Seabird Mitigation and the Prevalence of *Campylobacter* spp. at Oyster Farms in the Northern Gulf of Mexico

by

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ABSTRACT

Off-bottom oyster farming provides surface area for seabird perching. Regulatory agencies have concerns about bacterial contamination of oysters from seabird excrement and require operational plans aimed at bird mitigation; however, the effectiveness of many bird deterrents have not been validated. An evaluation of the bird populations at an oyster farm and assessment of a simple, inexpensive, non-lethal bird deterrent were conducted alongside an investigation into the prevalence of *Campylobacter* spp. in farmed oysters and birds interacting with the floating gear. Seabirds, such as pelicans, cormorants, terns, and gulls were abundant year-round but the use of a deterrent reduced bird-cage interactions by 85%. *Campylobacter* was isolated from 12 of 206 bird fecal samples and from 10 of 66 oyster samples. Isolates shared the highest 16S rDNA sequence identities with *C. lari*-like species whose pathogenicities are unknown. Strain-level identification is needed to determine their seafood safety risk. Overall, the simple bird deterrent was effective and may be incorporated to meet operational plan requirements, however the risk of oyster contamination with pathogenic *Campylobacter* species requires further investigation.

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LIST OF ABBREVIATIONS

US	United States
GOM	Gulf of Mexico
nGOM	northern Gulf of Mexico
CDC	Center for Disease Control
FDA	United States Food and Drug Administration
ISSC	Interstate Shellfish Sanitation Conference
NSSP	National Shellfish Sanitation Program
ADPH	Alabama Department of Health
AUSL	Auburn University Shellfish Laboratory
PCR	Polymerase chain reactions

CHAPTER 1: INTRODUCTION TO OYSTER AQUACULTURE AND THE BIRD PROBLEM

1.1 Eastern Oysters and Aquaculture

Oysters are sessile, benthic invertebrates which primarily colonize the intertidal zone creating oyster beds or reefs. As filter feeders oysters provide essential ecosystem services through water quality enhancement, while the reef structures create habitat for other invertebrates and fishes and protect shorelines from erosion due to wave action and storms (Coen et al., 2007; Grabowski and Peterson, 2007; Plunket and La Peyre, 2005). Additionally, oysters are harvested as seafood and are considered a delicacy. The oyster market has traditionally been supported through wild harvest, however wild stocks have been in decline since the late 20th century due to the effects of climate change (Cole et al., 2021; Parker et al., 2017) and anthropogenic stressors (Rothschild et al., 1994; Wilberg et al., 2011), causing an estimated 84% reduction in oyster reef habitat worldwide (McAfee and Connell, 2021).

The Eastern oyster, *Crassostrea virginica*, is a 'true oyster' of the family Ostreidae whose range extends from the Gulf of St. Lawrence in Canada to the coast of Brazil (Kennedy et al., 1996). However, there is an evident declining pattern in wild Eastern oyster populations in the northern Gulf of Mexico (nGOM). Apalachicola Bay, Florida historically supported a productive oyster reef but experienced a collapse in 2012 and has yet to recover (Pine III et al., 2015). In 2020, the Florida Fish and Wildlife Conservation Commission closed oyster harvest in this area through December of 2025 to allow the oyster reefs to rebuild (Florida Fish and Wildlife Conservation

Commission, 2020). Harvest in Alabama during 2005 exceeded one million pounds but fell to less than 30,000 pounds four years later. Due to changes in harvesting regulations, numbers in Alabama have rebounded, with nearly 285,000 harvested pounds reported in 2022 (NOAA Fisheries Office of Science and Technology, 2022), but are still well below historical levels. Oyster harvests in Mississippi have fallen since 2011 to approximately one tenth of the average number of sack landings reported in the decade prior (2000-2010: 278,839 sacks per year; 2011-2019: 30,442 sacks per year) and continue to decline (Rider, 2024). In 2022, Louisiana reported over 7.2 million pounds of meat harvested which accounted for 31.4% of the nation's oyster landings by weight, but was still below the twenty year (2003-2022) average of 11 million meat pounds (Louisiana Wildlife & Fisheries, 2024).

Resulting from the decline in natural populations, Eastern oyster aquaculture has gained popularity as an alternative means to meet consumer demand and reinstate some of the vital ecosystem services that oysters provide. In 2019, the Eastern oyster wild harvest and aquaculture industries in the United States (US) were valued at $143 million dollars (Food and Agriculture Organization of the United Nations, 2021). Innovation in oyster aquaculture technology has allowed farmed oysters to meet growing consumer demand while also improving the quality and consistency of the product. Wave and mechanical tumbling, which toss the oysters around, break off the fragile growing edge and encourage the animals to grow a deeper cup. This process results in a more desirable shell shape and improves uniformity and meat quality, and therefore oysters grown in aquaculture receive a premium price in the half shell raw market (Walton et al., 2013).

The two primary methods of commercial oyster aquaculture are on-bottom culturing and off-bottom culturing. On-bottom culturing involves growing oysters on the seafloor, mimicking environmental conditions that a wild reef experiences but protecting oysters from predators using baskets or shelves. Off-bottom culturing includes any method in which the oysters do not occupy the seafloor and are suspended in the water column (Walton and Swann, 2021). Holding oysters in the water column increases food availability and decreases the likelihood of sedimentation/siltation and predation (Walton et al., 2013). Additionally, it allows farmers ease of access to the oysters so that they can tumble, desiccate, and change bags more efficiently, all of which improve the appearance and growth rate of the animals. Off-bottom techniques are particularly suited for the nGOM due to the fine, muddy sediment which can accumulate and smother oysters grown using on-bottom methods (Grice, 2018).

There are three main types of off-bottom oyster aquaculture gear used in the US: adjustable long line systems, floating bags, and floating cages (Fig. 1.1). The adjustable long line system is comprised of rows of plastic pylons along which a plastic line, usually encapsulated in a dripper tube to increase durability, is ran. Along this line, bags of oysters are hung to feed in the water column. The line can then be raised or lowered to appropriate attachment points on the pylons to alter the bags' positions in the water column or desiccate the oysters. This culture method was originally developed in Australia but has been adopted across the US as an efficient method to farm at large scale. The floating bag system is comprised of a plastic lattice oyster bag with two small floats or buoys attached directly to the sides or ends of the bags. These floats keep the bag directly underneath the water's surface. This method is most typically used in the northern climates, as the floats can be removed to sink the bags to the bottom, avoiding freezing waters and

rough weather conditions (Mallet et al., 2009). The floating cage system, which is the most common gear in Alabama and Mississippi, is comprised of anchored mudlines to which aluminum cages are attached via leads and bridles. Each cage is subdivided into six bays with shelves for holding oyster bags, and has two large, plastic pontoons attached on top. The pontoons function to keep the cage neutrally buoyant just below the water's surface so that the oysters are constantly submerged. In doing so, the pontoons sit above the water.

Figure 1.1. Floating oyster aquaculture gear used in the northern Gulf of Mexico. A) Adjustable long line; B) floating cage; C) floating bag. Pictures courtesy of AUSL.

As farms expand their production capacity, more floating gear is added which greatly increases the surface area at the farm site. Sea and shore birds find the floating pontoons to be a favorable resting place and are often seen interacting with these structures (Fig 1.2). Types of birds frequently found in association with floating oyster aquaculture gear include terns, gulls, pelicans, and cormorants. These birds are coastal species who nest on land and forage in marine or estuarine environments (Bugoni et al., 2005; Gallardo et al., 2009; Hatch et al., 1999; Lamb et al., 2020), making farm sites a convenient loafing spot during feeding and nesting periods.

Figure 1.2. Floating gear inundated with seabirds including cormorants (back), pelicans (center), and terns and gulls (front).

1.2 The Bird Problem

Birds perching on floating gear and other hard structures found at farm sites (i.e. pylons or buoys) defecate on or near the structures, leading to exposure of cultured oysters to fecal material. Oysters accumulate bacteria from the surrounding water, including potential human pathogens, during filter feeding. In the past 10 years (2011-2021), there were 185 foodborne outbreaks associated with the consumption of raw oysters, leading to nearly 1,200 illnesses, 46 hospitalizations, and 3 deaths (CDC, 2023). Of those with identified etiology (175 outbreaks), 118 were attributed to *Vibrio* species (*Vibrio parahaemolyticus*, *V. vulnificus*, *V. cholerae*), 46 to noroviruses, 3 each to *Campylobacter* and *Giardia*, 2 to *Salmonella*, and 1 each to *Staphylococcus*, rotavirus, and sapovirus. *Vibrio* are naturally occurring marine organisms that are often abundant in waters where oysters are cultured (Brands et al., 2005), but the other pathogens likely originate from other sources, such as animals (including humans), runoff, and wastewater discharge (Costantini et al., 2006; Willis et al., 2013; Pouillot et al., 2022).

Wild birds are potential vectors of human pathogens and there is concern that their presence at farm sites increases the possibility of zoonotic disease contamination (Benskin et al., 2009; Clayton and Moore, 1997). Gulls (*Larus* spp.) harbor verocytotoxin-producing *Escherichia coli* 0157 (VTEC 0157) (Ejidokun et al., 2006; Makino et al., 2000; Wallace et al., 1997), while both terns (*Sterna* spp.) and gulls are documented carriers of *Salmonella enterica* Typhimurium serotypes (Kapperud et al., 1998; Penfold et al., 1979; Thornley et al., 2003), both of which cause human gastroenteritis. Large flocks of migratory waterfowl (*Anseriformes* spp.) and gulls increase the concentration of fecal coliforms in waters where they roost (Benton et al., 1983; Hussong et

al., 1979; Luechtefeld et al., 1980; Pacha et al., 1988; Yogasundram et al., 1989). However, a meta-analysis conducted by Smith et al. (2020) notes that the risk of enteric pathogen spillover has not yet been accurately assessed as the majority of studies analyze the presence of pathogenic bacteria at the genus level, whereas strain-level identification is often needed to confirm pathogenicity. Studies also fail to note that the pathogen must survive at an infectious dose outside the host organism.

1.3 Perching Birds and Seafood Safety

Seafood safety regulation in the US falls under the jurisdiction of the United States Food and Drug Administration (FDA). In 1982 the Interstate Shellfish Sanitation Conference (ISSC), which is a voluntary, national group of state and federal officials as well as members of the shellfish industry, was formed to focus on sanitation of molluscan shellfish. Through the ISSC, the National Shellfish Sanitation Program was enacted which sets national standards (i.e., NSSP Guide for the Control of Molluscan Shellfish or the NSSP Model Ordinance) to improve sanitation of shellfish involved in interstate commerce (NSSP, 2019). Proposals can be submitted to the ISSC to recommend additions or changes to the Model Ordinance. The members of the ISSC meet biannually to discuss these changes, and the state officials then vote on whether to adopt them. These standards are then implemented at the state level, where states can set stricter requirements than stated in the NSSP if desired.

In 2017, the concern around pathogen contamination from bird interactions with aquaculture gear prompted an amendment to the NSSP Model Ordinance to include a clause addressing this issue

(NSSP, 2017). The current Model Ordinance states that, should the state regulators determine the oyster farm attracts sufficient birds that their fecal material poses a human health risk, oyster farmers must have an operational plan to address the attraction of birds to aquaculture gear (NSSP, 2019). However, the lack of literature defining the risk of seabirds to oyster consumers has led to ambiguity in the enforcement of regulations. As a result of the lack of data to inform humane and efficient bird mitigation on floating oyster farms, it is currently sufficient for farmers to implement a bird mitigation strategy which might be ineffective. Currently so long as farmers are attempting to address the issue, many states deem the farm compliant, even if birds are still present.

The purpose of this thesis is to describe bird interactions with floating oyster aquaculture gear, effectiveness of deterrents, and potential human pathogen presence transmission between seabirds and cultured oysters. In Chapter 1, I quantified the abundance and frequency at which seabirds interact with floating oyster gear and tested whether a simple, inexpensive, non-lethal bird deterrent is an effective strategy in reducing the number of bird-gear interactions. In Chapter 2, I investigated the prevalence of *Campylobacter* bacteria in fecal matter collected from seabirds found at oyster farm sites and from oysters cultured in off-bottom floating cages to evaluate whether birds are a source of *Campylobacter* contamination in cultured oysters. The overall goals of this thesis are to increase understanding of potential seafood safety issues associated with seabirds at oyster farms and inform best practices for bird mitigation in oyster aquaculture.

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CHAPTER 2: BIRD INTERACTIONS WITH FLOATING OYSTER AQUACULTURE GEAR AND THE EFFICIENCY OF A SIMPLE, INEXPENSIVE, NON-LETHAL BIRD DETERRENT

2.1 Introduction

The current National Shellfish Sanitation Program (NSSP) Model Ordinance requires farmers to create a plan focused on minimizing seabird interaction with floating oyster gear to protect consumers from potential food safety risks (NSSP, 2019). This plan may include bird mitigation or deterrent strategies. Mitigation techniques include sinking the gear to below the water level to eliminate the perching surface for a period to reduce potential pathogens or restricting harvest during times of bird interactions. Restricting harvest is not a feasible strategy as farms may have birds present year-round (Matvey, pers. observation). In addition, sinking the gear requires substantial labor in an industry that already suffers from workforce limitations. Therefore, most farmers are choosing to implement deterrents in the form of innovative gear designs and the addition of physical structures that prevent birds from landing on floating gear.

There are three primary types of non-lethal bird deterrents: auditory, visual, and physical (Fig 2.1). Auditory deterrents function by using sounds to scare away birds. They use loud booms or blasts as well as the distress cries of birds, and they can be programmed to emit cries specific to the problematic species present. A reduction in auditory deterrent effectiveness has been observed in studies tracking the effect on large nuisance species, such as double-crested cormorants, and it has been observed that birds become accustomed to auditory deterrents (Christensen-Dalsgaard, 2019). Birds on catfish aquaculture ponds have been observed to learn the timing of automated

auditory deterrents and flee the farm site just before the blast goes off, and then promptly return afterward to resume poaching aquaculture crops (Mitch Anderson, Fly Away Bird Solutions, pers. corres). To avoid this issue, Lehoux and Bélanger (1995) suggested that the deterrent should be programmed to go off at random intervals. Even in these cases, the cannons release air before going off, so the birds learn to leave and return following discharge (Rivadeneira et al., 2018). Auditory deterrents that emit bird distress calls are also effective but target only one species at a time. Additional disadvantages of auditory deterrents include noise pollution and the requirement of a steady surface to attach the device. Ultrasonic sound (> 18 kHz) devices, outside the human audible range, are not heard by several bird species making them ineffective (Avery and Werner, 2017; Seamans et al., 2013; Soldatini et al., 2008) and the birds become accustomed to the devices (Soldatini et al., 2008). In addition, it is unclear how many auditory deterrents would be needed to sufficiently deter birds from a given surface area or how often techniques would have to be altered to avoid acclimation.

Visual deterrents rely on the predator avoidance behaviors of the birds to scare them from their perch or prevent landing in the first place. A popular strategy to implement is a kite that mimics an eagle when blowing in the wind. The issues with this deterrent type include the requirement of sufficient wind to keep the kite moving but not too much wind, which can destroy it. Kites must also be moved to different locations to prevent acclimation, and they are ineffective against larger birds such as pelicans and cormorants. However, the kites are relatively inexpensive and are effective against smaller birds such as terns (Navy Cove Oyster Farm, pers. communication). Additionally, more nuanced types of visual deterrents exist, such as automated laser systems that use beams of light to project images or trace programmed paths (Glahn et al., 2000). Lasers are

effective because they operate at a wavelength that birds can perceive while not being harmful to the eyes. They activate a flight response from what the bird recognizes as a potential threat or disturbance, prompting the bird to avoid the laser. Laser bird deterrents cause minimal disturbance (Blackwell et al., 2002; Glahn et al., 2000). A disadvantage of this deterrent type is a lack of efficiency during daylight hours, requiring some adaptation in the current technology to improve effectiveness during the day (Melvin et al., 2016). Additionally, these laser deterrents are relatively expensive compared to other mitigation strategies.

Physical deterrents rely on providing a physical barrier to prevent birds from landing on gear. Physical deterrents often entail fixing some structure to the cage, such as spikes, wires, or sweeps, that cause discomfort to the birds. Comeau et al. (2009) tested the efficiency of a physical bird deterrent, which was a length of plastic triangles attached to the top of the pontoon of floating bags, and found these systems to be effective at preventing cormorants from landing on floating gear. Bird spiders are similar to industrial bird deterrents that might be implemented in cityscapes. They are comprised of a bouquet of lightweight wires that fan out from a stem attached to the cages. The wires then sway with wind and wave action, brushing against birds and startling them (birdbgone.com/bird-spider-260/). Spinning deterrents act much like wind vanes, and they use flags or other objects of high surface area that extend from a central axis and catch the breeze to spin on top of floating cages and discourage bird landings (Cunningham et al., 2024). Unfortunately, the effectiveness of physical bird deterrents may be influenced by bird size and the number of birds at a site (Bird Barrier, 2021). These types of deterrents can also increase the difficulty of working the gear by adding more steps of deterrent removal or workarounds.

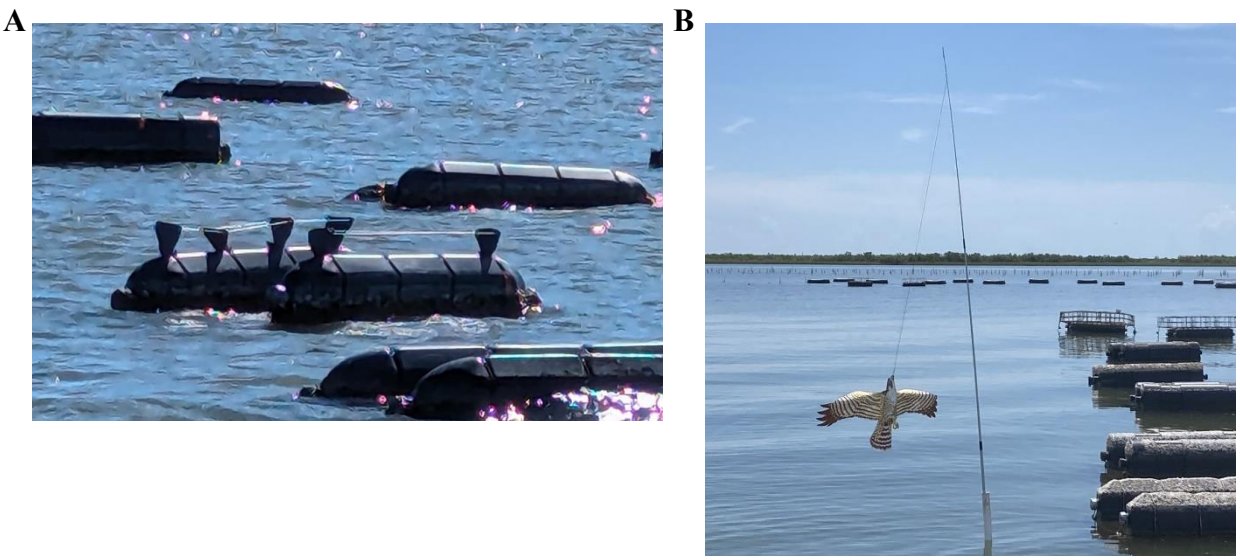

Figure 2.1. Examples of bird deterrents. A) A wire deterrent constructed to block birds from landing on top of pontoons B) A predatory kite visual deterrent set up at a floating oyster farm site.

There are only a handful of studies that evaluate the efficiency of bird deterrents in the context of floating oyster gear (Comeau et al., 2009; Cunningham et al., 2024; Tobin et al., 2002). However, few offer conclusive evidence of deterrent efficiency across multiple bird species. As farm sites may attract different types of birds (pelicans, cormorants, terns, and gulls west of Mobile Bay, Alabama versus primarily terns east of the bay; Navy Cove Oyster Farm, personal communication), it is important to understand 1) the types of birds that frequent oyster farms and 2) the effectiveness of deterrents across these bird species. The purpose of this study was to monitor the abundance and diversity of seabirds interacting with floating cage gear and evaluate the efficiency of a simple, inexpensive, nonlethal bird deterrent in coastal Alabama.

2.2 Methods

2.2.1 Experimental Field Design

Two experimental floating cage lines were deployed in July of 2023 at the Auburn University experimental oyster farm site in Bayou Sullivan, AL (30.364631, -88.215715) in the Mississippi Sound (Fig 2.2). Three floating cages were attached to each line 1.2 meters apart from one another. The treatment line was outfitted with three floating cages (Go Deep International, New Brunswick, Canada) that had bird deterrents attached to them. In comparison, the control line had three non-modified cages installed as per industry standard practice. Lines were approximately 67 meters from one another and oriented in parallel. Each line was installed in parallel to a row of pylons inside of the farm block in an east-west orientation (Fig 2.3). Floating cage lines were reinstalled when necessary, such as in the case of heavy winds or storm events.

2.2.2 Simple Bird Deterrent Design

The floating cages used in this experiment had two pontoon floats, each measuring 56.5” long and 6” wide. The simple bird deterrent (Fig 2.4) consisted of two pieces of 9 mm diamond plastic lattice fastened together to create a 65” long x 15” wide sleeve. The sleeve was fitted over each of the pontoons on a floating cage by attaching it to the frame using plastic zip ties. Plastic zip ties (15” x 0.25”, Sherill Electronic Systems Inc, Birmingham, AL) were then attached along the top of the lattice, protruding upwards and cut to 4-5” at an approximately 45° angle, in alternating lines to cover the top of the pontoon. This pattern led to a total of 45 zip ties per floating cage.

Plastic zip ties were used as they were inexpensive and unlikely to injure any bird that might still land on the deterrent cage.

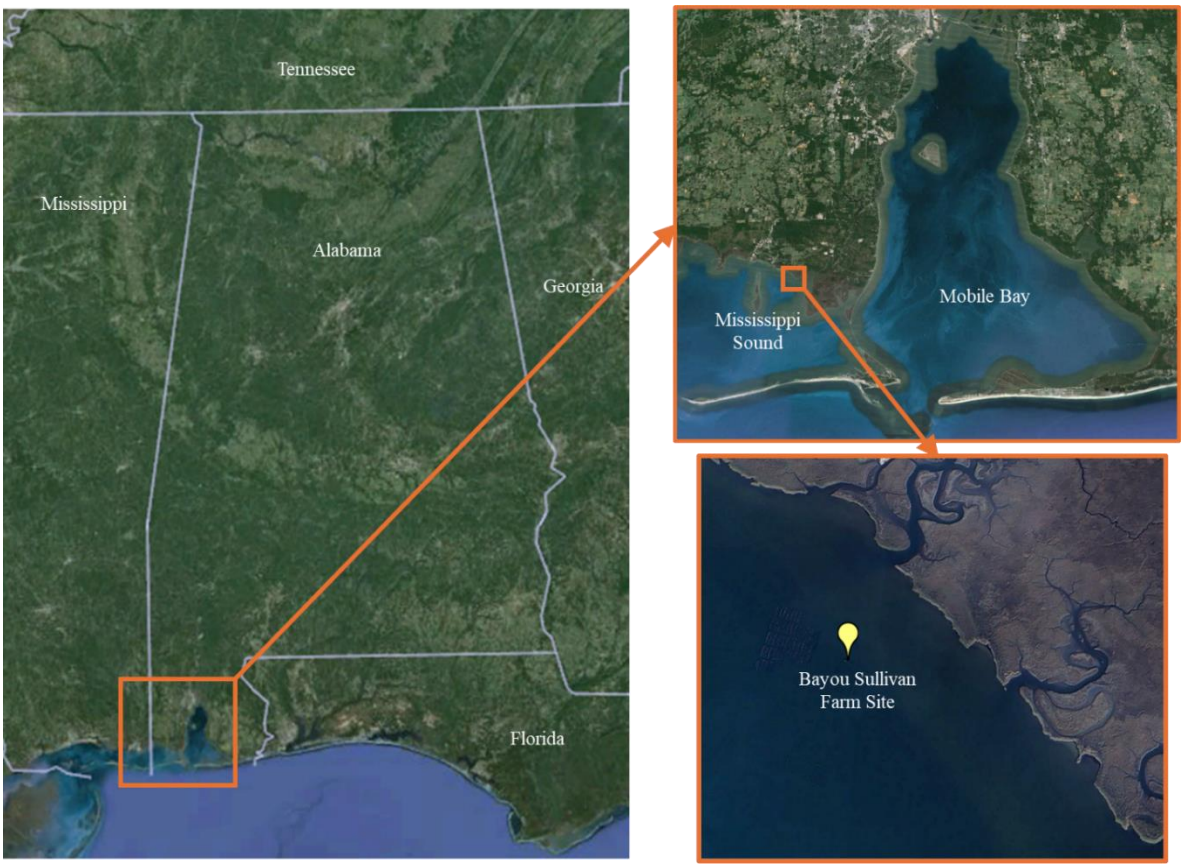

Figure 2.2. Map of the study area within the Mississippi Sound in the Northern Gulf of Mexico. Images from Google Earth Pro (v7.3.6.9796).

