CHAPTER 7

RAPID ASSESSMENT OF BIODIVERSITY IN ESTUARINE BENTHIC COMMUNITIES: OBJECTIVE SURROGATE SELECTION

7.1 Introduction

There is currently a strong international focus on developing a range of surrogates for the rapid assessment of biodiversity. Such tools are urgently required to assist the conservation of biodiversity, which has become a global priority with the realisation that biodiversity is declining at rates greater than those of the mass extinction events punctuating the fossil record (McCann 2000). Despite every major phylum of animals having marine representatives and some groups, such as the cnidarians and echinoderms, being entirely marine (Ruppert & Barnes 1994), most of the work on biodiversity surrogates has concentrated on terrestrial fauna. Therefore, the ongoing development of reliable biodiversity surrogates in marine and estuarine waters is crucial in providing a streamlined approach to monitoring and assessment, which would aid the representative and adequate conservation of biodiversity.

7.1.1 Conserving Biodiversity in Australian Waters

The definition of biodiversity is extremely broad and covers many levels of organization. Therefore, mapping, monitoring and conserving marine biodiversity is difficult (Olsgard et al. 2003). To conserve and manage the biodiversity of oceans, estuaries and coastal waters in Australia a system of marine protected areas (MPAs) has been established and an important priority of these MPAs is to conserve a representation of species diversity (Vanderklift et al. 1998).

Protective zoning of local coastal waters, including estuaries, first commenced in 1991 with the Solitary Islands Marine Reserve and continued with the declaration of the SIMP in 1998. Given

the lack of biological and ecological data for the region at that time, decisions about the location of areas of high protection were based on "educated guesswork" and issues other than biodiversity (Smith 2005). It appears that such management practices are not uncommon as, globally, MPAs continue to be selected opportunistically and without prior comprehensive surveys of their biodiversity (Vanderklift et al. 1998; Banks & Skilleter 2002; Giangrande 2003). These practices of establishing protected areas without adequate initial data on the distribution of biodiversity have raised questions regarding their effectiveness at conserving biodiversity (Vanderklift et al. 1998; Banks & Skilleter 2002). Of particular concern, is their effectiveness in addressing the objectives of comprehensive and adequate conservation. Blair (1999) suggests that the primary reason behind such management practices is that the practical implementation of conservation strategies is often done under conditions of limited funding, information and time. This has partially contributed to the ongoing issue of the current lack of species inventory data for most Australian marine habitats, as obtaining such data over large areas is costly and time-consuming (Banks & Skilleter 2002; Smith 2005). Compounding the problem of a lack of data on the on the diversity and distribution of biota, is the current shortage of relevant taxonomic expertise (Chapman 1998; Giangrande 2003). This is particularly relevant in marine and estuarine environments, where the majority of fauna are invertebrates that can usually only be identified to species by specialists (Olsgard & Somerfield 2000).

Although there is obviously a need to improve basic inventory data, accumulating complete species inventories for regions is not an option for the foreseeable future (Margules & Pressey 2000). Therefore, surrogates that represent species diversity will have to be found if the conservation of species diversity remains a primary objective of MPAs (Vanderklift et al. 1998). Government commitments to the development of a national representative system of MPAs based on the principles of comprehensiveness, adequacy and representativeness means that the development of biodiversity surrogates at fine scales (i.e. habitats) will have an increasingly important role in the identification of suitable sites for MPAs (Banks & Skilleter 2002). This urgent need to develop reliable diversity surrogates, that provide cost-effective data for assessing the biodiversity status of marine habitats, has received increasing attention in recent years (Banks & Skilleter 2002; Gladstone & Davis 2003; Smith 2005).

7.1.2 Surrogate Measures for Species Diversity

Species richness (number of species) is a fundamental measurement of community and regional diversity, underlying many ecological models and conservation strategies (Gotelli & Colwell 2001). Therefore, measurements of species richness are the most common method for quantifying biodiversity (May 1994; Olsgard et al. 2003). However, the identification of organisms to species level is one of the greatest constraints in terms of time and cost in ecological studies (Giangrande 2003). This is especially true for studies of marine and estuarine communities as they contain many poorly known groups. The prevalence of poorly known groups is likely due to some phyla receiving little attention as they are perceived to have no economic or applied research value and, consequently, many invertebrate organisms remain undescribed (Giangrande 2003). This obviously imposes major limitations on assessments of species diversity.

Biodiversity surrogates are quantities that are more easily determined than, but which correlate strongly with, species richness and reflect species level community patterns (Olsgard & Somerfield 2000). The extensive work involved in sorting and identifying benthic invertebrate samples to species level, in addition to the need for taxonomic expertise, means that community analyses are labour-intensive, time-consuming and costly (Le V. dit Durell et al. 2005). If it can be shown that analyses of taxonomic groups that are quickly and easily identified, are comparable to a full species analysis, then a great deal of time and labour may be saved (Olsgard & Somerfield 2000). These groups may be derived from either a subset of the data, such as a particular phylum, or from changing taxonomic resolution so that identifications are made only to higher taxa such as families or phyla. In reference to terrestrial reserve management, Margules and Pressey (2000) argue that there is no "best" surrogate as the decision on which to use will depend on many factors, including: the data that are available; the resources for data analysis; and the ability to collect new data. This is also true for marine and estuarine environments, especially when developing reliable surrogates for species diversity in new habitats or regions. For example, the process of developing surrogates is reliant upon baseline information on the actual species diversity being available, against which the surrogate data can be adequately assessed.

Various levels of taxonomic resolution and subsets of species assemblages have been successfully used as biodiversity surrogates in terrestrial environments (Balmford et al. 1996; Oliver & Beattie 1996; Blair 1999). More recently, there has been an increasing focus on applying these methods in a marine context (Vanderklift et al. 1998; Ward et al. 1999; Olsgard & Somerfield 2000; Olsgard et al. 2003; O'Hara 2001; Smith 2005). A number of these studies focussed on marine soft-sediment communities. However, the application of such approaches in many estuarine habitats, including subtidal estuarine sediments, remain unexplored. Hence, although the potential of marine biodiversity surrogates has been recognised for over a decade, the pressing issue of identifying reliable surrogates for a wide variety of estuarine habitats remains. As such, it has been agreed (Vanderklift et al. 1998; Olsgard et al. 2003) that further investigations are necessary to examine the application of a range of species diversity surrogates in different locations, habitats and at different spatial scales.

According to Olsgard et al. (2003), three main types of surrogates have been used for predicting species richness, including: (i) richness among higher taxa such as genera and families (i.e. surrogates derived from using a lower taxonomic resolution); (ii) richness among indicator groups (i.e. subsets of the total fauna data); and (iii) the use of environmental variables to describe habitat diversity as an indirect measure of biodiversity. The former two biotic surrogates are considered in this study.

i) Higher Taxa

Although the identification of organisms to the level of species is often the ideal in studies of marine biodiversity, there are often situations where such a fine level of taxonomic discrimination may be impossible (Olsgard & Somerfield 2000). For example, the taxonomy of many groups in Australia is not well known, with much of the invertebrate fauna undescribed. Hence, taxonomic resolution usually varies among phyla, with the better known groups (e.g. molluses and crustaceans) identified to a finer taxonomic level than the lesser known groups (e.g. nematodes and nemerteans) (Chapman 1998).

