Mercury Levels in Freshwater Fish: Estimating Concentration with Fish Length to Determine Exposures Through Fish Consumption

Callum Hoyt Backstrom¹ · Kate Buckman¹ · Emily Molden² · Celia Y. Chen¹

Received: 13 June 2019 / Accepted: 23 January 2020 / Published online: 11 February 2020 © Springer Science+Business Media, LLC, part of Springer Nature 2020

Abstract

Methylmercury (MeHg) is a neurotoxic pollutant that bioaccumulates and biomagnifies in aquatic food webs, impacting the health of piscivorous wildlife and human consumers of predatory fish. While fish mercury levels have been correlated with various biotic and abiotic factors, many studies only measure adults to characterize the health of locally fished populations, omitting information about how local fish bioaccumulate mercury relative to their growth. In this study, we sought to establish length: total mercury (THg) concentration relationships in juvenile and adult fish of four genera (sunfish, yellow perch, white perch, and killifish) across six freshwater pond systems of Nantucket Island to determine safe consumption sizes across species and environmental conditions. A wide length range (2-21 cm) was utilized to develop linear regression models of ln-THg versus fish length. In most cases, different genera within the same pond indicated similar slopes, supporting that all four genera share comparable features of feeding and growth. Comparing individual species across ponds, differences in ln-THg versus fish length were attributable to known environmental Hg-modulators including surface water MeHg levels, pH, and watershed area. Referencing human health and wildlife criteria, our results confirm that numerous Nantucket freshwater ecosystems contain elevated fish THg levels, which could impact the health of not only piscivorous wildlife in all measured ponds but also recreational fishers in at least two measured systems. Future studies should measure THg levels across juvenile and adult fish to detect potential differences in the slope of THg concentration across fish length relevant for local consumption advice.

Methylmercury (MeHg) is a neurotoxic pollutant that bioaccumulates and biomagnifies in food webs throughout freshwater ecosystems. In North America, elemental mercury (Hg (0)) is emitted to the atmosphere primarily through the

Electronic supplementary material The online version of this article (https://doi.org/10.1007/s00244-020-00717-y) contains supplementary material, which is available to authorized users.

Callum Hoyt Backstrom chb@backstromlaw.com

> Kate Buckman Kate.L.Buckman@dartmouth.edu

Emily Molden emily@nantucketlandcouncil.org

Celia Y. Chen Celia.Y.Chen@dartmouth.edu

¹ Department of Biological Sciences, Dartmouth College, HB 6044, 78 College Street, Hanover, NH 03755, USA

² Nantucket Land Council, 6 Ash Lane, Nantucket, MA 02554, USA burning of coal and other fossil fuels (Sundseth et al. 2017). In addition to anthropogenic atmospheric sources, mercury can be released by natural sources, such as rock weathering (while minimal), and industrial or mining sources (which can be large, but localized) (AMAP/UNEP 2013; Sundseth et al. 2017). While runoff and discharge from rivers can introduce elemental mercury to freshwater systems directly (Obrist et al. 2018; AMAP/UNEP 2013), the elemental mercury that enters the atmosphere also is deposited in marine and freshwater surfaces through dust, rainfall, and snow, where anaerobic microbes can convert its ionic form (Hg^{2+}) into a bioavailable form, methylmercury (MeHg) (Harris et al. 2007; Obrist et al. 2011). Elevated MeHg levels in fish have not only been linked to reductions in reproductive performance, growth, and survival in piscivorous birds (Nocera and Taylor 1998; Evers et al. 2005; Scheuhammer et al. 2008; Eagles-Smith et al. 2018) and mammals (Hinck et al. 2009) but also to deleterious effects in human consumers (Sheehan et al. 2014; World Health Organization 2013). In humans, MeHg exposure from consuming aquatic fish can cause neurological effects, impaired fetal and infant



growth, and cardiovascular disease (Grandjean et al. 2005; Mergler et al. 2007; Karagas et al. 2012). All 50 U.S. states have mercury advisories for fish consumption in effect, with advisories varying across statewide and localized levels (i.e., for specific water bodies in some states) (USEPA 2011).

While many studies measure total mercury (THg) levels in a range of legal-length adult fish to inform advisories (Simonin et al. 2008; Rose et al. 1999; Eagles-Smith et al. 2015; Sackett et al. 2013), authors rarely explore the length-THg relationship over a wider range of fish size from juveniles to adults (Burger and Gochfeld 2011). Changes in THg concentrations from juvenile to adult stages could be critical for modeling maximum catch lengths for safe consumption and to predict how adult fish of different species increase THg levels over further increases in length. We sought to capture a wide range of fish, including smaller juveniles (~2-10 cm) to characterize mercury levels in a variety of species over increasing length. By characterizing mercury levels in fish populations across length, we intended to develop a more dependable, informative way to predict which species are safe for consumption, and at what sizes. In doing so, we also intended to advance our understanding of how a combination of biotic and abiotic factors influences the concentration of MeHg in different fish species across different ecosystems.

Nantucket, a small (273 km²) island approximately 48.3 km off of the coast of Cape Cod, MA, provided an opportunity to characterize an understudied collection of freshwater pond systems, both in terms of MeHg bioavailability as well as wildlife and human exposure. Due to elevated concentrations of Hg in biota, such as fish, birds, and mammals (Whittier et al. 2002; Evers et al. 2003), many of the lakes and streams in the Northeast United States have been labeled "biological Hg hotspots" (Evers et al. 2007), demanding particular attention from a scientific as well as policymaking perspective (Driscoll et al. 2007). Elevated MeHg levels have even been found in recreational and subsistence fisheries of the isolated islands off of Cape Cod, including Martha's Vineyard (Purdy 2009) and Nantucket (MA DEP 2000a, b). However, neither island has any known historic point source of industrial Hg pollution (Purdy 2009; Nantucket Historical Association). These remote island ecosystems allow us to investigate the extent to which regional Hg pollution impacts isolated pond systems through atmospheric deposition alone.

Many abiotic and biotic factors influence the bioavailability and bioaccumulation of Hg through aquatic ecosystems. The concentration of a pond's bioavailable MeHg pool is in part linked to abiotic environmental factors: fish THg has been shown to correlate positively with wetland area (Rudd 1995; Rose et al. 1999; Simonin et al. 2008; Grigal 2002; Gabriel et al. 2009), freshwater surface area (Rose et al. 1999; Rudd 1995; Kidd et al. 2012), and

watershed area (Rose et al. 1999; Rudd 1995). Fish THg appears to correlate negatively with pond pH (Kamman et al. 2005; Rose et al. 1999; Chen et al. 2005; Simonin et al. 2008) and specific conductivity (Julian and Gu 2014). Anaerobic sediment conditions and increased sulfate levels also can spur the growth of sulfate-reducing bacteria, the major microbial group that mediates mercury methylation via co-metabolism (Benoit et al. 2003; Gilmour et al. 1998). MeHg levels in surface water have been found to best correlate with pond biota MeHg levels (Morway et al. 2017; Clayden et al. 2014). Fish MeHg concentration also has been found to correlate with the following biotic factors: fish length, trophic level, and feeding mode, as well as pond productivity. Fish length correlates positively with fish THg concentration (Cizdziel et al. 2002; Gabriel et al. 2009; Burger and Gochfeld 2011). Across freshwater and marine systems, fish THg levels also increase with fish trophic level (Sonesten 2003; Lavoie et al. 2013; Chumchal and Hambright 2009; Burger and Gochfeld 2011; Ward et al. 2012). Differences in THg concentration between species have been linked to differences in pelagic and benthic feeding strategies, which reflect differences in fish prey trophic level (Piraino and Taylor 2009). Higher pond nutrient levels may buffer MeHg levels in harvested fish through the compounding effects of both biodilution in primary producers (Pickhardt et al. 2002; Kamman et al. 2004; Miller et al. 2012) and somatic growth dilution of MeHg in both zooplankton and fish through accelerated growth (Karimi et al. 2007; Ward et al. 2010).

In this study, we determined the relationship between length and THg concentration in four fish genera across six freshwater pond systems of Nantucket to address the following four questions:

- 1. In the same pond, do different fish species differ in their relationship between THg concentration and length?
- 2. Across different ponds, does the same fish species bioaccumulate THg differently?
- 3. Are across-pond differences in fish THg bioaccumulation "slope" and magnitude related to pond environmental factors?
- 4. How do these findings relate to potential wildlife and human exposure?

By collecting many fish across a range of lengths, we examined THg bioaccumulation based on fish genus (pooling species known to share similar ontogenetic features, trophic level, and feeding behavior), length, and source pond. We then examined the relationship of the slope and intercept of THg concentration in each genus/pond considering biotic and abiotic variables known to be predictors of THg bioaccumulation.

Materials and Methods

Collection Sites

Nantucket has more than 30 distinct pond systems hosting a range of fish species across numerous genera that are captured recreationally and consumed by piscivorous wildlife. These species include yellow perch (Perca flavescens), white perch (Morone americana), and sunfish (Lepomis gibbosus and L. macrochirus). In 1995 and 2000, state studies detected THg levels in fish from four Nantucket ponds exceeding the EPA human health criterion of 0.30 mg/kg (USEPA 1997), with fish THg levels as high as 1.27 mg/kg in Miacomet Pond (MA DEP 2000a, b). However, state mercury measurements were limited to these 2 years, and each year's investigation surveyed a different assortment of ponds. Furthermore, only 2-13 adult (mean length 17.7-53.5 cm) fish from each system, primarily yellow and white perch, were measured for THg (MA DEP 2000a, b).