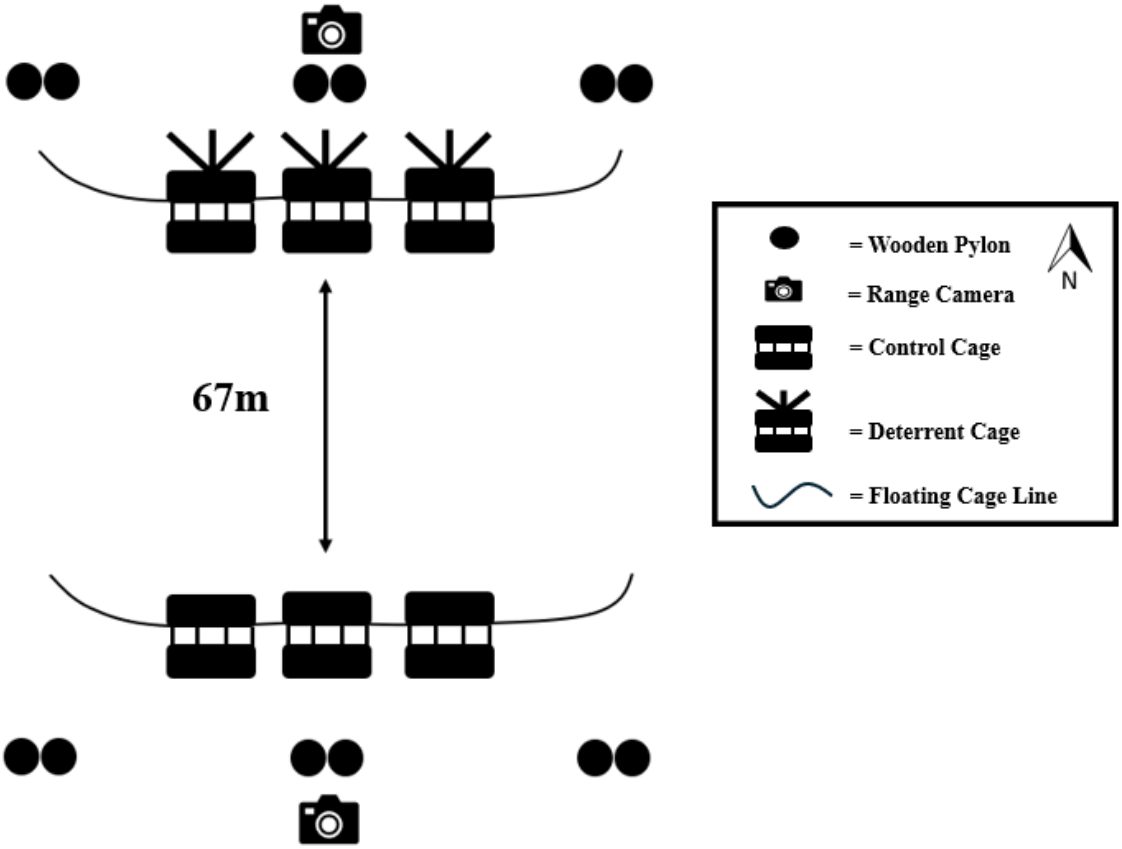

Figure 2.3. Floating cage experimental design used to determine the effectiveness of bird deterrents. The northern line is the deterrent treatment, and the southern line is the non-deterrent control.

Figure 2.4. Zip tie deterrent cage design.

2.2.3 Bird Interaction Monitoring

For this study I defined a bird interaction as a bird perched or sitting on top of a floating cage. Bird interactions, including abundance and diversity, were monitored using RangeCam 4G Wide, Barn Owl Tech range cameras (Barn Owl Tech, Colorado Springs, CO, USA). A range camera was attached to the pylon nearest the middle of each line, facing towards the line. The distance between the cage and the camera varied with the tide but was within 15-30 ft on average. Each camera was set to capture 12 MP photos every 30 minutes between 0600 and 1930 daily. Bird diversity data was collected from July 1, 2023, until March 31, 2024, excluding the dates between February 3 and February 27, 2024. During this time, cameras lost power and failed to capture images. Images from February 1-2 and 28-29, 2024 were included in the bird diversity analysis, although the

abundance of birds present during February is likely underestimated. All photos were analyzed to quantify and identify any birds present. Photo resolution was too low to reliably identify smaller birds, specifically of the family *Laridae,* to the species level. As a result, this family was broken down into two broad groups "terns" (*Sterna*: *S, sandvicensis, S. hirundo, S. antillarum, S. forsteri*; *Thalasseus*: *T. maximus*; *Hydroprogne*: *H. caspia*) and "gulls" (*Larus; L. atricilla, L. argentatus, L. delawarensis*) for further analysis. Presumptive bird species were identified and included in the results, but their interactions were not analyzed statistically.

2.2.4 Data Analysis

As deterrents are meant to prevent birds from interacting with floating gear and may impact birds in a species-specific manner, bird observations from cages with deterrents are unlikely to accurately represent bird populations on oyster farms. Therefore, when describing bird populations at the Bayou Sullivan farm site, only control cages were considered. The total number of bird observations, as well as observations for each abundant bird group (i.e., pelicans, cormorants, terns, and gulls), on each control cage was determined for each month. Control cage data was tested for normality using the Shapiro-Wilk test and for homogeneity of variance using Levene's Test for Equality of Variance (Levene's). Data for pelicans, cormorants, and terns did not meet the assumption of normality and were square root transformed to meet this assumption. A one-way ANOVA was used to determine if the number of bird observations differed by month, followed by a Tukey's HSD posthoc test where significant. Data for the month of February was incomplete but was included in the analysis of species richness.

To visualize bird interactions over the course of a day, the total number of bird observations, as well as observations for each abundant bird group (i.e., pelicans, cormorants, terns, and gulls), on each control cage throughout the study was determined for each half-hour increment. Control cage data was tested for normality using the Shapiro-Wilk test and for homogeneity of variance using Levene's Test. Data for cormorants and gulls did not meet the assumption of normality and were square root transformed to meet this assumption prior to analysis. A one-way ANOVA was used to determine if number of bird observations differed by time of day, followed by a Tukey's HSD posthoc test where significant.

To determine the effectiveness of the simple deterrent, the total number of bird observations for each cage (controls and deterrents) was determined for each month. As this study was not concerned about the interactions among months and treatments (for example, it was not relevant whether the number of birds on the control cages during December was different than the number of birds on deterrent cages during January), effectiveness within each month was determined using a Student's t-test. Monthly data was tested for normality using the Shapiro-Wilk test and for homogeneity of variance using Levene's Test. Data did not meet the assumption of normality and was square root transformed prior to analysis. P-values were corrected for multiple t-tests using the Holm-Bonferroni method.

2.3 Results

2.3.1 Bird Diversity

Throughout the course of the study, a total of 20,797 bird observations were recorded in camera images, with 18,011 counted from control cages (Table 2.1). The most commonly observed birds were brown pelicans (*Pelecanus occidentalis*), followed by Terns (presumptive species include royal terns (*Thalasseus maximus*), sandwich terns (*Thalasseus sandvicensis*), common terns (*Sterna hirundo*), least terns (*Sternula antillarum*), Caspian terns (*Hydroprogne caspia*), and Forster's Terns (*Sterna forsteri*)), double-crested cormorants (*Nannopterum auritum*), gulls (presumptive species include laughing gulls (*Larus atricilla*), ring-billed gulls (*Larus delawarensis*), and herring gulls (*Larus argentatus*)), snowy egrets (*Egretta thula*), ruddy turnstones (*Arenaria interpres*), great blue herons (*Ardea herodias*), and black skimmer (*Rynchops niger*).

The number of bird observations differed significantly by month ($F(8,18) = 232.2$, $p < 0.001$). Birds were observed interacting with cages the most during the month of September, and less frequently during the months of January and March (when not considering February due to camera malfunction) (Fig. 2.5). The abundances of common bird groups all varied significantly by month. Brown pelicans were the predominate species and were most abundant during the months of July, September, and October ($F(8,18) = 686.6$, $p < 0.001$) (Fig. 2.6A). Double-crested cormorants dominated control cages during the months of December, January, and March but were also frequently observed in November ($F(8,18) = 118.7$, $p < 0.001$) (Fig 2.6B). The most gulls were observed during the months of December and January ($F(8,18) = 81.45$, $p < 0.001$) (Fig. 2.6C), with a majority of these being laughing gulls (Fig. 2.7A). Terns were the most observed group in the months of August and November but were observed most frequently in October ($F(8,18) = 180$, $p < 0.001$) (Fig. 2.6D). Within the terns, royal terns were seen most frequently (Fig. 2.7B).

Table 2.1. Diversity of birds interacting with floating oyster aquaculture gear.

Treatment	Bird Group	Jul '23	Aug '23	Sep '23	Oct '23	Nov '23	Dec '23	Jan '24	Feb '24	Mar '24	Total
Control	**Pelicans**	1,907	685	5,367	1,852	290	101	6	0	74	10,282
	Terns	141	1,002	240	1,685	787	430	77	13	119	4,494
	Cormorants	1	0	25	36	704	563	319	165	591	2,404
	Gulls	63	37	0	13	22	203	292	45	53	728
	Other										
	Great blue herons	1	0	0	0	1	0	0	0	1	3
	Ruddy turnstones	0	0	0	0	1	6	5	0	0	12
	Snowy egrets	0	0	0	0	0	6	80	0	1	87
	Black skimmers	1	0	0	0	0	0	0	0	0	1
	Control Totals	2,114	1,724	5,632	3,586	1,805	1,309	779	223	839	18,011
Deterrent	**Pelicans**	133	275	1,993	270	15	0	0	0	1	2,687
	Terns	3	25	8	0	1	0	0	1	0	38
	Cormorants	0	0	0	0	4	0	2	0	0	6
	Gulls	6	1	0	0	4	0	4	2	4	21
	Other										
	Great blue herons	0	0	1	0	0	0	0	0	2	3
	Ruddy turnstones	0	0	0	0	0	0	0	0	0	0
	Snowy egrets	0	0	0	0	20	0	6	3	2	31
	Black skimmers	0	0	0	0	0	0	0	0	0	0
	Deterrent Totals	142	301	2,002	270	44	0	12	6	9	2,786
	Grand Total	2,256	2,025	7,634	3,856	1,849	1,309	791	229	848	**20,797**

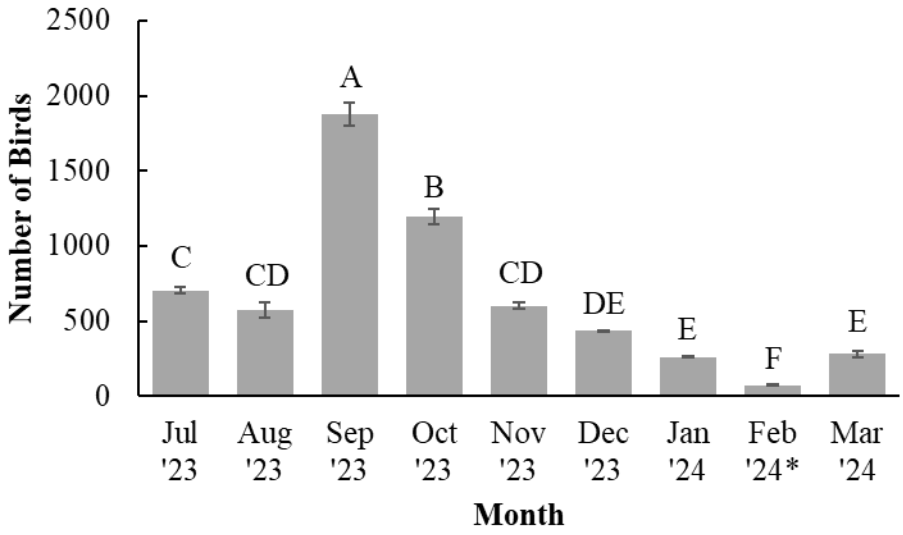

Figure 2.5. Average (± SE) number of birds observed monthly across all cages over the course of the study. Letters denote significant differences among months. Note: February's abundances are likely underestimated as data was missing due to camera malfunctions.

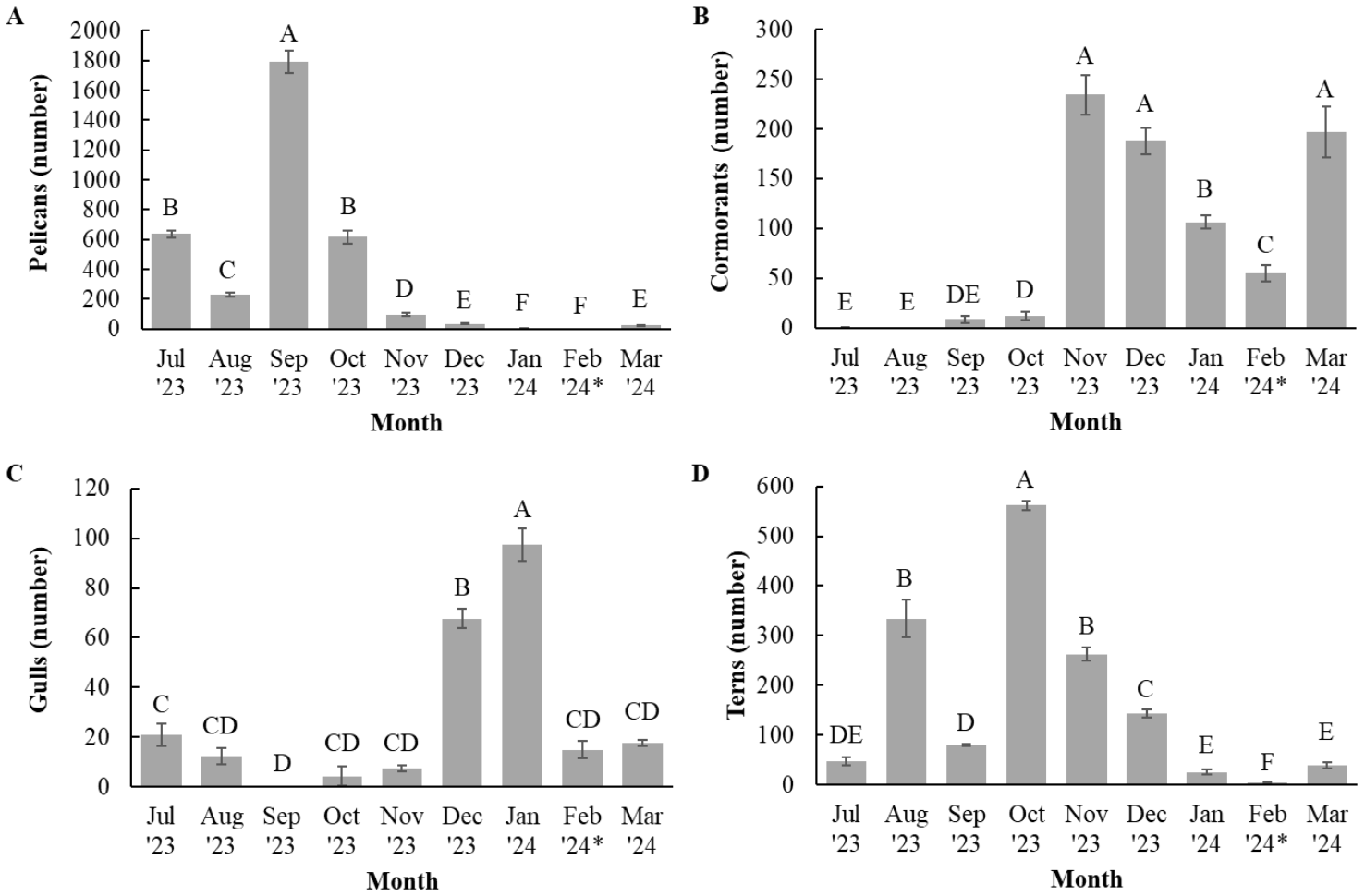

Figure 2.6. Average (± SE) number of birds by presumptive species observed each month across all cages over the course of the study. A) Pelicans; B) Terns, C) Cormorants; D) Gulls.

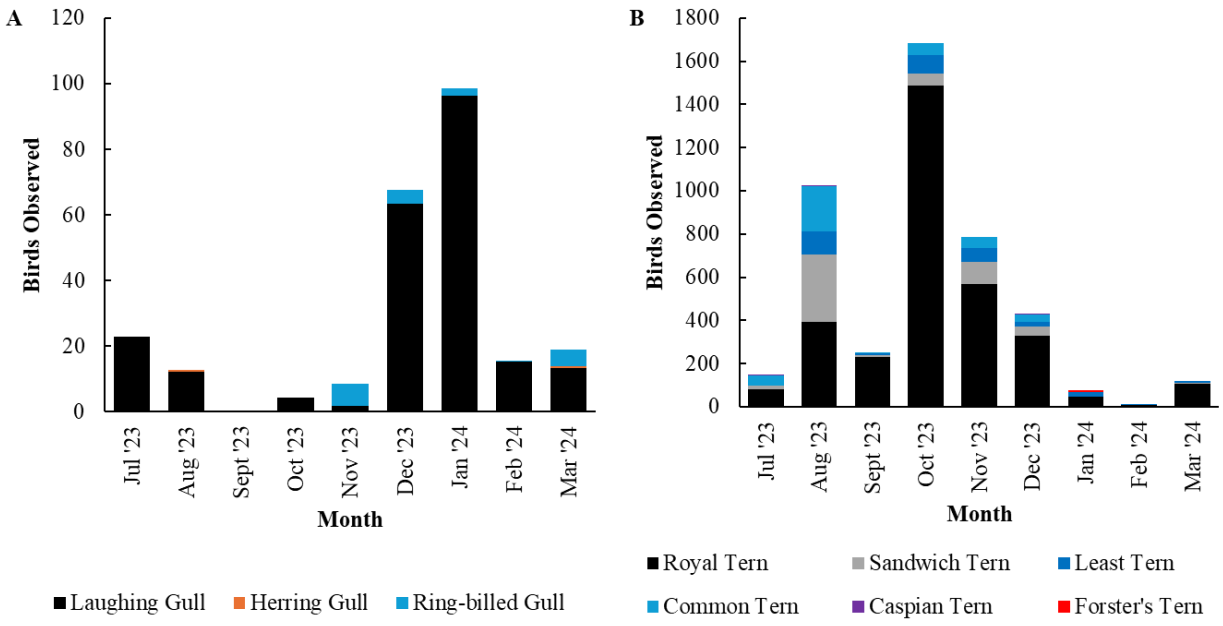

Figure 2.7. Monthly observations of presumptive species within the A) Gulls and B) Terns.

Bird observations changed throughout the day, with the highest number of birds observed peaking in the mornings (8:00 h – 9:30 h), and the numbers dwindling throughout the day ($F(27,56) = 201$, $p < 0.001$) (Fig 2.8; Table 2.2). Species-specific patterns can be observed (for statistical results, see Table 2.2), with Brown Pelicans populating the farm site around 07:30 h, peaking between 08:00 h and 10:00 h and slowly tapering off in abundance as the day progressed ($F(27,56) = 97.5$, $p < 0.001$) (Fig 2.9A). Double-Crested Cormorants were present on the farm site in a bimodal pattern, peaking between 09:00-10:30 h and 13:00-14:30 h ($F(27,56) = 80.8$, $p < 0.001$) (Fig 2.9B), although numbers of Cormorants were statistically similar from 08:30 h to 16:00 h. Gulls were mostly present in the mornings between 08:00 h and 09:00 h, with only occasional sightings after 12:30 h ($F(27,56) = 29.0$, $p < 0.001$) (Fig 2.9C). While Laughing Gulls were present throughout the day, Ring-Billed Gulls were most abundant in the mornings and Herring Gulls were rarely captured interacting with floating cages (Fig. 2.10A). Terns were observed to occupy the farm in

a tri-modal pattern, with higher abundance in the mornings (7:30-8:30 h), reappearing midday (11:30 h), then once again arriving in lower abundances late afternoon (16:30-17:00 h) ($F(27,56) = 40.3$, $p < 0.001$) (Fig 2.9D). All presumptive Tern species followed a similar pattern (Fig. 2.10B).

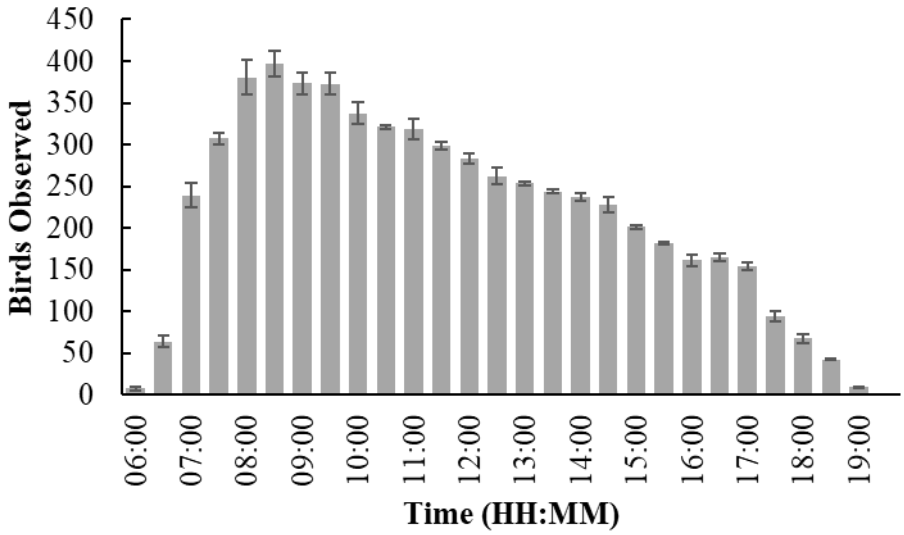

Figure 2.8. Average (± SE) number of birds observed each hour across all cages over the course of the study. Significant differences among times are shown in Table 2.2.

