Comparability of Bioaccumulation Within the Sanddab Feeding Guild in Coastal Southern California

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ABSTRACT

Most assessments of fish tissue contamination in southern California are site specific, resulting in the assessment of ecologically or bathymetrically different species of unknown comparability. Previous studies have not addressed whether contaminant concentrations are comparable among ecologically similar species (i.e., a guild), even though individual species might occur at different depths. To assess whether a guild approach might be useful for comparing relative fish contamination among sites with different species, we collected samples of 4 species of the sanddab guild at 22 sites where species pairs co-occurred. Sampling was conducted using 7.6-m (headrope) otter trawls in July and August of 1997. Total DDT concentrations were determined from homogenized whole fish composites. Analysis focused upon three questions: (1) are tissue contaminant levels in co-occurring sanddab guild species pairs correlated? (2) if so, are the relationships linear and uniform, or are corrections needed to relate responses in one species to another? and (3) how does the variability in bioaccumulation among species, sites, and ages compare to that within same-aged individuals of a species at a site? Log-transformed DDT concentrations were highly correlated among all species pairs within the sanddab guild. All of the relationships were linear over the range observed, with slopes not statistically distinguished from unity. The variability in response among species was about 4 times the variability encountered among replicates within species, but was 15 times smaller than the variability among the sites sampled. Together, these results suggest that the sanddab guild, which is represented on soft bottoms throughout the southern California coastal shelf, can be used as a "superspecies" in regional assessments of fish tissue contamination that require assessment of relative condition among sites inhabited by different species.

INTRODUCTION

Concentrations of dichloro-diphenyl-trichloroethane (DDT) in fish tissues on the Palos Verdes Shelf have historically been among the highest in the nation (Mearns *et al.* 1988). Most of this contamination can be traced to manufacturing-related discharges that ceased in the early 1970s. Although tissue contaminant levels have decreased substantially since that time (Mearns *et al.* 1988, SCCWRP *et al.* 1992, SCCWRP 1994, Schiff and Allen 1997), commercial fishing of white croaker (*Genyonemus lineatus*) on the Palos Verdes Shelf is still banned because of high DDT concentrations in edible muscle tissue and DDT-contaminated fish are still present in local markets (Gold *et al.* 1998).

While extensive data have been collected to document fish contamination, these data are not easy to integrate for a regional assessment of the extent of tissue contamination in the Southern California Bight (SCB) and the relative degree of contamination among different

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areas. Although the use of different tissues (liver or muscle) contributes to the difficulty of comparisons, the primary impediment for same-tissue comparisons is the dissimilarity in fish species collected by the various monitoring efforts. Some of this dissimilarity reflects disparate programmatic goals (e.g., pelagic vs. benthic fish); most of it reflects the limited bathymetric distribution of individual species on the southern California coastal shelf. A recent trawl study of the southern California coastal shelf found that no individual species occurred over more than 68% of the shelf (Allen *et al.* 1998).

An alternative approach for achieving a regional assessment and comparison among sites is to process and compare tissue samples from a group of ecologically similar species (i.e., a guild). Although species with different feeding habits often have different contaminant concentrations, species at the same trophic level generally have similar contaminant levels (Young and Mearns 1978). In addition, closely related species at similar trophic levels may show similar bioaccumulation because of similarities in diet, movements, and ability to metabolize contaminants (Mann and Ajani 1991).