We collected summer (July–August 2017) measurements of fish and water quality from six different ponds on Nantucket Island used for recreational fishing: Tom Nevers (TNP); Miacomet (MP); Washing (WP); Gibbs (GP); Long (LP); and Head of Hummock (HHP) (Fig. 1). Permission to access these ponds was granted by the Nantucket Conservation Foundation. Historically, these pond systems have been listed as eutrophic or hyper-eutrophic, as determined by a Chlorophyll *a* (Chl *a*) or total phosphorus (TP)-based Carlson's Trophic State Index (TSI) (Carlson 1977; Sutherland and Molden 2017). HHP and LP are more brackish, whereas MP, TNP, GP, and WP are freshwater systems. Nantucket Land Council (NLC) water quality measurements have been sporadic, covering only 1–2 ponds annually and missing measurements for some ponds since 2009 (Sutherland and Molden 2017).

Fish Sample Collection

Juvenile fish of four genera, yellow perch (Perca flavescens), white perch (Morone americana), killifish (Fundulus majalis and F. diaphanus), and sunfish (Lepomis gibbosus and L. macrochirus), were collected in accordance with a scientific collection permit granted from the Massachusetts Department of Fish and Wildlife (Permit #186.17SCF). All four genera share trophic levels and ontogenetic shifts in predation preferences from juvenile stages to adulthood. Yellow perch, white perch, and both sunfish species are commonly captured and consumed within recreational fisheries. Yellow perch, bluegill, and pumpkinseed are secondary consumer fish with a lifespan of 4-7 years (Gabriel et al. 2009). Yellow perch reach an average length of 10.0-25.5 cm (CABI 2018c), while bluegill and pumpkinseed reach an average length of 20.1 and 20.4 cm, respectively (CABI 2018a, NJDEP 2012). All three species share the same diet within



Fig. 1 Maps of Nantucket Island, both from Google Earth satellite imagery (upper left) and from ArcGIS software (bottom right). The watersheds relevant to this study's pond systems are denoted in orange the same trophic level (3-4), consuming phyto- and zooplankton as juveniles and switching to benthic macroinvertebrates and small fish in adulthood (Ethier et al. 2008). White perch most commonly reach 12.7–17.8 cm in length (Riede 2004) and consume primarily invertebrates throughout their lifetime, with an ontogenetic shift from crustaceans and smaller insects in juvenile stages to crabs, shrimp, and small fish in adulthood (Mason et al. 2006). F. majalis and F. heteroclitus (similar to F. diaphanus) reach top lengths of approximately 18 and 13-15 cm, respectively, with the maximum lifespan of F. heteroclitus recorded at approximately 4 years (Fernández-Delgado 1989). Both F. majalis and F. heteroclitus are omnivorous, with gut contents of F. heteroclitus indicating a diet of detritus, algae, amphipods, copepods, and insects (Allen et al. 1994). Due to the known ontogenetic, morphological, and trophic similarities between the species of killifish (Fundulus majalis and F. diaphanus) and sunfish (Lepomis gibbosus and L. macrochirus), we grouped the species within each genus for all further analyses.

Fish were captured from pond shorelines with a $4' \times 10'$ seine net (mesh size ~ 1 mm) from 9 AM–12 PM on mornings from August 6–15, 2017. Fish were assumed to swim freely throughout pond systems, and thus all fish were considered representative of a random sample of each pond. We collected fish from a wide range of lengths across genera and ponds to encapsulate the growth of small juvenile to adult fish. After collection, the fish were transported live by bucket to a processing site for euthanasia and bagging. All fish were euthanized and placed on dry ice in a cooler according to the Institutional Animal Care and Use Committee (IACUC) guidelines. Fish were stored at -20 °C until analyzed for mercury content.

Fish Sample Mercury Analysis

We used measurements of fish total mercury (THg) as a proxy for MeHg, because MeHg has been found to comprise up to 98–99% of the total mercury in fish (Wiener et al. 2003; Bloom 1992). All fish selected for mercury analysis were measured for length, washed with ultra-pure (18Mohm) water, and stored in preweighed glass vials. For those fish too large to fit within the vials (all sunfish > 8 cm, all yellow/white perch > 10 cm), a white-muscle filet sample was extracted from the left shoulder of each fish (approximately size $1 - \times 1 - \times 2$ -cm, located 1 cm above the pectoral fin). This filet was washed and placed within its own sample vial. After determining the wet weight of each vialed fish sample, vials were placed in a freeze-dryer (Labconco Freezone) for a minimum of 48 h. Each freeze-dried vial was then reweighed to determine the fish sample dry mass. The dry fish samples were then homogenized using ceramic scissors. A Milestone Direct Mercury Analyzer (DMA-80) was used to measure the total mercury content of each dried, homogenized fish sample. All data used for statistical analysis were converted to a wet-weight basis: THg (mg/kg) was converted to wet weight by multiplying the THg (mg/kg) DMA-80 measure of each fish by the dry-to-wet weight ratio of that fish. Certified standard reference materials (TORT2, DORM4) and a sample duplicate were analyzed every 10–20 sample runs, and all recoveries averaged within 5% of reference values (TORT2% recovery = 105 ± 0.9 , N = 30; DORM4% recovery = 103 ± 0.9 , N = 30; sample duplicate RPD = 4.4 ± 1.1 , N = 19).

Statistical Analysis

For each pond, fish THg (mg/kg, wet-weight) (i.e., THg) was plotted against fish length (cm) by genus. The distribution of fish THg was normalized within and across genera and pond categories using a natural-log transformation. We conducted a series of simple linear regressions to determine whether the species within each pond exhibited significant linear relationships between ln-THg and fish length in terms of both slope and intercept at the two-sided $\alpha = 0.05$ level. Those species within each pond exhibiting a significant relationship between ln-THg and length were then compared to one another in a series of multivariable regression analyses: one set comparing the regressions of different genera *within* each pond, and another comparing the regressions of fish in the same genus *across* their different source ponds.

To determine whether there was a significant difference in the intercept and slope of fish ln-THg versus fish length (cm) among genera within the same pond, the first multivariable regression model included an interaction term between fish length and genus. The error rate for the two-sided P value given for the model interaction term was set to $\alpha = 0.10$. If the interaction term yielded a two-sided P < 0.10, the multivariable regression model with the interaction term was used to determine the difference in slope and intercept between each pairwise comparison of genera within the same pond. For each set of pairwise comparisons within the multivariable regression model, the regression of a single pond genus was compared as a reference to the other pond genera regressions. This process was repeated, using another pond genus regression as the designated reference of comparison, until all possible combinations of regression pairs were compared to one another within the model.

To determine whether there was a significant difference in the magnitude and slope of fish genus ln-THg versus fish length *across different source ponds*, the second multivariable regression model included an interaction term between fish length and pond. If the interaction term yielded a twosided P < 0.10, the multivariable regression model with the interaction term was used to determine the difference in slope and intercept between regressions for the same fish species between ponds.

For those genera that did not display significant regression lines across their source ponds, we conducted a series of one-way ANOVAs to compare genus THg (mg/kg) of fish with similar lengths (target = 5-10 cm) across different source ponds. To ensure that fish length was comparable across ponds, we conducted an additional series of one-way ANOVAs to compare the mean lengths of fish from each of the ponds in the first ANOVA. Each one-way ANOVA analysis was followed by a Tukey's HSD post-hoc analysis to identify which pond category fish were significantly different in terms of either THg or length. The two-sided type I error rate for all ANOVA analyses was set to $\alpha = 0.05$. All analyses were conducted in the JMP 13 statistical software program.

Fish Stable Isotope Analysis

To determine whether genus trophic level varied by pond, we measured the stable isotope ratio (δ^{15} N and δ^{13} C) of dry tissue from sample fish as a metric of both trophic level and benthic/pelagic food source (Kidd et al. 2012; Piraino and Taylor 2009; Jardine et al. 2013; Fry et al. 1999). Fish similar in length (fish length \bar{x} =6.6, SE=0.12 cm, *n*=54), were selected across genera and pond systems for isotope analyses (*n*=3–5 fish per genus/pond combination). Dry tissue (1.25–1.50 mg) from each fish was packed in tin foil cups. An internal lab standard and five duplicates were included to ensure measurement precision. All samples were analyzed for δ^{15} N and δ^{13} C values by continuous flow Isotope Ratio Mass Spectrometer (IRMS) at the Stable Isotope Facility of the University of California, Davis.

Water Quality Sample Collection

To assess the nutrient conditions in each pond, anchored kayaks were used to sample sites from the center region of each pond. In accordance with past Nantucket Land Council water quality measurements, HHP, GP, TNP, and WP were analyzed at a single site at the center of each pond deemed representative of the system. Because LP and MP are larger, longer, and narrower, a central site as well as two additional sites equidistant from the relative center of each pond was measured, again at the same locations used historically by the Nantucket Land Council (Fig. 2).

Each site was measured twice: once in late July/early August (July 25–August 2), and again in late August (August 22–29). The following in situ sampling methods replicate the past methods found in Sutherland and Molden's NLC report (2017). Site latitude and longitude were measured using a Garmin GPS 60TM unit to ensure site fidelity across measurement dates. To determine whether each site water column was stratified, a Yellow Springs Instrument (YSI) ProODOTM optical dissolved oxygen meter was used to record vertical profiles of water temperature (C) and dissolved oxygen (mg/L) at 0.3- or 0.6-m intervals (depending on the overall depth) from surface to bottom.

Since the water columns of all but one site were well mixed both thermally and in terms of oxygen concentration, a hose was used to draw an integrated sample from the whole water column for water chemistry and Chl a analyses. For each site, two to three separate integrated water samples were combined into a single polyethylene jug, which was then mixed before the homogenized sample was poured into three clean, pre-rinsed polyethylene amber bottles: one 500-mL bottle for N and P-based water chemistry analyses, and two 250-mL bottles for Chl a analyses. All bottles were immediately stored on ice. A subsample of the homogenized water from the jug was then analyzed for specific conductivity (μ S) and pH (s.u.) using an Ultrameter IITM (Mylon L Company). For the one site and collection time where we determined that the water column was stratified based on temperature and oxygen saturation (GP1), a horizontal Van Dorn Sampler was used to repeat the same measurement and bottling procedures separately for both the epilimnion and the hypolimnion.