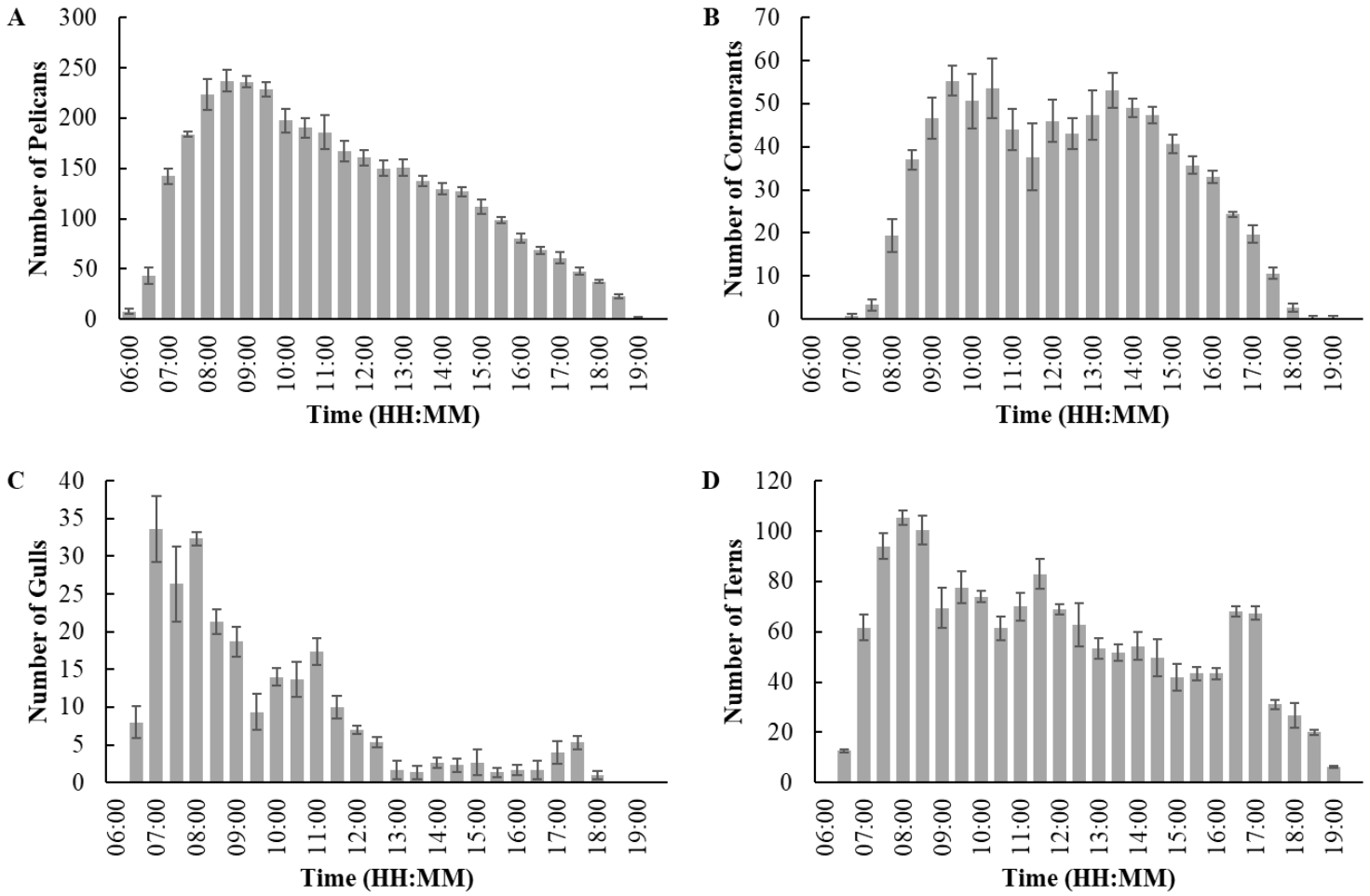

Figure 2.9. Average (± SE) number of birds by group observed each hour across all cages over the course of the study. A) Pelicans; B) Cormorants, C) Gulls; D) Terns. Significant differences among times are shown in Table 2.2.

Table 2.2. Results from Tukey's HSD tests comparing bird abundances over the course of a day. Each group (pelicans, cormorants, etc.) was analyzed separately with a one-way ANOVA. Observations were not significantly different between times if they shared a letter.

Time	Pelicans	Cormorants	Gulls	Terns	Total
6:00	opq	h	l	m	n
6:30	lmnop	h	defghi	lm	lm
7:00	fgh	gh	a	defgh	ghi
7:30	cdef	fg	ab	abc	cde
8:00	abc	de	a	a	ab
8:30	a	abc	abc	ab	a
9:00	a	a	abcd	cdef	ab
9:30	ab	a	cdefgh	bcde	ab
10:00	abcd	a	bcde	cdef	bc
10:30	bcde	a	bcdef	defgh	cd
11:00	cde	ab	abcd	cdef	cd
11:30	defg	abc	cdefg	abcd	cdef
12:00	defg	a	defghij	def	defg
12:30	efgh	ab	efghijk	defgh	efgh
13:00	efgh	a	ijkl	efghi	fgh
13:30	ghi	a	jkl	fghi	ghi
14:00	ghi	a	ghijkl	efghi	ghi
14:30	ghi	a	ghijkl	fghij	hij
15:00	hij	ab	ghijkl	hijk	ijk
15:30	ijk	abcd	jkl	ghijk	jk
16:00	jkl	abcd	hijkl	ghijk	k
16:30	klm	bcde	ijkl	defg	k
17:00	klmn	cde	fghijk	defg	k
17:30	lmno	ef	efghijk	ijkl	l
18:00	mnopq	fgh	kl	jkl	lm
18:30	nopq	gh	l	klm	mn
19:00	pq	gh	l	lm	n
19:30	q	h	l	m	n

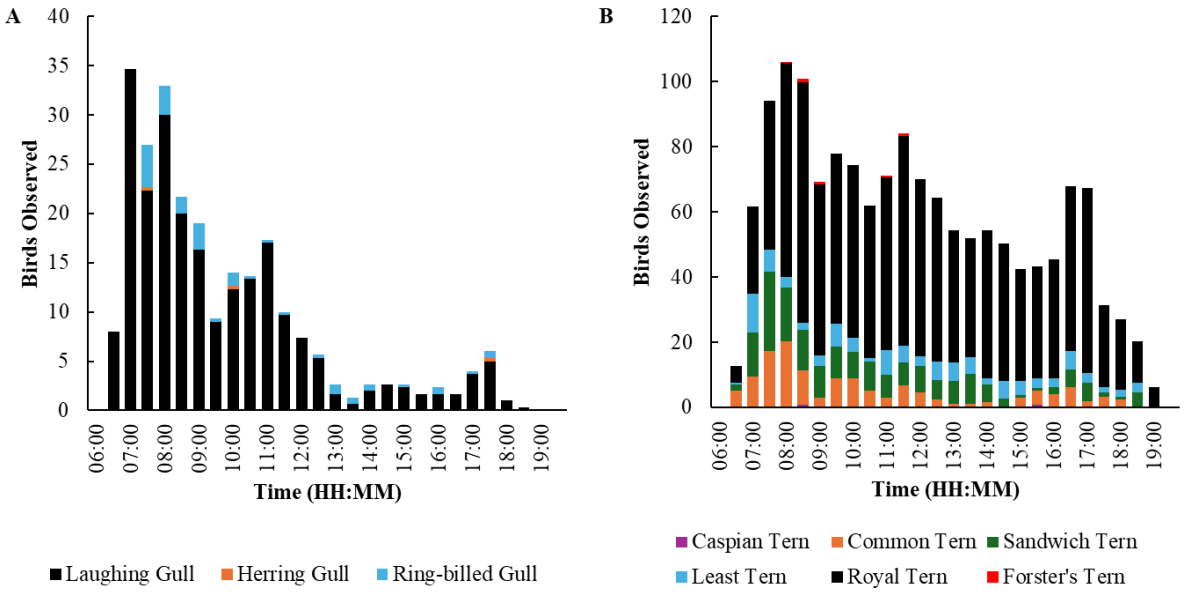

Figure 2.10. Hourly observations of presumptive species within the A) Gulls and B) Terns

2.3.2 Deterrent Efficiency

Bird deterrents were effective in reducing bird-cage interactions (Fig. 2.11). Greater than 73% of birds found on the farm during any given month were observed on control cages (July = 93.70%, August = 85.13%, September = 73.77%, October = 93.00%, November = 97.62%, January = 98.67%, February = 98.67%, March = 98.94%). The simple bird deterrent resulted in an 84.5% reduction in bird interactions on average compared to control cages. Deterrents were most effective in reducing terns, gulls, and double-crested cormorants (Fig. 2.12; Table 2.3), but less effective in reducing brown pelican and snowy egret interactions. There was no apparent effect of the deterrent on great blue heron perching behavior.

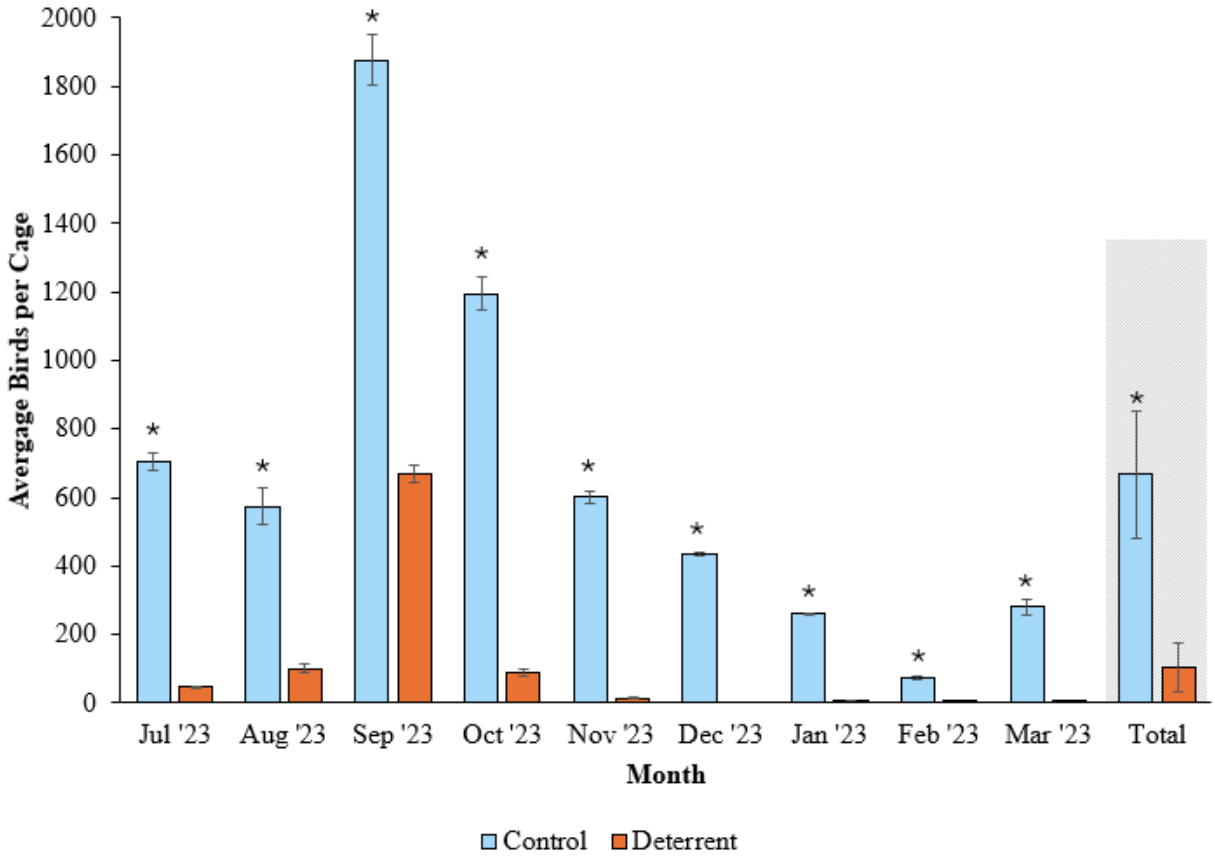

Figure 2.11. Effectiveness of the bird deterrent over the course of the study. The average (± SE) number of birds observed is shown for each sampling month. The averages (± SE) for the whole study are shown in the total column highlighted in gray.

Figure 2.12. Images captured denoting the effectiveness of the deterrent cages. A) comparison of Brown Pelican density per treatment on 9/10/2023 at 09:00 h; B) comparison of Double-Crested Cormorant density per treatment on 3/6/2024 at 09:30 h; C) comparison of Tern density per treatment on 10/30/2023 at 08:30 h. Left, deterrent cages; Right, control cages.

Table 2.3. Total number of each bird group observed on all replicates of each treatment cage over 9 months and the effectiveness of the deterrent in percent reduction.

Bird Group	Control	Deterrent	Percent Reduction
Terns	4,494	28	99.38%
Gulls	728	21	97.13%
Pelicans	10,282	2,687	73.87%
Cormorants	2,404	6	99.75%
Others			
Ruddy Turnstones	12	0	100.00%
Snowy Egrets	87	31	64.37%
Great Blue Herons	3	3	0.00%
Black Skimmers	1	0	100.00%
Total	**18,011**	**2,786**	**84.53%**

2.4 Discussion

The increase in popularity of off-bottom oyster aquaculture in the nGOM within the last ten years (Petrolia, 2023) has the potential to drive change in shoreline usage by sea- and shorebirds as well as migratory waterfowl. Aquaculture gear attracts seabirds to areas in which they would not otherwise congregate as a result of the increase in surface area available for perching (Butler, 2003; Meire, 1993; Roycroft et al., 2004). The seafood safety concerns surrounding the potential deposition of fecal contaminants around floating oyster gear, that may accumulate within oysters destined for the raw market, prompted recommendations by regulatory agencies advising that farms reduce the frequency of bird interactions with farm gear (NSSP, 2019). To accurately assess potential health risks and identify efficient ways to deter bird roosting at farms, it is necessary to identify the community of birds that regularly visit oyster aquaculture sites. In this study, birds populated floating gear throughout the year and the species diversity observed was congruent with species richness of the nGOM as described in Gallardo et al. (2009) and Burger (2017). This study

demonstrated that, while birds frequently interact with floating oyster cages, bird abundance can be significantly reduced using simple, inexpensive physical deterrents.

Data is reported herein as average birds observed, but it should be noted these numbers do not refer to individual birds, as the same individual is likely present in multiple photographs. However, this strategy of determining abundance has been used in studies on fishes and demonstrates a direct linear relationship with true abundance (Schobernd et al., 2014; Bacheler et al., 2014). Therefore, the monthly and hourly patterns observed in this study are likely to be an accurate representation of bird populations visiting the farm site.

The community of birds observed at the Bayou Sullivan farm site was dominated by brown pelicans, terns, and double-crested cormorants. The number of birds able to fit on a pontoon at a given time was dependent of the species. For a cage entirely comprised of brown pelicans, up to eight individuals were observed on one cage at a time. During our study, double-crested cormorants were never observed to exceed 6 individuals per cage despite their smaller body size. This is likely due to their sunning/drying behaviors, which involve spreading out their wings while resting. This study also demonstrated clear seasonal patterns in bird groups visiting the farm. The high abundance of brown pelicans found on the farm sites during the fall may be due to migratory behaviors, as recent literature notes partial migrations of brown pelicans in lower Alabama are driven by increases in foraging effort due to declining food supply (Lamb et al., 2020; Lamb et al., 2020). Daily interactions between brown pelicans and floating gear tend to be highest in the morning and taper off as the day goes on, which may be indicative of gear use as resting perches during foraging hours. During the late summer through early fall, camera data indicated that brown

pelicans displaced other species in favor of forming monospecific groups. However, from late fall to early spring, they were often found sharing the site with other species. The winter months, in which brown pelicans were less abundant on floating gear, coincided with increased roosting by double-crested cormorants.

Double-crested cormorants (hereafter referred to as cormorants) are a migratory species that travels from Canada and the Great Lakes down to the Southeast and Gulf coasts where they compete with local species, including brown pelicans, for wintering habitat (Hatch et al., 1999). The southern migration period begins in October and cormorants return north starting in February; this migration pattern was observed during this study. The cormorants gather in daily resting areas and, in doing so, develop high-density monospecific groups (Mendall, 1936). However, during this study, cormorants were observed at the farm site in a semidiurnal pattern, with abundances peaking in late morning and again in early afternoon. Cormorants have not been reported as inherently hostile towards other species of seabirds and are often observed co-nesting with other species, primarily pelicans, gulls, and herons (Somers et al., 2011). However, photo data and personal on-farm observations suggest that cormorants preferentially target landing spots that are away from perching birds or may displace other species when choosing a loafing spot. The overwhelming dominance of cormorants at oyster farms during the wintering months is likely driven by migration patterns, their predisposition to forming monospecific groups, and relative indifference towards other seabird species.

Of the group terns, the royal terns were the most frequently identified species and were often found in con-specific groups when resting on cages. Royal terns are shorebirds that are endemic to the

Gulf of Mexico and forage in estuarine environments (McGinnis and Emslie, 2001). Their congregation on floating gear occurred primarily in late summer through late fall and they most often visited farm sites in the morning. Buckley and Buckley (1974) noted that adults and juveniles forage separately and observed juvenile royal terns roosting in shoreline habitats at the highest density from 06:00-08:59 h, while adults were found in the highest density from 09:00-11:59 h. In this study a roughly trimodal distribution of terns at the farm site throughout the day was observed, with the highest density overlapping with the foraging times of both juveniles and adults (07:00-08:30 h). From these observations, I hypothesize that floating oyster farm sites act as a convenient resting ground during foraging hours. The increase in density of terns present around 11:30 h, marking the end of the adult foraging period, supports this claim, however the subsequent increase in the afternoon (16:00-17:00 h) is less clear, with literature suggesting a less refined pattern of afternoon feeding observed in con-specific terns (Bugoni et al., 2005).

Gulls were observed at the farm site in high density in the morning, coinciding with typical foraging behavior (Isaksson et al., 2016). Gulls were found on farm gear primarily in winter, accounting for a smaller proportion of birds present during the months in which pelicans were most abundant. This can likely be explained as displacement by or competition with larger pelicans. Although cormorants were also abundant in the winter, gulls were present earlier in the mornings, peaking between 07:00 h and 08:00 h, with cormorant presence thereafter increasing until approximately 09:30 h. Large gulls, such as herring gulls and ring-billed gulls, visited the farm site individually or in small monospecific cohorts of <5 individuals.

Apart from ruddy turnstones, which were observed foraging on the biofouling growing on cages during boat trips to the farm sites, birds appeared to be using floating gear as a resting perch for sleeping, drying/sunning themselves, or preening. This coincides with the results of Comeau et al. (2009) which found similar usage of floating cages by bird populations in the Northeast. The lack of active foraging behavior implies that birds are idle while on the farm. These habits result in fecal concentration on and around the cages; however, the risk associated with this material is still unknown.

The efficiency of techniques to mitigate bird interactions with aquaculture production is better studied in fish than in shellfish, as birds are active predators at fish production sites and during longline fishing expeditions. In fish aquaculture systems such as ponds, typical techniques for reducing birds include frightening strategies (noise or predator imitation) and full or partial exclusion, which entails constructing a large structure to impair or completely keep birds from accessing ponds (Curtis et al., 1996; Littauer et al., 1997; Mott and Boyd, 1995). While full exclusion techniques are not feasible for off-bottom oyster aquaculture, partial exclusion techniques, like the zip tie bird deterrent tested in this study, have been effective to varying degrees (Comeau et al., 2009; Cunningham et al., 2024). The simple, inexpensive, nonlethal deterrent used in this study significantly decreased bird interactions with floating cages by nearly 85%.

Deterrent efficiency was dependent on bird group, with some groups relatively unaffected. The deterrent used in this study was relatively ineffective in preventing cage interactions with snowy egrets; I hypothesize that the length of their legs prevents the plastic zip ties from disturbing them while perched. Great blue herons were observed to exclusively stand on the submerged metal

framing of the cage, in between the pontoons to which the deterrents were fixed. This rendered the deterrent functionally ineffective. It should be noted that only six great blue herons were observed during this study. The days in which pelicans, terns, and gulls were observed on deterrent cages were days of high bird abundance at the farm, indicating a negative relationship between bird numbers and deterrent efficiency. This pattern was most obvious in brown pelicans, which were often found on deterrent cages when all other perching spots at the site were taken by other birds. Lack of space and their social behaviors led to interactions with deterrent cages where, due to their larger bodies and feet, they were able to rest on the bendable plastic zip ties by weighing them down where perched.

Comeau et al. (2009) tested the efficiency of a simple physical bird deterrent in New Brunswick, Canada and found similar results to this study, with the implementation of deterrents significantly reducing the frequency of birds interacting with floating oyster gear. Their deterrent was AntiCormo (Bouctouche Bay Industries, Ltd., New Brunswick, Canada), a commercial bird deterrent made up of spikes attached to the gear floats, targeted to deter cormorants. This device was effective in reducing cormorant interactions by up to 100% at one location, with occasional interactions at a second site, suggesting a potential influence of site on deterrent efficiency. Cunningham et al. (2024) compared effectiveness of cormorant mitigation between six types of deterrents. Similar to this study, the use of any type of deterrent significantly reduced interactions. Analyzing the success of each specific type of gear, float-mounted triangles (Ketcham Supply, New Bedford, MA), Bird B Gone Spinning Bird Deterrent® (Bird B Gone, Irvine, CA), and Bird Spikes for Bird, Cat, Squirrel, Racoon Animals Repellent® (TANGTEA, Amazon.com) all had a higher probability of reducing bird interactions than the Scarem Kite® (Flyonte, Amazon.com)

(Cunningham et al., 2024). Each deterrent type has associated shortcomings. The Scarem Kite® relies heavily on sufficient wind at the farm site to keep the kite flying. Kite-like deterrents have been observed to lose efficiency if not repositioned around the farm site regularly (Navy Cove Oyster Farm, pers. communication). In addition, they may not be as effective against larger birds, explaining the difference in performance when compared to other deterrent types in the study by Cunningham et al. (2024). Physical bird deterrents, like the AntiCormo, triangles, or the simple, inexpensive deterrent used in this study can inconvenience farmers when working floating gear. The deterrent can interfere with gear movement or cause discomfort and injury to workers. Deterrents can be removed to avoid these issues when working the gear, however this significantly increases the time and effort associated with production in an industry that is already workforce limited.

It is important to note that during this study the cages were not desiccated, or flipped, to mitigate biofouling, as would be a regular practice in industry production. This standard practice would nullify the effect of our deterrent since the deterrent would be fully submerged. At this point, the cage is exposed, and this also alters the surface available for perching, as the birds would land on a wire mesh structure instead of a solid plastic one. Understanding bird interactions with the cage mesh would require a separate study for this area. However, previous studies have noted that bird interaction with desiccating cages mirrors, if not increases, that of cages without deterrents (Comeau et al., 2009).

This study demonstrated that a simple, inexpensive, nonlethal bird deterrent is effective at reducing bird interactions with off-bottom oyster aquaculture gear. Precision of bird monitoring would

benefit from the use of higher quality camera systems than those used in this study, as identification at the species level was sometimes difficult. As each farm site is likely to have a different community of birds, studies are required that evaluate the effectiveness of other types of bird deterrents in the nGOM to identify ones that are most effective at a particular farm site. States have varying interpretations of the NSSP Model Ordinance and regulate these interactions differently, so it is currently unclear how effective deterrents need to be to meet the guidance. In addition, some regulators have concerns over the safety of deterrents for the birds, particularly physical ones. Finally, there is insufficient data to develop a risk assessment regarding birds and oyster farming, and seafood safety concerns may be overestimated, so future studies should determine the risk of transfer of human pathogens through bird-gear interactions. Regardless, the presence of bird fecal material on floating gear is unsightly, particularly for an oyster farm that provides tours and tastings, and birds can carry human pathogens. This study demonstrated that a simple deterrent is effective at reducing the number of various bird species on floating oyster cages in the nGOM.

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CHAPTER 3: PREVALENCE OF *CAMPYLOBACTER* IN SEABIRDS AND OYSTERS AT OYSTER AQUACULTURE FARMS

3.1 Introduction

Campylobacter, a genus of Gram-negative, curved, microaerophilic bacteria (Tobolowsky et al., 2023), are the most common bacterial cause of human gastroenteritis worldwide and one of the leading causes of diarrheal disease globally (European Food Safety Authority, 2023; World Health Organization et al., 2013). *Campylobacter* are found in the gastrointestinal tracts of warm-blooded animals including poultry, cattle, wild birds, and rodents (Luechtefeld et al., 1980; Svedhem et al., 1981; Taylor et al., 2013). Infections of *Campylobacter* in humans, referred to as campylobacteriosis, most commonly occur through the consumption of contaminated animal and dairy products and usually involves infection with the species *Campylobacter jejuni* or *C. coli*, although other species of *Campylobacter* are recognized as emerging pathogens (Facciolà et al., 2017; Taylor et al., 2013). Acute infection typically results in diarrhea, fever, and dehydration, but can have long-term consequences including peripheral neuropathies, such as Guillain-Barré syndrome and Miller Fisher syndrome, and functional bowel diseases like irritable bowel syndrome (World Health Organization et al., 2013). In the US, there were 705 outbreaks of campylobacteriosis from 2011 to 2021, resulting in 5,951 reported cases, 431 hospitalizations, and 2 deaths as reported by the Center for Disease Control (CDC) National Outbreak Reporting System (CDC, 2023). In 2022, campylobacteriosis was the most reported zoonotic disease in the European Union (European Food Safety Authority, 2023).