The most promising guild for accomplishing a regional assessment in southern California is the sanddab guild. This guild consists of five flatfish species that form a depth displacement series: speckled sanddab (*Citharichthys stigmaeus*), Pacific sanddab (*Citharichthys sordidus*), longfin sanddab (*Citharichthys xanthostigma*), gulf sanddab (*Citharichthys fragilis*), and slender sole (*Eopsetta exilis*) (Allen 1982). All species but one (slender sole) is a sanddab (*Citharichthys* spp., Paralichthyidae); the slender sole is a pleuronectid. All members of the guild are small flatfishes with medium-sized mouths and are visual foragers that feed on a variety of benthic and near-bottom nektonic prey. Allen *et al.* (1998) found that 96% of the area between 10 and 200 m depth on the southern California coastal shelf contained at least one of these species. Three of the species, speckled sanddab (inner shelf, 10-25 m), Pacific sanddab (middle shelf, 25-100 m), and slender sole (outer shelf, 100-200 m), are temperate species that segregate along a depth gradient. Longfin sanddab and gulf sanddab are tropical species; longfin sanddab occurs on the inner/middle shelf zone and gulf sanddab on the middle/outer shelf zone.

Although guild members are generally spatially segregated, the distributions of two or more species overlap in limited areas. These areas provide the opportunity to assess the comparability of the contaminant accumulation between species. Here we examine whether sanddab guild species are sufficiently similar in their bioaccumulation of DDT to be treated as a group for assessing the extent of tissue contamination on the southern California coastal shelf. We assume that the species have limited movements and that tissue concentrations reflect exposure conditions. We focused upon whole fish in anticipation of future studies that will focus upon health risks to predators. The objectives of the study were to answer the following questions: (1) are tissue contaminant levels in co-occurring sanddab guild species pairs correlated? (2) if so, are the relationships linear and uniform, or are corrections needed to relate responses in one species to another? and (3) how does the variability in response among species, sites, and ages compare to the variability in response within species at a site?

METHODS

Whole fish samples of sanddab guild species were collected in July and August of 1997 at 22 stations located along the southern California coastal shelf (Figure 1). The sampling locations represent the range of sediment contamination along the coastal shelf (Schiff and Gossett 1998). In decreasing order of contamination, they were Palos Verdes Shelf, Santa Monica Bay, southern San Pedro Shelf, Dana Point, and Point Loma. All samples were collected using 7.6-m (headrope) otter trawls with 1.25-cm cod-end mesh towed for 10 min along isobaths. Fish were sorted into predetermined age classes (Table 1). Up to three composite samples of six fish per species/age class category were selected for all sanddab guild species collected at a site. Fish were

FIGURE 1. Southern California stations sampled for 1997 sanddab guild bioaccumulation comparability study.

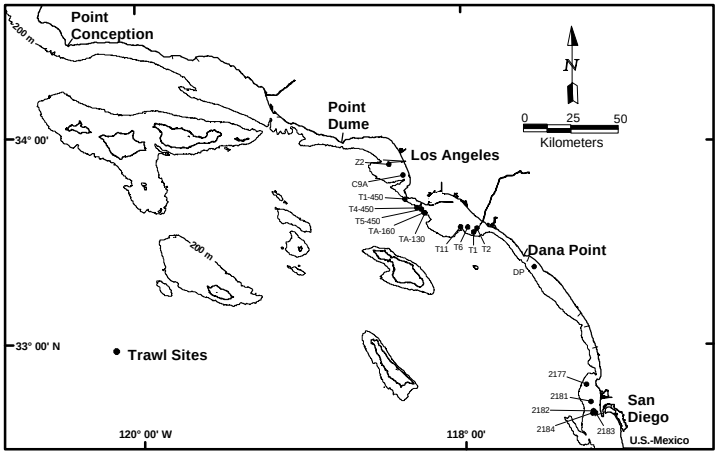

TABLE 1. Target size ranges of fish by species for whole fish composites in 1997 sanddab bioaccumulation comparability study (based on Arora 1951, Ford 1965, Hart 1973, Allen 1976, Eschmeyer *et al*. 1983, and Love 1996). *Estimated length ranges. Bold numbers indicate immature fish.