To measure the MeHg pond water concentration (ppm) in each pond, duplicate 500-mL whole water samples were collected in acid-cleaned amber glass bottles from each pond site during the second collection period. MeHg water samples were collected from the pond surface alongside kayaks by submerging each bottle top-first below the surface and then inverting the bottle upright. Using a clean hands–dirty hands method, all bottles were filled, capped, and then stored inside acid-washed bags. Within 2–3 h of collection, all water MeHg samples were acidified to 0.4% acid with 2 mL of Optima HCl. An additional amber-glass 500-mL bottle was filled with DI water and acidified as a field blank for analysis.

For Chl *a* analyses, the two 250-mL field collection bottles from each pond site were used to filter three separate 100-mL Chl *a* water samples with a Buchner funnel-handpump assembly and WhatmanTM 4.7-cm diameter Glass Microfiber Filter GF/F Circles with 0.6- to 0.8- μ m nominal particle retention. The whole filtration assembly was cleaned between filtrations from different sites. Each triplicate Chl *a* filter for each site was packaged in aluminum foil and bagged on ice. The samples were then shipped to the Darrin Freshwater Institute (Troy, NY) where all water nutrient samples, as well as all Chl *a* samples, were analyzed.

Water Quality Analysis

The Chl *a* concentration $(\mu g/L)$ of each pond site was measured via fluorimetry (Standard Methods 10200) as

Fig. 2 ArcGIS images of each pond watershed. Gibbs and Tom Nevers Ponds (center left panel) share the same watershed. Each watershed is denoted in orange, and fresh and forested wetlands are labeled in green/blue striped and flat green shading, respectively. Yellow dots denote the sites in each pond used for field measurements and water sample collections. The three separate sites used for each of the two larger ponds, Miacomet and Long (bottom panels) are labeled by site identification



an average across triplicate filter samples. A Carlson's Trophic State Index (TSI) was calculated using the average Chl *a* measure of each pond across collection dates to characterize the trophic status of each pond (Carlson 1977). The single 500-mL polyethylene amber bottle of water collected from each pond site was analyzed for the following nutrients: total phosphorus (TP, μ g/L) total nitrogen (TN, mg/L), nitrate (NO₃⁻, mg N/L), and ammonium (NH₄⁺, mg N/L). All nutrients were measured using standard methods of the Darrin Freshwater Institute. Total phosphorus was measured using persulfate oxidation (Ascorbic Acid Method, Standard Methods, 19th Ed,

4500-P E), total nitrogen was measured using a persulfate method (Standard Methods, 19th Ed., 4500-N D), nitrate was measured using ion chromatography (EPA method 300), and ammonium was measured using the phenate method (Standard Methods, 19th Ed., 4500-NH3 F). The Dartmouth TEA Core Lab measured the MeHg speciation (ng MeHg/L) of acidified surface water samples. A weighed, enriched isotope spike was added to the weighed water samples, which were then buffered with a citrate buffer (300 μ L of 2 M buffer). An ethylating reagent (40 μ L of 1% NaBH₄) was then added to each sample before being run directly on a MERX-ICP-MS system.

ArcGIS Watershed Data

To characterize the geographical features of each pond in relation to its watershed, we used shape files from remote sensing data provided by the Nantucket Island GIS Coordinator's office. Land cover features were differentiated in ArcGIS 2016. Hydrology and image classification overlays were used to quantify the surface area of each watershed, as well as the surface area of each pond. Within each watershed, we also quantified the surface area of freshwater—and forested—wetland.

Results and Discussion

By measuring the THg concentrations of fish spanning a range of lengths and species across Nantucket pond systems, we were able to identify differences in the intercept and slope of fish THg concentration with increasing length both across genera within ponds and within genera across ponds (see "Fish Tissue Concentrations", "Within-Pond Comparisons" and "THg Bioaccumulation Across Different Ponds and Environmental Factors" sections). These acrosspond comparisons of fish THg concentrations could then be related to measures of surface water MeHg levels and other environmental factors. Finally, we were able to use the regressions of fish In-THg concentration versus fish length to determine the lengths at which fish genera THg concentrations exceed the health criteria for human and wildlife consumers (see "Implications for Fish Consumption on Nantucket Island" section).

Fish Tissue Concentrations

A total of 318 juvenile fish of the four genera were collected across the six ponds, with 35–129 fish of at least two different genera collected from each pond. A total of 265 fish,

with a minimum of 5 fish from each genus/pond subcategory, were selected for analysis (Table 1). Almost all distributions of fish length by pond and genus were unimodal; just two genera from HHP (killifish and sunfish) exhibited bimodal length distributions, suggesting a maximum of two fish cohorts (i.e., age classes) across length.

In all ponds but LP, the majority or entirety of fish collected had THg levels (mg/kg wet-weight) greater than 0.02, the EPA advisory level for fish-eating birds (USEPA 2000). Notably, three fish from TNP (length 14.6, 15.1, and 16.6 cm) exhibited THg levels above 0.30 mg/kg wet-weight (0.37, 0.31, and 0.55 mg/kg, respectively)—the human health criterion for safe consumption (USEPA 1997). One of these TNP sunfish also exceeded the recreational fishery advisory for human consumption of 0.40 mg/kg (USFDA 1998).

A natural-log transformation of the fish THg concentrations yielded significant linear regressions of ln-THg versus fish length (cm) for at least one genus in all but one of the pond systems (Fig. 3). Most notably, all ponds in which we collected sunfish yielded significant linear regressions of In-THg versus fish length (cm), whereas killifish and white perch each exhibited significant regressions in only two of the three ponds where they were collected (Table 2). Furthermore, yellow perch only yielded a significant regression in MP (Table 2). In most cases where linear regressions were not observed, the sample datasets contained few fish or fish with lengths that were relatively similar and did not represent a wide range of lengths (Fig. 3). Hence, our inability to characterize some genus/pond sample subsets with significant linear regressions is likely due to insufficient sample size and/or length range within those subsets.

The distributions of all fish ln-THg concentrations and their residuals were normal despite the difference between whole body and filet sampling at the sunfish, yellow perch, and white perch cutoff lengths (8, 10, and 10 cm, respectively). Therefore, it appears that filet-subsampling larger

Table 1 Summary of fish from each pond selected for analysis, by genus

	(million)	Killifish			Yellow Pe	rch		White Perc	2h		Sunfish	
	length (cm)			length (cm)			length (cm)			length	length (cm)	
	Total,	Median	Range	Total,	Median	Range	Total,	Median	Range	Total,	Median	Range
Pond	n	(IQR)	(Min, Max)	n	(IQR)	(Min, Max)	n	(IQR)	(Min, Max)	n	(IQR)	(Min, Max)
LP	20	4.2 (3.5, 4.7)	(3.1, 5.5)	-	-	-	5	6.8 (6.5, 7.1)	(6.3, 7.2)	-	-	-
MP	16	6.5 (3.4, 7.4)	(3.0, 9.1)	13	5.5 (5.1, 6.4)	(4.8, 11.3)	-	-	-	20	3.5 (3.2, 4.3)	(2.8, 13.8)
HHP	31	7.1 (4.0, 8.4)	(2.8, 10.2)	8	7.3 (7.1, 7.5)	(6.7, 8.1)	7	5.6 (5.6, 12.3)	(5.0, 13.6)	39	9.0 (3.4, 10.2)	(2.7, 12.8)
GP	-	-	-	3	8.3 (7.3, 8.3)	(7.3, 8.3)	15	5.4 (4.7, 5.9)	(3.3, 13.7)	10	2.9 (2.8, 6.6)	(2.2, 17.6)
TNP	-	-	-	8	6.1 (6.0, 6.3)	(6.0, 6.3)	-	-	-	24	11.5 (6.4, 14.1)	(2.2, 20.7)
WP	-	-	-	2	14.7 (14.7, 14.7)	(14.7, 14.7)	-	-	-	34	9.5 (5.8, 12.5)	(3.0, 15.2)
Total	67			34			27			127		

Total selected subsample n = 265 fish

LP=Long Pond, MP=Miacomet Pond, HHP=Head of Hummock Pond, GP=Gibbs Pond, TNP=Tom Nevers Pond, WP=Washing Pond, IQR=Interquartile Range (i.e., Quartile 1 length, Quartile 3 length) about each median length value within each category



Fig. 3 Scatter plots of natural log-transform normalized fish THg concentration, wet-weight (mg/kg) versus fish length (cm), separated by pond system. Each point denotes a single fish. Simple linear

regression lines significant at the $\alpha = 0.05$ level are labeled by genus within each legend (see Table 2 for statistical summary)

Table 2 Summary of simple linear regression estimates of ln-total mercury concentration (ln(THg, mg/kg, wet-weight) versus fish length (cm),categorized by genus (see Fig. 3 for graphical outputs of all genus regressions by pond)

