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Using high-level identification of macroinvertebrates for pollution assessments: an example from Gamak Bay, on the southern coast of Korea

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ABSTRACT :*Although surveys of soft-bottom macrofauna are an important tool in assessing marine pollution, identifying organisms to the species level is time-consuming and therefore costly. One solution is to identify organisms to a higher taxonomic level. This study, using data from macrobenthic surveys in Gamak Bay, on the southern coast of Korea, shows that abundances measured at higher taxonomic levels than species can be adequate for pollution assessments. 'Second-stage' MDS and 'BIO-ENV' showed that aggregation of data to the level of family produces results that are close to those based on species-level identification. In severely polluted areas, a W statistic based on order-level aggregation was identical to that produced by species-level identification.Although these results could be used to make a general recommendation that the family level, at least, is a suitable level for faunal identification in pollution assessments, this will to a large extent depend on the objectives of each individual investigation. In surveys to assess pollution, nonetheless, analyzing the benthic community at a higher taxonomic level than species is efficient and cost-effective, and is sufficient to accomplish the assessment's objective.*

KEYWORDS :*higher-level taxa, Korea, macroinvertebrate, pollution assessment, taxonomic resolution*

I. INTRODUCTION

Surveys of macrobenthic community structure are often used to monitor the effects of pollution. These surveys conventionally require identification of organisms to the species level. Although surveys of soft-bottom macrofauna are important tools for monitoring marine pollution, they are often criticized for being excessively labor-intensive, costly, and relying on techniques that have remained unchanged for almost a century [1, 2, 3, 4]. Species identification is particularly time-consuming. One solution to this problem is to identify organisms to a higher taxonomic level. Several studies have assessed the feasibility of measuring abundances at higher-level taxa as an alternative to species-level identification [2, 5, 6, 7, 8, 9, 10, 11, 12, 13], and most have reported no loss of information when higher taxonomic levels were used. Warwick [5, 7] suggested that the results of community structure analyses based on higher taxa may more closely reflect gradients of contamination or stress than those based on species data, as natural environmental variables are more likely to affect community structure at the species level and may mask the effects of pollution. It is important to determine whether higher taxonomic levels still enable us to assess variations in community structure and to what taxonomic level it is necessary to identify organisms to meet a study's objectives. If the results of appropriate univariate or multivariate analyses of data from higher taxonomic levels are similar to those of species level, it would strongly indicate that identifications at these levels are sufficient in that particular investigation [13].

Studies comparing species-level and higher-level identifications have only been carried out in a few regions, including the North Sea and the Australian coast. To make general recommendations about the taxonomic resolution of environmental studies, such investigations must be conducted over a wider geographic area. In this study, the appropriateness of identifying the macrobenthos to higher-level taxa for pollution assessments along the coast of Korea was assessed, which has not been previously attempted. The study was conducted in Gamak Bay, on the southern coast of Korea; this body of water used to be one of the country’scleanest. In recent years, however, the water and sediment quality of the bay has rapidly deteriorated due to excessive mariculture in the area and increased sewage and effluent from adjacent cities and coastal industrial complexes. It is especially notable that the incidence of imposex in *Thais clavigera* females is 100% in the bay [14]. The Korean government is concerned about the degradation of the environment in the bay, and wishes to develop simple and highly repeatable methods for monitoring the impacts of mariculture in the area. Here the effects of assessing macrobenthic abundances at different taxonomic levels were examined, using different transformations in subsequent analyses of faunal patterns; environmental variables associated with the observed faunal patterns at different taxonomic levels were identified.

II. MATERIAL AND METHODS

This study is a reassessment of the research conducted by Koo et al. [15], an analysis of changes in macrobenthic community structure used to assess pollution levels in Gamak Bay. Macrobenthic and environmental data collected in the spring of 1999 were reanalyzed with their permission. The study area included 12 sites chosen based on a presumed pollution gradient from the interior to the exterior of the bay (Fig. 1). For comparative studies of faunal patterns at various taxonomic levels, *W* statistic [16] and ‘Second-stage’ multidimensional scaling (MDS) ordinations[10] were analyzed. Subsequent calculations were performed using the PRIMER package [17].