Common Name	Scientific Name	Centimeter Size Class Age 0	Age 1	Age 2	Max. Length (cm)
speckled sanddab	*Citharichthys stigmaeus*	**5-6**	7-8	8-9	17
longfin sanddab	*Citharichthys xanthostigma*	***5-8**	***9-13**	***14-16**	25
Pacific sanddab	*Citharichthys sordidus*	**5-8**	**9-13**	**14-16**	41
gulf sanddab	*Citharichthys fragilis*	***5-6**	*7-8	*8-9	14
slender sole	*Eopsetta exilis*	***5-8**	***9-10**	***10-12**	35

rinsed in seawater, wrapped in aluminum foil, placed in labeled plastic bags, and frozen.

In the laboratory, whole fish composites were thawed and removed from the foil. Each fish was measured to centimeter size class (standard length), weighed individually to the nearest gram, rinsed in deionized water to remove visible particles, and shake dried. Individual fish weights were summed to give a composite weight. Whole fish composite samples were homogenized in a blender, with 0.5 or 1.0 L stainless steel or glass containers with silicone or BUNA rubber gaskets with Teflon (or aluminum foil-lined) lids. The composite fish and an equal weight of deionized water (to facilitate blending) were combined and blended for 2 to 5 min to obtain a smooth homogenate. Two equal-sized aliquots of homogenate were used to fill two wide-mouthed glass jars with Teflon-lined lids (and external labels) to three-fourths full or less; the remainder of the sample was discarded. Blenders were washed with nonionic soap and water, rinsed several times with deionized water, dried, and then rinsed with an appropriate solvent (e.g., methanol, ethanol, acetone) and dried. Samples were kept at -20° C (± 2° C) for up to six months to minimize possible degradation of target analytes.

Prior to chemical analysis, sample aliquots were thawed and thoroughly mixed to ensure a uniform homogenate. Total DDT was analyzed by four laboratories using either gas chromatography with electron capture detectors (GC-ECD) or ion-trap gas chromatography/mass spectrometry (GC/MS) with capabilities of achieving the detection limit of 10 ng/g wet weight (ww) (i.e., 10 ppb ww). Following analysis, the measured concentration was doubled to correct for the equal weight of water added to the sample during homogenization.

Relationships in log-transformed tissue DDT concentrations among equal-aged pairs collected at the same site for all species pairs were assessed using linear regression and Pearson product-moment correlation. The possible influences of age, species, and sites were assessed using a nested analysis of variance (ANOVA) model. Regression slopes were compared to unity to determine if direct comparability of concentrations was appropriate. Four components of variance (among replicate variance within same-age and same-species fish from the same site, among age class variance within same-species fish from the same site, among species variance within the same site, and among site variance) were estimated using the sums of squares from the nested ANOVA model.

The presence of DDT was not detected (i.e., was below the detection limit of 10 ng/g ww) in Pacific sanddabs at two sites in the survey (Table 2). Sites with Pacific sanddab "nondetects" were discarded for correlation and regression analyses. For the ANOVA, these sites were assigned half the detection limit (5 ng/g ww) to provide a conservative estimate of variance.

RESULTS

Seventy-seven composites representing 4 species and 22 stations were analyzed for DDT (Table 2); gulf sanddab was not analyzed because of its low occurrence in the survey. Equal-aged species pairs (not including replicates) occurred at 28 sites (Table 3). Age 1 was the most frequently collected age class; longfin sanddab/Pacific sanddab was the most frequent species pair; and Age 1 longfin sanddab/Pacific sanddab was the most frequent equal-age pair.

Mean DDT concentrations in composites ranged from nondetectable to 18,160 ng/g ww (Table 2). Mean concentrations of equal-aged species composites increased by three orders of magnitude from Point Loma to the Palos Verdes Shelf (Figure 2).

Contaminant concentration was highly correlated in every species pair (Table 4). The highest correlation ($r = 0.97$) was observed for the speckled sanddab/Pacific sanddab and longfin sanddab/Pacific sanddab pairs. The lowest correlation ($r = 0.68$) occurred in the slender sole/Pacific sanddab pair. Regression equations among species pairs were significant and positive; no slope differed significantly from unity (Table 4).