			Slope ((lı	n(THg, mg/kg W	'W))/cm)	Intercept (ln(THg, mg/kg WW))				
Genus	Pond	n	Estimate	Test Statistic	P-Value	Estimate	Test Statistic	P-Value		
Sunfish	TNP	24	0.111	$t_{df=22} = 8.31$	<0.0001	-2.91	$t_{df=22} = -18.9$	<0.0001		
	GP	10	0.094	$t_{df=8} = 5.65$	0.0005	-3.52	$t_{df=8} = -27.9$	<0.0001		
	MP	20	0.104	$t_{df=18} = 6.67$	<0.0001	-3.78	$t_{df=18} = -51.0$	<0.0001		
	WP	34	0.102	$t_{df=32} = 8.60$	<0.0001	-3.92	$t_{df=32} = -33.1$	<0.0001		
	HHP	39	0.272	$t_{df=37} = 16.8$	<0.0001	-5.85	$t_{df=37} = -43.6$	<0.0001		
Villifich	MD	16	0.246	+ -7.02	~0.0001	1 80	t = 14.0	~0.0001		
KIIIIISII		10	0.340	$t_{df=14} - 7.03$	<0.0001	-4.80	$l_{df=14}14.9$	<0.0001		
	HHP	31	0.291	$t_{df=29} = 13.5$	<0.0001	-5.50	$t_{df=29} = -36.9$	<0.0001		
W. Perch	GP	15	0.096	$t_{df=13} = 21.5$	<0.0001	-3.57	$t_{df=13} = -116.1$	<0.0001		
	HHP	7	0.201	$t_{df=5} = 4.02$	0.01	-5.21	$t_{df=5} = -12.5$	<0.0001		
V Porch	MP	13	0.110	$t_{11} = 5.47$	0 0002	-3.46	t= -25 8	<0.0001		
	IVIT	15	0.110	•df=11 - J. - 7	0.0002	-5.40	df=11 -23.0	-0.0001		

TNP=Tom Nevers Pond, GP=Gibbs Pond, MP=Miacomet Pond, WP=Washing Pond, HHP=Head of Hummock Pond, W. Perch=White Perch, Y. Perch=Yellow Perch

fish did not substantially change the relative magnitude of THg concentrations for larger fish across genera. In addition, despite the difference in maximum whole-body fish sample length used between sunfish and yellow/white perch (8 vs. 10 cm), all regression comparisons of these three genera within the same source ponds produced statistically parallel In-THg versus length regression slopes (Supplement Table 1). Additionally, the white perch and sunfish of HHP had regression slopes parallel to that of HHP killifish (Supplement Table 1), suggesting that the switch to filet sampling at larger white perch and sunfish lengths did not confound their comparison with the entirely whole-body sampled killifish regression. Thus, we believe that any confounding effect of the transition from whole body to filet sampling at larger fish length did not impact our comparisons between In-THg versus fish length regressions.

Within-Pond Comparisons

The first multivariable analysis compared the regressions of fish ln-THg versus fish length (cm) among genera within Miacomet Pond (MP), Head of Hummock Pond (HHP), and Gibbs Pond (GP) separately (Fig. 3; Supplement Table 1). We interpreted differences in regression slopes among genera as genus-based differences in the change in THg concentration (i.e., THg bioaccumulation) over fish length. Likewise, we interpreted differences in regression intercept among genera as genus-based differences in the relative magnitude of THg concentration across fish length. In GP, there was no significant difference in the regression slopes of white perch and sunfish (overall model $F_{3,21}=39.0$, P < 0.0001, slope comparison P=0.92). There also was no significant difference in ln-THg intercept between the two genera of GP (P=0.60). By contrast, there was a significant difference in ln-THg intercept between genus regressions in HHP ($F_2=3.78$, P < 0.0001; overall model $F_{5,71}=96.6$, P < 0.0001). The ln-THg intercepts of HHP white perch and sunfish were comparable (P=0.36), while that of HHP killifish differed from each of the other two genera (P=0.02, P < 0.0001 in pairwise comparisons with white perch and sunfish, respectively). However, there was no significant difference in regression slope among killifish, white perch, and sunfish from HHP ($F_2=2.08$, P=0.13). Hence, there was no significant interaction between fish length and genus in HHP.

The within-pond comparisons of fish ln-THg versus fish length in GP and HHP suggest that the slope of THg concentration with increasing fish length (i.e., the THg bioaccumulation) is consistent across genera within each pond (Fig. 3; Supplement Table 1). Notably, sunfish and white perch from GP had virtually identical ln-THg versus length regressions in terms of both slope and intercept, suggesting that both the slope and magnitude of THg concentration with increasing length are the same for both genera. Our stable isotope measurements show that the genera within both GP and HHP have similar or overlapping mean- δ^{13} C ratios (Fig. 4), supporting that the genera within each pond share similar feeding behaviors. While differences in δ^{15} N ratio between individual genera in both GP and HHP were



Fig. 4 Mean stable isotope values for fish from different pond systems. More negative δ^{13} C values suggest a more pelagic source of diet, whereas more positive δ^{13} C values suggest a more benthic source of diet. Higher δ^{15} N values suggest a higher overall trophic level of feeding. LP=Long Pond, MP=Miacomet Pond, HHP=Head of Hummock Pond, WP=Washing Pond, GP=Gibbs Pond, and

TNP=Tom Nevers Pond. W. Perch=white perch, Y. Perch=yellow perch. N=10 killifish (N=5 HHP, 5 MP), 15 white perch (N=5 LP, 5 GP, 5 HHP), 18 yellow perch (N=5 MP, 3 GP, 5 HHP, 5 TNP), 11 Sunfish (N=3 HHP, 3 TNP, 5 WP). Standard error bars denote one standard error from the mean

more considerable, it does not appear that these potential differences in trophic level among genera had an effect on THg bioaccumulation slope across genera in either pond. Since all four genera are known to consume phyto- and zooplankton, followed by invertebrates at higher juvenile ontogenetic stages, these findings reflect that the different genera within each pond share the same relative level of THg bioaccumulation over increasing length.

While the regression slopes of killifish, white perch, and sunfish from HHP were all statistically similar, white perch and sunfish regressions showed a significantly different ln-THg intercept from that of the killifish regression for HHP (Fig. 3; Supplement Table 1). The intercepts of lake-specific regressions of fish THg concentration versus trophic level (measured as $\delta^{15}N$) have been used to estimate and compare mercury levels at the base of lake food webs (Sackett et al. 2013). Similarly, our pond In-THg intercepts could reflect differences in "initial" concentrations of fish THg (i.e., at length 0 cm) for the same species across systems. However, different fish species regressions within the same pond can easily vary in In-THg intercept, most likely due to differences in trophic level or metabolic activity among individuals of the smallest collection sizes (Sonesten 2003). In HHP, white perch (length = 5.0-13.6 cm) had a notably higher minimum length than sunfish (length = 2.7 - 12.8 cm) and killifish (length = 2.8-10.1 cm). The differences in ln-THg intercept could reflect an underrepresented shift in THg concentration between fish of 2.7-2.8 cm and fish of 5.0 cm. Therefore, while comparing the In-THg intercept of the same fish species across systems might reveal system-specific differences in fish mercury concentrations, we cannot effectively compare the In-THg intercepts of different fish species within the same pond.

Surprisingly, killifish from MP exhibited a THg bioaccumulation slope over three times as high as that for either yellow perch or sunfish (Fig. 3; Supplement Table 1). The overall model for MP indicated a significant difference in the MP regressions of fish ln-THg versus fish length, based on fish genus ($F_{5,43}$ =52.2, P < 0.0001). There was a significant interaction between fish length and genus in MP (F_2 =19.0, P < 0.0001). There also was a significant difference in ln-THg intercept between genus regressions of MP (F_2 =10.6, P < 0.0001). The ln-THg intercepts of MP killifish and yellow perch were comparable (P=0.56), whereas the ln-THg intercept of MP sunfish differed from each of the other two genera (both P < 0.0001).

Killifish are thought to share the same macroinvertebrate diet as sunfish and yellow perch and can actually feed lower on the food web by also consuming algae and detritus. The observed killifish ln-THg versus length regression slope conflicts with predictions based on diet. Our stable isotope analysis (Fig. 4), which included both killifish and yellow perch from MP, suggests that while both genera have fairly comparable δ^{13} C ratio values, killifish from MP had notably higher δ^{15} N than yellow perch. Hence, while both killifish and yellow perch may share a more benthic feeding strategy (Piraino and Taylor 2009), MP killifish may nonetheless feed at a higher trophic level (Kidd et al. 2012; Piraino and Taylor 2009), increasing their Hg bioaccumulation. As discussed for the fish regressions of HHP, the significant difference between In-THg intercepts of MP sunfish and killifish/yellow perch may be due to variations in ontogenetic shift across individuals of the small lengths captured within each genus. The minimum size of sampled MP yellow perch (length = 4.8 - 11.3 cm) was substantially longer than those of either sunfish (2.8-13.8 cm) or killifish (3.0-9.1 cm). Differences in trophic level or metabolic rate among smaller individuals of the different MP genera could explain differences in In-THg intercepts among MP fish regressions.

Despite the variability in ln-THg *intercept* among genus ln-THg versus length regressions within the same pond, most genus regressions shared similar bioaccumulation *slopes* within the same pond. We found comparative differences in the projected ln-THg intercept of genera from HHP and MP, and in the regression slope of killifish from MP. Yet, our within-pond comparisons suggest that all measured genera from MP, GP, and HHP that are fished recreationally (i.e., sunfish, white perch, and yellow perch) bioaccumulate THg at a similar degree over increasing length (i.e., share similar within-pond bioaccumulation slopes).

THg Bioaccumulation Across Different Ponds and Environmental Factors

The second multivariable analysis compared, across ponds, each individual genus fish ln-THg versus fish length (cm) regression for sunfish, killifish, and white perch (Fig. 5, Table 3). The overall sunfish model indicated a significant difference in sunfish In-THg versus length based on source pond ($F_{9,117} = 148.6, P < 0.0001$). There was a significant interaction between sunfish length and pond ($F_4 = 29.7$, P < 0.0001) and a significant difference in intercept between sunfish regressions ($F_4 = 35.1$, P < 0.0001). While TNP had a significantly higher sunfish regression intercept than the other four ponds, the HHP sunfish regression had a much lower In-THg intercept than any of the other sunfish source ponds, and GP, MP, and WP were all comparable in sunfish regression slope and intermediate in sunfish In-THg intercept relative to the extremes of TNP and HHP (all significant P < 0.01). Because the ln-THg versus fish length slope was statistically similar across TNP, WP, MP, and GP, the difference in overall magnitude of sunfish THg levels across these regressions suggests a difference in MeHg exposure across pond systems.

