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Assessing river health in south-western Australia: comparison of macroinvertebrates at family level with Chironomidae at species level

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Introduction

In response to growing community concern about declining water quality in the Nation's rivers and streams, the Australian Government established the National River Health Program (NRHP) in 1992. The first objective of the NRHP, to assess and monitor the ecological condition of Australian rivers, was met by the development of the Australian River Assessment Scheme (AUSRIVAS); a set of predictive models which use changes in assemblages of aquatic macroinvertebrates to rapidly bio-assess the ecological condition of the Nation's rivers.

AUSRIVAS is based on the British RIVPACS model, which uses aquatic macroinvertebrates as indicators of river health (WRIGHT et al. 1984, WRIGHT 1995) and has been successful in assessing river condition on a national scale (ARMITAGE et al. 1987). Cost-effective rapid bioassessment (RBA) is a priority of the NRHP. For this reason AUSRIVAS uses macroinvertebrates identified to family level, which is considered adequate for discrimination in RBA, and is less time-consuming than other approaches (MARCHANT et al. 1995, WRIGHT 1995, WRIGHT et al. 1995, BOWMAN & BAILEY 1997). Although based on RIVPACS, AUSRIVAS differs in that specific riverine habitats are sampled and processed separately. The change to specific habitat sampling was based on HUMPHRIES et al. (1996) and PARSONS & NORRIS (1996).

Habitat and bioregion-specific models were constructed following a series of standardised protocols. Firstly, Reference sites were classified into groups of sites with similar community composition, stepwise discriminant function analysis was then used to identify environmental variables that best predicted the sites to the correct group. The number of families expected (E) to occur at a site was then calculated by multiplying the probability of a site belonging to a classification group by the probability of a site occurring in that group then summing the products. Only taxa with a probability of ≥50% of occurring at a site were considered when calculating E values (SIMPSON & NORRIS in press).

The ecological condition of a site then may be tested in the appropriate model by calculating the ratio of observed to expected (O/E) number of families. To simplify output, O/E ratios were allocated to Bandings based on the 10th percentiles of mean O/E values for each model (X, an enriched fauna with more taxa than expected; A, equivalent to reference condition; B, mildly impacted; C, moderately impacted; D, severely impacted).

In Western Australia, 188 Reference sites considered to be undisturbed or minimally disturbed, and 20 Impact sites, specifically chosen because of observable disturbances in the immediate vicinity (e.g. effluent inputs, land clearance, stock access), were sampled in wet and dry seasons in 1994 and 1995. Resulting data from the Reference sites were used to construct habitat-specific models, and the sensitivity of the models was tested using data from the Impact sites.

Testing showed that models distinguished between undisturbed and severely disturbed sites, but did not reliably detect subtle impacts (SMITH et al. 1998). It is considered that the high error rate is partly a consequence of identifying macroinvertebrates to family level, and species level identifications could lead to greater resolution. Samples in which all macroinvertebrates were taken to species level were not available, however, for a subset of the channel habitat data set, all larvae of Chironomidae collected for the four sampling trips, were identified to species. Chironomidae are a major component of the fauna of streams and rivers in south-western Australia accounting for up to 40% of the total taxa (EDWARD 1986, STOREY & EDWARD 1989). Therefore, Chironomidae identified to species level (CS) were used in a comparison with macroinvertebrates identified to family level (MF) to determine if the former had the potential to better identify impacted sites.

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Methods

Field sampling

The subset of the channel habitat data set consisted of 45 Reference and five Impact sites from 50 rivers or streams across the south coastal/karri forest region of Western Australia. Sites were sampled in wet (September; Trips 1 and 3) and dry (January; Trips 2 and 4) seasons in 1994 and 1995. Samples were collected according to a national protocol (DAVIES 1994). Basically, macroinvertebrates were collected with a D-framed net (350 mm wide, 250 mm high, with 250-µm mesh), with separate samples taken from each of four habitats (riffle, channel, macrophytes and pool rocks) where the habitat constituted ≥10% of a nominated 100-m reach. The channel habitat was sampled using a kick/sweep technique over 10 m of the habitat. Samples were live-picked in the field for 30 min. A magnifying visor (×2) and fine forceps or pipette were used to remove animals from successive small aliquots of the sample dispersed in a large white tray in filtered stream water. Animals were preserved in 70% alcohol and subsequently identified in the laboratory. At each site, 44 physical and chemical variables were measured, for use in discriminant function analysis (SMITH et al. 1998).

