

Supporting Information for

Estimating Mercury Exposure of Piscivorous Birds and Sport Fish Using Prey Fish Monitoring

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Supporting Information

EXPERIMENTAL SECTION

Grebe Sampling. We sampled grebes and fish at 25 lakes and reservoirs (hereafter termed *lakes*) throughout California from April through October during 2012 (13 lakes) and 2013 (12 lakes; **Figure S1**). We captured an average of 14 grebes per lake (range: 2-38 grebes) with night-lighting techniques.^{1,2} Briefly, we shined a high-powered spot light at grebes, which sometimes can disorient the bird long enough for capture with a long-handled net from a moving boat. We held birds in individual animal crates lined with towels (Plastic Pet Carrier, C Specialties Inc., Indianapolis, Indiana, USA) until processing and we released them near the site of capture. Western grebes and Clark's grebes were differentiated by plumage. We weighed each grebe with a digital bench scale (Ohaus ES6R, Ohaus Corporation, Parsippany, New York, USA) or spring scale (Pesola Spring Scales, Pesola Ag, Baar, Switzerland). We measured the distance from the back of the bird's head to the tip of the culmen, short tarsus length (tarsometatarsus bone), and culmen depth at the proximal end of the nares with digital calipers (Fowler electronic digital calipers, Newton, Massachusetts, USA), and flattened wing length with a wing board. We described wing molt by classifying each of the 10 primary feathers on the right wing with a value from 0 through 5: 0 represented an old feather grown the prior year, 1 represented a missing feather or a new feather that had not yet emerged from the feather quill, 2 represented a new feather $< \frac{1}{3}$ the length of a fully-grown feather, 3 represented a new feather between $\frac{1}{3}$ and $\frac{2}{3}$ the length of a fully-grown feather, 4 represented a new feather $> \frac{2}{3}$ the length of a fully grown feather, and 5 represented a new, fully-grown feather. We banded each bird with stainless steel U.S. Geological Survey leg bands to identify recaptures.

We obtained lake attribute data (lake area [ha], lake perimeter [km], and elevation [m]) from the U.S. Geological Survey National Hydrography Dataset (<http://nhd.usgs.gov>) and the California Department of Fish and Wildlife (ftp://ftp.dfg.ca.gov/BDB/GIS/California_Lakes).

Mercury Determination. THg concentrations were determined on a Milestone DMA-80 Direct Mercury Analyzer (Milestone, Monroe, Connecticut, USA) or a Nippon MA-3000 Direct Mercury Analyzer (Nippon Instruments North America, College Station, Texas, USA) following Environmental Protection Agency Method 7473,³ using an integrated sequence of drying, thermal decomposition, catalytic conversion, and then amalgamation, followed by atomic absorption spectroscopy. THg concentrations were determined at three different laboratories depending on tissue type: 1) bird eggs were analyzed at the U.S. Geological Survey, Dixon Field Station Environmental Mercury Laboratory (Dixon, California), 2) bird blood was analyzed at the U.S. Geological Survey, Corvallis Field Station Environmental Mercury Laboratory (Corvallis, Oregon), and 3) fish were analyzed at Moss Landing Marine Laboratories (Moss Landing, California).

Quality assurance measures included analyses of at least two certified reference materials (either dogfish muscle tissue [DORM], dogfish liver [DOLT], or lobster hepatopancreas [TORT] certified by the National Research Council of Canada, Ottawa, Canada), two system and method blanks, three continuing calibration verifications, two duplicates, and two spiked duplicates per batch. Recoveries (mean \pm SD) for blood samples were 99.2% \pm 0.4% ($n=34$) for certified reference materials, 99.2% \pm 0.5% ($n=52$) for calibration verifications, and 101.7% \pm 1.0% ($n=26$) for matrix spikes. Absolute relative percent difference for blood samples averaged 4.7% \pm 1.1% ($n=22$) for duplicates and 4.6% \pm 1.4% ($n=13$) for matrix spike duplicates. Recoveries (mean \pm SD) for egg samples were 100.0% \pm 4.3% ($n=28$) for certified reference materials, 98.1% \pm 2.2% ($n=32$) for calibration verifications, and 99.0% \pm 1.8% ($n=24$) for matrix spikes. Absolute relative percent

difference for egg samples averaged $3.1\% \pm 1.7\%$ ($n=21$) for duplicates and $1.3\% \pm 1.0\%$ ($n=12$) for matrix spike duplicates. Recoveries (mean \pm SD) for prey fish samples were $96.3\% \pm 4.8\%$ ($n=27$) for certified reference materials, $97.0\% \pm 6.6\%$ ($n=10$) for calibration verifications, and $96.2\% \pm 11.4\%$ ($n=54$) for matrix spikes. Absolute relative percent difference for prey fish averaged $8.0\% \pm 6.5\%$ ($n=27$) for duplicates and $4.1\% \pm 3.8\%$ ($n=27$) for matrix spike duplicates. Recoveries (mean \pm SD) for sport fish samples were $95.0\% \pm 5.9\%$ ($n=16$) for certified reference materials, $96.1\% \pm 7.0\%$ ($n=57$) for calibration verifications, and $97.7\% \pm 8.1\%$ ($n=32$) for matrix spikes. Absolute relative percent difference for sport fish averaged $5.6\% \pm 6.0\%$ ($n=16$) for duplicates and $4.9\% \pm 3.3\%$ ($n=16$) for matrix spike duplicates.

