

PREVALENCE OF *CAMPYLOBACTER* IN WILD BIRD POPULATIONS

by

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EPIGRAPH

“We have a choice to use the gift of our lives to make the world a better place.”

Jane Goodall

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ABSTRACT

Campylobacter bacteria have had a significant impact on human health, being responsible for the majority of food borne illnesses and gastroenteritis worldwide (3). Especially within poultry such as chickens and turkeys, *Campylobacter* infections have played a large role in causing infection within human populations due to the consumption of undercooked meat. Wild birds have been thought to factor into the epidemiology of this bacterium, although few studies have estimated the prevalence of *Campylobacter* species within wild birds of the United States. This study evaluated the overall occurrence of three *Campylobacter* species – *C. jejuni*, *C. coli*, and *C. lari* – from 333 out of 914 wild bird fecal samples collected at Tri-State Bird Rescue and Research in Newark, Delaware. Samples were plated on *Campylobacter* selective agar, confirmed by catalase and oxidase tests and examined under a light microscope, followed by multiplex-PCR and Multi-locus sequencing typing PCR to identify *Campylobacter* species. Prevalence rates of *Campylobacter* from nine avian families averaged 7.5% overall with rates ranging widely between different families. Crows (*Corvus brachyrhynchos* and *Corvus ossifragus*) had the highest prevalence, followed by laughing gulls (*Larus atricilla*) and blue jays (*Cyanocitta cristata*) with considering only groups of species where sample size was at least greater than 7 individuals. All positive samples were *Campylobacter jejuni*. It remains somewhat unknown as to why certain species are more prone to carrying the bacterium than others, although feeding habits and ecological niches occupied by individual species are sure to play a role. With possible implications of wild birds

transmitting the bacterium to other avian species such as chickens and other poultry or even directly to humans, this study provided valuable baseline values of the occurrence of the bacterium within selected wild bird populations.

Chapter 1

INTRODUCTION

Enteropathogens, such as those found in the *Campylobacter* genus, are one of the most common disease causing agents in regard to food borne illnesses worldwide (3). *Campylobacter jejuni*, recognized as the main pathogen for humans, appears to be the most prevalent cause of bacterial gastroenteritis throughout the world, including the United States (25). *Campylobacter* outbreaks are usually isolated, sporadic events rather than organized outbreaks (3). Once infected, humans tend to experience a wide variety of symptoms ranging from abdominal pain and sometimes nausea, to vomiting and occasionally bloody diarrhea. These symptoms usually last around seven days until a person has fully recovered. Due to the generalized symptoms and overall feelings of malaise, *Campylobacter* infections often go undiagnosed and unreported. Therefore, estimates of 2.4 million infected people annually in the United States or about 1% of the population, according to the Center of Disease Control and their Foodborne Diseases Active Surveillance Network may be dramatically underestimated. Campylobacteriosis is the most common antecedent infection for Guillain-Barré syndrome (13).

Campylobacteriosis peaks during the summer months, and children and young adults are more prone to infection than other age groups within the population (9). In a recent study by French *et al.* (2009), wild bird fecal samples were collected on and around children's playgrounds in a New Zealand city, yielding *Campylobacter jejuni* in 12.5% of the 192 samples. This may indicate that frequent hand-mouth contact could cause children to be more prone to the disease. Another valuable aspect of the

aforementioned study is the consideration of wild birds as an active route of infection of *Campylobacter*.

Even within recent news, *Campylobacter* species in wild birds have been shown to be responsible for causing human illness. In Alaska, USA, undercooked peas consumed by humans had been infected with *Campylobacter* by Sandhill Cranes (*Grus canadensis*) inhabiting the area around the pea fields (27). Fecal matter of the cranes present on the undercooked peas was determined to be the cause of the outbreak as this is what harbored the bacterium. This was demonstrated with molecular techniques by the Center for Disease Control and Prevention (27).

Within bird populations such as mature poultry and similar avian food animals such as ducks and turkeys, *Campylobacter* infections are nonpathogenic, meaning they do not cause disease and thus avian species are simply carriers. This also holds true for wild birds carrying the bacterium - the disease is silent and the animal does not exhibit any symptoms (2). This especially makes detection of the bacterium challenging. Around 50% of all commercial broiler and turkey flocks are estimated to carry the *Campylobacter* bacterium, posing a potential threat to consumers if the meat is handled inappropriately or undercooked after leaving slaughter plants (17, 6, 12, 18, 1).

