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Beyond catch location, individual fish traits add little predictive power for DDX and PCBs in Southern California sport fishes

Toni Sleugh [a,*], Lillian McGill [a], Rasmus Swalethorp [a], Kiirah Green [a], Brendan S. Talwar [a], Charles S. Wong [b], Wenjian Lao [b], Ken Schiff [b], Brice X. Semmens [a]

[a] Scripps Institution of Oceanography, University of California, San Diego, CA, USA
[b] Southern California Coastal Water Research Project, Costa Mesa, CA, USA

A B S T R A C T

Legacy contaminants (DDX and PCBs) persist in fishes of the Southern California Bight, yet most consumption advisories rely on species- and region-level averages that ignore within-species variation among harvested individuals. We evaluated whether individual traits improve prediction of contaminant burden in a "fish in hand," and whether any gains can be achieved using information available to anglers at capture (e.g., size, region) versus traits requiring post-hoc laboratory analysis (e.g., age, stable-isotope–inferred trophic ecology). Using individually sampled, angler-caught fish collected across the Southern California Bight with associated metadata, we compared five nested predictive frameworks of increasing complexity, from species alone to models adding region, angler-measurable traits (length, lifestyle), spatially explicit sediment-contamination estimates, and laboratory-derived age and trophic-isotope metrics. Region — when informed by underlying sediment contaminant burden maps — substantially improved predictions of individual contaminant concentrations, whereas fish length contributed little additional predictive power. Among laboratory-assessed traits, isotope-derived trophic ecology provided the largest improvement, but gains were modest relative to location-based models. Overall, our results indicate limited potential for individual traits beyond catch location to meaningfully refine advisories, and support place-based guidance that leverages spatial contaminant prediction tools to inform safer consumption of recreationally caught fish.

1. Introduction

In the Southern California Bight (SCB), ocean dumping was historically a prevalent method of waste management, with municipal, industrial, and military waste disposed of through sewage outfalls and at-sea dumping at deep-water disposal sites (Bascom, 1982; Kivenson et al., 2019; Schmidt et al., 2024). This practice led to widespread contamination throughout the SCB (Allen, 2006; Kivenson et al., 2019). The Palos Verdes Shelf (PVS) Superfund Site was formed by decades of such dumping through the Los Angeles County sewage system (Chartrand et al., 1985; Kehoe and Jacobson, 2003). More recently, the legacy of historical deep-water disposal of industrial waste at designated dump sites (Fig. 1; Schmidt et al., 2024) has reemerged as a public health and environmental concern (Kivenson et al., 2019; Xia, 2020). In particular, there is now widespread interest in the impacts of Stockholm Convention on Persistent Organic Pollutants (POPs) (2001), chemicals that are persistent, widely distributed, able to bioaccumulate, and toxic to humans and wildlife. Two of the most ubiquitous POPs in the SCB are dichlorodiphenyltrichloroethane (DDT), a pesticide that was instrumental in decreasing infection rates of insect-borne diseases, and polychlorinated biphenyls (PCBs), a group of industrial compounds used as coolants and additives in electrical equipment, hydraulic oils, and fire retardants (Curley et al., 1979; Kehoe and Jacobson, 2003; Ododo and Wabalo, 2019). DDT primarily entered the SCB marine environment through targeted industrial waste disposal at PVS and deep-water dumpsites, while PCBs entered through sewer outfalls and runoff, producing distinct contamination gradients for each contaminant across the region (McGill et al., 2024; Schmidt et al., 2024). Following the passing of the Ocean Dumping Act and the banning of DDT and PCBs in the 1970s, both inputs of contaminants and levels of contamination in water, sediments, and biota declined markedly (USEPA, 2024); however, POPs remain widespread in the SCB and continue to pose health risks to the environment and the people who depend on it (Allen, 2006; Kehoe and Jacobson, 2003; Schiff et al., 2000; Schmidt et al., 2024).

Because PCBs and DDX (DDT and its six most commonly monitored breakdown products: *o,p* – and *p,p* - DDD, DDE, and DDT, along with DDMU and DDNU) are hydrophobic, they readily sorb to suspended and settled particles. These particles settle into marine sediments, which function as both a sink and a long-term source of these chemicals. Thus, DDX and PCBs can persist for decades while remaining bioavailable to organisms via remobilization through bioturbation (Karickhoff and Morris, 1985) or sediment resuspension (Oliver et al., 1989).

* Corresponding author.
E-mail address: tsleugh@ucsd.edu (T. Sleugh).

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Biomagnification results in the greatest exposure to PCBs and DDX in biota at higher trophic levels (Evans et al., 1991; Kidd et al., 1998), such as recreationally important fishes or humans. Species closely associated with the sediment also face chronic exposure to high levels of POPs (Ciesielski et al., 2016; Leblanc, 1995). Stable isotope analysis provides time-integrated estimations of basal carbon sources ($\delta^{13}C$) and trophic position ($\delta^{15}N$), allowing us to quantify the impacts of biomagnification and differential resource use on a fish's contaminant burden (Kidd et al., 2001; Kurle and Worthy, 2002). Previous research suggests that $\delta^{13}C$ and $\delta^{15}N$ are important predictors of POPs in aquatic systems, with differences in bioaccumulation between benthic and pelagic fishes (Jardine et al., 2006; Kidd et al., 2001; Lopes et al., 2011).

Contaminant loading in Southern California's recreationally important fishes has been well studied, with routine monitoring of relevant species and environmental factors at the regional, state, and federal levels (Klasing and Brodberg, 2008; Klasing et al., 2009; McGill et al., 2024; McLaughlin et al., 2020). Monitoring from 2018 revealed that while average concentrations of DDX and PCBs in fishes have continued to decline, high variability persists within species and across locations (McLaughlin et al., 2020). Species-level monitoring efforts typically use composite sampling, where many individuals of a species are combined into one sample. This doesn't allow for consideration of individual-level variables that may impact a fish's contaminant burden, such as size, age, or diet (McLaughlin et al., 2018). This is a notable limitation in the SCB, where recreationally caught fishes are often generalist predators, with highly variable sizes, ages, and diets within a species (Allen et al., 2006; Horn and Ferry-Graham, 2006). Indeed, PCBs and DDX show greater intraspecific variation than other monitored pollutants such as mercury, yet routine monitoring efforts do not account for this variation when evaluating contaminant burden (McLaughlin et al., 2020). An analysis of previous monitoring data showed that while sediment contamination explains the majority of variation in composite DDX concentrations, that relationship was mediated by other factors, such as trophic ecology and species-specific habitat use (McGill et al., 2024). Beyond species-level traits, individual characteristics may be important to forming a holistic understanding of how POPs vary across Southern California's fishes. The extent to which individual characteristics can refine contaminant predictions is especially relevant to anglers, who make seafood consumption decisions based on the "fish in hand."