Data analysis

All analyses were based on presence/absence data. For MF and CS data sets for each sampling trip, mean taxa richness was calculated for Reference and Impact sites. Three-way ANOVA under the GLM procedure of SAS (1987) was used to test for significant differences between trip, site and taxonomic level. Prior to analysis, data were $\log_{10}(x+1)$ transformed to achieve normal distributions and equality of variances. Tukey's HSD range tests (DAY & QUINN 1989) were applied to distinguish between levels of the main factors where significant differences were found.

To identify between-site differences in community assemblages for MF and CS, each data set was ordinated by Semi-Strong Hybrid multidimensional scaling (SSH) using the Pattern Analysis Package, PATN (BELBIN 1995). Only taxa that occurred at more than 10% of sites in any data set were included in each analysis to avoid 'low-occurrence' taxa having a disproportionate effect on the results (GAUGH 1982). For each analysis, similarity between each site was calculated using the Bray–Curtis association measure on the presence/absence of taxa at each site. The Principal Axis Correlation (PCC) option in PATN then was used to calculate gradients in taxa richness and water quality parameters through each ordination. Monte Carlo randomisations (n = 100) of the data were performed to test the significance of these gradients. To test the degree of separation of Reference and Impact sites in each ordination, the Analysis of Similarity (ANOSIM) option in PATN (BELBIN 1995) was invoked. This uses Monte-Carlo randomisations of the data to compare mean within and between group variation in dissimilarity.

To quantify the difference between Reference and Impact sites in each data set (i.e. are Reference sites more or less similar to Impact sites for MF or CS data), the mean dissimilarity for all pair wise comparisons between each Impact site and all Reference sites was calculated for each trip and each data set. Two-way ANOVA, by taxonomic level (MF vs. CS) and sampling trip was then used to test for significant differences in dissimilarity (arcsin transformed), with Tukey's HSD range tests applied to distinguish between levels of the main factors where significant differences were found.

Model banding, derived from the channel habitat models was determined for all a priori Impact sites by running each MF data set through the appropriate AUSRIVAS model; Trips 1 and 3 through the wet season and Trips 2 and 4 through the dry season channel habitat model. Ordination plots were then plotted for MF and CS data sets for each trip, indicating positions of Impact sites, annotated with Model Bandings.

The banding assigned to a site run through the AUSRIVAS models depends upon the taxa present at the site and the frequency of occurrence of taxa at the Reference sites in each classification group in the model. Therefore, Chi-square contingency table analysis was used to test for significant differences in the frequency of occurrence of each taxon between Impact and Reference sites. This was applied to each trip and for all taxa for MF and CS data sets.

Results

ANOVA detected significantly more taxa for MF compared to CS data sets, but with no significant difference in richness between the 45 Reference and the five Impact sites (Table 1, Fig. 1). There was a significant temporal effect, with greater taxa richness in Trip 4 compared to Trip 2. There were no other between-trip differences and the interaction terms were not significant. Although there was no overall difference between Reference and Impact sites, there were fewer species of Chironomidae at Impact compared to Reference sites in Trips 1 and 2, but not in Trips 3 or 4 (Fig. 1).

Ordination of each data set for each trip indicated relatively good separation of Impact from

Table 1. Three-way ANOVA and Tukey's Multiple Range tests for between taxonomic level (macroinvertebrate at family (MF) and Chironomidae at species (CS)), site type and sampling trip differences in taxa richness. Main effects not significantly different at $\alpha < 0.05$ are underlined by a common line; ns, not significant; *P < 0.05; **P < 0.01; ***P < 0.001. Data were $\log_{10}(x + 1)$ transformed prior to analysis.

Effect	df	F	P	Tukey's Test			
Taxonomic level	1	53.04	***		MF	>	CS
Site type	1	2.45	ns		Reference	=	Impact
Sampling trip	3	3.59	*	T4	T3	T1	T2
Taxonomy × Type	1	3.73	ns				
Taxonomy × Trip	3	0.72	ns				
Type × Trip	3	1.42	ns				
Taxonomy × Type × Trip	3	1.08	ns				

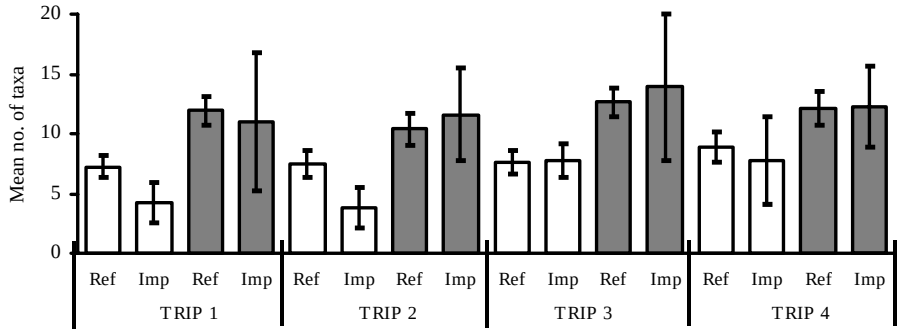

Fig. 1. Between sampling trip, taxonomic level and site type differences in mean taxa richness (±95% C.I.). Open columns are for Chironomidae at species level and shaded columns are for Macroinvertebrates at family level. Ref, reference sites; Imp, impact sites.