The exceptionally high magnitude of fish THg concentrations in TNP could be explained by a higher available



Fig. 5 Linear regressions of natural log-transformed fish THg, wetweight (mg/kg) versus fish length (cm), by genus: sunfish (left), white perch (middle), and killifish (right). Each line denotes the set of fish from the labeled pond. Killifish and white perch from Long Pond (LP) lacked significant regression lines (NS) and are thus portrayed as independent points. Differences in lettered pairs assigned to each pond regression denote significant differences in slope (lowercase)

or intercept (uppercase) between regressions, as tabulated in Table 3. Slope and intercept letters assigned to comparisons of pond regressions are exclusive to each genus. Regression lines for genera from Tom Nevers Pond (TNP) and Head of Hummock Pond (HHP), of particular relevance due to their heightened magnitude (TNP) or slope (HHP) of bioaccumulation, have been colored red and green, respectively

Table 3 Slope, intercept linear components and comparative *P*-values obtained from multivariable regression models of fish ln-THg (mg/kg, wet-weight) versus fish length (cm), based on pond (see Fig. 5 for graphical output)

			Pond for Comparison										
		Slong Intercent	I I	Tom Ne	vers (TNP) Gibl	os (GP)	Miaco	met (MP)	Washi	ng (WP)	Head of Hu	mmock (HHP)
Genus Pond		(Letter ID)	Reference	Slope	Intercept	Slope	Intercept	Slope	Intercept	Slope	Intercept	Slope	Intercept
Sunfish	TNP	0.111, -2.91 (a, A)	TNP			0.44	<0.0001	0.83	<0.0001	0.64	<0.0001	<0.0001	<0.0001
	GP	0.094, -3.52 (a, B)	GP	0.44	<0.0001			0.76	0.30	0.69	0.005	<0.0001	<0.0001
	MP	0.104, -3.78 (a, BC)	MP	0.83	<0.0001	0.76	0.30			0.96	0.24	<0.0001	<0.0001
	WP	0.102, -3.92 (a, C)	WP	0.64	<0.0001	0.69	0.005	0.96	0.24			<0.0001	<0.0001
	HHP	0.272, -5.85 (b, D)	HHP	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001		
			1										
Killifish	MP	0.346, -4.80 (a, A)	MP									0.29	<0.0001
Contraction of the second	HHP	0.291, -5.50 (a, B)	1										
			i										
W. Perch	GP	0.096, -3.57 (a, A)	GP									0.007	<0.0001
	HHP	0.201, -5.21 (b, B)	1										

Differences in lettered pairs assigned to each pond regression denote significant differences in slope (lowercase) or intercept (uppercase) between regressions. Slope and intercept letters assigned to comparisons of pond regressions are exclusive to each genus. The "Reference" column ID of each row corresponds to the reference pond regression compared to the slopes and intercepts of the other pond regressions in the subsequent columns. Bold values denote significant differences in slope or intercept between the two ponds within each comparison

MP=Miacomet Pond, HHP=Head of Hummock Pond, GP=Gibbs Pond, TNP=Tom Nevers Pond, WP=Washing Pond, W. Perch=white perch

pool of pond MeHg. Surface water MeHg levels of TNP (mean = 0.146 ng/L) were more than ten times as high as in HHP (Fig. 6). This could be due to a combination of a lower pH (mean = 6.89, range = 6.51-7.27) and a substantially higher percent watershed wetland cover in TNP (Supplement Table 2; Supplement Fig. 1). The low pH may be attributable to organic humic and fulvic acids leaching into the pond from surrounding regions of vegetation, as indicated by TNP's dark watercolor and low transparency (Sutherland

and Molden 2017). Our relatively low measurements of TNP Secchi depth (16.1% visibility of total water depth across measurements) are indicative of these earlier observations. Most of the wetland area of the Tom Nevers-Gibbs Pond watershed is labeled as "forested" and woody-cranberry bog wetland. GP is used to flood the cranberry bogs in the watershed for harvesting season, and a single outflow channels this floodwater through a stretch of forested wetland into TNP to the south end of the watershed (Sutherland and



Fig. 6 Comparisons of pond features across study systems: **a** surface water MeHg concentraion (ng/L), and **b** chlorophyll *a* (μ g/L) for each pond. GP=Gibbs Pond, HHP=Head of Hummock Pond, LP=Long Pond, MP=Miacomet Pond, TNP=Tom Nevers Pond, and WP=Washing Pond. All averages are reported as means across measurements from two collection dates. Sample size *n*=2 measurements of water MeHg from each pond. Sample size *n*=2 for chlo-

rophyll *a* from a single site of GP, HHP, TNP, and WP (1 measurement per collection date), n=6 measurements from 3 separate sites of both MP and LP (3 measurements per collection date, 1 at each site). Chlorophyll *a* measurements are reported as averages of triplicate sub-samples collected at each site on each of the 2 collection dates. Bars denote ranges of minimum and maximum values

Molden 2017). Acidic waters containing tannins (i.e., dissolved organic complexes similar to humic and fulvic acids) from forested areas have been correlated with above-average fish THg concentrations (Kamman et al. 2005). Additionally, the most important variety of microbes capable of methylating mercury from Hg²⁺ to MeHg is sulfate-reducing bacteria (Benoit et al. 2003; Gilmour et al. 1998), which thrive in reducing environments, such as freshwater wetlands (Chen et al. 2009). Wetland area has been shown to correlate positively with fish THg concentrations (Rudd 1995; Rose et al. 1999; Simonin et al. 2008; Grigal 2002; Gabriel et al. 2009). Because the wetland percent area of the Tom Nevers-Gibbs Pond watershed (21.7%) is notably higher than the surface area of TNP itself (1.66% of watershed area), the effect of organic inputs could be compounded by a high amount of wetland area available for Hg methylation.

While larger ponds are typically correlated with higher fish THg concentrations (Rose et al. 1999; Rudd 1995; Kidd et al. 2012), smaller ponds like TNP may exhibit heightened MeHg concentrations due to the greater proportion of allochthonous organic material influx from the watershed relative to pond water volume (Greenfield et al. 2001). The elevated water MeHg concentration of TNP corresponds to the higher intercept of the TNP sunfish regression, supporting that the sunfish of TNP have higher THg levels than sunfish from GP, MP, or WP due to higher environmental MeHg bioavailability, rather than a higher slope of THg concentration with increasing fish length.

The THg comparison of "medium"-length yellow and white perch supports the relative magnitudes of fish THg levels derived from the parallel sunfish regressions (Fig. 7). For most yellow perch and most fish collected from LP, Hg concentration was not related to fish length. Thus, we isolated "medium"-sized yellow and white perch (5-10 cm) from each of their source ponds to produce two sets of ANO-VAs comparing fish THg (mg/kg) by source pond (Fig. 7). There was a significant difference in medium-sized fish THg among source ponds for both genera ($F_{3,25} = 88.9$, P < 0.0001 for yellow perch, $F_{2.15} = 120.0$, P < 0.0001 for white perch). Yellow perch from TNP had significantly higher mean THg ($\bar{x} = 0.083$, SE = 0.002 mg/kg) than those from GP ($\bar{x} = 0.047$, SE = 0.002 mg/kg), MP ($\bar{x} = 0.059$, SE = 0.002 mg/kg, and HHP ($\bar{x} = 0.016$, SE = 0.004 mg/kg; all P < 0.0001). Medium-sized GP and MP yellow perch had comparable mean THg (P=0.17) but were both significantly higher in mean THg than the medium-sized yellow perch from HHP (P < 0.0001). Similarly, white perch from GP had significantly higher mean THg ($\bar{x} = 0.048$, SE = 0.002 mg/ kg) than white perch from HHP (\bar{x} =0.0184, SE=0.002 mg/ kg; P < 0.0001), which had significantly higher mean THg than those from LP ($\bar{x} = 0.007$, SE = 0.002 mg/kg; P = 0.007). Both across-pond comparisons of mediumlength fish were conservative: in both yellow and white perch analyses, the ponds with the longer mean fish samples had lower mean fish THg concentration, eliminating the chance that differences in capture size among mediumlength fish might have confounded the differences in THg concentration among different source ponds.

The relatively lower THg concentrations in mediumlength white and yellow perch from HHP belie the higher slope of THg concentration found in genera across HHP (Fig. 5; Table 3). While the yellow and white perch ANOVA comparisons suggest that fish from HHP have relatively low THg levels (Fig. 7), comparing sunfish revealed that the ln-THg versus length regression slope of sunfish from HHP was over twice as high as that from any of the other sunfish

Fig. 7 An across-pond comparison of fish THg (mg/ kg, wet- weight) (top) and fish length (cm) (bottom) in "medium" size- class individuals (5-10 cm) of both a yellow perch (left) and **b** white perch (right). TNP=Tom Nevers Pond, MP = Miacomet Pond, GP=Gibbs Pond, HHP=Head of Hummock Pond, and LP=Long Pond. Sample size n = 29 total yellow perch (8) from TNP, 10 from MP, 3 from GP, and 8 from HHP) and 18 total white perch (8 from GP. 5 from HHP, and 5 from LP)



source ponds (TNP, GP, MP, and WP) (all comparisons P < 0.0001), which were all characterized by statistically parallel slopes (Fig. 5; Table 3). Similarly, the multivariable model for white perch indicated a significant difference between the white perch regressions of GP and HHP $(F_{3,18}=39.1, P < 0.0001)$. White perch from HHP had over twice the regression slope (0.201 (ln-THg)/cm) and a significantly lower intercept (-5.21 ln-THg) than white perch from GP (slope = 0.096 (ln-THg)/cm, intercept = -3.57ln-THg) (P = 0.007, P < 0.0001 respectively). The multivariable model for killifish also indicated a significant difference between the killifish regressions of MP and HHP $(F_{3,43} = 120.6, P < 0.0001)$. Yet, the ln-THg versus length regression slope of killifish from HHP was statistically comparable to that of killifish from MP. While killifish from MP exhibited a higher intercept (-4.80 ln-THg) than killifish from HHP ($-5.50 \ln$ -THg; P < 0.0001), there was no significant difference in regression slope between killifish of MP and HHP (P = 0.29). Because all HHP regression slopes are comparable to the anomalously high regression slope of MP killifish, all genera from HHP seem to bioaccumulate mercury at a heightened slope relative to genera of other ponds. Our comparison of medium-length perch across ponds reveals how size-controlled analyses can overlook these important changes in relative THg concentrations across a range of fish lengths.

