



An analysis of the importance of taxonomic level in the assessment of annelid communities in a Mexican lagoon

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ABSTRACT.—Assessing taxonomic sufficiency (TS) is useful for developing rapid and reliable procedures in marine impact assessment and monitoring. The coastal lagoon Estero de Urías has been subjected to the effects of several anthropogenic activities (shrimp farms, a thermoelectric plant, a slaughterhouse, a fish processing factory, a harbor, and urban sewage) for several decades, thus it is a candidate for TS application. The characterization of this lagoon through the study of soft-bottom annelids has identified zones subjected to different degrees of organic pollution, which lead to the need for monitoring. TS involves the identification of taxa to higher taxonomic levels than species (e.g., genus or family) without losing statistically relevant information. This study investigated the degree to which reduced taxonomy can be used to detect anthropogenic effects in a lagoon through the analyses of published and unpublished data of polychaetes and oligochaetes. Multidimensional scaling (MDS) ordinations, pairwise Spearman correlation tests, “second-stage” MDS ordination, analysis of similarity (ANOSIM), and BIO-ENV analyses revealed that, in general, results obtained at species, genus, and family levels followed similar patterns. Analyses performed at the genus and family levels were as effective as those performed at the species level and followed similar trends to those found in previous studies. Therefore, further analyses using family-level data are recommended for monitoring and characterization of this tropical coastal lagoon.

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Analyses of macrobenthic infaunal communities normally involve identification of organisms to species level, but consistent and accurate identification to such level requires considerable training and years of experience (Snelgrove and Grassle 1995), and it is also an expensive and time-consuming task (Fiori and Soares-Gomes 2001). Ferraro and Cole (1995) found that faunal identification time spent at the genus, family, order, and phylum levels was reduced by 25%, 55%, 80%, and 95%, respectively, compared to the total time spent identifying at the species level.

Taxonomic sufficiency (TS) is the process of identifying taxa to the highest possible taxonomic category (genus, family, order, etc.) without losing statistically significant information during, for example, assessment of pollution impact (Maurer 2000). It entails using the highest taxonomic level necessary for meeting study aims without

sacrificing relevant information. In recent years, TS has been frequently used in pollution studies and was thoroughly discussed by Dauvin et al. (2003), Terlizzi et al. (2003), and Marrero et al. (2013), among others.

Some studies support the TS perspective for environmental monitoring programs when the responses to stress gradients can be detected at higher taxonomic levels (Olsgard et al. 1997). Nevertheless, many environmental variables (e.g., depth and sediment type) also can influence macrobenthic community structure, and it has not always been easy to separate the effects produced by these variables from those produced by anthropogenic activities (Underwood 2000). Human effects tend to modify community composition at a higher taxonomic level than natural environmental variables, whose influence on fauna is reflected mainly by species replacement (Warwick 1988, Olsgard et al. 1997, Olsgard and Somerfield 2000, Ajmal-Khan 2006). Determination of the resultant changes in benthic community structure has been one of the mainstays in monitoring the biological effects of marine pollution (Warwick 1988). According to Ajmal-Khan (2006), when stress increases due to anthropogenic activities, it successively affects species, genera, and families. Consequently, the community's response to increased stress is often manifested at higher taxonomic levels. Thus, the taxonomic level required to detect changes in the community could depend on the degree of environmental alteration.

Several TS studies analyzing samples at the phylum, family, genus, and species levels have had similar results, suggesting that relevant information is not often lost when analyses are performed at higher levels (Warwick 1988, Ferraro and Cole 1990, Ellis 1995, Drake et al. 1999, Olsgard and Somerfield 2000, Fiori and Soares-Gomes 2001, Hernández-Arana et al. 2003, Muniz and Pires-Vanin 2005, Ajmal-Khan 2006, Domínguez-Castanedo et al. 2007, Bevilacqua et al. 2009, Marrero et al. 2013). Another advantage of TS is that sometimes expertise in monitoring program technical staff is lacking for identifying a broad spectrum of invertebrate taxa (Fiori and Soares-Gomes 2001). Training of personnel to accurately sort at higher taxonomic levels is relatively rapid thus lowering the risk of misclassification and also increasing program efficiency. Moreover, personnel without previous high-level taxonomic expertise may be engaged to do the sorting work (Olsgard and Somerfield 2000, Ajmal-Khan 2006). The choice to use the species or higher taxonomic levels depends on the research objectives. Descriptive and comparative studies require the species-level, especially in environments where knowledge is scarce; while for monitoring benthic communities studies, the identification to family level is often probably sufficient (Gomez Gesteira et al. 2003).