Reference sites for both MF and CS data (Fig. 2a–d). There was some overlap, and the Reference sites that ordinated amongst Impact sites tended to have elevated salinities (≥3 ppt). These levels of salinity (either natural or anthropogenic in origin) are known to adversely affect aquatic fauna and indicated that not all Reference sites were undisturbed (for MF and CS data). Therefore, these saline sites were a posteriori classed as Impacted. ANOSIM detected significant separation of Impact/Saline sites from Reference sites in all ordinations except one (MF – Trip 1, $P < 0.0001$; Trip 2, $P < 0.01$; Trip 3, $P < 0.0001$; Trip 4, $P < 0.04$; CS – Trip 1, $P < 0.0001$; Trip 2, $P < 0.0001$; Trip 3, $P < 0.01$; Trip 4, $P < 0.1$). Generally, there was tighter clustering of Impact sites in ordinations of CS as opposed to MF data (Fig. 2a–d). This was supported by significantly greater dissimilarity between Impact and Reference sites for CS as opposed to MF data. Also, there was a greater change in taxa composition between Impact and Reference sites for CS compared to MF data (Table 2, Fig. 3).

PCC identified significant gradients in taxa richness (number of taxa in MF and number of species in CS), with the gradients running towards the Reference and away from the Impact/Saline sites in each ordination. There were also significant gradients in conductivity (EC) in each ordination, directed towards the Impact and Saline sites (Fig. 2).

When Model Bandings were superimposed on the ordinations, Impact/Saline sites identified by the models as impacted (Bands B, C or D) were not distinctly separated from the unimpacted Reference sites (Fig. 2a–d). In most instances the reverse was true; Impact and Saline sites registered by the model as unimpacted (Bands X and A), were separated from