Based on Chl a measure, all of the pond systems were characterized by the Carlson Trophic State Index as eutrophic, and GP was characterized as hypereutrophic (Supplement Table 2). Because HHP exhibited some of the highest Chl *a* concentrations ($\bar{x} = 27.0$, range = $21.7-32.3 \mu g/L$), the higher bioaccumulation slope across fish from HHP cannot be explained by nutrient biodilution. In fact, GP, which had over twice the mean Chl a concentration as HHP ($\bar{x} = 64.9$, range = $63.5-66.3 \mu g/L$), expressed a sunfish In-THg versus length regression with a slope parallel to those sunfish regressions of the much lesseutrophic TNP, MP, and WP (mean Chl a = 9.6, 7.4, and12.9 µg/L, respectively). Because white perch from HHP expressed twice the regression slope of white perch from GP, this trend appears in both sunfish and white perch across their respective source ponds.

Hg biodilution effects have been observed in zooplankton (Chen et al. 2005; Miller et al. 2012) and fish (Simonin et al. 2008) across lakes ranging from oligotrophic to lower or upper-range eutrophic $[0.7-13.7 \ \mu g/L$ in Chen et al. (2005),

2.8–11.0 µg/L in Miller et al. (2012), 0.4–46.2 µg/L in Simonin et al. (2008)]. However, the Carlson's TSI labels of "eutrophic" and "hyper-eutrophic" used to characterize each pond system encompass a broad range of Chl *a* concentrations (7.3–56 µg/L and 56–155 + µg/L, respectively) that may obscure marked differences in Chl *a* between eutrophic pond systems. For example, the same "eutrophic" label encompasses a greater than 8-fold difference between the mean 6.1 µg/L Chl *a* measured in TNP from 2014 to 2016 and the mean 50.1 µg/L Chl *a* measured in HHP from 2009 to 2013. Our results suggest that differences in productivity across the observed eutrophic to hyper-eutrophic range (7.4–64.9 µg/L) do not appear to influence the slope of fish THg bioaccumulation with increasing fish length across Nantucket ponds.

Unlike the anomalously high Hg bioaccumulation slope of killifish in MP, all three genus regressions from HHP (sunfish, killifish, and white perch) share comparable THg bioaccumulation slopes. While all of the genera of HHP yielded mean $\delta^{15}N$ stable isotope values that are comparable to those of genera across all other pond systems (Fig. 4), it is possible that baseline signatures of $\delta^{13}C$ and $\delta^{15}N$ in HHP food webs are much lower than other ponds, leading to deflated $\delta^{15}N$ values relative to fish trophic level. Future investigations should analyze the stable isotope signatures of zoo- and phytoplankton, macroalgae, and macroinvertebrates from fish pond systems to normalize for differences in ambient $\delta^{13}C$ and $\delta^{15}N$ across pond systems.

Despite the higher slope of THg concentration with increasing fish length across genera of HHP, this pond had relatively low surface water MeHg levels (mean = 0.012 ng/L) (Fig. 6), which could be due to a combination of high pH and specific conductivity (i.e., salinity) (Supplement Fig. 1). The biannual oceanic openings of Hummock Pond raise both the pH and the salinity of the entire pond system, including HHP (Curly 2002), which may reduce the pool of Hg²⁺ available for microbial methylation (Xun et al. 1987; Julian and Gu 2014). Yet, at greater fish lengths, genera from HHP expressed ln-THg concentrations comparable to those from ponds with higher aqueous MeHg levels (Figs. 5 and 6). Thus, our findings from HHP support that surface water MeHg levels cannot be used as the only variable to predict biota THg levels across systems. Although our measurements of environmental predictors were limited (n = 2-6 total measurements of each metric perpond; Supplemental Table 2; Supplement Fig. 1), all measurements of Chl a, pH, and specific conductivity matched general trends in each pond derived from historical measurements (Sutherland and Molden 2017).

Both our within-pond and across-pond fish comparisons suggest that regressions of fish ln-THg concentration versus fish length can reveal important differences both in the magnitude and slope of THg bioaccumulation. Fish ln-THg concentration has been found to increase linearly with fish length across species in previous studies (Sonesten 2003, Cizdziel et al. 2002). Similarly, linear regressions of fish THg versus fish stable nitrogen isotope ratio have been used to characterize the THg versus trophic level relationship of various pond biota (Kidd et al. 2012). Our findings support that these regression-based techniques can provide a crucial understanding of the changes in the slope of THg concentration with increasing fish length that might be hidden in size-controlled studies (e.g., our analysis of medium-length perch in Fig. 7). State measurements of local fish THg levels that are limited to a narrow length range of adult individuals (MA DEP 2000a, b) might miss length-based differences in the slope of THg bioaccumulation across different pond systems, especially in the absence of smaller fish lengths. Most regression-based analyses of fish In-THg versus fish length (Cizdziel et al. 2002), log-THg versus fish length (Sackett et al. 2013) or fish THg versus fish weight (Gilmour and Riedel 2000; Mason et al. 2006) focus on or only measure fish greater than 10 cm in length, which could misrepresent variations in fish MeHg levels at lower trophic levels during their juvenile stages. Given that we were able to replicate our regression analyses across different systems with relatively few fish across a length range (as few as 7 fish from 5.0 to 13.6 cm in the case of white perch from HHP), our findings suggest that In-THg versus fish length regressions could inform studies beyond the ecological range of characteristics found on Nantucket.

Implications for Fish Consumption on Nantucket Island

Our findings have implications for our understanding of local environmental health and the development of public health policy for fish consumption on Nantucket Island. Using the significant genus linear regressions derived from each pond, we projected the length at which fish from each regression exceed the EPA criterion for piscivorous birds (0.02 mg/kg), the general human health limit (0.30 mg/kg), and the recreational fisheries limit for human consumption (0.40 mg/kg) (Table 4). For all recreational fisheries species collected, the projected lengths at which fish exceed the recreational human fisheries health limit are located within the maximum adult length range (40.0 cm for pumpkinseed sunfish (CABI 2018a), 39.0-40.5 cm for bluegill sunfish (CABI 2018b), 50.0 cm for yellow perch (Frimodt 1995), and 49.5 cm for white perch (Page and Burr 1991). Furthermore, the length at which pond fish exceed the advisory limit for piscivorous birds was very low (max = 7.1 cm for sunfish in HHP), with all fish from some ponds (TNP, GP) projected as exceeding safe limits for bird consumption. Hence, local piscivorous bird species, such as the snowy egret (Egretta

			Fish Length at Which THg Exceeds Health Criterion (cm)					
Genus	Pond	Regression Equation	Piscivorous Birds (0.02 mg/kg)	General Human Health (0.30 mg/kg)	Recreational Human Fishers (0.40 mg/kg)			
Sunfish	TNP	$\ln[THg] = 0.111(cm) - 2.91$	0 ^{ab}	15.4 ª	18.0 ^a			
	GP	$\ln[THg] = 0.094(cm) - 3.52$	0 ^{ab}	24.6	27.7			
A week	MP	$\ln[THg] = 0.104(cm) - 3.78$	0 ^{ab}	24.8	27.5			
	WP	$\ln[THg] = 0.102(cm) - 3.92$	0.08 ^a	26.6	29.4			
	HHP	$\ln[THg] = 0.272(cm) - 5.85$	7.12 ª	17.1	18.1			
W. Perch	GP	$\ln[THg] = 0.096(cm) - 3.57$	0 ^{ab}	24.6	27.6			
	HHP	$\ln[THg] = 0.201(cm) - 5.21$	6.46 ^a	19.9	21.4			
Y. Perch								
	MP	$\ln[THg] = 0.110(cm) - 3.46$	0 ^{ab}	20.5	23.1			
V V								
Killifish	MP	$\ln[THg] = 0.346(cm) - 4.80$	2.57 ª	N/A^1	N/A^1			
	HHP	$\ln[THg] = 0.291(cm) - 5.50$	5.46 ª	N/A^1	N/A^1			

 Table 4
 A summary of the Nantucket pond fish lengths (cm) projected to exceed USEPA health criterion for piscivorous birds, general human health, and recreational human fishers

TNP=Tom Nevers Pond, GP=Gibbs Pond, MP=Miacomet Pond, WP=Washing Pond, HHP=Head of Hummock Pond, W. Perch=White Perch, Y. Perch=Yellow Perch

^aProjected length limit is within the range of fish that we collected. All other projected lengths are within the known size ranges of each genus ^bFor length values reported as zero, the regression indicates that a fish of any length would exceed the limit

¹Since killifish are not harvested in fisheries of any kind, projected lengths for the general human health and recreational fishing criteria were omitted

thula) and the great egret (*Ardea alba*) that frequent these systems (Nantucket Conservation Foundation 2018), also might be susceptible to heightened MeHg exposure.