Annelids, especially polychaetes, play a major role in the functioning of benthic communities in terms of nutrient recycling, reworking of marine sediments, and redistribution of organic matter (Hutchings 1998, Muniz and Pires 2000, Venturini et al. 2011). They are often the numerically dominant macrobenthic taxon in these sediments in terms of abundance and diversity, and may constitute more than half of the organisms in soft-bottom habitats (Muniz et al. 1998, Muniz and Pires 1999, 2000). Polychaetes and oligochaetes also have been used as indicators of different degrees of pollution due to their strong dominance in perturbed environments including those impacted by urban sewage (Pearson and Rosenberg 1978, Hily and Glémarec 1990, Méndez et al. 1998, Olsgard and Somerfield 2000, Gamito 2008, Ferrando et al. 2010, Ferrando and Méndez 2011, among others).

Estero de Urías is a coastal lagoon that is permanently exposed to multiple anthropogenic disturbances, including shrimp farms, a thermoelectric plant, a slaughterhouse, a fish processing factory, a harbor, and urban sewage. Most of these anthropogenic features cause eutrophication at the sediment (Ochoa-Izaguirre et al. 2002). Therefore, the lagoon is a suitable ecosystem to detect organic pollution impact through the study of benthic organisms. Méndez (2002) and Ferrando and Méndez (2011) characterized the lagoon through the study of annelid communities based on samples collected during 1997 and 2008, respectively. Specific zones related to different anthropogenic activities were distinguished during the two periods of time: non-perturbed or slightly perturbed zones (fringed by mangrove trees and in the mouth of the coastal lagoon, which receives the effect of marine water); a temporarily-perturbed zone (close to the thermoelectric plant, which discharges hot water into the lagoon); and perturbed to very perturbed zones, which receive wastes from the shrimp farm, the fish processing factory, the slaughterhouse, and urban sewage. The aim of the present study was to determine if the use of a higher taxonomic level for annelids (species, genus, or family) was sufficient for further monitoring of the effects of anthropogenic activities in the Estero de Urías coastal lagoon.

MATERIALS AND METHODS

STUDY AREA.—Estero de Urías is a tropical coastal lagoon located in the state of Sinaloa (Mexico), along the southeast coast of the Gulf of California, near the city of Mazatlán. Its depth ranges from 1 to 3 m, except for the navigation channel, where it can reach 12 m. The climate is tropical/subtropical with two contrasting seasons: the rainy season (July–October) and the dry season (November–June). The mean annual temperature and annual rainfall are 25 °C and 800 mm, respectively (Ochoa-Izaguirre et al. 2002).

SAMPLING.—Sediment samples were collected at six sites subjected to the effect of the different anthropogenic activities characterized in previous studies: site 1 receives wastes from the Don Jorge shrimp farm; site 2 is located in an area surrounded by mangrove trees and receives wastes from small shrimp farms; site 3 is subjected to the effects of hot water coming from the José Aceves Pozos thermoelectric plant; site 4 is located in front of a fish processing factory and a slaughterhouse; site 5 receives urban sewage from polluted wetland known as El Infiernillo; and site 6 is located in front of the Mazatlán harbor and fishing fleet, and is influenced by marine water (Fig. 1).

Pooled data of the six sites for all the time periods were analyzed: February and April 1997 (Méndez 2002), February and August 2008 (Ferrando and Méndez 2011), and October 2008 (unpubl data). Temporal variation in TS was not analyzed here. Sediment was collected with a 26.5 × 12.5 cm Van Veen Grab Sampler (one replicate in 1997 and two replicates in 2008) and sieved through a 0.5-mm mesh. The retained material was fixed with a 4% formaldehyde solution and preserved in 70% ethanol (Hobson and Banse 1981). Annelids were sorted and counted using a Leica S6E stereoscopic microscope. Polychaetes were identified to species level according to taxonomic keys (see Méndez 2002 and Ferrando and Méndez 2011). The lack of regional identification keys for oligochaetes did not permit their identification to species level. Therefore, the distinction of the different taxa belonging to this group was