Statistical Analysis: Bird Body Condition Index. The body condition index was estimated as an individual's residual mass divided by its mass, where an individual's residual mass was calculated as the residual from a linear regression model of bird mass and structural body size. Structural body size of birds was calculated using a principal components analysis (PCA) of three structural body size measurements (length in mm of back of head to tip of culmen, short tarsus, and culmen depth) for each grebe species and sex. The PCA indicated that structural body size measurements were correlated as expected, and the first principal component (PC1) accounted for 54% (male) and 50% (female) of the morphological variation in western grebes and 56% (male) and 51% (female) of the morphological variation in Clark's grebes. Eigenvector weights of PC1 were positive and ranged from 0.41 to 0.67 (male) and 0.47 to 0.64 (female) for western grebes and from 0.50 to 0.63 (male) and 0.55 to 0.59 (female) for Clark's grebes.

Statistical Analysis: Akaike Information Criterion. We evaluated models using second-order Akaike Information Criterion (AICc) and considered the model with the smallest AICc to be the most parsimonious.⁴ We used AICc differences between the best model and each of the other candidate models ($\Delta AICc$) to determine the relative ranking of each model. For biological importance, we considered models for which $\Delta AICc \leq 2$. We used Akaike weights (w_i) to examine the weight of evidence that the selected model was the best model within the set of candidate models. We used evidence ratios to compare the relative weight of support between models. For brevity in the tables, we present only the set of best models that were within $\Delta AICc \leq 2$ (those considered for biological importance), the null model, and each model that was similar to the best model except one of the variables in the best model was removed (see Tables S3-S5).

Statistical Analysis: Adjusted Relative Variable Importance. We assessed the relative importance of each variable by summing Akaike weights across models that incorporated the same variable.⁴ Because the variables were not completely balanced in the candidate model set, and therefore had different prior variable weights, we further adjusted this relative variable importance by comparing the difference in final (or posterior) relative variable weight with its initial (or prior) weighting. Prior weighting represents the expected variable weight if all models in the candidate model set were equally weighted and was calculated as the proportion of models within the candidate model set in which a given variable was present. Adjusted relative variable importance was thus calculated as the log-odds ratio of the posterior (P) and prior (P_0) variable weights

$$\left(\ln \left[\frac{\left(\frac{P}{1-P} \right)}{\left(\frac{P_0}{1-P_0} \right)} \right] \right)$$
. Adjusted relative variable importance values that exceeded 0 had posterior weights

that were greater than was expected by their prior weighting and were considered to be important, and values less than 0 had posterior weights that were less than was expected by their prior weighting and were considered to be unimportant.

RESULTS

Predictive Equations: Grebe Blood. THg concentrations in grebe blood ($\mu\text{g/g ww}$) can be estimated using model-averaged coefficients from our full candidate model set:

$$(S1) \ln\left(\overline{GrebeBloodTHg_{\mu\text{g}_{ww}}}\right) = \beta_0 + 0.706 \left(\ln\left(\overline{PreyFishTHg_{\mu\text{g}_{dw}}}\right) \right) + 0.000408(\text{DayofYear} - 181) \\ - 0.0000258(\text{DayofYear} - 181)^2 + 0.00416(\text{LakePerimeter}_{km}) \\ - 0.00000270(\text{LakeArea}_{ha}) - 0.0496(\text{LakeShapeIndex}) \\ - 0.0000250(\text{LakeElevation}_m)$$

Where β_0 is a species and sex-specific coefficient that incorporates the potential effects of bird mass, body condition, and wing molt score. To uniquely predict THg concentrations by grebe species and sex, β_0 can be estimated using one of these four equations:

Western grebe females:

$$\beta_0 = 0.811 + 0.0000216(\text{Mass}) - 0.0698(\text{Molt}) + 0.00897(\text{Molt}^2) \\ - 0.0151(\text{BodyCondition})$$

Western grebe males:

$$\beta_0 = 1.01 + 0.0000216(\text{Mass}) - 0.0698(\text{Molt}) + 0.00897(\text{Molt}^2) \\ - 0.0151(\text{BodyCondition})$$

Clark's grebe females:

$$\beta_0 = 1.05 + 0.0000216(\text{Mass}) - 0.0698(\text{Molt}) + 0.00897(\text{Molt}^2) \\ - 0.0151(\text{BodyCondition})$$

Clark's grebe males:

$$\beta_0 = 1.24 + 0.0000216(\text{Mass}) - 0.0698(\text{Molt}) + 0.00897(\text{Molt}^2) \\ - 0.0151(\text{BodyCondition})$$

To estimate β_0 coefficient for each equation, we used species and sex-specific means for bird mass and body condition, and mode for wing molt score. Mean mass of western grebes was 1,055 g for females and 1,311 g for males. Mean mass of Clark's grebes was 1,021 g for females and 1,271 g for males. Mean body condition index of western grebes was -0.0156 for females and -0.0119 for males. Mean body condition index of Clark's grebes was -0.0109 for females and -0.00734 for males. Given the highly skewed nature of wing molt scores (87% of all grebes were captured prior to molt and therefore had a wing molt score of 0), we used the mode of molt score (0) for model prediction. Using these values, β_0 was estimated to be 0.834 for female western grebes, 1.04 for male western grebes, 1.07 for female Clark's grebes, and 1.27 for male Clark's grebes.

