Phthiraptera and Acari Collected from 13 Species of Waterfowl from Alabama and Georgia

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Valentina R. Garbarino[1,*], Joshua W. Campbell[1], Joseph O'Brien[2],
Heather C. Proctor[3], and Bilal Dik[4]

Abstract - Waterfowl, including ducks, geese, rails and others, are host to a great diversity of ectosymbiotic arthropods. In this study, we collected ectosymbionts from waterfowl and analyzed taxon richness and total abundance to determine whether there were differences in the mite and louse assemblages of waterfowl of different species, genera, sexes, and feeding behaviors. Data were collected from 53 individual birds from 13 waterfowl species and 5 waterfowl genera taken from Georgia and Alabama. A total of 11 louse species and 7 feather and nasal mite species were collected from the waterfowl samples. *Fulica americana* (American Coot) harbored the highest louse abundance and taxon richness but had the lowest abundance of mites. Most significant results were driven by the *Fulica* assemblage. Significant sex differences were detected only between male and female anseriform birds, in which female hosts demonstrated higher mean numbers of ischnoceran lice than male hosts. No significant differences in mite abundance between waterfowl sex or genera were observed, but more mite taxa were found on diving waterfowl than on dabbling species. These data will help to provide a foundation for future research on the ecology of waterfowl ectosymbionts in the southeastern United States.

Introduction

Obligatory ectosymbionts are organisms that live on the surface of a host's body, which provides all of the necessities for the maintenance and proliferation of all life stages (Boyd 1951). Birds host many ectosymbionts: some are parasites, some are commensals, and some may be mutualists (Proctor 2003). These include flies, lice, fleas, mites, and ticks (Proctor and Lynch 1993). Fossil evidence has shown that lice (Wappler et al. 2004) and mites (Dalgleish et al. 2006) associated with waterfowl were in existence as early as 44 million years ago. These and other ectosymbionts coevolved with their hosts, specializing for the specific micro-environments present on different host birds (Wappler et al. 2004).

Within the Order Phthiraptera (lice), two suborders parasitize birds: Amblycera and Ischnocera (Ash 1960). Amblyceran lice have shorter, thicker bodies (Boyd 1951), live directly on the surface of the host's skin, feed on fragments of

[1]High Point University, 833 Montlieu Avenue, High Point, NC 27262. [2]USDA- Forest Service, Forestry Sciences Laboratory, 320 Green Street, Athens, GA 30602-2044. [3]University of Alberta, CW405 Biological Sciences Building, 116 Street and 85th Avenue, Edmonton, AB, Canada T6G 2E9. [4]Selçuk Üniversitesi, Veteriner Fakültesi, Parazitoloji Anabilim Dalı, Alaaddin Keykubat Kampüsü, 42250-Selçuklu, Konya, Turkey. [*]Corresponding author - valentina.garbarino@hotmail.com.

skin and secretions, and chew on emerging tips of new feathers to obtain blood (Ash 1960). Ischnoceran lice vary in body shape but are often narrower than Amblyceran lice (Boyd 1951), and tend to live and feed on the non-living parts of the host's feathers (Ash 1960). Both can be harmful to their individual host, but Amblycera tend to cause more irritation to the host and can elicit an immune response or cause infection when their excrement interacts directly with open areas of the host's skin (Møller and Rózsa 2005). Feeding damage caused by Ischnocera can decrease the host's attractiveness to mates by altering plumage color, and negatively affects thermoregulatory and flying capabilities (Vas et al. 2011). Heavy louse loads may result in increased effort in preening, reducing time available for obtaining food or mates (Brown et al.1995), and can increase the chances of hosts being parasitized by endoparasites transmitted by louse vectors (Bartlett 1993). Differences in ectosymbiont loads on birds exist based on host behavior, sex, and relative size (Felso and Rózsa 2007, Galván et al. 2007, Kleindorfer and Dudaniec 2009).