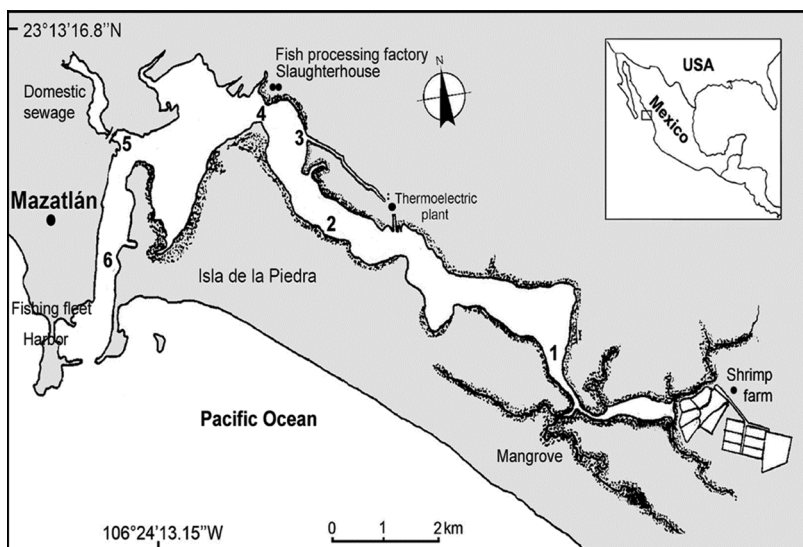


Figure 1. Estero de Urías coastal lagoon off western Mexico showing the six sampling sites subjected to the effects of different anthropogenic influences.

performed using morphological differences (e.g., hook and body shapes, and presence or absence of capillary chaetae).

Additional samples were collected for sediment analyses (one sample per site). Organic matter percentages in sediments were obtained following the ignition loss method (Dean 1974). About 200 g of sediments were sieved through a 2-mm mesh (to separate gravel from sand) and a 0.0625-mm mesh (to separate sand from mud). Grain sizes were expressed as percentages of mud, sand, and gravel (Folk 1965). Sediment temperature was measured with a digital CE model KM43F thermometer. Depth was measured with a graduated plumb line.

DATA ANALYSES.—According to Terlizzi et al. (2003), data for TS should be analyzed using ordination models, which show taxonomic aggregation, and non-parametric multivariate tests, which are complementary methods for further interpretation. In the present study, both test types were applied following the procedures proposed by Somerfield and Clarke (1995) and Olgsgard et al. (1997). Annelid abundances were standardized prior to TS analysis using one replicate (samples collected in 1997) and the mean values of two replicates (samples of 2008). Because quantifying temporal variation was not the aim here, all the abundances per site were pooled and aggregated to the levels of species, genus, and family.

Ranked matrices of similarities among samples were constructed using the Bray-Curtis similarity index (Bray and Curtis 1957) with the following transformations: none, square root, fourth root, and presence/absence (Olgsgard et al. 1997). According to Clarke (1993), transformations are used to reduce contributions to similarity by dominant taxa, thereby increasing the importance of the less abundant taxa in the analyses. Ordination of sampling sites was achieved by non-metric multidimensional scaling diagrams (MDS), and the goodness of fit of the resulting two-dimensional plots was measured using Kruskal's stress formula 1 (Kruskal and Wish 1978, Clarke

and Green 1988). Sample 4d (site 4 during February 1997) was eliminated from this analysis because it was the only one lacking annelids.

The Spearman rank correlation (ρ) was computed between the corresponding elements of each pair of matrices (generated using similarity of Bray-Curtis), and the significance of the correlation was determined by a permutation procedure (9999 permutations) using the PRIMER program RELATE (Clarke and Warwick 2001). To visualize these interrelationships, these rank correlations between the corresponding elements of pairs of matrices were used as input similarities in the creation of “second-stage” MDS ordinations, where the distance between taxonomic levels reflects the degree to which the similarity matrices are correlated (Somerfield and Clarke 1995).