Most notably, sunfish from TNP and HHP have a lower length at which THg concentrations exceed the human health criterion (In other words, smaller fish from these systems relative to others should be eaten with caution) (Table 4). (In other words, smaller fish from these systems relative to others should be eaten with caution.) The sunfish lengths exceeding the human health criterion in these ponds are lower than the mean lengths of adult sunfish (20.1 and 20.4 cm for bluegill and pumpkinseed, respectively). White perch from HHP also exhibit lower lengths exceeding advisory limits for human consumption than those found in GP. The higher magnitude of THg concentration across length in TNP, and the higher slope of THg concentration with fish length in HHP, appear to both heighten the advisory risk for consuming fish from these pond systems to a similar extent.

Conclusions

This study confirms that numerous Nantucket Island freshwater pond ecosystems contain relatively elevated levels of mercury, which could pose a health concern not only for the island's piscivorous wildlife but also for recreational fishers in at least two of the studied systems. By collecting a large sample of fish representing a wide range of lengths (2.2–20.7 cm) and four genera, we were able to develop simple linear regression models of ln-THg versus fish length that provided a detailed account of the intercept (i.e., magnitude) and slope (i.e., bioaccumulation) of THg concentration among fish within each pond system. We found that most juvenile fish mercury levels were high enough to adversely affect piscivorous wildlife on Nantucket, a discovery that was overlooked by previous mercury surveys that tested only fish within recreational catch limits. Future studies should continue to measure THg concentrations in a range of smaller fish to determine whether ln-THg versus fish length regressions reveal differences in the slope of THg bioaccumulation with increasing fish length that may be relevant for local environmental and human health policy.

Acknowledgments The authors thank Kaitlyn Shaw, water resource ecologist of the Town of Nantucket, and Nathan Porter, GIS coordinator of the Town of Nantucket, for providing historical water quality and ArcGIS data. They also extend thanks to Forrest Town and the Dartmouth Geography Department for providing the ArcGIS software necessary for their morphometric analyses, as well as the Dartmouth TEA Core Lab for their help with all mercury measurements. The authors also thank the Dartmouth Office of Undergraduate Advising and Research for their support through the Kaminsky Family Fund Award, the Dartmouth Department of Biological Sciences for their support through the Thomas B. Roos Memorial Fund, and the Dartmouth Superfund Research Program funded by NIH Grant Number P42 ES007373 from the National Institute of Environmental Health Sciences to Dr. Celia Chen. Comments from an anonymous reviewer were greatly appreciated. Finally, the authors thank many Backstrom and Hoyt family members for their assistance collecting fish in the field.

References

- Allen EA, Fell PE, Peck MA et al (1994) Gut contents of common mummichogs, *Fundulus heteroclitus L.*, in a restored impounded marsh and in natural reference marshes. Estuaries 17:462. https://doi.org/10.2307/1352676
- AMAP/UNEP (2013) Technical background report for the global mercury assessment (2013). Arctic Monitoring and Assessment Programme and United Nations Environment Programme, Geneva, Switzerland
- Benoit J, Gilmour C, Heyes A, Mason RP, Miller C (2003) Geochemical and biological controls over methylmercury production and degradation in aquatic ecosystems. In: Chai Y, Braids OC (eds) Biogeochemistry of environmentally important trace elements. ACS symposium series no. 835. American Chemical Society, Washington, DC, pp 262–297
- Bloom NS (1992) On the chemical form of mercury in edible fish and marine invertebrate tissue. Can J Fish Aquat Sci 49:1010–1017. https://doi.org/10.1139/f92-113
- Burger J, Gochfeld M (2011) Mercury and selenium levels in 19 species of saltwater fish from New Jersey as a function of species, size, and season. Sci Total Environ 409:1418–1429. https://doi. org/10.1016/j.scitotenv.2010.12.034
- CABI (2018a) Invasive species compendium: *Lepomis gibbosus* (pumpkinseed). https://www.cabi.org/isc/datasheet/77080. Accessed 11 May 2018
- CABI (2018b) Invasive species compendium: *Lepomis macrochirus* (bluegill). https://www.cabi.org/isc/datasheet/77082. Accessed 14 May 2018
- CABI (2018c) Invasive species compendium: Perca flavescens (yellow perch). https://www.cabi.org/isc/datasheet/70036. Accessed 12 May 2018

- Carlson RE (1977) A trophic state index for lakes. Limnol Oceanogr 22:361–369. https://doi.org/10.4319/lo.1977.22.2.0361
- Chen CY, Stemberger RS, Kamman NC et al (2005) Patterns of Hg bioaccumulation and transfer in aquatic food webs across multilake studies in the northeast US. Ecotoxicology 14:135–147. https://doi.org/10.1007/s10646-004-6265-y
- Chen CY, Driscoll CT, Kamman NC (2009) Mercury hotspots in freshwater ecosystems: drivers, processes, and patterns. Terr Aquat Environ Ch 9:143–166
- Chumchal MM, Hambright KD (2009) Ecological factors regulating mercury contamination of fish from Caddo Lake, Texas, USA. Environ Toxicol Chem 28:962. https://doi.org/10.1897/08-197.1
- Cizdziel JV, Hinners TA, Pollard JE et al (2002) Mercury concentrations in fish from Lake Mead, USA, related to fish size, condition, trophic level, location, and consumption risk. Arch Environ Contam Toxicol 43:309–317. https://doi.org/10.1007/ s00244-002-1191-6
- Clayden MG, Kidd KA, Chételat J et al (2014) Environmental, geographic and trophic influences on methylmercury concentrations in macroinvertebrates from lakes and wetlands across Canada. Ecotoxicology 23:273–284. https://doi.org/10.1007/ s10646-013-1171-9
- Curly T (2002) Hummock Pond annual report, 2002. Marine & Coastal Resource Department, Nantucket Island
- Driscoll CT, Han Y-J, Chen CY et al (2007) Mercury contamination in forest and freshwater ecosystems in the Northeastern United States. Bioscience 57:17–28. https://doi.org/10.1641/B570106
- Eagles-Smith CA et al (2015) Spatial and temporal patterns of mercury concentrations in freshwater fish across the Western United States and Canada. Sci Total Environ. https://doi.org/10.1016/j. scitotenv.2016.03.229
- Eagles-Smith CA, Silbergeld EK, Basu N et al (2018) Modulators of mercury risk to wildlife and humans in the context of rapid global change. Ambio 47:170–197. https://doi.org/10.1007/ s13280-017-1011-x
- Ethier ALM, Scheuhammer AM, Bond DE (2008) Correlates of mercury in fish from lakes near Clyde Forks, Ontario, Canada. Environ Pollut 154:89–97
- Evers DC, Taylor KM, Major A, Taylor RJ, Poppengha H, Scheuhammer AM (2003) Common loon eggs as indicators of methylmercury availability in North America. Ecotoxicology 12:69–81
- Evers DC, Burgess NM, Champoux L et al (2005) Patterns and interpretation of mercury exposure in freshwater avian communities in Northeastern North America. Ecotoxicology 14:193–221. https://doi.org/10.1007/s10646-004-6269-7
- Evers DC, Han Y-J, Driscoll CT et al (2007) Biological mercury hotspots in the Northeastern United States and Southeastern Canada. Bioscience 57:29–43. https://doi.org/10.1641/B570107
- Fernández-Delgado C (1989) Life-history patterns of the salt-marsh killifish *Fundulus heteroclitus (L.)* introduced in the estuary of the guadalquivir river (South West Spain). Estuar Coast Shelf Sci 29:573–582. https://doi.org/10.1016/0272-7714(89)90011-5
- Frimodt C (1995) Multilingual illustrated guide to the world's commercial coldwater fish. Fishing News Books, Osney Mead, Oxford, England, p 215
- Fry B, Mumford PL, Tam F et al (1999) Trophic position and individual feeding histories of fish from Lake Okeechobee, Florida. Can J Fish Aquat Sci 56:11
- Gabriel MC, Kolka R, Wickman T et al (2009) Evaluating the spatial variation of total mercury in young-of-year yellow perch (*Perca flavescens*), surface water and upland soil for watershed–lake systems within the southern Boreal Shield. Sci Total Environ 407:4117–4126. https://doi.org/10.1016/j.scitotenv.2009.03.019
- Gilmour CC, Riedel GS (2000) A survey of size-specific mercury concentrations in game fish from Maryland fresh and estuarine

waters. Arch Environ Contam Toxicol 39:53–59. https://doi. org/10.1007/s002440010079

