

**WESTERN CAPE RIVER AND CATCHMENT
SIGNATURES**

DM Schael • JM King

WRC Report No. 1303/1/05



Water Research Commission



WESTERN CAPE RIVER AND CATCHMENT SIGNATURES

Report to the Water Research Commission

by

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WRC Report No. 1303/1/05
ISBN No.: 1-77005-372-7

OCTOBER 2005

This Report 1303/1/03 and CD are obtainable from:

Water Research Commission
Private Bag X03
Gezina
0031
Pretoria, South Africa

The Report and CD emanate from the Water Research Commission research project K5/1303: "The nature of catchment and river signatures, the affect on these of different disturbances, and the management implications"

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Executive Summary

Introduction

In a previous Water Research Commission Project (final report 754/1/01 "Assessing the ecological relevance of a spatially-nested geomorphological hierarchy for river management": King & Schael 2001) invertebrate data were collected from headwater reaches (mountain streams and foothills) of 17 relatively undisturbed (here called Least Disturbed or LD) sites and 11 disturbed (D) sites in the Western Cape, all sites being located within the Fynbos bioregion. In each site up to 12 invertebrate samples were taken from the full available range of hydraulic conditions (substratum-flow combinations), with ancillary physico-chemical data taken at the level of sampling area or site. A species list was compiled for each of the LD sites, from its set of invertebrate samples. These lists were used in multivariate similarity analyses to search for sites that were similar in terms of their invertebrate assemblages. The hypothesis put forward was that the sites would cluster by geomorphological/biological zones, that is, into a mountain-stream group of invertebrates and a foothill group. Instead, the sites clustered by catchment, with a second division by channel bed form (bedrock or alluvial). River zone only appeared at the third level of division. Within any one catchment, with the invertebrate samples dealt with individually instead of pooled, each sample clustered with others from its site and separate from those of other sites. These distinctions have been termed catchment and river signatures.

The possible implications of such signatures are wide: traditional management of South African rivers recognises all headwater systems within any one biome as being essentially the same. With this reasoning, some rivers could potentially be sacrificed to land and water developments with the knowledge that other similar rivers remained. The data from King & Schael (2001), however, suggested that this assumption may not be true and that all rivers may be different, in ways as yet not understood. The small follow-up project reported on here was thus designed to investigate the nature and causes of the river/catchment signatures, and to assess if there were management implications.

The study was a desktop one, confined to additional analyses of the database compiled in the original project (King & Schael 2001). A number of univariate and multivariate analyses were done to address the project objectives as listed below, investigating the nature of the species assemblages, their secondary environmental causes, and the effect of disturbance on catchment signatures as noted in King and Schael (2001).

Project Objectives

The project objectives, as agreed in the original contract between the University of Cape Town and the Water Research Commission are summarised below.

1. Explain the nature and proximal causes of catchment and river signatures.

2. Identify, if possible, the underlying causes of the catchment and river signatures.
3. Describe the link between various kinds of disturbance and the progressive loss of catchment and river signatures.
4. Reach consensus with other researchers on the management implications of the finding of Objectives 1 – 3, and transfer the conclusions to the management arena.
5. Assess the influence (if any) of the selection of sampling points within a site on SASS scores. Validate the present biomonitoring techniques, or suggest modifications if necessary to enhance standardised sampling.
6. Refine the database framework (MS Access program interface) for wide user-ship in scientific and technical management arenas; complete user interface for easy data access and additions.

These objectives have been addressed in full and are reported on in this document. Chapter 1 provides the background and impetus for the research. Objectives 1 – 3 are addressed in Chapters 2 – 5, and objective 5 in Chapter 6. Improvements to the database are reported in Chapter 7. Objective 4 was addressed through a workshop at the University of Cape Town attended by a select group of research scientists, which is reported in Chapter 8. Conclusions and recommendations appear in Chapter 9.

Are catchment signatures real or an artefact of the research? (Chapter 2)

The main objective of this chapter was to investigate whether the catchment signatures described by King & Schael (2001) were an artefact created either by the sampling regime or by the process used for identifying the invertebrates to species level. It was deemed possible that a bias in the results could have been brought about by the combinations of habitats sampled in each site: sites within any one catchment could have had a similar suite of available habitats and this could have resulted in their invertebrate samples grouping together. Alternatively, sites/catchments could have appeared more similar or dissimilar than they really were because their invertebrates had been identified by different staff. Several permutations of the data set were, therefore, analysed in an attempt to detect any possible bias. First, the habitat types were standardised for all LD sites by selecting only those habitats that were common to all sites. The invertebrate assemblages of these habitat types were re-analysed using hierarchical clustering, multi-dimensional scaling (MDS) plots and analysis of similarity (ANOSIM). Second, the same set of habitat-types was used, but their invertebrate samples were analysed using different combinations of taxonomic levels (species to family) and groups (e.g. only the mayflies), to detect any possible bias in the data. Through all these permutations of the data, the catchment signatures persisted. Only the Chironomidae (midges) displayed a weak catchment signature, reflecting their good dispersal abilities and their ubiquitous presence across the landscape. In summary, the catchment was shown to be the landscape feature that best explained invertebrate species distributions.