To detect differences among sampling sites at the different taxonomic levels with and without transformation, the one-way analysis of similarities permutation test (ANOSIM) (Clarke and Green 1988, Clarke 1993) was performed with 9999 permutations. Bonferroni correction was applied to reduce the type I error by dividing the experiment-wise P value ($\alpha = 0.05$) by the number of comparisons made (Napierala 2012). The statistic R is close to zero when no differences between communities are apparent and increases to a maximum of 1 as communities become dissimilar (Dernie et al. 2003). Following recommendations from Somerfield and Clarke (1995) and Olsgard et al. (1997), we analyzed the non-significant ($P > 0.05$) pairwise tests ($\alpha = 0.05$ divided by 1 comparison, after Bonferroni correction). In this case, this significance level indicates that faunal composition between pairs of stations did not differ significantly. To determine the relationships between patterns in community structure and combinations of environmental variables, the BIO-ENV multivariate procedure (Clarke and Ainsworth 1993) was applied. It calculates rank correlations between a similarity matrix derived from biotic data and different matrices derived from various subsets of environmental variables, thereby identifying the variables most correlated with the observed biotic structure (Olsgard et al. 1997). This procedure was conducted with the PRIMER 6.0 program (v6.1.6), using 9999 permutations and the Euclidean distance as a resemblance measure. The analyzed environmental variables were depth, sediment, temperature, and percentages of organic matter, mud, sand, and gravel.

RESULTS

Because analysis of temporal variability was not our objective, abundance data of all the time periods were condensed in a single matrix to evaluate annelid TS in the focal lagoon. This matrix contained a total of 98 species grouped in 70 genera and 30 families of annelids. Table 1 presents the number of families, genera, and species over the study. Sites 2 and 6 had the highest annelid species richness over the study (54 and 77, respectively) and were dominated by *Mediomastus californianus* Hartman, 1944, *Mediomastus ambiseta* (Hartman, 1947), *Prionospio heterobranchia* Moore, 1907, *Prionospio cirrifera* Wirén, 1883, *Ophelina acuminata* Oersted, 1843, and *Tharyx monilaris* Hartman, 1960. Sites 4 and 5 had the lowest species richness, represented mainly by oligochaetes. Sites 1 and 3, with intermediate numbers of taxa, were mainly dominated by *Capitella* “*capitata*” (Fabricius, 1780) and *Capitella* sp. The spionid *Streblospio benedicti* Webster, 1879 dominated zones with different

Table 1. Number of families, genera, species, total annelid abundance (individuals in five grabs), and dominant taxa in each collection site over the study.

Site	Description	Families	Genera	Species	Total abundance	Dominant taxa
1	Shrimp farm	13	22	29	1,190	<i>Streblospio benedicti</i> , <i>Capitella</i> “ <i>capitata</i> ”, <i>Capitella</i> sp.
2	Mangrove and small shrimp farms	20	37	54	1,001	<i>Mediomastus californianus</i> , <i>Mediomastus ambiseta</i> , <i>Prionospio heterobranchia</i>
3	Thermoelectric plant	14	26	32	656	<i>Oligochaeta</i> sp. 1, <i>Capitella</i> “ <i>capitata</i> ”
4	Fish factory and slaughterhouse	9	13	14	381	<i>Oligochaeta</i> sp. 1, <i>Streblospio benedicti</i>
5	Domestic sewage	6	7	9	78	<i>Oligochaeta</i> sp. 4, <i>Oligochaeta</i> sp. 2
6	Mouth of the coastal lagoon	27	59	77	1,509	<i>Prionospio cirrifera</i> , <i>Ophelina acuminata</i> , <i>Tharyx monilaris</i>

degrees of perturbation coming from the shrimp farm, the fish factory and the slaughterhouse.

MDS ordinations of matrices derived from untransformed data and with the three applied transformations appeared similar at the levels of species, genus, and family (Fig. 2), indicating that at these taxonomic levels and transformations, the overall patterns of community structure are retained. Stress values ranged between 0.11 and 0.13, indicating a useful representation.

Results of tests for differences between the similarity matrices derived from abundance of species, genera, and families showed high correlations among all taxonomic levels (Table 2). Although correlations slightly decreased as taxonomic levels increased, all correlations were statistically significant ($P < 0.001$), indicating that data aggregated to the different taxonomic levels presented similar patterns. Moreover, the different transformations did not show substantial effects compared with the untransformed data.