Most feather mites (Acari: Astigmata—Analgoidea and Pterolichoidea) feed on uropygial oils and adherent debris such as fungal spores, rather than feeding directly on feather material itself (Proctor 2003). In studies of wild birds, there is little evidence of negative effects of feather mites (Proctor 2003). In fact, correlational studies frequently show a positive relationship between high mite loads and health conditions when the host is not intensely infested (Blanco et al. 1997). It is plausible that mites, instead of being parasites, may actually be mutualists that function in removing excess body oils or potentially harmful organisms from their host's body (Dowling et al. 2001). However, the very large correlational study of Galván et al. (2012) found only a slight positive relationship between host condition and mite load, suggesting that, in most cases, feather mites are commensals.

Most recent multi-host surveys of avian ectosymbionts have focused on hosts in the Order Passeriformes, and have demonstrated correlations between ectosymbiont load and host social behavior and mass (Kleindorfer and Dudaniec 2009), size of uropygial gland and mite abundance (Galván et al. 2007), and host sex (Clayton et al. 1992). Areas that have been studied include ectosymbiont abundance (Sychra et al. 2008) and host physical and behavioral adaptations to combat ectosymbiont loads (Bush et al. 2011). Although a few studies have attempted to identify all ectosymbionts associated with certain waterfowl species (e.g., McDaniel et al. 1966, Mourik and Norman 1985), there is a lack of information on taxon richness and total ectosymbiont abundance for waterfowl in the southeastern United States.

In this study, we gathered 53 hunter-killed birds from 13 species, 5 genera, and two orders of aquatic birds (Anseriformes and Gruiformes) and removed all ectosymbionts. The purpose of this study was to examine ectosymbiotic abundance and taxon richness on several genera of waterfowl in the southeastern United States, and determine whether ectosymbiont load and diversity varied across waterfowl genus, sex, or feeding behavior.

Materials and Methods

Fifty-three hunter-killed waterfowl from thirteen waterfowl species were examined for ectosymbiont abundance and taxon richness. These included one species from the Order Gruiformes: *Fulica americana* Howard (American Coot) (*n* = 7), and twelve species from the Order Anseriformes: *Aix sponsa* L. (Wood Duck) (*n* = 10), *Anas acuta* L. (Northern Pintail) (*n* = 1), *Anas americana* Gmelin (American Wigeon) (*n* = 1), *Anas clypeata* L. (Northern Shoveler) (*n* = 2), *Anas crecca* L. (Green-winged Teal) (*n* = 5), *Anas platy-rhynchos* L. (Mallard) (*n* = 4), *Anas rubripes* Brewster (American Black Duck) (*n* = 1), *Anas strepera* L. (Gadwall) (*n* = 15), *Aythya americana* Eyton (Red-head) (*n* = 1), *Aythya collaris* Donovan (Ring-necked Duck) (*n* = 1), *Aythya marila* L. (Greater Scaup) (*n* = 3), and *Bucephala albeola* L. (Bufflehead) (*n* = 2). Waterfowl were legally harvested between November and December 2008–2011 from Cherokee and Morgan counties in Alabama and Floyd and McIntosh counties in Georgia. Harvested waterfowl were immediately retrieved after being shot, and placed individually into air-tight zip-lock bags. All birds appeared healthy and had no noticeable physical abnormalities, nor did they appear emaciated. Bagged waterfowl were frozen until they could be washed and examined. All waterfowl were sexed by plumage characteristics, except for American Coots, as these birds are not sexually dimorphic.

