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PREDICTING SPECIES RICHNESS FOR AUSTRALASIAN FRESHWATER MACROINVERTEBRATES: DO WE WANT TO KNOW?

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Abstract

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The identification of freshwater macroinvertebrates to family level is becoming increasingly popular for surveys, predictive models and pollution indices in Australia because it is quicker and cheaper than genus or species level identification, and it requires less specialised knowledge. Family richness has been used as a predictor of species richness for other taxonomic groups such as vertebrates, ants and plants and we were interested in seeing whether this might be a useful method for freshwater macroinvertebrates. Taxon lists from one Papua New Guinean and 34 Australian datasets from lentic and lotic waters were used to regress the number of families against the total number of taxa (species where possible). Also, the ability of the number of species and morphospecies within some orders (Coleoptera, Diptera, Ephemeroptera and Trichoptera) to predict overall species richness was investigated. The number of all families explained 91% of the variation in species richness. The number of species within each of the orders explained between 60 and 85% of the variation in overall species richness. We conclude that it would be possible to predict species richness in this way, particularly if sampling techniques and sampling effort were standardised. The terms 'species richness' and 'biodiversity' are often used synonymously although the former is only a subset of the latter. Some of the limitations and dangers of assessing species richness instead of biodiversity are discussed.

Introduction

Most freshwater studies addressing biodiversity have assumed that biodiversity and species richness are synonymous (e.g., Lang and Raymond, 1993; Allan and Flecker, 1993; but see Collier, 1993). Species richness is very expensive to determine using traditional methods and taxonomy. Rapid Biological Assessment (RBA) has been developed in order to over come these difficulties. RBA is based on either the use of morphospecies rather than formally named species (basic RBA) or on identifying either subsets of communities or only identifying to taxonomic levels higher than species (ordinal RBA: Beattie et al., 1993). We present an evaluation of how effective ordinal RBA is likely to be for freshwater invertebrate communities.

Ordinal RBA assumes that higher-taxon richness or the number of species in taxonomic subsets are closely related to overall species richness but this has rarely been tested. Williams and Gaston (1994) used family richness to predict species richness of British ferns, British butterflies, Australian passerine birds and North and Central American bats. They found that for each of these groups of organisms, family richness explained at least 79% of the variation in species richness and concluded that 'with careful choice of higher-taxon rank, it may be possible to redeploy effort from taxonomically intensive to taxonomically extensive surveys'. Andersen (1995) used a similar approach to estimate species richness of Australian ants using generic diversity.

We obtained taxon lists from 34 datasets throughout Australia and one from Papua New Guinea and used family richness for the whole community and the numbers of morphospecies within four orders (Coleoptera, Diptera, Ephemeroptera and Trichoptera) as predictors of community species richness.

Methods

The number of families, total number of taxa and the numbers of coleopteran, ephemeropteran, trichopteran and dipteran taxa were determined for 34 taxon lists from surveys throughout Australia and 1 from Papua New Guinea (Table 1). The Australian studies were from all states and one territory: Western Australia, 10; New South Wales, 9; Victoria, 5; Queensland, 3; Northern Territory, 3, South Australia, 2, Tasmania, 2. The types of freshwater system were also very varied and eight of

Table 1. Details of the 35 datasets.