Early terrestrial work that examined the use of higher taxa to rapidly assess biodiversity (Balmford et al. 1996; Oliver & Beattie 1996) found this method to be valuable because patterns of biodiversity were retained, despite the lower sampling effort. In marine environments, the higher taxa approach was first suggested by Warwick (1988a, b) as a cost-effective method for monitoring environmental impacts in soft-sediment habitats. It has since been widely utilised for

these purposes (Ferraro & Cole 1990; Gray et al. 1990; Platt et al. 1990; Warwick & Clarke 1991; Agard et al. 1993) and has proven particularly successful, as many anthropogenic effects appear to occur at taxonomic levels higher than species (Warwick 1988a, b; Smith & Simpson 1993). Alternatively, higher taxa have been found to effectively replicate spatial patterns of benthic assemblages in estuaries (Chapman 1998; MacFarlane & Booth 2001) and preliminary studies in Australia have also supported the use of higher taxa in assessing the diversity of benthic infauna in a large marine embayment (Vanderklift et al. 1998). Clearly, however, many questions remain regarding the ability of higher taxa to reflect species patterns in either marine or estuarine biodiversity and conservation studies.

ii) Indicator Groups

An alternative to identifying fauna to higher taxa is to identify only subsets of fauna to species. These subsets are usually an abundant and well-known phylum, class or order. For example, when assessing coastal biodiversity, both fish and invertebrate assemblages have been found to be effective in predicting marine species richness (Ward et al. 1999). This study also considered these indicator groups to be particularly cost-effective, as developing a detailed inventory of the total species diversity would have been prohibitively expensive. Molluscs have also been found to be effective biodiversity indicators in surveys of Australian rocky shore invertebrates (Gladstone et al. 2002; Smith 2005) and because of their prevalence in estuaries, may also prove useful in these habitats. In marine soft sediments, Olsgard & Somerfield (2000) examined polychaete species richness as a surrogate for total species richness and found that little information was lost when comparing ecological patterns. Similarly, various polychaete orders have been assessed for their ability to predict the species richness of all polychaetes in benthic assemblages (Olsgard et al. 2003).

The current study explored the application of both of these surrogate approaches to reliably reflect the species level diversity of infauna in subtidal estuarine sediments. This was accomplished by comparing various indicator groups and levels of taxonomic resolution to determine which surrogate(s): i) most accurately predicted the species richness across estuaries and ii) best reflected the ecological patterns of the full species assemblage. The most promising surrogates were further examined to evaluate if they were consistently the best surrogates over time and could reliably detect significant spatial differences.

7.2 Methods

The analyses for this study used the data that had previously been collected for the major spatial component of this thesis (refer to 'Chapter 4' for a detailed description of the study design and sampling methods). In brief, macrofaunal samples were collected from nine estuaries in the SIMP, during the summer of 2003. Five samples were collected from unvegetated, subtidal sediments at three sites in each estuary. Species level data were aggregated into higher taxa (genus, family, order and phyla). These classifications were based on Beesley et al. (2000) for the polychaetes, Beesley et al. (1998) for the molluscs and Poore (2004) for the crustaceans. The remaining fauna were classified as accurately as possible using the available resources, mainly Rupert & Barnes (1994) and local reference collections. For the indicator groups, species level data were aggregated into three groups of dominant organisms. These were the polychaetes, molluscs and crustaceans, which were clearly the dominant taxa as they contributed 34, 29 and 19 % of the total species, respectively. In comparison, all other groups contributed to less that 5 % of total species. Comparisons of how well these surrogate datasets correlated with species level data were made using both univariate and multivariate techniques.

7.2.1 Statistical Analyses

7.2.1.1 Species Richness

Data were pooled within each site (n = 5) as the major taxa were not present in all individual samples. Simple linear regression analyses were used to determine how well the richness of higher taxa surrogates correlated with species richness (Balmford et al. 1996). The strength of the relationship between the higher taxa and species richness could then be evaluated by comparing the resultant correlation coefficients (r). The coefficients of determination (r^2) were used to indicate the proportion of the variation in species richness that could be accounted for by the variation of each higher taxon (Fowler et al. 1998). These methods were also used to comparatively assess correlations of each indicator group with total species richness (Olsgard et al. 2003). However, as the indicator groups are subsets of the total species richness data there is a degree of autocorrelation. To alleviate this, additional analyses were required to correlate each indicator group with all other taxa (i.e. exclude the indicator group from the total species richness data) (Olsgard et al. 2003; Smith 2005).

7.2.1.2 Species Assemblage

Species assemblage and surrogate assemblage data were square-root transformed and the Bray-Curtis similarity measure was used to generate a similarity matrix for each assemblage in PRIMER (Clarke & Gorley 2001). The RELATE routine was then used to determine the degree of agreement between individual, surrogate similarity matrices and the similarity matrix for all species. This method has previously been used to correlate marine and estuarine species assemblages with higher taxa (Olsgard & Somerfield 2000; MacFarlane & Booth 2000; O'Hara 2001) and indicator groups (Somerfield & Clarke 1995; O'Hara 2001; Smith 2005). The Spearman rank correlation coefficient (ρ) produced by this procedure enabled a comparative assessment of how well each surrogate assemblage reflected patterns in the full species assemblage. An identical match between two assemblages is indicated by a value of $\rho = 1$, whereas no relationship between two assemblages in indicated by $\rho = 0$. The RELATE routine also calculates the significance of ρ (i.e. tests if the relationship is significantly different from zero) using a simple permutation test (Clarke & Gorley 2001). To be able to conduct these analyses with the indicator group surrogates, data were pooled within sites (n = 5) as each group contained some samples with zero counts (Clarke & Gorley 2001). Unfortunately, pooling within sites still did not eliminate all zero counts for the crustaceans, which consequently had to be excluded from these analyses.

7.2.1.3 Replication of Spatial Patterns

Balmford et al. (1996) state that justifying the use of species diversity surrogates requires good evidence that the surrogates mirror species level spatial differences. Therefore, to verify the adequacy of the surrogates that best reflected species level data, some of the multivariate analyses that revealed significant differences in Chapter 4 were re-analysed using surrogate data. Specifically, these analyses involved testing for differences in community structure between two estuary types and between the individual estuaries nested within each estuary type. Data were square-root transformed, then used to construct a Bray-Curtis similarity matrices. Two-dimensional ordinations of assemblages were created using non-metric multidimensional scaling (nMDS) and significance testing was conducted on each similarity matrix using a one-way analysis-of-similarity (ANOSIM). These analyses did not require the specific level of detail given in Chapter 4. Therefore, the analyses were condensed at both spatial scales by not differentiating between the three sites in each estuary (i.e. analyses included all 15 samples from each estuary).

The correlation between total species richness and the surrogate that suggested the greatest potential was reproduced to construct a simple linear regression equation, which could be used as a predictive model for the January sampling time (Smith 2005).

7.2.1.4 Temporal Consistency of Surrogate Results

One of the most important criteria of an effective surrogate, or model, for predicting biodiversity is that it is general enough to be applicable at different times (Leathwick et al. 1996; Lehmann et al. 2002). Accordingly, all higher taxa and indicator group surrogates were re-tested using data that had been collected in July 2003, using identical field methods. The statistical methods described above were used to assess whether the previously determined, optimum surrogate remained the optimum surrogate for reflecting: (i) species richness; and (ii) species assemblages at this time. Note that both the crustacean and mollusc indicator groups had to be excluded from comparisons with the full species assemblage using the RELATE routine. This was because some zero counts were still present, even after data were pooled within sites.