This conclusion supports the findings of Wishart *et al.* (2002), who reported that the genetic structure and flow of selected invertebrates and fish revealed that catchments in the Fynbos bioregions of the Western Cape were unique entities.

That study and this one identify catchment as an important large-scale unit with biological and ecological significance and, in fact, Wishart *et al.* (2002) regarded catchments as the best functional unit for conservation of instream biota.

What characteristics of the data set cause the catchment signatures (Chapter 3)

Investigation of the characteristics of the invertebrate data that produced catchment signatures revealed that there was no one over-riding cause. It was concluded that the signatures were not caused by unique species within each catchment, nor by a unique mix of taxa in each catchment, nor by unique proportions of the same set of taxa within each catchment. Instead, the signatures were caused by subtle changes of species within each major taxon group from catchment to catchment. As an example, of the 11 stonefly species collected in the study, three occurred only in the Eerste-Molenaars catchment group, one only in the Olifants-Berg group, and the Breede had a mixture of these species. Those stonefly species in the Eerste-Molenaars group were shredders, whilst those in the other two catchment groups were deposit feeders, suggesting fundamental differences in the ecological functioning of the sites. Of interest was the maintenance of the basic proportional presence of each major taxon group through all the species changes: in comparisons of the major catchment groups, for instance, the percentage of the taxa that were true flies held at 29-44%, whilst stoneflies always contributed 4-9%.

Of all the analyses, the only one that eradicated the catchment signatures was that using functional feeding groups (FFGs). In this analysis, species and morph species of each invertebrate taxon is replaced by the manner of feeding it employs. This resulted in the samples re-grouping in a way that coarsely reflected a split between mountain and foothill sites and thus reflected the more commonly held view that the main division of invertebrate assemblages is between the various longitudinal zones of the river. The two sets of results described above suggest that sites in each of the river zones (mountain or foothill) were functioning in a similar way, with the same proportions of the major invertebrate groups, even though the actual mix of species differed.

What effect does disturbance have on catchment signatures? (Chapter 4)

Although the original similarity analyses (King & Schael 2001) revealed that most disturbed (D) sites were distinctly different from the least-disturbed (LD) sites, the subsequent analyses in this project did not reveal a clear picture of what caused this. Most D sites had similar invertebrate densities, levels of diversity and species richness to the LD sites. Standard measures used to detect differences between reference (LD) sites and D sites, such as % ephemeropterans, plecopterans and trichopterans (EPT), number of families, % dipterans and % non-insects, also did not demonstrate statistical differences, although box plots did show small differences between the two.

Once again, subtle changes of species, rather than shifts in major taxonomic groups, distinguished D from LD sites, and the overall impression was that even though the D sites were

showing visual signs of disturbance, this was not sufficiently intense, except for one or two sites, to cause major changes in invertebrate assemblages. Thus, an array of disturbances, such as a picnic area, a dam with downstream water loss, agricultural land and a bull-dozed riverbed (Table 4.1), did not appear to be having a major affect on ecosystem functioning (as judged by invertebrate assemblages), whilst a dam with a bottom release of very cold water (Holsloot), and an infestation of grey poplar (*Cecilia*) appeared to be more intense disturbances causing the early stages of more substantial ecosystem change.

What are the underlying environmental factors causing the catchment signatures? (Chapter 5)

The shifts in species in LD sites from catchment to catchment must be caused by underlying environmental conditions. Possible environmental candidates are water chemistry, the presence or absence of fish, biogeographical influences such as temperature, topography and rainfall, or paleogeographical influences such as past drainage networks. These were assessed in terms of their possible contributions to catchment signatures. The main catchment signatures were caused by: 1) the Olifants and Berg River sites, which clustered together; 2) the Eerste and Molenaars Rivers sites, which clustered together; 3) the Breede River sites; 4) the Palmiet River site; and 5) the Table Mountain sites, which were in different small catchments but clustered together.