Major sources for infection of broiler chickens, turkey flocks and other avian species stem from fecal matter contaminated with the bacterium. As the bacterium is spread primarily through the fecal-oral route within bird populations but also within human populations, water contaminated with fecal matter can also be a source of infection (2, 30). Rats, wild birds, house flies and even milk have been shown to be responsible for *Campylobacter* outbreaks (4,10). In the United Kingdom, Campylobacteriosis has been traced to wild birds pecking door step milk bottles and infecting milk used for human consumption (4, 21). With a low dose of bacterium being

required for infection in humans along with difficult detection in avian species, *Campylobacter* may be of higher health concern than so far estimated.

The *Campylobacter* bacterium is a Gram negative rod with characteristic gull-wing morphology (22). Four species of *Campylobacter* have been identified as the most common causes of human enteritis (*Campylobacter jejuni*, *Campylobacter coli*, *Campylobacter lari*, and *Campylobacter upsaliensis*) (4). Pathogenicity factors such as lipid A moiety in the cell wall, a flagellar antigen, possibilities of exhibiting the use of a cytotoxin or enterotoxin, as well as L-fucose receptors help the bacterium in establishing an infection in the human gut (4).

Most *Campylobacter* species thrive in temperatures around 42° Celsius, making a bird the ideal environment for the bacterium to grow in with birds' high core body temperature averaging around 42° Celsius as well. Wild birds have been frequently targeted as potential vectors for transmitting the bacterium to poultry, humans, and even cattle (25, 8, 16, 20, 28, 14). With rather limited research on the overall prevalence of *Campylobacter* in wild bird populations and with implications towards the transmittance of *Campylobacter* to humans in part through infections of poultry and food animals, this study will help establish baseline values of *Campylobacter* infection in wild birds in the United States. The goal of this study is to evaluate the occurrence of three of the most common human disease causing strains of the *Campylobacter* genus – *C. jejuni*, *C. coli*, and *C. lari* – which are also commonly present in wild birds in the United States. In addition, this study is looking for potential relationships between the orders, families, and habitats of birds previously studied and how results may vary in different parts of the world.

Chapter 2

MATERIAL AND METHODS

2.1 Sample Collection

Because *Campylobacter* is an enteric pathogen carried in and shed from the intestine, wild bird fecal samples were collected at the wild bird rehabilitation facility, Tri-State Bird Rescue and Research, in Newark, Delaware. I collected fecal samples under standardized procedures similar to procedures used by Waldenström *et al.* (25). For smaller birds such as songbirds and all the way up to smaller shorebirds, fecal samples were collected from clean paper towels in admission boxes or playpens at Tri-State Bird Rescue and Research. Samples were collected with sterile standard cotton swabs and immediately placed in a charcoal medium containing test tube (Transwab; BioDisc, Solna, Sweden). For larger birds such as raptors, waterfowl or other birds that will most likely not defecate during handling procedures, sterile standard cotton swabs were inserted into the cloaca 1 to 2 cm in order to collect a fecal sample. After collection, swabs were broken off and left in the charcoal medium test tube and stored in a regular refrigerator (4-7° Celsius) for 12-24 hours until transferred to a -70° Celsius freezer where all samples were stored until time of analysis for up to 9 months.

For each bird sampled, an identification number was assigned along with a record of age, sex if known, body condition (overweight, normal, underweight, emaciated), weight in grams, location where the bird was found, primary injury and secondary injury. I recorded age as either hatch year, or after hatch year, along with more specific age indicators of naked nestling, nestling, fledgling, downy for waterfowl,

brancher for hawks and owls, juvenile, immature, or adult. For some species, such as Bald Eagles (*Haliaeetus leucocephalus*), specific age could sometimes be indicated in years due to specific plumage variations.