7.3 Results

The 94 species that comprised the total January dataset were represented by 88 genera, 66 families, 26 orders and eight phyla. Species were primarily represented by polychaetes (32), molluscs (28) and crustaceans (18), whilst the remaining fauna consisted of oligochaetes, nemerteans, nematodes, echiurans, phoronids, insects a gobiid fish (Fig. 1). Polychaetes were dominated by the families Nereididae, Spionidae, Orbiniidae, Capitellidae, Opheliidae and Sabellidae. Molluscs primarily consisted of bivalves from the families Galeommatidae and Trapezidae, and cerithid, batillarid, nassariid and hydrobiid gastropods. Melitid amphipods, urohaustorid isopods, leptocheliid tanaids and decapods contributed the most to crustacean abundances.

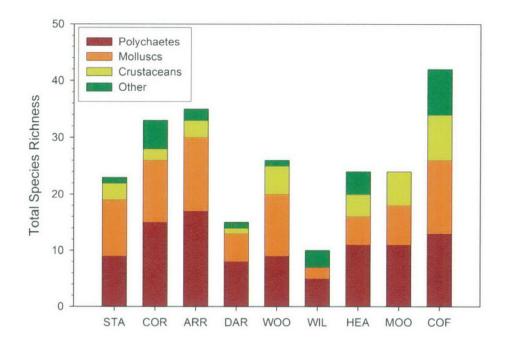


Fig. 7.1 Contribution of dominant faunal groups to the total macrofaunal species richness in each estuary during January 2003. Estuary names are abbreviated to their first three letters.

7.3.1 Species Richness Representation

The total species richness was found to be significantly correlated (P < 0.001) with the richness of each of the higher taxa (Fig. 2) and indicator groups (Fig. 3). Similarly, a significant relationship was observed for the richness of each of the polychaete, mollusc and crustacean indicator groups when correlated with the species richness of all other taxa (P = 0.001; 0.002; 0.001, respectively) (Fig. 3). Particularly high correlation coefficients were returned for the genus, family and order level higher taxa (r = 0.994; 0.986; 0.965, respectively) (Table 1). Note that there is less than a 1 % difference between these values for genus and family, which each accounted for more than 97 % of the variation in species richness ($r^2 = 0.989$; 0.973, respectively). The strongest relationship between an indicator group and total species richness was produced by the polychaetes (r = 0.835). However, this result was not stronger than that for either the genus- family- or order-level higher taxa. Each of the indicator groups was not as effective at predicting all other species, as they were at predicting the total species richness (i.e. inclusive of themselves).

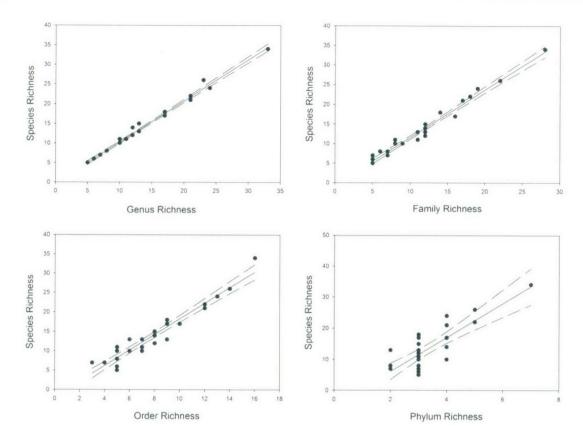


Fig. 7.2 The richness of the higher taxa surrogates correlated with the total species richness. Each point represents samples (n = 5) pooled within a site.

Table 7.1 Correlation coefficients (r) and coefficients of determination (r^2) for analyses between the richness of each surrogate and the total species richness, as well as between the richness of the indicator group surrogates and all other species. Significant correlations are shown in bold.

| | Total species richness | | All other taxa | |
|------------------|------------------------|----------------|----------------|-------|
| | r | r ² | r | r^2 |
| Higher Taxa | | | | |
| Genus | 0.994 | 0.989 | - | - |
| Family | 0.986 | 0.973 | - | - |
| Order | 0.965 | 0.931 | - | _ |
| Phylum | 0.816 | 0.666 | - | - |
| Indicator Groups | | | | |
| Polychaetes | 0.835 | 0.697 | 0.581 | 0.338 |
| Molluscs | 0.805 | 0.648 | 0.568 | 0.323 |
| Crustaceans | 0.749 | 0.561 | 0.613 | 0.376 |

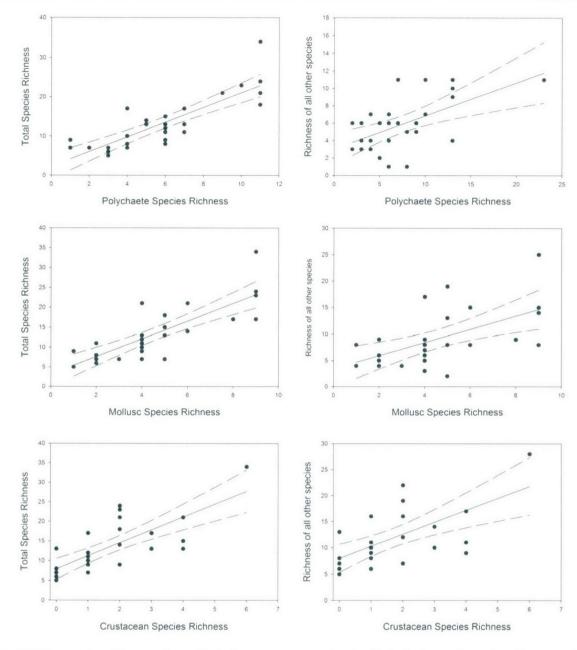


Fig. 7.3 The species richness of specific indicator group correlated with both the total species richness and the species richness of all other taxa. Each point represents samples (n = 5) pooled within a site.

7.3.2 Species Assemblage Representation

The degree of concordance between the full species assemblage and the genus-level assemblage was extremely high ($\rho = 0.998$) and remained very high ($\rho = 0.938$) when compared to the family-level assemblage (Table 2). Thereafter, the correlation coefficient for the remaining higher taxa declined rapidly with reducing taxonomic resolution. However, despite the reduction in the correlation coefficients, the relationship with the species assemblage remained highly

significant (P=0.001) for all higher taxa surrogates. Similarly, there was a significant relationship when comparing the full species assemblage to the polychaete and molluscs indicator groups (P=0.001). Of these, the polychaetes resulted in the strongest relationship ($\rho=0.836$). However, this was still less than that for either the genus- or family-level higher taxa (Table 2).

Table 7.2 Spearman rank correlation coefficients (ρ) and significance results produced, using the RELATE routine, by comparing higher taxa and indicator group assemblages with the full species assemblage.

| | Spearman rank correlation coefficient (ρ) | P |
|------------------|--|-------|
| Higher Taxa | | |
| Genus | 0.998 | 0.001 |
| Family | 0.938 | 0.001 |
| Order | 0.486 | 0.001 |
| Phylum | 0.270 | 0.001 |
| Indicator Groups | | |
| Polychaetes | 0.836 | 0.001 |
| Molluscs | 0.499 | 0.001 |
| Crustaceans | - | - |

7.3.3 Replication of Spatial Differences

As the genus and family level higher taxa were the surrogates that best represented both species richness and species assemblages, these were the two surrogates that were used to examine the effectiveness of using surrogate data to replicate spatial differences. In assessing community patterns at both the estuary type (Fig. 4) and estuaries nested within estuary type (Fig. 5) spatial scales, the species and genus level nMDS ordinations were almost identical. Obvious differences between each estuary type were still observed at the family level (Fig. 4c), despite evidence of some overlapping samples. Distinct groupings among individual estuaries nested within each type remained consistent using the family level of taxonomic resolution (Fig. 5c,f). Similarly, among the intermittently closed and permanently open estuary types, the overall patterns observed at the species and genus levels (i.e. the position of one estuary in relation to another within an ordination) also remained consistent at the family level. For example, within the intermittent closed estuaries (Fig. 5a-c) Willis Creek remained tightly grouped and completely separated from all other estuaries at all levels of taxonomic resolution.