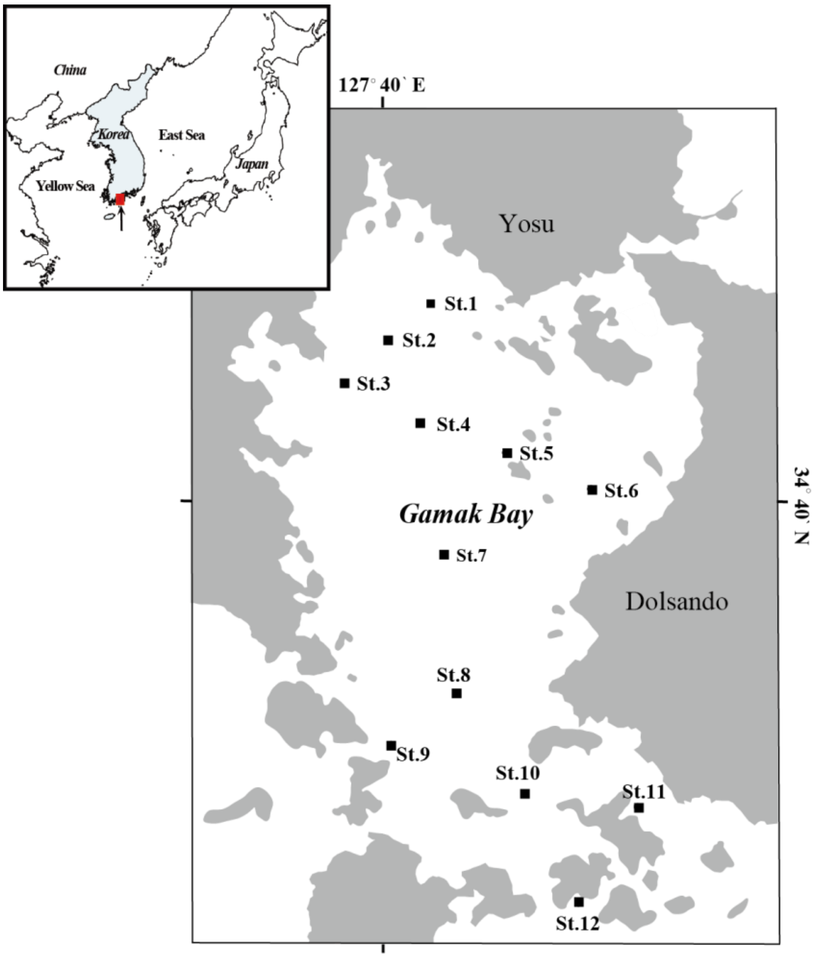


Fig. 1.Location and layout of the study site inGamak Bay, on the Southern coast of Korea

Macrobenthic abundance and biomass were aggregated to the levels of genus, family, order, class, and phylum. *W* statistics derived from an ABC curve analysis [18], which compares *k*-dominance curves for abundance and biomass, were applied to the various taxonomic levels. The *W* statistic involves summing the differences between the ranked cumulative percentages of abundance and biomass values. Ranked matrices of similarities among samples were constructed using the Bray–Curtis similarity measure and the following transformations: none, square root, fourth root, and presence/absence. Ordination was by non-metric MDS, and the goodness-of-fit of the resulting two-dimensional plots was measured. The multivariate patterns obtained were compared using the methods of Somerfield and Clarke [10], whereby rank correlations between the corresponding elements of pairs of matrices themselves become the elements of a second similarity matrix, which is then used as an input matrix for 'second-stage' MDS. The Spearman rank correlation was used for relationships between taxonomic levels.

The relationships between patterns in the multivariate community structure and combinations of environmental variables were examined using the BIO-ENV procedure [19], which calculates rank correlations between a similarity matrix derived from biotic data and matrices derived from various subsets of environmental variables, thereby defining suites of variables most closely correlated with the observed biotic structure. The following environmental variables were used: waterdepth, sediment temperature (Tem), sediment particle size (Mz), dissolved oxygen content (DO), and salinity of bottomwater (S), and chemical data including carbon (C),nitrogen (N), tributyltin (TBT), polychrolinated biphenyl(PCB), polycyclic aromatic hydrocarbon (PAH), and organochlorinepesticide (OCP) contents of surface sediments.

III. RESULTS AND DISCUSSION

For comparison with the species-level analysis, *W* statistics were calculated for the same data aggregated to genus, family, order, class, and phylum levels (Fig. 2). At the genus and family levels the values were virtually identical to the species values at all sites, so that there would have been absolutely no loss of information had the samples originally been sorted into genus or family levels. Pearson correlation coefficients were high (>0.998) among species, genus, and family levels (Table 1). Values derived at the order, class, and phylum levels deviated from those at the level of species, although in three of the twelve sites (Sites 1, 2, and 3, regarded as being severely polluted; [15]), values at the order level were the same as at species level.