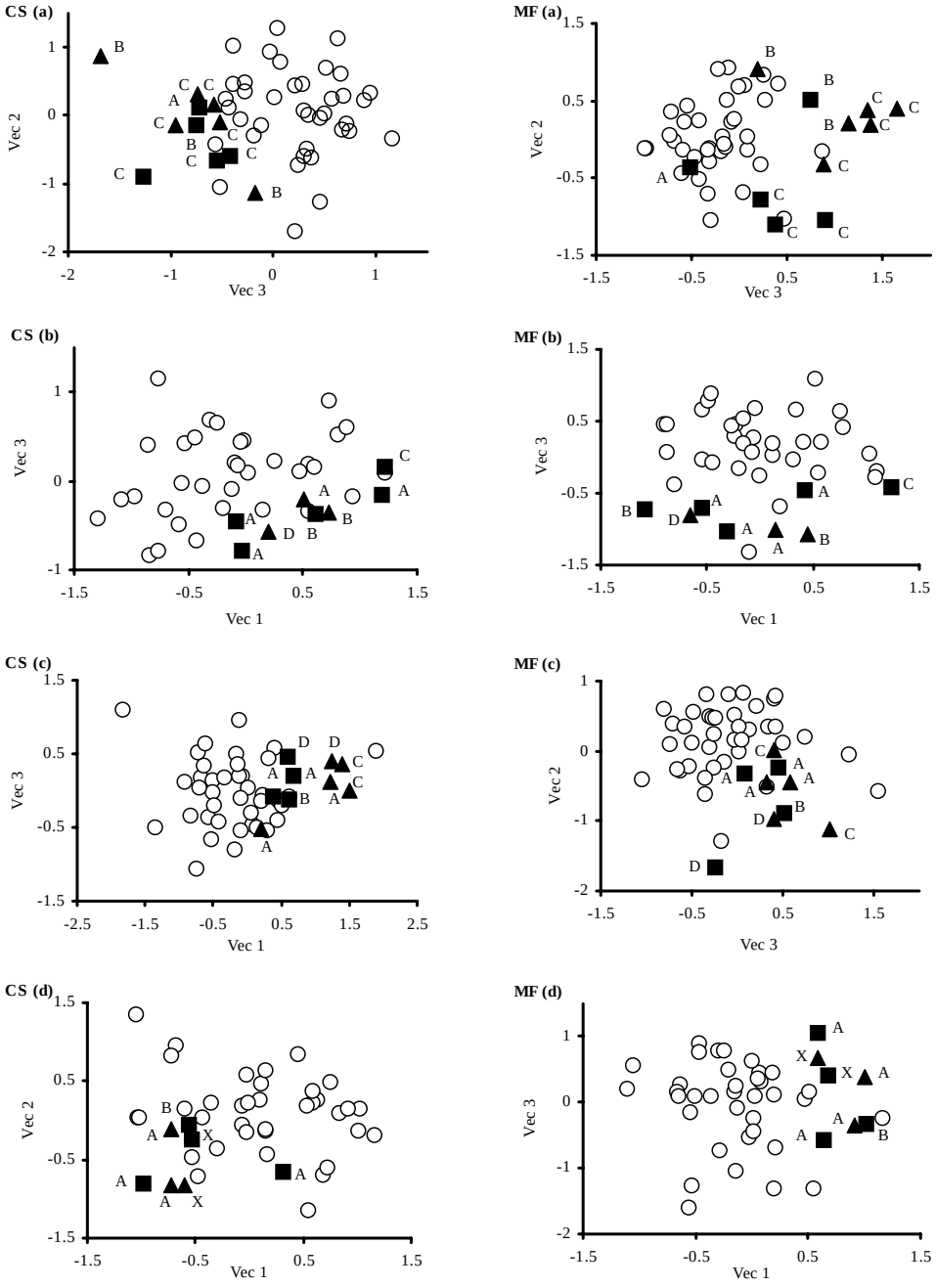

Fig. 2. Multidimensional scaling ordinations of Chironomidae at Species (CS) and Macroinvertebrate at Family (MF) data sets for sampling trips 1 (a), 2 (b), 3 (c) and 4 (d), indicating Reference (O), Impact (■) and Saline (▲) sites (≥3 ppt salinity when sampled). Letters beside Impact and Saline sites are model bandings derived from the testing of MF data through the AUSRIVAS models (X, taxa-enriched; A, reference condition; B, mildly impacted; C, moderately impacted; D, severely impacted).

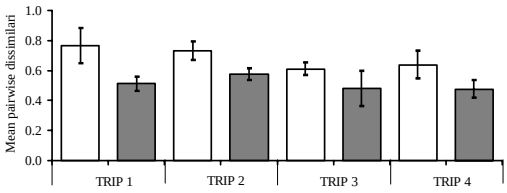

Fig. 3. Mean (±95% C.I.) pairwise dissimilarity between each impact site and all reference sites for each trip for Chironomidae at species level (open columns) and Macroinvertebrates at family level (closed columns).

Reference sites in ordination space.

Chi-square contingency table analysis detected significant differences in the frequency of occurrence of taxa between Reference and Impact/Saline sites. For CS, 13 taxa demonstrated significant differences, with nine taxa decreasing and four taxa increasing in occurrence at Impact/Saline sites (Table 3). For MF, 11 taxa demonstrated significant differences, with seven taxa decreasing and four taxa increasing in occurrence at Impact/Saline sites (Table 4). Seasonality in the fauna meant that few taxa had significant differences in all four sampling trips. However, many taxa had significant differences in one season (e.g. declined in occurrence at Impact/Saline sites in Trips 1 and 3 or in Trips 2 and 4), with no difference in the other season.

Discussion

Ordination of samples demonstrated significant separation of a priori Impact, and a posteriori Saline sites from Reference sites, indicating differences in the composition of taxa between these groups. This separation occurred for both the MF and CS data sets. Even though samples separated in ordination space, the AUSRIVAS models frequently recorded Impact/Saline sites as not impacted based on family-level composition (Banding X or A). Impact sites were preselected, based on observable disturbances in the immediate vicinity of each site, and there was every expectation that taxa composition at these sites would reflect these disturbances. Similarly, an a posteriori level of 3 ppt salinity in the water was selected, above which fauna at sites was affected by salinity. BAYLY & WILLIAMS (1973) have previously identified this level as the upper limit of salinity for freshwater fauna. However, the models often failed to register the changes in family assemblage composition identified in the ordinations as sufficiently large as to be impacted. This inability of the AUSRIVAS models to detect changes in taxa assemblages is obviously of concern, particularly as salination of inland waters as a result of land clearance and rising water tables is a major land use issue in south-western Australia (FROEND et al. 1997). Chi-square analysis indicated that changes in MF assemblages were real, with taxa both increasing and decreasing in occurrence at impacted sites. However, in most instances, the loss of families did not appear to be sufficient for the models to register an impact. As SMITH et al. (1998) suggest, the AUSRIVAS models are good at detecting severe impacts, but inadequate at detecting mild changes. Part of the limitation of the AUSRIVAS approach is that not all taxa are used in the models. For instance, the models only consider taxa with a greater than 50% probability of occurrence at Reference sites, and they do not consider taxa which are only present at impacted sites (e.g. Dugesiidae, Planorbidae and Sphaeriidae for MF, and *Polypedilum nubifer* for CS data).

