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Effective waterbird deterrents for floating oyster farms: implications for water quality and *Campylobacter* presence

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ABSTRACT: Floating oyster aquaculture gear offers roosting sites for waterbirds, which defecate on crops, potentially degrading water quality by introducing fecal coliforms and pathogens that pose human health risks, like pathogenic *Campylobacter* spp. (e.g. *C. jejuni, C. lari, C. coli*). We evaluated the effectiveness of bird deterrents in reducing waterbird density and examined whether bird density was associated with fecal coliform concentrations in water and oyster meat, as well as with the presence of pathogenic *Campylobacter* spp. in oyster meat. From 3 July to 13 November 2024, we conducted weekly waterbird surveys at 6 floating farms in New England (USA) to compare waterbird densities between areas of farms with and without deterrents. We concurrently sampled water (n = 212 samples), bird feces (n = 123), and oysters (n = 112). The most common waterbird species observed on farms were common tern *Sterna hirundo* (n = 2660), herring gull *Larus argentatus* (n = 1599), double-crested cormorant *Nannopterum auritum* (n = 1089), laughing gull *Leucophaeus atricilla* (n = 761), common eider *Somateria mollissima* (n = 88), and great black-backed gull *Larus marinus* (n = 59). We found that waterbird density was higher (β = 3.29, credible interval = 2.41−4.19) on farm sections without deterrents; however, density was not associated with fecal coliform levels in water or oyster meat, nor with the presence of *Campylobacter* spp. in oyster meat. Only 3 fecal samples tested positive for *Campylobacter* spp. Our research suggests that waterbird feces are not the sole cause of water quality degradation or *Campylobacter* outbreaks on oyster farms.

KEY WORDS: Water quality · Food safety · Pathogens · Shellfish aquaculture · Waterbird abundance · *Crassostrea virginica*

1. INTRODUCTION

Aquaculture for shellfish production has expanded rapidly across New England (USA) over the past 2 decades (NMFS 2024). Currently, eastern oysters *Crassostrea virginica* (hereafter, oysters) dominate production and are widely consumed as a popular seafood (Botta et al. 2020, Goetsch 2023). Floating aquaculture gear (hereafter, floating gear) has become increasingly popular among oyster farmers because it requires less labor to reduce biofouling and increases crop access to nutrients (Fitridge et al. 2012). While floating gear offers advantages, it also attracts waterbirds, which frequently use oyster farms as roosting sites (Callier et al. 2018, Caron et al. 2023). Waterbirds defecate on floating gear and are suspected sources of water contamination and pathogenic *Campylobacter* spp. (e.g. *C. jejuni, C. lari, C. coli;* hereafter, *Campylobacter*), which pose a potential risk to human health, particularly when oysters are consumed raw (Caron et al. 2023).

Water quality is routinely monitored throughout the USA to indicate when and where there are potential risks to human health (FDA 2023). For example, states conduct regular water sampling around oyster farms to assess fecal coliform concentrations, which

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are used as indicators of water quality (FDA 2023). On a broad scale, elevated fecal coliform concentrations in water bodies often result from major rain events that cause sewage overflows into coastal waters where aquaculture occurs (Leight et al. 2016, Leight & Hood 2018, McGinnis et al. 2018); however, at a local scale, waterbird feces may also contribute to water contamination (Converse et al. 2012, Safaie et al. 2021). Temporary farm closures caused by elevated fecal coliform levels impose economic burdens on farmers, when they are prevented from selling their crops (Evans et al. 2016, Leight et al. 2016). Although regulatory agencies do not distinguish between sources of fecal coliforms (e.g. human sewage versus waterbird feces) during water quality monitoring, farmers are nonetheless required to implement waterbird deterrent plans to improve water quality on oyster farms that attract birds (FDA 2023). Studies evaluating the effectiveness of deterrents have demonstrated that various techniques can reduce waterbird density (Comeau et al. 2009, Safaie et al. 2021); however, biologists have not investigated the effectiveness of waterbird deterrents in improving water quality at oyster farms and the extent to which birds using floating farms pose a risk to food safety.

Although routine water quality testing focuses on detecting fecal coliform concentrations, it does not include surveillance of other pathogens that may pose risks to human health. For example, *Campylobacter* can be present in oyster crops (Endtz et al. 1997, Whyte et al. 2004), with raw oyster consumption leading to hospitalizations (Caron et al. 2023); however, not all *Campylobacter* species are harmful to humans (Costa & Iraola 2019). When outbreaks occur, farms are temporarily closed regardless of the *Campylobacter* species present (Caron et al. 2023, FDA 2023). Routine sampling is then conducted to determine the presence or absence of *Campylobacter*, and farms are only reopened once the genus is no longer detected. While there are many sources of *Campylobacter* (Denis et al. 2011, Mughini-Gras et al. 2016, Mulder et al. 2020), bird feces are the primary source in some areas (Mughini-Gras et al. 2016, Shrestha et al. 2019, Mulder et al. 2020). To our knowledge, no study has evaluated whether spatial and temporal changes in waterbird density affect *Campylobacter* presence and fecal coliform concentrations in oyster crops.

Here, we conducted an experimental study to evaluate the effectiveness of using waterbird deterrents on floating oyster farms in Rhode Island and Massachusetts, USA, to reduce waterbird density and in turn, evaluate the influence on key water quality indices. Our primary objectives were to (1) assess the effectiveness of deterrents in reducing waterbird density, (2) examine the relationship between waterbird density and fecal coliform concentrations in water and oyster meat, and (3) investigate the impact of waterbird density on the presence of *Campylobacter* in oyster meat. We hypothesized that (1) waterbird deterrents would effectively reduce waterbird densities, (2) fecal coliform concentrations in water and oyster meat would be higher in sections without deterrents, and (3) the presence of *Campylobacter* would be higher in oyster meat in sections without deterrents.

