Polychaete community structure of Indian west coast shelf, Arabian Sea

Ellis[1] introduced the concept of taxonomic sufficiency (TS) in which identification is required only to the level that indicates the community response. Warwick[2,3] applied TS in studying the pollution effects on marine benthic communities and suggested that natural variables, such as water depth and sediment type affect community structure mainly by species replacement, whereas anthropogenic effects are detectable at higher taxonomic levels. Later, this approach was used in oil and sewage pollution impact studies on benthos[4–6] and it was recommended that the TS concept was appropriate to identify the effects of pollution on marine communities. As TS moves progressively to species, costs, in terms of the expertise and time needed to identify organisms, decrease[4]. It is quicker and easier to train personnel to sort higher taxonomic levels than species, and the risk of potential taxonomic classification error is lower at a higher level of identification[7]. Ferraro and Cole[4,8] hypothesized that when a given stress increases, it successively affects individuals, species, genera and families and thus, the communities response to increasing stress is manifested at higher and higher taxonomic levels.

Later, TS was adopted to study the relationships among spatial patterns of benthic community in natural environment[9–11]. De Biasi et al.[9] recommended that the family level is taxonomically sufficient for habitats with strong gradients in eco-physiological stress. Dethier and Schoch[10] reported that even weak estuarine gradients can drive family level patterns. The present study investigates the scope of TS in benthic fauna of continental shelf off the west coast of India, where our study[12] has shown that the depth and natural environmental gradients influence the distribution and abundance of polychaetes. The object of this study was to know whether taxonomic resolutions, generic and family in the polychaetes, can explain community variation along the depth gradient similar to the higher resolution data set.

Infaunal macrobenthic samples for the present study were collected onboard the Fishery and Oceanographic Research Vessel (FORV) *Sagar Sampada*, owned by the Ministry of Earth Sciences, Government of India. Two cruises (Cruise No. 162 and 192A) were conducted along the western continental shelf of India (8°3′96″N and 77°21′96″E to 21°56′99″N and 67°57′69″E). The first cruise (during 16 February 1998 to 6 March 1998) covered 62 stations from 13 transects (T) and the second (20–28 February 2001) covered 13 stations from three transects (T5, 9 and 13). Benthic samples were collected from 75 stations at 30, 50, 100 and 200 m depths at each transect using Smith Mc Intyre grab (0.1 m^2 bite area; Figure 1). Additional samples were collected at ~75 m from selected transects (T3, T7, T10, T11, T12 and T14), where the distance between 50 and 100 m depths was greater than 30 nautical miles. Initially, specimens were sorted and being the dominant group, polychaetes were identified down to species level using the identification key developed by Day[13].
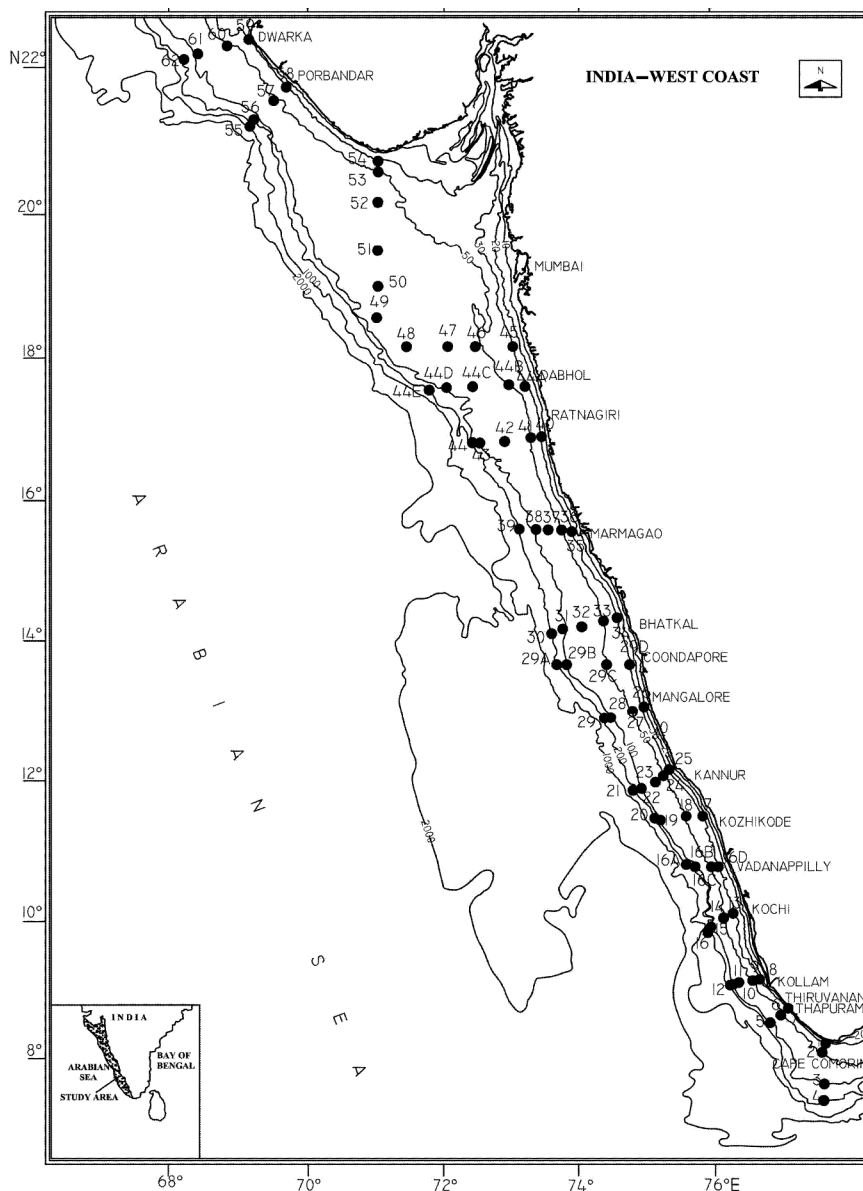

