Trophic Magnification of PCBs and Its Relationship to the Octanol–Water Partition Coefficient

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Abstract: We investigated polychlorinated biphenyl (PCB) bioaccumulation relative to octanol—water partition coefficient ($K_{OW}$) and organism trophic position (TP) at the Lake Hartwell Superfund site (South Carolina). We measured PCBs (127 congeners) and stable isotopes ($\delta^{15}N$) in sediment, organic matter, phytoplankton, zooplankton, macroinvertebrates, and fish. TP, as calculated from $\delta^{15}N$, was significantly, positively related to PCB concentrations, and food web trophic magnification factors (TMFs) ranged from 1.5–6.6 among congeners. TMFs of individual congeners increased strongly with log $K_{OW}$, as did the predictive power ($r^2$) of individual TP-PCB regression models used to calculate TMFs. We developed log $K_{OW}$-TMF models for eight food webs with vastly different environments (freshwater, marine, arctic, temperate) and species composition (cold- vs warmblooded consumers). The effect of $K_{OW}$ on congener TMFs varied strongly across food webs (model slopes 0.0–15.0) because the range of TMFs among studies was also highly variable. We standardized TMFs within studies to mean = 0, standard deviation (SD) = 1 to normalize for scale differences and found a remarkably consistent $K_{OW}$ effect on TMFs (no difference in model slopes among food webs). Our findings underscore the importance of hydrophobicity (as characterized by $K_{OW}$) in regulating bioaccumulation of recalcitrant compounds in aquatic systems, and demonstrate that relationships between chemical $K_{OW}$ and bioaccumulation from field studies are more generalized than previously recognized.

Introduction

Persistent organic contaminants (OCs) are widespread in the environment and pose serious health risks to humans and wildlife.1,2 Regulatory agencies have long relied on bioconcentration factors (BCFs) or bioaccumulation factors (BAFs) to evaluate risks and manage toxic substances,3 but trophic magnification factors (TMFs) derived from stable isotope analysis are increasingly used to quantify biomagnification of OCs in the environment.4 TMFs, which measure the average biomagnification of contaminants through food webs, have a number of advantages over traditional BCFs and BAFs because they are not prone to uncertainty in measurement of water concentrations, they account for ecological complexity in trophic interactions, and they measure biomagnification across entire food webs rather than for individual species.3–6

In spite of the widespread application of the TMF approach, challenges remain in identifying general patterns in biomagnification among ecosystems and food webs. TMFs for a given OC can vary widely among studies depending on the types of consumers (e.g., poikilotherms or homeotherms) included in the analysis, the range of trophic levels investigated, and other factors.7–9 These issues arise not only when comparing the magnitude of biomagnification among systems for single contaminants, but also when investigating biomagnification related to physical/chemical properties of OCs themselves.

The n-octanol–water partition coefficient ($K_{OW}$) is a primary regulator of biomagnification of recalcitrant compounds like PCBs in aquatic food webs.10,11 Compound $K_{OW}$s are constant among different environments, although they vary slightly with temperature12 and salinity.13 However, TMFs for PCBs increase sharply (up to 15×) with each unit increase in log $K_{OW}$ in some

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Table 1. Scientiﬁc values for each food web component. Organic matter: \( \text{MM} \), Macromia, \( \text{mi} \), midge; \( \text{zo} \), zooplankton. Fish: \( \text{bb} \), black buffalo; \( \text{bh} \), black bullhead; \( \text{bc} \), black crappie; \( \text{bg} \), bluegill; \( \text{ca} \), common carp; \( \text{cc} \), channel catﬁsh; 
\( \text{ds} \), dollar sunﬁsh; \( \text{fc} \), ﬂathead catﬁsh; \( \text{gs} \), green sunﬁsh; \( \text{gz} \), gizzard shad; \( \text{hc} \), highﬁn carpsucker; \( \text{lb} \), largemouth bass; \( \text{rb} \), redbreast sunﬁsh; \( \text{rs} \), redear sunﬁsh; \( \text{ts} \), threadfins shad; \( \text{wb} \), white bass; \( \text{ws} \), whiteﬁn shiner; \( \text{wm} \), warmouth; \( \text{yp} \), yellow perch. Parameters for regression models are provided in Table 1. Scientiﬁc names are provided in SI Table S1.