Using individually sampled, angler-caught fish collected across the SCB, we compared five predictive frameworks spanning (i) species as the only predictor, (ii) status-quo advisory predictors (species, region), (iii) point-of-capture predictors (species, region, length, and lifestyle), (iv) point-of-capture predictors augmented with spatially explicit sediment contamination estimates, and (v) a comprehensive model adding laboratory-derived age and isotope metrics. By analyzing individual-level data, we aimed to identify drivers of inter- and intraspecific variation in contaminant burden that could allow consumers to better assess which fish are more or less safe to eat. We modeled the relative importance of biological and ecological variables in predicting a fish's contaminant burden, evaluated variability in contaminant concentrations within and across species, and explored the power of increasingly complex models to predict [PCBs] and [DDX] in fish.

2. Methods

2.1. Sample collection & processing

We collected recreationally important fish samples in collaboration with the Pfleger Institute of Environment Research (PIER), which gathered discarded, fileted fish carcasses from commercial passenger fishing vessels across the SCB (Fig. 1). This CPFV sampling effort produced a total of 1165 fishes from 16 species (Fig. 1). From this larger sample, we selected six priority species based on their catch abundance and consumption popularity, the distribution of fish size and catch locations, and the number of fish available: Kelp Bass (*Paralabrax clathratus*), Pacific Bonito (*Sarda chiliensis*), Vermilion Rockfish (*Sebastes miniatus*), Bocaccio Rockfish (*Sebastes paucispinis*), Pacific Chub Mackerel (*Scomber japonicus*), and Pacific Sanddab (*Citharichthys sordidus*). From each species, we selected approximately 40 individuals of various sizes and regions. We sampled white muscle tissue, liver tissue, and sagittal otoliths from each individual fish.

Forage fishes were collected from commercial bait barges across the SCN and during routine sampling by the NOAA Southwest Fishery Science Center's Coastal-Pelagic Fish Survey. Similarly to the recreational fishes, we removed sagittal otoliths from each individual Pacific Sardine (*Sardinops sagax*) and Northern Anchovy (*Engraulis mordax*). However, the small size of the forage fishes required them to be analyzed as whole-

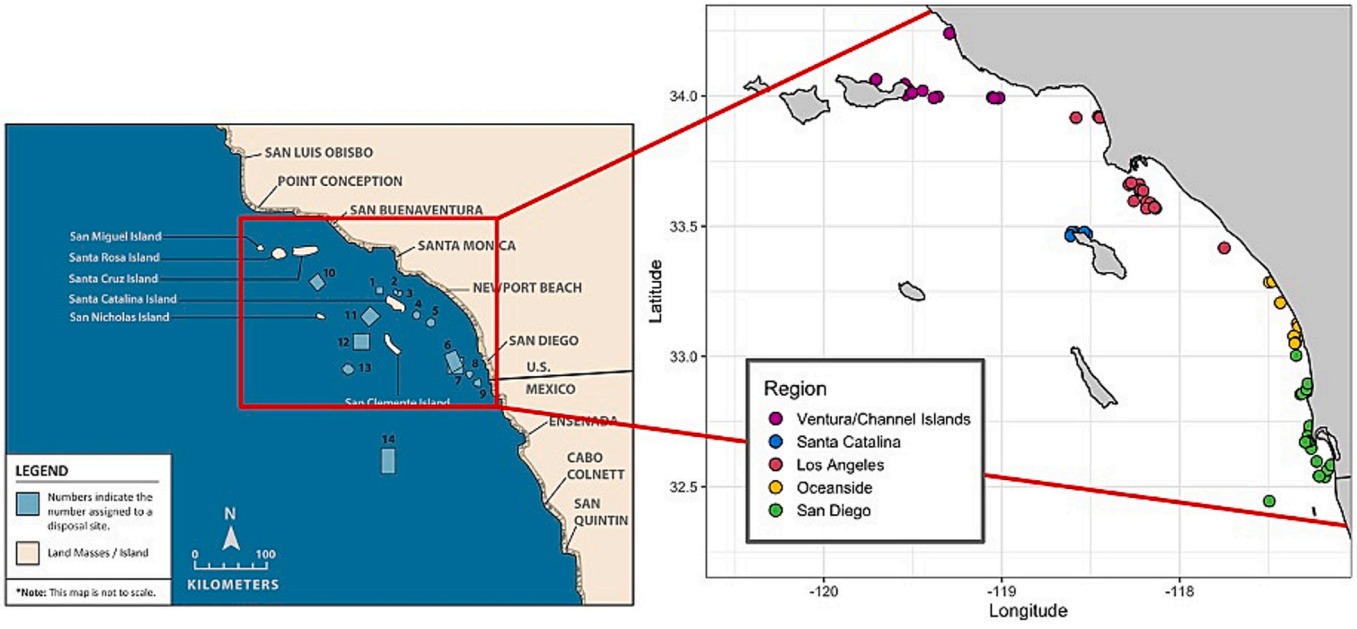


Fig. 1. Environmental Protection Agency (EPA) map of historical dumpsites in Southern California (left), and map of fish sampling locations (right) with each point representing an individual fish and colors representing the five sampling regions.

body composites of ten and six individuals, respectively. For more details on sample collection and processing, see the Extended Methods section of the Supporting Information.

2.2. Stable isotope analysis

Muscle tissue samples were kept at −80 °C until processing. We freeze-dried the samples before homogenizing them with a glass pestle. The dry weight was recorded before the sample was placed into tin foil capsules for bulk stable isotope analysis. These samples were sent to the Stable Isotope Facility at UC Davis for bulk $\delta^{13}C$ and $\delta^{15}N$ isotope analysis (*13C and 15N Analysis of Solids by EA-IRMS, 2020*). The mean absolute accuracy for calibrated reference materials was ±0.10 ‰ for $\delta^{13}C$ and ± 0.08 ‰ for $\delta^{15}N$. The mean standard deviation for reference material replicates was ±0.11 ‰ for $\delta^{13}C$ and ± 0.09 ‰ for $\delta^{15}N$.