Sources of *Campylobacter* infection in humans typically stem from the consumption of contaminated or undercooked dairy and poultry products (D'aoust, 1989; Hopkins and Scott, 1983; Taylor et al., 2013). However, campylobacteriosis outbreaks have also been reported from water and agricultural crops contaminated by wild bird populations (Benton et al., 1983; Gardner et al., 2011). In a 2011 report by the CDC and Alaska Department of Health and Social Services, 45 cases of campylobacteriosis were linked to the consumption of locally grown raw peas contaminated with *C. jejuni* by sandhill cranes (*Grus canadensis*), which were observed grazing and defecating in pea fields during the harvest period (Gardner et al., 2011). Wild birds, especially those with large migratory ranges, are of primary concern in studies evaluating enteric pathogen spillover because of their potential as long-distance vectors. Migratory behavior was found to significantly impact the likelihood of *Campylobacter* prevalence in birds depending on whether the animal was a winter, summer, or stopover migrator (Kwon et al., 2017). Broiler chickens are also a natural host for thermophilic *Campylobacter* species, which colonize their gut in large quantities as a commensal organism and pose a food safety risk (Hopkins and Scott, 1983; Sahin et al., 2015). However, *Campylobacter* species have been isolated in seabirds and waterfowl as well. A study by Benton et al. (1983) attributed the contamination of a major water supply to gulls roosting at the reservoir, while Luechtefeld et al. (1980) isolated *C. jejuni* from 156 of 445 migratory ducks. There are minimal studies concerning *Campylobacter* isolation from shellfish and fewer contextualizing *Campylobacter* presence at oyster farm sites.

Campylobacter spp. have been previously isolated from oysters (Jurinovic et al., 2022; Teunis et al., 1997; Wilson and Moore, 1996); however unlike other livestock, there is a lack of literature on *Campylobacter* in shellfish. Oysters are a particular topic of interest regarding seafood safety as

they are frequently eaten raw, increasing the consumers' exposure to potential pathogens. There have been 9 outbreaks of campylobacteriosis attributed to raw oyster consumption since 2011 (CDC, 2023). In 2021, the Rhode Island Department of Health reported an outbreak of *C. jejuni* resulting in eight cases of campylobacteriosis attributed to the consumption of raw oysters from an off-bottom oyster farm. After eliminating other sources of contamination, including shore-based runoff, wastewater treatment systems, and nearby agricultural or livestock operations, the report implicated the contamination to seabirds roosting nearby during the harvest period (Caron et al., 2023). However, no samples were tested to verify the presence of *Campylobacter* in the birds roosting in the area. The lack of substantial data to inform risk assessment of bird-oyster interactions has led to tension between oyster farmers and regulators. The presence of seabirds at oyster farms has triggered sanitation concerns for regulatory agencies. The potential for seabirds to introduce human pathogens to the farm site and then for oyster to accumulate these pathogens as a result of filter feeding has caused alterations in the National Shellfish Sanitation Program (NSSP) Model Ordinance to address the problem of seabirds at floating oyster aquaculture sites.

Our previous studies confirmed that the implementation of a simple, inexpensive, non-lethal bird deterrent significantly reduced the number of birds interacting with floating oyster farm gear. However, preemptively requiring the use of deterrents incurs additional labor and costs to the industry which already operates under heavy regulation. Studies outlining the presence of *Campylobacter* in seabirds and oysters held in floating aquaculture gear are required to generate a risk assessment for these wildlife interactions. This study aims to determine the prevalence of *Campylobacter* in seabirds and cultured oysters in the northern Gulf of Mexico (nGOM).

3.2 Methods

3.2.1 Oyster Tissue Sampling

Floating oyster cages were deployed as described in Chapter 1. Each floating cage contained four bags, one in each corner and leaving the center two positions empty, stocked with 90 oysters per bag. Oyster densities declined during the sampling period due to removal of samples and mortalities. When bags reached ≤ 70 oysters they were restocked to 90 oysters, approximately every 3 months. To avoid the impacts of air drying on bacterial populations within the oysters, no desiccation was performed during the study. Therefore, to reduce biofouling and allow adequate water flow throughout the experiment, all bags were replaced simultaneously approximately every 3 months. Water quality data, including temperature, salinity, and dissolved oxygen, was collected using an EXO3 YSI sonde (Yellow Springs, OH, USA). Water quality was consistently monitored throughout the study, excluding a small window between Jan 5 – Jan 10, 2024, where sonde equipment was removed from the field for maintenance.

Three oysters were sampled from each of the four bags in every cage at least monthly, resulting in 6 oyster samples comprised of twelve oysters each (n = 3 for control cages, n = 3 for deterrent cages) at each sampling event. Oysters were scrubbed to remove organic matter and biofouling. Morphometric data for each oyster, including shell height, width, and length (Fig. 3.1), was collected using digital calipers.

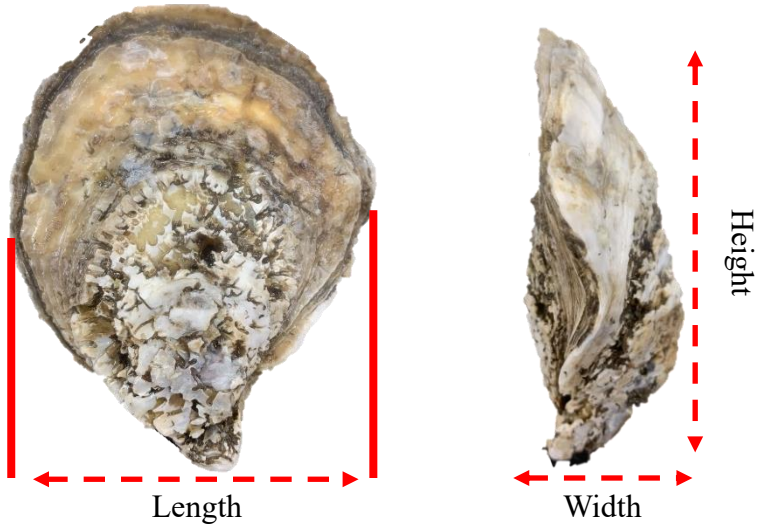

Figure 3.1. Diagram depicting oyster measurements collected during the study.

All twelve oysters from a single cage were shucked and blended at low speed for one minute into a homogenate, resulting in three homogenized samples of control oysters and three homogenized samples of deterrent cages. These homogenates were weighed prior to processing. Each homogenate was then inoculated in 225 mL of enrichment broth (13.8 g Bolton Broth Base added to 500 mL DI water; autoclaved at 15 psi, 121 °C, 15 min; cooled to 50°C; added 1 vial of rehydrated Bolton Broth Supplement and 25 mL of lysed horse blood and mixed well) (CDC, 2001) and split evenly into two 300 mL Erlenmeyer flasks at approximately 112.5 mL each. Flasks were loosely covered with aluminum foil and incubated in microaerophilic conditions, achieved by incubating flasks inside 6-liter BD GasPak™ EZ containers (Sparks, MD, USA) with the associated oxygen-fixing sachets (BD GasPak™ CampyPak sachets, Sparks, MD, USA) as per manufacturer protocols. Sachets produced atmospheric conditions within the air-tight container with approximately 5-15% oxygen. Incubation conditions were specified in the US Food and Drug Administration (FDA) Bacteriological Analytical Manual for Campylobacter (CDC, 2001). In

short, flasks were maintained at 30°C for three hours, were then increased to 37°C for two hours, and finally set at 42°C for 28 hours. After incubation, 20 µL from each flask was streaked on CHROMagar™ Campylobacter (CHROMagar, Paris, France) and incubated for 48 hours at 42°C in microaerophilic conditions. Plates were examined for growth and the number of unique morphologies, based on colony size, shape, color, and margin, was determined. According to the manufacturer, *Campylobacter* spp. colonies grown on CHROMagar™ Campylobacter are individual, red, and circular or irregular colonies, whereas other microbes would appear blue or be inhibited; however, the protocol only reports on the colonies of *C. coli*, *C. jejuni*, and *C. lari*. Therefore, to ensure collection of any *Campylobacter* capable of growing on the plates, all unique morphologies were further analyzed. Morphologies identified during the study are described in Appendix I. For each sample, five isolates of each unique morphology were re-streaked on CHROMagar™ Campylobacter and incubated at 42°C for 48 hours in microaerophilic conditions. DNA was collected from isolates by heat extraction. Briefly, a single colony was resuspended in 100 µL of nuclease-free water and heated to 95°C for 15 minutes. After heating, samples were centrifuged at 1000 *rcf* for 5 minutes and supernatants were collected. Supernatants were stored in 96 well plates at -80°C for later use in PCR analysis. Remaining colonies from each isolate were preserved in freezing media (2.62 g Bolton Broth Base added to 95 mL DI water, 10 mL Fetal Bovine Serum and 10 mL glycerol; autoclaved at 15 psi, 121°C, 15 min) (CDC, 2001) and stored at -80°C.

3.2.2 Seabird Fecal Matter Sampling

Approximately nine fecal samples were collected opportunistically from seabirds visiting the farm site on a weekly basis. The sample collection protocol involved riding out to the farm by boat, identifying an individual bird to the species level, then scaring it off its perch and quickly approaching to check for fresh fecal material. Fecal samples were considered fresh if defecation was witnessed or if the material was wet upon discovery. Feces were collected using sterile cotton swabs into sterile 1.5 mL microcentrifuge tubes. Samples were brought back to the lab and resuspended 1:3 in Phosphate Buffered Saline (PBS) (Butcher and Stintzi, 2017). A 1:10 dilution was made in PBS, after which both dilutions were plated on Campylobacter CHROMagar™ and incubated for 48 hours in microaerophilic conditions at 42°C. Plates were scrutinized for colony growth as described above. Five isolates of each unique morphology on plates with growth were collected, re-streaked on Campylobacter CHROMagar™, and incubated for 48 hours in microaerophilic conditions at 42°C. DNA was collected from re-streak growth via heat extraction as described above and remaining colonies were preserved in freezing media and stored at -80°C as previously described.

3.2.3 Bacterial Colony Identification

To ensure amplifiable DNA was recovered from heat extracts, PCR was performed on the 16S rDNA using primer set 27F (5'-AGAGTTTGATCCTGGCTCAG-3') and 1492R (5'-GGTTACCTTGTTACGACTT-3') (Ludwig, 2007) (Tables 3.1 and 3.2). A negative control of sterile water was included in each reaction. DNA was visualized on a 1% agarose gel using electrophoresis (PCR Product ~ 1400 bp). Remaining PCR products were stored at -80°C. If 16S

rDNA amplification was unsuccessful, the colonies were restreaked from frozen stocks, and heat extractions and PCR were repeated to obtain quality, amplifiable DNA.

Following confirmation of amplifiable DNA, isolates were screened using *Campylobacter* specific multiplex PCR according to Yamazaki-Matsune (2007) (Tables 3.3 and 3.4) and visualized as above. The *Campylobacter* specific multiplex contained seven PCR primer sets, including a *Campylobacter* genus set (C412F-C1228R; 816 bp) and six sets for *Campylobacter* species (*C. hyointestinalis* subsp. *hyointestinalis* (HYO1F-HYOFET23SR; 611 bp), *C. coli* (CC18F-CC519R; 502 bp), *C. fetus* (MG3F-CF359R; 359 bp), *C. lari* (CLF-CLR; 251 bp), *C. jejuni* ((C-1)-(C-3); 161 bp), *C. upsaliensis* (CU61F-CU146R; 86 bp)). A negative control of sterile water was included in each reaction. Positive controls were only available for *C. jejuni*. Isolates that were confirmed as *Campylobacter*, showing amplification in the multiplex PCR, were further analyzed using sequencing. 16S rDNA amplicons from confirmed isolates were purified following the ExoSAP-IT™ (ThermoFisher Scientific, Waltham, MA) or ExoProStar (Cytiva, Marlborough, MA) protocols and subjected to Sanger sequencing at Eurofins Genomics (Louisville, KY).

Table 3.1. PCR mixture used for amplification of the 16S rDNA.

Reagent	**Vol. per rxn (µL)**
Sterile Water	8.0
GoTaq colorless master mix (2X)	10
27F primer (10 µM)	0.5
1492R primer (10 µM)	0.5
Template DNA	1.0
Total Reaction Volume	20

Table 3.2. Thermal cycler program for amplifying the 16S rDNA.

Step	Temperature	Time
1	95°C	5 min
2	95°C	30 sec
3	51°C	30 sec
4	72°C	1 min
5	Repeat 2-4	40x
6	72°C	7 min
7	4°C	Hold

Table 3.3. PCR mixture used for amplification of the CampID Multiplex PCR.

Reagent	Vol. per rxn (µL)
Sterile Water	11
GoTaq colorless master mix (2X)	12.5
CampID primers (10 µM)	
C412F	
C1228R	
HYO1F	
HYOFET23SR	
CC18F	
CC519R	
MG3F	0.5
CF359R	
CLF	
CLR	
C-1	
C-3	
CU61F	
CU146R	
Template DNA	1
Total Reaction Volume	25

Table 3.4. Thermal cycler program for amplifying the CampID Multiplex PCR.

Step	Temperature	Time
1	95°C	15 min
2	95°C	30 sec
3	58°C	1.5 min
4	72°C	1 min
5	Repeat 2-4	25x
7	10°C	Hold

3.2.4 Data Analysis

Oyster growth metrics (height, length, width, and wet weight) were analyzed using linear regression models in RStudio (v2023.06.01).

Sequence analysis was conducted after aligning and trimming all sequences to a common length (617 bp) in BioEdit (v5.0.9). Using the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST), sequences were evaluated for similarity to isolates cataloged in the rRNA/ITS database and filtered to only compare to sequences from type material.

To test the relatedness of isolates from birds and oysters, phylogenetic analysis was conducted using a bootstrapped consensus Neighbor-Joining tree of 500 iterations created in MEGA11 (v11.0.13). The phylogenetic tree included isolates collected from oysters and birds, as well as downloaded, aligned, and trimmed sequences of the closest type strains resulting from NCBI BLAST comparison and *Arcobacter nitrofigilis* as an outgroup. Identical isolates based on 100% 16S rDNA sequence within a sample were represented by a single isolate in the phylogenetic tree.

3.3 Results

3.3.1 Oyster Growth

Oysters evaluated during the study had an initial pooled (12 oysters) wet tissue weight of 168.6 g which increased at a rate of 0.73 (± 35.21 g, 95% C.I.) grams per day with no significant differences between control and deterrent cages (p = 0.95). There were no significant differences in shell width, shell length, or shell height between treatments (p = 0.686, p = 0.683, p = 0.442, respectively) or cages (p = 0.635, p = 0.0874, p = 0.930, respectively). There was no significant difference in oyster mortality between cage treatments (p = 0.16), with ~3 dead individuals (5.5%) removed per restocking event. Restocking of bags was necessary on two occasions (10/18/2023 and 1/24/2024).

3.3.2 Water Quality

Temperature during the study period varied from 4.19 °C on 1/21/2024 to 35.53 °C on 8/1/2023 (Fig. 3.2). Salinity ranged from 3.42 PSU on 3/1/2024 to 31.68 on 11/12/2023. Dissolved oxygen ranged from 1.17 mg/L on 8/3/2023 to 17.85 mg/L on 2/22/2024. Water quality parameters on the days when oysters were sampled are shown in Table 3.5.

Table 3.5. Water quality parameters on days when oyster samples were collected.

Date (MM/DD/YYYY)	Temperature (°C)	Salinity (PSU)	Dissolved Oxygen (mg/L)
08/01/2023	32.42	22.49	4.81
08/17/2023	30.10	24.10	6.69
08/30/2023	30.15	23.94	4.92
09/13/2023	30.22	21.75	5.21
09/26/2023	28.34	23.15	5.43
10/11/2023	23.59	27.86	5.29
11/08/2023	20.99	27.80	7.43
12/06/2023	15.30	24.23	8.60
01/11/2024	11.32	20.59	9.21
01/31/2024	12.54	16.37	9.45
03/06/2024	18.59	6.88	5.46

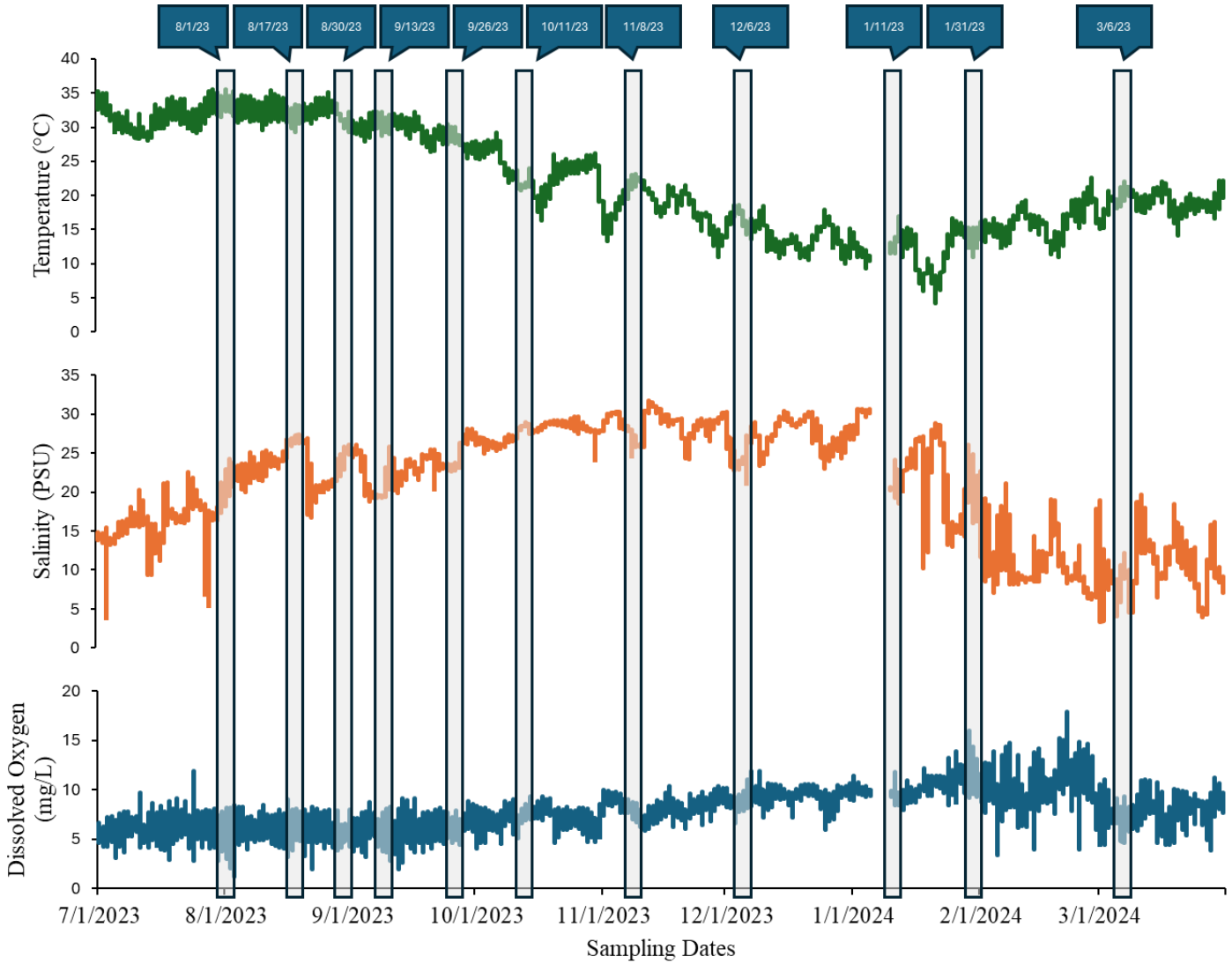

Figure 3.2. Water quality data over the course of the experiment. Gray bars indicate dates on which oyster samples were taken.

3.3.3 Campylobacter in Birds

Fecal matter was collected from 206 birds over the course of the study. *Campylobacter* isolation resulted in an overall positivity rate of 5.82% (12/206) (Table 3.6). Positive samples were collected from royal terns (n=5), brown pelicans (n=4), least terns (n=1), common terns (n=1), and ruddy turnstones (n=1). Samples collected from Caspian terns (n=6), sandwich terns (n=22), laughing gulls (n=3), great blue herons (n=1), and double-crested cormorants (n=2) were negative for *Campylobacter*. Multiplex results showed that 6 isolates resulted in species-specific banding patterns for *C. coli*, 1 matched patterns for *C. jejuni*, and 3 isolates had bands matching with both of these species (Table 3.7).

Table 3.6. Bird fecal material tested and positivity rate for *Campylobacter* by species over the course of the study.

Species	Number Sampled	Number Positive	% Positive
Caspian Tern (*Hydroprogne caspia*)	6	0	0.00
Common Tern (*Sterna hirundo*)	10	1	10.00
Sandwich Tern (*Thalasseus sandvicensis*)	22	0	0.00
Least Tern (*Sternula antillarum*)	13	1	7.69
Royal Tern (*Thalasseus maximus*)	98	5	5.10
Brown Pelican (*Pelecanus occidenatlis*)	50	4	8.00
Laughing Gull (*Leucophaeus atricilla*)	3	0	0.00
Great Blue Heron (*Ardea herodias*)	1	0	0.00
Double-crested Cormorant (*Nannopterum auritus*)	2	0	0.00
Ruddy Turnstone (*Arenaria interpres*)	1	1	100.00
Total	**206**	**12**	**5.82**

Positive samples from brown pelicans were collected during May and September 2023. All four positive samples most closely resembled the species *C. lari* subspecies *concheus* in 16S rDNA sequence identity (>99.68%) (Table 3.7). Positive samples (n=5) from royal terns were collected during July, September, and November 2023. Two samples in July, as well as one sample from September, most closely matched the species *C. lari* subspecies *concheus* in sequence identity (>99.19%). Two other samples collected from royal terns, one collected in July and the other during November, were more closely related to *C. ornithocola* in sequence identity (>99.39%). The sample collected from a least tern and a common tern in August 2023 both resembled *C. ornithocola* in sequence identity (>99.5% and >99.85%, respectively). The sample collected from a ruddy turnstone during November 2023 most closely resembled *C. lari* subspecies *concheus* in sequence identity (>99.69%). However, all isolates shared high (>97%) similarity with multiple species of *Campylobacter*, including *C. armoricus*, *C. aviculae*, *C. bilis, C. coli*, *C. hepaticus, C. insulaenigrae*, *C. jejuni*, *C. lanienae C. lari* subsp. *concheus*, *C. lari* subsp. *lari*, *C. novaezeelandiae*, *C. ornithocola*, *C. peloridis*, *C. subantarcticus*, *C. taeniopygiae*, and *C. volucris* (Appendix II).

3.3.4 Campylobacter in Oysters

Oysters were positive for *Campylobacter* in 15.15% of samples (10/66) (Table 3.8). Oyster tissue positivity occurred most frequently during the months of September and November. During three sampling events, oysters collected from control cages grew *Campylobacter* after tissue enrichment. A single positive deterrent sample was collected at each of 2 sampling events. Multiplex results showed that 3 isolates resulted in species-specific banding patterns for *C. coli*, 1 isolate matched

banding patterns for *C. jejuni*, and 2 isolates had bands matching with both of these species (Table 3.9). Oyster isolate sequences were most similar to *C. lari* subsp. *concheus* (4 samples), *C. volucris* (5 samples), and *C. ornithocola* (2 samples) according to NCBI BLAST (Table 3.9) but shared high (>97%) sequence similarity to the same species reported previously for bird fecal isolates (Appendix III).