The “second-stage” MDS ordination’s stress value was 0.03, indicating an excellent representation. The associated diagram shows a “fan pattern” with a clear separation of groups horizontally for taxonomic levels and vertically for transformations (Fig. 3), which indicates that the effects of transformations and taxonomic resolution operated independently.

Values of the ANOSIM for differences among groups (sampling sites at the different taxonomic levels, with and without transformations) are shown in Table 3. All differences were statistically significant ($P < 0.003$) after Bonferroni correction ($P < 0.05/15$). The ANOSIM statistic for a global test of differences among groups (R) was also significant. Comparisons of pairwise tests ($P > 0.05$ after Bonferroni correction) indicated that sites 2 with 6, sites 3 with 4, and sites 4 with 5 were always associated due to the similitude of their faunal composition. Also sites 1 with 3 and sites 1 with 4 were associated in most of the cases.

BIO-ENV analyses indicated that percentages of mud, organic matter, and gravel had the highest overall correlation at all taxonomic levels. Independent analyses for each one of these variables (Table 4) using the different taxonomic levels and

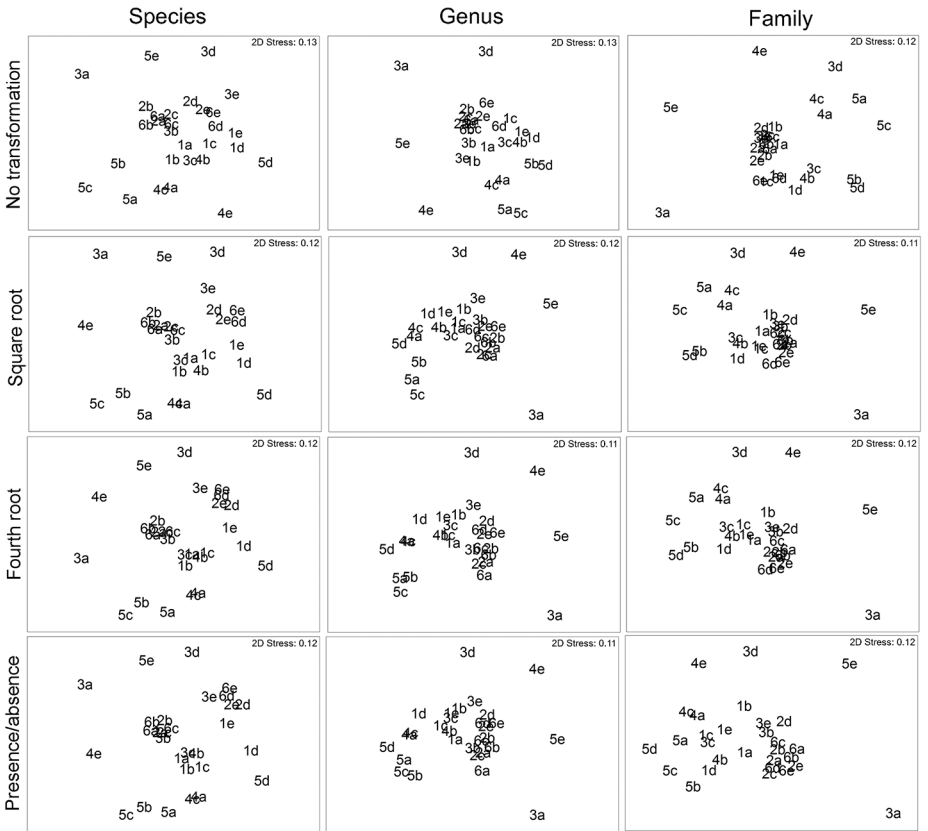


Figure 2. Multidimensional scaling ordinations (Bray-Curtis similarity index) representing the six sampling sites with untransformed and transformed abundances of species, genera, and families (Numbers = sampling sites; a = August 2008; b = October 2008; c = February 2008; d = February 1997; e = April 1997). Site 4d was omitted from analyses due to the absence of annelids.

Table 2. Pairwise Spearman correlations (ρ) between similarity matrices (Bray-Curtis) derived from abundance of species (SP), genera (GEN), and families (FAM) using no transformations (NT), and square root (2), fourth root (4), and presence/absence (P/A) transformations. All the correlations were statistically significant at $P < 0.001$ as determined by 9999 permutations (RELATE).