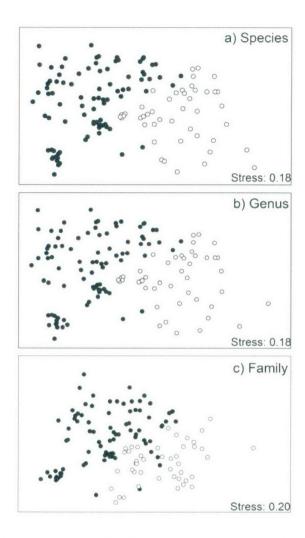


Fig. 7.4 Two-dimensional nMDS ordinations of differences between intermittently closed and permanently open estuary types. Graphs show analyses of the same samples identified using different levels of taxonomic resolution: a) species; b) genus; and c) family. Samples are represented by filled circles for the intermittently closed estuaries and open circles for the permanently open estuaries.

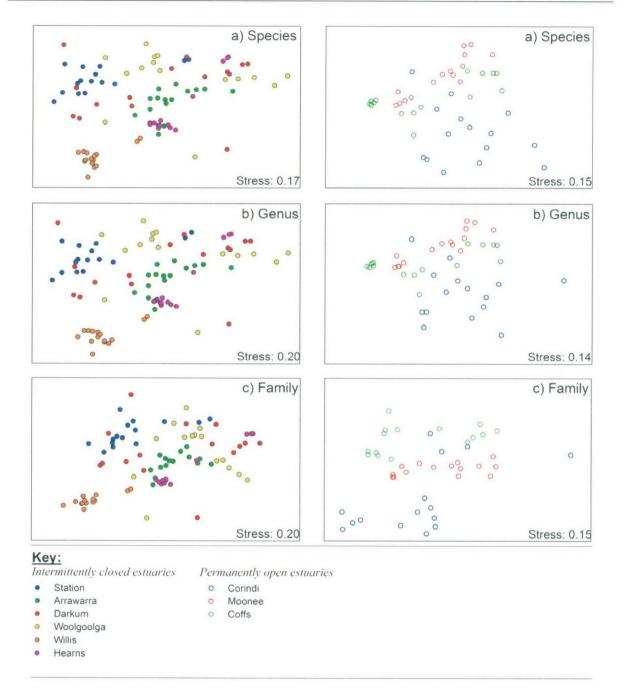


Fig. 7.5 Two-dimensional nMDS ordinations of differences between the individual estuaries nested within both the intermittently closed and permanently open estuary types. Ordinations show analyses of the same samples identified using either species, genus or family levels of taxonomic resolution.

ANOSIM results confirmed that the differences between estuary types and between the individual estuaries nested within each type were relatively consistent with the varying higher

taxa (Table 3). Highly significant differences (P = 0.001) were evident at both spatial scales for all three levels of taxonomic resolution. This means that the spatial differences observed using the species level of taxonomic resolution were still detected when fauna were identified only to the level of genus or family. Although the differences remained significant, the R-values reduced slightly with the reduction in taxonomic resolution for the analyses testing for differences between estuary types. These changes suggest that the communities were slightly more similar at the family level, which may not have been as effective at detecting discrete differences between some samples. Interestingly, this was not the case for the results among each of the intermittently closed and permanently open estuaries. At this scale, the family R-values were greater than those for genus and, for the permanently open estuaries, even greater than the species level R-value (Table 3).

Table 7.3 Non-metric multidimensional (nMDS) scaling stress values and analysis of similarity (ANOSIM) results testing for differences between the faunal communities of intermittently closed and permanently open estuary types, as well as between the individual estuaries nested within each type. Analyses were conducted three times using a different level of taxonomic resolution each time.

| Factors | Taxonomic resolution | 2D nMDS stress | ANOSIM test statistic (R) | P |
|-----------------------|----------------------|----------------|---------------------------|-------|
| Estuary types | Species | 0.18 | 0.403 | 0.001 |
| | Genus | 0.18 | 0.400 | 0.001 |
| | Family | 0.20 | 0.336 | 0.001 |
| Intermittently closed | Species | 0.17 | 0.632 | 0.001 |
| estuaries | Genus | 0.20 | 0.519 | 0.001 |
| | Family | 0.20 | 0.549 | 0.001 |
| Permanently open | Species | 0.15 | 0.368 | 0.001 |
| estuaries | Genus | 0.14 | 0.322 | 0.001 |
| | Family | 0.15 | 0.377 | 0.001 |

Overall, both the genus and family higher taxa surrogates accurately reflected species richness, species assemblages and spatial differences. Although the results were slightly better for genus, additional practical considerations, such as the potential time or expertise saved in identifications, had to be taken into account. During the identification of the samples used in this study, it took approximately twice as long to identify fauna to species as it did to identify fauna to family. This equates to a time savings of 50 %. In contrast, in comparison to species, genus

level identifications only resulted in a time savings of 5-8 %. The extensive time savings in identifying fauna to family would be further reflected in an overall reduction of the costs involved in running a biodiversity monitoring programme with this surrogate. On this basis, the family level of higher taxonomic resolution was selected as the best of both the higher taxa and indicator group surrogates. Accordingly, to produce a simple model predicting overall total species richness of individual estuaries, the linear regression correlating family richness with total species richness was reproduced, generating the following regression equation:

Total Species Richness =
$$0.555 + 0.21$$
 Family Richness

This model accounted for approximately 97 % of the variation in species richness ($r^2 = 0.973$) with a narrow confidence interval at 95 % (Fig. 6).

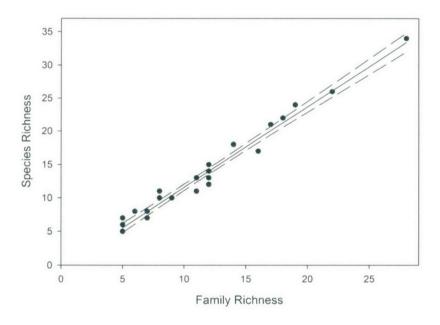


Fig. 7.6 Family richness correlated with total species richness. Regression equation: Total Species Richness = 0.555 + 0.21 (Family richness); $r^2 = 0.973$. Data points represent information from individual sites within estuaries, where 5 samples were pooled within each site.

7.3.4 Temporal Consistency of Surrogate Results

When compared to the initial January samples, fewer species (67) were collected during the July sampling period. These species represented 67 genera, 55 families, 23 orders and eight phyla. Polychaetes (19), molluscs (20) and crustaceans (19) remained the dominant faunal groups (Fig. 7). A total of 33 of the species present in January were not collected in the July sampling, whereas only nine of the species collected in July were not present in the January samples. All of the fauna that were observed on only one sampling occasion were generally rare, with most being recorded as singletons. The fauna collected in July comprised just one polychaete and one mollusc that were not collected in January. In contrast, the crustaceans appeared more variable, including six species that had not been collected previously.

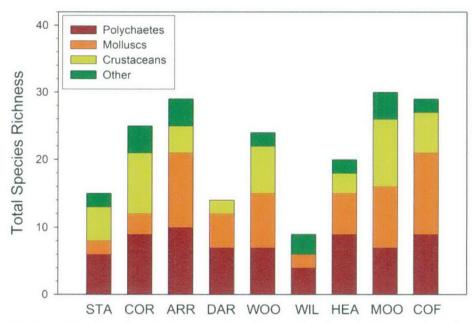


Fig. 7.7 Contribution of dominant faunal groups to the total macrofaunal species richness in each estuary during July 2003. Estuary names are abbreviated to their first three letters.