2.3. Sample extraction and analysis

All individual Kelp Bass, Pacific Chub Mackerel, Pacific Sanddab, Vermilion Rockfish, and Pacific Bonito had a liver sample, and about half of them had a matching muscle sample. Bocaccio Rockfish samples were exclusively muscle tissue, and Northern Anchovy and Pacific Sardine were whole body composite samples. Because of the high lipid content and higher detection rate of toxicants in liver tissue compared to muscle, we chose to focus our analysis on liver samples where possible. Because the lipid-normalized contaminant data yielded relatively similar estimates for DDX (Supplemental Fig. 1), we were able to directly compare lipid-normalized muscle and liver samples. All muscle and liver samples were analyzed in collaboration with the Southern California Coastal Water Research Project, and additional details can be found in the Extended Methods section of the Supporting Information.

2.4. Modeling POPs in fish

We fit five Bayesian linear mixed-effect models to evaluate the potential of different biological and ecological variables to predict lipid-normalized DDX and PCB concentrations. The variables spanned a range of accessibility, with some being available in the moment to anglers and others requiring costly post-hoc laboratory analysis. The variables considered for each model included proxies for trophic position (age, length, and $\delta^{15}N$), resource utilization (species, lifestyle: benthic vs. pelagic, and $\delta^{13}C$), and environmental exposure to contaminants (estimated PCB or DDX concentrations in sediment ($[PCB_{sed}]$ or $[DDX_{sed}]$) and region). Based on existing regional datasets, we generated continuous sediment DDX and PCB concentrations across a spatial array with a spatiotemporal generalized linear mixed-effects model, as described in McGill et al. (2024). OEHHA has issued marine consumption advisories in Southern California for fish caught between Ventura Harbor and San Mateo Point (Klasing et al., 2009); however, the region groupings used in these models encompassed the entire SCB, including the Channel Islands, Oceanside, and San Diego. Age, total length (TL), $\delta^{13}C$, and $\delta^{15}N$ were normalized by the mean and standard deviation within species before being input into the model to allow for comparison across species on a standardized scale. All fish and sediment contaminant values were transformed as $\log(x + 1)$. Species from which over 50% of samples yielded no detectable levels of DDX or PCBs were excluded from the models. In practice, this resulted in Bocaccio Rockfish and Pacific Sardine being excluded from PCB models only. All candidate models were left-censored, meaning non-detect values were constrained to fall between zero and the lipid-normalized reporting limit (0.5 ng/g ww / $\%lipid_{ind}$). Missing values of $\delta^{15}N$ ($n = 2$) and $\delta^{13}C$ ($n = 3$) were imputed using Multiple Imputation by Chained Equations (MICE). Individuals with no age estimates ($n = 52$) were excluded from candidate models for comparison purposes, including all Pacific Bonito samples.

Candidate models were chosen to reflect increasingly complex ways of predicting contaminant burden in fish (Table 1). The base model uses only a random effect of species to predict fish contaminant burden. A consumption advisory model includes random effects of both species and region, reflecting that many current advisories are developed using composite species sampling and catch region to estimate contaminant burden. We considered two fisher-friendly models; the first includes data that is accessible to fishers at the point of capture – namely species, region, length (relative to others of its species), and lifestyle (benthic or pelagic), while the second model also uses spatial sediment pollutant estimates ($[PCB_{sed}]$ and $[DDX_{sed}]$) under the assumption that anglers have access to internet apps (e.g. SaferSeafood) that leverage these spatial data in prediction (Hahn et al., 2025). Finally, the resource-intensive model adds stable isotope values and age to assess the predictive power of a model that includes costly laboratory data. $\delta^{15}N$ enrichment allows us to examine relative trophic level, while $\delta^{13}C$ enrichment is an indicator of feeding ecology. In the SCB, higher $\delta^{13}C$ values reflect reliance on trophic pathways supported by benthic or nearshore primary production, and lower values indicate feeding in pelagic or offshore systems (e.g., phytoplankton-based production) (Kurle and Worthy, 2002). For models including length, age, or $\delta^{15}N$ (both fisher-friendly models and the resource-intensive model), an interaction of benthic or pelagic lifestyle was used to capture the different exposure pathways experienced by benthic and pelagic fish.

The "brms" R package was used to build and fit the candidate models. Model performance was compared via leave-one-out cross-validation using the "loo" R package (Table 1) (Burkner, 2017, 2018, 2021; Vehtari et al., 2024). We assessed model predictive power by

Table 1
Candidate model comparison for DDT and PCBs with ΔELPD (expected log pointwise predictive densities), ΔELPD standard error, and residual variation (σ). Models with a ΔELPD of 0 (cells with grey background) are considered the strongest predictors of DDX or PCBs in fishes.

Candidate Model	Fixed Effects	Random Effects	DDX ΔELPD	DDX ΔELPD SE	DDX σ	PCB ΔELPD	PCB ΔELPD SE	PCB σ
Base Model (species only)	–	Species	−37.5	9.8	1.50 [1.35, 1.67]	−1.0	2.7	1.49 [1.31, 1.71]
Consumption Advisory Model	–	Species, Region	−1.4	2.9	1.23 [1.11, 1.38]	−1.8	2.5	1.49 [1.31, 1.71]
Fisher Friendly Model	Length*Lifestyle	Species, Region	−2.7	4.0	1.24 [1.12, 1.38]	−0.9	1.5	1.47 [1.30, 1.68]
Fisher Friendly w/ SaferSeafood Model	Length*Lifestyle, Sediment Contamination	Species, Region	−1.1	4.0	1.22 [1.10, 1.36]	**0**	**0**	**1.47 [1.29, 1.68]**
Resource Intensive Model	$\delta^{15}N$*Lifestyle, Sediment Contamination, $\delta^{13}C$, Age*Lifestyle	Species, Region	**0**	**0**	**1.20 [1.08, 1.34]**	−2.8	2.2	1.49 [1.31, 1.71]

looking at residual variation (DDT σ and PCB σ; variation unexplained by the model), and expected log pointwise predictive densities (EPLD, which measures the ability of the model to predict missing data points, with consideration of over-fitting). Posterior predictions, with all other variables being held constant, were performed for total length, $\delta^{13}C$, $\delta^{15}N$, and both [PCB_{sed}] and [DDX_{sed}] to examine the impact of each predictor without being influenced by the others. All analyses were run using R version 4.5.0 (R Core Team, 2025).

To compare the variability captured by individual sampling to that of composites, we focused on Vermilion Rockfish, a species for which samples were well distributed across the SCB and had a 100% detection rate for both DDX and PCBs. We used bootstrap sampling of our individual data to simulate traditional composites, organized by region only, and more complex composites, selected by region, age, and size, in that order. We then compared the mean and standard deviation of both composite types to the mean and standard deviation of our individual samples for each region. Additionally, we compared the observed contaminant concentrations in this study with those from previous monitoring data reported by the SCB 2018 Regional Monitoring Program (Bight '18).

