Parasite Communities in Populations of Greater and Lesser Scaup in Green Bay, WI

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Introduction

- Greater (*Aythya marlia*) and Lesser (*Aythya affinis*) Scaup populations have decreased across North America
- Non-native trematodes (flatworm parasites) have been linked to major scaup die-offs near the Mississippi River.
- Scaup have abundant and diverse parasite communities based on their diet and behavior.
- Our study focused on the Green Bay, WI area and specifically investigated trematodes including potentially pathogenic species.
- We tested the hypothesis that demographic variables such as sex, age, and species differences and timing of migration could explain variation in parasite communities.

Fig. 1. Hunter-donated Lesser Scaup specimen prior to dissection in lab.

Methods

- Waterfowl: Greater Scaup and Lesser Scaup
  - 20 birds in total from Green Bay, WI Area
  - Hunter donated in 2019 and 2020
- Procedures
  - Recorded Species, Age, Sex and Date of Harvest
  - Specimens were dissected using standardized protocols (Lutz et al. 2017)
    - Organs and other tissues were separated individually to collect endoparasites (Figs. 1 and 2)
  - Parasites found were identified using 10-60X magnification to lowest taxonomic level and counted
- 2020 data analyzed using Generalized Linear Models in R.

Fig. 2 Researchers Nicole and Gina set up dissection area with separate dishes for each organ and tissue for parasite isolation.

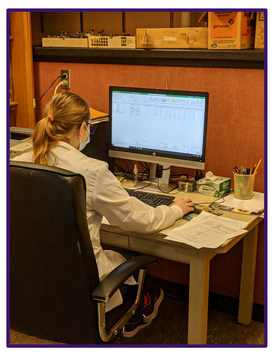

Fig.3 Researcher Allison entering data prior to statistical analysis.

Results

Overall trematode prevalence was 90% (18 of 20 hosts with at least one trematode). Parasite Intensity ranged from 1-169 worms. We discovered 12 morphotypes of trematodes including the three potentially pathogenic taxa.

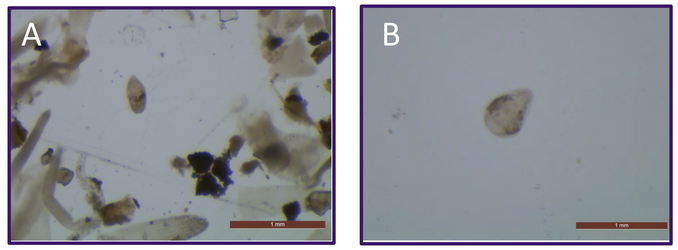

Fig.4 Potentially pathogenic trematodes (A) *Leyogonimus* sp. and (B) *Sphaeridiotrema* sp. extracted from a Scaup intestine. Scale bar = 1 mm.

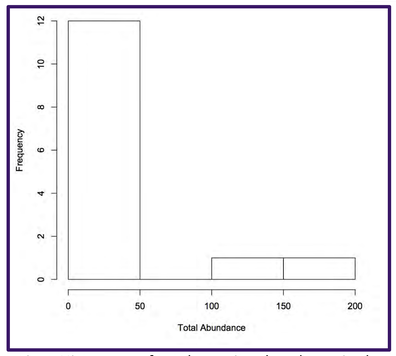

Fig. 5 Histogram of total parasite abundance in the 2020 Scaup data. The graph shows a negative binomial distribution and based on this we ran generalized linear models for our statistical test.

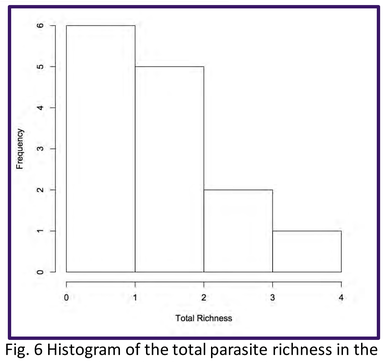

Fig. 6 Histogram of the total parasite richness in the 2020 Scaup data. This dataset was also negative binimal. Total richness varied from 1-4 parasite taxa. Based on generalized linear models, none of our tested variables were statistically significant.

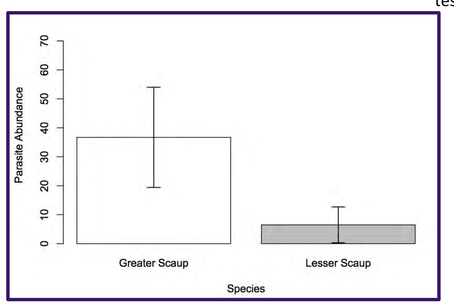

Fig. 7 Average parasite abundance in Greater Scaup and Lesser Scaup. Greater Scaup, on average, had higher parasite abundance than the Lesser Scaup. This difference was statistically significant (P=0.0526).

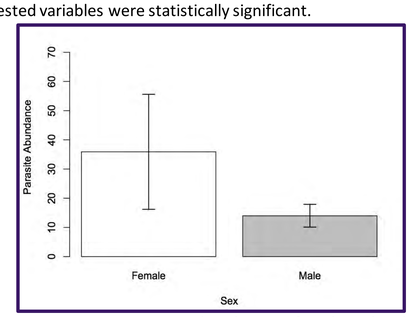

Fig. 8 Average parasite abundance in female and male Greater Scaup. Females, on average, had higher parasite abundance than males. This data was marginally significant (P=0.06225).

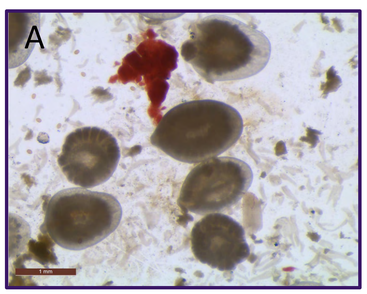

Fig. 9 Potentially pathogenic trematode (A) *Cyathocotyle* sp. and a representative of the most common family of trematode observed (B) Echinostomatidae extracted from a Scaup intestine.

Discussion

- We uncovered a diverse and abundant community of trematodes in both species of scaup. We found the three non-native pathogenetic trematodes that have been linked to higher mortality rates in Lesser Scaup in the Mississippi River area in Wisconsin and Illinois and American Coot and Lesser Scaup in the Shawano Lake, WI area (England et al. 2018, Hermann and Sorensen 2011, Ross 2008).
- In order to test all host variables, we analyzed data from 2020 because 2019 data did not include host age.
- Our results indicated that the abundance of parasites was greater in Greater Scaup p = 0.05026 (Fig. 7) suggesting that there are species specific differences in exposure or physiological suitability for parasites.
- Among Greater Scaup, females are about twice as infected than males with p = 0.06225. (Fig. 8). This could be due to diet difference because female waterfowl consume more snails for the calcium content and snails are key intermediate hosts in the parasite life cycles (Lozano 1991).
- None of our predictor variables were significant for parasite richness, though our study was limited by some identifications to the family or genus level. DNA analysis is needed to properly ID some parasites.
- Some trematodes were only found in a single host and our analysis could not account directly for these rare species.
- Further research will help understand the distribution of pathogenic species and the native Scaup parasite community in the understudied Green Bay, WI region.

References

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