	SP NT	SP 2	SP 4	SP P/A	GEN NT	GEN 2	GEN 4	GEN P/A	FAM NT	FAM 2	FAM 4
SP 2	0.985										
SP 4	0.956	0.990									
SP P/A	0.918	0.965	0.990								
GEN NT	0.882	0.863	0.835	0.801							
GEN 2	0.881	0.884	0.868	0.841	0.985						
GEN 4	0.868	0.886	0.882	0.865	0.954	0.989					
GEN P/A	0.837	0.866	0.876	0.873	0.906	0.953	0.985				
FAM NT	0.805	0.791	0.769	0.743	0.896	0.883	0.857	0.818			
FAM 2	0.809	0.808	0.793	0.770	0.905	0.912	0.901	0.869	0.983		
FAM 4	0.794	0.804	0.798	0.782	0.888	0.913	0.918	0.902	0.938	0.982	
FAM P/A	0.717	0.736	0.742	0.737	0.813	0.851	0.876	0.886	0.831	0.903	0.963

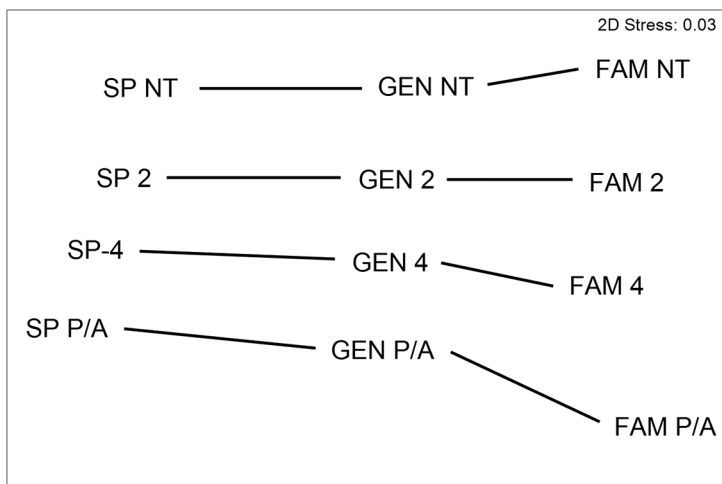


Figure 3. “Second-stage” multidimensional scaling of inter-matrix rank correlations (pairwise Spearman correlations from Table 2) (SP = species; GEN = genera; FAM = families; NT = no transformation; 2 = square root; 4 = fourth root; P/A = presence/absence).

transformations revealed that these variables had higher correlation with biotic matrices, pointing them as the main environmental factors responsible for annelid distribution. These patterns were consistent for untransformed data, square root-transformed, fourth root-transformed, and presence/absence-transformed data.

DISCUSSION

The taxonomic resolution necessary for monitoring the tropical coastal lagoon Estero de Urías via annelid community assessment was evaluated according to methods proposed by Somerfield and Clarke (1995) and Olsgard et al. (1997). In general, results obtained with untransformed and transformed data at the species, genus, and family levels provided similar findings. All levels resulted in similar patterns in terms of correlations between similarity matrices among taxonomic levels, sampling site grouping, and the main environmental variables influencing annelid distribution.

The idea of TS has been widely supported in marine environments. Bevilacqua et al. (2009) stated that differences at regional or larger scales in higher taxa are commonly observed in marine invertebrates. Terlizzi et al. (2003) demonstrated that little information is lost when macrobenthic specimens inhabiting subtidal soft bottoms are identified at phylum level. They suggested that at polluted sites, it might be less expensive to investigate the presence and abundance of some families or orders as “indicators” of disturbance, rather than examining the issue at the species level. Because polychaetes have been widely used as indicators of organic pollution (Pearson and Rosenberg 1978) and have different feeding guilds that are generally represented in each family (Fauchald and Jumars 1979, Gambi and Giangrande 1985), our results are consistent with Terlizzi et al.’s (2003) assessment. Moreover, Olsgard and Somerfield (2000) stated that the use of TS is likely to be most advantageous if species level baseline studies have already been completed, which has occurred in our case (Méndez 2002, Ferrando and Méndez 2011), thus allowing comparisons to extend to the results obtained at genus and family levels.