2. MATERIALS AND METHODS

2.1. Study site

We conducted research on 3 oyster farms located in the central portion of Narragansett Bay, Rhode Island, USA, and 3 farms in Buzzards Bay, Massachusetts (i.e. one farm in each of the northwest, northeast, and southeast regions of Buzzards Bay), from 3 July to 13 November 2024. Given the locations of our study sites, all surrounding landmasses were highly urbanized. A total of 4 farms were growing oysters to market size (i.e. 5–7 cm in shell length; hereafter, grow-out sites; Rhode Island = 3 farms, Massachusetts = 1 farm) and 2 held oyster seed (i.e. 2.5–5 cm in shell length; hereafter, nursery sites; Massachusetts = 2 farms). We ensured that enough oysters were collected at each site to provide sufficient tissue mass for bacteriological analysis (see Sections 2.4 and 2.5). All farms used floating gear that offered roosting sites for birds and were known, based on previous years, to support higher abundances of roosting waterbirds than surrounding areas. During our field season, the mean number of cages with associated floats at grow-out sites was 292 (range = 50–630) and 92 (range = 85–200) at nursery sites. Water depths ranged from 3 to 14 m at grow-out sites and were 0.6 and 1.8 m at nursery sites. Distance from shoreline ranged from 20 to 400 m at grow-out sites and was 30 and 56 m at nursery sites. The exact locations and ownership of the 6 participating farms were kept confidential in exchange for their willingness to participate in this study that entailed intensive monitoring of waterbird presence and water quality at their farms. The heterogeneity in landscape context for the 6 farms, which included deeper large bays as well as shallower coastal areas, represented the typical variation in waters used for oyster farming in this region.

2.2. Waterbird deterrents

We deployed waterbird deterrents on 1 section of each farm. Because gear type, water depth, and site characteristics varied among farms, we implemented different deterrent methods tailored to each location. On grow-out sites, we extended 2 pieces of bungee cord ~10 cm above each float on the oyster cages. At 1 nursery site, we installed an elevated monofilament grid system, using PVC pipe to support the monofilament, positioned ~2.5 m above a portion of the farm. This deterrent allowed the farmer to continue working the farm by boat, as the monofilament was positioned high enough above the farm to permit access. Lastly, we placed 2 coyote decoys along the shoreline at the second nursery site to deter waterbirds from a section of the farm close to the shoreline. All deterrents were randomly placed on one edge of each farm (e.g. the outer 2 longlines). We deployed a mean of 22 deterrents (range = 10–50 cages) on cages at grow out sites and a mean of 157 deterrents (range = 85–200 cages) on cages at nursery sites. Importantly, cage design was consistent within each farm, and the only difference was the presence or absence of deterrents on otherwise identical cages.

2.3. Waterbird survey protocol

The same 2 observers conducted weekly land-based waterbird surveys at all study sites over the 20 wk study period. Within each week, we conducted 2 surveys at each farm: 1 during the high tide cycle and 1 during the low tide cycle. During each survey, the observer used a 20–60× spotting scope to census the number of each waterbird species roosting on floating gear. We did not include birds roosting on other structures or on the water in the analyses outlined below. Observers conducted each survey from the same fixed location on the shoreline and surveyors used as much time as needed to identify all birds roosting on floating gear (max. survey time = 60 min, mean survey time = 14 min). All farms were located at open-water sites, providing an unobstructed view; therefore, we assumed perfect detection of all waterbird species. For each survey, we calculated waterbird density separately for the sections of the farms that had deterrents (hereafter, with deterrent) or did not (hereafter, without deterrent). We estimated waterbird density by dividing the total waterbird count by the total cage surface area available for roosting.

2.4. Sample collection

We collected water, oyster, and bird fecal samples concurrently with weekly waterbird surveys from 8 August to 11 November 2024 for microbial analysis. In some instances, bird surveys and microbial sampling occurred simultaneously. When simultaneous sampling was not possible, we always conducted bird surveys and collected water, oyster, and bird fecal samples within the same week, and usually within 1 or 2 d of each other. While we acknowledge that this lack of alignment complicates the interpretation of microbial data in relation to bird density (as described in Section 2.6), our sampling scheme mirrors those used by regulatory agencies monitoring *Campylobacter* outbreaks potentially linked to bird density (Caron et al. 2023), and operates at a finer temporal scale than routine fecal coliform monitoring (i.e. approximately monthly). We collected 30 oysters from 3 randomly selected oyster cages (i.e. 10 oysters per cage) in sections with and without bird deterrents. The oysters from each treatment were placed in a single zip-lock bag (i.e. with-deterrent samples stored separately from without-deterrent samples) and stored on ice in a cooler. Waterbird fecal samples were obtained from the same cages where oysters were collected using sterile sponges (EZ-Reach™ SPLIT polyurethane sponge sampler, World Bioproducts) by swabbing a ~10 × 10 cm area of each cage where feces were present. Three sponges (i.e. 1 sponge used per cage) were pooled into 1 bag for analysis (i.e. with-deterrent samples stored separately from without-deterrent samples), and the bags were placed on ice in a cooler. Two ~100 ml water samples were collected from beneath the cages where oysters were harvested (i.e. 30–60 cm below the water surface), one in an area with and one without deterrents. Additionally, a control ~100 ml water sample was taken ~10 m up current of the cages, based on the tidal direction. The collected water samples were stored on ice in a cooler. Because deterrents were placed along farm edges, treatment areas (i.e. with and without deterrents areas) were often adjacent. To minimize potential carryover effects, we randomly sampled without-deterrent cages located away from with-deterrent cages.