Figure 1. The location of sampling stations in the west coast Indian shelf.
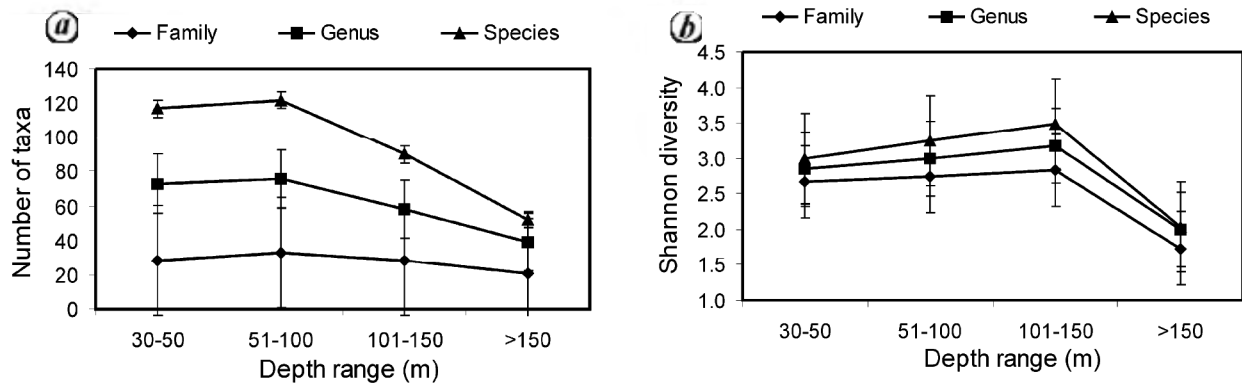
Figure 2. Depth-wise variations in different taxonomic levels of polychaetes (*a*) in taxa richness and (*b*) in Shannon diversity. Bars show standard deviation.

Univariate and multivariate community analyses were performed using PRIMER (Plymouth Routines in Multivariate Ecological Research; version 5) with the polychaete species abundance matrix. One way ANOSIM (analysis of similarity) was carried out to test differences found in the communities (square-root transformed data) between different depth habitats[14]. For the convenience of analysis and interpretation, the data from all transects were pooled into specific depth ranges, i.e., 30–50 m (19 stations), 51–100 m (29 stations), 101–150 m (13 stations) and >150 m (14 stations).

The data set consisted of 12,518 individuals belonging to 32 families, 94 genera and 165 species of polychaetes. The number of species per genus and per family varied widely in the samples; 60 genera and nine families were represented by one species only. The most speciose families were Eunicidae (22 species), Spionidae (14 species) and Terebellidae (11 species). Spionidae $(187 \pm 311.4$ ind. $m^{-2})$, Magelonidae $(171.5 \pm 721.5$ ind. $m^{-2})$ and Eunicidae $(65.8 \pm 66.4$ ind. $m^{-2})$ were numerically the dominant families. Correlation analyses indicate a slightly closer relationship between species and genus $(r = 0.98; P < 0.001)$ than between species and family $(r = 0.94; P < 0.001)$ and genus and family $(r = 0.95; P < 0.001)$. Shannon diversity $(H'(\log 2))$ ranged from nil to 4.64. Over 82% of the stations had diversity of more than two.

In the west coast Indian shelf, a depth-wise variation in polychaetes was evident[12]. Average taxa richness at each level of resolution with respect to depth gradient also indicated (Figure 2 *a*) a reduction in number with increase in depth. Family showed stronger negative correlation with depth $(r = -0.54; P < 0.001)$ than genus $(r = -0.42; P < 0.001)$ and

species $(r = -0.43; P < 0.001)$. Highest number of taxa was recorded from 51 to 100 m depth (122 species, 76 genera and 32 families) and lowest in >150 m depth (52 species, 39 genus and 20 families). The number of genera ranged from 62% (30–50 and 51–100 m) to 75% (>150 m) of the number of species whereas the number of families ranged from 24% (30–50 m) to 38% (>150 m) of the number of species. As in the case of taxa richness, average diversity at each level of resolution followed similar pattern in the depth gradient (Figure 2 *b*) with higher values in 101–150 m and steep decline towards depth >150 m. Species and genus level diversity showed a maximum difference of 1.2 whereas species and family difference was 1.5 (both in stations 10, 51–100 m).