Table 3. Values of one-way ANOSIM statistic (R) for global tests for differences between groups (sampling sites at the different taxonomic levels, with and without transformations) in each matrix (differences were significant at $P < 0.003$ in all cases after Bonferroni correction calculated as 0.05/15), and pairwise tests in which $P < 0.05$ (after Bonferroni correction calculated as 0.05/1) with 9999 permutations.

Level	No transformation			Square root			Fourth root			Presence/absence		
	Sites	R	P	Sites	R	P	Sites	R	P	Sites	R	P
Species	Global R = 0.278			Global R = 0.275			Global R = 0.246			Global R = 0.205		
	1, 4	0.212	0.079	1, 4	0.228	0.056	1, 3	0.170	0.103	1, 2	0.268	0.056
	2, 3	0.100	0.167	2, 3	0.072	0.246	1, 4	0.184	0.079	1, 3	0.064	0.270
	2, 6	0.056	0.310	2, 6	-0.016	0.421	2, 3	0.012	0.429	1, 4	0.094	0.206
	3, 4	0.032	0.341	3, 4	0.044	0.341	2, 6	-0.080	0.635	1, 6	0.310	0.071
	3, 6	0.086	0.167	3, 6	0.054	0.286	3, 4	0.052	0.302	2, 3	0.020	0.389
	4, 5	0.064	0.222	4, 5	0.072	0.222	3, 5	0.244	0.071	2, 6	-0.154	0.825
							3, 6	0.042	0.333	3, 4	0.052	0.317
							4, 5	0.072	0.246	3, 5	0.254	0.056
										3, 6	-0.010	0.460
										4, 5	0.074	0.246
Genus	Global R = 0.334			Global R = 0.365			Global R = 0.371			Global R = 0.342		
	1, 3	0.186	0.056	1, 3	0.198	0.063	1, 3	0.170	0.063	1, 3	0.114	0.135
	1, 4	0.198	0.063	2, 6	0.048	0.294	2, 6	-0.064	0.627	1, 4	0.092	0.175
	2, 6	0.132	0.151	3, 4	0.008	0.437	3, 4	0.016	0.413	2, 3	0.182	0.063
	3, 4	-0.016	0.524	4, 5	0.066	0.286	4, 5	0.110	0.151	2, 6	-0.074	0.643
	4, 5	0.014	0.333							3, 4	0.006	0.413
										3, 6	0.172	0.079
										4, 5	0.100	0.143
Family	Global R = 0.267			Global R = 0.321			Global R = 0.353			Global R = 0.340		
	1, 3	0.160	0.071	1, 3	0.140	0.079	1, 3	0.056	0.262	1, 3	-0.024	0.540
	1, 6	0.192	0.175	2, 3	0.104	0.095	2, 6	0.108	0.214	1, 4	0.092	0.175
	2, 3	0.052	0.230	2, 6	0.148	0.151	3, 4	0.036	0.357	2, 6	0.066	0.286
	2, 6	0.224	0.079	3, 4	0.060	0.246	3, 5	0.200	0.063	3, 4	0.072	0.254
	3, 4	0.044	0.333	3, 5	0.160	0.111				3, 5	0.200	0.071
	3, 5	0.138	0.135	4, 5	0.188	0.056						
	4, 5	0.142	0.103									

ANOSIM highlighted sites where the faunistic composition was equivalent. In general, such associations corresponded to sites receiving different kinds and differing degrees of perturbation, like the perturbed and very perturbed zones receiving the effects of anthropogenic activities or the non-perturbed or slightly perturbed zones located in the mouth of the lagoon and close to mangrove swamps. Because similar results were obtained through the analyses of data generated by species, genus, and family matrices, we can conclude that genus and family levels have enough information to characterize the study area. Also, percentages of organic matter, mud, and gravel were the environmental variables that best explained the annelid community distribution patterns in Estero de Urías. The similar results obtained at species, genus, and family levels as they related to environmental variables suggests that no substantial information was lost at genus and family levels, supporting the TS approach. Moreover, these results are consistent with previous observations from Méndez (2002) and Ferrando and Méndez (2011) using other tools like canonical correspondence analysis at the species level. Our findings are consistent with TS

Table 4. Summary of results from independent BIO-ENV analyses considering only the environmental variables with the highest overall correlation. Data in table correspond to the higher correlations (R , significant when $P < 0.05$) of organic matter (OM), gravel (GRA) and depth (DEP) with the biotic matrices constructed at the different taxonomic levels and transformations examined (statistical significance was determined via 9999 permutations and the Euclidean distance as a resemblance measure).