The largest source of variability was among sites and the smallest source was among replicates within species (Table 5). The variability among sites was about 60 times the variability among replicates within a species. The variability among species was about 4 times the variability among replicates, but was 12% of the variability among the sites sampled. The variability among age classes was about twice the variability among replicates; these variances were not significantly different.

DISCUSSION

The objective of this study was to determine if sanddab guild species are sufficiently similar in their accumulation of DDT to be treated as a group in assessing the extent of fish contamination on the southern California coastal shelf. The results from this study support this premise because (1) DDT concentrations in sanddab guild species were highly correlated; (2) they had linear relationships that could not be statistically distinguished from unity; and (3) the relative variability in concentrations was much less across species than across sites.

Correlations were higher among all *Citharichthys* species pairs than in the slender sole/Pacific sanddab pair, which may be due to the closer phylogenetic relationship of the sanddab species. However, some of this difference may reflect conditions in the areas where the species pairs were collected. The slender sole/Pacific sanddab pair was captured exclusively on the Palos Verdes Shelf, which has the highest sediment concentration of DDT in the SCB (Schiff and Gossett 1998). No other species pair was collected from this area and the range of tissue concentrations against which the other species pairs were compared was substantially lower.

Correlations for two of the species pairs (speckled sanddab/longfin sanddab and longfin sanddab/Pacific sanddab) were based upon a cluster of tissue samples with concentrations less than 125 ng/g ww and a single sample at a concentration near 500 ng/g ww. In one case, significance of the correlation depended upon inclusion of that single data point. Despite the heavy reliance upon a single data point, we believe these relationships are meaningful. Although speckled sanddab and longfin sanddab samples were collected only at sites with low contamination, both species had

TABLE 2. Mean DDT in sanddab guild species by age class and station off southern California in 1997 sanddab bioaccumulation comparability study. (n = no. composites; nd = nondetect; ww = wet weight)

		Mean Total DDT								
		Citharichthys sordidus		*Citharichthys xanthostigma*		*Citharichthys stigmaeus*		*Eopsetta exilis*		Total
Station	Age Class	n	(ng/g ww)	n	(ng/g ww)	n	(ng/g ww)	n	(ng/g ww)	n
Z2	1	3	531.5	3	534.9	2	472.5	-	-	8
C9A	0	2	199.6	-	-	1	174.9	-	-	3
DP	1	-	-	4	69.9	2	25.8	-	-	6
2177	1	3	nd	3	30.7	-	-	-	-	6
2181	1	1	nd	1	36.0	-	-	-	-	2
2182	0	1	24.0	1	24.0	-	-	-	-	2
2183	1	3	13.5	3	36.7	-	-	-	-	6
2184	1	1	28.0	1	38.0	-	-	-	-	2
T1	2	2	51.5	2	79.9	2	93.6	-	-	6
T11	2	2	25.8	2	68.9	-	-	-	-	4
T2	1	-	-	2	64.0	2	30.3	-	-	4
T2	2	-	-	2	117.0	2	20.5	-	-	4
T6	1	2	21.6	2	53.1	2	24.3	-	-	6
T1-450	2	1	10,040	-	-	-	-	1	3,050	2
T4-450	1	1	17,140	-	-	-	-	1	10,400	2
T4-450	2	1	18,160	-	-	-	-	1	11,980	2
T5-450	1	1	13,920	-	-	-	-	1	8,350	2
T5-450	2	1	9,600	-	-	-	-	1	10,800	2
TA-130	1	1	7,010	-	-	-	-	1	1,460	2
TA-130	2	1	5,120	-	-	-	-	1	2,730	2
TA-160	1	1	9,050	-	-	-	-	1	1,640	2
TA-160	2	1	5,630	-	-	-	-	1	4,070	2
Total		29		26		13		9		77

TABLE 3. Number of comparisons of sanddab guild species pairs by age class, sanddab comparability study. CST = speckled sanddab (*Citharichthys stigmaeus*); CX = longfin sanddab (*Citharichthys xanthostigma*); CSO = Pacific sanddab (*Citharichthys sordidus*); EE = slender sole (*Eopsetta exilis*).