2.2 Sample Analysis

Samples were cultivated at the University of Kalmar Section of Zoonotic Ecology and Epidemiology within the School of Pure and Applied Natural Sciences in Sweden by methods previously used by Waldenström *et al.* (25). Each sample was plated on *Campylobacter*-selective blood-free, charcoal based agar plates and incubated at 42° Celsius under microaerophilic conditions for about 48 hours. After inspecting plates, if bacteria were positive for catalase and oxidase and exhibited an inability to grow in oxygen rich environments, they were observed under the light microscope. If Gram negative gull-shaped rods were observed, the bacteria were considered to be *Campylobacter* and were then further isolated on blood agar plates incubated at 42° Celsius for 24-48 hours. Isolates from these plates were then prepared for polymerase chain reactions.

One method used for *Campylobacter* species identification was a Multiplex polymerase chain reaction (MX-PCR) with specific primers for *C. jejuni* and *C. coli* developed by Vandamme *et al.* (23) but was instead performed with 25µl volumes as performed in the study by Waldenström *et al.* (25). Samples were then tested using a PCR specific for *C. lari* as developed by Lawson *et al.* (15). Products were separated on a 1.5% Agarose electrophoretic gel. Bands at 760bp indicate *C. jejuni*, bands at 350bp indicate *C. coli*, and bands at 561bp indicated *C. lari*. Reference strains for confirmed positives were used in all PCR reactions to act as controls. Samples categorized as positive *Campylobacter* species that did not appear positive in the aforementioned PCR analyses underwent further characterization. A multi-locus sequencing typing PCR

(MLST-PCR) reaction directed at *C. jejuni* was performed on these samples aimed at the AspA housekeeping gene loci following an extraction (26).

Chapter 3

RESULTS

3.1 Samples Collected

Tri-State Bird Rescue and Research receives birds from a wide variety of areas and towns and states outside of Newark, Delaware. 914 fecal samples of birds coming into the rehabilitation facility were collected, with birds originally from towns throughout Delaware, Maryland, Virginia, North Carolina, Pennsylvania, and New Jersey. These 914 samples were representative of 14 orders, 43 families, and 105 species (TABLE 1). Of these 914 samples collected, 333 were chosen for analysis based on previous research indicating common positives of *Campylobacter* species in certain orders and families (5, 11, 26, 29, 24). The remaining samples will be analyzed in the near future but are not part of this specific study. These 333 fecal samples were representative of 6 orders, 10 families, and 32 species (TABLE 1).

3.2 Samples Analyzed

Overall, 25 out of 333 or 7.5% of the analyzed samples tested positive for *Campylobacter* species. 7.3% of the analyzed samples tested positive for *Campylobacter jejuni*. One *Campylobacter* positive sample did not test positive for *C. jejuni*, *C. coli*, or *C. lari* with a MX-PCR and did not test positive for *C. jejuni* with a MLST-PCR directed at the AspA loci of the selected species, and was thus unable to be identified to species. With the exception of this unknown *Campylobacter* species sample, the only *Campylobacter* species present, *C. jejuni* was seen within 5 different orders, 6 families,

and 8 species (TABLE 2). Species of birds that tested positive for any *Campylobacter* species included the American robin (*Turdus migratorius*), blue jay (*Cyanocitta cristata*), American crow (*Corvus brachyrhynchos*), fish crow (*Corvus ossifragus*), mallard duck (*Anas platyrhynchos*), laughing gull (*Larus atricilla*), red-tailed hawk (*Buteo jamaicensis*), and dunlin (*Calidris alpina*). Crows (*Corvus brachyrhynchos* and *Corvus ossifragus*) had the highest prevalence, followed by laughing gulls (*Larus atricilla*) and blue jays (*Cyanocitta cristata*) when considering only groups of species where sample size was at least greater than 7 individuals.

A statistical test was not able to be performed due to low numbers of positive samples within most species or families from the United States.

Chapter 4

DISCUSSION

The goal of this study was to establish general values for the prevalence of *Campylobacter* in wild birds within Delaware and surrounding states on the East Coast of the United States. Rates of *Campylobacter* species within the range of species and families of birds tested was similar to previous research from around the world. With all families sampled – with the exception of Gaviidae and Mimidae which did not have previous data in regards to *Campylobacter* readily available – prevalence rates could be clearly identified. The distribution of *Campylobacter* for individual taxa of birds differed among orders and families.