2.5. Sample processing

The concentration of fecal coliforms was measured in oyster meat samples as most probable number per gram (MPN g^{-1}), following the United States Food

and Drug Administration Bacteriological Analytical Manual (Feng et al. 2020), and in water samples as most probable number per 100 milliliters (MPN 100 ml^{-1}), according to Standard Methods for the Examination of Water and Wastewater, Method 9223 (Standard Methods Committee of the American Public Health Association et al. 2017). For oyster processing, 30 oysters from either the with- or without-deterrent section of each farm were placed in a sanitized strainer and rinsed with 70% ethanol while being shaken. After 5 min of exposure to ethanol, oysters were shucked and the oyster meat was aseptically removed and transferred into a sterile sample bag (Whirl-Pak®, Nasco) for analysis. The isolation and detection of pathogenic *Campylobacter* species — as presence/absence in 25 g oyster samples and presence/absence per swab for bird feces sponge swabs — were performed using pre-enriched samples analyzed using the BAX® System Real-Time PCR Assay for *C. jejuni*, *C. coli*, and *C. lari*, following the validated method described in the Association of Official Analytical Collaboration Research Institute Performance Tested Method Certificate No. 040702 (AOAC Research Institute 2015). For each analysis, oysters were collected from 3 different cages and combined into a single composite sample prior to pre-enrichment, with separate composites prepared for cages with and without bird deterrents. Bird feces present on the cages from which oysters were collected were swabbed and likewise combined into a single composite sample prior to pre-enrichment. An aliquot of the enriched samples was used for qualitative determination of *Campylobacter* DNA presence. We note that this BAX assay does not differentiate between these 3 species. Microbiological analysis was performed by Eurofins Microbiology Laboratories New England (North Kingstown, RI).

To confirm the efficacy of the sampling protocol, a *Campylobacter* inoculum was added to separate oyster meat and sponge swab samples as positive controls. *Campylobacter* detection was performed following selective enrichment and is therefore interpreted as a qualitative measure of presence or absence. To verify that the sample processing and enrichment protocol supported pathogen recovery, a *Campylobacter* cocktail (*C. jejuni*, *C. lari*, and *C. coli*) was cultured and added to oyster and feces swab samples to confirm survival through processing and successful detection, thereby validating the sample handling methodology. This qualitative method measures whether detectable DNA from the target pathogenic *Campylobacter* species is present in the enriched sample; it does not quantify bacterial load or counts.

2.6. Analytical methods

We used Bayesian generalized linear mixed models to analyze our waterbird survey, fecal coliform concentration, and *Campylobacter* data sets. We fit models using the 'brms' package (Bürkner 2017) in program R version 4.4.1 (R Core Team 2025). We fit our waterbird density model using the hurdle lognormal response distribution and the logit link function to estimate the probabilities of obtaining a value of zero (e.g. probability that waterbird density is zero; hereafter, hurdle probability). In addition, we used the 'identity link' function to estimate the regression coefficients for fixed effects (Bürkner 2017). We fit our waterbird density model as:

$$\begin{aligned}\text{identity}(x_i) = \alpha + \beta1 \times \text{date}_i + \beta2 \times \text{date}^2{}_i + \\ \beta3 \times \text{treatment}_i + \beta4 \times \text{shoreline distance}_i + \\ \beta5 \times \text{tide}_i + \text{site identity} + \text{survey identity}\end{aligned} \quad (1)$$

where x_i is the predicted waterbird density for survey i given the corresponding fixed and random effects. α is the intercept and each β represents the regression coefficient of each fixed effect. All fixed effects included in this model were selected based on their biological relevance for predicting bird abundance. Date (i.e. day of year) and its quadratic term (i.e. $date^2$) were included to detect temporal trends or peaks in waterbird density across the field season (King et al. 2012, Becker et al. 2016, Anderson et al. 2019). We included treatment as a categorical variable that indicated whether the survey observations were from with- or without-deterrent sections of each farm. We included distance to shoreline (i.e. shoreline distance) in the model as a continuous variable because some waterbird species may select for resources located closer to the shoreline (Henry & Cumming 2017). We included tide cycle (i.e. high versus low) as a categorical variable in the model as the foraging patterns of many waterbirds are driven by tide cycles (Urmy & Warren 2018, Boardman & Ruesink 2023, Gutowsky et al. 2023). Site and survey identities (hereafter, ID) were included as random effects to account for spatial and temporal variation that was unexplained by fixed effects.

We also fit 2 models for fecal coliform concentrations in water using the hurdle lognormal response distribution and the identity link function to estimate regression coefficients for fixed effects. The first model included waterbird density as a fixed effect and included only water samples collected from the with- and without-deterrent areas because we did not count waterbirds in the control areas. The second model excluded waterbird density as a fixed effect

and retained water samples from all 3 sampling areas (i.e. control, with-deterrent, without-deterrent areas). These models were specified as follows:

$$\text{identity}(y^1{}_i) = \alpha + \beta1 \times \text{date}_i + \beta2 \times \text{date}^2{}_i + \beta3 \times \text{treatment}_i + \beta4 \times \text{shoreline distance}_i + \beta5 \times \text{water depth}_i + \beta6 \times \text{precipitation}_i + \beta7 \times \text{water temperature}_i + \beta8 \times \text{waterbird density}_i + \text{site ID} + \text{survey ID} \quad (2)$$

$$\text{identity}(y^2{}_i) = \alpha + \beta1 \times \text{date}_i + \beta2 \times \text{date}^2{}_i + \beta3 \times \text{treatment}_i + \beta4 \times \text{shoreline distance}_i + \beta5 \times \text{water depth}_i + \beta6 \times \text{precipitation}_i + \beta7 \times \text{water temperature}_i + \text{site ID} + \text{survey ID} \quad (3)$$

where $y^1{}_i$ and $y^2{}_i$ are the predicted fecal coliform concentrations in water sample *i* given the corresponding fixed and random effects: $y^1{}_i$ retained waterbird density as a fixed effect and $y^2{}_i$ did not. Date and its quadratic term were included to detect temporal trends or seasonal peaks in fecal coliform concentrations (Carstens & Amer 2019, Zhang et al. 2020, 2021). Treatment was included in the model, as we predicted fecal coliform concentrations would be reduced on the sections of farms with deterrents. Shoreline distance was considered because shorelines are often linked to increased urbanization, which is expected to result in higher fecal coliform concentrations of farms located closer to these areas (Zhang et al. 2020, Orr et al. 2023). Water depth was included given that deeper areas are typically associated with greater flow, while shallower areas tend to have reduced flow and increased resuspension rates; thus, higher fecal coliform concentrations were anticipated in shallower, low-flow waters (Portnoy & Allen 2006). We included mean weekly precipitation (i.e. mean daily precipitation within a week; hereafter, precipitation) in the model, as major rain events elevate fecal coliform concentrations due to sewage overflow (Zimmer-Faust et al. 2018, Zhang et al. 2020). We collected precipitation data from the National Oceanic and Atmospheric Administration that were specific to the town in which each study site was located. Water temperature was incorporated, as cooler water conditions are known to promote fecal coliform growth (Chigbu et al. 2004). Finally, site and survey IDs were included as random effects to account for spatial and temporal variation not explained by the fixed effects. We also used the first linear predictor (i.e. identity($y^1{}_i$)) to model fecal coliform concentrations in oyster meat.