Because of the standardised approach

Table 2. Two-way ANOVA and Tukey's Multiple Range tests for between sampling trip and between taxonomic level (macroinvertebrate at family (MF) and Chironomidae at species (CS)), differences in mean pairwise dissimilarity between each Impact site and all reference sites. Main effects not significantly different at $\alpha < 0.05$ are underlined by a common line; ns, not significant; *P < 0.05; **P < 0.01; ***P < 0.001.

Effect	df	F	P	Tukey's Test			
Taxonomic level	1	27.31	***		CS	>	MF
Sampling trip	3	2.96	*	T4	T3	T1	T2
Taxonomy × Trip	3	1.23	ns				

Table 3. Chi-square contingency table analysis of differences in occurrence of each species of Chironomidae between reference and impact/saline sites for each trip. Values in parentheses are the number of samples in each group (reference and impact); values alongside each taxa are the percent of reference/impact sites at which each species was recorded; P values indicate Chi-square significance; ns, not significant; *P < 0.05; **P < 0.01; ***P < 0.001.

Sub-family	Species	Trip 1 Ref/Impact		Trip 2 Ref/Impact		Trip 3 Ref/Impact		Trip Ref/Impact	
		(38/11)	p	(34/8)	p	(39/9)	p	(36/7)	p
Aphroteniinae									
	Aphroteniella filicornis Brundin	16/0	ns	3/0	ns	33/0	*	6/0	ns
	Aphroteniella tenuicornis Brundin	3/0	ns	3/0	ns	-/-	-	-/-	-
Chironominae									
	?*Chernovskiia* sp. MRHI-C11	-/-	-	3/0	ns	3/0	ns	3/0	ns
	Chironomini ?genus ?sp. MRHI-C1	3/0	ns	-/-	-	-/-	-	-/-	-
	Chironomini ?genus ?sp. MRHI-C4	3/0	ns	-/-	-	-/-	-	-/-	-
	Chironomini ?genus ?sp. V12	39/0	*	32/0	ns	23/0	ns	64/0	**
	Chironomus aff. *alternans* Walker	11/55	**	76/50	ns	10/78	***	64/57	ns
	Chironomus occidentalis Skuse	0/9	ns	0/13	*	3/22	*	0/14	*
	Cladopelma curtivalva Kieffer	0/18	**	26/0	ns	8/11	ns	19/43	ns
	Cladotanytarsus sp. VSC12	5/18	ns	3/0	ns	8/11	ns	8/14	ns
	Cryptochironomus griseidorsum Kieffer	3/9	ns	12/38	ns	0/22	**	31/57	ns
	Demicryptochironomus sp. nov. V14	5/0	ns	3/0	ns	-/-	-	8/0	ns
	Dicrotendipes sp.	-/-	-	3/0	ns	0/22	**	0/14	*
	Dicrotendipes sp. V47	3/45	***	38/13	ns	8/22	ns	42/43	ns
	Harrisius nr *montanus* (Skuse)	5/0	ns	12/0	ns	13/0	ns	14/0	ns
	Harrisius sp. V40	-/-	-	-/-	-	3/0	ns	-/-	-
	Kiefferulus intertinctus Skuse	-/-	-	3/13	ns	0/11	*	0/14	*
	Nilothauma sp. V21	8/0	ns	-/-	-	-/-	-	6/0	ns
	Paracladopelma sp. VCD10	24/0	ns	21/13	ns	23/0	ns	17/29	ns
	Polypedilum nubifer (Skuse)	0/9	ns	0/50	***	0/11	*	0/57	***
	Polypedilum sp. MRHI-C7	5/0	ns	3/0	ns	8/0	ns	3/0	ns
	Polypedilum sp. MRHI-P1	3/9	ns	-/-	-	0/11	*	-/-	-
	Polypedilum sp. V3	37/36	ns	44/0	*	41/11	ns	47/29	ns
	Polypedilum sp. V33	61/0	***	32/0	ns	56/33	ns	47/14	ns
	Rheotanytarsus ?*underwoodi* Glover	42/18	ns	32/13	ns	28/0	ns	39/0	*
	Riethia sp. nov.V4	53/0	**	62/13	*	51/0	**	53/14	ns
	Riethia sp. nov.V5	16/0	ns	21/0	ns	31/0	ns	22/0	ns
	Stempellina ?*australiensis* Freeman	21/0	ns	15/0	ns	18/0	ns	36/0	ns
	Stenochironomus ?*anomalus* Freeman	-/-	-	-/-	-	-/-	-	3/0	ns
	? *Stictochironomus* sp. MRHI-C8	5/0	ns	6/0	ns	5/0	ns	8/0	ns
	Tanytarsini ?genus ?sp.V13	16/0	ns	6/0	ns	3/0	ns	6/0	ns
	Tanytarsus spp.	71/64	ns	68/75	ns	87/89	ns	83/86	ns
Orthocladiinae									
	Austrobrillia longipes Freeman	3/0	ns	-/-	-	-/-	-	-/-	-
	Botryocladius bibulmun (in press)	32/0	*	18/0	ns	33/0	*	19/14	ns
	Botryocladius freemani (in press)	5/0	ns	-/-	-	5/0	ns	-/-	-
	?*Chaetocladius* sp. VSC9	11/0	ns	-/-	-	-/-	-	3/0	ns
	Cricotopus ?*albitibia* (Walker)	-/-	-	-/-	-	-/-	-	0/14	*
	Cricotopus annuliventris (Skuse)	29/64	*	26/13	ns	31/56	ns	22/14	ns
	Nanocladius sp. MRHI-O1	8/0	ns	-/-	-	-/-	-	-/-	-
	Orthocladiinae ?genus /sp. MRHI-O2	0/9	ns	3/0	ns	0/11	*	-/-	-
	Orthocladiinae ?genus ?sp. V15	-/-	-	6/0	ns	-/-	-	6/0	ns
	Orthocladiinae ?genus ?sp. V44	-/-	-	-/-	-	-/-	-	3/0	ns
	Orthocladiinae ?genus ?sp. VND1	5/0	ns	-/-	-	5/0	ns	-/-	-