Different percentage rates of the occurrence of *C. jejuni* as compiled by Waldenström *et al.* from a variety of studies throughout Europe were compared to data obtained in this study (26). Overall, family Accipitridae and Laridae showed similar trends to European studies. Family Accipitridae exhibited a 2% versus a 3% prevalence and family Laridae a 24% versus a 23% prevalence. Other families exhibited a great variety of prevalence. Family Anatidae exhibited a 2% prevalence from our samples, while European data suggested a 27% prevalence. Family Corvidae a 25% versus a 51% prevalence, and family Turdidae exhibited a 3% versus a 14% prevalence. Only families with a positive sample size greater than 7 were considered in order to be able to make some inferences in terms of the entire family.

The Corvidae (crows and blue jays in this study) showed the highest prevalence of *Campylobacter* out of all birds samples. About 40% of all crows carried

Campylobacter jejuni. Opportunistic feeding habits as well as foraging close to human development likely influenced the prevalence of *Campylobacter* in the Corvidae. Further MLST-PCR directed at various housekeeping genes of *Campylobacter* species could ultimately lead to the identification of sequence types and if they stem from human, poultry, or wild bird strains of the bacterium. A study conducted in Japan showed a 34% occurrence of *Campylobacter* in crow species from various regions with their crop contents consisting of up to 100% human refuse or garbage (11). Although blue jays (*Cyanocitta cristata*) are known to feed mostly on nuts, seeds, and small vertebrates, their foraging behavior could still influence the way they come in contact with the *Campylobacter* bacterium. From our collected data, all blue jays positive for *Campylobacter* were hatch year birds. This again seems to indicate that through a food item or foraging behavior, adult blue jays transfer the bacterium to their young. It is also possible that siblings within a nest may transfer the bacterium to each other as parents remove fecal sacs. As fecal sacs get picked up by parents and subsequently food is picked up with the beak and distributed to the young, the bacterium could be transferred to all members of a nest.

The Laridae had similar prevalence rates between our study (24%) to that of previous studies in Sweden (26). Quessy and Messier discovered a prevalence rate of 15.9% within ring-billed gulls (*Larus delawarensis*), the only Laridae species they evaluated for *Campylobacter* (19). Gulls tested in this study came from different environments (i.e. isolated beaches or parking lots) which may have influenced the occurrence of *Campylobacter*. Gulls are opportunistic feeders and many have adapted to living in close proximity to humans, often using trash bins and city dumps as foraging grounds where the prevalence of *Campylobacter* may be higher. Again, although not analyzed in this study, it would be interesting to see if sequence types and clonal

complexes correspond to human isolated *Campylobacter* within the same geographic area in order to determine if wild birds carry original *Campylobacter* strains as compared to human or poultry related strains.

The Turdidae had a much lower prevalence rate (3%) than previous research in Sweden indicated (14%)(25). Only the American robin (*Turdus migratorius*) was infected with *Campylobacter*. I did not detect *Campylobacter* in other thrushes such as Eastern bluebirds (*Sialis sialis*), Swainson's thrushes (*Catharus ustulatus*), Veerys (*Catharus fuscescens*) and wood thrushes (*Hylocichla mustelina*). With similar feeding habits and prey items among these species, we cannot answer the question as to why the American robin proved to carry a higher prevalence rate of *Campylobacter*. It could be suggested that closer proximity to humans may play a role in acquisition of the bacterium in connection with ground feeding foraging habits of American robins in human inhabited areas.

Due to their gregarious feeding habits as well as frequent contact with standing water and water edges, the Anatidae have been shown to carry the *Campylobacter* bacterium more frequently than other families (25). A previous study conducted in Louisiana, USA concluded a 12.9% prevalence rate of *Campylobacter jejuni* in the order Anseriformes, which includes family Anatidae. Even though waterfowl are expected to have higher rates of *Campylobacter* prevalence, the prevalence rate in this study was rather low (2%).

I only detected one species of *Campylobacter* (*C. jejuni*) from wild birds in this study. Throughout the world, researchers have found different *Campylobacter* species in wild birds, specifically isolating *C. jejuni*, *C. lari*, and *C. coli* from certain gull and thrush species among others (25)(19). The same families were tested in this study, yet only revealed to be positive for *C. jejuni*, but not *C. coli* or *C. lari*.