Figure 1. Relationship between trophic position (TP) and PCB concentrations (ng g\(^{-1}\) lipid) for the Lake Hartwell food web. Symbols represent mean values for each food web component. Organic matter: \( \text{bi} \), bioﬁlm; \( \text{cp} \), CPOM; \( \text{ph} \), phytoplankton. Invertebrates: \( \text{ac} \), Asian clam; \( \text{go} \), gomphidae; \( \text{ma} \), Macromia, \( \text{mi} \), midge; \( \text{zo} \), zooplankton. Fish: \( \text{bb} \), black buffalo; \( \text{bh} \), black bullhead; \( \text{bc} \), black crappie; \( \text{bg} \), bluegill; \( \text{ca} \), common carp; \( \text{cc} \), channel catﬁsh; 
\( \text{ds} \), dollar sunﬁsh; \( \text{fc} \), ﬂathead catﬁsh; \( \text{gs} \), green sunﬁsh; \( \text{gz} \), gizzard shad; \( \text{hc} \), highﬁn carpsucker; \( \text{lb} \), largemouth bass; \( \text{rb} \), redbreast sunﬁsh; \( \text{rs} \), redear sunﬁsh; \( \text{ts} \), threadfins shad; \( \text{wb} \), white bass; \( \text{ws} \), whiteﬁn shiner; \( \text{wm} \), warmouth; \( \text{yp} \), yellow perch. Parameters for regression models are provided in Table 1. Scientiﬁc names are provided in SI Table S1.

food webs but show little or no increase in others.\(^9,14\) It is unclear if these differences (i.e., apparent overall dependence of the TMF upon the \( K_{OW} \) of the chemical) are related to ecological differences among food webs or to methodological differences among studies.

We investigated patterns of PCB biomagniﬁcation in Lake Hartwell (South Carolina), a warm-temperate reservoir with a legacy of severe contamination.\(^1\)\(^5\) Our ﬁrst objective was to characterize PCB biomagniﬁcation within the Lake Hartwell food web, and we expected that PCB concentrations would increase with trophic position (TP). Next, we quantiﬁed the dependence of the TMF upon the \( K_{OW} \) for PCB congeners and the predictive power (i.e., coefﬁcient of determination, \( r^2 \)) explained by TP-PCB regression models. TMFs and predictive power of TP on congener concentrations should increase with hydrophobicity.\(^16\)\(^\text{ff} \)\(^11\) Finally, we used an innovative approach to analyze or interpret \( \log K_{OW} - \text{TMF} \) relationships from Lake Hartwell and other published studies to describe the generality of \( K_{OW} \) effects on PCB biomagniﬁcation.

EXPERIMENTAL SECTION

Study Area. Lake Hartwell was contaminated with PCBs from the Sangamo-Weston capacitor plant located on a tributary 25 km upstream of the reservoir. The plant discharged \( \sim 181.4 \) t of PCBs, primarily Aroclors 1016, 1242, and 1254, into the aquatic environment from 1955 to 1977.\(^15\) The Twelvemile Creek arm (TCA) of Lake Hartwell (Supporting Information (SI) Figure S1) remains heavily contaminated with PCBs.\(^16\)\(^\text{ff} \)\(^18\) Sediment concentrations generally range from \( \sim 500 - 6500 \) ng g\(^{-1}\) (dry weight) in the TCA,\(^16\) peaking near the top of the reservoir and then gradually declining down-lake.\(^18\) The TCA has mostly ﬁne-grained sediments (sand, silt and clay), and macrophytes are uncommon due to ﬂuctuating water levels, steep banks, and high turbidity.