Dataset	Author(s)	Year	Area	State	Type
1	Bennison, Hillman and Suter	1989	Murray River and tributaries	NSW/SA	lowland river
2	Boulton	1988	Werribee River	VIC	intermittent
3	Boulton	1988	Lerderderg River	VIC	intermittent
4	Boulton and Lloyd	1991	Lower River Murray	SA	lowland river
5	Bunn, Edward and Loneragan	1986	Northern jarrah forest streams	WA	intermittent
6	Charlton (unpublished)	1994	Millstream Delta	WA	lowland river
7	Chessman and Growns, J.	1994	Williams River and tributaries	NSW	lotic
8	Chessman, McEvoy and Growns (unpublished)	1992	Upper Nepean River and tributaries?	NSW	lotic
9	Chessman, Growns, J., Hardwick and Holleley	1994	Warung Management Area	NSW	lotic
10	Chessman, Growns, J., Hardwick, Holleley, Jackson and McEvoy	1994	Dorrigo Management Area	NSW	lotic
11	Chessman, O'Connor and Holleley	1995	Tenterfield Management Area	NSW	lotic
12	Cosser	1988	Gowrie Creek*	QLD	lotic
13	Davis, Rosich, Bradley, Growns, J., Schmidt, and Cheal	1993	Perth wetlands*	WA	lentic
14	Davis, Barmuta and Balla	1988a	Serpentine River*	WA	lotic
15	Davis, Barmuta and Balla	1988b	Dirk Brook	WA	lotic
16	Davis, Harrington and Friend	1993	George Gill Range	NT	intermittent
17	De Deckker and Williams	1982	Tasmanian salt lakes	TAS	saline
18	Doeg	1984	Mitta Mitta River	VIC	lotic
19	Growns, I.	1992	Sutton catchment	WA	intermittent
20	Growns, I.	1992	Lewin catchment	WA	intermittent
21	Growns, I. and Davis	1994	Carey Brook	WA	lotic
22	Lake and Pearson (unpublished)	1988	Birthday Creek	QLD	lotic
23	Lake and Pearson (unpublished)	1988	Yuccabine Creek	QLD	lotic
24	Marchant	1982	Magela Creek	NT	billabong
25	Marchant, Mitchell and Norris	1984	Lower LaTrobe River and tributaries*	VIC	lowland river
26	Metzeling, Graesser, Suter and Marchant	1984	Upper LaTrobe River and tributaries	VIC	lotic
27	Norris, Lake and Swain	1982	South Esk River*	TAS	lotic
28	Norris, Moore, Maher and Wensing	1993	Lake MacKenzie	NSW	lentic

Table 1 Continued

29	Norris, Moore, Maher and Wensing	1993	Lake Windamere	NSW	lentic
30	Outridge	1987	Magela Creek	NT	billabong
31	Pen and Potter (unpublished)	1990	Collie River*	WA	lotic
32	Robson (unpublished)	1990	Julimar Forest	WA	lotic
33	Towns	1985	Brown Hill Creek	SA	intermittent
34	Wright and Chessman (unpublished)	1992	Blue Mountains*	NSW	lotic
35	Yule	1995	Konaiano Creek	PNG	lotic

PNG = Papua New Guinea
*some sites polluted

the studies had at least some sites that were polluted (Table 1).

The total number of taxa for each study was taken as the number of recognised taxonomic units (RTUs) for that study, e.g., where chironomid larvae were not identified beyond family, this was counted as one RTU. Immature and unidentified taxa were not included unless they were the only RTU in that family or genus. Coleopteran adults and larvae were considered to be different RTU's unless they were both identified to the same published species name. Where identification was not taken even to family level, each group was taken as one RTU, e.g., Hydracarina.

Plots of the numbers of total taxa against the numbers of families and coleopteran, dipteran, ephemeropteran and trichopteran taxa were examined for outliers. The state in which each study occurred was superimposed on the plot of numbers of families, in order to look for any regional variation.

Linear regression was used to examine the relationships between the total numbers of taxa and the numbers of families and the numbers of coleopteran, ephemeropteran, trichopteran and dipteran taxa. All data were $\log_{10}(x+1)$ transformed and residuals were examined for normality using Normal Scores plots.

To test the predictive value of the regression of number of families versus total numbers of taxa, data on numbers of families and species for single sites were used from Marchant et al. (1995). The data from the lower La Trobe and Thomson Rivers and the upper La Trobe River were not used for this test as they had been used in the calculation of the regression equation. Percentage error in prediction of species richness was calculated by subtracting the number of predicted species from the actual number of species, so that a negative error means that more species were predicted than were actually recorded. Percentage error was plotted against number of families to identify any systematic errors.

Results

All regressions were highly significant. The number of families explained 91% of the variation in the number of total taxa (Table 2). The number of taxa from the taxonomic sub-groups were poorer predictors of total numbers of taxa with the numbers of coleopteran taxa giving the best result (Table 2).

For most states, not enough datasets were available to assess regional variation. However, the plot suggested that, for the datasets available, lotic systems in south-west Western Australia had low species richness, whereas those in NSW had consistently high species richness (Fig. 1). There was no evidence that the different states showed different relationships between species and family richness, i.e. the intercepts and slopes of the lines for each state appeared very similar (Table 2).