Another aspect to consider in regards to this study is the fact that samples were collected at a rehabilitation facility. This may have artificially increased the rates of prevalence for certain species since individual birds may not have been a proper representation of the overall population due to an injury. For example, if a hawk has an injury that dramatically decreases its chances of survival (i.e. a broken wing), it may resort to different prey items or food choices simply to stay alive. These can then harbor *Campylobacter* more or less frequently. If a bird has been on the ground for an extended period of time, other opportunistic infections such as *Salmonella* may occur as well, paving the way for the bird to soon harbor a variety of bacterial infections it would not normally have contracted. However, healthy hatch year birds may also have simply fallen out of a nest and then immediately been picked up by humans and brought into the clinic. Here, infection would not have necessarily occurred simply because of an injury due to the short time span between falling out of a nest and being brought to a rehabilitation facility.

It is unknown how frequently humans and poultry are actually infected with *Campylobacter* isolates from birds. There have been few instances where small outbreaks could actually be traced to wild birds (27). However, the potential remains for wild birds to act as vectors in carrying and spreading diseases such as *Campylobacter*, especially with birds that migrate thousands of miles across the globe. Overall occurrence of *Campylobacter* species was still low considering the variety of ecological guilds wild birds can occupy. The question, however, does remain in regards to the importance of *Campylobacter* in wild birds and how it could potentially infect human populations with novel strains of the bacterium. This study was only a small step taken towards that direction in identifying the prevalence of *Campylobacter* within different species of birds

in order to someday determining the actual influence wild birds have on the epidemiology and ecology of the *Campylobacter* bacterium.

TABLE 1: Species of wild birds of samples collected, analyzed, and ones that tested positive for *Campylobacter jejuni*

ORDER/FAMILY	SPECIES	Total Collected	Total Screened	Total positive <i>C. jejuni</i>
Gaviiformes				
Gaviidae	<i>Gavia immer</i>	7	2	
Pelecaniformes				
Sulidae	<i>Morus bassanus</i>	9		
Phalacrocoracidae	<i>Phalacrocorax auritus</i>	1		
Ciconiiformes				
Ardeidae	<i>Nycticorax nycticorax</i>	3	2	
	<i>Egretta caerulea</i>	1		
	<i>Bubulcus ibis</i>	2	1	
	<i>Egretta thula</i>	1		
	<i>Ardea alba</i>	4	1	
	<i>Ardea herodias</i>	16	3	
Threskiornithidae	<i>Plegadis falcinellus</i>	1		
Anseriformes				
Anatidae	<i>Cygnus olor</i>	1	1	
	<i>Branta canadensis</i>	25	25	
	<i>Aix sponsa</i>	9	9	
	<i>Anas platyrhynchos</i>	21	21	1
	<i>Anser "domesticus"</i>	1	1	
	<i>Anas "domesticus"</i>	1	1	
Falconiformes				
Cathartidae	<i>Cathartes aura</i>	6		
	<i>Coragyps atratus</i>	3		
Accipitridae	<i>Pandion haliaetus</i>	22	20	
	<i>Circus cyaneus</i>	1	1	
	<i>Haliaeetus leucocephalus</i>	13	12	
	<i>Accipiter striatus</i>	1	1	
	<i>Accipiter cooperii</i>	9	9	
	<i>Buteo platypterus</i>	1		
	<i>Buteo lineatus</i>	6	5	
	<i>Buteo jamaicensis</i>	10	8	1
Falconidae	<i>Falco sparverius</i>	14		
	<i>Falco peregrinus</i>	3		
Galliformes				
Phasianidae	<i>Alectoris chukar</i>	1		

Table 1 (continued)