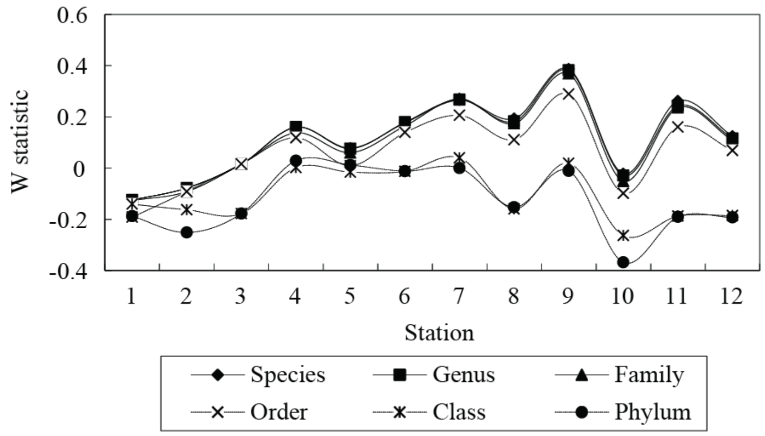


Fig. 2.*W* statistics for each site, using different taxonomic levels

MDS ordinations of matrices derived from square root-transformed abundances of various taxonomic levels were similar at the levels of species, genus, and family (Fig. 3), indicating that the overall patterns of community structure are retained at these levels. This is also seen in the high correlation values between the species level and the levels of genus and family, with respective correlation coefficients of 0.998 and 0.978. Even at the order level there was a 0.931 correlation with species-level data. The ordination plots at the levels of class and phylum were less similar, and their correlation coefficients with species-level patterns were 0.715 and 0.745, respectively.

Table 1.Pearson’s correlation coefficients of the *W* statistics of each taxon

	Species	Genus	Family	Order	Class
Genus	0.999				
Family	0.998	0.999			
Order	0.981	0.985	0.985		
Class	0.549	0.577	0.575	0.593	
Phylum	0.588	0.612	0.61	0.636	0.953

To examine whether there are consistent differences in the way in which patterns change with changes in taxonomic level and transformation, ‘second-stage’ MDS ordination was applied. Rank correlations between similarity matrices based on different taxonomic levels and different transformations tended to be lower between matrices derived from higher-taxon abundances using strong transformations. The plots produced a fan-pattern, showing separation of groups horizontally for taxonomic levels and vertically for transformations (Fig. 4). While both affected the results of subsequent analyses, this showed that the effects of each were different and unrelated. Matrices derived from species, genus and family abundances constructed using the same transformation tended to cluster together, indicating that transformation had more of an effect than the level to which abundances were identified, although as the taxonomic level increased the effects of subsequent transformations became stronger.