Water chemistry data from DWAF gauging weirs in all the studied catchments for which it was available revealed that regional water chemistry differences did not appear to be a possible cause of the catchment signatures.

Fish can have significant effects on invertebrate population structure and so data from CapeNature were used to search for possible correlations between the presence of native and alien fish and the catchment signatures. The tentative conclusions, based on few data, suggest that the presence of both native and alien fish plays some role in the catchment signatures, but other environmental variables are also implicated.

One such variable could be the geographical location of sites. The catchments stretch from the Olifants in the north, to the Palmiet in the south, and to the Table Mountain group in the south-west (Figure 5.3). The MDS plot of invertebrate assemblages from LD sites can be re-orientated to coincide with this geographical layout (Figure 5.4), suggesting that the catchment signatures may be at least partly attributable to biogeographical distribution patterns. Knowing that the signatures are caused by species replacing species within each major taxonomic group (Chapter 3), these replacements could be a result of some species reaching the edge of their distributional ranges and being replaced by others. On assessing individual taxa, however, some were shown to be confined to the north or south, or absent from Table Mountain, but the majority were either wide-spread across the region or scattered, and so again there was no clear picture of species distributions causing the catchment signatures.

Paleogeographically, the Olifants and Berg systems are thought to have once had a common estuary, and this may have caused their grouping together to provide one catchment signature.

Table Mountain was once an isolated island off mainland Africa, which may account for its studied rivers – though in different small catchments - sharing a common catchment signature. At present no suggestion can be made as to why the Molenaars sites clustered with the Eerste sites rather than with those from the Breede, which is its parent river. Much remains unknown and unexplained about the causes of the signatures and an exploration of “river capture” and past drainage networks is just one avenue of research that could be followed to shed further light on them.

In conclusion, despite some positive correlations and avenues revealed for further research, none of the analyses reported here provide proof of a single environmental driver for the catchment signatures. Rather, the signatures appear to be the result of complex interactions of many variables over long geological time.

The effect of sampling point selection and identification on SASS scores (Chapter 6)

The data used in this study were not collected using SASS techniques. They were used, however, to assess if the choice of sampling points for a SASS collection could affect the resulting SASS score. Different permutations of sampling points had little impact on the outcome in terms of computed scores, producing essentially the same results as those of Dallas (2001) and fairly similar to Dickens & Graham (2002).

A further outcome of this analysis was the demonstration that a SASS score does not detect physical degradation of a river, and indeed was not designed to do so, being designed to assess pollution levels. Researchers should therefore avoid using SASS as an index of river health in terms of physical disturbance.

Catchment and river signatures workshop (Chapter 8)

A workshop was held at the University of Cape Town with the delegates being a mix of scientists and managers. The presenters represented different disciplines in river science: invertebrates, fish, riparian vegetation and conservation planning. Each came with their own data sets and suggestions on the nature of catchment and/or river signatures, resulting in a range of ideas on what caused them. The invertebrate and fish specialists found signatures in biotic data, the vegetation specialists in a combination of biotic and physical data (species, geology, soils) and the conservation specialist in purely physical data. It was concluded that biotic river and catchment signatures do exist and reflect biodiversity at the landscape level, but there was no clarity on how they form and what they indicate about the functioning of individual catchments.

It was agreed that catchment/river signatures do have management implications, especially in the Reserve Determination process within South Africa's current water law. Managers need further clarity, however, on the validity of these signatures across disciplines and for the rest of South Africa. Although it is recognised that further research is needed to confirm the nature, validity and importance of signatures, it was recommended that catchments be better integrated into

classifications of rivers at the second hierarchical level, after ecoregions but before longitudinal zones.

In summary, the main conclusions and recommendations from the workshop are as follows.

- River and catchment signatures appear to reflect biodiversity at the catchment/landscape level.
- Catchments should be represented in river classification systems at a high level – after ecoregion but before longitudinal zone.
- Conservation targets need to be addressed per catchment, with more than one river conserved per catchment.
- Integration of investigations on signatures should occur across disciplines. This could be done via a collaborative proposal that used both historical and new field data for a series of common study sites.
- Catchment and river signatures need to be validated for other parts of the country and for lower rivers. This may require collection of new data combined with analysis of historical species data.

General conclusions (Chapter 9)

River and catchment signatures are real. As shown in this project, they are biotic fingerprints of upper rivers and catchments in the Western Cape, distinguishing each from the others. There is no reason to believe they do not exist in other parts of South Africa and, indeed, elsewhere although this remains to be shown. Lower rivers may also have biotic signatures, but as a majority of lower rivers are considerably degraded the data of natural conditions needed to detect the signatures may be largely missing.