Table 3. *contd*.

Sub-family	Species	Trip 1 Ref/Impact		Trip 2 Ref/Impact		Trip 3 Ref/Impact		Trip Ref/Impact	
		(38/11)	p	(34/8)	p	(39/9)	p	(36/7)	p
	?Par*alimnophyes pullulus* (Skuse)	3/18	ns	21/0	ns	10/22	ns	14/0	ns
	?*Paralimnophyes* sp. V31	16/0	ns	6/0	ns	31/0	ns	11/0	ns
	Stictocladius sp. V70	-/-	-	3/0	ns	3/0	ns	6/0	ns
	Stictocladius uniserialis Freeman	32/0	*	18/0	ns	33/0	*	31/0	ns
	genus nr *Stictocladius* sp. V35	-/-	-	-/-	-	3/0	ns	-/-	-
	Thienemanniella sp. V19	42/45	ns	18/0	ns	67/56	ns	25/14	ns
Tanypodinae									
	Ablabesmyia sp. MRHI-TA8	-/-	-	0/13	*	-/-	-	-/-	-
	Ablabesmyia sp. V37	24/0	ns	15/0	ns	13/0	ns	6/0	ns
	Alotanypus dalyupensis Freeman	-/-	-	3/13	ns	-/-	-	-/-	-
	Apsectrotanypus ?*maculosus* Freeman	26/0	*	24/0	ns	15/0	ns	22/0	ns
	Larsia ?*albiceps* Johannsen	-/-	-	3/0	ns	-/-	-	3/0	ns
	Paramerina levidensis (Skuse)	21/18	ns	41/13	ns	56/22	ns	58/43	ns
	Pentaneura sp. nov. V10	13/0	ns	3/0	ns	18/0	ns	8/0	ns
	Pentaneurini ?genus ?sp. MRHI-TA1	11/0	ns	3/0	ns	5/0	ns	-/-	-
	Pentaneurini ?genus ?sp. MRHI-TA7	3/0	ns	-/-	-	3/0	ns	-/-	-
	Procladius paludicola Skuse	0/36	***	24/75	**	5/33	*	31/100	**
	Procladius villosimanus Kieffer	0/9	ns	-/-	-	3/11	ns	0/14	*
	Tanypodinae ?genus ?sp. MRHI-TA3	3/0	ns	3/0	ns	0/11	*	3/0	ns
	?*Zavrelimyia* sp. V20	13/0	ns	12/0	ns	3/0	ns	14/0	ns

adopted for data collection in the field, where family data were recorded as presence/absence, it was not possible to quantify Chironomidae at the species level. This restricted the possible analyses. Changes in the abundance of some species of Chironomidae were obvious during live-picking. For instance, *Chironomus* aff. *alternans* and *Procladius paludicola* were present at most sites (see Table 3), but were super-abundant at Impact sites. If these data were available, it is likely that the Chironomidae would have indicated even greater between-site differences than reported here.