3. Results

Across all 251 samples, DDX was detected in all but ten (one individual Pacific Chub Mackerel, 5 Northern Anchovy composites, and 4 Pacific Sardine composites). PCBs were detected in 189 of the samples, with non-detect samples being especially common in Northern Anchovy, Pacific Sardine, and Bocaccio Rockfish. Non-lipid normalized values of [DDX_{fish}] in liver tissue ranged from <0.5 to 2150 ng/g ww (144.1 ± 285.4, mean ± SD), while [DDX_{fish}] in muscle tissue ranged from <0.5 to 250 ng/g ww (11.4 ± 36.0). Values for [PCB_{fish}] ranged from <0.5 to 489 ng/g ww (55.1 ± 77.6) in livers and < 0.5 to 105 ng/g ww (8.82 ± 15.4). The most common congener of DDX detected in fish was *p,p'*-DDE, and for PCBs, it was PCB153. The least common DDX congener was *o,p*-DDD (Supplemental Fig. 2 & 3). Compared to data from Bight '18, our sample revealed individuals with higher levels of DDX than were captured in composite data; detection rates were similar between the two studies, but we found muscle [DDX] as high as 250 ng/g ww where Bight '18 reported 123 ng/g ww in their composite with the highest concentrations (McLaughlin et al., 2020). For PCBs, our detection rate was slightly higher than in 2018 (73% to 75%), and the range of concentrations in composites was much more comparable to that of our individual samples (<0.5–106 ng/g ww in composites, <0.5–105 ng/g ww in individuals). Bight '18 reported high variability in PCB concentrations in the sampled species and regions, which was also true for our individual samples. Composites simulated to match methods from Bight '18 showed that mean values of [DDX] and [PCBs] for Vermilion Rockfish were almost identical to those of carefully selected composites and individual samples. However, the standard deviations for individually selected samples were much higher than those for either composite type, indicating that composite sampling may obscure individual fish with contaminant concentrations much higher or lower than average (Supplementary Fig. 6).

For DDX, 98.9% (n = 187) of the muscle tissue sampled would be considered safe for daily consumption (DDX: < 220 ng/g ww), with only two Vermilion Rockfish caught off of Los Angeles falling into the 2–6 servings per week category (Fig. 2). For PCBs, 72.5% (n = 137) of samples would be considered safe for daily consumption (PCBs: < 9 ng/g ww), with 20.1% (n = 38) of samples in the 2–6 servings a week category and 5.8% (n = 11) in the 1 serving a week category (Klasing and Brodberg, 2008). None of the muscle samples would be considered unsafe to eat based on ATLs for either DDX or PCBs, consistent with results from the 2018 Regional Monitoring effort (Klasing and Brodberg, 2008; McLaughlin et al., 2020). As expected, the non-lipid-normalized

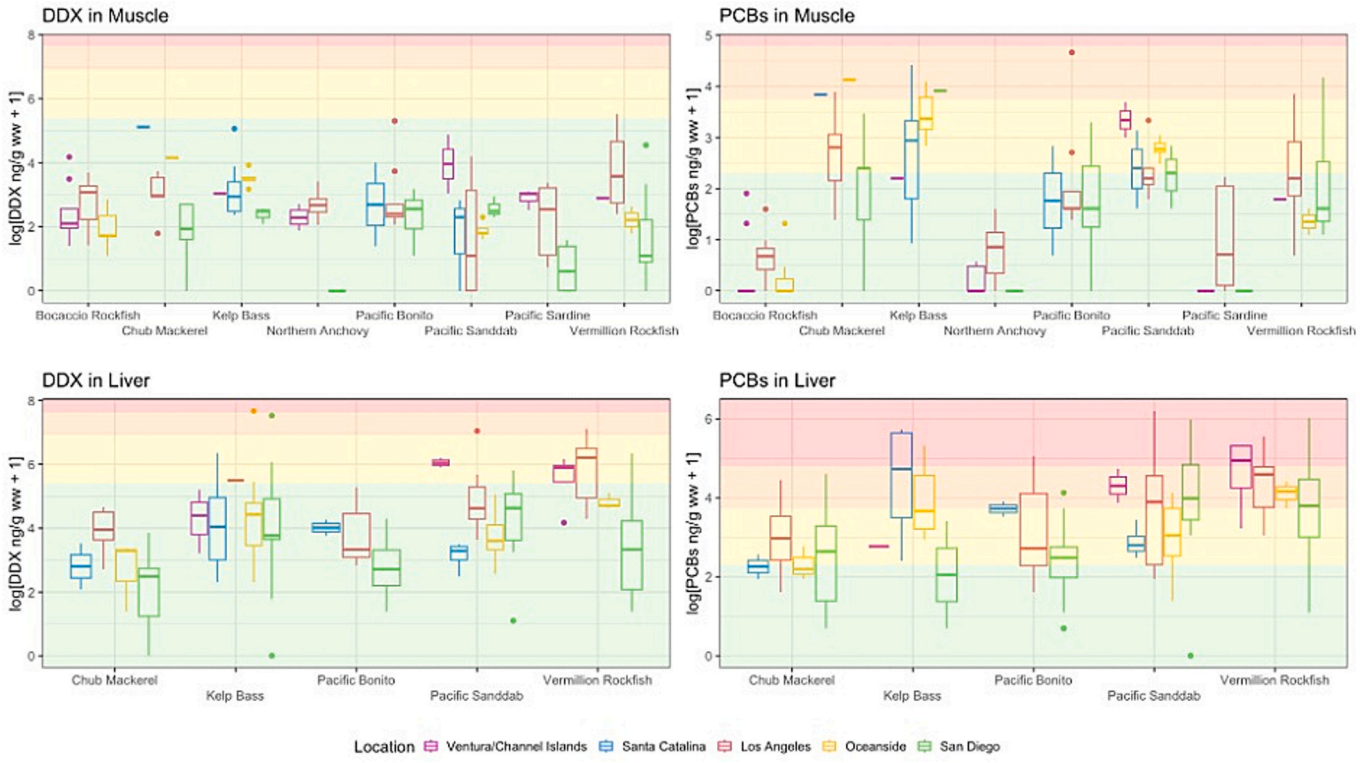


Fig. 2. Boxplot of non-lipid normalized (ng/g ww) DDX (left) and PCB (right) concentrations in muscle (top) and liver (bottom) tissue. Box colors represent location. Background colors indicate the Advisory Tissue Level (ATL) based on OEHHA limits (green: safe to consume one serving daily; yellow: 2–6 servings per week; orange: one serving per week; red: unsafe to consume). ATLs are determined using data only from muscle tissue and provide recommendations for how frequently to consume one serving (8 oz. skinless filet) of fish. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

concentrations of DDX and PCBs were higher in liver than muscle samples, likely because of the higher lipid content of the liver. Lipids, on average, made up approximately 34.4% of liver samples, but only 11.1% of muscle samples. As a result, concentrations of POPs in liver samples were more likely to exceed ATLs for daily consumption (Fig. 2); however, it is important to note that these advisories are only meant to provide advice on how frequently to consume skinless filets, making us unable to interpret consumption advice based on data from liver samples.