Because state and federal agencies use fecal coliform concentrations in water to assess water quality (FDA 2023), we fit simple linear models to evaluate whether fecal coliforms in seawater (i.e. predictor variable) were associated with fecal coliforms in oyster meat (i.e. response variable). To investigate site-level relationships, we fit a separate model for each study site. We considered linear relationships with $p < 0.05$ to be statistically significant and assessed model fit using R^2 values, with values >0.7 indicating strong correlations and values <0.4 indicating weak correlations. We log transformed both the response and predictor variables prior to fitting models.

We fit 2 models investigating the probability of *Campylobacter* being detected in fecal and oyster meat samples using a Bernoulli distribution with a logit link function to estimate regression coefficients for fixed effects:

$$\text{logit}(z_i) = \alpha + \beta1 \times \text{date}_i + \beta2 \times \text{date}^2{}_i + \beta3 \times \text{treatment}_i + \beta4 \times \text{shoreline distance}_i + \beta5 \times \text{water depth}_i + \beta6 \times \text{precipitation}_i + \beta7 \times \text{water temperature}_i + \beta8 \times \text{waterbird density}_i + \text{site ID} + \text{survey ID} \quad (4)$$

where z_i is the probability that *Campylobacter* would be present in sample *i*, given the fixed and random effects. We used the same fixed and random effects in our *Campylobacter* models as in the fecal coliform concentration models, because our predictions were largely the same. We fit waterbird density, fecal coliform, and *Campylobacter* models by running 3 Markov chain Monte Carlo (MCMC) chains of 5000 iterations, discarding 2000 iterations during the warm-up period, and saved each iteration. We ensured MCMC chains converged by examining trace plots and by using the Gelman-Rubin statistic ($\hat{R} < 1.05$; Gelman & Rubin 1992). For each global model, we fit a null model including only random effects. We compared models using the 'loo' package to calculate expected log pointwise predictive density values (hereafter, ELDP; Vehtari et al. 2017, 2024). The interpretation of ELPD differences is analogous to that of the widely applicable information criterion (WAIC; Watanabe 2010) values, where lower values indicate better model fit. Additionally, when the standard error of the ELPD difference overlaps zero, there is no meaningful difference in model fit (Bürkner 2017). We report 95% credible intervals (hereafter, CRI; i.e. alpha level = 0.05) and posterior means for regression coefficients (hereafter, β), for Bayesian generalized linear mixed models.

3. RESULTS

We completed a total of 164 land-based waterbird surveys and documented 24 different species at aqua-

culture farms from 3 July to 13 November 2024. All species observed perching on floating gear belonged to the tern, gull, cormorant, and waterfowl guilds. More specifically, the primary species we encountered roosting on floating oyster farms across our entire survey period were common tern *Sterna hirundo* (n = 2660 total individuals), herring gull *Larus argentatus* (n = 1599), double-crested cormorant *Nannopterum auritum* (n = 1089), laughing gull *Leucophaeus atricilla* (n = 761), common eider *Somateria mollissima* (n = 88), and great black-backed gull *Larus marinus* (n = 59). Species abundance varied across study sites both spatially and temporally (Fig. 1). Some sites consistently supported higher waterbird abundance, while others remained low, and temporal fluctuations in abundance were evident at most sites throughout the field season. Few waterbirds were observed on farm sections equipped with deterrents (Fig. 2).

Our global waterbird density model outcompeted the null model (ELPD = −25.9, SE = 8.3; Table 1). The hurdle probability (i.e. probability waterbird density is zero) was 0.46 (CRI = 0.41, 0.53), indicating that waterbirds were present at farms during approximately half of the surveys. The absence of deterrents had a positive effect (β = 3.29, CRI = 2.41, 4.19) on waterbird density, resulting in higher waterbird density on oyster cages without deterrents (μ = 0.02, CRI = 0.01, 0.06; Fig. 3). Low tide had a weak negative effect (β = −0.42, CRI = −0.76, −0.08) on waterbird density; waterbird density was lower during low tide cycles. All other fixed effects had insignificant effects on waterbird density.

We collected a total of 212 water and 112 oyster meat samples from 6 August to 13 November 2024. Water samples included 76 up-current control samples (i.e. outside the farm), 74 without-deterrent samples, and 62 with-deterrent samples. Oyster samples included 68 without-deterrent samples, and 44 with-deterrent samples. Mean fecal coliform concentrations in the water were 13.8 MPN 100 ml^{-1} (median = 0.0 MPN 100 ml^{-1}), with a maximum observed value of 1732.9 MPN 100 ml^{-1}. Mean fecal coliform concentrations in the oyster meat were 46.9 MPN g^{-1} (median = 0.0 MPN g^{-1}) and exceeded >1100 MPN g^{-1} on 3 occasions at only 1 of 6 farms (Figs. 1 & 2).

Both models used to predict fecal coliform concentrations in water did not outperform the null model, as indicated by overlapping ELPD standard errors (model with up-current control: ELPD = −0.9, SE = 2.6; model without up-current control: ELPD = −2.4, SE = 5.5; Table 1). The model used to predict fecal coliform concentrations in oyster meat also failed to outcompete the null model (ELPD = −3.7, SE = 5.9). Therefore, our model fixed effects failed to explain the observed variation in fecal coliform concentrations in water and oyster meat.