3.3.5 Phylogenetic Analysis of Campylobacter Isolates

Isolate relatedness was determined using a neighbor-joining phylogenetic tree (Fig. 3.3). Oyster samples collected in September 2023 clustered in two groups: one group of three isolates with similarity to *C. lari* subsp. *lari* and *C. novaezeelandiae*, and another with four isolates similar to *C. lari* subsp. *concheus*. Oyster samples in October 2023 clustered into three groups: two with sequence similarity to *C. ornithocola* and *C. subantarcticus*, two to *C. volucris*, and one with similarity to *C. lari* subsp. *concheus*. Oyster samples collected in January clustered with *C. lari* subsp. concheus. Royal tern isolates clustered with *C. jejuni* and *C. lari* subsp. *concheus*. Common and least tern isolates clustered with *C. jejuni*, *C. ornithocola*, and *C. subantarcticus*. Brown pelican isolates and ruddy turnstone isolates clustered with *C. lari* subsp. *concheus*.

Table 3.7. Nearest identity of *Campylobacter* isolates from bird fecal material based on multiplex and BLAST results.

			Multiplex	BLAST		
Sample Date	**Bird Species**	**Common Name**	**Matching Banding Pattern**	**Closest Sequence Match**	**Accession Number**	**Percent Identity**
05/22/2023	*P. occidentalis*	Brown Pelican	*C. coli*	*C. lari* subsp. *concheus*	NR_042683.1	99.68%
05/22/2023	*P. occidentalis*	Brown Pelican	*C. coli*	*C. lari* subsp. *concheus*	NR_042683.1	99.68%
05/30/2023	*P. occidentalis*	Brown Pelican	*C. coli*	*C. lari* subsp. *concheus*	NR_042683.1	99.68%
09/05/2023	*P. occidentalis*	Brown Pelican	*Campylobacter* spp.	*C. lari* subsp. *concheus*	NR_042683.1	99.69%
07/11/2023	*T. maximus*	Royal Tern	*C. jejuni*	*C. lari* subsp. *concheus*	NR_042683.1	99.19%
07/17/2023	*T. maximus*	Royal Tern	*C. coli*	*C. lari* subsp. *concheus*	NR_042683.1	99.85%
07/23/2023	*T. maximus*	Royal Tern	*C. coli* *C. jejuni*	*C. ornithocola*	NR_156985.1	99.39%
09/05/2023	*T. maximus*	Royal Tern	*Campylobacter* spp.	*C. lari* subsp. *concheus*	NR_042683.1	99.85%
10/04/2023	*T. maximus*	Royal Tern	*C. coli*	*C. ornithocola*	NR_156985.1	99.69%
08/07/2023	*S. antillarum*	Sandwich Tern	*C. coli* *C. jejuni*	*C. ornithocola*	NR_156985.1	99.54%
08/07/2023	*S. hirundo*	Common Tern	*C. coli* *C. jejuni*	*C. ornithocola*	NR_156985.1	99.85%
11/06/2023	*A. interpres*	Ruddy Turnstone	*C. coli*	*C. lari* subsp. *concheus*	NR_042683.1	99.69%

Table 3.8. Oyster samples tested and positivity rate for *Campylobacter* over the course of the study.

	# positives (n = 3)			
Date	**Samples**	**Control**	**Deterrent**	
08/01/2023	6	0	0	
08/17/2023	6	0	0	
08/30/2023	6	0	0	
09/13/2023	6	3	0	
09/26/2023	6	2	0	
10/11/2023	6	3	1	
11/07/2023	6	0	0	
12/06/2023	6	0	0	
01/11/2024	6	0	0	
01/31/2024	6	0	1	
03/06/2024	6	0	0	**Incidence**
Total	**66**	**8**	**2**	**15.15%**

3.4 Discussion

Shellfish are highly efficient filter feeders which concentrate microorganisms and chemicals from the surrounding water (Jiang et al., 2023; Ke and Wang, 2001; Unzueta-Martínez et al., 2022). They are also a popular seafood delicacy which are often, in the case of oysters especially, consumed raw or undercooked. This carries an inherent risk to consumers, and concerns for the transfer of known human pathogens, such as *Escherichia*, *Vibrio*, and norovirus are stressed by regulatory agencies (FDA, ISSC, NSSP) (Contreras-Rodríguez et al., 2019). However, there has been insufficient research conducted concerning interactions between the genus *Campylobacter* and oysters. The campylobacteriosis outbreak in Rhode Island during 2021, attributed to raw oyster

consumption contaminated with fecal material from roosting seabirds (Caron et al., 2023), emphasized the need to explore interactions between floating oyster aquaculture gear and seabirds. Chapter 1 established that seabirds interact frequently with off-bottom oyster aquaculture. Previous research suggests these interactions may influence seafood safety through bacterial contamination resulting from bird fecal matter entering the water near the growing oysters. However, data on the presence of *Campylobacter* in the seabird species visiting oyster farms is scarce.

Seabird diversity observed at oyster aquaculture sites changes throughout the year (Chapter 1) which may alter the risk of oyster contamination if *Campylobacter* are carried more frequently in some bird species than others. From bird fecal samples collected at the oyster aquaculture farm sites, *Campylobacter* was isolated from 12 of 206 individuals sampled across all species present. Reports of *Campylobacter* concentrations isolated from seabirds vary between studies (Moriarty et al., 2011). In this study the most positive individuals were found among the royal terns, followed by the brown pelicans. With this study design, it is difficult to assess which birds have the highest positivity rate, as sample sizes across bird species were unequal. Future studies would benefit from a more targeted approach versus the opportunistic one used in this study.

Table 3.9. Nearest identity of *Campylobacter* isolates from oysters based on BLAST results.

			Multiplex	BLAST		
Sample Date	**Sample Name**	**Cage Type**	**Matching Banding Pattern**	**Closest Sequence Match**	**Accession Number**	**Percent Identity**
09/13/2023	OTS 15	Control	*Campylobacter* spp.	*Campylobacter volucris*	NR_116923.1	99.78%
09/13/2023	OTS 16	Control	*Campylobacter* spp.	*Campylobacter volucris*	NR_116923.1	99.78%
09/13/2023	OTS 17	Control	*Campylobacter* spp.	*Campylobacter volucris*	NR_116923.1	99.78%
09/26/2023	OTS 19	Control	*C. coli*	*Campylobacter lari* subsp. *concheus*	NR_118522.1	98.44%
09/26/2023	OTS 20	Control	*C. coli*	*Campylobacter lari* subsp. *concheus*	NR_118522.1	97.08%
10/11/2023	OTS 23	Control	*C. coli*	*Campylobacter lari* subsp. *concheus*	NR_118522.1	98.49%
10/11/2023	OTS 24	Control	*Campylobacter* spp.	*Campylobacter volucris*	NR_116923.1	99.41%
10/11/2023	OTS 25	Control	*Campylobacter* spp.	*Campylobacter volucris*	NR_116923.1	98.82%
			C. coli *C. jejuni*	*Campylobacter ornithocola*	NR_156985.1	99.34%
10/11/2023	OTS 26	Treatment	*C. coli* *C. jejuni*	*Campylobacter ornithocola*	NR_156985.1	98.68%
01/31/2024	OTS 41	Treatment	*C. jejuni*	*Campylobacter lari* subsp. *concheus*	NR_118522.1	99.80%

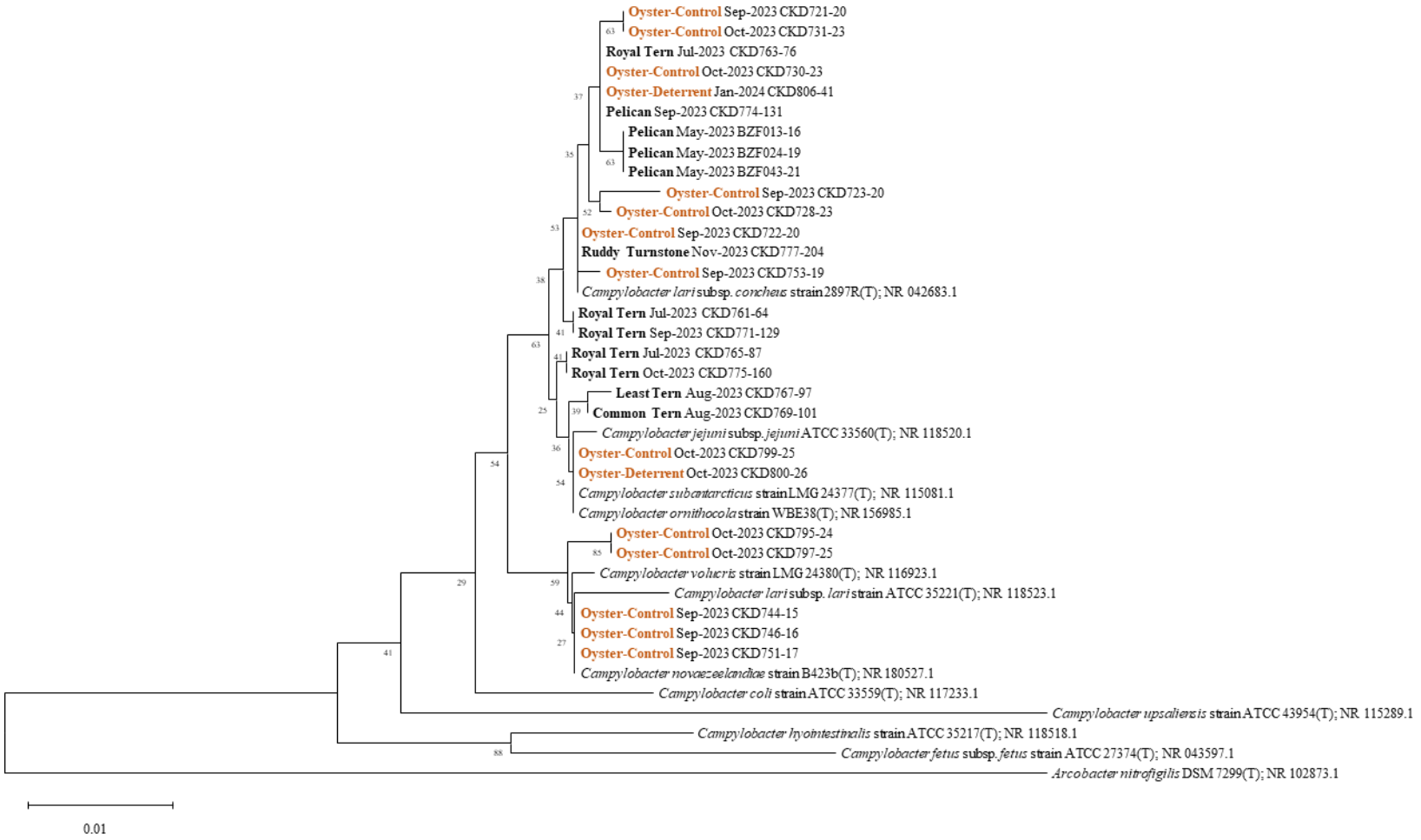

Figure 3.3. Neighbor-joining tree of isolates collected in this study based on 16S rDNA sequence. Nearest neighbor type strains are included.

Most *Campylobacter* isolates, collected from brown pelicans and ruddy turnstones, were nearest in sequence identity to *Campylobacter lari* subsp. *concheus* (≥99.68%) after comparison with the NCBI BLAST database. Royal terns, least terns, and common terns harbored isolates that were most similar to *C. ornithocola* (≥99.51%) and *C. lari* subsp. *concheus* (≥99.35%). However, all sequences matched multiple *Campylobacter* species at >97% similarity, making it difficult to identify them to the species level. Speciation of bacteria using 16S rDNA sequencing is subject to error because, while it is an effective method of differentiating unrelated species, it might not be as effective when parsing out closely related or recently diverged species (Fox et al., 1992; Janda and Abbott, 2007; Olm et al., 2020). The isolates collected during this study are especially at risk of misidentification given that the taxa are so closely related, with >70% total gene conservation between members, and their recent reclassification (Costa and Iraola, 2019; Miller et al., 2014). The lack of sequenced genomes documented for each species reduces the precision of NCBI BLAST comparisons. 16S rDNA sequencing was used in combination with a *Campylobacter* genus specific multiplex designed by Yamazaki-Matsune et al. (2007) to increase the precision of speciation; however, the multiplex PCR results past the genus-level banding were inconsistent and many isolates did not amplify with multiple bands, limiting our ability to use this technique for this purpose. Ultimately, the sequence results revealed that isolates evaluated were highly similar to species of *Campylobacter* that were not evaluated in the original development of the multiplex PCR, as Yamazaki-Matsune et al. (2007) aimed to distinguish the most common species implicated in human illness. The multiplex PCR was reliable to confirm that isolates were *Campylobacter* prior to sequencing; however, some isolates resulted in banding patterns that matched both *C. jejuni* and *C. coli*. Therefore, primers should be assessed with all type strains included in the phylogenetic analysis in this study to ensure the species-specific primers are not cross-reactive

with other *Campylobacter* species. Alternative techniques to 16S rRNA sequencing which achieve higher precision include DNA gyrase subunit B (*Gyr*B) gene sequencing (Iv et al., 2011), 16S-23S rDNA internal transcribed spacer region sequencing (Khan and Edge, 2007), as well as multilocus sequence typing methods (Miller et al., 2012), pulse-field gel electrophoresis, and amplified fragment length polymorphism techniques (On et al., 2008).

Isolates collected from bird feces and oysters clustered with type strains of *C. lari* subsp. *concheus* and *C. ornithocola*, while other isolates collected from oyster samples clustered with type strains of *C. volucris*. All three of these species are highly related and were recently reclassified from *C. lari* (now *C. lari* subsp. *lari*) into novel taxa due to phenotypic and genetic differences (Costa and Iraola, 2019). Cases of campylobacteriosis are most commonly the result of infection by *C. jejuni* or *C. coli*, however cases of bacteremia with *C. lari* have been documented to occur sporadically, with most occurring in patients who are undergoing immunosuppressant treatment, are immunocompromised, or have underlying complications (Martinot et al., 2001). Three outbreaks of campylobacteriosis attributed to *C. lari* have been recorded by the CDC since 2011, only one of which was connected to the consumption of raw oysters (CDC, 2023). Strains of *C. lari* subsp. *concheus*, originally described by Debruyne et al. (2009), were first isolated from shellfish and humans, but there is insufficient data regarding their pathogenicity. No cases of campylobacteriosis have been attributed to infection by *C. lari* subsp. *concheus* (CDC, 2023). *Campylobacter ornithocola* was isolated from fecal samples collected from wild birds in urban parks of Valdivia, Chile. Much like *C. lari* subsp. *concheus*, its pathogenicity remains unknown and no cases of campylobacteriosis from this species have been documented (Cáceres et al., 2017; CDC, 2023). *Campylobacter volucris* was first isolated from a fecal swab from black-headed gulls

(*Larus ridibundus*) in southern Sweden. The pathogenicity of *C. volucris* also remains unknown and this species is not associated with any cases of campylobacteriosis (CDC, 2023; Debruyne et al., 2010). It is unknown if the isolates of *Campylobacter* recovered from birds and oysters during this study are human pathogens, as they could not be reliably speciated and there is insufficient literature to support either conclusion. However, the original isolation of the related type strains from birds suggests that these *Campylobacter* species may be normal members of the bird gastrointestinal microbial community.

It is interesting to note that while only one unique isolate of *Campylobacter* (based on similar morphology on CHROMagar™ *Campylobacter* and 100% 16S rDNA identity across multiple isolates from each bird) was ever isolated within an individual bird, one oyster did harbor multiple isolates. This suggests that birds do not carry a high diversity of *Campylobacter*, while oysters' role as filter feeders may enable them to uptake multiple strains of *Campylobacter*. In addition, with the exception of one royal tern and one brown pelican isolate, bird isolates did not share 100% sequence identity with isolates collected from oysters. This finding may be due to the opportunistic sampling of a small number of birds at each date, limiting the recovery of the full *Campylobacter* diversity present in birds. It is also possible that the isolates found in oysters come from other sources. Future studies should continue to collect isolates from birds as well as water and sediment to get a clear picture of the source of *Campylobacter* in oysters.

Campylobacter collected from both bird feces and oysters roughly clustered into five groups when compared using a Neighbor-Joining phylogenetic tree. The first group clustered around *C. volucris*, *C. lari* subsp. *lari* and *C. novaezeelandiae* and was comprised of isolates collected from

control oysters during September 2023. As reported in Chapter 1, September and October had the highest number of bird interactions for our farm site. However, no bird isolates clustered directly with these groups, so other non-point sources of contamination cannot be excluded. No collected isolates directly clustered with known human pathogens, indicating these strains may not be of human health concern. *Campylobacter* was disproportionately isolated from oyster samples collected from each gear type, with 8 of 10 positive isolates sourced from control cages, suggesting that isolates from oysters may originate from birds and that transmission could be decreased by using bird deterrents. However, isolation of *Campylobacter* from two deterrent cages, despite the significant reduction of birds present on deterrent gear, emphasizes the need for further investigation into the positivity rate of birds and other potential sources of contamination.

The Alabama Department of Health issues oyster harvest closures in response to various factors, such as high rainfall and wastewater treatment plant output. Oyster sample collection on January 31, 2024, occurred one day after ADPH had issued a closure due to rainfall and *Campylobacter* was isolated from one sample collected from a deterrent cage. Other sampling did occur during an ADPH mandated closure resulting from potential sewage discharge (December 6, 2023) however no *Campylobacter* was isolated. Additionally, there were no obvious relationships between measured water parameters and oyster positivity. These results do not rule out run-off or wastewater as sources of *Campylobacter*, or an environmental influence on *Campylobacter* uptake/purging in oysters, but more thorough testing is needed to draw conclusions about these relationships.

Variation in *Campylobacter* isolation rates between bird species has been hypothesized to be the result of species dietary habits and niche occupation (Fuirst et al., 2018). Sources of *Campylobacter* in species like cormorants might be more difficult to pinpoint as their migratory behavior exposes them to various locations that may differ in human pathogen loads. A similar problem might be present in brown pelicans. While a Schreiber and Mock (1988) banding study found that Louisiana brown pelicans were not observed to travel as far as Florida, supporting the notion brought up by a King et al. (2013) study which hypothesizes that metapopulations of brown pelicans might exist nearby to each other without interacting, other populations from the Northeast undergo long distance migrations and use the nGOM as rest stops (Kwon et al., 2017). These populations might be more problematic because of the undefined risk they bring along with them as stopover migrators (Kwon et al., 2017).

Bird presence at the farm site was highly influenced by weather, as birds were not found in times of high wind and rough surf. Therefore, fecal samples could not always be collected weekly as planned. Samples from cormorants were underrepresented during this study as the study design did not accommodate for their unique excretory behavior. Cormorants were observed to project fecal matter far away from themselves when defecating or while leaving from perch, with fecal matter scarcely landing on the structure. This made sample collection from cormorants extremely difficult so, despite the birds being abundant on the floating gear, this study cannot draw conclusions regarding the risk of *Campylobacter* transmission from cormorants. Future studies will devise a different sampling technique to get good representation from this bird group.

This study isolated *Campylobacter* from both seabirds and oysters sampled at floating oyster aquaculture farms. After phylogenetic analysis, results cannot rule out seabirds found on these farm sites as a source of *Campylobacter* contamination in oysters. It is important to note that oyster samples were enriched and as few as one bacterial cell could lead to a positive sample, so the presence of *Campylobacter* is not indicative of an infectious dose. The presence of bacteria within the genus *Campylobacter* at oyster farm sites does not denote an inherent risk of human infection and future investigations into the pathogenicity of the strains isolated during this study are necessary to accurately determine risk. In the meantime, there is a need for optimized monitoring tools and procedures for pathogenic *Campylobacter* in the interest of the growing oyster aquaculture industry and consumer safety.

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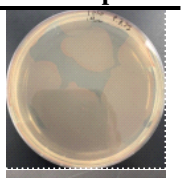
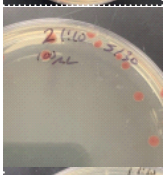
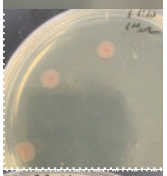
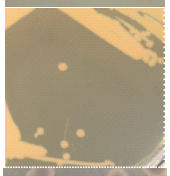
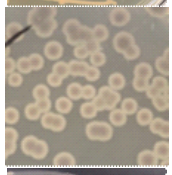
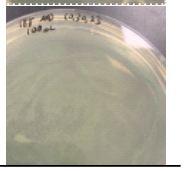
CHAPTER 4: CONCLUSIONS

Results from this study show that bird abundance and diversity at oyster farm sites change throughout the year. This information should be used by farmers to increase farm resiliency by implementing dynamic bird mitigation plans to address seasonal changes. I found that the use of a simple, inexpensive, non-lethal bird deterrent was effective in reducing the number of seabirds interacting with floating oyster gear, clearly outlining its efficiency as bird mitigation technique when applied in compliance with NSSP Model Ordinance regulation. Other deterrent technologies have shown similar promise but still require thorough investigation as to their efficiency and shortcomings. I also determined that *Campylobacter* bacteria are present in fecal matter collected from seabirds found roosting on floating oyster aquaculture gear, however the incidence was low (5.82%). *Campylobacter* bacteria were also present in oysters grown in aquaculture settings with low incidence. Through phylogenetic analysis of isolate relatedness, I concluded that *Campylobacter* isolated from bird fecal matter and oysters were more related to species of *Campylobacter* whose human pathogenicity is currently unknown than those of reported human pathogens, suggesting that these species may be normal inhabitants of the bird gastrointestinal microbial community and do not necessarily represent risks to human health. The discovery of identical 16S rDNA sequences in isolates from birds and oysters does not rule out the possibility of transmission of *Campylobacter* from seabirds during roosting on floating oyster aquaculture gear, but other potential sources should be investigated. Future research is required to determine whether these strains are pathogenic. Overall, available data from these studies and others is insufficient to deem bacterial contamination of cultured oysters by roosting seabirds a significant seafood safety risk.

APPENDICES

Appendix I. Morphologies of isolates collected from CHROMAgar Campylobacter.

ID	Size	Shape	Color	Margin	Amplification with *Campylobacter* primers	Example
1	Swarmer	irregular	light red to pinkish	entire	Yes	
2	3-4mm diameter	irregular	Red-bourgandy center, lighter red middle, opaque white/translucent edge	entire	Yes	
3	3.5-5mm diameter	irregular	Red center, pink middle, opaque white boundary	entire	Yes	
4	>0.5mm diameter	irregular	reddish-pink with translucent boundary	entire	Yes	
5	2-3mm diameter	irregular	light pink center surrounded by yellow tinge	entire	Yes	
6	2-3mm diameter	irregular	Grey-blue center with white boundary	entire	No	
7	3-4mm diameter	irregular	Blue-green center with white boundary	entire	No	
8	Swarmer	irregular	Blue-green	entire	No	

Appendix II. Type strains matching at > 97% identity or above to *Campylobacter* isolates from birds collected in this study. All type strain matches were described as partial sequences of 16S ribosomal RNA.

