the riverine habitat and disrupt the movement of host fish.

Re-introduction in Illinois

INHS researchers are studying the viability of re-establishing populations of northern riffleshells using mussels displaced by construction.

The Hunter Station Bridge on the Allegheny River in Pennsylvania is scheduled for removal in 2018. Perhaps the last location with a large population of northern riffleshells, it was estimated

that this project would directly impact over 25,000 mussels.

INHS researcher Jeremy Tiemann identified two rivers within the historic range of the northern riffleshell in Illinois that had protected areas, diverse high-quality mussel assemblages, and populations of host fish. In 2010, researchers attached PIT (Passive Integrated Transponder) tags to 150 individuals gathered from the bridge site in Pennsylvania and released them in the Salt Fork and Middle Fork of the Vermilion River in east-central Illinois. After a year and a half, 80% of the individuals in this pilot study were able to be located again.

In 2012, INHS researchers were part of a multi-state team that gathered 3,900 mussels from under the Hunter Station Bridge. After quarantine and tagging, 1,200 northern riffleshells were hand planted by a team of volunteers in the Salt Fork and Middle Fork rivers. Monitoring of these populations will help shape future conservation efforts for freshwater mussels in our state.

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The Naturalist's Apprentice

Mussel Crossword

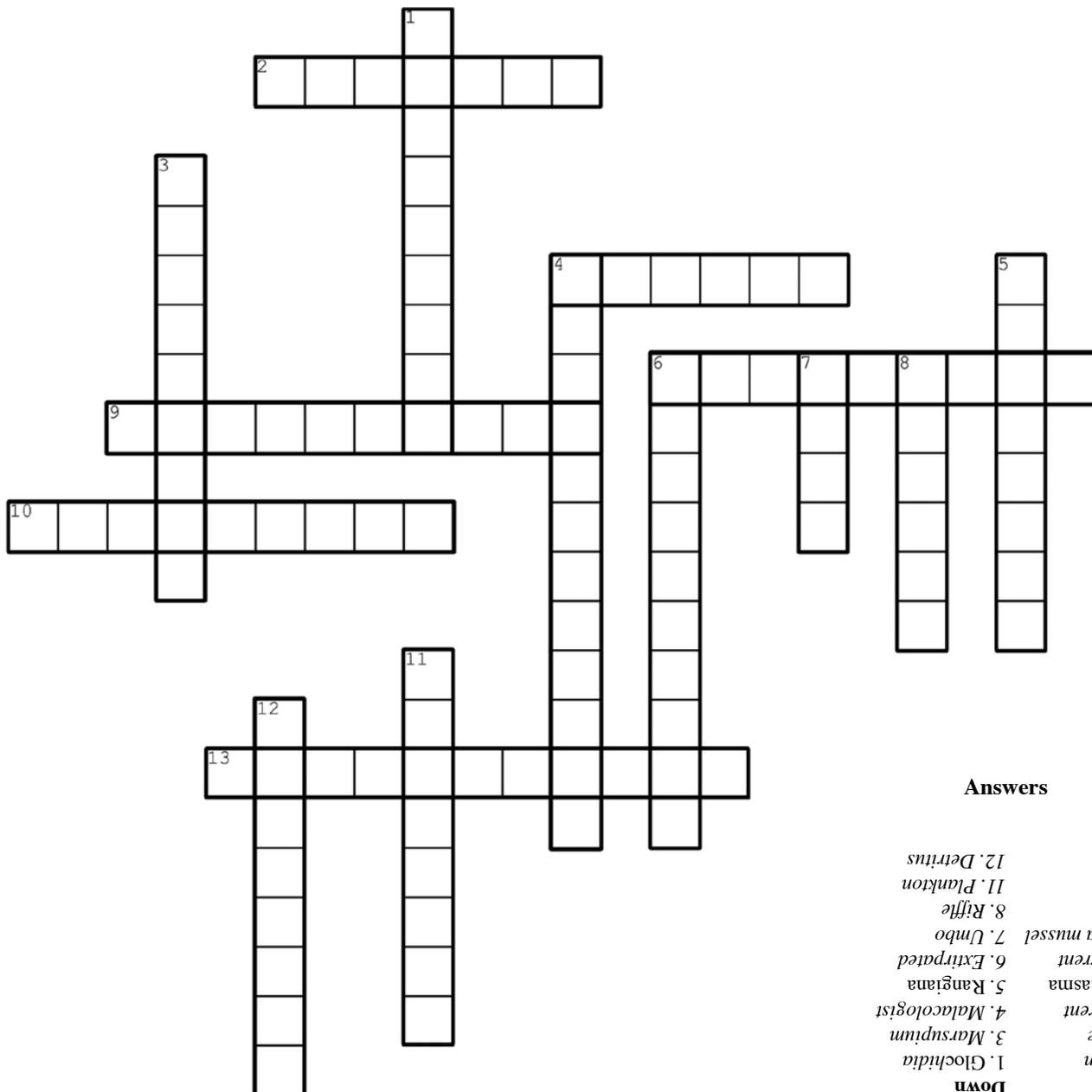
Jen Mui

Across

2. a host fish for northern riffleshell larvae
4. the soft tissue covering the body of the mussel
6. aperture used to excrete waste
9. with 5 down, scientific name of the northern riffleshell
10. aperture used to bring water and nutrients into the mussel
13. an exotic species that covers native mussel species

Down

1. larval stage of freshwater mussel lifecycle
3. brood pouch in female mussel
4. scientist that studies mussels
5. with 9 across, scientific name of the northern riffleshell
6. term for a species that is locally extinct
7. the oldest portion of the mussel shell, also called a beak
8. shallow, oxygen rich habitat in streams
11. small floating organisms eaten by mussels
12. organic debris from decaying organisms



Answers

- Across**
2. Sculpin
 4. Mantle
 9. Epitriangula
 10. Incurrent
 13. Zebra mussel
- Down**
1. Glochidia
 3. Marsupium
 4. Malacologist
 5. Excurent
 6. Extrapated
 7. Umbo
 8. Riffle
 11. Plankton
 12. Detritus

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Blood Parasites

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defined as the number of infected birds out of the total number sampled. Intensity was defined as the number of parasitized blood cells out of the total number of blood cells examined.