Differences in community similarity among various depth ranges for each level of taxonomic resolution were tested using one-way analysis of similarity (ANOSIM, Table 1). Differences between depth ranges were significant for 30–50 and >150 m, and 51–100 and >150 m for all the three taxonomic levels. Evaluation of *R*-statistics suggests that the above depth-wise differences are increasing from the species level to the family level of taxonomic resolution. Moreover, for family level, difference was found to be significant for 101–150 and >150 m as well. The *R*-values suggest the greatest community differences at the family level of aggregation (Table 1).

Studies on TS of macrobenthos in natural environments have reported in estuarine gradients[9,10] and rocky shore[11]. The present study applies TS to a wider domain of Indian continental shelf, where our previous study of infaunal macrobenthos of shelf waters of west coast of India[12] with high resolution spe-

cies level data showed a depth-wise decrease in polychaetes. The present study confirmed that in the western continental shelf of India, genus and family aggregations of polychaetes show similar community response as that of species on a depth gradient in this environment. Our high resolution data showed significant community differences (ANOSIM) between shallow depths and shelf edge (30–50 and >150 m, and 51–100 and >150 m), whereas the low resolution data (family level) further separated the communities between 101–150 and >150 m depth ranges. This is in accordance with the study of Dethier and Schoch[10], in which they explained weak estuarine gradients with family level patterns. The present study has no scope to take the taxonomic level higher than family (as only polychaetes are considered), however, studies have reported the insufficiency of order and higher levels in explaining the community structure[9,15], and De Biasi *et al.*[9] concluded that family is a taxonomically sufficient descriptor for habitats with strong gradients of eco-physiological stress.

The extent to which taxonomic aggregation affects multivariate analyses may also depend on the way in which species are distributed amongst the family[16]. In this study, three families (Eunicidae, Spionidae and Terebellidae) were considerably more speciose (29% of the total species) than the others and these families along with Magelonidae (this was represented by one species only) together contributed over 53% of the total individuals. This gives validation to results obtained from the analysis of higher taxa which show analogous results to those based on species level.

The major benefit of being able to detect community patterns at higher taxonomic

Table 1. Community analyses using one-way ANOSIM (with 999 permutations) for comparisons among different depths for species, genus and family levels of the samples

Species level
Global R: 0.193; $P < 0.001$

Depth range	30–50 m	Pair-wise R-statistics		
		51–100 m	101–150 m	>150 m
30–50 m	0	0.018	0.151	0.385
51–100 m		0	0.018	0.483
101–150 m			0	0.164
>150 m				0

Genus level
Global R: 0.185; $P < 0.001$

Depth range	30–50 m	Pair-wise R-statistics		
		51–100 m	101–150 m	>150 m
30–50 m	0	0.015	0.121	0.43
51–100 m		0	–0.007	0.505
101–150 m			0	0.203
>150 m				0

Family level
Global R: 0.194; $P < 0.001$

Depth range	30–50 m	Pair-wise R-statistics		
		51–100 m	101–150 m	>150 m
30–50 m	0	0.049	0.057	0.522
51–100 m		0	–0.031	0.522
101–150 m			0	0.268
>150 m				0

levels is the clear saving in time, expertise needed and low cost of identification[4,10]. Information obtained by more accurate taxonomic identification is considered redundant while the same inference is drawn when animals are identified to a higher taxon[3]. Studies have reported that the cost of family-level identification is 50–55% less than species level identification[8,9]. Dethier and Schoch[10] opined that savings in effort put into taxonomic detail can profitably be transferred to field sampling effort. Identification to the family level also avoids errors in identification, which are much more common at the species level.

On the other hand, care has to be taken in implementing such an approach for a regular protocol. Maurer[17] aroused several anxieties about the taxonomic sufficiency approach, for example, the exclusion of rare species can seriously violate results from general ecological observation leading to the unacceptable losses of ecological information. Essentially, a species list is an irreplaceable tool to know the functioning of ecosystem. However, as De Biasi et al.[9] opined, a correct identification to a higher taxonomic level would be better than an incorrect identification to the species level. Being fast,

lower resolution results can give a general picture about the benthic ecosystem which, in turn, can be utilized for developing a subsequent sampling programme, if the aim of the study demands.

In the present study, family level information followed a similar pattern of species in explaining the community structure and was found to be sufficient to explain the depth gradient in the continental shelf. So we propose, for the monitoring and impact assessment studies of macrobenthos, the TS can be employed in the Arabian Sea for a rapid evaluation of human impact.

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