Turning to lipid-normalized values in both muscle and liver samples, there were four samples of Northern Anchovy and five of Pacific Sardine that had undetectable levels of both DDX and PCBs. Kelp Bass had both the highest mean (7.74 ± 1.61 ng/g lipid) and individual (12.5 ng/g lipid) lipid-normalized concentrations of DDX, while Pacific Sardine had the lowest mean (5.24 ± 2.47 ng/g lipid). For PCBs, Vermilion Rockfish had the highest mean (6.16 ± 1.05 ng/g lipid) and individual (8.30 ng/g lipid) lipid-normalized concentrations, and Pacific Sardine again had the lowest mean (1.59 ± 2.25) (Table 2). As expected, the species for which we analyzed muscle tissue only (Bocaccio Rockfish) or whole-body composites (Northern Anchovy and Pacific Sardine) had much lower rates of detection of both DDX and PCBs than species with liver samples.

The species-only base model was the worst predictor of DDX in fish, with high residual variation and a lower ELPD than the other models (Table 1). Predictive power greatly improved in the consumption advisory model, with the added random effect of location decreasing residual variation by 0.27 and increasing ELPD by 37.5. The first fisher-friendly model performed almost identically to the consumption advisory model; however, the SaferSeafood model, which included estimates of sediment contamination, performed slightly better than both. The resource-intensive model was the best predictor of DDX in fish, although still performing only slightly better than the consumption advisory model and the two fisher-friendly models (Table 1). Regarding PCBs, all five models performed almost identically, with no evidence of differences in residual variation. ELPD values for PCB models are also largely similar but suggest that the resource-intensive model is the worst predictor (Table 1).

The resource-intensive model for DDX showed that intercepts for Los Angeles and Ventura were the highest, while Santa Catalina had a much lower intercept. Intercepts for species were more variable, with Kelp Bass and Pacific Bonito having the highest intercepts, followed by Pacific Chub Mackerel, Bocaccio Rockfish, and Vermilion Rockfish. Pacific Sardine, Northern Anchovy, and Pacific Sanddab had the three lowest intercepts, though credible intervals for all species (excluding Kelp Bass) overlapped zero (Supplemental Fig. 4). [DDX_{sed}] showed strong evidence for a positive slope. $\delta^{13}C$ and $\delta^{15}N$ enrichment in benthic fish had similarly positive slopes, although the credible interval for $\delta^{15}N$ included zero. In contrast, $\delta^{15}N$ in pelagic fish had a negative slope. Total length had an effect size near zero in both benthic and pelagic fishes, with credible intervals overlapping zero. Age had a negligible effect on DDX in benthic fish, but there was evidence for a positive effect on DDX in pelagic fish (Fig. 3).

The resource-intensive model for PCBs revealed very little regional variation in PCBs, with each of our five locations having effect sizes with 95% credible intervals including zero. Similarly, variation across species was low, although a high number of non-detects gave Northern Anchovy a relatively low intercept estimate (Supplemental Fig. 4). As with DDX, $\delta^{13}C$ and [PCB_{sed}] had positive effect sizes, and age had a negligible effect on PCBs in benthic fishes. In contrast, age in pelagic fishes had a negative effect size, along with TL in both benthic and pelagic species (Fig. 3).

4. Discussion

Although several decades have passed since the cessation of DDX and PCB industrial use and dumping in Southern California, these contaminants are still widespread. Current efforts to evaluate the environmental and public health impacts of pollutants in marine fish happen at a coarse spatial scale and focus on species averages rather than individual fish. Previous research has shown that trends in contaminant burden based on individual traits, such as size or trophic ecology, could help refine advisories (Baptista et al., 2013; Leblanc, 1995; Lopes et al., 2011; McGill et al., 2024). Evaluating the extent to which individual traits predict contaminants is necessary to improve our understanding of contaminant transport in the marine environment and the efficacy of

Table 2
Summary of data collected for each species, including lipid-normalized [DDX] and [PCBs]. Variables include $\delta^{13}C$, $\delta^{15}N$, lifestyle, age, and total length (TL).

Species	Lifestyle	n	Tissue Type	DDX (mean ± SD, range), ng/ g lipid	PCBs (mean ± SD, range), ng/g lipid	$\delta^{13}C$ (mean ± SD, range)	$\delta^{15}N$ (mean ± SD, range)	Age (mean ± SD, range), yrs	TL (mean ± SD, range), cm
Kelp Bass	Benthic	38	Liver	7.74 ± 1.61 [5.43, 12.5]	4.02 ± 3.17 [<0.5, 8.01]	−17.14 ± 0.85 [−18.6, −16.0]	15.9 ± 0.74 [14.6, 17.9]	10 ± 3 [5, 20]	39.4 ± 4.08 [34.5, 51.9]
		22	Muscle	7.03 ± 0.96 [5.88, 9.54]	5.56 ± 2.39 [<0.5, 7.46]				
Vermilion Rockfish	Benthic	41	Liver	6.80 ± 1.55 [3.89, 10.1]	6.16 ± 1.05 [4.46, 8.30]	−17.8 ± 0.67 [−19.9, −16.7]	15.8 ± 0.63 [14.5, 17.0]	6 ± 3 [2, 15]	31.5 ± 10.03 [16.8, 47.8]
		20	Muscle	6.68 ± 2.08 [<0.5, 10.1]	6.15 ± 0.99 [3.88, 8.45]				
Pacific Chub Mackerel	Pelagic	26	Liver	5.82 ± 1.43 [<0.5, 8.41]	5.75 ± 0.76 [3.77, 6.94]	−18.7 ± 1.15 [−21.6, −16.9]	15.0 ± 0.45 [14.3, 15.9]	2 ± 1 [1,3]	28.3 ± 4.11 [23.3, 40.5]
		13	Muscle	5.77 ± 0.99 [4.04, 6.99]	5.56 ± 1.21 [2.86, 7.16]				
Pacific Bonito	Pelagic	40	Liver	6.16 ± 1.03 [3.89, 8.47]	5.63 ± 1.32 [2.35, 8.22]	−18.3 ± 0.990 [−21.2, −16.9]	16.4 ± 1.06 [14.6, 18.4]	–	47.8 ± 16.7 [26.5, 71.0]
		22	Muscle	6.19 ± 1.12 [4.32, 8.54]	5.39 ± 1.40 [2.81, 7.90]				
Pacific Sanddab	Benthic	37	Liver	5.93 ± 0.98 [4.19, 8.00]	5.24 ± 1.24 [2.58, 8.14]	−18.5 ± 0.63 [−19.6, −16.9]	15.3 ± 0.5 [14.4, 16.6]	4 ± 1 [1.67, 6]	21.7 ± 5.90 [9.90, 29.8]
		18	Muscle	4.70 ± 2.43 [<0.5, 7.72]	5.83 ± 0.760 [3.73, 6.85]				
Bocaccio Rockfish	Benthic	24	Muscle	7.12 ± 0.66 [5.25, 8.02]	2.01 ± 2.46 [<0.5, 5.60]	−18.0 ± 1.21 [−21.2, −16.6]	16.9 ± 0.6 [15.1, 17.8]	4 ± 1 [2, 6.5]	41.1 ± 9.89 [27, 57]
Northern Anchovy	Pelagic	30	Whole-body composite	6.03 ± 2.43 [<0.5, 7.70]	2.51 ± 2.43 [<0.5, 6.22]	−17.7 ± 0.27 [−18.2, −17.11]	14.1 ± 0.28 [13.7, 14.7]	1 ± 1 [0,3]	10.0 ± 1.43 [6.86, 12.43]
Pacific Sardine	Pelagic	39	Whole-body composite	5.24 ± 2.47 [<0.5, 8.32]	1.59 ± 2.25 [<0.5, 5.47]	−17.1 ± 0.41 [−17.7, −16.2]	13.9 ± 0.22 [13.5, 14.5]	1 ± 0.2 [1, 1.83]	10.5 ± 4.69 [2.43, 15.5]