We can simplify the equation even further by assuming equal composition of grebes among species and sexes, and the four specific β_0 coefficients can be replaced with the average grebe β_0 coefficient of 1.05. Thus, the final equation to predict THg concentrations in grebe blood is:

$$\begin{aligned}
\text{(S2)} \quad \ln\left(\text{GrebeBlood}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{ww}}}\right) = & \\
& 1.05 + 0.706\left(\ln\left(\text{PreyFish}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{dw}}}\right)\right) + 0.000408(\text{DayofYear} - 181) \\
& - 0.0000258(\text{DayofYear} - 181)^2 + 0.00416(\text{LakePerimeter}_{\text{km}}) \\
& - 0.00000270(\text{LakeArea}_{\text{ha}}) - 0.0496(\text{LakeShapeIndex}) \\
& - 0.0000250(\text{LakeElevation}_{\text{m}})
\end{aligned}$$

where $\text{PreyFish}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{dw}}}$ is the least squares mean THg concentration in prey fish at a lake.

We can further simplify this equation by using median values for date and mean values for lake attributes. When we do so, the simplified equations to predict THg concentrations in grebe blood are:

$$\begin{aligned}
\text{(S3)} \quad \ln\left(\text{GrebeBlood}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{ww}}}\right) &= 1.11 + 0.706\left(\ln\left(\text{PreyFish}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{dw}}}\right)\right) \\
\text{(S4)} \quad \ln\left(\text{FemaleWesternGrebeBlood}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{ww}}}\right) &= 0.895 + 0.706\left(\ln\left(\text{PreyFish}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{dw}}}\right)\right) \\
\text{(S5)} \quad \ln\left(\text{MaleWesternGrebeBlood}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{ww}}}\right) &= 1.10 + 0.706\left(\ln\left(\text{PreyFish}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{dw}}}\right)\right) \\
\text{(S6)} \quad \ln\left(\text{FemaleClark'sGrebeBlood}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{ww}}}\right) &= 1.13 + 0.706\left(\ln\left(\text{PreyFish}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{dw}}}\right)\right) \\
\text{(S7)} \quad \ln\left(\text{MaleClark'sGrebeBlood}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{ww}}}\right) &= 1.33 + 0.706\left(\ln\left(\text{PreyFish}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{dw}}}\right)\right)
\end{aligned}$$

Predictive Equations: Grebe Eggs. For predicting THg concentrations in grebe eggs ($\mu\text{g/g}$ fww), we implemented a similar approach and predicted models for each unique combination of grebe species (western grebe, Clark's grebe, and unknown) and egg collection type (random and abandoned). The egg-specific coefficients in the model (β_0) were species, egg collection type, and nest initiation date. There was no difference in model predictions by grebe species or egg collection type, therefore we assumed equal composition of Clark's grebes and western grebes eggs as well as random and abandoned eggs. Lastly, we used the median nest initiation date for all eggs collected (median day of year was 211). Thus, the final equation to predict THg concentrations in grebe eggs is:

$$\begin{aligned}
\text{(S8)} \quad \ln\left(\text{GrebeEgg}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{fww}}}\right) & \\
&= -1.49 + 0.569\left(\ln\left(\text{PreyFish}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{dw}}}\right)\right) + 0.00197(\text{LakePerimeter}_{\text{km}}) \\
&+ 0.00000846(\text{LakeArea}_{\text{ha}}) + 0.0421(\text{LakeShapeIndex}) \\
&- 0.00000977(\text{LakeElevation})
\end{aligned}$$

We can further simplify this equation by using median values for date and mean values for lake attributes. When we do so, the equation to predict THg concentrations in grebe eggs is:

$$\text{(S9)} \quad \ln\left(\text{GrebeEgg}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{fww}}}\right) = -1.21 + 0.569\left(\ln\left(\text{PreyFish}\overline{\text{THg}}_{\frac{\mu\text{g}}{\text{g}}_{\text{dw}}}\right)\right)$$

Predictive Equations: Sport Fish. For predicting THg concentrations in sport fish ($\mu\text{g/g dw}$), we again implemented a similar model-averaging approach and predicted models for the two most abundant species of sport fish. The final equations to predict THg concentrations in sport fish are:

$$(S10) \ln\left(\text{SportFishTHg}_{\frac{\mu\text{g}}{\text{g}}\text{dw}}\right) = -0.630 + 0.00621(\text{TotalLength}_{\text{mm}}) \\ + 0.768\left(\ln\left(\text{PreyFishTHg}_{\frac{\mu\text{g}}{\text{g}}\text{dw}}\right)\right) + 0.0000205(\text{LakeArea}_{\text{ha}}) \\ - 0.000658(\text{LakeElevation}_{\text{m}}) - 0.000140(\text{LakePerimeter}_{\text{km}}) \\ - 0.0202(\text{LakeShapeIndex}) + 0.000309(\text{DayofYear} - 204) \\ + 0.00000161(\text{DayofYear} - 204)^2$$

$$(S11) \ln\left(\text{LargemouthBassTHg}_{\frac{\mu\text{g}}{\text{g}}\text{dw}}\right) = -0.237 + 0.00649(\text{TotalLength}_{\text{mm}}) \\ + 0.768\left(\ln\left(\text{PreyFishTHg}_{\frac{\mu\text{g}}{\text{g}}\text{dw}}\right)\right) + 0.0000205(\text{LakeArea}_{\text{ha}}) \\ - 0.000658(\text{LakeElevation}_{\text{m}}) - 0.000140(\text{LakePerimeter}_{\text{km}}) \\ - 0.0202(\text{LakeShapeIndex}) + 0.000309(\text{DayofYear} - 204) \\ + 0.00000161(\text{DayofYear} - 204)^2$$

$$(S12) \ln\left(\text{RainbowTroutTHg}_{\frac{\mu\text{g}}{\text{g}}\text{dw}}\right) = -0.865 + 0.00608(\text{TotalLength}_{\text{mm}}) \\ + 0.768\left(\ln\left(\text{PreyFishTHg}_{\frac{\mu\text{g}}{\text{g}}\text{dw}}\right)\right) + 0.0000205(\text{LakeArea}_{\text{ha}}) \\ - 0.000658(\text{LakeElevation}_{\text{m}}) - 0.000140(\text{LakePerimeter}_{\text{km}}) \\ - 0.0202(\text{LakeShapeIndex}) + 0.000309(\text{DayofYear} - 204) \\ + 0.00000161(\text{DayofYear} - 204)^2$$