When predicting species richness, most of the higher taxa continued to perform well using the July dataset (Table 4). The exception to this was the phylum level, which revealed a substantial decline in the correlation coefficient, from 0.816 to 0.499. In comparison, the correlation coefficient for the genus level improved from 0.994 to 1.000. This was due to each of the species in the July samples belonging to a different genus; therefore, the species and genus level datasets were identical at this time. The relationship between family richness and total species richness was very consistent, with the amount of variation explained by the family-level taxa

differing by only 1.0 %. The indicator groups were not as consistent in their ability to predict species richness and the richness of all other species (Table 4). From January to July, the correlation coefficients for all three groups decreased considerably when predicting total species richness and they did not reveal any significant relationships when correlated with the richness of all other species.

Table 7.4 Product-moment correlation coefficients (r) for comparisons of the richness of higher taxa and indicator groups with: (i) the total species richness of each site; and (ii) all other species at each site. Results are shown for both the January and July 2003 samples. Significant correlations are indicated by bold font.

| | Total species richness | | All other species | |
|------------------|------------------------|-----------|-------------------|-----------|
| | January 2003 | July 2003 | January 2003 | July 2003 |
| Higher Taxa | | | | |
| Genus | 0.994 | 1.000 | - | - |
| Family | 0.986 | 0.976 | - | - |
| Order | 0.965 | 0.912 | - | - |
| Phylum | 0.816 | 0.499 | - | - |
| Indicator Groups | | | | |
| Polychaetes | 0.835 | 0.464 | 0.581 | 0.032 |
| Molluscs | 0.805 | 0.657 | 0.568 | 0.152 |
| Crustaceans | 0.749 | 0.628 | 0.613 | 0.105 |

The strength of the relationship between assemblage data pooled to higher taxa and that of the species level improved for all except family in the July samples (Table 5). Of the indicator groups, only the polychaetes could be compared to the July species assemblage. This was due to both the mollusc and crustacean datasets containing zero counts, even when samples were pooled within sites. The resultant correlation coefficient for the polychaetes ($\rho = 0.799$) was not as strong as that for the January sampling period ($\rho = 0.836$). Overall, the best relationship between the full species assemblage pattern and that of any of the surrogates was produced by the genus assemblage ($\rho = 1.000$). However, as in the results for predicting species richness, the genus level data was identical to the species data as each species collected on this occasion belonged to a different genus. The next best relationship between the species and surrogate assemblage patterns was produced by the family-level data ($\rho = 0.895$). These results, together with the results for predicting species richness, indicate that data aggregated to genus and family higher taxa were the most consistent surrogates, each having a strong relationship with species richness and species assemblage patterns for both the January and July datasets.

Table 7.5 Spearman rank correlation coefficients (ρ) produced by comparing higher taxa and indicator group assemblages with the full species assemblage in January and July 2003.

| | January 2003 | July 2003 |
|------------------|--------------|------------------|
| Higher Taxa | | |
| Genus | 0.998 | 1.000 |
| Family | 0.938 | 0.895 |
| Order | 0.486 | 0.596 |
| Phylum | 0.270 | 0.396 |
| Indicator Groups | | |
| Polychaetes | 0.836 | 0.799 |
| Molluscs | 0.499 | - |
| Crustaceans | _ | |

7.4 Discussion

This study comparatively assessed the ability of 7 diversity surrogates, 4 higher taxa and 3 indicator groups, to predict both species richness and reflect multivariate, species level community patterns. In some instances the indicator groups were unable to reflect the patterns of the entire species assemblage as the respective subsets of data for these particular indicator groups contained some sites with zero counts (i.e. not all indicator groups were present in all sites). These instances included all of the crustacean datasets and the July mollusc dataset. Such data are unable to be analysed by the RELATE procedure and the absence of these particular indicator groups from sites, immediately suggests that more adequate and more generally applicable surrogates are required. All the indicator groups did, however, correlate significantly with the total species richness and the richness of all other species. The polychaetes presented the strongest relationship, explaining 69.7 % of the variation in total species richness. However, they only explained 33.8 % of the variation of all other species. This result was weaker than expected as polychaetes have been shown to be able to predict up to 86.7 % of the variation in the richness of all other species in some soft sediment communities (Olsgard et al. 2003).

Significant correlations with species richness were also observed for all of the higher taxa surrogates. In fact, higher taxa showed a greater potential as surrogates for predicting the total

species richness, as three of the four levels of taxonomic resolution (genus, family and order) each explained more of the variation in species richness (98.9 %, 97.3 % and 93.1 %, respectively) than the best indicator group, the polychaetes. This is consistent with the findings of Balmford et al. (1996) who showed that, in terrestrial habitats, family-level richness was better at total species richness than various indicator groups. Whilst there is little information available that compares both higher taxa and indicator groups as diversity surrogates in marine environments, Vanderklift et al. (1998) and Olsgard et al. (2003) have examined the effectiveness of various higher taxa at predicting the species richness of benthic invertebrates. They found that the richness of the genus or family taxonomic levels, and order richness in Olsgard et al. (2003), strongly correlated with species richness and they emphasised the potential value of these taxonomic levels for the rapid assessment of species diversity.

In addition to the strong correlations observed between the higher taxa and species richness, especially at the level of genus and family, the higher taxa also correlated strongly with specieslevel community patterns. Again, this was especially the case for the genus- and family-levels, with the genus-level resulting in almost no loss of information. The strength of the relationship with the species-level community structure declined rapidly with decreasing taxonomic resolution for order and phyla. O'Hara (2001) presents comparable results, whereby genus and family higher taxa correlate well with species assemblages; then this relationship weakens considerably when taxonomic resolution is further reduced. Similar to the species richness results, the best relationship between an indicator group and the species-level community assemblage was produced by the polychaetes. However, this relationship was not as strong as that for either the genus- or family-level assemblages. In four out of five study areas, Olsgard and Somerfield (2000) likewise found a much closer relationship between family- and specieslevel assemblages when compared to the relationship between the species and polychaete assemblages. At the one area where polychaetes performed better than the family level assemblage, there was only a 1.6 % difference between the resultant correlation coefficients. The same area also had a seven-year pollution history due to anthropogenic influences, which may have altered the natural community to favour a greater diversity or dominance of polychaete species (Olsgard & Somerfield 2000).

Not only were the genus- and family-level higher taxa the most promising surrogates for reflecting species richness and species assemblages, they were also able to detect the same

significant spatial differences that were produced when conducting analyses using species level data. Specifically, as with the species-level results, the genus and family higher taxa were sensitive enough to detect highly significant differences between intermittently closed and permanently open estuaries, as well as between the individual estuaries within each estuary type. Both Chapman (1998) and Olsgard and Somerfield (2000) also found that grouping benthic fauna into broader taxonomic categories preserved quantitative patterns of spatial variability and significant differences between sites. Similarly, it is also widely documented that anthropogenic impacts are also usually detected at higher taxonomic levels (Warwick 1998 a, b; Ferraro & Cole 1990; Gray et al. 1990; Platt et al. 1990; Warwick et al. 1990; Agard et al. 1993), therefore the sensitivity of such studies is not compromised by reducing taxonomic resolution. The ability of higher taxa to reflect natural and anthropogenic spatial differences highlights the flexibility of these particular surrogates and supports their potential wider applications in estuarine ecology.