Species Pair	Age Class	Sites	No. Sites
CST/CX	1	Z2, DP, T2, T6	4
CST/CX	2	T1, T2	2
CST/CSO	1	Z2, T6	2
CST/CSO	2	T1	1
CX/CSO	0	C9A, 2182	2
CX/CSO	1	Z2, 2177, 2181, 2183, 2184, T6	6
CX/CSO	2	T1, T11	2
CSO/EE	1	T4-450, T5-450, TA-130, TA-160	4
CSO/EE	2	T1-450, T4-450, T5-450, TA-130, TA-160	5
Total			28

very similar concentrations to Pacific sanddab found at the more contaminated Santa Monica Bay site (Z2), where all three species occurred together (Table 2). The increase in contamination in these two species followed the trajectory of Pacific sanddab contamination from less to more contaminated sites up to this point (Figure 2).

Many fish tissue studies normalize contaminant concentrations by lipid content. Our analysis used non-normalized values because our long-range interest focuses upon predator risk from consumption of whole fish, for which normalization would not be appropriate. However, we did measure lipids and found that the correlation between species was higher for three of the four comparisons without lipid normalization. Slender sole/Pacific sanddab was the only comparison for which lipid normalization improved the relationship ($r = 0.69$ to $r = 0.84$; $p = <0.05$ to $p = <0.01$).

FIGURE 2. Total DDT concentration in whole fish composites of sanddab guild species: Pacific sanddab (*Citharichthys sordidus*); longfin sanddab (*Citharichthys xanthostigma*); speckled sanddab (*Citharichthys stigmaeus*); and slender sole (*Eopsetta exilis*). Age 1 fish from Station T2 are designated T2(1) and Age 2 fish are designated T2(2); all fish from all other stations are of a single age class.

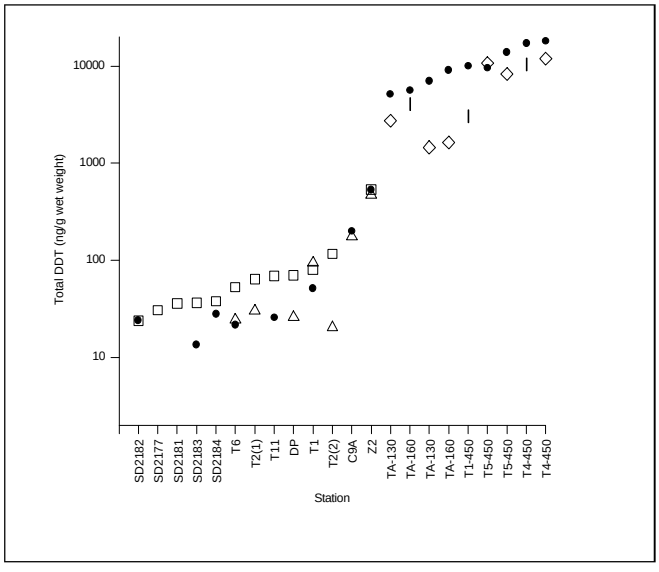

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FIGURE 3. Comparison of total DDT concentration between whole fish composites for sanddab guild species pairs of the same age collected at the same southern California stations. Sanddab guild species — Pacific sanddab (*Citharichthys sordidus*); longfin sanddab (*Citharichthys xanthostigma*); speckled sanddab (*Citharichthys stigmaeus*); slender sole (*Eopsetta exilis*).