We can further simplify these equations by using median values for date, 350 mm for total length, and mean values for lake attributes. When we do so, the equations to predict THg concentrations in sport fish are:

$$(S13) \ln\left(\text{SportFishTHg}_{\frac{\mu\text{g}}{\text{g}}\text{dw}}\right) = 1.06 + 0.768\left(\ln\left(\text{PreyFishTHg}_{\frac{\mu\text{g}}{\text{g}}\text{dw}}\right)\right)$$

$$(S14) \ln\left(\text{LargemouthBassTHg}_{\frac{\mu\text{g}}{\text{g}}\text{dw}}\right) = 1.56 + 0.768\left(\ln\left(\text{PreyFishTHg}_{\frac{\mu\text{g}}{\text{g}}\text{dw}}\right)\right)$$

$$(S15) \ln\left(\text{RainbowTroutTHg}_{\frac{\mu\text{g}}{\text{g}}\text{dw}}\right) = 0.783 + 0.768\left(\ln\left(\text{PreyFishTHg}_{\frac{\mu\text{g}}{\text{g}}\text{dw}}\right)\right)$$

Predictive Models' Fit. We compared model-averaged predictions to our individual raw THg concentrations and found good agreement for both the complex model (see **Figure S3** in the Supporting Information) as well as the simplified model that only included THg concentrations in prey fish. For the complex model, predicted THg concentrations were correlated with raw THg concentrations observed in grebe blood ($R^2 = 0.61$, $n=353$; **Figure S3a**), grebe eggs ($R^2 = 0.47$,

$n=101$; **Figure S3b**), and sport fish ($R^2 = 0.83$, $n=230$; **Figure S3c**). For the simplified model that only included THg concentrations in prey fish, model fit was only slightly reduced for predicted THg concentrations in grebe blood ($R^2 = 0.52$, $n=353$) and grebe eggs ($R^2 = 0.43$, $n=101$), indicating that the simplified equation be used to predict THg concentrations in adult grebe blood and eggs. However, there was a substantial reduction in model fit for the simplified sport fish model ($R^2=0.29$), indicating the importance of the additional sport fish variables, such as sport fish species, total length, and lake attributes.

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Table S1. Common names, scientific names, sample sizes, and proportion of prey fish species sampled in California during 2012–2013.

Common Name	Scientific Name	Sample Size	Percentage of Total Prey Fish Sampled
bluegill	<i>Lepomis macrochirus</i>	150	30%
Mississippi silverside	<i>Menidia audens</i>	110	22%
threadfin shad	<i>Dorosoma petenense</i>	70	14%
golden shiner	<i>Notemigonus crysoleucas</i>	40	8%
Sacramento perch	<i>Archoplites interruptus</i>	27	5%
Sacramento sucker	<i>Catostomus occidentalis</i>	20	4%
tui chub	<i>Gila bicolor</i>	18	4%
blue chub	<i>Gila coerulea</i>	10	2%
hitch	<i>Lavinia exilicauda</i>	10	2%
largemouth bass	<i>Micropterus salmoides</i>	10	2%
pumpkinseed sunfish	<i>Lepomis gibbosus</i>	10	2%
redeer sunfish	<i>Lepomis microlophus</i>	10	2%
smallmouth bass	<i>Micropterus dolomieu</i>	10	2%
Tahoe sucker	<i>Catostomus tahoensis</i>	10	2%

Table S2. Common names, scientific names, sample sizes, and proportion of sport fish species sampled in California during 2012–2013.

Common Name	Scientific Name	Sample Size	Percentage of Total Sport Fish Sampled
largemouth bass	<i>Micropterus salmoides</i>	156	68%
rainbow trout	<i>Oncorhynchus mykiss</i>	40	17%
brown trout	<i>Salmo trutta</i>	12	5%
smallmouth bass	<i>Micropterus dolomieu</i>	12	5%
Eagle Lake rainbow trout	<i>Oncorhynchus mykiss aquilarum</i>	10	4%

Table S3. Ranking of candidate model set describing western grebe and Clark's grebe blood total mercury (THg) concentrations ($n=353$ grebes) at 25 lakes in California during 2012–2013. Akaike's Information Criterion (AIC_c) was used to rank models. Lake was a random effect in all models. We present only the top models that were within $\Delta AIC_c \leq 2$, the null model (shaded), and each model that was similar to the top model except one of the variables in the top model was removed (only shaded if $\Delta AIC_c > 2$). The + denotes an additive effect. k indicates the number of parameters in the model, including the intercept. $-2\log L$ indicates the $-2\log$ -likelihood of the model. ΔAIC_c represents the difference in the value between AIC_c of the current model and the value for the most parsimonious model. Akaike weight (w_i) represents the likelihood of the model given the data, relative to other models in the candidate set (model weights sum to 1.0). The evidence ratio represents the weight of evidence that the top model is better than the selected model, given the candidate model set.