Of the 77 Mourning Doves sampled, 44.2% (34/77) were infected with at least one parasite genus and had the most intense infection, ranging from 0.002–5.14% infected red blood cells. Blood parasite infections were seen in 73% (11/15) of the Wild Turkeys and exhibited high intensity infections ranging from 0.001–3.48% of cells infected.

These results are comparable with a study conducted in 1995 on Wild Turkeys from South Carolina where 100% of the turkeys examined were infected (n=76) but exhibited a lower infection intensity (0.001–.046%) than in our study.

Wood Ducks and Canada Geese had an infection prevalence of 5.4% (6/111) and 11.8% (2/17), respectively. Our study differs with previous studies done in Michigan where 100% of the Canada Goose goslings were infected and up to 87% avian mortality was documented. Overall parasite prevalence and prevalence by parasite genera are shown in Table 1.

There were no significant differences in parasitemia due to age or sex in our sampled birds. However, we did observe trends towards hatch-year birds having more intense infections than after-hatch year birds, and males having more intense infections than females. Future studies to better assess the role of landscape and environmental factors (temperature, soil moisture, and land usage) on parasite transmission and infection rates in both avian and vector communities as well as monitoring hematozoa

related mortalities would be beneficial to the overall understanding of hematozoa ecology.

This study was conducted by Kendall Annetti who completed her undergraduate honors project with the UIUC Departments of Animal Sciences and Integrative Biology in the lab of Dr. Nohra Mateus-Pinilla at the Illinois Natural History Survey. Funding was provided by the Wildlife Restoration Project W-146-R, James Scholar Honors Program at the University of Illinois (LAS and ACES), ISAS, the Robert H. Davis Undergraduate Research Prize, and the National Wild Turkey Federation. Assistance was provided by Illinois hunters, Samantha Carpenter and Aaron Yetter at INHS, and IDNR biologists Wade Louis, Darryl Coates, and Dan Newhouse.

Kendall Annetti, UIUC and Nohra Mateus-Pinilla, INHS

Table 1. Parasite prevalence for Wood Ducks, Canada Geese, Mourning Doves, and Wild Turkeys from Illinois birds sampled in 2010 and 2011.

Order and Species	No. Sampled (n)	Infected n [%]	Prevalence of infection by parasite genera (%)		
			H.	P.	L.
Anseriformes					
Wood Duck <i>Aix sponsa</i>	111	6 (5.4%)	3.6	2.7	0
Canada Goose <i>Branta canadensis</i>	17	2 (11.8%)	0	11.8	0
Columbiformes					
Mourning Dove <i>Zenaidura macroura</i>	77	34 (44.2%)	36.4	10.4	2.6
Galliformes					
Wild Turkey <i>Meleagris gallopavo</i>	15	11 (73.3%)	53.3	60.0	13.3
Total	222	23.9 (%)	18.0	10.0	1.8

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