We now know that the signatures are due to unique mixes of species per river and catchment from a regional pool of mostly common species, but still have very little understanding of what caused the specific mixes and what their significance is. The signatures do not appear to be strongly correlated with water chemistry, the presence or absence of native or alien fish, systematic biogeographic species changes across the region or paleogeographic influences, although all of these seem to play some role. Rather the signatures are probably the result of complex interactions of the above and other variables over many millions of years.

Many questions thus remain unanswered to a large degree because we do not have sufficient understanding of the biology and habitat requirements of riverine species to attempt further interpretation of the signatures data set. Some additional insights have emerged however.

- Perennial rivers have more stable aquatic communities than non-perennial ones and therefore may be expected to have much clearer signatures. This would make them more amenable to assessment of whether or not human disturbance is affecting them.
- Alien fauna and flora appear to be breaking down the biotic signatures, homogenising at least fish and plant communities and presumably reducing biodiversity.

- Rivers appear to have abiotic signatures too: their complex mix of geomorphological, hydrological, chemical and thermal attributes may be of use to distinguish them from each other. The question of whether or not these abiotic signatures are good surrogates for the biotic ones lies at the heart of the national planning to conserve freshwater biodiversity.

The main management implications of river and catchment signatures are as follows.

- It cannot be assumed that all rivers within an ecoregion are much the same and thus that a random selection of them can be sacrificed to development with no implications for biodiversity. Biodiversity could be being reduced at the community/landscape level through catchments not being recognised as unique entities.
- More than one river within each catchment needs to be conserved at a very low level of disturbance so that further research on signatures and its links to biodiversity has access to replicate study sites.
- The signatures could be used to detect very early levels of degradation of sensitive or important river systems, as it will detect change earlier than standard techniques such as %EPT or SASS scores.
- With further data collection, the signatures could be used to grade and compare different kinds of disturbance on a scale from negligible impact to very severe impact.

Recommendations (Chapter 9)

Recommendations for future work and consideration are as follows.

- The catchment should be high in the hierarchical levels of river classification for biodiversity management – higher than longitudinal zone – because rivers within one bioregion or ecoregion are not all the same. Individual catchments within any one ecoregion, bioregion, geomorphological region or hydrological region (whichever is being used to partition the country) need to be represented in any system of conserved rivers.
- There should be more than one completely undisturbed river in each catchment so that biodiversity is conserved at the community/landscape level and so that future research on signatures and its links to biodiversity has access to replicate sites per catchment.
- Historical records of biotic distributions (such as those at the Albany Museum) should be used to confirm that river and catchment signatures exist in other parts of the country.
- The validity of signatures across disciplines should be researched through a multidisciplinary research programme. The catchment should be high in the hierarchical levels of river classification for biodiversity using shared study sites. This would strengthen understanding of their nature and possibly their causes.
- Full understanding of why catchments and rivers are biologically distinct will not be possible without a deeper understanding of the biology of riverine species. Such research should become an essential component of all relevant research and consultancy work at an appropriate level of commitment.

Acknowledgments

The research in this report emanated from a project funded by the Water Research Commission and entitled:

THE NATURE OF CATCHMENT AND RIVER SIGNATURES, THE AFFECT ON THESE OF DIFFERENT DISTURBANCES, AND THE MANAGEMENT IMPLICATIONS.

The Steering Committee responsible for this project consisted of the following persons:

Dr SA Mitchell	Water Research Commission (Chairman)
Mr ND Impson	CapeNature
Ms C Thirion	RQS, Department of Water Affairs and Forestry
Prof CG Palmer	Institute for Water Research, Rhodes University
Dr HF Dallas	Freshwater Consulting Group
Dr HL Malan	Freshwater Research Unit, University of Cape Town
Mr B Hohls	RQS, Department of Water Affairs and Forestry

Their advice and guidance are gratefully acknowledged.

Sincere thanks to the following people for their help with data manipulation and entry: Barry Donohue, Silke Bollmohr, Ayanda Ntalo and Tammy Robinson. The database consultant for the design of the query centre and modification of data entry program was Corné Stoltz. The Department of Water Affairs and Forestry, RQS directorate, is thanked for providing the water chemistry data from their sampling sites within our study area. Dean Impson of CapeNature supplied the alien fish presence/absence data related to the study sites.