A total of 110 paired samples of fecal coliform concentrations were collected from both water and oyster meat samples (without deterrent = 66, with deterrent = 44). To assess the relationship between these 2 metrics, we fit linear models separately for each of the 6 study sites (Fig. 4). We found fecal coliform concentrations in the water had significant positive effects (MA Nursery Site B, p = 0.0338; MA Grow-Out Site A, $p < 0.001$) on fecal coliform concentrations in oyster meats at 2 farms; however, the correlation was weak at one farm (R^2 = 0.27; Fig. 4, MA Nursery Site B) and strong at another (R^2 = 0.93; Fig. 4, MA Grow-Out Site A).

We collected a total of 123 waterbird fecal samples in addition to oyster meat samples (n = 112) to test for the presence of *Campylobacter*. A total of 3 fecal samples tested positive for *Campylobacter* (Figs. 1 & 2); however, none of the oyster meat samples tested positive. Given the limited number of positive fecal samples, we did not attempt to fit *Campylobacter* models (Table 1). All 3 positive detections of *Campylobacter* in fecal samples occurred in October at different farms and all were on sections without deterrents (Figs. 1 & 2). Only 1 study site (i.e. RI Grow-Out Site A) had higher waterbird abundance, relative to other observations at that same site, prior to the time of the positive detection (Fig. 1). Additionally, fecal coliform concentrations in water were below action levels around the time of detections (range 0–6.3 MPN 100 ml^{-1}).

4. DISCUSSION

In this study, we found that waterbird density in eastern oyster floating gear farms was reduced by various deterrent techniques, supporting our initial hypothesis that waterbird density would be lower in sections of farms equipped with deterrents. However, we found weak evidence that fecal coliform concentrations and the presence of pathogenic *Campylobacter* species would be higher in sections with higher waterbird density. For our fecal coliform concentration models, none of the fixed effects, including waterbird density, were significant predictors of fecal coliform concentrations in water or oyster meat. We were unable to fit *Campylobacter* models because *Campylobacter* was never detected in the 112 oyster samples and was detected in only 3 (out of 123 samples) water-

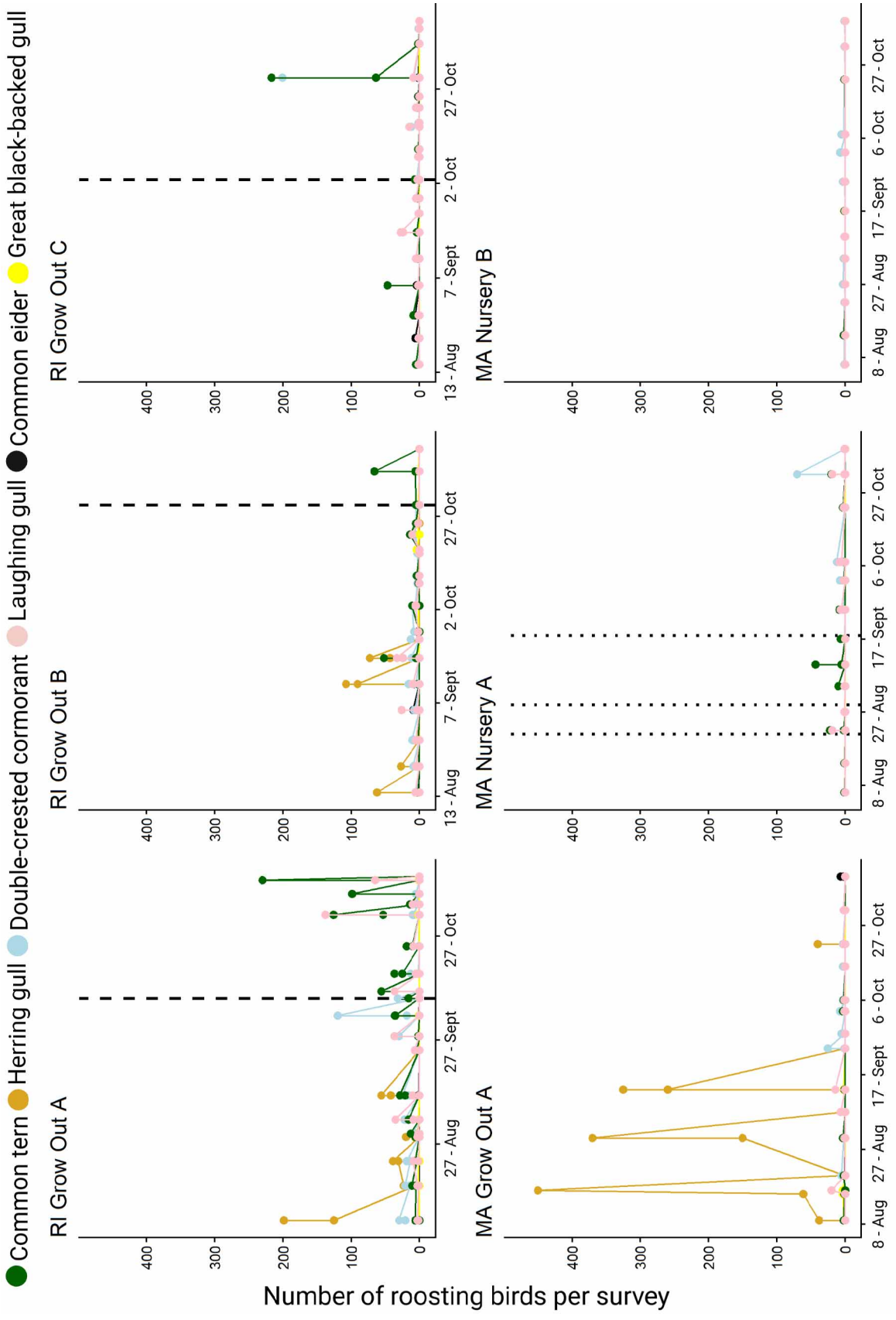

Fig. 1. Abundance of 6 waterbird species commonly observed roosting on floating gear oyster farms in Rhode Island and Massachusetts from 3 July to 13 November 2024. Vertical black dashed lines indicate the dates when waterbird fecal samples collected from the surface of oyster cages tested positive for pathogenic *Campylobacter* spp. Black dotted lines show dates when fecal coliform concentrations in oyster meat exceeded 1100 minimal probably number (MPN) g^{-1}. Plot labels indicate the state (RI: Rhode Island; MA: Massachusetts) in which each farm was located and the type of farm (grow-out versus nursery)