Waterfowl were placed into a sealed bucket of soapy water and manually agitated for approximately 5 minutes. The water was decanted and filtered through a 53-μm sieve. This agitation process was done twice for each bird. After two soap washes, each bird was thoroughly rinsed, and the rinse water was also filtered through the 53-μm sieve. The material accumulated in the sieve was transferred to 70% ethanol and examined. All ectosymbionts were counted and initially sorted into morphotaxa using a dissecting microscope. Representatives of each morphospecies were prepared and identified to the lowest taxonomic level possible. Lice were cleared in 10% KOH for 24 hours, washed in distilled water for one day, and then in consecutive solutions of 70, 80, 90, and 99% alcohol for 24 hours each before mounting. Lice samples were mounted on slides using Canadian balsam under an Olympus SZ60 microscope, and identified using a Leica DM 750 microscope. Lice were identified using Castro and Cicchino (1983), Cicchino and Emerson (1983), Clay (1935, 1953), Clay and Hopkins (1954, 1960), Eichler (1976), Eichler et al. (1980, 1981), Emerson (1955), Keler (1960), Kellogg (1896), Nelson and Price (1965), and Price (1971, 1974). Mites were cleared overnight in 80% lactic acid, mounted in PVA medium (catalogue number 6371A, BioQuip Products, Rancho Dominguez, CA), and cured on a slide-warmer at 45 °C for four days prior to being examined using a DIC illuminated compound microscope. Feather mites were identified to genus using Gaud and Atyeo (1996), and to finer levels using more specific taxonomic literature. Rhinonyssid (nasal) mites were identified using Knee and Proctor (2010). Voucher specimens

of lice have been stored in the louse collection of the Parasitology Department of the veterinary facility of Selcuk University in Konya, Turkey, and representative samples of mites have been stored in the Auburn University invertebrate collection.

Ectosymbiont abundance and taxon richness data were analyzed with GLM (Statistix 9 program, Analytical Software, Tallahassee, FL) to conduct one-way ANOVAs with common ($n \geq 4$) waterfowl species, feeding behavior (dabbling vs. diving), genus, and sex as the independent variables and ectosymbiont abundance and taxon richness as dependent variables. Tukey's multiple comparison procedure in the same program was used to determine differences in relative abundances and taxon richness. Buffleheads ($n = 2$), Northern Pintail ($n = 1$), American Wigeon ($n = 1$), Northern Shoveler ($n = 2$), and American Black Duck ($n = 1$) were excluded for some tests due to low sample size of these waterfowl species.

To examine ectosymbiont assemblage structure, we used non-metric multidimensional scaling analysis (NMDS) of trends in abundance of ectoparasites in the waterfowl samples. We chose NMDS because this method is more robust to variability in underlying distribution patterns in species responses than are eigenvalue-based ordination techniques (Clarke 1993, Gaiser et al. 1998). We also performed Multi-response permutation procedures (MRPP) on the ectosymbiont data to test for differences in assemblages among waterfowl genera and sex. MRPP is a nonparametric test of differences in taxon composition/relative abundance between two or more groups. For both the NMDS and MRPP, we used Bray-Curtis/Sørensen distance measures, as these reduce the effect of outliers on the analysis (McCune and Grace 2002). American Coots were not separated or analyzed by sex, because they cannot be accurately sexed by traditional methods (Shizuka and Lyon 2008) as their plumage was not sexually dimorphic and internal characteristics were underdeveloped and ambiguous during our sampling period.

Results

A total of 2094 avian lice and 24,892 bird-associated mites were collected from the 53 waterfowl individuals. Twenty-nine percent of the lice collected were Amblycera, and 71% were Ischnocera. Eleven louse (Table 1) and seven mite species (Table 2) were identified from the waterfowl samples. Five additional louse morphotaxa were collected as immatures that could not be positively identified. Total ectosymbiont abundance did not differ among waterfowl genera ($P = 0.69$) or between the two categories of feeding behavior (dabbling or diving; $P = 0.31$).

Lice

Overall, lice were found in significantly higher abundances ($P = 0.001$) on *Fulica* compared to other waterfowl genera, a pattern holding true for both

Table 1. List of louse species/taxa found on waterfowl species. Numbers in table indicate the total number of lice of that taxon collected. Number in parentheses is the number of waterfowl hosts they were collected from. Louse species identified only to genus could not be identified to species because samples were from nymphal stages.