To identify which of the biodiversity surrogates displayed the greatest potential, a number of criteria need to be addressed. Firstly, the surrogate has to be representative of other taxa (Noss 1990; Pearson 1994; Caro & O'Doherty 1999) by adequately predicting both species richness and reflecting community patterns within the estuaries tested. Genus-level data achieved the most closely correlated results for both species richness and community patterns, with almost no loss of information. The family level also satisfied this criterion as it performed very strongly throughout all the analyses used. Secondly, to be effective, the practical advantages of individual surrogates also had to be considered. This means that the reasons behind deciding to use diversity surrogates in the first place, namely, benefits of savings in time and taxonomic expertise, had to be taken into account. Although negligible information was lost using the genus level, similar amounts of time and specialist expertise are required to identify fauna to genus in comparison to species (Warwick 1988a, b; Giangrande 2003). In contrast, family-level identifications achieved time savings of up to 50 % for benthic samples in both this and other studies (Chapman 1993; Ferraro & Cole, 1995). In this study, the time taken to sort and identify samples was estimated to be reduced by approximately 50 % for family and only 5-8 % for genus identifications, when compared to identifying all fauna to species. The substantial time savings that are achieved when identifying fauna to family are particularly important in macrofaunal studies as most resources are spent processing samples in the laboratory (Chapman 1993). From this practical point of view, the family-level higher taxon was therefore deemed to be the best surrogate as: fauna can be quickly and easily identified; species-level diversity was accurately predicted; and patterns of community variation were retained.

In the comparison of results from both the January and July sampling times, the genus- and family-level higher taxa consistently produced the best results. Therefore, selection of the best surrogate from the second sampling time again came down to the efficiency of each of these higher taxa in saving time and taxonomic expertise. As a result, the family level higher taxon was also the best surrogate for the July data, further supporting its application as an effective and efficient biodiversity surrogate in estuarine soft sediments.

Additional advantages of using the family-level higher taxon as a biodiversity surrogate are that it meets the desirable criteria for indicators of biodiversity that were recommended by Noss (1990). These include factors such as sensitivity to environmental change, a wide geographic distribution, cost-effectiveness in sampling and relevance to ecologically significant phenomena. At the time, these criteria were suggested primarily in regard to the use of indicator groups as diversity surrogates; however, they are equally applicable to higher taxa surrogates. As a modification of the taxonomic resolution used in a study, the nature of higher taxa means that they automatically cover the full geographic distribution of the species assemblage. In fact, higher taxa usually have a much greater geographical spread than species, which increases their potential for wider applications. The family-level higher taxon used here is also cost-efficient and sensitive to spatial change; however, further investigation will be required to determine if this particular measure is able to detect temporal changes. Perhaps the most important advantage of using family-level taxonomic resolution as a surrogate for species diversity, is that it will make this type of rapid assessment more accessible to a range of ecologists, since it provides a reduced need for an in-depth knowledge of a range of disparate taxa (Smith 2005).

This objective examination of methods for rapidly assessing biodiversity has validated the potential for reduced taxonomic resolution to the level of family to save resources, both time and taxonomic expertise. This will, consequently, enable better management of estuarine resources in-line with MPA conservation objectives by ensuring that species diversity is adequately assessed. The time saved by the relative ease with which fauna can be identified to family, suggests that using this level of taxonomic resolution may provide an extremely cost-effective method for estimating the macrofaunal diversity of estuarine benthic environments.

This relationship should also be retained if perturbation occurs as this study incorporated estuaries covering a range of modification, from near pristine to highly impacted. Other studies (Chapman 1998; MacFarlane & Booth 2001) have also supported the ability of family-level taxonomic resolution to reflect estuarine macrofaunal community structure across a range of anthropogenic influences. However, the identification of indicators of species diversity requires not only the demonstration of the potential of a surrogate, as addressed by this study, but also rigorous testing in other localities and at different ecological scales (Balmford et al. 1996). This provides direction for continuing the assessment of the application of the family-level higher taxon as a surrogate for rapidly measuring species diversity in estuarine soft-sediments.

On a final note, although the use of diversity surrogates has many advantages, authors have cautioned that care should be taken not to consider the use of diversity surrogates as an excuse to limit resources. This is primarily because, when evaluating biodiversity between different areas, it is ultimately the distribution of species and the identities of those species, in addition to the interactions of species with each other and the environment, that are of interest (Olsgard & Somerfield 2000; Giangrande 2003). Further, in regions such as Australia the use of either higher taxa or indicator groups that are well known will not help in addressing the relatively poor knowledge of local fauna (Hutchings 1999). As noted by Smith and Simpson (1993), it may thus be necessary to reach a compromise between management and scientific objectives in the selection of appropriate taxonomic resolution in such studies. When working with higher taxa another important consideration that should be kept in mind is that taxonomic levels, other than species, are classifications that are made up for the convenience of biologists and have no biological meaning. For example, the concept of a family in the polychaetes may not be similar to that used in the molluscs; therefore, higher taxa may not be equivalent units that are comparable across faunal groups (Hutchings 1999).

CHAPTER 8

SYNTHESIS

8.1 Description of Spatial and Temporal Community Patterns

It has repeatedly been acknowledged that estuarine management in Australia is hindered by the lack of long-term data describing how communities vary over space and time in intermittently closed estuaries (Hutchings 1999; Moverley & Hirst 1999; NSWEPA 2000; Roy et al. 2001; HRCNSW 2002; Gladstone et al. 2002). Therefore, using benthic macrofaunal communities as the primary indicators, the principal aims of this study were to: (i) determine the community variation between intermittently closed and permanently closed estuary types; (ii) investigate how this relationship between estuary types changes over time; (iii) examine the spatial variation within each estuary type; and (iv) explore temporal variation within estuaries that represent not only different estuary types but also a range in the frequency and duration of entrance closures. These aims were designed to address the overall objective of gaining a greater understanding of the ecology of intermittently closed estuaries.

At the commencement of the study, the entrances of the intermittently closed estuaries examined had been closed for an extended period. At that time, the initial prediction made was that the ecology of the intermittent estuaries would differ to that of nearby permanently open estuaries and that these differences would be evident in their benthic macrofaunal communities. The patterns of community structure observed in the early stages of the project strongly supported this prediction, even with extremely variable assemblages within each estuary type. Further, these assemblage differences between the two estuary types persisted throughout the study, even when all estuary entrances were open, strongly supporting the idea that the two estuary types are different from an ecological point of view.

Although the two estuary types remained significantly different, there were times when they were more similar than at other times. This temporal variation in their relationship did not display regular seasonal or annual variation. Instead, it correlated well with the number of intermittent estuaries that were closed at each sampling time; the two estuary types were most similar when all estuaries were open and most dissimilar when many of the intermittent estuaries were closed. The strength of this relationship was surprising considering that the "number of closed estuaries" is instantaneous information and does not take into account the duration that individual estuaries had been either open or closed prior to sampling.

There are a number of mechanisms by which the state of an estuary's entrance is likely to be important in determining benthic community structure. Firstly, extended closure can have a major effect on a range of important parameters due to the lack of marine influence. The change in the hydrodynamic environment affects both physico-chemical (e.g. water movement, salinity) and biological (e.g. recruitment, trophic supply) processes. The variability in a wide range of variables that were unmeasured in this study (e.g. nutrient loads, retention of pollutants) is also likely to play a key role in determining the distribution and abundance of macrofauna in the intermittent estuaries. It was therefore proposed that, in these systems, only fauna that are able to withstand relatively extreme ranges of physico-chemical conditions, for extended periods, would survive during such lengthy closures. While this has been found to be true for estuarine fish communities (Pollard 1994; Griffiths 2001; Young & Potter 2002), few studies had examined long-term temporal changes of benthic communities in intermittent estuaries, particularly in relation to extended closure. The current study revealed that the effects of entrance closure were greatest at the lower sites of estuaries, though community responses were variable between estuaries. During closure, the lower sites of some intermittently closed estuaries became quite depauperate whereas, at others, the community became dominated by fauna that were otherwise more commonly associated with sites further upstream. These findings support the patterns observed in the fish communities of Australian intermittently closed estuaries (Pollard 1994; Griffiths 2001; Young & Potter 2002) in that, much of the fauna present while an estuary is open, will then be excluded during entrance closure and, in some circumstances, replaced by fauna that are more tolerant of closure conditions.