Transformation	Species			Genus			Family		
	Variables	R	P	Variables	R	P	Variables	R	P
None	MUD	0.241	0.002	MUD	0.361	0.001	MUD	0.327	<0.001
	MUD, OM	0.241	0.002	GRA, MUD	0.360	0.001	GRA, MUD	0.326	<0.001
				MUD, OM	0.358	0.001	MUD, OM	0.326	<0.001
				GRA, MUD, OM	0.358	0.001	GRA, MUD, OM	0.325	<0.001
Square root	MUD	0.245	0.005	MUD	0.368	<0.001	MUD	0.347	<0.001
	MUD, OM	0.245	0.001	GRA, MUD	0.367	<0.001	GRA, MUD	0.346	<0.001
	GRA, MUD, OM	0.245	0.001	MUD, OM	0.366	<0.001	MUD, OM	0.345	<0.001
				GRA, MUD, OM	0.366	<0.001	GRA, MUD, OM	0.344	<0.001
Fourth root	MUD	0.238	0.001	MUD	0.374	<0.001	MUD	0.349	<0.001
	MUD, OM	0.238	0.002	GRA, MUD	0.373	<0.001	GRA, MUD	0.348	<0.001
	GRA, MUD, OM	0.238	<0.001	MUD, OM	0.372	<0.001	MUD, OM	0.347	<0.001
				GRA, MUD, OM	0.372	<0.001	GRA, MUD, OM	0.346	<0.001
Presence/absence	MUD	0.226	0.002	MUD	0.379	<0.001	MUD	0.332	<0.001
	MUD, OM	0.225	0.001	GRA, MUD	0.378	<0.001	GRA, MUD	0.331	<0.001
	GRA, MUD, OM	0.225	0.002	MUD, OM	0.376	<0.001	DEP, MUD	0.329	<0.001
	GRA, MUD	0.225	0.002	GRA, MUD, OM	0.376	<0.001	MUD, OM	0.329	<0.001
				DEP, MUD	0.376	<0.001	GRA, MUD, OM	0.328	<0.001

approaches used in marine macrobenthos environments near sources of pollution, in which little information loss has been reported when genus or family level data are used instead of species level data (i.e., Warwick 1988, Gray et al. 1990, Agard et al. 1993, Ferraro and Cole 1995, Somerfield and Clarke 1995, Olsgard et al. 1997, Baldó et al. 1999, Drake et al. 1999, Karakassis and Hatziyanni 2000, Gomez Gesteira et al. 2003, Muniz and Pires-Vanin 2005, Marrero et al 2013, among others). In particular, the use of family level has been supported by Olsgard and Somerfield (2000) and Terlizzi et al. (2003) because it could represent the best accuracy and precision given funding and time constraints. Moreover, Gomez Gesteira et al. (2003) have argued that family level data are generally sufficient for monitoring pollution effects in in-fralittoral soft-bottom environments, which is the case in our study area.

In addition to taxonomic aggregation, several studies have demonstrated that data transformation can influence the results of analyses, as their effects can vary across habitats and environmental conditions. Also, mathematical transformations of data and low taxonomic accuracy can interact to decrease the potential of multivariate tools to perceive changes in assemblages (Terlizzi et al. 2003). Nevertheless, it has been also suggested that, in some cases, no transformation provides the “best view” of the assemblage structure (Bevilacqua et al. 2009). Our results suggested that, in general, transformations did not exert substantial influence compared to the use of untransformed data.

In conclusion, our study indicated that the use of genus or family level data did not lead to relevant information loss in relation to species level data. Thus, our results are consistent with previous studies that referred to soft-bottom annelids, indicating that genus and family level data without any transformation provide sufficient information to characterize the Estero de Uriás coastal lagoon. It is important to note that in this exercise, we did not examine temporal changes. Therefore, our conclusions might have been different if we had explicitly investigated changes over time. We recommend the use of family level data for further monitoring programs, which will allow sampling of annelids at more sites, with higher periodicity, and at reduced costs.

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