Model	k	$-2\log L$	AIC_c	ΔAIC_c	w_i	Evidence ratio	Cumulative weight
THg Prey Fish + Species + Sex + Molt + Lake Perimeter	7	545.25	559.58	0.00	0.02	1.00	0.02
THg Prey Fish + Species + Sex + Lake Perimeter	6	547.40	559.64	0.06	0.02	1.03	0.04
THg Prey Fish + Species + Sex + Molt + Lake Perimeter + Molt ²	8	543.61	560.03	0.45	0.02	1.25	0.06
THg Prey Fish + Species + Sex + Date + Lake Perimeter + Date ²	8	543.77	560.19	0.62	0.02	1.36	0.08
THg Prey Fish + Species + Sex + Molt + Lake Perimeter + Lake Shape	8	544.26	560.67	1.10	0.01	1.73	0.09
THg Prey Fish + Species + Sex + Date + Molt + Lake Perimeter + Date ²	9	542.17	560.69	1.12	0.01	1.75	0.11
THg Prey Fish + Species + Sex + Lake Perimeter + Lake Shape	7	546.49	560.81	1.24	0.01	1.85	0.12
THg Prey Fish + Species + Sex + Molt + Lake Perimeter + Lake Shape + Molt ²	9	542.55	561.08	1.50	0.01	2.12	0.13
THg Prey Fish + Species + Sex + Date + Lake Perimeter + Lake Shape + Date ²	9	542.68	561.20	1.62	0.01	2.25	0.14
THg Prey Fish + Species + Sex + Date + Lake Perimeter + Lake Area + Lake Shape + Date ²	10	540.74	561.39	1.81	0.01	2.47	0.15
THg Prey Fish + Species + Sex + Lake Perimeter + Lake Area + Lake Shape	8	544.97	561.39	1.81	0.01	2.47	0.16
THg Prey Fish + Species + Sex + Molt + Lake Perimeter + Lake Area + Lake Shape	9	542.88	561.41	1.83	0.01	2.50	0.17
THg Prey Fish + Species + Sex + Date + Lake Perimeter	7	547.09	561.42	1.84	0.01	2.51	0.17
THg Prey Fish + Species + Sex + Date + Molt + Lake Perimeter + Date ² + Molt ²	10	540.80	561.45	1.87	0.01	2.55	0.18
THg Prey Fish + Species + Sex + Body Condition + Lake Perimeter	7	547.15	561.47	1.90	0.01	2.58	0.19
THg Prey Fish + Species + Sex + Molt + Lake Area	7	547.23	561.55	1.97	0.01	2.68	0.20
THg Prey Fish + Species + Sex + Date + Molt + Lake Perimeter + Lake Shape + Date ²	10	540.95	561.59	2.01	0.01	2.74	0.21
THg Prey Fish + Species + Sex + Molt	6	550.76	563.00	3.42	0.00	5.54	0.48
THg Prey Fish + Sex + Molt + Lake Perimeter	6	558.86	571.10	11.53	0.00	318.27	0.99
THg Prey Fish + Species + Molt + Lake Perimeter	6	559.45	571.70	12.12	0.00	428.11	0.99
Species + Sex + Molt + Lake Perimeter	6	576.77	589.02	29.44	0.00	2.47×10^6	1.00
Null (Lake as random effect)	2	608.62	612.66	53.08	0.00	3.36×10^{11}	1.00

Table S4. Ranking of candidate model set describing western grebe and Clark's grebe egg total mercury (THg) concentrations ($n=101$ eggs) at 7 lakes in California during 2012–2013. Akaike's Information Criterion (AIC_c) was used to rank models. Lake was a random effect in all models. We present only the top models that were within $\Delta AIC_c \leq 2$, the null model (shaded), and each model that was similar to the top model except one of the variables in the top model was removed (only shaded if $\Delta AIC_c > 2$). The + denotes an additive effect. k indicates the number of parameters in the model, including the intercept. $-2\log L$ indicates the $-2\log$ -likelihood of the model. ΔAIC_c represents the difference in the value between AIC_c of the current model and the value for the most parsimonious model. Akaike weight (w_i) represents the likelihood of the model given the data, relative to other models in the candidate set (model weights sum to 1.0). The evidence ratio represents the weight of evidence that the top model is better than the selected model, given the candidate model set.

Model	k	$-2\log L$	AIC_c	ΔAIC_c	w_i	Evidence ratio	Cumulative weight
THg Prey Fish + Date + Lake Perimeter	5	110.29	120.92	0.00	0.04	1.00	0.04
THg Prey Fish	3	114.71	120.95	0.03	0.04	1.02	0.08
THg Prey Fish + Lake Perimeter	4	112.95	121.37	0.45	0.03	1.25	0.11
THg Prey Fish + Date	4	113.23	121.65	0.73	0.03	1.44	0.14
THg Prey Fish + Lake Area	4	113.35	121.76	0.84	0.03	1.52	0.17
THg Prey Fish + Date + Lake Area	5	111.25	121.88	0.96	0.02	1.62	0.19
THg Prey Fish + Lake Shape	4	113.51	121.93	1.01	0.02	1.65	0.21
THg Prey Fish + Egg Type	4	113.57	121.99	1.06	0.02	1.70	0.24
THg Prey Fish + Egg Type + Lake Perimeter	5	111.75	122.38	1.46	0.02	2.07	0.26
Date + Lake Area + Lake Shape	5	111.96	122.59	1.67	0.02	2.30	0.28
THg Prey Fish + Date + Lake Perimeter + Lake Area	6	109.84	122.73	1.81	0.02	2.47	0.29
THg Prey Fish + Date + Lake Shape	5	112.17	122.80	1.88	0.02	2.56	0.31
THg Prey Fish + Date + Lake Perimeter + Date ²	6	109.94	122.83	1.91	0.02	2.60	0.32
THg Prey Fish + Egg Type + Lake Area	5	112.20	122.83	1.91	0.02	2.60	0.34
THg Prey Fish + Date + Date ²	5	112.22	122.86	1.93	0.02	2.63	0.35
THg Prey Fish + Date + Lake Perimeter + Lake Shape	6	109.96	122.86	1.94	0.02	2.63	0.37
THg Prey Fish + Egg Type + Date + Lake Perimeter	6	110.21	123.11	2.19	0.01	2.98	0.38
Date + Lake Perimeter	4	119.88	128.30	7.37	0.00	39.92	0.94
Null (Lake as random effect)	2	125.43	129.55	8.63	0.00	74.72	0.97