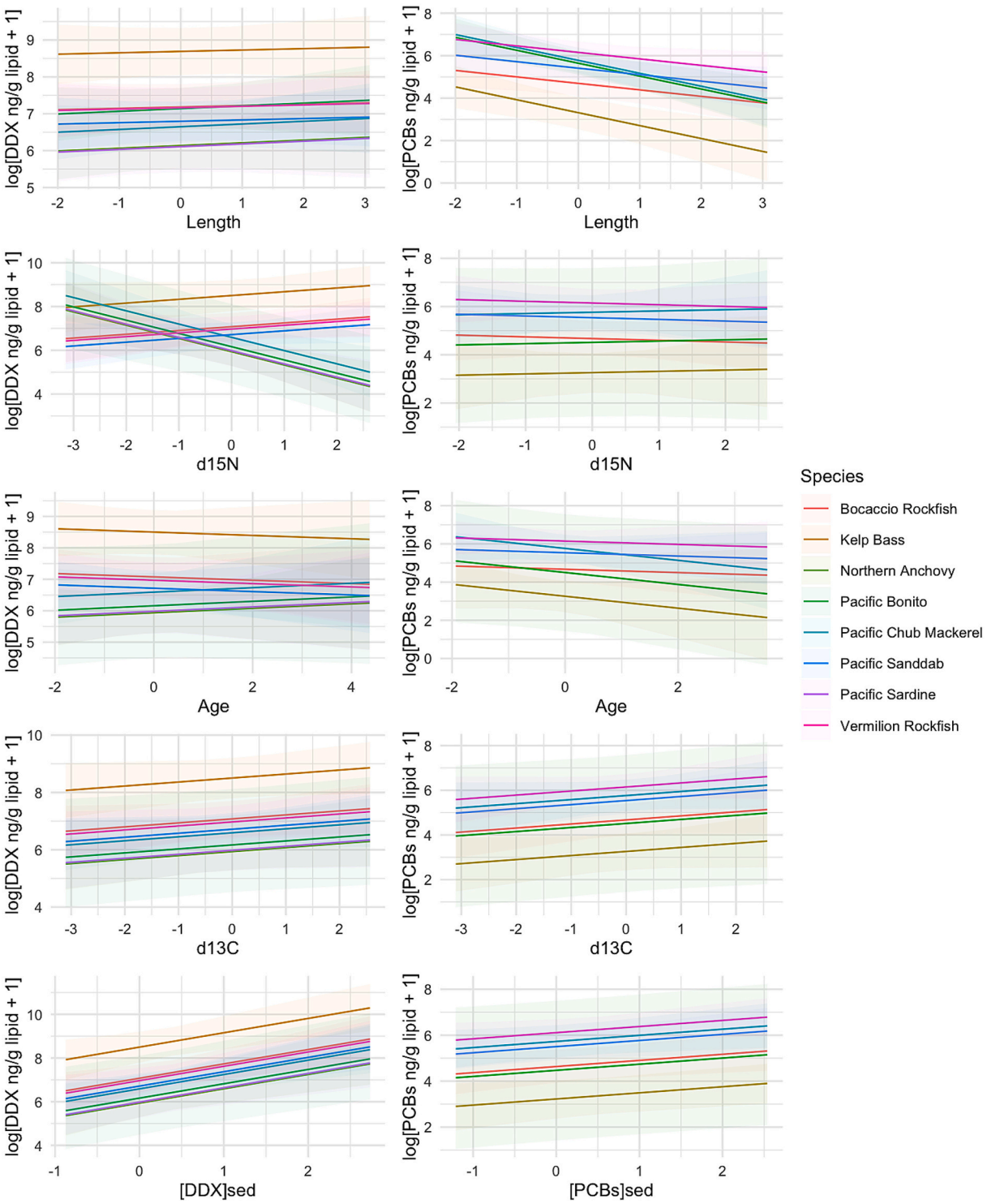


Fig. 3. Posterior predictions of lipid-normalized (ng/g lipid) concentrations of DDX (left) and PCBs (right) when all variables are held constant except, from top to bottom: total length, $\delta^{15}N$, age, $\delta^{13}C$, and sediment contamination. Colors represent species and ribbons are 95% credible intervals. Length, $\delta^{15}N$, and age include a lifestyle (benthic vs. pelagic) interaction. Bocaccio Rockfish, Kelp Bass, Pacific Sanddab, and Vermilion Rockfish are categorized as benthic, while Pacific Chub Mackerel, Northern Anchovy, Pacific Bonito, and Pacific Sardine are considered pelagic.

existing advisories. While this study showed that these individual traits do impact fish contaminant burden, they add little extra explanatory power beyond current advisories based on species and region. Comparing individual data to both simulated composites and prior composite data suggests that composites can accurately capture average contaminant levels in fish but may also obscure individual fish with unusually high or low concentrations, particularly for DDX. A comparison of data from this study to Bight '18 confirms that concentrations of DDX and PCBs have generally decreased over time, although intraspecies variability remains high across the region (Supplementary Fig. 5; McGill et al., 2024; McLaughlin et al., 2020). Observed contaminant concentrations do not necessarily follow trends as expected - our highest detected [DDX] came from a Vermilion Rockfish off the coast of Los Angeles, and it had much higher [DDX] than older, larger,

and higher trophic position fish from the same region, including those caught on the same fishing trip. This high individual variability may, by chance, expose anglers to greater concentrations of DDX or PCBs than expected based on composite sampling. For this reason, individual sampling is an important tool for estimating within-composite variability and accounting for these highly contaminated fish in advisory development and routine monitoring.