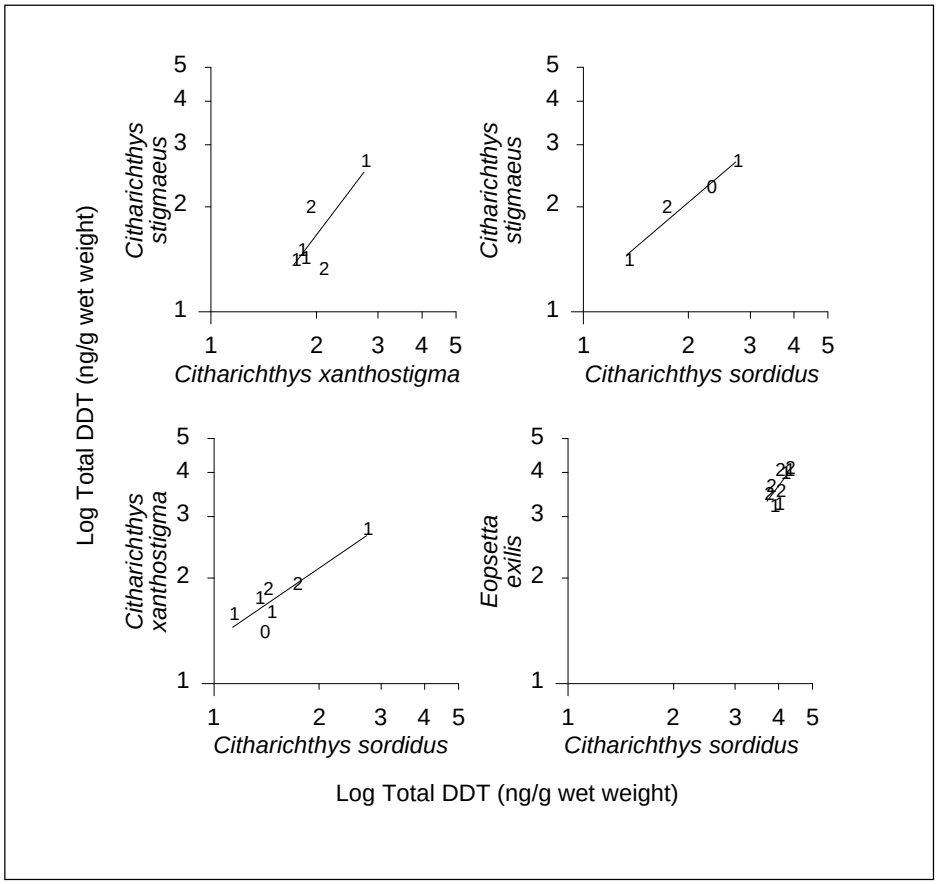

TABLE 4. Results of correlation and regression analyses of log-transformed total DDT concentrations in same-age pairs of sanddab guild species in sanddab bioaccumulation study. CST = speckled sanddab (*Citharichthys stigmaeus*); CX = longfin sanddab (*Citharichthys xanthostigma*); CSO = Pacific sanddab (*Citharichthys sordidus*); EE = slender sole (*Eopsetta exilis*).

Species Pair	n	Regression Equation	r	p
CST/CX	6	CST = -0.18 + (1.32*CX)	0.849	< 0.05
CST/CSO	4	CST = 0.06 + (0.86*CSO)	0.976	< 0.05
CX/CSO	7	CX = 0.12 + (0.69*CSO)	0.938	< 0.01
EE/CSO	9	EE = -0.25 + (1.35*CSO)	0.694	< 0.05
Total	26			

TABLE 5. Analysis of variance of log total DDT concentrations in whole fish samples among sites, species, ages, and replicates in sanddab bioaccumulation study, 1997. (n.s. = not significant at p = 0.05).

Source of Variation	df	SS	MS	Fs	p
Among sites	17	22.36	1.32	59.77	<<0.001
Among species	30	2.58	0.09	3.91	<0.001
Among ages	13	0.49	0.04	1.72	n.s.
Among replicates	38	0.84	0.02	—	
Total	98	26.26			