Bird ID	Sample Date	Bird Species	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
16	5/22/2023	Pelecanus occidentalis	Campylobacter lari subsp. concheus strain CCUG 55786	1129	1129	100%	0	99.68%	1436	NR_118522.1
			Campylobacter lari subsp. concheus strain 2897R	1129	1129	100%	0	99.68%	1501	NR_042683.1
			Campylobacter ornithocola strain WBE38	1118	1118	100%	0	99.35%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1118	1118	100%	0	99.35%	1485	NR_115081.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1112	1112	100%	0	99.19%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1112	1112	100%	0	99.19%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1112	1112	100%	0	99.19%	1341	NR_041834.1
			Campylobacter insulaenigrae strain CCUG 48653	1101	1101	100%	0	98.87%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1101	1101	100%	0	98.87%	1469	NR_114914.1
			Campylobacter volucris strain LMG 24380	1101	1101	100%	0	98.87%	1482	NR_116923.1
			Campylobacter insulaenigrae NCTC 12927	1101	1101	100%	0	98.87%	1341	NR_043608.1
			Campylobacter novaezeelandiae strain B423b	1096	1096	100%	0	98.70%	1510	NR_180527.1
			Campylobacter hepaticus strain HV10	1090	1090	100%	0	98.54%	1470	NR_152703.1
			Campylobacter bilis strain VicNov18	1090	1090	100%	0	98.54%	1495	NR_181124.1
			Campylobacter aviculae strain MIT17-670	1090	1090	100%	0	98.54%	1457	NR_180417.1
			Campylobacter taeniopygiae strain MIT10-5678	1090	1090	100%	0	98.54%	1450	NR_180416.1
			Campylobacter jejuni strain DSM 4688	1086	1086	98%	0	99.01%	1327	NR_117760.1
			Campylobacter armoricus strain CA656	1074	1074	100%	0	98.06%	1510	NR_180483.1
			Campylobacter lari subsp. lari strain ATCC 35221	1074	1074	100%	0	98.06%	1435	NR_118523.1
			Campylobacter lari strain DSM 11375	1074	1074	100%	0	98.06%	1338	NR_117762.1
			Campylobacter lari subsp. lari strain NCTC 11352	1074	1074	100%	0	98.06%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1074	1074	100%	0	98.06%	1441	NR_043034.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1420	NR_117233.1
			Campylobacter coli strain DSM 4689	1068	1068	100%	0	97.89%	1342	NR_117761.1
			Campylobacter coli strain LMG 6440	1068	1068	100%	0	97.89%	1341	NR_041835.1
			Campylobacter lari subsp. lari strain CCUG 23947	1066	1066	100%	0	97.73%	1459	NR_118653.1
			Campylobacter lari strain JCM2530	1062	1062	100%	0	97.73%	1435	NR_112241.1
			Campylobacter peloridis strain 2314BVA	1057	1057	100%	0	97.57%	1497	NR_042684.1
			Campylobacter lanienae NCTC 13004	1051	1051	100%	0	97.41%	1467	NR_028698.1
			Campylobacter lanienae NCTC 13004 strain CCUG 44467	1040	1040	100%	0	97.08%	1434	NR_118521.1
			Campylobacter lanienae NCTC 13004	1040	1040	100%	0	97.08%	1340	NR_115704.1

Bird ID	Sample Date	Bird Species	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
19	5/22/2023	Pelecanus occidentalis	Campylobacter lari subsp. concheus strain CCUG 55786	1129	1129	100%	0	99.68%	1436	NR_118522.1
			Campylobacter lari subsp. concheus strain 2897R	1129	1129	100%	0	99.68%	1501	NR_042683.1
			Campylobacter ornithocola strain WBE38	1118	1118	100%	0	99.35%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1118	1118	100%	0	99.35%	1485	NR_115081.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1112	1112	100%	0	99.19%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1112	1112	100%	0	99.19%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1112	1112	100%	0	99.19%	1341	NR_041834.1
			Campylobacter insulaenigrae strain CCUG 48653	1101	1101	100%	0	98.87%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1101	1101	100%	0	98.87%	1469	NR_114914.1
			Campylobacter volucris strain LMG 24380	1101	1101	100%	0	98.87%	1482	NR_116923.1
			Campylobacter insulaenigrae NCTC 12927	1101	1101	100%	0	98.87%	1341	NR_043608.1
			Campylobacter novaezeelandiae strain B423b	1096	1096	100%	0	98.70%	1510	NR_180527.1
			Campylobacter hepaticus strain HV10	1090	1090	100%	0	98.54%	1470	NR_152703.1
			Campylobacter bilis strain VicNov18	1090	1090	100%	0	98.54%	1495	NR_181124.1
			Campylobacter aviculae strain MIT17-670	1090	1090	100%	0	98.54%	1457	NR_180417.1
			Campylobacter taeniopygiae strain MIT10-5678	1090	1090	100%	0	98.54%	1450	NR_180416.1
			Campylobacter jejuni strain DSM 4688	1086	1086	98%	0	99.01%	1327	NR_117760.1
			Campylobacter armoricus strain CA656	1074	1074	100%	0	98.06%	1510	NR_180483.1
			Campylobacter lari subsp. lari strain ATCC 35221	1074	1074	100%	0	98.06%	1435	NR_118523.1
			Campylobacter lari strain DSM 11375	1074	1074	100%	0	98.06%	1338	NR_117762.1
			Campylobacter lari subsp. lari strain NCTC 11352	1074	1074	100%	0	98.06%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1074	1074	100%	0	98.06%	1441	NR_043034.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1420	NR_117233.1
			Campylobacter coli strain DSM 4689	1068	1068	100%	0	97.89%	1342	NR_117761.1
			Campylobacter coli strain LMG 6440	1068	1068	100%	0	97.89%	1341	NR_041835.1
			Campylobacter lari subsp. lari strain CCUG 23947	1066	1066	100%	0	97.73%	1459	NR_118653.1
			Campylobacter lari strain JCM2530	1062	1062	100%	0	97.73%	1435	NR_112241.1
			Campylobacter peloridis strain 2314BVA	1057	1057	100%	0	97.57%	1497	NR_042684.1
			Campylobacter lanienae NCTC 13004	1051	1051	100%	0	97.41%	1467	NR_028698.1
			Campylobacter lanienae NCTC 13004 strain CCUG 44467	1040	1040	100%	0	97.08%	1434	NR_118521.1
			Campylobacter lanienae NCTC 13004	1040	1040	100%	0	97.08%	1340	NR_115704.1

Bird ID	Sample Date	Bird Species	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
21	5/30/2023	Pelecanus occidentalis	Campylobacter lari subsp. concheus strain CCUG 55786	1129	1129	100%	0	99.68%	1436	NR_118522.1
			Campylobacter lari subsp. concheus strain 2897R	1129	1129	100%	0	99.68%	1501	NR_042683.1
			Campylobacter ornithocola strain WBE38	1118	1118	100%	0	99.35%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1118	1118	100%	0	99.35%	1485	NR_115081.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1112	1112	100%	0	99.19%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1112	1112	100%	0	99.19%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1112	1112	100%	0	99.19%	1341	NR_041834.1
			Campylobacter insulaenigrae strain CCUG 48653	1101	1101	100%	0	98.87%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1101	1101	100%	0	98.87%	1469	NR_114914.1
			Campylobacter volucris strain LMG 24380	1101	1101	100%	0	98.87%	1482	NR_116923.1
			Campylobacter insulaenigrae NCTC 12927	1101	1101	100%	0	98.87%	1341	NR_043608.1
			Campylobacter novaezeelandiae strain B423b	1096	1096	100%	0	98.70%	1510	NR_180527.1
			Campylobacter hepaticus strain HV10	1090	1090	100%	0	98.54%	1470	NR_152703.1
			Campylobacter bilis strain VicNov18	1090	1090	100%	0	98.54%	1495	NR_181124.1
			Campylobacter aviculae strain MIT17-670	1090	1090	100%	0	98.54%	1457	NR_180417.1
			Campylobacter taeniopygiae strain MIT10-5678	1090	1090	100%	0	98.54%	1450	NR_180416.1
			Campylobacter jejuni strain DSM 4688	1086	1086	98%	0	99.01%	1327	NR_117760.1
			Campylobacter armoricus strain CA656	1074	1074	100%	0	98.06%	1510	NR_180483.1
			Campylobacter lari subsp. lari strain ATCC 35221	1074	1074	100%	0	98.06%	1435	NR_118523.1
			Campylobacter lari strain DSM 11375	1074	1074	100%	0	98.06%	1338	NR_117762.1
			Campylobacter lari subsp. lari strain NCTC 11352	1074	1074	100%	0	98.06%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1074	1074	100%	0	98.06%	1441	NR_043034.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1420	NR_117233.1
			Campylobacter coli strain DSM 4689	1068	1068	100%	0	97.89%	1342	NR_117761.1
			Campylobacter coli strain LMG 6440	1068	1068	100%	0	97.89%	1341	NR_041835.1
			Campylobacter lari subsp. lari strain CCUG 23947	1066	1066	100%	0	97.73%	1459	NR_118653.1
			Campylobacter lari strain JCM2530	1062	1062	100%	0	97.73%	1435	NR_112241.1
			Campylobacter peloridis strain 2314BVA	1057	1057	100%	0	97.57%	1497	NR_042684.1
			Campylobacter lanienae NCTC 13004	1051	1051	100%	0	97.41%	1467	NR_028698.1
			Campylobacter lanienae NCTC 13004 strain CCUG 44467	1040	1040	100%	0	97.08%	1434	NR_118521.1
			Campylobacter lanienae NCTC 13004	1040	1040	100%	0	97.08%	1340	NR_115704.1

Bird ID	Sample Date	Bird Species	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
64	7/11/2023	Thalasseus maximus	Campylobacter lari subsp. concheus strain 2897R	1134	1134	100%	0	99.84%	1501	NR_042683.1
			Campylobacter lari subsp. concheus strain CCUG 55786	1134	1134	100%	0	99.84%	1436	NR_118522.1
			Campylobacter ornithocola strain WBE38	1123	1123	100%	0	99.51%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1123	1123	100%	0	99.51%	1485	NR_115081.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1118	1118	100%	0	99.35%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1118	1118	100%	0	99.35%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1118	1118	100%	0	99.35%	1341	NR_041834.1
			Campylobacter insulaenigrae strain CCUG 48653	1112	1112	100%	0	99.19%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1112	1112	100%	0	99.19%	1341	NR_043608.1
			Campylobacter insulaenigrae NCTC 12927	1112	1112	100%	0	99.19%	1469	NR_114914.1
			Campylobacter taeniopygiae strain MIT10-5678	1107	1107	100%	0	99.03%	1450	NR_180416.1
			Campylobacter novaezeelandiae strain B423b	1101	1101	100%	0	98.87%	1510	NR_180527.1
			Campylobacter aviculae strain MIT17-670	1096	1096	100%	0	98.70%	1457	NR_180417.1
			Campylobacter volucris strain LMG 24380	1096	1096	100%	0	98.70%	1482	NR_116923.1
			Campylobacter jejuni strain DSM 4688	1092	1092	98%	0	99.18%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1090	1090	100%	0	98.54%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1085	1085	100%	0	98.38%	1470	NR_152703.1
			Campylobacter armoricus strain CA656	1079	1079	100%	0	98.22%	1510	NR_180483.1
			Campylobacter lari strain DSM 11375	1079	1079	100%	0	98.22%	1338	NR_117762.1
			Campylobacter coli strain DSM 4689	1079	1079	100%	0	98.22%	1342	NR_117761.1
			Campylobacter lari subsp. lari strain ATCC 35221	1079	1079	100%	0	98.22%	1435	NR_118523.1
			Campylobacter coli strain ATCC 33559	1079	1079	100%	0	98.22%	1435	NR_118511.1
			Campylobacter lari subsp. lari strain NCTC 11352	1079	1079	100%	0	98.22%	1341	NR_115700.1
			Campylobacter coli strain ATCC 33559	1079	1079	100%	0	98.22%	1420	NR_117233.1
			Campylobacter lari subsp. lari strain ATCC 35221	1079	1079	100%	0	98.22%	1441	NR_043034.1
			Campylobacter coli strain LMG 6440	1079	1079	100%	0	98.22%	1341	NR_041835.1
			Campylobacter lari subsp. lari strain CCUG 23947	1072	1072	100%	0	97.89%	1459	NR_118653.1
			Campylobacter lari strain JCM2530	1068	1068	100%	0	97.89%	1435	NR_112241.1
			Campylobacter peloridis strain 2314BVA	1062	1062	100%	0	97.73%	1497	NR_042684.1
			Campylobacter iguaniorum strain 1485E	1040	1040	100%	0	97.08%	1503	NR_134706.1

Bird ID	Sample Date	Bird Species	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
76	7/17/2023	Thalasseus maximus	Campylobacter lari subsp. concheus strain 2897R	1134	1134	100%	0	99.84%	1501	NR_042683.1
			Campylobacter lari subsp. concheus strain CCUG 55786	1134	1134	100%	0	99.84%	1436	NR_118522.1
			Campylobacter ornithocola strain WBE38	1123	1123	100%	0	99.51%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1123	1123	100%	0	99.51%	1485	NR_115081.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1118	1118	100%	0	99.35%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1118	1118	100%	0	99.35%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1118	1118	100%	0	99.35%	1341	NR_041834.1
			Campylobacter novaezeelandiae strain B423b	1101	1101	100%	0	98.87%	1510	NR_180527.1
			Campylobacter insulaenigrae strain CCUG 48653	1101	1101	100%	0	98.87%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1101	1101	100%	0	98.87%	1341	NR_043608.1
			Campylobacter insulaenigrae NCTC 12927	1101	1101	100%	0	98.87%	1469	NR_114914.1
			Campylobacter aviculae strain MIT17-670	1096	1096	100%	0	98.70%	1457	NR_180417.1
			Campylobacter taeniopygiae strain MIT10-5678	1096	1096	100%	0	98.70%	1450	NR_180416.1
			Campylobacter volucris strain LMG 24380	1096	1096	100%	0	98.70%	1482	NR_116923.1
			Campylobacter jejuni strain DSM 4688	1092	1092	98%	0	99.18%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1090	1090	100%	0	98.54%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1085	1085	100%	0	98.38%	1470	NR_152703.1
			Campylobacter armoricus strain CA656	1079	1079	100%	0	98.22%	1510	NR_180483.1
			Campylobacter lari strain DSM 11375	1079	1079	100%	0	98.22%	1338	NR_117762.1
			Campylobacter lari subsp. lari strain ATCC 35221	1079	1079	100%	0	98.22%	1435	NR_118523.1
			Campylobacter lari subsp. lari strain NCTC 11352	1079	1079	100%	0	98.22%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1079	1079	100%	0	98.22%	1441	NR_043034.1
			Campylobacter coli strain DSM 4689	1074	1074	100%	0	98.06%	1342	NR_117761.1
			Campylobacter coli strain ATCC 33559	1074	1074	100%	0	98.06%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1074	1074	100%	0	98.06%	1420	NR_117233.1
			Campylobacter coli strain LMG 6440	1074	1074	100%	0	98.06%	1341	NR_041835.1
			Campylobacter lari subsp. lari strain CCUG 23947	1072	1072	100%	0	97.89%	1459	NR_118653.1
			Campylobacter lari strain JCM2530	1068	1068	100%	0	97.89%	1435	NR_112241.1
			Campylobacter peloridis strain 2314BVA	1062	1062	100%	0	97.73%	1497	NR_042684.1
			Campylobacter lanienae NCTC 13004	1046	1046	100%	0	97.24%	1467	NR_028698.1
			Campylobacter iguaniorum strain 1485E	1040	1040	100%	0	97.08%	1503	NR_134706.1

Bird ID	Sample Date	Bird Species	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
87	7/23/2023	Thalasseus maximus	Campylobacter ornithocola strain WBE38	1129	1129	100%	0	99.68%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1129	1129	100%	0	99.68%	1485	NR_115081.1
			Campylobacter lari subsp. concheus strain 2897R	1129	1129	100%	0	99.68%	1501	NR_042683.1
			Campylobacter lari subsp. concheus strain CCUG 55786	1129	1129	100%	0	99.68%	1436	NR_118522.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1123	1123	100%	0	99.51%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1123	1123	100%	0	99.51%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1123	1123	100%	0	99.51%	1341	NR_041834.1
			Campylobacter insulaenigrae strain CCUG 48653	1118	1118	100%	0	99.35%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1118	1118	100%	0	99.35%	1341	NR_043608.1
			Campylobacter insulaenigrae NCTC 12927	1118	1118	100%	0	99.35%	1469	NR_114914.1
			Campylobacter taeniopygiae strain MIT10-5678	1112	1112	100%	0	99.19%	1450	NR_180416.1
			Campylobacter novaezeelandiae strain B423b	1107	1107	100%	0	99.03%	1510	NR_180527.1
			Campylobacter aviculae strain MIT17-670	1101	1101	100%	0	98.87%	1457	NR_180417.1
			Campylobacter volucris strain LMG 24380	1101	1101	100%	0	98.87%	1482	NR_116923.1
			Campylobacter jejuni strain DSM 4688	1098	1098	98%	0	99.34%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1096	1096	100%	0	98.70%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1090	1090	100%	0	98.54%	1470	NR_152703.1
			Campylobacter armoricus strain CA656	1085	1085	100%	0	98.38%	1510	NR_180483.1
			Campylobacter lari strain DSM 11375	1085	1085	100%	0	98.38%	1338	NR_117762.1
			Campylobacter lari subsp. lari strain ATCC 35221	1085	1085	100%	0	98.38%	1435	NR_118523.1
			Campylobacter lari subsp. lari strain NCTC 11352	1085	1085	100%	0	98.38%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1085	1085	100%	0	98.38%	1441	NR_043034.1
			Campylobacter lari subsp. lari strain CCUG 23947	1077	1077	100%	0	98.06%	1459	NR_118653.1
			Campylobacter coli strain DSM 4689	1074	1074	100%	0	98.06%	1342	NR_117761.1
			Campylobacter coli strain ATCC 33559	1074	1074	100%	0	98.06%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1074	1074	100%	0	98.06%	1420	NR_117233.1
			Campylobacter lari strain JCM2530	1074	1074	100%	0	98.06%	1435	NR_112241.1
			Campylobacter coli strain LMG 6440	1074	1074	100%	0	98.06%	1341	NR_041835.1
			Campylobacter peloridis strain 2314BVA	1068	1068	100%	0	97.89%	1497	NR_042684.1
			Campylobacter iguaniorum strain 1485E	1040	1040	100%	0	97.08%	1503	NR_134706.1
			Campylobacter helveticus strain ATCC 51209	1040	1040	100%	0	97.08%	1435	NR_118517.1

Bird ID	Sample Date	Bird Species	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
97	8/7/2023	Sternula antillarum	Campylobacter ornithocola strain WBE38	1129	1129	100%	0	99.68%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1129	1129	100%	0	99.68%	1485	NR_115081.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1123	1123	100%	0	99.51%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1123	1123	100%	0	99.51%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1123	1123	100%	0	99.51%	1341	NR_041834.1
			Campylobacter insulaenigrae strain CCUG 48653	1118	1118	100%	0	99.35%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1118	1118	100%	0	99.35%	1341	NR_043608.1
			Campylobacter lari subsp. concheus strain 2897R	1118	1118	100%	0	99.35%	1501	NR_042683.1
			Campylobacter lari subsp. concheus strain CCUG 55786	1118	1118	100%	0	99.35%	1436	NR_118522.1
			Campylobacter insulaenigrae NCTC 12927	1118	1118	100%	0	99.35%	1469	NR_114914.1
			Campylobacter taeniopygiae strain MIT10-5678	1112	1112	100%	0	99.19%	1450	NR_180416.1
			Campylobacter novaezeelandiae strain B423b	1107	1107	100%	0	99.03%	1510	NR_180527.1
			Campylobacter aviculae strain MIT17-670	1101	1101	100%	0	98.87%	1457	NR_180417.1
			Campylobacter volucris strain LMG 24380	1101	1101	100%	0	98.87%	1482	NR_116923.1
			Campylobacter jejuni strain DSM 4688	1098	1098	98%	0	99.34%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1096	1096	100%	0	98.70%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1090	1090	100%	0	98.54%	1470	NR_152703.1
			Campylobacter armoricus strain CA656	1085	1085	100%	0	98.38%	1510	NR_180483.1
			Campylobacter lari strain DSM 11375	1085	1085	100%	0	98.38%	1338	NR_117762.1
			Campylobacter lari subsp. lari strain ATCC 35221	1085	1085	100%	0	98.38%	1435	NR_118523.1
			Campylobacter lari subsp. lari strain NCTC 11352	1085	1085	100%	0	98.38%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1085	1085	100%	0	98.38%	1441	NR_043034.1
			Campylobacter lari subsp. lari strain CCUG 23947	1077	1077	100%	0	98.06%	1459	NR_118653.1
			Campylobacter lari strain JCM2530	1074	1074	100%	0	98.06%	1435	NR_112241.1
			Campylobacter peloridis strain 2314BVA	1068	1068	100%	0	97.89%	1497	NR_042684.1
			Campylobacter coli strain DSM 4689	1062	1062	100%	0	97.73%	1342	NR_117761.1
			Campylobacter coli strain ATCC 33559	1062	1062	100%	0	97.73%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1062	1062	100%	0	97.73%	1420	NR_117233.1
			Campylobacter coli strain LMG 6440	1062	1062	100%	0	97.73%	1341	NR_041835.1
			Campylobacter iguaniorum strain 1485E	1040	1040	100%	0	97.08%	1503	NR_134706.1
			Campylobacter helveticus strain ATCC 51209	1040	1040	100%	0	97.08%	1435	NR_118517.1

Bird ID	Sample Date	Bird Species	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
101	8/7/2023	Sterna hirundo	Campylobacter ornithocola strain WBE38	1134	1134	100%	0	99.84%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1134	1134	100%	0	99.84%	1485	NR_115081.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1129	1129	100%	0	99.68%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1129	1129	100%	0	99.68%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1129	1129	100%	0	99.68%	1341	NR_041834.1
			Campylobacter insulaenigrae strain CCUG 48653	1123	1123	100%	0	99.51%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1123	1123	100%	0	99.51%	1341	NR_043608.1
			Campylobacter lari subsp. concheus strain 2897R	1123	1123	100%	0	99.51%	1501	NR_042683.1
			Campylobacter lari subsp. concheus strain CCUG 55786	1123	1123	100%	0	99.51%	1436	NR_118522.1
			Campylobacter insulaenigrae NCTC 12927	1123	1123	100%	0	99.51%	1469	NR_114914.1
			Campylobacter taeniopygiae strain MIT10-5678	1118	1118	100%	0	99.35%	1450	NR_180416.1
			Campylobacter novaezeelandiae strain B423b	1112	1112	100%	0	99.19%	1510	NR_180527.1
			Campylobacter aviculae strain MIT17-670	1107	1107	100%	0	99.03%	1457	NR_180417.1
			Campylobacter volucris strain LMG 24380	1107	1107	100%	0	99.03%	1482	NR_116923.1
			Campylobacter jejuni strain DSM 4688	1103	1103	98%	0	99.51%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1101	1101	100%	0	98.87%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1096	1096	100%	0	98.70%	1470	NR_152703.1
			Campylobacter armoricus strain CA656	1090	1090	100%	0	98.54%	1510	NR_180483.1
			Campylobacter lari strain DSM 11375	1090	1090	100%	0	98.54%	1338	NR_117762.1
			Campylobacter lari subsp. lari strain ATCC 35221	1090	1090	100%	0	98.54%	1435	NR_118523.1
			Campylobacter lari subsp. lari strain NCTC 11352	1090	1090	100%	0	98.54%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1090	1090	100%	0	98.54%	1441	NR_043034.1
			Campylobacter lari subsp. lari strain CCUG 23947	1083	1083	100%	0	98.22%	1459	NR_118653.1
			Campylobacter lari strain JCM2530	1079	1079	100%	0	98.22%	1435	NR_112241.1
			Campylobacter peloridis strain 2314BVA	1074	1074	100%	0	98.06%	1497	NR_042684.1
			Campylobacter coli strain DSM 4689	1068	1068	100%	0	97.89%	1342	NR_117761.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1420	NR_117233.1
			Campylobacter coli strain LMG 6440	1068	1068	100%	0	97.89%	1341	NR_041835.1
			Campylobacter iguaniorum strain 1485E	1046	1046	100%	0	97.24%	1503	NR_134706.1
			Campylobacter helveticus strain ATCC 51209	1046	1046	100%	0	97.24%	1435	NR_118517.1
			Campylobacter helveticus strain NCTC 12470	1040	1040	100%	0	97.08%	1341	NR_115702.1
			Campylobacter cuniculorum DSM 23162 = LMG 24588 strain 1	1040	1040	100%	0	97.08%	1390	NR_043784.1