The plot of total number of taxa against the number of coleopteran taxa (Fig. 2a) showed that Carey Brook (study 21) and the Serpentine River (14) had lower proportions of beetle taxa than would have been expected and the Collie River (31) had a higher proportion than would

Table 2. Regression results of predictions of total numbers of taxa using log (x+1) transformed data.

Independent variable	n	Intercept	Slope	r^2
Number of families:				
All datasets	35	−0.488	1.530	0.91
NSW	9	−0.730	1.671	0.98
VIC	6	0.062	1.298	0.80
WA	10	−0.046	1.260	0.83
Number of coleopteran taxa	35	1.174	0.713	0.85
Number of dipteran taxa	35	0.981	0.732	0.70
Number of trichopteran taxa	35	1.356	0.606	0.68
Number of ephemeropteran taxa	35	1.573	0.632	0.60

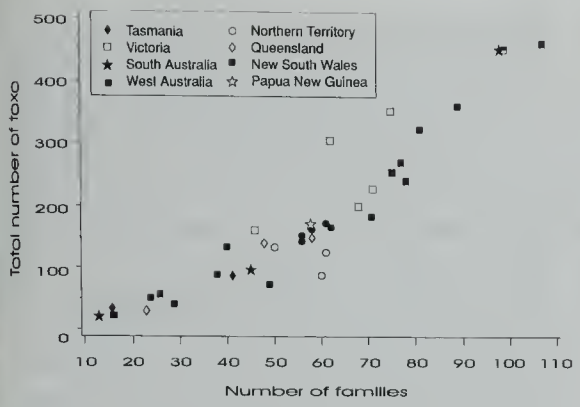

Figure 1. Plot of total number of taxa against number of families for the 35 studies. The state in which the study was done is overlaid.

have been expected. All these 3 areas are in south-west Western Australia. The same plot for dipteran taxa (Figure 2b) showed that Carey Brook had a high proportion of Diptera whereas the Werribee (study 2) and Lerderderg rivers (study 3), which are both ephemeral rivers in Victoria, had low proportions of dipteran larvae. This plot also showed a marked difference in the proportions of Diptera between the Williams River (study 7) and the River Murray and tributaries (study 1), although they both had similar total numbers of taxa. The plot for Ephemeroptera (Figure 2c) indicated that the River Murray and tributaries, the Perth wetlands (study 13) and the Werribee and Lerderderg Rivers had low numbers compared to their total numbers of taxa. The trichopteran plot (Figure 2d) indicated that the River Murray and tributaries had low numbers of caddis whereas the Werribee and Lerderderg Rivers had high numbers compared to their total numbers of taxa.

The prediction of species richness from family richness for 19 single sites (data from Marchant et al., 1995) gave a mean error of −7.7% (standard error, 2.5) with a maximum error of −31%. The plot of percent error against number of families showed that roughly half of the sites were predicted to within 10% of the actual species richness (Fig. 3). Also, 14 out of the 19 predictions were for more species than actually occurred.