- Gilmour CC, Riedel GS, Ederington MC et al (1998) Methylmercury concentrations and production rates across a trophic gradient in the northern Everglades. Biogeochemistry 40:327–345. https:// doi.org/10.1023/A:1005972708616
- Grandjean P, Cordier S, KjellströmT et al (2005) Health effects and risk assessments. Dynamics of Mercury Pollution at Regional and Global Scales Part IV: 511–538
- Greenfield BK, Hrabik TR, Harvey CJ, Carpenter SR (2001) Predicting mercury levels in yellow perch: use of water chemistry, trophic ecology, and spatial traits. Can J Fish Aquat Sci 58:1419–1429. https://doi.org/10.1139/cjfas-58-7-1419
- Grigal DF (2002) Inputs and outputs of mercury from terrestrial watersheds: a review. Environ Rev 10:1–39. https://doi. org/10.1139/a01-013
- Harris RC, Rudd JWM, Amyot M et al (2007) Whole-ecosystem study shows rapid fish-mercury response to changes in mercury deposition. Proc Natl Acad Sci 104:16586–16591. https://doi. org/10.1073/pnas.0704186104
- Hinck JE, Schmitt CJ, Chojnacki KA, Tillitt DE (2009) Environmental contaminants in freshwater fish and their risk to piscivorous wildlife based on a national monitoring program. Environ Monitor Assess 152:469–494. https://doi.org/10.1007/s1066 1-008-0331-5
- Jardine TD, Kidd KA, O'Driscoll N (2013) Food web analysis reveals effects of pH on mercury bioaccumulation at multiple trophic levels in streams. Aquat Toxicol 132–133:46–52. https://doi. org/10.1016/j.aquatox.2013.01.013
- Julian P, Gu B (2014) Mercury accumulation in largemouth bass (*Micropterus salmoides* Lacépède) within marsh ecosystems of the Florida Everglades, USA. Ecotoxicology 24:202–214. https ://doi.org/10.1007/s10646-014-1373-9
- Kamman NC, Lorey PM, Driscoll CT et al (2004) Assessment of mercury in waters, sediments, and biota of New Hampshire and Vermont Lakes, USA, sampled using a geographically randomized design. Environ Toxicol Chem 23:1172. https://doi. org/10.1897/03-170
- Kamman NC, Burgess NM, Driscoll CT et al (2005) Mercury in freshwater fish of Northeast North America: a geographic perspective based on fish tissue monitoring databases. Ecotoxicology 14:163– 180. https://doi.org/10.1007/s10646-004-6267-9
- Karagas MR, Choi AL, Oken E et al (2012) Evidence on the human health effects of low level methylmercury exposure. Environ Health Perspect 120:799–806
- Karimi R, Chen CY, Pickhardt PC et al (2007) Stoichiometric controls of mercury dilution by growth. Proc Natl Acad Sci 104:7477– 7482. https://doi.org/10.1073/pnas.0611261104
- Kidd KA, Muir DCG, Evans MS et al (2012) Biomagnification of mercury through lake trout (*Salvelinus namaycush*) food webs of lakes with different physical, chemical and biological characteristics. Sci Total Environ 438:135–143. https://doi.org/10.1016/j.scito tenv.2012.08.057
- Lavoie RA, Jardine TD, Chumchal MM et al (2013) Biomagnification of mercury in aquatic food webs: a worldwide meta-analysis. Environ Sci Technol 47:13385–13394. https://doi.org/10.1021/ es403103t
- MA DEP (2000a) Fish toxics monitoring public requests and year 2 watershed surveys. Massachusetts Department of Environmental Protection, Division of Watershed Management and Environmental analysis
- MA DEP (2000b) Islands watershed 2000 water quality assessment report. Massachusetts Department of Environmental Protection, Division of Watershed Management
- Mason RP, Heyes D, Sveinsdottir A (2006) Methylmercury concentrations in fish from tidal waters of the Chesapeake Bay. Arch

Environ Contam Toxicol 51:425–437. https://doi.org/10.1007/ s00244-004-0230-x

- Mergler D, Anderson HA, Chan LH et al (2007) Methylmercury exposure and health effects in humans: a worldwide concern. AMBIO J Hum Environ 36:3–11
- Miller EK, Chen C, Kamman N et al (2012) Mercury in the pelagic food web of Lake Champlain. Ecotoxicology 21:705–718. https ://doi.org/10.1007/s10646-011-0829-4
- Morway ED, Thodal CE, Marvin-DiPasquale M (2017) Long-term trends of surface-water mercury and methylmercury concentrations downstream of historic mining within the Carson River watershed. Environ Pollut 229:1006–1018. https://doi. org/10.1016/j.envpol.2017.07.090
- Nantucket Conservation Foundation (2018) Snowy and Great Egret. https://www.nantucketconservation.org/birds-overview/snowy -and-great-egret/. Accessed 14 May 2018
- Nantucket Historical Association: Research Library: Archival collections, Photographs, Nantucket Genealogy. https://www.nha.org/ library/index.html. Accessed 11 May 2018
- NJDEP (2012) Bluegill: *Lepomis macrochirus*. Division of Fish and Wildlife, New Jersey, USA. http://www.state.nj.us/dep/fgw/pdf/ fishfact/bluegill.pdf. Accessed 1 May 2018
- Nocera JJ, Taylor PD (1998) In situ behavioral response of common loons associated with elevated mercury (Hg) exposure. Ecol Soc 2:10
- Obrist D, Johnson DW, Lindberg SE et al (2011) Mercury distribution across 14 U.S. forests. Part I: spatial patterns of concentrations in biomass, litter, and soils. Environ Sci Technol 45:3974–3981. https://doi.org/10.1021/es104384m
- Obrist D, Kirk JL, Zhang L et al (2018) A review of global environmental mercury processes in response to human and natural perturbations: changes of emissions, climate, and land use. Ambio 47:116–140. https://doi.org/10.1007/s13280-017-1004-9
- Page LM, Burr BM (1991) A field guide to freshwater fishes of North America north of Mexico. Houghton Mifflin Company, Boston
- Pickhardt PC, Folt CL, Chen CY et al (2002) Algal blooms reduce the uptake of toxic methylmercury in freshwater food webs. Proc Natl Acad Sci 99:4419–4423. https://doi.org/10.1073/pnas.072531099
- Piraino MN, Taylor DL (2009) Bioaccumulation and trophic transfer of mercury in striped bass (*Morone saxatilis*) and tautog (*Tautoga onitis*) from the Narragansett Bay (Rhode Island, USA). Mar Environ Res 67:117–128. https://doi.org/10.1016/j.maren vres.2008.12.006
- Purdy A (2009) Mercury bioaccumulation in freshwater fish of Martha's Vineyard: assessing the health of a tribal resource. Senior Honors Thesis, Dartmouth College
- Riede K (2004) Global register of migratory species from global to regional scales. Final Report of the R&D-Projekt 808 05 081. Federal Agency for Nature Conservation, Bonn, Germany
- Rose J, Hutcheson MS, West C et al (1999) Fish mercury distribution in Massachusetts, USA lakes. Environ Toxicol Chem 18:1370–1379. https://doi.org/10.1002/etc.5620180705
- Rudd JWM (1995) Sources of methylmercury to freshwater ecosystems: a review. Water Air Soil Pollut 80:697–713
- Sackett DK, Cope GW, Rice JA, Aday DD (2013) The influence of fish length on tissue mercury dynamics: implications for natural resource management and human health risk. Int J Environ Res Public Health 10:638–659. https://doi.org/10.3390/ijerph1002 0638
- Scheuhammer AM, Basu N, Burgess NM et al (2008) Relationships among mercury, selenium, and neurochemical parameters in common loons (*Gavia immer*) and bald eagles (*Haliaeetus leucocephalus*). Ecotoxicology 17:93–101. https://doi.org/10.1007/ s10646-007-0170-0
- Sheehan MC, Burke TA, Navas-Acien A et al (2014) Global methylmercury exposure from seafood consumption and risk of

developmental neurotoxicity: a systematic review. Bull World Health Org 92:254–269F. https://doi.org/10.2471/blt.12.116152

- Simonin HA, Loukmas JJ, Skinner LC, Roy KM (2008) Lake variability: key factors controlling mercury concentrations in New York State fish. Environ Pollut 154:107–115. https://doi.org/10.1016/j. envpol.2007.12.032
- Sonesten L (2003) Fish mercury levels in lakes—adjusting for Hg and fish-size covariation. Environ Pollut 125:255–265. https://doi. org/10.1016/S0269-7491(03)00051-4
- Sundseth K, Pacyna J, Pacyna E et al (2017) Global sources and pathways of mercury in the context of human health. Int J Environ Res Public Health 14:105. https://doi.org/10.3390/ijerph14010105
- Sutherland, JW, Molden E (2017) Nantucket Island Ponds and 2016 water quality: Tom Nevers, Gibbs, Little Weweeder, Maxcy, Washing, and North Head of Long Ponds. A summary of physical, chemical, and biological monitoring. Nantucket Land Council, Inc
- USEPA (1997) Mercury study report to congress. Volume VI: an ecological assessment for anthropogenic mercury emissions in the United States. Office of Air Quality Planning Standards and Office of Research and Development: EPA-452/R-97-008
- USEPA (2000) Guidance for assessing chemical contaminant for use in fish advisories—third edition, volume 2: risk assessment and fish consumption limits, 823-B-00-008. http://www.epa.gov/water science/fish/guidance.html. Accessed 1 May 2018
- USEPA (2011) National listing of fisheries advisories. EPA-820-F-13-058

- USFDA (Food and Drug Administration) (1998) Action levels for poisonous or deleterious substances in human food and animal feed. Industry Activities Staff Booklet, Washington, DC
- Ward DM, Nislow KH, Chen CY, Folt CL (2010) Reduced trace element concentrations in fast-growing juvenile atlantic salmon in natural streams. Environ Sci Technol 44:3245–3251. https://doi. org/10.1021/es902639a
- Ward DM, Mayes B, Sturup S et al (2012) Assessing element-specific patterns of bioaccumulation across New England lakes. Sci Total Environ 421–422:230–237. https://doi.org/10.1016/j.scito tenv.2012.01.058
- Whittier TR, Paulsen SG, Larsen DP et al (2002) Indicators of ecological stress and their extent in the population of northeastern lakes: a regional-scale assessment. Bioscience 52:235. https://doi. org/10.1641/0006-3568(2002)052%5b0235:ioesat%5d2.0.co;2
- Wiener JG, Krabbenhoft DP, Heinz GH, Scheuhammer AM (2003) Ecotoxicology of mercury. In: Hoffman DJ, Rattner BA, Burton GAJ, Cairns JJ (eds) Handbook of ecotoxicology, 2nd edn. Lewis, Boca Raton, FL
- World Health Organization (2013). Mercury and health. Available at: http://www.who.int/news-room/fact-sheets/detail/mercury-andhealth. Accessed 11 May 2018
- Xun L, Campbell NER, Rudd JWM (1987) Measurements of specific rates of net methyl mercury production in the water column and surface sediments of acidified and circumneutral lakes. Can J Fish Aquat Sci 44:750–757. https://doi.org/10.1139/f87-091