The Freshwater Research Unit, Zoology Department, University of Cape Town (UCT) provided office and support facilities for the duration of the project. Its members are thanked for their interest, support and fruitful discussions. Additionally, the Department of Botany at the University of Port Elizabeth offered the same support to Ms Schael throughout the project.

Professor John Field of the Zoology Department, UCT, discussed various aspects of the work with us during the course of the analyses, and read the complete draft of this report, providing much valued feedback. We are deeply grateful for his input. Also, sincere thanks to Professor George Branch, also of the Zoology Department, for discussion on aspects of the data analysis, and to Prof de Wit, Geological Sciences Department, UCT, who told us of the past history of the Klein Berg River, as a part of the Breede system. This instance of river capture might yield interesting data in the future on the persistence of catchment signatures in invertebrate community structure when a river becomes part of a different system.

The Water Research Commission is thanked for its financial and other support of this project. In particular we would like to thank our project manager, Dr Steve Mitchell, for his continuing support and guidance.

Capacity Building

The objective of this short-term project was to complete further analyses of an existing data set, and it was thus not particularly suited for extensive capacity building. Attempts were made to include post-graduates and under-graduates in various analytical tasks, but the response and interest was poor, and those who did become involved did not have the background to do advanced analyses so the project staff eventually had to complete this work themselves. Nevertheless, four post-graduate students did receive some training in data entry, data manipulation, databases and spreadsheets, as follows:

Barry Donohue (UCT)
Silke Bollmohr (UCT)
Tammy Robinson (UCT)
Ayanda Ntalo (UPE)

There were two more substantial contributions to capacity building. The first was via a PhD thesis by one of the project staff, Ms Denise Schael. This is titled *Distributions of physical habitats and benthic macro-invertebrates in Western Cape headwater streams at multiple spatial and temporal scales*. The thesis was submitted in August 2005 and passed as of November 2005.

The other major contribution was through a workshop held on 28 February 2005, titled *Western Cape river and catchment signatures: what are they and are there management implications?* A range of river scientists, covering the disciplines aquatic invertebrates, fish and riparian vegetation, made presentations of data sets they have that seem to suggest river and catchment signatures. This was followed by a structured half-day discussion addressing the two main topics in the workshop title. In total, eight people presented data sets and a total of 18 attended the workshop. The workshop report appears as Chapter 8 in the Final Report of Project K5/1303.

Technology Transfer

- The workshop described above.
- DMS presented a paper at SASAQs /ZSSA: Schael, D.M. and King, J. 2003. Catchment signatures: is every river different? Joint Conference of the Southern African Society of Aquatic Sciences and Zoology Society of Southern Africa, 30 June – 4 July 2003, Cape Town, South Africa. DMS received best student oral presentation award.

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List of Terms and Acronyms

<u>Term</u>	<u>Definition/Explanation</u>
ANOSIM	Analysis of similarity; a multivariate analysis to test if different groups are significantly different in terms of species composition; a name for the analysis module in the PRIMER package module.
ANOVA	Analysis of variance; univariate statistical analysis to test for significant difference between groups.
BIOENV	PRIMER module that matches biotic and environmental patterns.
Chironomidae	A family of non-biting midges.
CLUSTER	Hierarchical agglomerative clustering module in PRIMER.
Coleoptera	beetles
D	Disturbed river
Diptera	flies, midges and mosquitoes
DISCRIM	Reduced list of invertebrate species that were determined from a SIMPER analysis that were the top discriminating species between catchments and used in subsequent analyses.
DWAF	Department of Water Affairs and Forestry
Ephemeroptera	mayflies
EPT	Ephemeroptera, Plecoptera and Trichoptera
FFG	Functional feeding group
Flow Types	Visual assessment of what different flows look like; Appendix 1.A gives list and definitions.
Fr	Froude number, a dimensionless number which integrates mean water column flow and depth.
Hemiptera	true bugs
LD	Least-disturbed river
Lepidoptera	aquatic caterpillars
MDS	Non-metric multidimensional scaling; a module in PRIMER
Megaloptera	dobsonflies
NB	Near-bed current velocity; flow measured as near to the substratum as possible
Odonata	dragonflies and damselflies
Plecoptera	stoneflies
PRIMER	Plymouth Routines in Multivariate Ecological Research; a multivariate statistical package; Clarke & Warwick (1994)
RQS	Resource Quality Services directorate within DWAF
SASS	South African Scoring System; biomonitoring technique to detect water quality of rivers using macroinvertebrates
SIMPER	Similarity percentage; a module in PRIMER that examines the contribution of individual species to the similarity measure
Simuliidae	a family of black flies