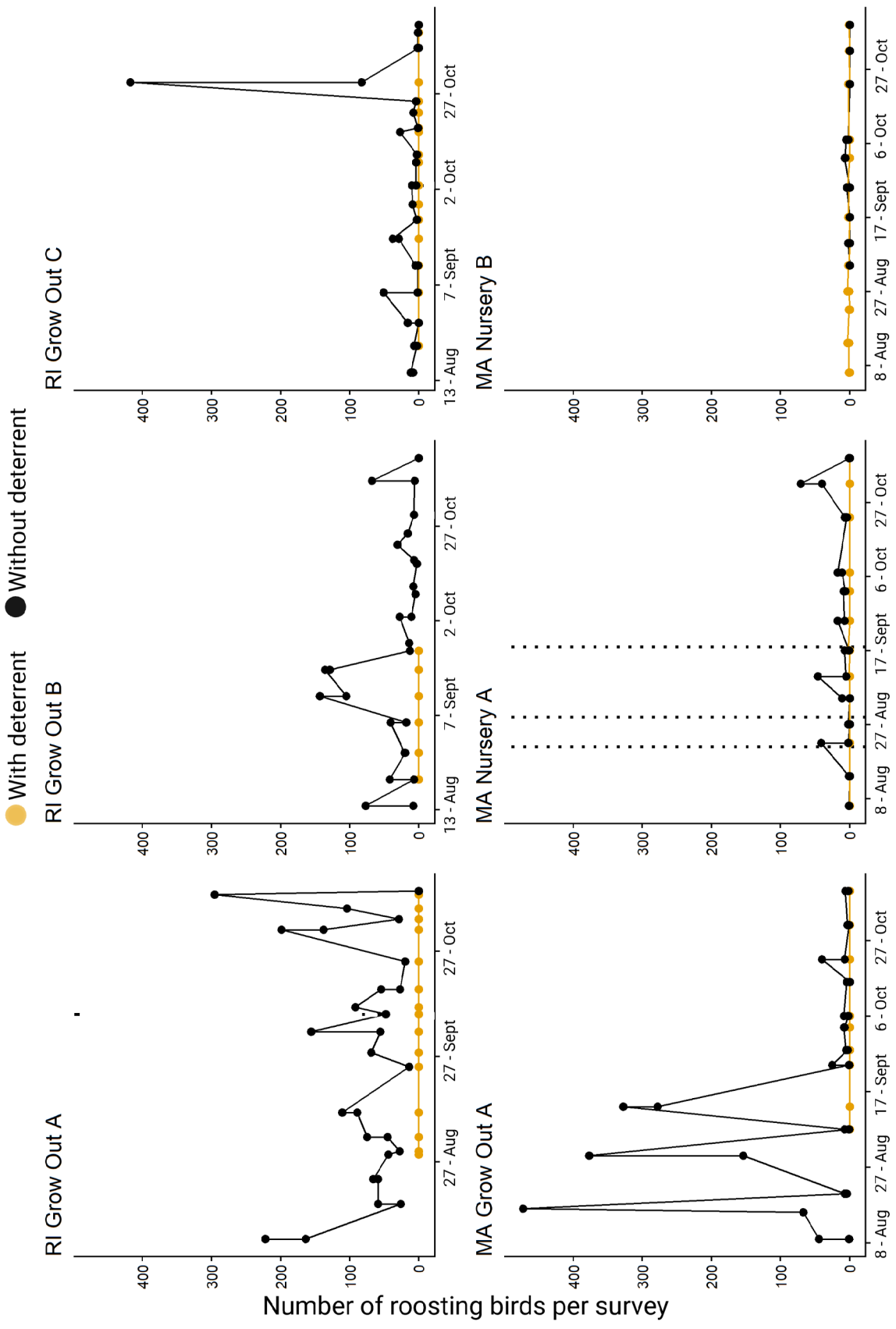

Fig. 2. Abundance of all waterbird species observed roosting on floating gear oyster farms in Rhode Island and Massachusetts from 3 July to 13 November 2024. Black dots indicate the number of birds roosting on cages without bird deterrents, while gold dots indicate the number of waterbirds roosting on cages equipped with bird deterrents. Other details as in Fig. 1

Table 1. Models used to explore the relationships between bird density, fecal coliform concentrations, and *Campylobacter* presence (i.e. response variables) and covariates

Models for	Response variable	Effects: Fixed	Effects: Random
Bird density	Bird density	Date + Date^2 + Treatment + Shoreline distance + Tide	Site ID + Survey ID
	Bird density	NULL	Site ID + Survey ID
Water	Fecal coliforms	Date + Date^2 + Treatment + Shoreline distance + Water depth + Precipitation + Water Temperature + Waterbird density	Site ID + Survey ID
	Fecal coliforms	Date + Date^2 + Treatment + Shoreline distance + Water depth + Precipitation + Water Temperature	Site ID + Survey ID
	Fecal coliforms	NULL	Site ID + Survey ID
Oyster	Fecal coliforms	Date + Date^2 + Treatment + Shoreline distance + Water depth + Precipitation + Water Temperature + Waterbird density	Site ID + Survey ID
	Fecal coliforms	NULL	Site ID + Survey ID
	Campylobacter	Date + Date^2 + Treatment + Shoreline distance + Water depth + Precipitation + Water Temperature + Waterbird density	Site ID+ Survey ID
	Campylobacter	NULL	Site ID + Survey ID
Bird feces models	*Campylobacter*	Date + Date^2 + Treatment + Shoreline distance + Water depth + Precipitation + Water Temperature + Waterbird density	Site ID + Survey ID
	Campylobacter	NULL	Site ID + Survey ID

bird fecal samples. We detected a relationship between fecal coliform concentration in water and oyster meat at only 2 of the 6 farms, and no relationship with *Campylobacter* presence.