MF data readily separated Impact/Saline sites from Reference sites in ordinations. This may have been because impacts were severe enough to cause the loss of families from some sites. The loss of entire families is more likely in south-western Australia because historically, biogeographic isolation on a geological time scale has resulted in a reduced diversity in the aquatic invertebrate fauna (BUNN & DAVIES, 1990), and many families now are represented by few species. Within these families, the likelihood of tolerant species replacing less tolerant species would be reduced. The same would not be so for eastern Australia, where most families are represented by many taxa. For example, in the Gripopterygidae, which disappear from Impact sites in the dry season, there are only three species in south-western Australia compared to at least 19 species in eastern Australia. Likewise, for the Baetidae two species contrasts to eight species and for the Leptophlebiidae four species contrasts to at least 19 species, between south-western and eastern Australia (BUNN & DAVIES, 1990).

This study agrees with the suggestion of SMITH et al. (1998) that the AUSRIVAS models detect severe but not subtle impacts. This is a concern since it is important that the models detect early changes in the ecological integrity of streams and rivers so that water resource managers can instigate remedial action. The study also indicates that the use of chironomid species data (and by inference species level identifications for all families), improves the discrimination between Reference and Impact sites. BARTON (1996) showed that using Chironomidae at the lowest practical taxonomic

Table 4. Chi-square contingency table analysis of differences in occurrence of each family of Macroinvertebrate between Reference and Impact sites for each trip. Values in parentheses are the number of samples in each group (Reference and Impact); values alongside each taxa are the percent of Reference/Impact sites at which each species was recorded; P values indicate Chi-square significance (ns, not significant; *P < 0.05; **P < 0.01; ***P < 0.001).

Family	Trip 1		Trip 2		Trip 3		Trip 4	
	Ref/Impact		Ref/Impact		Ref/Impact		Ref/Impact	
	(38/11)	p	(34/8)	p	(39/9)	p	(36/7)	p
Aeshnidae	37/9	ns	6/0	ns	38/22	ns	19/0	ns
Ancylidae	-/-	-	6/0	ns	3/0	ns	3/0	ns
Aphroteniinae	18/0	ns	6/0	ns	33/0	*	6/0	ns
Athericidae	11/0	ns	12/0	ns	13/0	ns	11/0	ns
Atriplectididae	5/0	ns	-/-	-	3/0	ns	-/-	-
Baetidae	16/0	ns	12/0	ns	13/0	ns	3/14	ns
Caenidae	34/45	ns	21/50	ns	36/56	ns	42/57	ns
Corydalidae	3/0	ns	3/0	ns	3/0	ns	3/0	ns
Ceinidae	11/73	***	9/38	*	15/89	***	11/57	**
Ceratapogonidae	71/45	ns	41/63	ns	85/56	ns	64/86	ns
Chironomini	100/91	ns	100/100	ns	97/100	ns	97/100	ns
Coenagrionidae	-/-	-	0/25	**	-/-	-	-/-	-
Corduliidae	18/0	ns	32/13	ns	23/11	ns	39/43	ns
Corixidae	0/9	ns	12/75	***	3/33	**	8/57	**
Culicidae	0/9	ns	9/13	ns	3/11	ns	6/0	ns
Curculionidae	3/0	ns	-/-	-	-/-	-	-/-	-
Dugesiidae	0/18	**	0/13	*	0/11	*	-/-	-
Dytiscidae	29/27	ns	56/50	ns	38/56	ns	69/57	ns
Ecnomidae	32/36	ns	29/50	ns	36/44	ns	31/57	ns
Empididae	21/9	ns	9/0	ns	8/0	ns	11/0	ns
Ephydridae	-/-	-	0/13	*	-/-	-	3/0	ns
Erpobdellidae	-/-	-	0/13	*	-/-	-	-/-	-
Gomphidae	8/18	ns	6/38	*	5/11	ns	8/43	*
Gordiidae	3/0	ns	-/-	-	3/0	ns	3/0	ns
Glossiphoniidae	-/-	-	-/-	-	0/11	*	-/-	-
Gripopterygidae	71/18	**	12/0	ns	72/11	**	17/0	ns
Gyrinidae	-/-	-	-/-	-	-/-	-	6/14	ns
Heteroceridae	-/-	-	-/-	-	0/11	*	-/-	-
Hydrophilidae	0/9	ns	6/13	ns	0/11	*	0/29	**
Hydropsychidae	24/18	ns	24/0	ns	21/11	ns	19/14	ns
Hydroptilidae	5/9	ns	26/0	ns	5/11	ns	39/57	ns
Hydrobiosidae	8/9	ns	9/0	ns	10/0	ns	17/0	ns
Hydridae	-/-	-	-/-	-	0/11	*	-/-	-
Hyriidae	-/-	-	3/0	ns	3/0	ns	6/0	ns
Leptoceridae	74/9	***	62/63	ns	72/56	ns	75/57	ns
Lestidae	-/-	-	3/0	ns	3/0	ns	-/-	-
Leptophlebiidae	82/0	***	71/0	***	79/0	***	75/0	***
Lumbriculidae	-/-	-	3/25	*	-/-	-	-/-	-
Lymnaeidae	3/0	ns	-/-	-	-/-	-	-/-	-
Mesoveliidae	-/-	-	3/0	ns	-/-	-	-/-	-
Megapodagrionidae	18/0	ns	12/0	ns	18/0	ns	14/0	ns
Naididae	-/-	-	3/13	ns	-/-	-	-/-	-
Neoniphargidae	5/0	ns	-/-	-	-/-	-	6/0	ns
Notonectidae	-/-	-	0/50	***	-/-	-	0/14	*
Neurorthidae	-/-	-	3/0	ns	-/-	-	-/-	-
Orthocladiinae	89/73	ns	65/13	**	92/78	ns	72/14	**