<u>Term</u>	<u>Definition/Explanation</u>
Substratum Types	Visual assessment of substratum types by size categories; Appendix 1.B gives the list and definitions
Trichoptera	caddisflies
WRC	Water Research Commission
Hydracarina	water mites

1. INTRODUCTION

In a recent study of the ecological relevance of a geomorphological scheme for river classification (King & Schael 2001), the data collected on aquatic invertebrates showed that each catchment and river had a distinct species assemblage. The invertebrates were collected from headwater reaches (mountain streams and foothills) of 17 relatively undisturbed (here called Least Disturbed or LD) rivers and 11 disturbed (D) rivers in the Western Cape (Table 1.1). All of the sites are located within the Fynbos bioregion of the Western Cape (Figure 1.1). In each site up to 12 invertebrate samples were taken from the full range of hydraulic conditions (substratum-flow combinations) available, with ancillary physico-chemical data taken at the level of sampling area or site (Table 1.2). A species list was compiled for each of the LD sites, from its set of invertebrate samples. These lists were used in multivariate similarity analyses to search for sites that were similar in terms of their invertebrate assemblages. It had been expected that the sites would cluster by geomorphological/biological zones, that is, into a mountain-stream group of invertebrates and a foothill group. Instead, the sites clustered by catchment, with a second division by substratum (bedrock or alluvial), and river zone only appearing at the third level of division (Figure 10.4; King & Schael 2001). Within any one catchment, with the invertebrate samples dealt with individually instead of pooled, each sample clustered with others from its site and separate from those of other sites. These distinctions have been termed catchment and river signatures.

The possible implications of such signatures are wide: traditional management of South African rivers recognises all headwater systems within any one biome as being essentially the same. With this reasoning, some rivers could potentially be sacrificed to land and water developments with the knowledge that other similar rivers remained. The data from King & Schael (2001), however, suggested that this assumption may not be true and that all rivers may be different, in ways as yet not understood.

This small follow-up project was therefore approved by the Water Research Commission, to further investigate the nature and causes of the river/catchment signatures. The study was a desktop one, confined to additional analyses of the database compiled in the original project. It focussed on the following main investigations.

The signatures could have one or more direct causes. They could be:

- artefacts of the collecting and analytical techniques;
- real, and due to some characteristic of the species data, possibly:
 - unique species in each catchment/river;
 - unique combinations from a common pool of species;
 - unique proportions of the same or different sets of species.

Outside the actual distribution of species, the signatures must also have one or more indirect causes. The environmental drivers could be:

- biogeographical;
- geochemical;
- other.

Another finding of the original project was that disturbance affected the catchment (and possibly river) signatures: D rivers, chosen to represent a range of different disturbances, had lost their catchment signatures to varying degrees depending on the type of disturbance they were experiencing. A further investigation involving D rivers thus focused on the following:

- the impact of disturbance on the characteristic species assemblage of a catchment;
- if different kinds of disturbances change species assemblages in different ways;
- the potential for using any trends to help prediction of the impact on rivers of different kinds of disturbance.

Table 1.1. River sites studied between November 1996 and February 1998. The biological zone was determined from 1:50 000 maps prior to visiting each site, using the altitude and gradient guidelines of Brown *et al.* (1996). The catchment each site is located in is given; the sites designated Table Mtn are each in different small catchments, but located on Table Mountain. The contribution to particular analysis goals is listed under "Purpose". Modified from King & Schael (2001).