Ultimately, the model comparison results show that the current consumption advisory strategy effectively captures broad patterns in recreational fish contaminant burden. Although including individual-level covariates improved predictive power, the more complex models performed only slightly better than the consumption advisory model for DDX. Finer-scale resolution data for region, including exact catch location as it relates to spatial maps of sediment burden, may further improve the predictive power of advisories and is already available to anglers through the SaferSeafood app (Hahn et al., 2025). The PCB models all performed similarly poorly, suggesting that other variables not included in these models may be better suited to predicting a contaminant that is much more dispersed in SCB sediments than DDX. In particular, variables related to environmental exposure, such as movement ecology and habitat use, may be better predictors of PCB concentrations than trophic or ontogenetic traits given the diffuse nature of PCB contamination and the high variability that may obscure trophic relationships. Globally, PCB concentrations in fishes do not have a significant relationship with trophic level or habitat on the species level, likely due to their higher regional variability than other persistent, bioaccumulative, and toxic contaminants (Bonito et al., 2016). The high individual variability observed in our data and residual variability in our models highlights the complex nature of contaminant exposure and transfer in marine environments.

Intraspecific trophic ecology, measured via stable isotope analysis, was an important driver of contaminant burden in fish. Across all of the species and both POPs, we saw evidence of a positive relationship between $\delta^{13}C$ and contaminant burden, indicating that fishes that depend more on benthic and/or nearshore primary production (higher $\delta^{13}C$ values) have higher contaminant burdens than fish of the same species that depend more on pelagic and/or offshore primary production (lower $\delta^{13}C$ values) (Kurle and Worthy, 2002). Because sediments are the primary sink for POPs, it follows that fishes that are more closely associated with the sediment or that are trophically linked to benthic primary production have increased exposure to POPs, a pattern consistent with previous research (Kidd et al., 2001; Lopes et al., 2011). Predicted relationships between [DDX] and $\delta^{15}N$ differed between benthic and pelagic fish: benthic fish had a slightly positive relationship between [DDX] and $\delta^{15}N$, while pelagic fish had a negative relationship (Fig. 3). This suggests that benthic fish, which experience chronic exposure to DDX from contaminated sediments and benthic primary production, have higher rates of DDX bioaccumulation than pelagic fish. Additionally, pelagic primary producers likely have lower [DDX] than benthic ones, resulting in pelagic fish being exposed to DDX less frequently and at lower levels than benthic fish (Ciesielski et al., 2016; McGill et al., 2024). Two factors that are likely to increase a fish's PCB burden are sediment contamination and $\delta^{13}C$, further suggesting that a fish's physical or trophic relationship to the sediment are stronger controls on fish [PCBs] burdens than size or trophic level in the SCB (Evans et al., 1991; Leblanc, 1995; Lopes et al., 2011). Interestingly, we found evidence of a slightly negative relationship between $[PCB]_{fish}$ and length in both benthic and pelagic fishes. It is not clear from this study what is driving the negative relationship between total length and [PCBs], but it may be related to growth dilution or seasonal variations in PCBs that coincide with growth periods (Berninger and Tillitt, 2019; James and Kleinow, 2014; Sijm et al., 1992). In other systems, size, age, and trophic position have well-established strong positive relationships with [PCBs], making these results unusual (Baptista et al., 2013; Evans et al., 1991; Leblanc, 1995; Takeuchi et al., 2009).

Sediments in the SCB have clearly conserved the original signature of DDX dumping, but that spatial pattern is much less distinct in the fishes sampled here (McGill et al., 2024; Schmidt et al., 2024). Both within and across species, we found high concentrations of POPs in areas with low estimated sediment contamination and vice versa. There may be many reasons why the signature of dumping is less conserved in fishes than in sediments, with the most likely being the tertiary nature of exposure in fishes. For the species sampled here, and many other recreationally important fishes, diet is their primary source of exposure to POPs (Leblanc, 1995). Because they are classified as secondary and tertiary consumers, the concentrations of POPs in their tissues may be influenced by their own movement or the movement of their prey species (Allen et al., 2006; Horn and Ferry-Graham, 2006; Wolfe and Lowe, 2015). While sediment contamination does clearly play a strong role in estimating contamination in fishes, contaminants have dispersed across the SCB more readily in fishes than in sediments (Fig. 4). However, the footprint of dumping is still clear. DDX had very specific points of entry at PVS and deepwater dumpsites, near which fish tended to have higher $[DDX]_{fish}$, while PCBs, which had more diffuse sources across the SCB, show no clear spatial patterns in $[PCB]_{fish}$ (Schiff et al., 2000). Current consumption advisories heavily rely on capture location, which is likely appropriate for benthic species with high site fidelity, but may be less applicable to migratory pelagic species like Pacific Bonito and Pacific Chub Mackerel (Collins et al., 1980; Fitch, 1955; Froese and Pauly, 2023; Klasing et al., 2009).

The majority of fish in our sample had detectable levels of DDX, PCBs, or both, although all of the muscle tissue sampled here fell within levels considered safe for human consumption in moderation (Bonito et al., 2016; Klasing and Brodberg, 2008; McGill et al., 2024). Even so, chronic exposure to POPs in consumers of recreationally caught fishes in the SCB leaves them at low, but cumulative, risk of developing health complications such as organ damage, immune and endocrine system disruption, birth defects, and cancer (Mengistu et al., 2025; Ododo and Wabalo, 2019; Oguntimehin et al., 2026; Thi Thuy, 2015). This study shows that existing monitoring methods of analyzing composites by species and region are effective but can be improved by including additional individual-level sampling. Evidence for higher contaminant concentrations in benthic-associated fishes may also help anglers make more informed risk-benefit decisions about their fish consumption. Existing fish consumption advisories and outreach among recreational and subsistence anglers is essential, especially those who may be eating whole fish, against the advice of consumption advisories, which recommend eating only skinless filets (Klasing and Brodberg, 2008). However, previous seafood consumption surveys in the region have shown that anglers eat their catch in a variety of ways, including some that contradict OEHHA's recommendations (Southern California Coastal Water Research Project (SSCWRP) et al., 1994; U.S. Environmental Protection Agency (USEPA) et al., 2014). For example, anglers who consume the fattier parts of a fish, such as the skin, head, or organs, may be exposed to higher concentrations of contaminants than are found in muscle tissue (Klasing and Brodberg, 2008). Consumption of these more lipid-rich parts of a fish, represented in this study by liver samples, may expose consumers to unsafe levels of contaminants, and managers should consider offering advice specific to this type of consumption.