| | Amblycera | | | | | | | Ischnocera | | | | | | | | |
	Hs[1]	Hc[1]	Hl[1]	Pp[1]	Ts[1]	Tq[1]	Ls[2]	As[3]	Ac[3]	Am[3]	Ad[3]	Ai[3]	Fs[3]	Fl[3]	It[3]	Ra[3]
Order Anseriformes																
Aix sponsa (Wood Duck)		7 (3)			8 (5)			56 (6)		54 (7)		69 (9)				
Anas acuta (Northern Pintail)	4 (1)				5 (1)			1 (1)								
Anas americana (American Wigeon)								5 (1)								
Anas crecca (Green-winged Teal)						3 (3)			8 (2)							
Anas clypeata (Northern Shoveler)								6 (1)	8 (2)			11 (2)				
Anas platyrhynchos (Mallard)					2 (1)			5 (2)	23 (4)			115 (4)				
Anas rubripes (American Black Duck)									12 (1)		1 (1)					
Anas strepera (Gadwall)	8 (2)					39 (12)		95 (11)	199 (15)			400 (10)				
Aythya americana (Redhead)			9 (1)					22 (1)		4 (1)		48 (1)				
Aythya collaris (Ring-necked Duck)								12 (1)		4 (1)	2 (1)	4 (1)				
Aythya marila (Greater Scaup)								1 (1)		5 (2)		12 (2)				
Bucephala albeola (Bufflehead)								1 (1)				2 (1)				
Order Gruiformes																
Fulica americana (American Coot)				521 (7)			1 (1)						155 (7)	119 (6)	184 (7)	650 (6)

[1]Menoponidae: Hs = *Holomenopon* sp., Hc = *Holomenopon clauseni* Price, Hl = *Holomenopon leucoxanthum* Burmeister, Pp = *Pseudomenopon pilosum* Scopoli, Ts = *Trinoton* sp., Tq = *Trinoton querquedulae* L.
[2]Laemobothriidae: Ls = *Laemobothrion* sp.
[3]Philopteridae: As = *Anaticola* sp., Ac = *Anaticola crassicornis* Scopoli, Am = *Anaticola mergiserrati* De Geer, Ad = *Anatoecus dentatus* Scopoli, Ai = *Anatoecus icterodes* Nitzsch, Fs = Fulicoffula sp., Fl = *Fulicoffula longipila* Kellogg, It = *Incidifrons transpositus* Kellogg, Ra = *Rallicola advenus* Kellogg.

Table 2. List of mite species/taxa found on waterfowl species. All are feather mites except for Rhinonyssidae, which are nasal mites. Numbers in table indicate the total number of mites of that taxon collected. Number in parentheses is the number of waterfowl hosts they were collected from. Species names in parentheses are the most likely species due to adult stages being unavailable.

	Alloptidae	Avenzoariidae	Freyanidae	Pterolichidae		Analgidae	Rhinonyssidae
	Brephosceles sp.	Bdellorhynchus polymorphus Trouessart	Freyana anatina Koch	Grallobia sp. (G. fulicae Trouessart)	Grallolichus proctogamus Trouessart	Megninniella sp. (M. gallinulae Buchholz)	Rhinonyssus rhinolethrum Trouessart
Order Anseriformes							
Aix sponsa (Wood Duck)	1259 (9)	51 (2)	2924 (10)				1 (1)
Anas acuta (Northern Pintail)	176 (1)		41 (1)				
Anas americana (American Wigeon)	53 (1)		383 (1)				
Anas crecca (Green-winged Teal)	113 (4)		1069 (5)				
Anas clypeata (Northern Shoveler)	34 (2)	56 (2)	302 (2)				
Anas platyrhynchos (Mallard)	7 (1)	152 (2)	1473 (4)				
Anas rubripes (American Black Duck)	33 (1)		776 (1)				
Anas strepera (Gadwall)	1184 (15)		11,092 (15)				
Aythya americana (Redhead)	16 (10)	49 (1)	287 (1)				
Aythya collaris (Ring-necked Duck)	31 (1)	119 (1)	196 (1)				
Aythya marila (Greater Scaup)	387 (3)	192 (3)	705 (3)				
Bucephala albeola (Bufflehead)	3 (1)	18 (1)	57 (2)				
Order Gruiformes							
Fulica americana (American Coot)	581 (6)		393 (4)	326 (5)	97 (4)	256 (6)	

Amblycera ($P < 0.0001$) and Ischnocera ($P = 0.005$) when examined separately (Fig.1). Louse taxon richness was also significantly ($P < 0.001$) higher on *Fulica* compared to other waterfowl genera. *Anaticola* was the only louse genus found on all species of Anseriformes (Table 1). Female Anseriformes hosted significantly more ischnoceran lice than did male Anseriformes ($P = 0.046$).