Bird ID	Sample Date	Bird Species	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
129	9/5/2023	Thalasseus maximus	Campylobacter lari subsp. concheus strain 2897R	1134	1134	100%	0	99.84%	1501	NR_042683.1
			Campylobacter lari subsp. concheus strain CCUG 55786	1134	1134	100%	0	99.84%	1436	NR_118522.1
			Campylobacter ornithocola strain WBE38	1123	1123	100%	0	99.51%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1123	1123	100%	0	99.51%	1485	NR_115081.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1118	1118	100%	0	99.35%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1118	1118	100%	0	99.35%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1118	1118	100%	0	99.35%	1341	NR_041834.1
			Campylobacter insulaenigrae strain CCUG 48653	1112	1112	100%	0	99.19%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1112	1112	100%	0	99.19%	1341	NR_043608.1
			Campylobacter insulaenigrae NCTC 12927	1112	1112	100%	0	99.19%	1469	NR_114914.1
			Campylobacter taeniopygiae strain MIT10-5678	1107	1107	100%	0	99.03%	1450	NR_180416.1
			Campylobacter novaezeelandiae strain B423b	1101	1101	100%	0	98.87%	1510	NR_180527.1
			Campylobacter aviculae strain MIT17-670	1096	1096	100%	0	98.70%	1457	NR_180417.1
			Campylobacter volucris strain LMG 24380	1096	1096	100%	0	98.70%	1482	NR_116923.1
			Campylobacter jejuni strain DSM 4688	1092	1092	98%	0	99.18%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1090	1090	100%	0	98.54%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1085	1085	100%	0	98.38%	1470	NR_152703.1
			Campylobacter armoricus strain CA656	1079	1079	100%	0	98.22%	1510	NR_180483.1
			Campylobacter lari strain DSM 11375	1079	1079	100%	0	98.22%	1338	NR_117762.1
			Campylobacter coli strain DSM 4689	1079	1079	100%	0	98.22%	1342	NR_117761.1
			Campylobacter lari subsp. lari strain ATCC 35221	1079	1079	100%	0	98.22%	1435	NR_118523.1
			Campylobacter coli strain ATCC 33559	1079	1079	100%	0	98.22%	1435	NR_118511.1
			Campylobacter lari subsp. lari strain NCTC 11352	1079	1079	100%	0	98.22%	1341	NR_115700.1
			Campylobacter coli strain ATCC 33559	1079	1079	100%	0	98.22%	1420	NR_117233.1
			Campylobacter lari subsp. lari strain ATCC 35221	1079	1079	100%	0	98.22%	1441	NR_043034.1
			Campylobacter coli strain LMG 6440	1079	1079	100%	0	98.22%	1341	NR_041835.1
			Campylobacter lari subsp. lari strain CCUG 23947	1072	1072	100%	0	97.89%	1459	NR_118653.1
			Campylobacter lari strain JCM2530	1068	1068	100%	0	97.89%	1435	NR_112241.1
			Campylobacter peloridis strain 2314BVA	1062	1062	100%	0	97.73%	1497	NR_042684.1
			Campylobacter iguaniorum strain 1485E	1040	1040	100%	0	97.08%	1503	NR_134706.1

Bird ID	Sample Date	Bird Species	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
131	9/5/2023	Pelecanus occidentalis	Campylobacter lari subsp. concheus strain 2897R	1134	1134	100%	0	99.84%	1501	NR_042683.1
			Campylobacter lari subsp. concheus strain CCUG 55786	1134	1134	100%	0	99.84%	1436	NR_118522.1
			Campylobacter ornithocola strain WBE38	1123	1123	100%	0	99.51%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1123	1123	100%	0	99.51%	1485	NR_115081.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1118	1118	100%	0	99.35%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1118	1118	100%	0	99.35%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1118	1118	100%	0	99.35%	1341	NR_041834.1
			Campylobacter novaezeelandiae strain B423b	1101	1101	100%	0	98.87%	1510	NR_180527.1
			Campylobacter insulaenigrae strain CCUG 48653	1101	1101	100%	0	98.87%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1101	1101	100%	0	98.87%	1341	NR_043608.1
			Campylobacter insulaenigrae NCTC 12927	1101	1101	100%	0	98.87%	1469	NR_114914.1
			Campylobacter aviculae strain MIT17-670	1096	1096	100%	0	98.70%	1457	NR_180417.1
			Campylobacter taeniopygiae strain MIT10-5678	1096	1096	100%	0	98.70%	1450	NR_180416.1
			Campylobacter volucris strain LMG 24380	1096	1096	100%	0	98.70%	1482	NR_116923.1
			Campylobacter jejuni strain DSM 4688	1092	1092	98%	0	99.18%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1090	1090	100%	0	98.54%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1085	1085	100%	0	98.38%	1470	NR_152703.1
			Campylobacter armoricus strain CA656	1079	1079	100%	0	98.22%	1510	NR_180483.1
			Campylobacter lari strain DSM 11375	1079	1079	100%	0	98.22%	1338	NR_117762.1
			Campylobacter lari subsp. lari strain ATCC 35221	1079	1079	100%	0	98.22%	1435	NR_118523.1
			Campylobacter lari subsp. lari strain NCTC 11352	1079	1079	100%	0	98.22%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1079	1079	100%	0	98.22%	1441	NR_043034.1
			Campylobacter coli strain DSM 4689	1074	1074	100%	0	98.06%	1342	NR_117761.1
			Campylobacter coli strain ATCC 33559	1074	1074	100%	0	98.06%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1074	1074	100%	0	98.06%	1420	NR_117233.1
			Campylobacter coli strain LMG 6440	1074	1074	100%	0	98.06%	1341	NR_041835.1
			Campylobacter lari subsp. lari strain CCUG 23947	1072	1072	100%	0	97.89%	1459	NR_118653.1
			Campylobacter lari strain JCM2530	1068	1068	100%	0	97.89%	1435	NR_112241.1
			Campylobacter peloridis strain 2314BVA	1062	1062	100%	0	97.73%	1497	NR_042684.1
			Campylobacter lanienae NCTC 13004	1046	1046	100%	0	97.24%	1467	NR_028698.1
			Campylobacter iguaniorum strain 1485E	1040	1040	100%	0	97.08%	1503	NR_134706.1

Bird ID	Sample Date	Bird Species	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
160	10/4/2023	Thalasseus maximus	Campylobacter ornithocola strain WBE38	1129	1129	100%	0	99.68%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1129	1129	100%	0	99.68%	1485	NR_115081.1
			Campylobacter lari subsp. concheus strain 2897R	1129	1129	100%	0	99.68%	1501	NR_042683.1
			Campylobacter lari subsp. concheus strain CCUG 55786	1129	1129	100%	0	99.68%	1436	NR_118522.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1123	1123	100%	0	99.51%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1123	1123	100%	0	99.51%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1123	1123	100%	0	99.51%	1341	NR_041834.1
			Campylobacter insulaenigrae strain CCUG 48653	1118	1118	100%	0	99.35%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1118	1118	100%	0	99.35%	1341	NR_043608.1
			Campylobacter insulaenigrae NCTC 12927	1118	1118	100%	0	99.35%	1469	NR_114914.1
			Campylobacter taeniopygiae strain MIT10-5678	1112	1112	100%	0	99.19%	1450	NR_180416.1
			Campylobacter novaezeelandiae strain B423b	1107	1107	100%	0	99.03%	1510	NR_180527.1
			Campylobacter aviculae strain MIT17-670	1101	1101	100%	0	98.87%	1457	NR_180417.1
			Campylobacter volucris strain LMG 24380	1101	1101	100%	0	98.87%	1482	NR_116923.1
			Campylobacter jejuni strain DSM 4688	1098	1098	98%	0	99.34%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1096	1096	100%	0	98.70%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1090	1090	100%	0	98.54%	1470	NR_152703.1
			Campylobacter armoricus strain CA656	1085	1085	100%	0	98.38%	1510	NR_180483.1
			Campylobacter lari strain DSM 11375	1085	1085	100%	0	98.38%	1338	NR_117762.1
			Campylobacter lari subsp. lari strain ATCC 35221	1085	1085	100%	0	98.38%	1435	NR_118523.1
			Campylobacter lari subsp. lari strain NCTC 11352	1085	1085	100%	0	98.38%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1085	1085	100%	0	98.38%	1441	NR_043034.1
			Campylobacter lari subsp. lari strain CCUG 23947	1077	1077	100%	0	98.06%	1459	NR_118653.1
			Campylobacter coli strain DSM 4689	1074	1074	100%	0	98.06%	1342	NR_117761.1
			Campylobacter coli strain ATCC 33559	1074	1074	100%	0	98.06%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1074	1074	100%	0	98.06%	1420	NR_117233.1
			Campylobacter lari strain JCM2530	1074	1074	100%	0	98.06%	1435	NR_112241.1
			Campylobacter coli strain LMG 6440	1074	1074	100%	0	98.06%	1341	NR_041835.1
			Campylobacter peloridis strain 2314BVA	1068	1068	100%	0	97.89%	1497	NR_042684.1
			Campylobacter iguaniorum strain 1485E	1040	1040	100%	0	97.08%	1503	NR_134706.1
			Campylobacter helveticus strain ATCC 51209	1040	1040	100%	0	97.08%	1435	NR_118517.1

Bird ID	Sample Date	Bird Species	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
204	11/6/2023	Arenaria interpres	Campylobacter lari subsp. concheus strain 2897R	1140	1140	100%	0	100.00%	1501	NR_042683.1
			Campylobacter lari subsp. concheus strain CCUG 55786	1140	1140	100%	0	100.00%	1436	NR_118522.1
			Campylobacter ornithocola strain WBE38	1129	1129	100%	0	99.68%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1129	1129	100%	0	99.68%	1485	NR_115081.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1123	1123	100%	0	99.51%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1123	1123	100%	0	99.51%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1123	1123	100%	0	99.51%	1341	NR_041834.1
			Campylobacter novaezeelandiae strain B423b	1107	1107	100%	0	99.03%	1510	NR_180527.1
			Campylobacter insulaenigrae strain CCUG 48653	1107	1107	100%	0	99.03%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1107	1107	100%	0	99.03%	1341	NR_043608.1
			Campylobacter insulaenigrae NCTC 12927	1107	1107	100%	0	99.03%	1469	NR_114914.1
			Campylobacter aviculae strain MIT17-670	1101	1101	100%	0	98.87%	1457	NR_180417.1
			Campylobacter taeniopygiae strain MIT10-5678	1101	1101	100%	0	98.87%	1450	NR_180416.1
			Campylobacter volucris strain LMG 24380	1101	1101	100%	0	98.87%	1482	NR_116923.1
			Campylobacter jejuni strain DSM 4688	1098	1098	98%	0	99.34%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1096	1096	100%	0	98.70%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1090	1090	100%	0	98.54%	1470	NR_152703.1
			Campylobacter armoricus strain CA656	1085	1085	100%	0	98.38%	1510	NR_180483.1
			Campylobacter lari strain DSM 11375	1085	1085	100%	0	98.38%	1338	NR_117762.1
			Campylobacter lari subsp. lari strain ATCC 35221	1085	1085	100%	0	98.38%	1435	NR_118523.1
			Campylobacter lari subsp. lari strain NCTC 11352	1085	1085	100%	0	98.38%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1085	1085	100%	0	98.38%	1441	NR_043034.1
			Campylobacter coli strain DSM 4689	1079	1079	100%	0	98.22%	1342	NR_117761.1
			Campylobacter coli strain ATCC 33559	1079	1079	100%	0	98.22%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1079	1079	100%	0	98.22%	1420	NR_117233.1
			Campylobacter coli strain LMG 6440	1079	1079	100%	0	98.22%	1341	NR_041835.1
			Campylobacter lari subsp. lari strain CCUG 23947	1077	1077	100%	0	98.06%	1459	NR_118653.1
			Campylobacter lari strain JCM2530	1074	1074	100%	0	98.06%	1435	NR_112241.1
			Campylobacter peloridis strain 2314BVA	1068	1068	100%	0	97.89%	1497	NR_042684.1
			Campylobacter iguaniorum strain 1485E	1046	1046	100%	0	97.24%	1503	NR_134706.1
			Campylobacter lanienae NCTC 13004	1040	1040	100%	0	97.08%	1467	NR_028698.1

Appendix III. Type strains matching at > 97% identity or above to *Campylobacter* isolates from oysters collected in this study. All type strain matches were described as partial sequences of 16S ribosomal RNA.

Sample	Sample Date	Cage Treatment	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
OTS 15	9/13/2023	Control	Campylobacter novaezeelandiae strain B423b	1140	1140	100%	0	100.00%	1510	NR_180527.1
			Campylobacter volucris strain LMG 24380	1134	1134	100%	0	99.84%	1482	NR_116923.1
			Campylobacter ornithocola strain WBE38	1118	1118	100%	0	99.35%	1444	NR_156985.1
			Campylobacter armoricus strain CA656	1118	1118	100%	0	99.35%	1510	NR_180483.1
			Campylobacter lari subsp. lari strain ATCC 35221	1118	1118	100%	0	99.35%	1435	NR_118523.1
			Campylobacter lari strain DSM 11375	1118	1118	100%	0	99.35%	1338	NR_117762.1
			Campylobacter subantarcticus strain LMG 24377	1118	1118	100%	0	99.35%	1485	NR_115081.1
			Campylobacter lari subsp. lari strain NCTC 11352	1118	1118	100%	0	99.35%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1118	1118	100%	0	99.35%	1441	NR_043034.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1112	1112	100%	0	99.19%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1112	1112	100%	0	99.19%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1112	1112	100%	0	99.19%	1341	NR_041834.1
			Campylobacter lari subsp. lari strain CCUG 23947	1110	1110	100%	0	99.03%	1459	NR_118653.1
			Campylobacter lari subsp. concheus strain CCUG 55786	1107	1107	100%	0	99.03%	1436	NR_118522.1
			Campylobacter lari strain JCM2530	1107	1107	100%	0	99.03%	1435	NR_112241.1
			Campylobacter lari subsp. concheus strain 2897R	1107	1107	100%	0	99.03%	1501	NR_042683.1
			Campylobacter peloridis strain 2314BVA	1101	1101	100%	0	98.87%	1497	NR_042684.1
			Campylobacter insulaenigrae strain CCUG 48653	1096	1096	100%	0	98.70%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1096	1096	100%	0	98.70%	1469	NR_114914.1
			Campylobacter insulaenigrae NCTC 12927	1096	1096	100%	0	98.70%	1341	NR_043608.1
			Campylobacter aviculae strain MIT17-670	1090	1090	100%	0	98.54%	1457	NR_180417.1
			Campylobacter taeniopygiae strain MIT10-5678	1090	1090	100%	0	98.54%	1450	NR_180416.1
			Campylobacter jejuni strain DSM 4688	1086	1086	98%	0	99.01%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1085	1085	100%	0	98.38%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1079	1079	100%	0	98.22%	1470	NR_152703.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1420	NR_117233.1
			Campylobacter coli strain DSM 4689	1068	1068	100%	0	97.89%	1342	NR_117761.1
			Campylobacter cuniculorum DSM 23162 = LMG 24588 strain 150B	1068	1068	100%	0	97.89%	1390	NR_043784.1
			Campylobacter coli strain LMG 6440	1068	1068	100%	0	97.89%	1341	NR_041835.1
			Campylobacter helveticus strain ATCC 51209	1062	1062	100%	0	97.73%	1435	NR_118517.1
			Campylobacter helveticus strain NCTC 12470	1057	1057	100%	0	97.57%	1341	NR_115702.1
			Campylobacter iguaniorum strain 1485E	1051	1051	100%	0	97.41%	1503	NR_134706.1
			Campylobacter helveticus strain D5248	1051	1051	100%	0	97.41%	1439	NR_025948.1

Oyster ID	Sample Date	Cage	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
16	9/13/2023	Control	Campylobacter novaezeelandiae strain B423b	1140	1140	100%	0	100.00%	1510	NR_180527.1
			Campylobacter volucris strain LMG 24380	1134	1134	100%	0	99.84%	1482	NR_116923.1
			Campylobacter ornithocola strain WBE38	1118	1118	100%	0	99.35%	1444	NR_156985.1
			Campylobacter armoricus strain CA656	1118	1118	100%	0	99.35%	1510	NR_180483.1
			Campylobacter lari subsp. lari strain ATCC 35221	1118	1118	100%	0	99.35%	1435	NR_118523.1
			Campylobacter lari strain DSM 11375	1118	1118	100%	0	99.35%	1338	NR_117762.1
			Campylobacter subantarcticus strain LMG 24377	1118	1118	100%	0	99.35%	1485	NR_115081.1
			Campylobacter lari subsp. lari strain NCTC 11352	1118	1118	100%	0	99.35%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1118	1118	100%	0	99.35%	1441	NR_043034.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1112	1112	100%	0	99.19%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1112	1112	100%	0	99.19%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1112	1112	100%	0	99.19%	1341	NR_041834.1
			Campylobacter lari subsp. lari strain CCUG 23947	1110	1110	100%	0	99.03%	1459	NR_118653.1
			Campylobacter lari subsp. concheus strain CCUG 55786	1107	1107	100%	0	99.03%	1436	NR_118522.1
			Campylobacter lari strain JCM2530	1107	1107	100%	0	99.03%	1435	NR_112241.1
			Campylobacter lari subsp. concheus strain 2897R	1107	1107	100%	0	99.03%	1501	NR_042683.1
			Campylobacter peloridis strain 2314BVA	1101	1101	100%	0	98.87%	1497	NR_042684.1
			Campylobacter insulaenigrae strain CCUG 48653	1096	1096	100%	0	98.70%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1096	1096	100%	0	98.70%	1469	NR_114914.1
			Campylobacter insulaenigrae NCTC 12927	1096	1096	100%	0	98.70%	1341	NR_043608.1
			Campylobacter aviculae strain MIT17-670	1090	1090	100%	0	98.54%	1457	NR_180417.1
			Campylobacter taeniopygiae strain MIT10-5678	1090	1090	100%	0	98.54%	1450	NR_180416.1
			Campylobacter jejuni strain DSM 4688	1086	1086	98%	0	99.01%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1085	1085	100%	0	98.38%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1079	1079	100%	0	98.22%	1470	NR_152703.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1420	NR_117233.1
			Campylobacter coli strain DSM 4689	1068	1068	100%	0	97.89%	1342	NR_117761.1
			Campylobacter cuniculorum DSM 23162 = LMG 24588 strain 150B	1068	1068	100%	0	97.89%	1390	NR_043784.1
			Campylobacter coli strain LMG 6440	1068	1068	100%	0	97.89%	1341	NR_041835.1
			Campylobacter helveticus strain ATCC 51209	1062	1062	100%	0	97.73%	1435	NR_118517.1
			Campylobacter helveticus strain NCTC 12470	1057	1057	100%	0	97.57%	1341	NR_115702.1
			Campylobacter iguaniorum strain 1485E	1051	1051	100%	0	97.41%	1503	NR_134706.1
			Campylobacter helveticus strain D5248	1051	1051	100%	0	97.41%	1439	NR_025948.1

Oyster ID	Sample Date	Cage	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
17	9/13/2023	Control	Campylobacter novaezeelandiae strain B423b	1140	1140	100%	0	100.00%	1510	NR_180527.1
			Campylobacter volucris strain LMG 24380	1134	1134	100%	0	99.84%	1482	NR_116923.1
			Campylobacter ornithocola strain WBE38	1118	1118	100%	0	99.35%	1444	NR_156985.1
			Campylobacter armoricus strain CA656	1118	1118	100%	0	99.35%	1510	NR_180483.1
			Campylobacter lari subsp. lari strain ATCC 35221	1118	1118	100%	0	99.35%	1435	NR_118523.1
			Campylobacter lari strain DSM 11375	1118	1118	100%	0	99.35%	1338	NR_117762.1
			Campylobacter subantarcticus strain LMG 24377	1118	1118	100%	0	99.35%	1485	NR_115081.1
			Campylobacter lari subsp. lari strain NCTC 11352	1118	1118	100%	0	99.35%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1118	1118	100%	0	99.35%	1441	NR_043034.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1112	1112	100%	0	99.19%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1112	1112	100%	0	99.19%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1112	1112	100%	0	99.19%	1341	NR_041834.1
			Campylobacter lari subsp. lari strain CCUG 23947	1110	1110	100%	0	99.03%	1459	NR_118653.1
			Campylobacter lari subsp. concheus strain CCUG 55786	1107	1107	100%	0	99.03%	1436	NR_118522.1
			Campylobacter lari strain JCM2530	1107	1107	100%	0	99.03%	1435	NR_112241.1
			Campylobacter lari subsp. concheus strain 2897R	1107	1107	100%	0	99.03%	1501	NR_042683.1
			Campylobacter peloridis strain 2314BVA	1101	1101	100%	0	98.87%	1497	NR_042684.1
			Campylobacter insulaenigrae strain CCUG 48653	1096	1096	100%	0	98.70%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1096	1096	100%	0	98.70%	1469	NR_114914.1
			Campylobacter insulaenigrae NCTC 12927	1096	1096	100%	0	98.70%	1341	NR_043608.1
			Campylobacter aviculae strain MIT17-670	1090	1090	100%	0	98.54%	1457	NR_180417.1
			Campylobacter taeniopygiae strain MIT10-5678	1090	1090	100%	0	98.54%	1450	NR_180416.1
			Campylobacter jejuni strain DSM 4688	1086	1086	98%	0	99.01%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1085	1085	100%	0	98.38%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1079	1079	100%	0	98.22%	1470	NR_152703.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1420	NR_117233.1
			Campylobacter coli strain DSM 4689	1068	1068	100%	0	97.89%	1342	NR_117761.1
			Campylobacter cuniculorum DSM 23162 = LMG 24588 strain 150B	1068	1068	100%	0	97.89%	1390	NR_043784.1
			Campylobacter coli strain LMG 6440	1068	1068	100%	0	97.89%	1341	NR_041835.1
			Campylobacter helveticus strain ATCC 51209	1062	1062	100%	0	97.73%	1435	NR_118517.1
			Campylobacter helveticus strain NCTC 12470	1057	1057	100%	0	97.57%	1341	NR_115702.1
			Campylobacter iguaniorum strain 1485E	1051	1051	100%	0	97.41%	1503	NR_134706.1
			Campylobacter helveticus strain D5248	1051	1051	100%	0	97.41%	1439	NR_025948.1

Oyster ID	Sample Date	Cage	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
19	9/26/2023	Control	Campylobacter lari subsp. concheus strain CCUG 55786	1131	1131	99%	0	100.00%	1436	NR_118522.1
			Campylobacter lari subsp. concheus strain 2897R	1131	1131	99%	0	100.00%	1501	NR_042683.1
			Campylobacter ornithocola strain WBE38	1120	1120	99%	0	99.67%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1120	1120	99%	0	99.67%	1485	NR_115081.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1114	1114	99%	0	99.51%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1114	1114	99%	0	99.51%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1114	1114	99%	0	99.51%	1341	NR_041834.1
			Campylobacter novaezeelandiae strain B423b	1098	1098	99%	0	99.02%	1510	NR_180527.1
			Campylobacter insulaenigrae strain CCUG 48653	1098	1098	99%	0	99.02%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1098	1098	99%	0	99.02%	1469	NR_114914.1
			Campylobacter jejuni strain DSM 4688	1098	1098	98%	0	99.34%	1327	NR_117760.1
			Campylobacter insulaenigrae NCTC 12927	1098	1098	99%	0	99.02%	1341	NR_043608.1
			Campylobacter aviculae strain MIT17-670	1092	1092	99%	0	98.86%	1457	NR_180417.1
			Campylobacter taeniopygiae strain MIT10-5678	1092	1092	99%	0	98.86%	1450	NR_180416.1
			Campylobacter volucris strain LMG 24380	1092	1092	99%	0	98.86%	1482	NR_116923.1
			Campylobacter bilis strain VicNov18	1086	1086	99%	0	98.69%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1081	1081	99%	0	98.53%	1470	NR_152703.1
			Campylobacter armoricus strain CA656	1075	1075	99%	0	98.37%	1510	NR_180483.1
			Campylobacter lari subsp. lari strain ATCC 35221	1075	1075	99%	0	98.37%	1435	NR_118523.1
			Campylobacter lari strain DSM 11375	1075	1075	99%	0	98.37%	1338	NR_117762.1
			Campylobacter lari subsp. lari strain NCTC 11352	1075	1075	99%	0	98.37%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1075	1075	99%	0	98.37%	1441	NR_043034.1
			Campylobacter coli strain ATCC 33559	1070	1070	99%	0	98.20%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1070	1070	99%	0	98.20%	1420	NR_117233.1
			Campylobacter coli strain DSM 4689	1070	1070	99%	0	98.20%	1342	NR_117761.1
			Campylobacter coli strain LMG 6440	1070	1070	99%	0	98.20%	1341	NR_041835.1
			Campylobacter lari subsp. lari strain CCUG 23947	1068	1068	99%	0	98.04%	1459	NR_118653.1
			Campylobacter lari strain JCM2530	1064	1064	99%	0	98.04%	1435	NR_112241.1
			Campylobacter peloridis strain 2314BVA	1059	1059	99%	0	97.88%	1497	NR_042684.1
			Campylobacter iguaniorum strain 1485E	1037	1037	99%	0	97.22%	1503	NR_134706.1
			Campylobacter lanienae NCTC 13004	1031	1031	99%	0	97.06%	1467	NR_028698.1