River #	River Name	Catchment	Zone	Date	Latitude	Longitude	Purpose
1	Jan Dissels	Olifants	Foothill	6-Mar-97	32 13 38	18 59 24	Reference Condition
2	Rondegat	Olifants	Foothill	5-Mar-97	32 22 08	19 03 06	Reference Condition
3	Noordhoek	Olifants	Foothill	4-Feb-98	32 40 13	19 04 09	Disturbance: bulldozing
4	Middeldeer	Olifants	Foothill	5-Feb-98	32 41 06	19 16 48	Disturbance: agriculture
5	Grootrivier	Olifants	Foothill	4-Mar-97	32 38 39	19 24 35	Disturbance: agric / road
6	Steenbok	Brede	Mountain	26-Feb-97	33 32 57	19 08 37	Reference Condition
7	Wolwekloof	Brede	Mountain	12-Mar-97	33 33 45	19 07 45	Reference Condition
8	Wit	Brede	Foothill	25-Feb-97	33 39 05	19 06 29	Reference Condition
9	Molenaars	Molenaars	Foothill	22-Jan-97	33 43 50	19 07 00	Reference Condition
10	Elands	Molenaars	Mountain	13-Feb-97	33 44 02	19 06 58	Reference Condition
11	Elandspad	Molenaars	Mountain	24-Jan-97	33 45 39	19 10 09	Reference Condition
12	Holsloot	Brede	Foothill	30-Jan-98	33 50 09	19 15 11	Disturbance: Dam
13	Du Toits	Brede	Mountain	18-Mar-97	33 56 13	19 10 10	Reference Condition
14	Bakkerskloof	Berg	Mountain	20-Feb-97	33 49 13	19 02 48	Reference Condition
15	Zachanashoek	Berg	Mountain	21-Feb-97	33 49 39	19 02 13	Reference Condition
16	Wemmershoek	Berg	Foothill	22-Jan-98	33 51 11	19 02 29	Disturbance: Dam
17	Berg	Berg	Foothill	19-Feb-97	33 58 24	19 04 38	Interbasin transfer
18	Eerste 1	Eerste	Mountain	15-Jan-97	33 59 37	18 58 37	Reference Condition
19	Langrivier	Eerste	Mountain	17-Jan-97	33 59 16	18 58 02	Reference Condition
20	Swartboskloof	Eerste	Mountain	13-Jan-97	33 59 18	18 57 25	Reference Condition
22	Lourens	Lourens	Foothill	20-Jan-98	34 04 00	18 54 01	Disturbance: agriculture
23	Palmiet	Palmiet	Mountain	12-Feb-98	34 06 20	19 03 17	Disturbance: dam/ weir
24	Dwars	Palmiet	Mountain	3-Feb-97	34 17 09	18 56 11	Reference Condition
25	Davidskraal	Davidskraal	Foothill	29-Jan-97	34 20 50	18 55 17	Disturbance: weir/ dam/ retaining walls
26	Window	Table Mtn	Mountain	20-Nov-96	33 59 06	18 26 08	Disturbance: botanical garden
27	Newlands	Table Mtn	Mountain	13-Dec-96	33 58 03	18 26 40	Reference Condition
28	Cecilia Ravine	Table Mtn	Mountain	8-Jan-98	33 59 48	18 25 11	Disturbance: alien trees
29	Disa	Table Mtn	Mountain	15-Jan-98	34 00 25	18 23 31	Reference Condition