ORDER/FAMILY	SPECIES	Total Collected	Total Screened	Total positive <i>C. jejuni</i>
Meleagrididae	<i>Meleagris gallopavo</i>	2		
Gruiformes				
Rallidae	<i>Rallus longirostris</i>	3		
Charadriiformes				
Charadriidae	<i>Charadrius vociferus</i>	5	5	
Scolopacidae	<i>Calidris alpina</i>	1	1	1
Laridae	<i>Larus atricilla</i>	17	15	5
	<i>Larus delawarensis</i>	3	3	
	<i>Larus argentatus</i>	3	3	
Sternidae	<i>Thalasseus maximus</i>	1		
	<i>Sterna forsteri</i>	1		
	<i>Sterna antillarum</i>	1		
Rynchopidae	<i>Rynchops niger</i>	1		
Alcidae	<i>Uria aalge</i>	1		
Columbiformes				
Columbidae	<i>Columba livia</i>	18		
	<i>Zenaida macroura</i>	27		
Strigiformes				
Tytonidae	<i>Tyto alba</i>	1		
Strigidae	<i>Bubo virginianus</i>	19		
	<i>Strix varia</i>	3		
	<i>Otus asio</i>	10		
	<i>Aegolius acadicus</i>	1		
Caprimulgiformes				
Caprimulgidae	<i>Caprimulgus carolinensis</i>	1		
Apodiformes				
Apodidae	<i>Chaetura pelagica</i>	4		
Trochilidae	<i>Archilochus colubris</i>	12		
Piciformes				
Picidae	<i>Melanerpes carolinus</i>	3		
	<i>Colaptes auratus</i>	10		
	<i>Picoides pubescens</i>	3		
	<i>Dryocopus pileatus</i>	2		

Table 1 (continued)

ORDER/FAMILY	SPECIES	Total Collected	Total Screened	Total positive <i>C. jejuni</i>
Passeriformes				
Tyrannidae	<i>Contopus virens</i>	2		
	<i>Sayornis phoebe</i>	3		
	<i>Myiarchus crinitus</i>	1		
	<i>Tyrannus tyrannus</i>	4		
Alaudidae	<i>Eremophila alpestris</i>	1		
Hirundinidae	<i>Tachycineta bicolor</i>	2		
	<i>Progne subis</i>	7		
	<i>Hirundo rustica</i>	16		
Bombycillidae	<i>Bombycilla cedrorum</i>	10		
Troglodytidae	<i>Troglodytes aedon</i>	9		
	<i>Thryothorus ludovicianus</i>	20		
Mimidae	<i>Dumetella carolinensis</i>	35		
	<i>Mimus polyglottos</i>	19		
	<i>Toxostoma rufum</i>	1	1	
Turdidae	<i>Sialia sialis</i>	8	8	
	<i>Hylocichla mustelina</i>	2	2	
	<i>Cathartus fuscescens</i>	2	2	
	<i>Catharus ustulatus</i>	2	2	
	<i>Turdus migratorius</i>	122	122	5*
Paridae	<i>Baeolophus bicolor</i>	3		
	<i>Poecile atricapillus</i>	2		
Corvidae	<i>Cyanocitta cristata</i>	30	30	5
	<i>Corvus brachyrhynchos</i>	7	7	3
	<i>Corvus ossifragus</i>	10	10	3
Sturnidae	<i>Sturnus vulgaris</i>	37		
Passeridae	<i>Passer domesticus</i>	39		
Vireonidae	<i>Vireo solitarius</i>	1		
	<i>Vireo olivaceus</i>	1		
Fringillidae	<i>Carpodacus mexicanus</i>	19		
	<i>Carduelis tristis</i>	12		
Parulidae	<i>Parula americana</i>	1		
	<i>Dendroica pensylvanica</i>	1		
	<i>Dendroica magnolia</i>	1		
	<i>Dendroica coronata</i>	1		
	<i>Mniotilta varia</i>	1		
	<i>Dendroica caerulescens</i>	1		
	<i>Wilsonia canadensis</i>	1		
	<i>Seiurus aurocappilus</i>	2		

Table 1 (continued)

ORDER/FAMILY	SPECIES	Total Collected	Total Screened	Total positive <i>C. jejuni</i>
	<i>Geothlypis trichas</i>	2		
Thraupidae	<i>Piranga olivacea</i>	1		
Emberizidae	<i>Pipilo erythrophthalmus</i>	1		
	<i>Spizella passerina</i>	6		
	<i>Ammodramus savannarum</i>	1		
	<i>Melospiza melodia</i>	10		
Cardinalidae	<i>Cardinalis cardinalis</i>	23		
Icteridae	<i>Agelaius phoeniceus</i>	3		
	<i>Quiscalus quiscula</i>	54		
	<i>Molothrus ater</i>	24		
	<i>Icterus spurius</i>	3		
	<i>Icterus galbula</i>	3		

*1 out of 5 positive samples was a positive *Campylobacter* species not identified as *C. jejuni* by MX-PCR or MLST-PCR

Family classifications taken from Clements' Birds of the World (7)

TABLE 2: Samples of wild bird species with specific information of ones that tested positive for *Campylobacter jejuni* but not for *C. coli* or *C. lari* along with the exception of one unknown *Campylobacter* species (*).