Waterbird species diversity on floating oyster gear was relatively low across most study sites. However, we suspect that waterbird diversity is higher beyond our temporal sampling frame, as previous research has shown that waterbird diversity increases throughout our study areas during the winter months (Bakner et al. 2025). The most common roosting species included cormorants, herring gulls, and common terns (Fig. 1) as documented in other studies (Comeau et al. 2009, Caron et al. 2023). Cormorant abundance remained relatively low throughout the field season (i.e. July to November), whereas herring gull abundance peaked in late summer, and common tern abundance peaked later in the fall (Fig. 1). These same birds have been implicated in affecting water quality in a variety of other contexts. For example, multiple studies have identified gulls *Larus* spp. as being localized sources of water pollution (Converse et al. 2012, Nevers et al. 2018, Safaie et al. 2021) and associated with temporary beach (i.e. freshwater lake) closures resulting from high fecal coliform detection (Edge & Hill 2007, Safaie et al. 2021). Other studies have shown that water quality, as indicated by *E. coli* concentrations, improves following the use of methods to reduce local gull abundance (Converse et al. 2012, Goodwin et al.

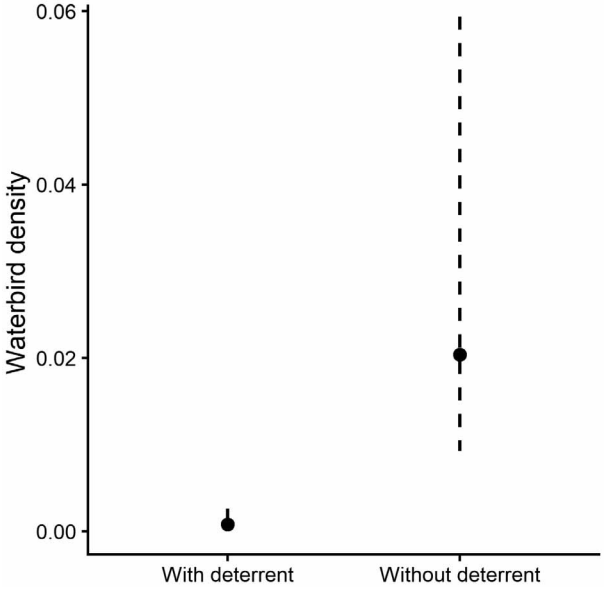

Fig. 3. Model predictions showing the density of waterbirds (birds per cage surface area) on sections of floating oyster farms with and without deterrents in Rhode Island and Massachusetts, based on data collected from 3 July to 13 November 2024. Points represent posterior means from a Bayesian generalized linear mixed model, and dashed lines indicate 95% credible intervals