Mean louse abundance was significantly ($P < 0.001$) higher on diving waterfowl than on dabbling birds. Amblyceran abundance was marginally greater on divers than dabblers ($P = 0.09$), while ischnoceran abundance was significantly greater ($P = 0.027$) on divers compared to dabblers. Diving birds also exhibited higher lice taxon richness ($P = 0.01$) compared to dabblers; however, this trend was probably driven by *Fulica*.

Mites

The most abundant species of feather mite collected was *Freyana anatina* Koch, comprising 79% of the collected mites. Only two taxa of feather mites were found on all species of waterfowl: *Freyana anatina* and members of the genus *Brephosceles* (Table 2). The mite taxa *Grallobia* sp., *Grallolichus proctogamus* Trouessart, and *Megniniella* sp. were found only on *F. americana*. A single specimen of nasal mite (Mesostigmata: Rhinonyssidae), *Rhinonyssus rhinolethrum* Trouessart, was found on *Aix sponsa* (Table 2).

Mite abundance showed no significant differences among waterfowl genera ($P = 0.27$; Fig. 2). However, several individual mite taxa were found in significantly higher abundances on certain waterfowl genera. For example, genus *Aythya* had significantly more *Bdellorhynchus* compared to all other Anseriformes and *Grallolichus proctogamus* was found only on *Fulica*. Overall, *Fulica*
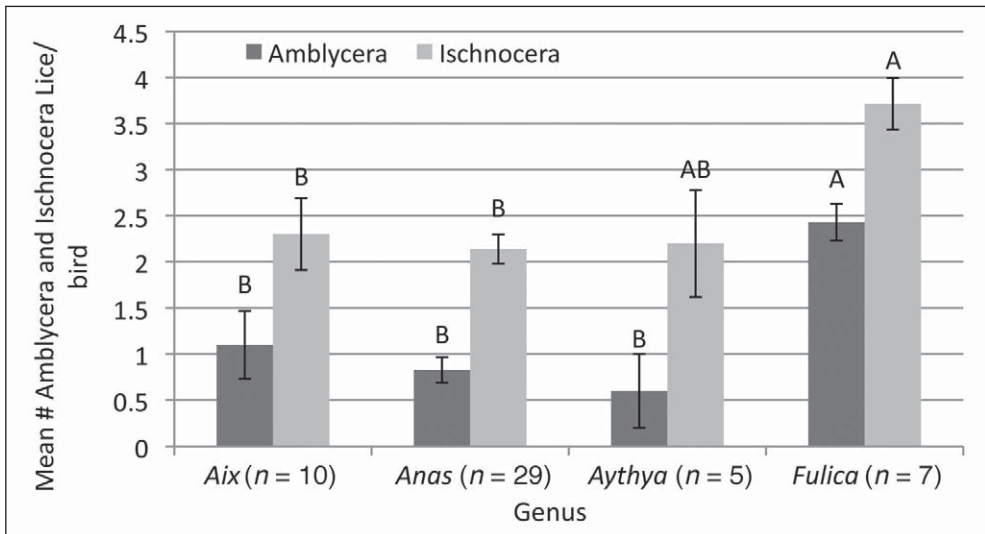