Food Web Characterization. Detailed methods for sample collection and storage are provided in the SI. We collected samples of sediment, organic matter, zooplankton, macroinvertebrates, and fish in Lake Hartwell in 2005 and 2006 (SI Figure S1). Organic matter sources for the food web included CPOM (coarse particulate organic matter), epiphytic algae (bioﬁlm), and phytoplankton. Zooplankton were pooled for analysis. The dominant taxa were Keratella sp. (Rotifera) and Diaptomidae (Calanoida, Copepoda); other abundant taxa are listed in the SI. Macroinvertebrate taxa included midges (nontanypodinae chironomids), odonates, and Asian clam (Corbicula ﬂuminica) (SI Table S1). We collected 21 fish species ranging from ﬁlter feeding planktivores to piscivores (SI Table S1). Subsamples of CPOM, bioﬁlm, phytoplankton, and zooplankton were removed for stable isotope analysis. Macroinvertebrate samples for PCB and stable isotope analysis were composites of multiple individuals. Fish were analyzed whole for PCBs, and skinless dorsal muscle tissue was analyzed for stable isotopes. Fish were analyzed individually except for...
small-bodied fishes (<150 mm total length) which were com-
posited for PCB and stable isotope analysis. Only adult fishes
were sampled to avoid variation in chemical signatures that
could be related to ontogenetic changes in diet.

**Analysis of PCBs, Lipids, and TOC.** Detailed methods for
sample extraction, PCB quantification, quality control pro-
dures, and total organic carbon (TOC) analysis are provided in
the SI. Analysis for PCB congeners was by gas chromatography/
mass spectrometry (GC/MS). This method quantified 118 GC
peaks representing 127 congeners (SI Table S2) which were
summed to calculate ∑PCBs. Approximate minimum detection
limits ranged from 0.01 to 0.1 ng g⁻¹ (wet weight, ww) among
congeners. A minimum of four surrogate standards (SS), includ-
ing CBs 14, 29, 34, 36, 61, 152, 186, and 192, were added to
samples prior to extraction. Recovery of SS was 67.3% (±17.7,
1SD). Reported concentrations were not corrected for recovery
efficiency because recoveries did not vary systematically among
samples or among congeners used as surrogate standards. An
aliquot of tissue extracts was analyzed for lipids using the gravi-
metric method and an aliquot CPOM samples was analyzed for
TOC by standard methods (SI).

**δ¹⁵N Analysis and Trophic Position Calculations.** Samples
for δ¹⁵N analysis were freeze-dried, milled, and homogenized.
Homogenates were combusted and reduced to N₂ with a CHN
analyzer (Carlo Erba NA 1500) with a continuous flow to an
isotope ratio mass spectrometer (Finnigan Delta). Atmospheric
N₂ was used as a δ¹⁵N reference standard. Reproducibility was
monitored using bovine liver (NIST No. 1577b) analyzed every
10 samples, and precision was 0.13% (1 SD) for δ¹⁵N.

Trophic position (TP) was determined following Post et al.²⁰
and Jardine et al.⁴ using the following equation:

\[ TP_{\text{consumer}} = \left[ (\delta^{15}N_{\text{consumer}} - \delta^{15}N_{\text{Asian clam}})/3.4 \right] + 2 \]  

(1)

where \( \delta^{15}N_{\text{consumer}} \) is the mean \( \delta^{15}N \) of the organism, mean
\( \delta^{15}N_{\text{Asian clam}} = 8.46 \) (0.12 SE), and 3.4 is the isotopic trophic
enrichment factor (i.e., the average difference, Δ15N, between an
animal and its diet). Long-lived primary consumers like Asian
clam are typically used to establish an isotopic baseline necessary
for calculating trophic position. It²² The trophic position of organic
matter sources was assigned a value of 1.0 to reflect their basal
position in the food web.