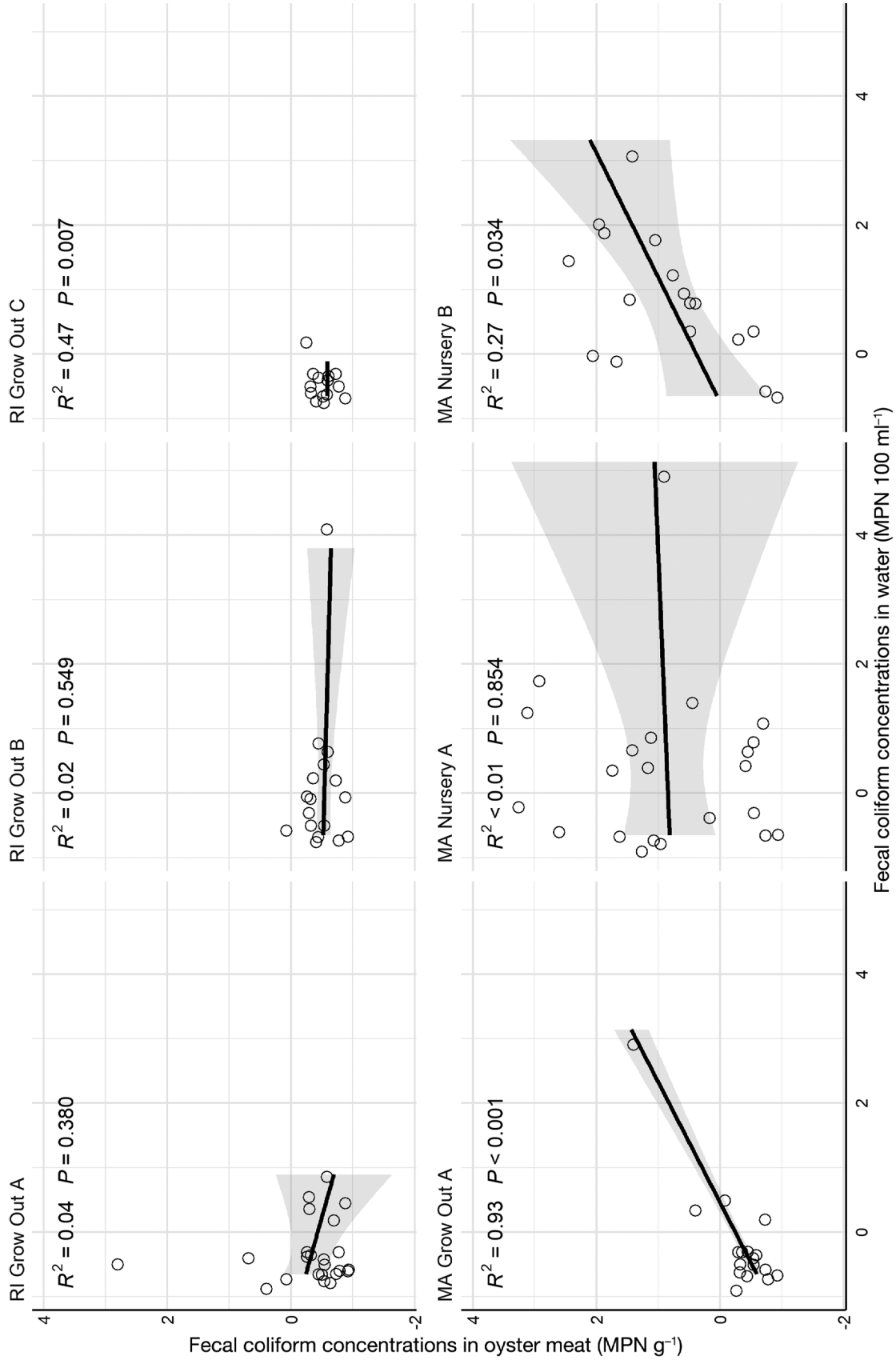

Fig. 4. Linear model predictions showing the relationships between fecal coliform concentrations in water and oyster meat at 6 floating oyster farms in Rhode Island and Massachusetts, based on data collected from 3 July to 13 November 2024. Black lines represent model predictions, gray shaded areas indicate 95% confidence intervals, and points represent raw data. Plot labels indicate the state (RI: Rhode Island; MA: Massachusetts) in which each farm was located and the type of farm (grow-out versus nursery). All axes are on the log-transformed scale

2016). While less is known about the effects of cormorant and common tern abundance on water quality, our results suggest these species did not have a notable impact on water quality in coastal oyster farms.

Fecal coliform concentrations in our study were relatively low throughout the sampling period. While routinely monitoring water quality, state and federal agencies initiate temporary farm closures when ≥10% of 30 water samples exceed 14 MPN 100 ml^{-1} (FDA 2023). In our study, we collected 3 water samples weekly (i.e. 1 each from the control, with-deterrent, and without-deterrent areas) at each farm and recorded only 12 instances throughout the whole study period (i.e. July–November) where fecal coliform concentrations exceeded this threshold. Of these, 10 samples came from a single nursery site in Massachusetts where oysters were not being grown for human consumption; the remaining 2 samples were from grow-out sites. The Massachusetts nursery site with elevated fecal coliform concentrations is a shallow site with limited tidal flushing, facilitating the accumulation of fecal coliforms. Additionally, the site is located near a heavily urbanized shoreline, which may have contributed additional sources of fecal contamination. Thus, while our results showed no relationship between waterbird density and fecal coliform concentrations, we also did not routinely detect elevated fecal coliform concentrations during our study period. The latter may be partially explained by infrequent precipitation events during our sampling period, as rainfall is often strongly correlated with increased fecal coliform concentrations due to stormwater runoff and overflow from human sewage (McGinnis et al. 2018, Zimmer-Faust et al. 2018, Zhang et al. 2020).

The presence of pathogenic *Campylobacter* species (e.g. *C. jejuni, C. lari, C. coli*) was detected in only 3 of 123 waterbird fecal samples and was not detected in any of the 112 oyster meat samples. Detection was performed using a qualitative PCR-based assay following selective enrichment to reliably detect *Campylobacter* DNA when present. In previous research in Rhode Island, high densities of cormorants and gulls were observed at one farm around the time of a *Campylobacter* outbreak in an oyster crop, and these species were suspected as being the source of contamination (Caron et al. 2023). In our study, a single positive detection of pathogenic *Campylobacter* species in feces occurred around the same time that cormorant abundance was >100 individuals at one farm with ~400 cages. Regarding study site differences in Rhode Island, the *Campylobacter* outbreak described by Caron et al. (2023) occurred in a shallow coastal lagoon with low flushing rates, whereas our Rhode Island study sites were located in deeper areas with higher flow and flushing rates. From our study and that of Caron et al. (2023), it remains unclear whether bird feces deposited into the water are the sole source of *Campylobacter* in oyster crops. Previous research suggests that *Campylobacter* survives better in cooler water temperatures, as these conditions promote entry into a nonculturable state in which metabolic activity is substantially reduced (Lázaro et al. 1999, González & Hänninen 2012, Bronowski et al. 2014). Interestingly, the only *Campylobacter* outbreak in oyster crops in Rhode Island to date occurred in September 2021, a period when water temperatures are warmer and survival is expected to be lowest (Caron et al. 2023). Notably, this timeframe coincides with peak oyster demand and the busy season for restaurants, when the risk of *Campylobacter* exposure from other sources, such as undercooked chicken consumption or cross-contamination in restaurant settings, may also be elevated. It is possible that *Campylobacter* contamination in oysters is more common than currently recognized but is only detected during months when oysters are more frequently harvested and consumed raw; hence, future studies should expand sampling beyond the temporal scope of our study and include additional sample collections to better capture the potential presence of *Campylobacter* in water and oyster meats throughout the year. To better understand the potential for *Campylobacter* to move from bird feces into oyster crops, we recommend including measurements of other environmental parameters (e.g. UV irradiation, rainfall, salinity, dissolved oxygen, height of the floats, and hydrodynamic conditions at the sites) in future field studies and conducting controlled mesocosm experiments across a range of water temperatures, flow rates, and *Campylobacter* concentrations. Furthermore, understanding indirect pathways, such as the potential movement of *Campylobacter* from sediments into oyster crops, would be best studied under controlled conditions. These experiments would help determine whether, and under what conditions, the pathogen is taken up into oyster tissue.

In this study, we demonstrated that bird deterrents can successfully reduce bird density on floating oyster farms. By reducing bird density, we expected improvements in water quality and a lower likelihood of disease occurrence due to the presence of fecal indicators in waterbird feces being reduced. However, our analyses indicated that bird density was not directly related to water quality (i.e. as determined by fecal

coliform levels) or the presence of pathogenic *Campylobacter* species. One limitation of our study was its temporal scale (i.e. weekly sampling). We selected a weekly scale because it offers finer resolution than the sampling schedule typically used by water quality regulators (i.e. approximately monthly). Future research could use the methods we outline here to replicate this study at an even finer temporal scale (e.g. daily) to determine whether higher-resolution data yield different insights. This implies that human health risks may remain unchanged until future studies identify clear relationships between pathogen sources and disease outbreaks; insights that would allow managers and oyster growers to better mitigate health risks.

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