Table S5. Ranking of candidate model set describing sport fish total mercury (THg) concentrations ($n=230$ fish) at 24 lakes in California during 2012–2013. Akaike's Information Criterion (AIC_c) was used to rank models. Lake was a random effect in all models. We present only the top models that were within $\Delta AIC_c \leq 2$, the null model (shaded), and each model that was similar to the top model except one of the variables in the top model was removed (only shaded if $\Delta AIC_c > 2$). The + denotes an additive effect and the \times denotes an interaction. k indicates the number of parameters in the model, including the intercept. $-2\log L$ indicates the $-2\log$ -likelihood of the model. ΔAIC_c represents the difference in the value between AIC_c of the current model and the value for the most parsimonious model. Akaike weight (w_i) represents the likelihood of the model given the data, relative to other models in the candidate set (model weights sum to 1.0). The evidence ratio represents the weight of evidence that the top model is better than the selected model, given the candidate model set.

Model	k	$-2\log L$	AIC_c	ΔAIC_c	w_i	Evidence ratio	Cumulative weight
THg Prey Fish + Species + Length + Lake Elevation + Lake Area + Species \times Length	14	248.52	278.48	0.00	0.14	1.00	0.14
THg Prey Fish + Species + Length + Lake Elevation + Species \times Length	13	251.15	278.84	0.36	0.12	1.20	0.26
THg Prey Fish + Species + Length + Lake Elevation + Lake Perimeter + Lake Area + Species \times Length	15	247.24	279.49	1.01	0.09	1.66	0.35
THg Prey Fish + Species + Length + Lake Elevation + Lake Area + Lake Shape + Species \times Length	15	247.44	279.68	1.21	0.08	1.83	0.42
THg Prey Fish + Species + Length + Lake Elevation + Lake Shape + Species \times Length	14	250.37	280.33	1.85	0.06	2.52	0.48
THg Prey Fish + Species + Length + Date + Lake Elevation + Lake Area + Species \times Length	15	248.13	280.37	1.90	0.06	2.58	0.54
THg Prey Fish + Species + Length + Lake Elevation + Lake Perimeter + Lake Shape + Species \times Length	15	248.54	280.79	2.31	0.04	3.17	0.58
THg Prey Fish + Length + Lake Elevation + Lake Area	6	271.80	284.18	5.70	0.01	17.28	0.88
THg Prey Fish + Species + Length + Lake Elevation + Lake Area	10	265.08	286.09	7.61	0.00	44.93	0.94
THg Prey Fish + Species + Length + Lake Area + Species \times Length	13	258.58	286.27	7.79	0.00	49.13	0.95
Species + Length + Lake Elevation + Lake Area + Species \times Length	13	274.89	302.58	24.10	0.00	1.71×10^5	1.00
THg Prey Fish + Species + Lake Elevation + Lake Area	9	391.46	410.28	131.80	0.00	4.18×10^{28}	1.00
Null (Lake as random effect)	2	455.61	459.67	181.19	0.00	2.21×10^{39}	1.00