**Data Analysis.** We calculated a TMF for individual congeners
and ∑PCBs following Fisk et al.⁸ and Jardine et al.⁴ We used linear
regression to determine the relationship between PCBs (lipid or
TOC normalized depending on matrices) and TP:

\[ \log_{10} \text{PCBlipid} = b + (m \times \text{TP}) \]  

(2)

The slope \( m \) of eq 2 was then used to calculate TMF:

\[ \text{TMF} = 10^m \]  

(3)

We used regression analysis to determine the effect of \( K_{OW} \)
on TMFs and the predictive power (\( r^2 \)) of TP-PCBlipid models.
Log \( K_{OW} \) values were from Hawker and Connell 1988.³¹ We
excluded coeluting congeners, congeners that occurred in <50% of
samples, and congeners detected in <75% of food web com-
ponents (i.e., organic matter types and individual taxa). This
resulted in a total of 64 congeners used in this analysis.

For comparison purposes, TMFs for a generalized lake food
web were calculated from chemical residues predicted using the
Arnot and Gobas²2 food web model. The generalized food web
consisted of phytoplankton, zooplankton, benthic invertebrates,
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Table 1. Continued

<table>
<thead>
<tr>
<th>congener</th>
<th>( \log K_{\text{ow}} )</th>
<th>TMF</th>
<th>slope</th>
<th>error</th>
<th>( r^2 )</th>
<th>( p )</th>
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<tr>
<td>PCB 151</td>
<td>6.64</td>
<td>5.78</td>
<td>0.76</td>
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<td>0.12</td>
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<td>0.10</td>
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<td>0.75</td>
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<tr>
<td>( \Sigma )PCB</td>
<td>3.09</td>
<td>0.49</td>
<td>0.07</td>
<td>0.68</td>
<td>&lt;0.0001</td>
<td></td>
</tr>
</tbody>
</table>

\( ^{a} \) Slope, error, \( r^2 \), and \( p \) values are for each TP-PCB regression model. Error term is standard error of the model slope. Relationships for log \( K_{\text{ow}} \) with TMF and \( r^2 \) are shown in Figure 2.

two forage fish, and a piscivorous fish with an assumed trophic position (TP) of 1, 2, 3, 3, 3, and 4, respectively. Steady-state solutions of the Arnot and Gobas model were found for the log \( K_{\text{ow}} \) of each PCB congener. Equation 2 was then used to develop a linear model relating TP and predicted residues for each congener. Subsequently, eq 3 was used to determine the TMF for the congener of interest based on the slope from eq 2 (the “m” parameter). Details of model parametrization are provided in the SI and include diets, composition (i.e., lipid, moisture, and nonlipid matter contents), and weights of the organism.

We also compared the relationship between \( K_{\text{ow}} \) and congener TMFs for Lake Hartwell to those from other field studies reporting TMFs for PCBs across a similar range of \( K_{\text{ow}} \). These included food webs from marine and freshwater systems, from arctic and temperate climates, and food webs comprised entirely of homeotherms (“warm”), homeotherms and poikilotherms (“whole”), and only poikilotherms (“cold”). We used linear regression to determine relationships between \( K_{\text{ow}} \) and raw TMFs derived from these studies. The range of TMFs varied strongly among studies, so we standardized TMFs within studies to mean = 0, SD = 1 to remove scale differences in the response of TMF factors to \( K_{\text{ow}} \) among food webs. We modeled standardized TMFs using analysis of covariance (ANCOVA) with \( K_{\text{ow}} \) as a continuous variable and individual food web studies as categorical variables.