Within each estuary type, the communities in individual estuaries were temporally variable but always distinguishable. The continued high degree of variation between the estuaries nested within each type was partly attributed to the equally variable physico-chemical conditions, which revealed differences at this scale for most water column variables and sediment variables. Physico-chemical variables, therefore, were also unique between individual estuaries throughout the study. Interestingly, seasonal variation in community structure was not consistent for each sampling year, which means that the changes observed were irregular. Temporal community differences in each estuary were due to changes in the abundance, or even simply the presence/absence, of the species that typically characterised each estuary. These comprised a core of nine discriminatory species that each contributed greatly to the temporal variation in four or more estuaries and included Armandia intermedia, Scoloplos normalis, Soletellina alba, Victoriopisa australiensis, Notomastus estuarius, Urohaustorius metungi, Simplisetia aequisetis, Arthritica helmsi and Orthoprionospio cirriformia. Most of these were also the species that continually contributed to the persistent spatial differences between estuary types and are, therefore, key indicators of community variation in these systems. A number of other species were also important contributors to temporal variation but tended to be estuary-specific. These were Batillaria australis and Cerithium coralium at Woolgoolga Lake, Fluviolanatus subtortus and Ascorhis tasmanica at Willis Creek, Australonereis ehlersi at Hearns Lake, Tellina imbellis and Nassarius jonasii at Coffs Creek, Trypaea australiensis at Moonee Creek, Trypaea australiensis, Nephtys gravieri and Mictyris longicarpus at Corindi River.

While each estuary was highly variable over time, this temporal variation did not detract from the persistent and long-term spatial individuality between estuaries, both biologically and physico-chemically, even among those of the same estuary type. Edgar and Barrett (2002) likewise found within-estuary temporal variation to be much lower than the spatial variation between estuaries. Ultimately, this is a reflection of the range in the values of intrinsic features that are specific to individual estuaries such as their catchment size and entrance dynamics, catchment uses and the degrees of both urbanisation and land clearance, as well as entrance and other estuary modifications.

8.2 The Processes Influencing Community Patterns

An understanding of the processes driving community patterns is essential if estuaries are to be effectively managed. Knowledge of these processes in intermittently closed estuaries, for example, can enable predictions to be made about the ecological effects of anthropogenic influences, such as artificially opening closed entrances.

The spatial and temporal differences observed throughout this study were most likely due to the long-term effects of repeated closures on either environmental and/or biological factors. However, the persistent assemblage differences between estuary types could not readily be directly linked with specific physico-chemical factors as each of the water column and sediment variables: (1) generally failed to reveal significant differences between estuary types; and (2) were highly variable, especially among the intermittently closed estuaries. Therefore, the data generated here do not provide strong explanatory power and, as demonstrated by the attempts made within this study, manipulative experiments at the scale required to show causality are generally either not logistically feasible or restricted by the sensitive and unpredictably dynamic nature of these environments. There are a number of additional factors that impede comparisons between biotic and abiotic trends in estuaries. When relating physico-chemical variables to biological patterns, there is a lack of knowledge about how environmental factors affect the biota (i.e. whether mean values or extremes require the greatest attention) (Edgar & Barrett 2002). For example, estuarine salinity can vary rapidly and ad hoc or occasional measurements may have little relevance to fauna when compared to seasonal extremes. The effects of environmental factors are further complicated to an unknown extent by biological interactions and virtually nothing is known about the biological regulation of macrofauna in estuaries over scales greater than hundreds of metres (i.e. < 1 km) (Edgar & Barrett 2002).

The variable nature of the physico-chemical parameters is influenced by entrance dynamics. The intermittently closed estuaries of the Solitary Islands Marine Park were each unique in their entrance dynamics and covered a broad range in the frequency and duration of entrances closures. This was despite the fact that these estuaries are all situated within a 30 km stretch of coast and, hence, also being largely exposed to very similar climatic conditions. Therefore, the most variable factor between the estuaries was catchment size, which appeared to affect entrance dynamics and, consequently, physico-chemical conditions. In fact, catchment size was

the environmental factor that correlated best with community structure. Thus, of the factors considered in this study, it appears that catchment size was most important in determining the differences in community structure between estuaries. The close association between catchment size and biotic patterns, however, also introduces unavoidable confounding into the interpretation of differences between estuary types. Catchment size, and hence the amount of runoff generated relative to waterway area, will determine how an estuary responds physically to rainfall, and therefore has an effect on chemical and biological processes (Haines 2004). Thus, small estuaries would be more likely than large estuaries to close during periods of reduced rainfall and patterns of difference between the two estuary types may simply reflect the effect of catchment size.

The results of the present study reflected this as: (i) the intermittently closed estuaries were generally smaller than the permanently open ones; and (ii) there appeared to be a relationship between catchment size and the frequency of entrance closure (Fig. 8.1). In addition to the differences between estuary types, the variability in catchment size within each estuary type may also explain the high degree of community variation between individual estuaries. Further, the high variability of community structure within the estuary types suggests the presence of a gradient both between and within types. Therefore, whilst at first appearances there are overall distinct community differences between the estuary types, at the scale of individual estuaries demarcation may not be as clear reflecting, instead, a continuum between types. This is again supported by the catchment size and entrance dynamics data as, although the estuary types were clearly distinguishable (Fig. 8.1a), there did appear to be a continuum from one estuary type to the other (Fig. 8.1b). Within the continuum for the estuaries examined, the change from one estuary type to the other specifically occurred at a catchment size 25 km2. This catchment size was both the smallest among the permanently open estuaries and the largest among the intermittently closed estuaries.

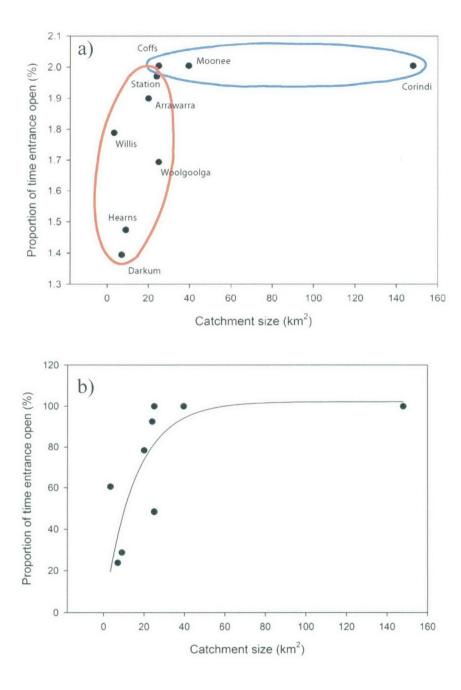


Fig. 8.1 The relationship between catchment size and the proportion of time estuary entrances were open with data points a) grouped by estuary type (red = intermittently closed; blue = permanently open) and b) linked by an asymptotic curve across the full range of catchment sizes.