Marine ecosystems are incredibly complex, and it is difficult to predict and examine the distribution of POPs. Further research is needed to examine contaminant exposure across the entire food web, from primary producers to tertiary carnivores, to better understand drivers of contaminant levels in fish. Even after including variables that account for trophic ecology, resource use, size, and environmental exposure, we saw high levels of variation between individuals of the same species, suggesting that additional explanatory variables remain to be identified, especially for PCBs. Results from this study suggest that environmental exposure, represented by sediment contamination, lifestyle, and $\delta^{13}C$, is an important predictor of contaminant burden in fishes; future studies should consider expanding on variables representing this exposure

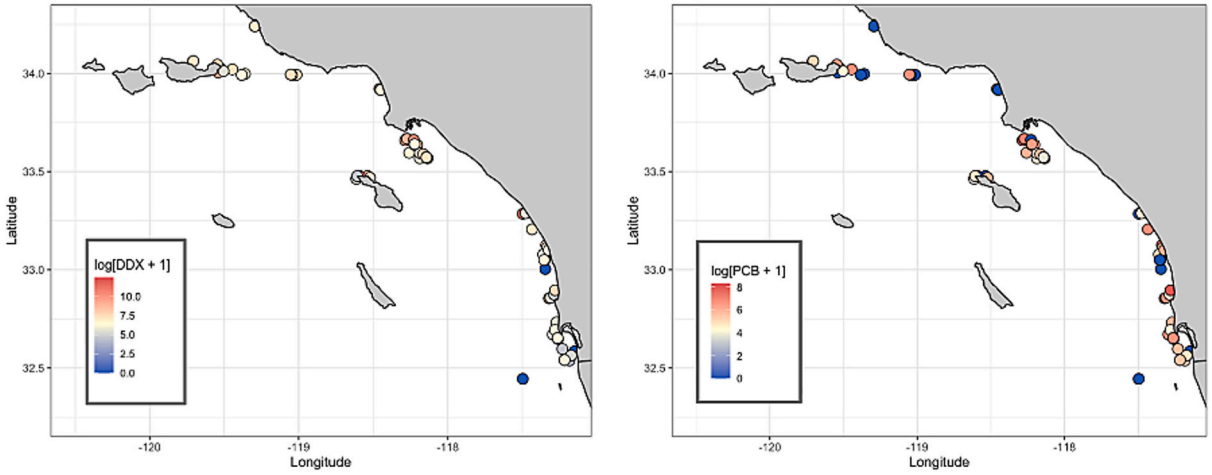


Fig. 4. Map of fish catch locations in the SCB. Point colors represent the concentration of DDX (left) and PCBs (right) detected in a fish relative to the mean concentration across all species (light yellow). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

pathway, such as movement ecology, habitat use, and more fine-scale primary production source analysis using compound-specific stable isotope analysis. Toxicokinetic and physiological variables have also been shown to be promising predictors of contaminant burden, especially in specific lipid-rich tissues that anglers may consume (Romanic et al., 2026). Because of the opportunistic nature of sampling in this study, all sampled recreationally important fishes were above the minimum size limits set by the California Department of Fish and Wildlife, and many had missing or damaged gonads from being filleted aboard CPFVs. Except for the forage fishes, our sample excludes larval and juvenile fishes, whose habitats and diets differ from their adult counterparts and may play a significant role in the contaminant burden that fish carry into maturity (Swank et al., 2021). Sex is another important missing variable; female fish can offload DDX and PCBs into their eggs and therefore can have lower contaminant burdens than their male counterparts, depending on maturity and time of year (Baptista et al., 2013; Conard et al., 2022; Lyons et al., 2019). Additionally, relying on catch from recreational party boat anglers meant that some species were excluded from our sample, including those that are considered less desirable, are labeled "Do Not Consume" by OEHHA, or are primarily popular with shore fishers. Future studies that include younger, sexed fish and account for seasonal variation will be essential in enhancing our understanding of variation in contaminant burden within and between fishes. This study focused specifically on Southern California, and the results reflect the impacts of the unique regional history of marine dumping; however, these methods are easily translated to other regions and may be a useful tool in evaluating the effectiveness of consumption advisories worldwide.

Southern California's history of ocean waste disposal continues to impact both environmental and public health. Fishes are an important part of the marine food web, often serving as a link between primary producers and consumers such as marine mammals, the California condor, and humans. This study helps better understand the connections between the ecology and biology of a fish and its contaminant burden, which can be used to update and inform future consumption advisories and monitoring efforts. Current consumption advisories may benefit from including more nuanced information about the behavior and ecology of a fish; however, the current advisory model performs similarly to models of increasing complexity. Angler outreach should be updated to include relevant information about the history of dumping, trophic transfer, and the risks of eating lipid-rich parts of their catch, to arm anglers with the knowledge they need to make the most informed consumption decisions. Current advisories based on species and region remain robust; the most promising near-term refinement is integrating spatially explicit sediment-burden estimates into angler-facing tools, rather than expanding laboratory-intensive sampling of individuals.

CRediT authorship contribution statement

Toni Sleugh: Writing – review & editing, Writing – original draft, Visualization, Supervision, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Lillian McGill:** Writing – review & editing, Methodology, Formal analysis. **Rasmus Swalethorp:** Writing – review & editing, Supervision, Resources, Investigation. **Kiirah Green:** Validation, Supervision, Project administration, Investigation, Data curation. **Brendan S. Talwar:** Writing – review & editing, Resources, Methodology, Data curation. **Charles S. Wong:** Writing – review & editing, Validation, Resources, Methodology, Investigation, Data curation. **Wenjian Lao:** Writing – review & editing, Validation, Resources, Methodology, Investigation, Data curation. **Ken Schiff:** Writing – review & editing, Validation, Resources, Methodology, Investigation, Data curation. **Brice X. Semmens:** Writing – review & editing, Supervision, Resources, Methodology, Funding acquisition, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.marpolbul.2026.120550.

Data availability

Data will be made available on request.

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