Oyster ID	Sample Date	Cage	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
20	9/26/2023	Control	Campylobacter lari subsp. concheus strain CCUG 55786	1140	1140	100%	0	100.00%	1436	NR_118522.1
			Campylobacter lari subsp. concheus strain 2897R	1140	1140	100%	0	100.00%	1501	NR_042683.1
			Campylobacter ornithocola strain WBE38	1129	1129	100%	0	99.68%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1129	1129	100%	0	99.68%	1485	NR_115081.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1123	1123	100%	0	99.51%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1123	1123	100%	0	99.51%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1123	1123	100%	0	99.51%	1341	NR_041834.1
			Campylobacter novaezeelandiae strain B423b	1107	1107	100%	0	99.03%	1510	NR_180527.1
			Campylobacter insulaenigrae strain CCUG 48653	1107	1107	100%	0	99.03%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1107	1107	100%	0	99.03%	1469	NR_114914.1
			Campylobacter insulaenigrae NCTC 12927	1107	1107	100%	0	99.03%	1341	NR_043608.1
			Campylobacter aviculae strain MIT17-670	1101	1101	100%	0	98.87%	1457	NR_180417.1
			Campylobacter taeniopygiae strain MIT10-5678	1101	1101	100%	0	98.87%	1450	NR_180416.1
			Campylobacter volucris strain LMG 24380	1101	1101	100%	0	98.87%	1482	NR_116923.1
			Campylobacter jejuni strain DSM 4688	1098	1098	98%	0	99.34%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1096	1096	100%	0	98.70%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1090	1090	100%	0	98.54%	1470	NR_152703.1
			Campylobacter armoricus strain CA656	1085	1085	100%	0	98.38%	1510	NR_180483.1
			Campylobacter lari subsp. lari strain ATCC 35221	1085	1085	100%	0	98.38%	1435	NR_118523.1
			Campylobacter lari strain DSM 11375	1085	1085	100%	0	98.38%	1338	NR_117762.1
			Campylobacter lari subsp. lari strain NCTC 11352	1085	1085	100%	0	98.38%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1085	1085	100%	0	98.38%	1441	NR_043034.1
			Campylobacter coli strain ATCC 33559	1079	1079	100%	0	98.22%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1079	1079	100%	0	98.22%	1420	NR_117233.1
			Campylobacter coli strain DSM 4689	1079	1079	100%	0	98.22%	1342	NR_117761.1
			Campylobacter coli strain LMG 6440	1079	1079	100%	0	98.22%	1341	NR_041835.1
			Campylobacter lari subsp. lari strain CCUG 23947	1077	1077	100%	0	98.06%	1459	NR_118653.1
			Campylobacter lari strain JCM2530	1074	1074	100%	0	98.06%	1435	NR_112241.1
			Campylobacter peloridis strain 2314BVA	1068	1068	100%	0	97.89%	1497	NR_042684.1
			Campylobacter iguaniorum strain 1485E	1046	1046	100%	0	97.24%	1503	NR_134706.1
			Campylobacter lanienae NCTC 13004	1040	1040	100%	0	97.08%	1467	NR_028698.1

Oyster ID	Sample Date	Cage	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
23	10/11/2023	Control	Campylobacter lari subsp. concheus strain CCUG 55786	1134	1134	100%	0	99.84%	1436	NR_118522.1
			Campylobacter lari subsp. concheus strain 2897R	1134	1134	100%	0	99.84%	1501	NR_042683.1
			Campylobacter ornithocola strain WBE38	1123	1123	100%	0	99.51%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1123	1123	100%	0	99.51%	1485	NR_115081.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1118	1118	100%	0	99.35%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1118	1118	100%	0	99.35%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1118	1118	100%	0	99.35%	1341	NR_041834.1
			Campylobacter novaezeelandiae strain B423b	1101	1101	100%	0	98.87%	1510	NR_180527.1
			Campylobacter insulaenigrae strain CCUG 48653	1101	1101	100%	0	98.87%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1101	1101	100%	0	98.87%	1469	NR_114914.1
			Campylobacter insulaenigrae NCTC 12927	1101	1101	100%	0	98.87%	1341	NR_043608.1
			Campylobacter aviculae strain MIT17-670	1096	1096	100%	0	98.70%	1457	NR_180417.1
			Campylobacter taeniopygiae strain MIT10-5678	1096	1096	100%	0	98.70%	1450	NR_180416.1
			Campylobacter volucris strain LMG 24380	1096	1096	100%	0	98.70%	1482	NR_116923.1
			Campylobacter jejuni strain DSM 4688	1092	1092	98%	0	99.18%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1090	1090	100%	0	98.54%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1085	1085	100%	0	98.38%	1470	NR_152703.1
			Campylobacter armoricus strain CA656	1079	1079	100%	0	98.22%	1510	NR_180483.1
			Campylobacter lari subsp. lari strain ATCC 35221	1079	1079	100%	0	98.22%	1435	NR_118523.1
			Campylobacter lari strain DSM 11375	1079	1079	100%	0	98.22%	1338	NR_117762.1
			Campylobacter lari subsp. lari strain NCTC 11352	1079	1079	100%	0	98.22%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1079	1079	100%	0	98.22%	1441	NR_043034.1
			Campylobacter coli strain ATCC 33559	1074	1074	100%	0	98.06%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1074	1074	100%	0	98.06%	1420	NR_117233.1
			Campylobacter coli strain DSM 4689	1074	1074	100%	0	98.06%	1342	NR_117761.1
			Campylobacter coli strain LMG 6440	1074	1074	100%	0	98.06%	1341	NR_041835.1
			Campylobacter lari subsp. lari strain CCUG 23947	1072	1072	100%	0	97.89%	1459	NR_118653.1
			Campylobacter lari strain JCM2530	1068	1068	100%	0	97.89%	1435	NR_112241.1
			Campylobacter peloridis strain 2314BVA	1062	1062	100%	0	97.73%	1497	NR_042684.1
			Campylobacter lanienae NCTC 13004	1046	1046	100%	0	97.24%	1467	NR_028698.1
			Campylobacter iguaniorum strain 1485E	1040	1040	100%	0	97.08%	1503	NR_134706.1

Oyster ID	Sample Date	Cage	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
24	10/11/2023	Control	Campylobacter novaezeelandiae strain B423b	1129	1129	100%	0	99.68%	1510	NR_180527.1
			Campylobacter volucris strain LMG 24380	1123	1123	100%	0	99.51%	1482	NR_116923.1
			Campylobacter ornithocola strain WBE38	1107	1107	100%	0	99.03%	1444	NR_156985.1
			Campylobacter armoricus strain CA656	1107	1107	100%	0	99.03%	1510	NR_180483.1
			Campylobacter lari subsp. lari strain ATCC 35221	1107	1107	100%	0	99.03%	1435	NR_118523.1
			Campylobacter lari strain DSM 11375	1107	1107	100%	0	99.03%	1338	NR_117762.1
			Campylobacter subantarcticus strain LMG 24377	1107	1107	100%	0	99.03%	1485	NR_115081.1
			Campylobacter lari subsp. lari strain NCTC 11352	1107	1107	100%	0	99.03%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1107	1107	100%	0	99.03%	1441	NR_043034.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1101	1101	100%	0	98.87%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1101	1101	100%	0	98.87%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1101	1101	100%	0	98.87%	1341	NR_041834.1
			Campylobacter lari subsp. lari strain CCUG 23947	1099	1099	100%	0	98.70%	1459	NR_118653.1
			Campylobacter insulaenigrae strain CCUG 48653	1096	1096	100%	0	98.70%	1435	NR_118519.1
			Campylobacter lari subsp. concheus strain CCUG 55786	1096	1096	100%	0	98.70%	1436	NR_118522.1
			Campylobacter insulaenigrae NCTC 12927	1096	1096	100%	0	98.70%	1469	NR_114914.1
			Campylobacter lari strain JCM2530	1096	1096	100%	0	98.70%	1435	NR_112241.1
			Campylobacter lari subsp. concheus strain 2897R	1096	1096	100%	0	98.70%	1501	NR_042683.1
			Campylobacter insulaenigrae NCTC 12927	1096	1096	100%	0	98.70%	1341	NR_043608.1
			Campylobacter taeniopygiae strain MIT10-5678	1090	1090	100%	0	98.54%	1450	NR_180416.1
			Campylobacter peloridis strain 2314BVA	1090	1090	100%	0	98.54%	1497	NR_042684.1
			Campylobacter aviculae strain MIT17-670	1079	1079	100%	0	98.22%	1457	NR_180417.1
			Campylobacter jejuni strain DSM 4688	1075	1075	98%	0	98.68%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1074	1074	100%	0	98.06%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1068	1068	100%	0	97.89%	1470	NR_152703.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1420	NR_117233.1
			Campylobacter coli strain DSM 4689	1068	1068	100%	0	97.89%	1342	NR_117761.1
			Campylobacter coli strain LMG 6440	1068	1068	100%	0	97.89%	1341	NR_041835.1
			Campylobacter helveticus strain ATCC 51209	1062	1062	100%	0	97.73%	1435	NR_118517.1
			Campylobacter cuniculorum DSM 23162 = LMG 24588 strain 150B	1062	1062	100%	0	97.73%	1390	NR_043784.1
			Campylobacter helveticus strain NCTC 12470	1057	1057	100%	0	97.57%	1341	NR_115702.1
			Campylobacter helveticus strain D5248	1051	1051	100%	0	97.41%	1439	NR_025948.1
			Campylobacter iguaniorum strain 1485E	1046	1046	100%	0	97.24%	1503	NR_134706.1

Oyster ID	Sample Date	Cage	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
25-A	10/22/2023	Control	Campylobacter novaezeelandiae strain B423b	1129	1129	100%	0	99.68%	1510	NR_180527.1
			Campylobacter volucris strain LMG 24380	1123	1123	100%	0	99.51%	1482	NR_116923.1
			Campylobacter ornithocola strain WBE38	1107	1107	100%	0	99.03%	1444	NR_156985.1
			Campylobacter armoricus strain CA656	1107	1107	100%	0	99.03%	1510	NR_180483.1
			Campylobacter lari subsp. lari strain ATCC 35221	1107	1107	100%	0	99.03%	1435	NR_118523.1
			Campylobacter lari strain DSM 11375	1107	1107	100%	0	99.03%	1338	NR_117762.1
			Campylobacter subantarcticus strain LMG 24377	1107	1107	100%	0	99.03%	1485	NR_115081.1
			Campylobacter lari subsp. lari strain NCTC 11352	1107	1107	100%	0	99.03%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1107	1107	100%	0	99.03%	1441	NR_043034.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1101	1101	100%	0	98.87%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1101	1101	100%	0	98.87%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1101	1101	100%	0	98.87%	1341	NR_041834.1
			Campylobacter lari subsp. lari strain CCUG 23947	1099	1099	100%	0	98.70%	1459	NR_118653.1
			Campylobacter insulaenigrae strain CCUG 48653	1096	1096	100%	0	98.70%	1435	NR_118519.1
			Campylobacter lari subsp. concheus strain CCUG 55786	1096	1096	100%	0	98.70%	1436	NR_118522.1
			Campylobacter insulaenigrae NCTC 12927	1096	1096	100%	0	98.70%	1469	NR_114914.1
			Campylobacter lari strain JCM2530	1096	1096	100%	0	98.70%	1435	NR_112241.1
			Campylobacter lari subsp. concheus strain 2897R	1096	1096	100%	0	98.70%	1501	NR_042683.1
			Campylobacter insulaenigrae NCTC 12927	1096	1096	100%	0	98.70%	1341	NR_043608.1
			Campylobacter taeniopygiae strain MIT10-5678	1090	1090	100%	0	98.54%	1450	NR_180416.1
			Campylobacter peloridis strain 2314BVA	1090	1090	100%	0	98.54%	1497	NR_042684.1
			Campylobacter aviculae strain MIT17-670	1079	1079	100%	0	98.22%	1457	NR_180417.1
			Campylobacter jejuni strain DSM 4688	1075	1075	98%	0	98.68%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1074	1074	100%	0	98.06%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1068	1068	100%	0	97.89%	1470	NR_152703.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1420	NR_117233.1
			Campylobacter coli strain DSM 4689	1068	1068	100%	0	97.89%	1342	NR_117761.1
			Campylobacter coli strain LMG 6440	1068	1068	100%	0	97.89%	1341	NR_041835.1
			Campylobacter helveticus strain ATCC 51209	1062	1062	100%	0	97.73%	1435	NR_118517.1
			Campylobacter cuniculorum DSM 23162 = LMG 24588 strain 150B	1062	1062	100%	0	97.73%	1390	NR_043784.1
			Campylobacter helveticus strain NCTC 12470	1057	1057	100%	0	97.57%	1341	NR_115702.1
			Campylobacter helveticus strain D5248	1051	1051	100%	0	97.41%	1439	NR_025948.1
			Campylobacter iguaniorum strain 1485E	1046	1046	100%	0	97.24%	1503	NR_134706.1

Oyster ID	Sample Date	Cage	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
25-B	10/22/2023	Control	Campylobacter ornithocola strain WBE38	1140	1140	100%	0	100.00%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1140	1140	100%	0	100.00%	1485	NR_115081.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1134	1134	100%	0	99.84%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1134	1134	100%	0	99.84%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1134	1134	100%	0	99.84%	1341	NR_041834.1
			Campylobacter lari subsp. concheus strain CCUG 55786	1129	1129	100%	0	99.68%	1436	NR_118522.1
			Campylobacter lari subsp. concheus strain 2897R	1129	1129	100%	0	99.68%	1501	NR_042683.1
			Campylobacter novaezeelandiae strain B423b	1118	1118	100%	0	99.35%	1510	NR_180527.1
			Campylobacter insulaenigrae strain CCUG 48653	1118	1118	100%	0	99.35%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1118	1118	100%	0	99.35%	1469	NR_114914.1
			Campylobacter insulaenigrae NCTC 12927	1118	1118	100%	0	99.35%	1341	NR_043608.1
			Campylobacter aviculae strain MIT17-670	1112	1112	100%	0	99.19%	1457	NR_180417.1
			Campylobacter taeniopygiae strain MIT10-5678	1112	1112	100%	0	99.19%	1450	NR_180416.1
			Campylobacter volucris strain LMG 24380	1112	1112	100%	0	99.19%	1482	NR_116923.1
			Campylobacter jejuni strain DSM 4688	1109	1109	98%	0	99.67%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1107	1107	100%	0	99.03%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1101	1101	100%	0	98.87%	1470	NR_152703.1
			Campylobacter armoricus strain CA656	1096	1096	100%	0	98.70%	1510	NR_180483.1
			Campylobacter lari subsp. lari strain ATCC 35221	1096	1096	100%	0	98.70%	1435	NR_118523.1
			Campylobacter lari strain DSM 11375	1096	1096	100%	0	98.70%	1338	NR_117762.1
			Campylobacter lari subsp. lari strain NCTC 11352	1096	1096	100%	0	98.70%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1096	1096	100%	0	98.70%	1441	NR_043034.1
			Campylobacter lari subsp. lari strain CCUG 23947	1088	1088	100%	0	98.38%	1459	NR_118653.1
			Campylobacter lari strain JCM2530	1085	1085	100%	0	98.38%	1435	NR_112241.1
			Campylobacter peloridis strain 2314BVA	1079	1079	100%	0	98.22%	1497	NR_042684.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1420	NR_117233.1
			Campylobacter coli strain DSM 4689	1068	1068	100%	0	97.89%	1342	NR_117761.1
			Campylobacter coli strain LMG 6440	1068	1068	100%	0	97.89%	1341	NR_041835.1
			Campylobacter iguaniorum strain 1485E	1051	1051	100%	0	97.41%	1503	NR_134706.1
			Campylobacter cuniculorum DSM 23162 = LMG 24588 strain :	1046	1046	100%	0	97.24%	1390	NR_043784.1
			Campylobacter helveticus strain ATCC 51209	1040	1040	100%	0	97.08%	1435	NR_118517.1

Oyster ID	Sample Date	Cage	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
26	10/11/2023	Deterrent	Campylobacter ornithocola strain WBE38	1140	1140	100%	0	100.00%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1140	1140	100%	0	100.00%	1485	NR_115081.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1134	1134	100%	0	99.84%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1134	1134	100%	0	99.84%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1134	1134	100%	0	99.84%	1341	NR_041834.1
			Campylobacter lari subsp. concheus strain CCUG 55786	1129	1129	100%	0	99.68%	1436	NR_118522.1
			Campylobacter lari subsp. concheus strain 2897R	1129	1129	100%	0	99.68%	1501	NR_042683.1
			Campylobacter novaezeelandiae strain B423b	1118	1118	100%	0	99.35%	1510	NR_180527.1
			Campylobacter insulaenigrae strain CCUG 48653	1118	1118	100%	0	99.35%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1118	1118	100%	0	99.35%	1469	NR_114914.1
			Campylobacter insulaenigrae NCTC 12927	1118	1118	100%	0	99.35%	1341	NR_043608.1
			Campylobacter aviculae strain MIT17-670	1112	1112	100%	0	99.19%	1457	NR_180417.1
			Campylobacter taeniopygiae strain MIT10-5678	1112	1112	100%	0	99.19%	1450	NR_180416.1
			Campylobacter volucris strain LMG 24380	1112	1112	100%	0	99.19%	1482	NR_116923.1
			Campylobacter jejuni strain DSM 4688	1109	1109	98%	0	99.67%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1107	1107	100%	0	99.03%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1101	1101	100%	0	98.87%	1470	NR_152703.1
			Campylobacter armoricus strain CA656	1096	1096	100%	0	98.70%	1510	NR_180483.1
			Campylobacter lari subsp. lari strain ATCC 35221	1096	1096	100%	0	98.70%	1435	NR_118523.1
			Campylobacter lari strain DSM 11375	1096	1096	100%	0	98.70%	1338	NR_117762.1
			Campylobacter lari subsp. lari strain NCTC 11352	1096	1096	100%	0	98.70%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1096	1096	100%	0	98.70%	1441	NR_043034.1
			Campylobacter lari subsp. lari strain CCUG 23947	1088	1088	100%	0	98.38%	1459	NR_118653.1
			Campylobacter lari strain JCM2530	1085	1085	100%	0	98.38%	1435	NR_112241.1
			Campylobacter peloridis strain 2314BVA	1079	1079	100%	0	98.22%	1497	NR_042684.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1068	1068	100%	0	97.89%	1420	NR_117233.1
			Campylobacter coli strain DSM 4689	1068	1068	100%	0	97.89%	1342	NR_117761.1
			Campylobacter coli strain LMG 6440	1068	1068	100%	0	97.89%	1341	NR_041835.1
			Campylobacter iguaniorum strain 1485E	1051	1051	100%	0	97.41%	1503	NR_134706.1
			Campylobacter cuniculorum DSM 23162 = LMG 24588 strain 1	1046	1046	100%	0	97.24%	1390	NR_043784.1
			Campylobacter helveticus strain ATCC 51209	1040	1040	100%	0	97.08%	1435	NR_118517.1

Oyster ID	Sample Date	Cage	Description	Max Score	Total Score	Query Cover	E value	% Identity	Accession Length	Accession
41	1/31/2024	Deterrent	Campylobacter lari subsp. concheus strain CCUG 55786	1134	1134	100%	0	99.84%	1436	NR_118522.1
			Campylobacter lari subsp. concheus strain 2897R	1134	1134	100%	0	99.84%	1501	NR_042683.1
			Campylobacter ornithocola strain WBE38	1123	1123	100%	0	99.51%	1444	NR_156985.1
			Campylobacter subantarcticus strain LMG 24377	1123	1123	100%	0	99.51%	1485	NR_115081.1
			Campylobacter jejuni subsp. jejuni ATCC 33560	1118	1118	100%	0	99.35%	1435	NR_118520.1
			Campylobacter jejuni subsp. doylei strain LMG 8843	1118	1118	100%	0	99.35%	1341	NR_043599.1
			Campylobacter jejuni strain NCTC 11351	1118	1118	100%	0	99.35%	1341	NR_041834.1
			Campylobacter novaezeelandiae strain B423b	1101	1101	100%	0	98.87%	1510	NR_180527.1
			Campylobacter insulaenigrae strain CCUG 48653	1101	1101	100%	0	98.87%	1435	NR_118519.1
			Campylobacter insulaenigrae NCTC 12927	1101	1101	100%	0	98.87%	1469	NR_114914.1
			Campylobacter insulaenigrae NCTC 12927	1101	1101	100%	0	98.87%	1341	NR_043608.1
			Campylobacter aviculae strain MIT17-670	1096	1096	100%	0	98.70%	1457	NR_180417.1
			Campylobacter taeniopygiae strain MIT10-5678	1096	1096	100%	0	98.70%	1450	NR_180416.1
			Campylobacter volucris strain LMG 24380	1096	1096	100%	0	98.70%	1482	NR_116923.1
			Campylobacter jejuni strain DSM 4688	1092	1092	98%	0	99.18%	1327	NR_117760.1
			Campylobacter bilis strain VicNov18	1090	1090	100%	0	98.54%	1495	NR_181124.1
			Campylobacter hepaticus strain HV10	1085	1085	100%	0	98.38%	1470	NR_152703.1
			Campylobacter armoricus strain CA656	1079	1079	100%	0	98.22%	1510	NR_180483.1
			Campylobacter lari subsp. lari strain ATCC 35221	1079	1079	100%	0	98.22%	1435	NR_118523.1
			Campylobacter lari strain DSM 11375	1079	1079	100%	0	98.22%	1338	NR_117762.1
			Campylobacter lari subsp. lari strain NCTC 11352	1079	1079	100%	0	98.22%	1341	NR_115700.1
			Campylobacter lari subsp. lari strain ATCC 35221	1079	1079	100%	0	98.22%	1441	NR_043034.1
			Campylobacter coli strain ATCC 33559	1074	1074	100%	0	98.06%	1435	NR_118511.1
			Campylobacter coli strain ATCC 33559	1074	1074	100%	0	98.06%	1420	NR_117233.1
			Campylobacter coli strain DSM 4689	1074	1074	100%	0	98.06%	1342	NR_117761.1
			Campylobacter coli strain LMG 6440	1074	1074	100%	0	98.06%	1341	NR_041835.1
			Campylobacter lari subsp. lari strain CCUG 23947	1072	1072	100%	0	97.89%	1459	NR_118653.1
			Campylobacter lari strain JCM2530	1068	1068	100%	0	97.89%	1435	NR_112241.1
			Campylobacter peloridis strain 2314BVA	1062	1062	100%	0	97.73%	1497	NR_042684.1
			Campylobacter lanienae NCTC 13004	1046	1046	100%	0	97.24%	1467	NR_028698.1
			Campylobacter iguaniorum strain 1485E	1040	1040	100%	0	97.08%	1503	NR_134706.1