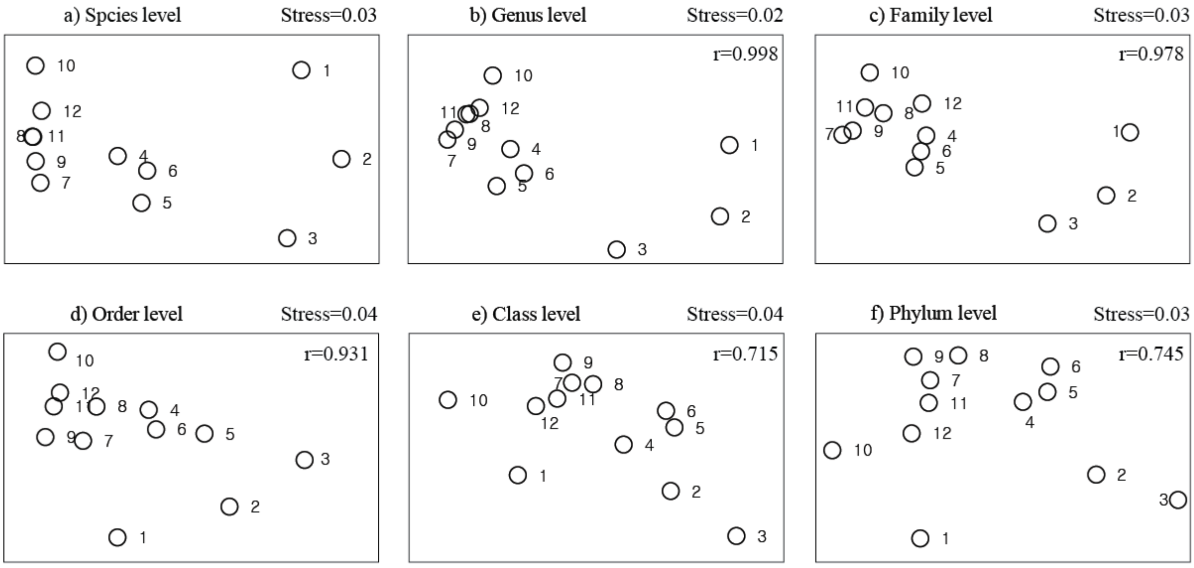


Fig. 3.Multidimensional scaling (MDS) ordinations of square root-transformed abundances of different taxonomic levels. The r-values are rank correlations between the underlying similarity matrices for species level and the levels of genus, family, order, class and phylum, respectively

The result of the BIO-ENV procedure showed that matrices derived from all taxonomic levels were most highly correlated with the environmental variables organic carbon (C), organochlorinepesticide (OCP), and tributyltin (TBT) (Table 2). The variables that gave the highest correlation (r_s= 0.796) were C and OCP combined with the matrices derived from species and genus levels, as well as OCP at the family level (r_s= 0.757). Increasing the taxonomic level degraded the match, implying that analyses utilizing the family level or below provide the best reflection of the relationship of faunal abundance to the measured environmental variables.

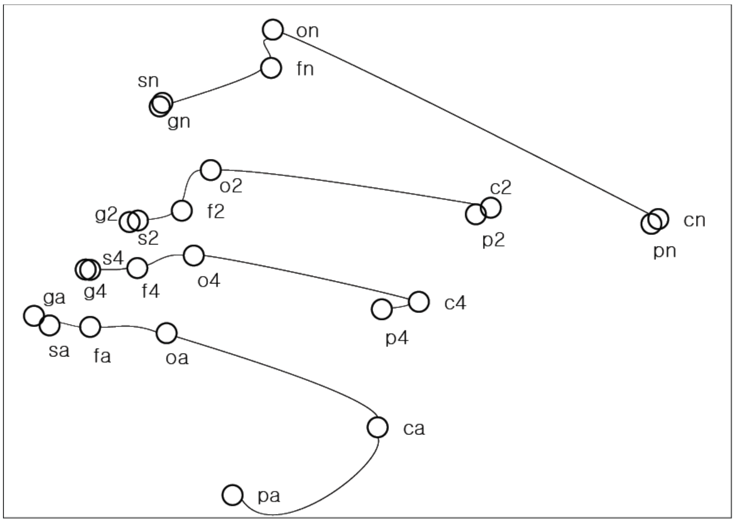
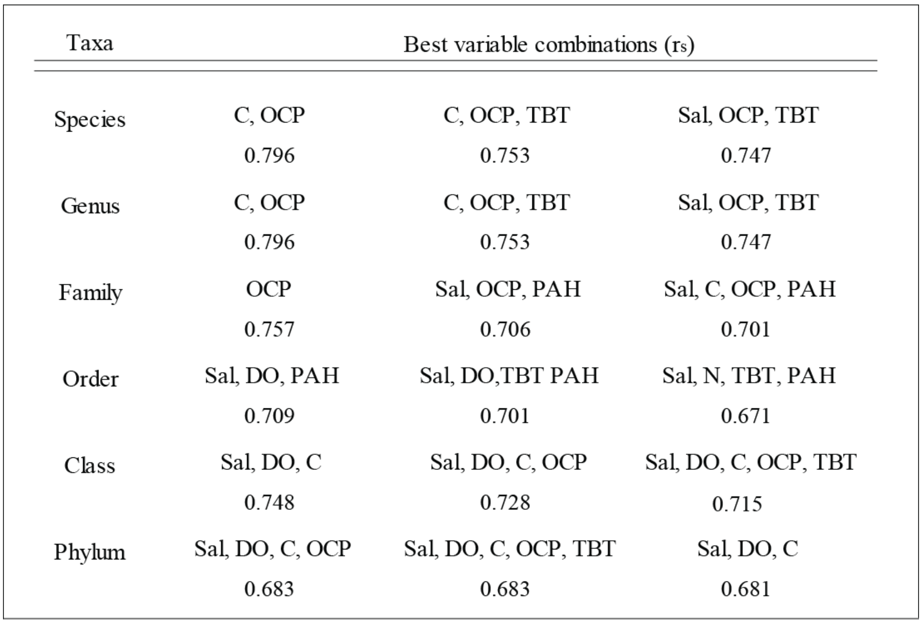


