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Changes in mercury exposure of marine birds breeding in the Gulf of Maine, 2008–2013

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ABSTRACT

Mercury is a potent contaminant that can disrupt an organism's behavior and physiology, ultimately affecting reproductive success. Over the last 100 years, environmental deposition of anthropogenic sourced mercury has increased globally, particularly in the U.S. Northeast region. Marine birds are considered effective bioindicators of ecosystem health, including persistent marine contaminants. Goodale et al. (2008) found that mercury exposure exceeded adverse effects levels in some marine bird species breeding across the Gulf of Maine. We re-examined mercury contamination in four species identified as effective bioindicators. Compared with the previous sampling effort, inshore-feeding species showed significant increases in mercury exposure, while one pelagic-feeding species remained stable. This suggests that a major shift may have occurred in methylmercury availability in inshore waters of the Gulf of Maine. Understanding environmental mercury trends in the Gulf of Maine, and its significance to marine birds and other taxa will require a dedicated, standardized, long-term monitoring scheme.

1. Introduction

Mercury is a potent environmental contaminant and an issue of great concern globally (UNEP, 2013). In the form of methylmercury, it accumulates in wildlife species and has serious neurological impacts that can disrupt an organism's behavior and physiology (Hawley et al., 2009; Moore et al., 2014; Kobiela et al., 2015), ultimately affecting reproductive success (Evers et al., 2008a; Jackson et al., 2011; Provencher et al., 2016). Globally, anthropogenic-sourced mercury increased enormously over the industrial period of the last 100 years or so (Schuster et al., 2002). Although there has been a downturn in atmospheric emissions in the last 20 years (Zhang et al., 2016), mercury deposition is still particularly pervasive in certain regions, such as the Arctic (Kirk et al., 2012), and the northeastern United States (Evers and Clair, 2005; Evers et al., 2007).

Oceans are particularly at risk to mercury contamination, due to the methylating actions of sulfate-reducing bacteria that thrive in marine surface waters (Fitzgerald et al., 2007), and the concentration of mercury in surface marine waters may have increased by two to three times (UNEP, 2013; Lamborg et al., 2014) over the last 100 years due to anthropogenic emissions. Once available in the ecosystem, methylmercury increases at each trophic level (known as biomagnification; Lavoie et al., 2013) and can become concentrated within individuals over time (known as bioaccumulation). Marine ecosystems are particularly sensitive to the effects of biomagnification and bioaccumulation as they are often highly structured systems with multiple trophic levels that increase methylmercury levels, particularly for the many long-lived, top predators (UNEP, 2002).

Because they are widespread, visible, relatively easily-accessible, well-studied, and represent a range of trophic levels, marine birds are considered useful and effective bioindicators of marine ecosystem health worldwide (Furness and Camphuysen, 1997; Burger and Gochfeld, 2004), including persistent marine contaminants such as mercury (Monteiro and Furness, 1995; Mallory and Braune, 2012; Provencher et al., 2014). The Gulf of Maine Seabird Contaminant Assessment Network (GOMSCAN) examined mercury contamination in a broad suite of seabird species ($n = 17$) breeding at islands across the Gulf of Maine ($n = 35$), and presented baseline data for the region for 2001–2006 (Goodale et al., 2008). The GOMSCAN data indicated that mercury exposure clearly exceeded adverse effects levels in individuals of some seabird species. Goodale et al. (2008) also made recommendations on future sampling methods, including (1) identification of effective bioindicator species to sample across multiple food webs, (2) determination of suitable sample sizes to detect change, and (3) an appropriate monitoring timeline to assess long-term temporal trends.

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Based on these recommendations, we examined the trend in mercury contamination at a range of trophic levels through the collection and analysis of marine bird egg and blood tissues from across the Gulf of Maine. Two species provide information on the inshore, benthic community – the Common Eider (*Somateria mollissima*), which forages coastally on largely sessile organisms, such as mollusks (Goudie et al., 2000), and the Black Guillemot (*Cepphus grylle*), which forages on small demersal fishes, such as rock eels (Butler and Buckley, 2002). Two species reflect the trophic extremes of the offshore marine community – the Leach's Storm-Petrel (*Oceanodroma leucorhoa*), which forages far offshore on surface plankton (Huntington et al., 1996), and the Double-crested Cormorant (*Phalacrocorax auritus*), which forages more inshore on large mid-water pelagic fishes that they catch at depth (Hatch and Weseloh, 1999). Specifically, we used data from this study (2013), and data for the same four focal species from the previous study (Goodale et al., 2008) to establish the first indication of the general trends in their mercury exposure, and examine what that may mean for the broader marine community in the Gulf of Maine.

2. Study area and methods

2.1. Study area

The Gulf of Maine is an international water body, terrestrially bounded and shared by three US states (Maine, New Hampshire, Massachusetts) and two Canadian provinces (New Brunswick, Nova Scotia). It is one of the most productive marine ecosystems in the world, with a rich blend of ecological, economic, recreational, and environmental resources (Sherman and Skjoldal, 2002). Marine birds nest on hundreds of islands in the Gulf of Maine, only a handful of which are managed specifically for these species (MDIFW, 1993).