Figure 1. Mean number (± SE) of Ischnocera and Amblycera lice per individual waterfowl of the four most abundant host genera. Within Amblycera and Ischnocera, columns with the same letter(s) are not significantly different at $P \geq 0.05$ according to Tukey's multiple comparison procedure.
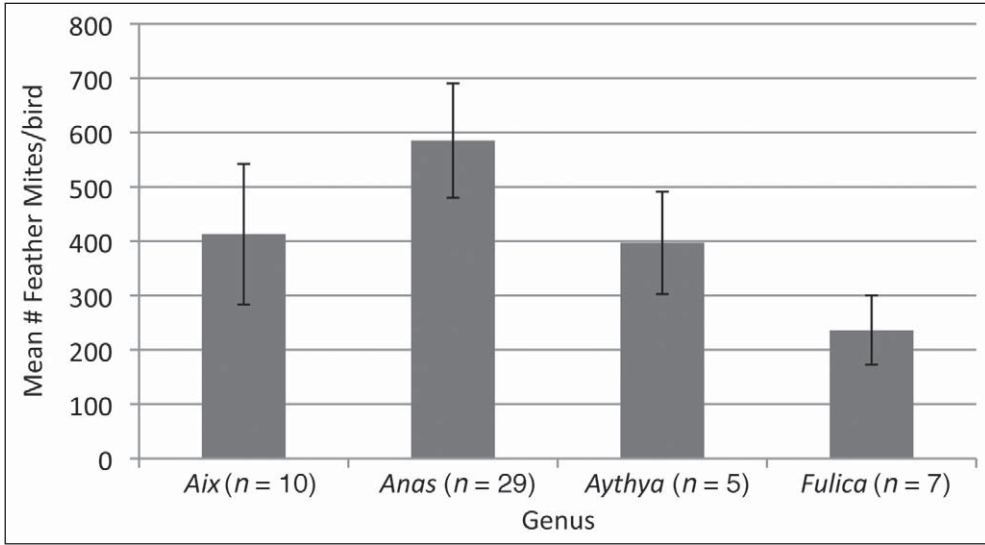
Figure 2. Mean number (± SE) of total feather mites per individual waterfowl of the four most abundant host genera.
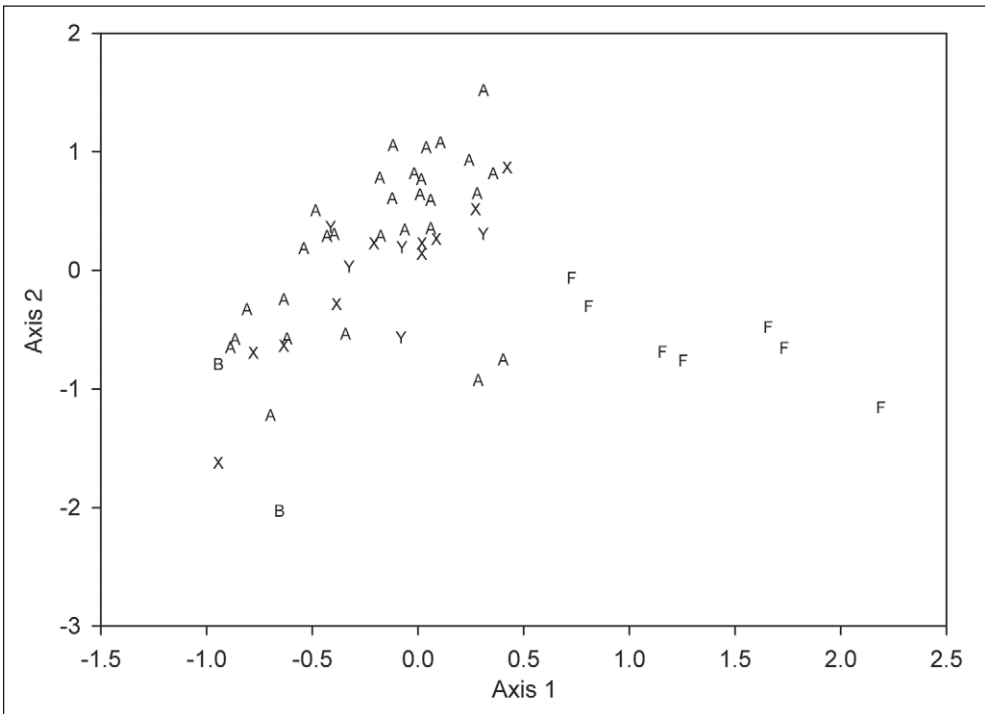