Fig. 4.‘Second-stage’ MDS ordination of inter-matrix rank correlation. Underlying similarity matrices derived from abundances of species (s), genus (g), family (f), order (o), class (c), and phylum (p) using square root (2), fourth root (4), absence/presence (a), or no (n) transformations (Stress value is 0.10)

The results described above show that the identification of organisms to the levels of genus and family still results in interpretable faunal structures. The most obvious drop in correlation values occurred in the order or class level, depending on the amount of pollution. The study area covered a pollution gradient from severely polluted interiors (sites 1, 2 and 3) to unpolluted exteriors [15]. Several authors (e.g. [2, 12, 13, 20, 21, 22]) have suggested that univariate and multivariate analyses based on higher taxa may more closely reflect pollution gradients than those based on species data, as species composition is more affected by natural environmental differences such as water depth and sediment grain size. They suggested that changes in higher taxonomic levels may be more relevant as a consequence of the hierarchical structure of biological responses to stress. This ‘hierarchic response to stress hypothesis’ proposes that, as stress increases, the adaptability of first the individual, and then species, genus, family, etc., is exceeded, and therefore as stress increases its impacts manifest at higher taxonomic levels. This implies that if disturbance increases in a particular area, the faunal gradients become stronger, and therefore identification of organisms to higher taxonomic levels should enable clearer taxonomic identification of changes in community structure. This may be a reason why the correlation of higher taxonomic levels (e.g., order level) with species level was greater at the more polluted sites in this study.

In 1986, the community ecology group at the IOC/GEEP workshop analyzed macrofauna data from a putative pollution gradient in Frierfjord and Lamgesunfjord, Norway [23]. They suggested that in studies of sublittoral benthic macrofaunal communities where strong gradients exist, little information is lost even if specimens are identified only to the level of phylum. The results of this study also indicate that the results of univariate and multivariate analyses from family level—or even order level where pollution is severe—are well reflective of variation at species level. Identifying patterns in soft-bottom benthic communities at varying levels of taxonomic discrimination is greatly important in view of the high potential for saving time and money in environmental monitoring [2]. In a study of microbenthic communities from the Southern California Bight, costs of genus-, family-, order- and phylum-level identification were 23, 55, 80 and 95% less than that of species-level identification [11]. However, the relationship between time saved and taxonomic level is not a straightforward one; time (and monetary) savings may vary from case to case. For example, in less polluted areas, there was an obvious drop in correlation values between matrices derived from species abundances and those derived from all higher taxonomic levels (e.g., Snorre 1989, Heidrun 1988 and Togi 1989 of the North Sea site in [13]), implying that identification to higher taxonomic levels was not sufficient in those areas. Therefore, higher-level taxa should only be used for environmental monitoring in cases where significant pollution gradients exist.

Table 2.Summary of results from BIO-ENV for data fromGamak Bay, comparing environmental variables andfauna to show the variables that best describe community patterns at different taxonomic levels



Taxa	Best variable combinations (r_s)		
Species	C, OCP	C, OCP, TBT	Sal, OCP, TBT
	0.796	0.753	0.747
Genus	C, OCP	C, OCP, TBT	Sal, OCP, TBT
	0.796	0.753	0.747
Family	OCP	Sal, OCP, PAH	Sal, C, OCP, PAH
	0.757	0.706	0.701
Order	Sal, DO, PAH	Sal, DO,TBT PAH	Sal, N, TBT, PAH
	0.709	0.701	0.671
Class	Sal, DO, C	Sal, DO, C, OCP	Sal, DO, C, OCP, TBT
	0.748	0.728	0.715
Phylum	Sal, DO, C, OCP	Sal, DO, C, OCP, TBT	Sal, DO, C
	0.683	0.683	0.681

IV. CONCLUSIONS

The results of the univariate and multivariate analyses applied in this study indicate that no information whatsoever would have been lost if organisms had been aggregated to any level at family or below. Moreover, in severely polluted areas, there was no substantial loss of information at the order level. Identification of fauna to a higher taxonomic level would obviate most of the time-consuming problems associated with the analysis of benthic samples for the purpose of assessing pollution effects. Therefore, in studies assessing pollution, it may be useful to aggregate macroinvertebrates to a higher taxonomic level than species. In baseline studies and ecologically orientated surveys, however, identification of organisms to the species level is still highly recommended.

V. ACKNOWLEDGEMENTS

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