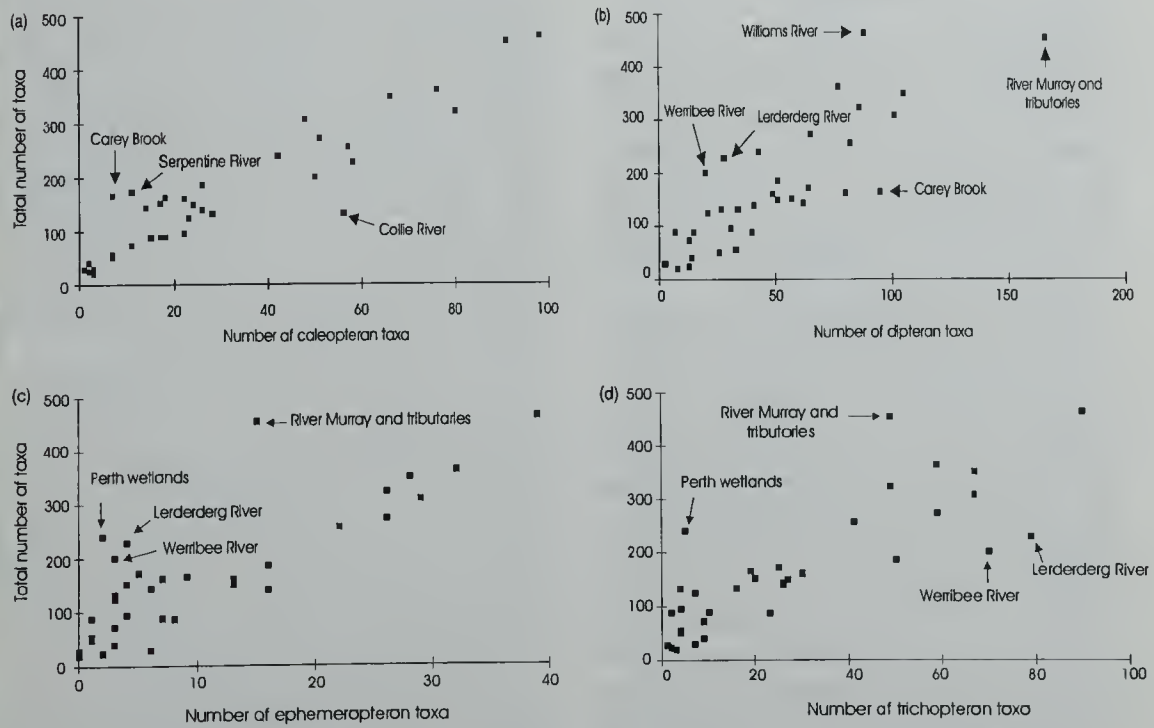

Figure 2. Plots of total number of taxa against numbers of taxa for (a) Coleoptera, (b) Diptera, (c) Ephemeroptera and (d) Trichoptera.

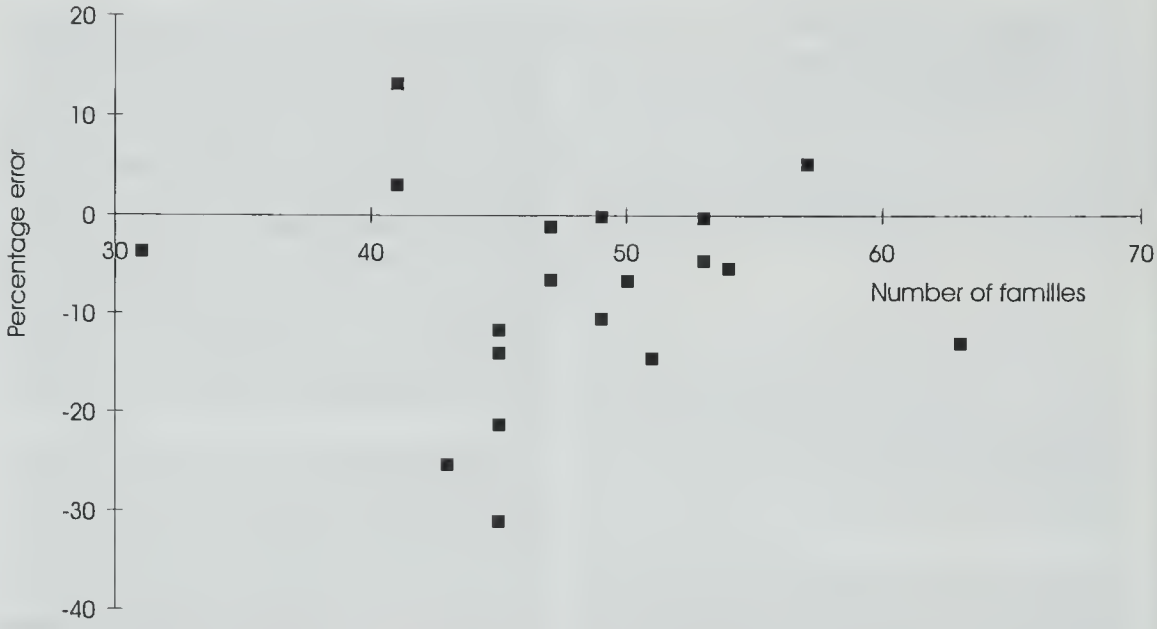

Figure 3. Plot of percentage error in prediction of species richness against number of families for the 19 single sites from Marchant et al. (1995).