RESULTS AND DISCUSSION

PCB Biomagnification in Lake Hartwell. Mean \( \Sigma \)PCBs in Lake Hartwell ranged from 30 to 16 800 ng g\(^{-1}\) wet weight among food web components (SI Table S1). Trophic relationships derived for consumers were typical for aquatic food webs with invertebrates having lower trophic position than fishes (Figure 1). Zooplankton had the highest trophic position (TP) among invertebrates. Trophic position of fishes varied from 2.5 to 4.0 (SI Table S1), but calculated values did not always confirm expectations based on published information on adult diets.

Top predators such as piscivores (largemouth bass, Micropterus salmoides and flathead catfish, Pylodictis olivaris) had high TP values, but TP was similarly high for other planktivorous (threadfin shad, Dorosoma petenense), omnivorous (black bullhead, Ameiurus melas), and inverteivorous (black buffalo, Ictiobus niger) fish that would be expected to have lower TP values (Figure 1).

Log PCB concentrations were linearly related to TP for individual congeners and \( \Sigma \)PCBs (Figure 1). Much of the variation in these models can be attributed to variability among fish species. For example, total PCBlipid concentrations varied 6-fold for fish with TP ∼3.0, similar to variation in \( \Sigma DDT \) concentrations for fish in Lake Malawi, Africa.

High variation within trophic levels can be partially explained by a weakness of the TP modeling approach. Calculation of TP assumes a common fractionation rate (\( \Delta \)15N) among consumers. However, \( \Delta \)15N varies widely among consumers, and violation of the assumption of constant \( \Delta \)15N causes measurement error in TP. Evidence for this type of error exists in Lake Hartwell. Black bullhead had higher TP than expected for an omnivore, and their PCB concentrations were much lower than models predicted (Figure 1). Likewise, warmouth had lower TP than expected for a generalized carnivore (consumers with a mixed diet of invertebrates and fish), and their PCB concentrations were typically measured above those predicted.
higher than predicted. Other ecological factors such as growth and elimination rates also regulate biomagnification of OCs in animals.\textsuperscript{29} These processes are largely independent of TP and could contribute unexplained variation in the TP relationship between K\textsubscript{OW} and congener TMFs varied among study areas (Table 1). The slope of the Lake Hartwell log K\textsubscript{OW} – TMF model was 1.88, indicating that TMFs approximately doubled with each unit increase in log K\textsubscript{OW}. The log K\textsubscript{OW} – TMF relationship for Lake Hartwell was in good agreement with that derived from the general model of lake food web data. TMFs derived from the Arnot and Gobas model demonstrated an increase in TMF with log K\textsubscript{OW}, but the relationship was not linear and there were significant deviations at low and high values of K\textsubscript{OW}. Trophic position (TP) explained 12–67% of the variation in PCB\textsubscript{lipid} concentrations (Table 1, Figure 2B). The r\textsuperscript{2} of TP-PCB\textsubscript{lipid} models also increased significantly with log K\textsubscript{OW} (r\textsuperscript{2} = 0.68, p < 0.0001), but the relationship was nonlinear (Figure 2B).

K\textsubscript{OW} is a measure of hydrophobicity and indicates partitioning potential, a fundamental property regulating biomagnification of recalcitrant OCs in the aquatic environment. The relationship between K\textsubscript{OW} and PCB bioaccumulation we observed is consistent with those from modeling studies, laboratory feeding experiments, and other food web studies. Biomagnification and half-lives of recalcitrant compounds typically increase for log K\textsubscript{OW} < 7.0, then decline due to reduced bioavailability and potentially inaccurate K\textsubscript{OW} estimates for these superhydrophobic OCs.\textsuperscript{7,10,30,32} We found a strong linear relationship between congener TMFs and log K\textsubscript{OW} in Lake Hartwell. Our criteria for developing log K\textsubscript{OW} – TMF models (excluding congeners occurring in <50% of samples and congeners occurring in <75% of food web components) excluded many octo- and nona-CBs, so there is uncertainty regarding the shape of the response for higher chlorinated congeners with higher K\textsubscript{OW}.