8.3 Implications for Management and Recommendations for Future Research

The results of this study present some clear advances in our conceptual understanding of estuarine systems and have implications for estuarine management. Firstly, the classification of estuary types has long been based on morphological, hydrological or entrance features. Previous authors (Schlacher & Wooldridge 1996a; Edgar et al 1999; Edgar et al. 2000; Edgar & Barrett 2003; Teske & Wooldridge 2003; Hirst 2004) have noted the need for biological relevance in various estuarine classifications. The results of this study support a biologically meaningful differentiation between, at least, permanently open barrier and intermittently closed estuary types. Having confirmed that intermittently closed estuaries examined are biologically distinct when compared to the permanently open estuaries, it is interesting to note some of the special features they exhibit. The biota of intermittently closed estuaries can be isolated for extended periods, experience extremes in their physico-chemical environment and may be subjected to atypical estuarine conditions, such as reverse salinity gradients. Still, the communities of most intermittently closed estuaries appear to be relatively robust, with many supporting either species or abundances that were not observed among the permanently open estuary type. The most notable examples of this were the very high abundances of Cerithium corallium and Batillaria australis in Woolgoolga Lake, as well as of Ascorhis tasmanica and Fluviolanatus subtotus in Willis Creek. The occurrence of reverse salinity gradients in closed estuaries again highlights the need to ensure that, in models of estuarine zonation, biologically relevant information is given priority, rather than continuing to use the traditional salinity-based classifications.

The remarkable individuality, both biologically and physico-chemically, displayed by the estuaries within each estuary type, reflects the fact that they represent a variety of intrinsic features. All of the estuaries, regardless of their current entrance status, varied in characteristics such as size, predominant catchment uses and degree of entrance modification. Hirst (2004), likewise, found that, over a regional scale, different estuaries are far from biologically and physico-chemically homogenous and highlighted the implications of this when considering effective estuarine classification and management. This high degree of variability stresses the need to take into account the implications of high levels of ecological heterogeneity between estuaries when considering effective estuarine classification and management (Edgar et al. 2000; HRCNSW 2002; Hirst 2004; Hastie & Smith 2006). For example, the long residence

time of water and sediments in intermittently closed estuaries, in particular, can make their faunal communities vulnerable to environmental degradation suggesting that, as a class, they require very careful management (McComb 1995).

A major priority for estuarine management in Australia is the urgent need for the establishment of a system of estuarine protected areas (Edgar et al. 2000). At a local level, the key outcomes of this study prompt some recommendations in regard to the management of the Solitary Islands Marine Park (SIMP). The management plans for the SIMP can only be based on the information that is available at the time they are written. Fortunately, zoning schemes are reviewed every five years and can, therefore, be adapted as the ecological knowledge of the park is expanded. The information from this study can be used to help marine park managers to meet the criteria of comprehensively, representatively and adequately conserving biodiversity. These criteria aim to ensure that marine protected areas: (i) protect their diversity of ecosystems and habitats; and (ii) protect typical species, in addition to the rare, threatened or charismatic ones. In relation to estuaries, there are a number of scales at which these criteria need to be addressed because the results presented here indicated distinct communities in different estuary types, between estuaries nested within each type and between sites along the length of each estuary.

Of the fifteen main estuaries in the SIMP, five are permanently open barrier estuaries whilst the remaining are intermittently closed estuaries. However, of the four estuaries in the SIMP that are afforded the highest level of protection (i.e. no take Sanctuary Zones), three are large permanently open barrier estuaries and only one is an intermittently closed estuary (Station Creek). Whilst this distribution of Sanctuary Zones might be proportional to the overall water area covered by each estuary type, it may be to the detriment of the unique communities of the intermittently closed estuaries. For example, this study revealed at least 13 of the species common in intermittently closed estuaries (Table 3.3.1.2) that were not detected in the Sanctuary Zones of the southern half of the marine park (i.e. Station Creek and Corindi River). Further, within the estuarine Sanctuary Zones, some habitats are poorly represented. With the exception of Corindi River, all Sanctuary Zone areas are only in the middle and upper reaches of estuaries. Thus, the only sandy substrate that is protected in the SIMP is a section on the northern side of Corindi River. Whilst I acknowledge that there are other factors to consider in the zonation of protected areas, especially the needs of recreational and commercial users, there are a number of steps that could be taken to alleviate the discrepancies in the current allocation

of protected areas within the SIMP. Specifically, Sanctuary Zones would need to be established so that they: 1) encompass the range of habitats along the length of estuaries; and 2) replicate the protection of these habitats across a number of estuaries within each of the two main estuary types.

Other applications for the results of this study stem from the preliminary examination conducted into the utility of surrogates for the rapid assessment of biodiversity. The development of reliable biodiversity surrogates in marine and estuarine waters is crucial in providing a streamlined approach to monitoring and assessment. For example, marine protected areas are often selected opportunistically and without prior comprehensive surveys of their biodiversity (Vanderklift et al. 1998; Banks & Skilleter 2002; Giangrande 2003). The primary reason behind such management practices is that the implementation of conservation strategies is often done under conditions of limited funding, information, time and taxonomic expertise (Chapman 1998; Blair 1999; Giangrande 2003). This has also partially contributed to the ongoing issue of the current lack of species inventory data for most Australian marine habitats, (Banks & Skilleter 2002; Smith 2005). Accumulating complete species inventories for regions is not an option for the foreseeable future (Margules & Pressey 2000) and, therefore, surrogates that represent species diversity will have to be found (Vanderklift et al. 1998)

This study identified the potential of using family level higher taxa to save resources, both time and taxonomic expertise, in biodiversity assessment. The time saved by the relative ease with which fauna can be identified to family suggests that using this level of taxonomic resolution may provide an extremely cost-effective method for monitoring and managing estuarine benthic environments. Other studies (Chapman 1998; MacFarlane & Booth 2001) have also supported the ability of family level taxonomic resolution to reflect estuarine macrofaunal community structure across a range of anthropogenic influences. However, it should be remembered that the use of either higher taxa will not help in addressing the relatively poor knowledge of local fauna (Smith & Simpson 1993; Hutchings 1999). In addition, the identification of indicators of species diversity requires not only the demonstration of their potential as a surrogate, as addressed by this study, but also rigorous testing in other localities and at different ecological scales (Balmford et al. 1996).

Finally, based on all the outcomes of this research, a number of issues have arisen that need to be addressed, providing direction for future estuarine research. Firstly, although clear patterns in space and time were defined within and between estuary types, the processes driving these patterns could not be definitively identified. Manipulative experiments are required to demonstrate causality; the unpredictably dynamic nature of intermittently closed estuaries hindered the attempts made here to begin to isolate the specific factors responsible for the differences in community structure. Still, the events on these occasions were unusual and, as such experiments are fundamental to understanding the ecology of estuaries in southeastern Australia, they should continue to be a focus of future research.

In addition, this study identified nine key discriminatory species that were consistently responsible for both the spatial differences between and within estuaries, as well as for the temporal changes within each estuary. These species are all common estuarine fauna along the coast of New South Wales (Hutchings et al. 1978; Atjinson et al. 1981; Jones et al. 1986; Jones 1987; Smith et al. 1994; Johnstone 1997; Smith 1997; Anderson 1998; McFarlane & Booth 2001; Sawtell 2002; Hirst 2004) and it suggested that their potential for the rapid assessment of environmental change in estuaries be examined further. This would be particularly useful for monitoring natural and anthropogenic disturbances, especially considering that, previously, changes in the benthic communities of intermittently closed estuaries could not be assessed at all, owing to the lack of baseline data.

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APPENDIX

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