Discussion

The number of families was a very good predictor of community species richness (i.e., total number of taxa) whereas the taxon richness for the four orders were not such good predictors; beetles were the best of the four. This suggests that analysing whole communities to coarse taxonomic levels may be more reliable than species level identification of indicator groups, if estimates of whole community species richness are wanted.

There was no evidence that there were different relationships between numbers of families and community species richness in different regions of Australia. However, there was some evidence that lotic systems in NSW had very high species richness whereas lotic systems in south-west Western Australia had low species richness. Bunn and Davies (1990) suggested that the low species richness of south-west Western Australian lotic systems may be due to the area's isolation, historical aridity and low primary productivity. Although low in numbers of species for many groups, this area has a very high proportion of endemics among its flora and fauna, including the lotic macroinvertebrates (CSIRO, 1992; Christensen, 1992). In contrast, high levels of species richness have previously been observed for tabanid diptera and odonates, as well as for other communities, on the north coast of NSW, which has been designated the Macpherson-Macleay overlap (CSIRO, 1991). MacArthur (1972) observed that lotic invertebrates are the principal exception to the rule that the tropics have greater biodiversity then temperate areas. However, Lake et al. (1994) found that two Queensland creeks had significantly higher species richness than streams of similar stream orders in Victoria. Our data did not show higher species richness for tropical areas but this may be due to the small number of datasets from the tropics in this study.

Several of the species lists showed that where communities are low in species numbers of one taxonomic group, they are high for another group. The intermittent Werribee and Lerderderg Rivers in Victoria had low numbers of dipteran larvae and mayfly nymphs but high numbers of caddis fly larvae. Carey Brook, a in south-west Western Australia, had low numbers of beetles but high numbers of dipteran larvae. There are doubtless historical and evolutionary reasons for these patterns but it is interesting to note that the overall relationship between numbers of families and community species richness was the same for these areas as for all the other studies.

The predictions of species richness for single sites were not good. Only about half of the predictions for single sites fell within 10% of the actual species richness and errors of up to 31% occurred. The majority of the predictions for single sites were for higher numbers of species than actually occurred. This may in part be because Marchant et al. (1995) included oligochaetes, trichads and mites as single taxa. However, several of the 35 studies used to calculate the regression equation also did this. The consistently high predicted species numbers are more likely to be because the predictions are for single sites whereas the regression was of studies of multiple sites in an area. The lower sampling effort for the single sites would be expected to obtain a lower proportion of species within each family compared to multiple site studies. For example, at most sites you would be likely to find beetles from the family Dytiscidae. However, there are likely to be different species of dytiscids at different sites. So a survey of several sites would find more species of dytiscids than a survey of only one site, whereas both surveys would record only one family for the different numbers of species. This highlights the care with which this type of predictive technique must be used.

Our results should be treated with some caution as the sampling intensity, methods and taxonomy varied among studies and the geographic distribution of the studies was uneven. However, we believe that we have shown that this approach would be highly successful in predicting the species richness of freshwater macroinvertebrates for an area. It might also show interesting patterns, such as the apparent high levels of species richness in northern NSW. In addition, our observation that where one group of organisms in a community has low species richness, another taxonomic group in the same community may have high species richness, has interesting evolutionary implications.

However, we are concerned that the almost exclusive focus on species richness in biodiversity assessment is unwarranted. Biodiversity is a difficult concept to define as it comprises many different ideas, of which species richness is only one. We need to know what the species are: an assessment of their endemicity, rarity, susceptibility to extinction and distribution can then be made, or at least attempted. It is also important to know where they fit into their community, i.e. whether they are needed for the continuing survival of other organisms, and whether they are an example of a scientifically important phenomenon, such as evolution (see Richardson, this volume). It is obviously impossible for all of this information to be obtained for all species, let alone in the time frames required by managers and legislators. However, this does not mean that species richness alone should be used as a surrogate for biodiversity. Scientists need to reach a consensus on what aspects of biodiversity need to be considered for conservation purposes and then communicate this to the wider community.

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