Contaminant K\textsubscript{OW} not only affects biomagnification via trophic transfer but also determines the power of TP to predict contaminant concentrations. Predictive power for PCB\textsubscript{lipid} models was maximized for log K\textsubscript{OW} values between 5.75 and 7.0. This curvilinear response in model r\textsuperscript{2} is expected because the predictive power of TP should be maximized for compounds where intake and fecal egestion elimination rate are the most important processes driving exposure and bioaccumulation.\textsuperscript{33}

The two large negative residuals in Figure 2B were for PCB 77 and 84, indicating that PC-PCB models had lower r\textsuperscript{2} than expected based on log K\textsubscript{OW} (see Table 1 for model parameters). The TP-PCB\textsubscript{lipid} model for PCB 77 also had a lower slope than other penta-CBs (data not shown). PCB 77 in particular\textsuperscript{37,38} is biotransformed in aquatic food webs.\textsuperscript{21,22,35,36} PCR 84 was detected in invertebrates in Twelvemile Creek (the stream delivering PCBs to Lake Hartwell) but not fish, suggesting that fish are able to metabolize PCB 84.\textsuperscript{40} We detected PCB 84 in 92% of fish samples from Lake Hartwell, but concentrations were ~2–5 fold lower than other penta-CBs (data not shown). Concentrations among fishes were highly variable and did not follow expected trophic relationships based on δ\textsuperscript{15N}. These results also suggest that metabolism by fish may disrupt food web bioaccumulation of PCB 84.

### Table 2. Linear Regression Models of Log K\textsubscript{OW} Versus TMFs for Various Food Webs

<table>
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<th>study area</th>
<th>food web</th>
<th>citation</th>
<th>n</th>
<th>slope</th>
<th>intercept</th>
<th>r\textsuperscript{2}</th>
<th>p</th>
</tr>
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<td>whole</td>
<td>8</td>
<td>10</td>
<td>4.7</td>
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<td>9</td>
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<tr>
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<td>2.8</td>
<td>1.9</td>
<td>1.53</td>
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<tr>
<td>China (reservoir)</td>
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<td>10</td>
<td>1.5</td>
<td>3.0</td>
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<td>12</td>
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<td>1.5</td>
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<td>1.9</td>
<td>0.16</td>
<td>-1.1</td>
</tr>
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</table>

*Data from Baffin Bay, Barents Sea, Beaufort-Chukchi Sea, and White Sea food webs were compiled by Borga et al. (ref 7 and Table 2). Models include TMFs calculated for PCBs 28, 31, 47, 52, 99, 101, 105, 118, 138, 149, 153, 180, and 194, although not all congeners were measured in each study. The same congeners were used when available for China (reservoir), Lake Hartwell, and Tokoyo Bay, but other congeners with similar chlorination state were substituted as necessary to ensure that a similar range of log K\textsubscript{OW} values were used among models. N refers to the total number of congeners used in models. Food web classifications: cold, food web comprised of polikothers (invertebrates and fish) only; warm, food web comprised of homeotherms (birds and mammals) only; whole, food web comprised of homeotherms and poikilotherms. References are for studies from which the data were compiled. Intercepts are for models that normalized K\textsubscript{OW} to the lowest value (K\textsubscript{OW} = 5.56, PCB 28). Model parameters for Lake Hartwell differ slightly from those in Figure 2A because only a subset of congeners was used for this analysis. Model r\textsuperscript{2} and p values are the same for models using TMFs and standardized TMFs.
food webs for each unit increase in log $K_{OW}$. The greatest increase was for a warm food web, followed by whole food webs. Model slopes were lowest for cold food webs except for the White Sea whole food web, where $K_{OW}$ had no effect. Variation in model slopes largely reflected variation in the range of TMFs among food webs (e.g., Barents Sea warm, TMFs = 5.4–28.4; Lake Hartwell, TMFs = 2.6–42.2). The $K_{OW}$ effect on standardized TMFs was consistent among food webs (Figure 3B). $K_{OW}$ was strongly linearly related with TMF (ANCOVA, full model: $F_{1,57} = 12.6, r^2 = 0.75, p < 0.0001$; $K_{OW}$: $F_{1,57} = 134.1, p = <0.0001$) and regression slopes did not differ among food webs (model slopes = 1.43–1.72, log $K_{OW}$ x food web: $F_{5,57} = 0.09, p = 0.99$). Mean slope for the whole model was 1.60 ($\pm 0.14$ SE) across food webs indicating that each unit increase in log $K_{OW}$ resulted in a 1.6x increase in the mean of the standardized TMF.