ORDER/FAMILY	SPECIES	AGE	SEX	BC	WEIGHT (g)	LOCATION FOUND	STATE	1° INJURY	2° INJURY
Anseriformes									
Anatidae	<i>Anas platyrhynchos</i>	HY/Downy	U	normal	35.3	Mendenhall	PA	NAI	-
Charadriiformes									
Laridae	<i>Larus atricilla</i>	HY/Juv	U	underwt	225	Milford	DE	OR	ST
	<i>Larus atricilla</i>	HY/Im	U	underwt	252	Long Neck	DE	OR	ST
	<i>Larus atricilla</i>	HY/Juv	U	underwt	206	Dewey	DE	OR	ST
	<i>Larus atricilla</i>	HY/Juv	U	underwt	200	Dewey Beach	DE	ST	GD
	<i>Larus atricilla</i>	HY/Juv	U	underwt	207	Dewey Beach	DE	OR	ST
Scolopacidae	<i>Calidris alpina</i>	AHY/A	U	normal	70.7		DE	OR	GD
Falconiformes									
Accipitridae	<i>Buteo jamaicensis</i>	HY/Im	M	emaciated	570	Smyrna	DE	GD	PA
Passeriformes									
Corvidae	<i>Corvus brachyrhynchos</i>	HY/FL	U	underwt	296	West Chester	PA	OR	GD
	<i>Corvus brachyrhynchos</i>	HY/Juv	U	underwt	377	Claymont	DE	OR	ST
	<i>Corvus brachyrhynchos</i>	HY/Juv	U	underwt	343	Wilmington	DE	ST	GD
	<i>Cyanocitta cristata</i>	HY/N	U	underwt	44.8	Harleysville	PA	ST	GD
	<i>Cyanocitta cristata</i>	HY/N	U	normal	53.1	Newark	DE	OR	ST
	<i>Cyanocitta cristata</i>	HY/Juv	U	normal	56.1	Mt. Lebanon	PA	NE	ST
	<i>Cyanocitta cristata</i>	HY/FL	U	underwt	61.1	Wilmington	DE	ST	NE
	<i>Cyanocitta cristata</i>	HY/FL	U	normal	57.3	Newark	DE	OR	GD
	<i>Corvus ossifragus</i>	HY/FL	U	normal	211	Gloucester Co.	NJ	ST	-
	<i>Corvus ossifragus</i>	HY/FL	U	underwt	227	Laurel	DE	FD	GD
	<i>Corvus ossifragus</i>	HY/Juv	U	normal	221	Perry Pointe	MD	FD	-
	<i>Corvus ossifragus</i>	HY/N	U	normal	174	Camden	DE	OR	GD

Table 2 (continued)

ORDER/FAMILY	SPECIES	AGE	SEX	BC	WEIGHT (g)	LOCATION FOUND	STATE	1° INJURY	2° INJURY
Turdidae	<i>Turdus migratorius</i>	HY/FL	U	underwt	42.6	Wilmington	DE	ST	GD
	<i>Turdus migratorius*</i>	HY/FL	U	normal	50.9	Wilmington	DE	NE	-
	<i>Turdus migratorius</i>	HY/Juv	U	normal	52.7	Middletown	DE	OR	NE
	<i>Turdus migratorius</i>	AHY/A	M	underwt	56	Essington	PA	ST	-
	<i>Turdus migratorius</i>	HY/FL	U	normal	42.6	Newark	DE	NE	OR

BC=body condition; Injury Codes: BE= behavioral, CO=contaminant, FD=feather damage, GD=general debilitation, NE=neurologic, OP=ophthalmic, OR=orthopedic, PA=parasites, RE=respiratory, ST=soft tissue damage, NAI= no apparent injury; Age: HY=hatch year, AHY=after hatch year, NN=naked nestling, N=nestling, FL=fledgling, B=brancher, JUV=juvenile, IM=immature, A=adult.

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