Table 4. *contd*.

Family	Trip 1		Trip 2		Trip 3		Trip 4	
	Ref/Impact		Ref/Impact		Ref/Impact		Ref/Impact	
	(38/11)	p	(34/8)	p	(39/9)	p	(36/7)	p
Palamonidae	13/18	ns	12/63	**	8/11	ns	8/43	*
Perthiidae	79/9	***	53/13	*	79/22	**	47/14	ns
Phreatoicopsidae	-/-	-	-/-	-	3/0	ns	-/-	-
Phreatoicidae	-/-	-	-/-	-	3/0	ns	-/-	-
Physidae	-/-	-	-/-	-	-/-	-	0/14	ns
Planorbidae	0/18	**	0/50	***	0/11	*	3/0	ns
Philorheithridae	3/0	ns	-/-	-	-/-	-	-/-	-
Parastacidae	16/0	ns	26/25	ns	36/11	ns	14/43	ns
Psychodidae	3/0	ns	-/-	-	-/-	-	-/-	-
Pyralidae	-/-	-	3/13	ns	-/-	-	3/0	ns
Richardsonianidae	-/-	-	3/13	ns	-/-	-	3/14	ns
Scirtidae	3/0	ns	-/-	-	0/11	*	3/0	ns
Simuliidae	74/36	*	18/0	ns	64/56	ns	17/14	ns
Sisyridae	-/-	-	-/-	-	3/0	ns	-/-	-
Sphaeriidae	0/18	**	0/13	*	0/11	*	0/14	*
Spongillidae	3/0	ns	-/-	-	-/-	-	3/0	ns
Stratiomyidae	-/-	-	-/-	-	-/-	-	3/14	ns
Tabanidae	-/-	-	-/-	-	-/-	-	0/14	*
Tanypodinae	63/45	ns	74/75	ns	69/67	ns	75/100	ns
Temnocephalidea	5/0	ns	12/0	ns	18/0	ns	8/0	ns
Tipulidae	37/9	ns	18/0	ns	28/22	ns	17/0	ns
Tubificidae	-/-	-	21/38	ns	33/11	ns	-/-	-
Acarina	92/36	***	74/50	ns	82/22	***	86/71	ns
Diptera	-/-	-	-/-	-	3/0	ns	-/-	-
Nematoda	8/9	ns	3/13	ns	8/11	ns	17/43	ns
Nemertea	0/9	ns	-/-	-	-/-	-	-/-	-
Oligochaeta	87/82	ns	41/25	ns	56/67	ns	86/86	ns
Odonata	3/0	ns	-/-	-	-/-	-	-/-	-
Veliidae	-/-	-	12/0	ns	3/0	ns	28/43	ns

level, significantly increased (39.5%) the sensitivity of Percent Model Affinity (PMA) for assessing the relative impact of agriculture on aquatic invertebrate communities. The priority of the Australian NRHP is rapid, cost-effective biomonitoring, and incorporating species and abundance data for Chironomidae, or other dominant families such as Leptoceridae (Trichoptera) would certainly increase costs. However, if future revised family-based models are unable to detect subtle impacts (i.e. commit Type II errors – not detecting an impact when one exists sensu FAIRWEATHER 1991), greater taxonomic resolution may need to be considered.

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