Figure 3. NMDS ordination of ectosymbiont community assemblages on individual waterfowl samples. Letters mark individual sample scores in ordination space and represent variation in ectosymbiont communities among the individual birds analyzed. Letters indicate the waterfowl genera of the samples: A = *Anas*, B-*Bucephala*, F = *Fulica*, X = *Aix*, Y = *Aythya*. The ordination shows that Axis 1 variation was driven mainly by the different ectosymbiont communities found on the Anatids versus *Fulica,* while Axis 2 variation was driven mainly by variation in the ectosymbiont communities within the Anatidae.

also harbored significantly higher mean taxon richness of feather mites (P = 0.001) compared to other host genera except *Aythya*. No significant difference was detected between mite abundance or richness relative to waterfowl sex.

The taxon richness of feather mites was significantly higher on divers than on dabblers ($P < 0.001$). Total mite abundance was greater on dabblers than divers, though not to a statistically significant degree ($P = 0.07$).

Ectosymbiont assemblage structure

In order to test the optimal dimensionality of the NMS ordination, we used a Monte Carlo test—a randomization procedure where the data matrix is shuffled and the ordination rerun. The original assemblage is compared to the set of randomly constructed assemblages to determine the optimal dimensionality of the NMDS. In our case, the results indicated a two-dimensional solution was optimal (final stress = 9.85, $P = 0.04$). The first two axes of the NMDS ordination explained 86.0% of the original variance, with axis 1 explaining 46% and axis 2 explaining an additional 37%. Apparently, ectoparasite assemblages were at least partially structured by waterfowl genus along Axis 1 (Figs. 3, 4). This finding is consistent with the MRPP, which indicated that there were significant differences in the ectosymbiont assemblages among waterfowl genera (A = 0.138,
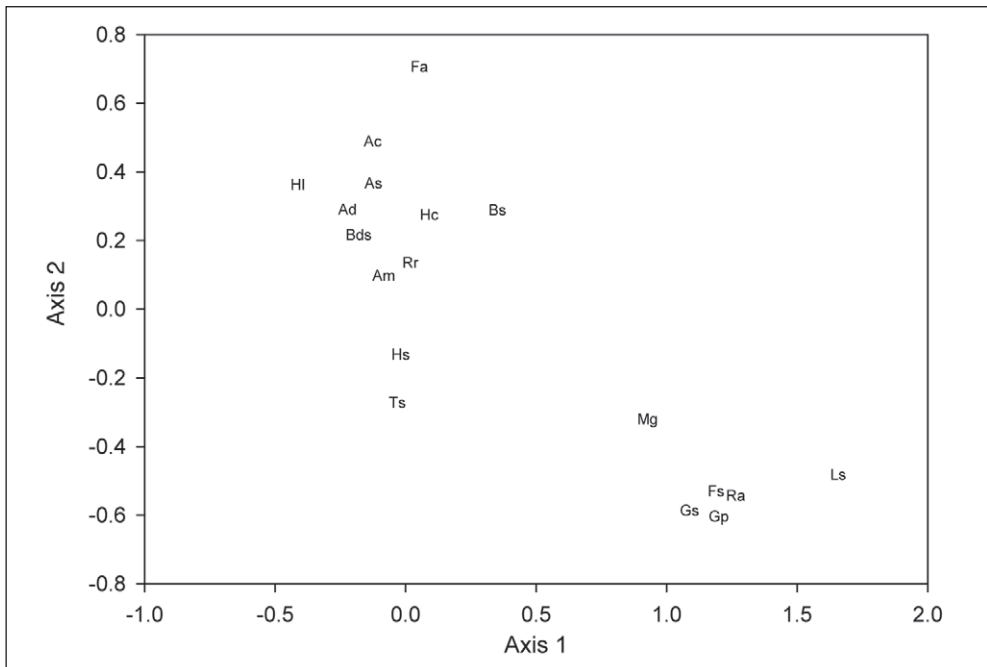

Figure 4. NMDS species scores for ectosymbionts. Labels indicate the first letter of the genus and species, or the first two letters of the genus where labels would be duplicated. As in Figure 3, variation in Axis 1 scores were driven by the different ectosymbiont taxa associated with the coots (cluster in the lower right of ordination), while variation in Axis 2 scores were driven by variation in taxa associated with the Anatidae (cluster in upper left of ordination).