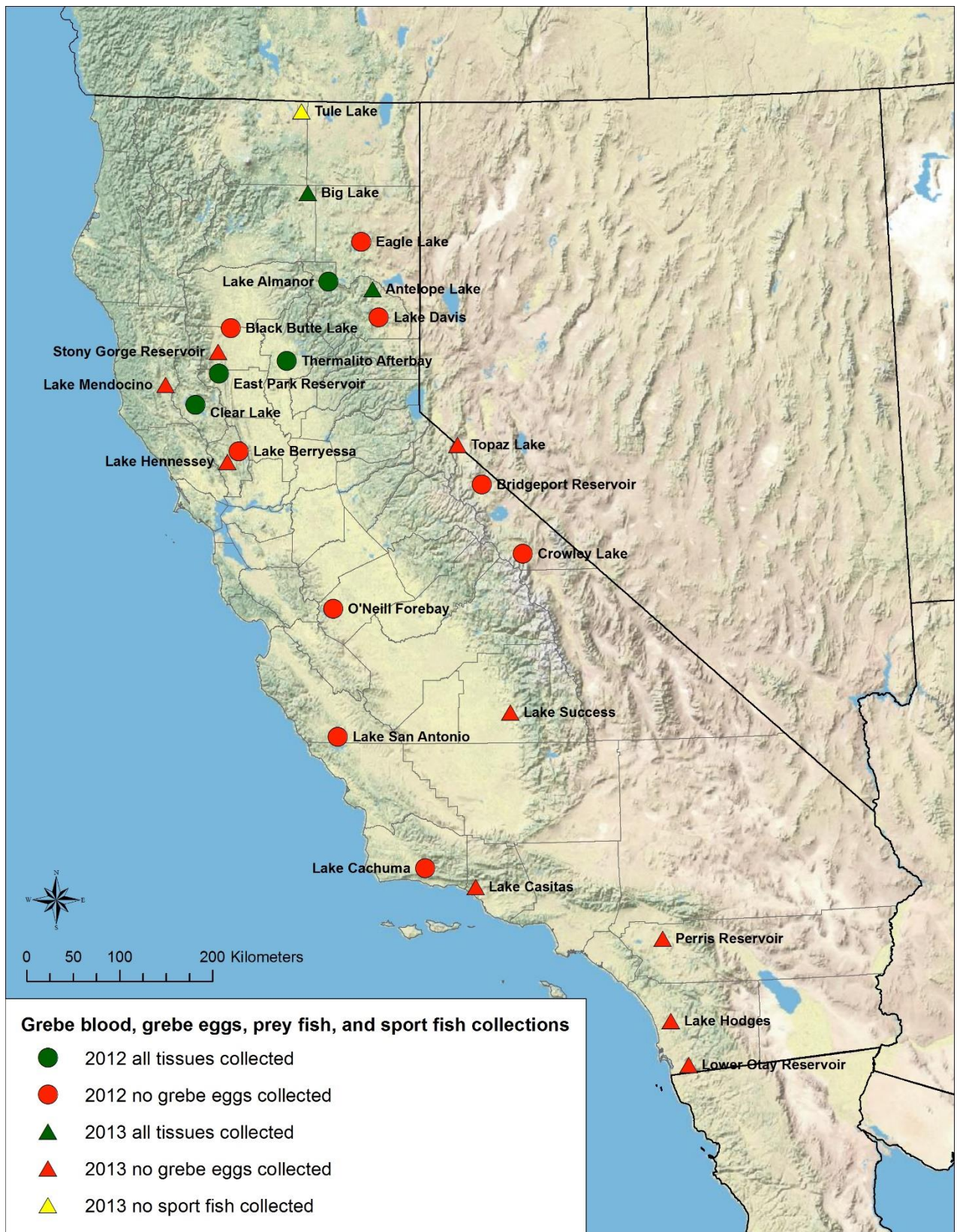


Figure S1. Map showing the 25 lakes and reservoirs that were sampled for grebes, sport fish, and prey fish in California, 2012–2013.