Because contaminant $K_{OW}$s are relatively constant in the environment, it was reasonable to expect that TMF dependence on $K_{OW}$ should be similar among food webs. However, the magnitude of the TMF response had not previously been compared among food webs. Comparisons are problematic due to ecological differences among food webs and methodological differences among studies. Regression models using raw TMFs indicated that food web type strongly affected the magnitude of the log $K_{OW}$ response. Regression slopes were steepest in a warm food web, intermediate in whole food webs, lowest in cold food webs, and nonsignificant for two food webs. Standardized TMFs demonstrated a consistent response (1.6x increase with each unit increase in log $K_{OW}$) among those food webs with a significant $K_{OW}$ effect. This generalized finding underscores the importance of hydrophobicity in regulating biomagnification of recalcitrant compounds in the environment.

**TMF Application.** Comparing TMFs across systems has yielded insight into important processes (e.g., comparing exposure at the base of the food web by comparing intercepts of the regressions,7), yet comparisons are challenging due to ecological differences among food webs and methodological differences among studies. For example, TMFs are typically higher in food webs having consumers with high lipid content, warm-blooded apex predators, and longer food chains.7,8,37 However, some differences in TMFs could result from different methodologies, such as the inclusion of basal organic matter when analyzing TP-PCB relationships (ref 41, this study). Comparisons of TMFs among studies would benefit from an approach similar to the one that we used to compare $K_{OW}$ effects among studies. That is, standardize TP and contaminant concentrations to their mean and variance within studies to remove scale differences among studies prior to making comparisons.

TMFs provide solid empirical evidence of biomagnification in the field, yet integrating TMF information into regulatory and risk management decision-making is an ongoing challenge.3 Currently, regulatory agencies assess bioaccumulation potential based on a chemical’s $K_{OW}$ and bioconcentration factor (BCF). Gobas et al.42 recently proposed a chemical assessment framework giving preference to TMF and BMF data over BCF and $K_{OW}$ since the TMF and BMF provide insights regarding the potential for a substance to biomagnify. This framework brings field measurements that are currently ignored into the assessment process. By including TMFs and BMFs in the framework, decisions on a chemical’s bioaccumulation potential can be based upon a much broader range of bioaccumulation data (lab and field) and will help to prevent or reduce the miscategorization of individual chemicals.

Figure 3. Effect of log $K_{OW}$ on raw (A) and standardized (B) TMFs for various PCB congeners. Asterisks in A indicate nonsignificant models, and these studies were excluded from ANCOVA (panel B). Regression lines in B are for individual cold, whole, and warm food webs. Food web classifications: cold, poikilotherms only; warm, homeotherms only; whole, homeotherms + poikilotherms. Data from: Beaufort-Chukchi Sea,23 Baffin Bay,23 Barents Sea,9 White Sea,14 Tokyo Bay,24 China reservoir.25
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ASSOCIATED CONTENT

Supporting Information. Sample collection, analytical methods for PCBs and TOC; modeling TMs for a generalized food web; characterization of fish trophic guilds; data for ΣPCBs, lipids, TOC, and TP; list of PCBs analyzed; and study area map. This material is available free of charge via the Internet at http://pubs.acs.org.

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