$P < 0.0001$). The ectosymbiont assemblage on *Fulica* differed from all other genera, and the assemblages on *Aythya* and *Bucephala* differed significantly, but no other genera were significantly different ($P = 0.05$). A test for differences (excluding *Fulica*) indicated that there were no differences in assemblages found on males versus females (A = 0.003, $P = 0.30$).

Discussion

Overall, American Coots (genus *Fulica*) hosted more lice than other genera of waterfowl, but fewer mites (excluding Buffleheads, genus *Bucephala*). The high louse load and low mite load on American Coots could be due to the competitive superiority of lice for the microenvironment of the host, or predation by lice on mites; lice can feed on smaller ectosymbionts or their eggs (Nelson and Murray 1971). American Coots also had the greatest taxon richness for lice and mites, probably contributing to the significantly greater taxon richness found in diving genera (*Aythya*, *Bucephala*, and *Fulica*) compared to dabbling genera (*Aix* and *Anas*). This contrasts with the work of Felso and Rózsa (2006), who found that louse taxon richness was significantly lower in clades of diving birds than non-diving birds. This discrepancy may be a function of the particular genera we included in this study and the smaller number of taxa included in our study.

Møller and Rózsa (2005) found higher abundances of amblyceran lice compared to ischnoceran lice on avian hosts. However, in our study, ischnoceran species tended to have higher abundances than amblyceran species. Out of the 53 avian hosts sampled, only 6 (11%) had slightly higher abundances of Amblycera than Ischnocera. Ischnoceran lice are presumably less irritating to waterfowl than amblyceran lice (Møller and Rózsa 2005). Therefore, they might not be removed by active preening and thus accumulate to greater population sizes. In particular, *Anaticola* spp. were found on every Anseriformes species surveyed. This finding suggests that this genus may be tolerated more than other lice, may be more difficult to remove, or may have greater dispersal abilities.

There was a significant difference between the waterfowl sexes of Anseriformes birds in ischnoceran lice loads: females had more lice than males. In other bird species, females prefer males with lower ectoparasite loads, whereas males selected mates independent of mate ectoparasite load (Clayton 1990). Preening plays a major role in host defense against lice (Møller and Rózsa 2005), and some studies suggest that males spend more time preening than females (Cotgreave and Clayton 1994), perhaps because of the greater selective value of healthy plumage. While this pattern has not been demonstrated in waterfowl, waterfowl with impaired preening ability do suffer from increased ectoparasite loads and reduced overall fitness (Cotgreave and Clayton 1994). So, perhaps the reduced lice load in males is a consequence of similar patterns of inter-sexual selection, where females select males with lower ectoparasite loads, healthier plumage, and increased overall fitness.

There is a competing hypothesis, however, for the difference in louse load between the waterfowl sexes. In the northern hemisphere, male waterfowl in the family Anatidae do not participate in parental care and have little to no direct contact with their young (Batt et al. 1992). Therefore, because lice are more dependent on vertical (parent-offspring) transmission than other ectoparasites (Bush and Clayton 2006), selection would favor lice that prefer females, or migrate from males to females during copulation. This theory could explain the greater lice load in females. Indeed, there is some evidence that lice can determine the sex of their host through hormonal cues (Foster 1968).

No significant difference was detected between feather mite abundance and waterfowl species or sex. Because of their small size, method of feeding, or the possible advantages associated with having higher mite loads, the mites might not be actively preened off by the host animal.

In conclusion, our study confirmed that there are differences in ectoparasite communities on different waterfowl genera and differences in ectoparasite abundance between sexes. Other patterns conflicted with previous studies, but were probably affected by unequal representation of waterfowl species across categories. Little information exists about the ecology of most of the lice and mite species that were collected. Further collection of ectosymbionts from waterfowl during different seasons and areas would undoubtedly increase knowledge about the natural histories of feather mite and lice species and their host associations.

Acknowledgments

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