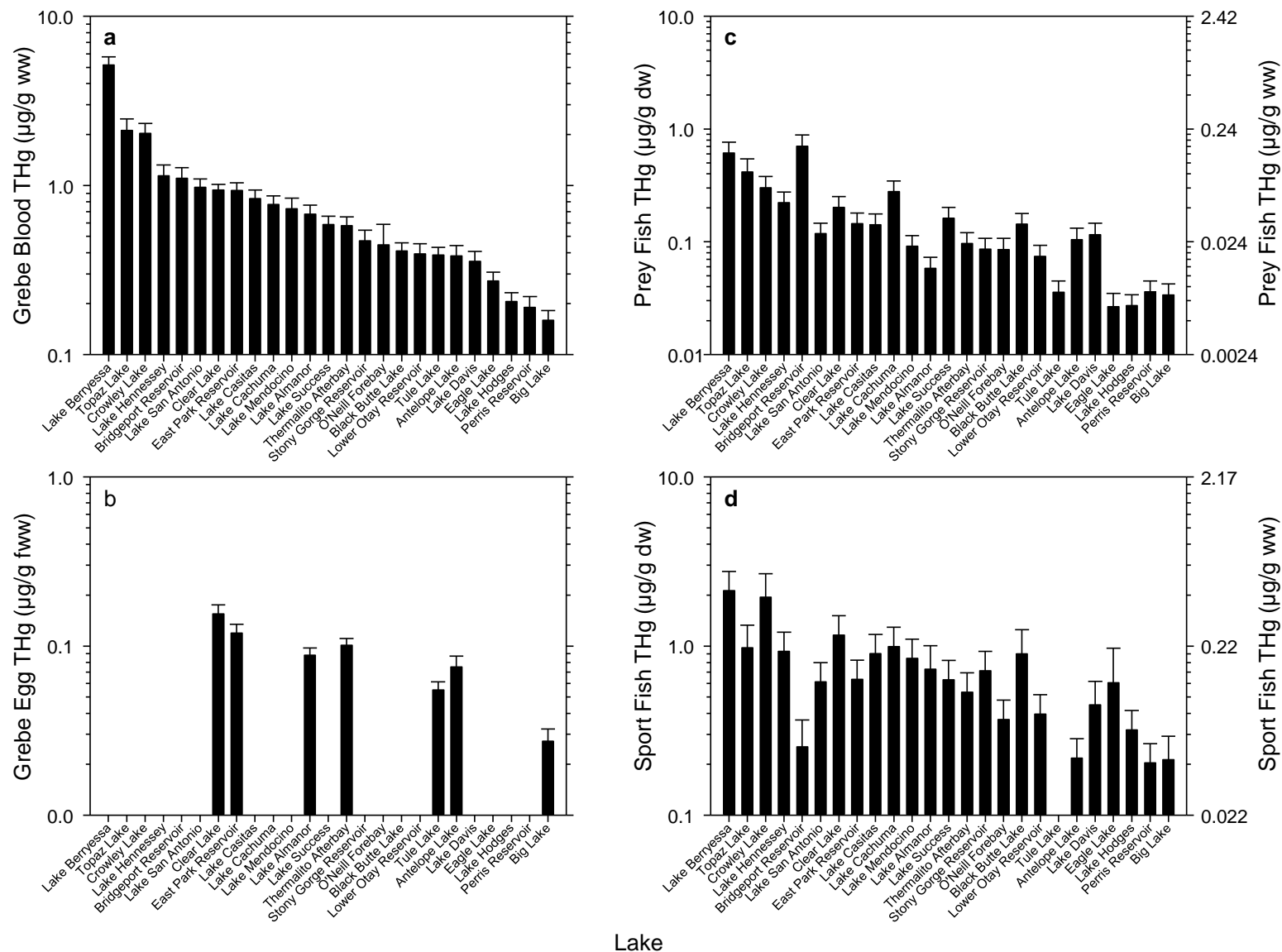


Figure S2. Total mercury concentrations (THg $\mu\text{g/g dw}$ [left axis] or THg $\mu\text{g/g ww}$ [right axis]) in (a) grebe blood, (b) grebe eggs, (c) prey fish, and (d) sport fish sampled at up to 25 lakes in California, 2012–2013. Values are least squares means \pm standard errors from separate models accounting for (a) grebe blood model: species and sex, with lake as a random effect; (b) grebe egg model: species and egg type, with lake as a random effect; (c) prey fish model: species, standard length, and species \times length interaction, with lake as a random effect; and (d) sport fish model: species, total length, and species \times length interaction, with lake as a random effect.

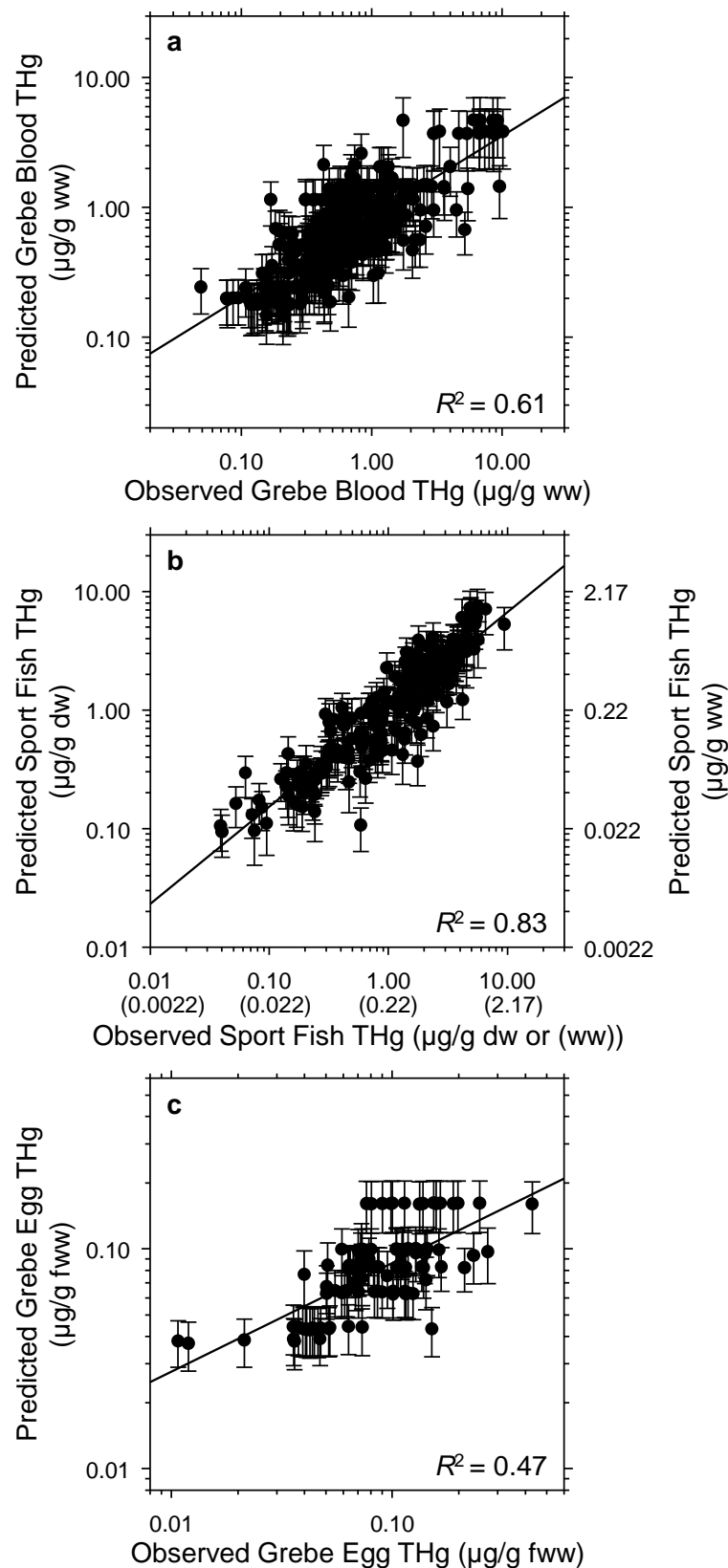


Figure S3. Model-predicted mean \pm standard errors total mercury concentrations (THg $\mu\text{g/g dw}$ [left axis] or THg $\mu\text{g/g ww}$ [right axis]) versus observed (raw) THg concentrations (THg $\mu\text{g/g dw}$ [top row] or THg $\mu\text{g/g ww}$ [bottom row]) in (a) grebe blood ($n=354$), (b) sport fish ($n=230$), and (c) grebe eggs ($n=101$) in California, 2012–2013. Model predictions were generated by using individual-specific data associated with the raw data point for all variables in the final model.