2.2. Sample collection

We collected egg or blood samples from four focal avian species from 8 island colonies spaced geographically across the Gulf of Maine (Fig. 1). In May–June of 2013, we collected 122 samples. Eggs were collected from nests of the Common Eider ($n = 32$) and Double-crested Cormorant ($n = 36$). Each egg was placed in a sealable polyethylene bag, and labeled on site. Blood samples were collected from adult Leach's Storm-Petrels ($n = 31$) and Black Guillemots ($n = 23$). Leach's Storm-Petrels were captured in a mist net as they visited their colony at night, while Black Guillemots were 'grubbed' from their nests in rock crevices. Blood sampling involved the puncture of the brachial vein of birds with a fine needle and collection of blood in 1–3 capillary tubes ($< 1.0\,cm^3$). The ends of each capillary tube were sealed with critocaps, and tubes were placed in labeled vacutainers for storage and transportation. Egg and blood samples were initially kept chilled, then frozen as soon after collection as possible, usually within 24–48 h, and stored at the Biodiversity Research Institute (BRI).

2.3. Mercury determination

All samples were later analyzed for total mercury concentrations at BRIs Wildlife Toxicology Laboratory, using a Direct Mercury Analyzer (DMA-80, Milestone Inc., Shelton, CT), and following EPA method 7473 (United States Environmental Protection Agency, 2007). During processing, we collected egg morphometrics (length, breadth, total egg weight, egg content weight, and volume), determined embryo development stage, and placed the contents in clean, labeled jars, before freeze-drying them. Eggs were homogenized prior to analysis, and egg mercury was measured as dry weight and converted to wet weight through percent moisture that we measured, using:

$$wet\ weight = (dry\ weight \times (100 - \%moisture))/100$$

2.4. Statistical analysis

To quantify the differences in mercury exposure among the four study species over space and time we constructed a general linear mixed model. This model used mercury levels as a response variable (log-transformed) then tissue type, species, study year, and site. Our mercury data were right-skewed and the log-transformation was successful in normalizing the distributions and made the liner mixed model framework appropriate. For 'tissue type', we only used samples of adult blood or eggs. Juvenile blood was collected for 28 individuals in the previous study, but, given the low mercury levels of the tissue and the inconsistent sampling across species, sites, and time periods, we removed these data from the analysis. 'Species' was a categorical variable consisting of the four study species. 'Study year' was a categorical variable assigning data from Goodale et al. (2008) as '2008' and data from the current study as '2013'. And 'site' was a random variable consisting of the 22 sites which represents undocumented differences between each of the breeding colonies, like spatial autocorrelation or unmeasured environmental covariates. Lastly, we included an interaction between species and study year to determine the trend in mercury levels over time by species. Tukey comparisons of least squared means were used to determine if there are any differences in groups within a categorical variable in a post-hoc test. Model fit was evaluated using an ANOVA comparison with the null model, r^2, and a visual assessment of the residuals. All statistical analyses were performed using JMP v.9.03 (SAS Institute Inc., Cary, NC).

3. Results

The fit of the general linear mixed model was good with an overall r^2 of 0.63 and visual checking of the residuals indicated a random spread that was uncorrelated with the fitted response. The variance associated with the random variable of colony site made up 31% of the total variation of the model, suggesting that there are many factors related to site that affect mercury levels that we did not explicitly test within the linear model, like spatial variance in mercury exposure.

In our general linear mixed model, we tested for the effect of tissue type, species, and year as fixed effects with the effect of year nested within species. We found that mercury concentrations in eggs were significantly higher than concentrations in adult blood across all species ($F_{1,242} = 9.17$, $p = .003$; Table 1). While not included in the model, a simple comparison of means between egg, adult blood, and juvenile blood indicates that juvenile blood has significantly lower Hg concentrations than the other two tissue types (ANOVA $F_{1,112} = 49.8$, $p < .001$; Table 2).

After we controlled for tissue type, total mercury concentrations were shown to vary considerably among species ($F_{3,31.8} = 13.5$, $p < .0001$), year ($F_{1,77.3} = 90.2$, $p < .0001$), and interaction of species and year ($F_{3,112.6} = 22.7$, $p < .0001$). Based on a Tukey test of least squared means for a post-hoc comparison, three of the four species showed significant increases in tissue mercury concentrations in 2013 when compared to 2008 (Fig. 2). All mercury concentrations presented in this section are predicted blood mercury (ww, μg/g) from the linear model (see Fig. 2). Common Eiders averaged 0.33 μg/g (95% Confidence Interval: 0.20, 0.53) in 2013 and 0.08 (0.05, 0.13) in 2008 (log-difference = 1.5 ± 0.26 μg/g, $p < .001$). Double-crested Cormorants were higher overall than eiders and averaged 0.84 μg/g (0.53, 1.35) in 2013 and 0.16 (0.10, 0.24) in 2008 (log-difference = 1.7 ± 0.13 μg/g, $p < .001$). Black Guillemots had a similar pattern to cormorants with an average of 0.65 μg/g (0.44, 0.97) in 2013 and 0.22 (0.13, 0.37) in 2008 (log-difference = 1.1 ± 0.30 μg/g Hg, $p = .01$). Only Leach's Storm Petrel showed no statistical difference between sampling occasions, 0.45 μg/g (0.30, 0.67) in 2013 and 0.47 (0.32, 0.69) in 2008. Their mean mercury concentration was the highest of all four focal species in 2008, and, despite remaining stable, was second to lowest in 2013, being surpassed by the Double-crested Cormorant and Black