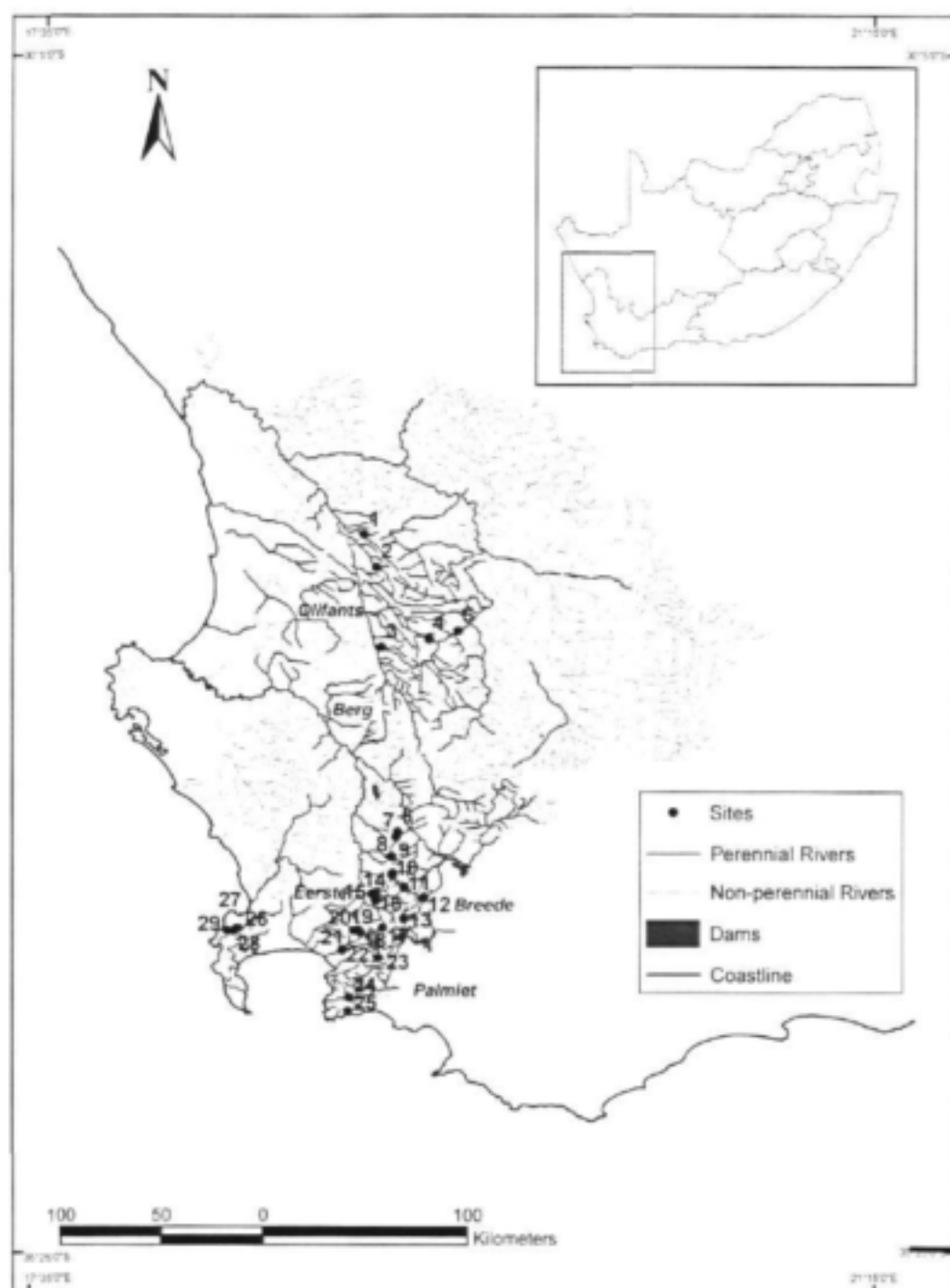


Figure 1.1 Map of the study sites in the Western Cape, South Africa.

Table 1.2 Summary of data collection methods. Details are in King & Schael (2001).

Data Type	Description
Flow and substrata mapping	Each site was delineated with tapes and substrata and flow types mapped (definitions and codes for substrata types and flow types in Appendix 1).
Invertebrate collection	All available flow-substratum combinations (hydraulic habitats) identified, and invertebrates collected from a sub-set of each. Kick and hand nets with 250µm-mesh used for different hydraulic habitats as appropriate, standardised to 2 – 3 minutes sampling at each. Invertebrate samples fixed and preserved in 4% formalin, and later transferred to 70% EtOH for storage.
Sample area hydraulic measurements	Depth, near-bed velocity and 0.6 velocity measured at 2 – 6 points within each sampled hydraulic habitat. Froude number calculated from depth and 0.6 velocity.
Sample area physical data	Flow-type and substrata (dominant and sub-dominant, degree of embeddedness) for each sampling area recorded.
Discharge measurements	One discharge transect at each site. 0.6 velocity measured at a minimum of ten points on each transect.
Site-level chemical parameters	Spot measurement of temperature, conductivity, pH and water colour at one spot per site.
Site-level physical assessment	Percent canopy cover, riparian vegetation type, submergent and emergent aquatic plant cover, moss cover and local channel features.
Invertebrate laboratory processing	Samples macro-sorted (by eye) for 1 hr, micro-sorted (with microscope) for 1 hr. All taxa identified to lowest practical level – usually species or morph-species. Specialists used for type-specimen or taxonomic group identification, and best resolution for ID (Appendix 2). Three different technical staff identified the invertebrates, with the bulk being done by the senior author of this report.

Reports on investigations of the above data form the bulk of this report. Chapter 2 summarises an assessment of whether or not the signatures were an artefact of the scientific techniques used. It was concluded that the signatures are real. Chapter 3 details analyses of the faunal data then undertaken to explain the catchment signatures. In Chapter 4, the effects of disturbance on catchment signatures are described. Chapter 5 addresses investigations of possible underlying environmental causes of the signatures. Three small additional tasks are also reported on. The influence of sampling point on SASS-type (South African Scoring System – Dickens & Graham 2002) scores (Chapter 6); further development of the database, to make it accessible to other users (Chapter 7); and report of a workshop designed to assess the possible wider occurrence, and implications, of catchment and river signatures (Chapter 8).

2. CATCHMENT SIGNATURES – REAL OR ARTEFACTS?

2.1 Introduction

Because of the nature of insect dispersal (Minshall 1984; Downes *et al.* 2000; Wishart *et al.* 2002), invertebrate assemblages from rivers within a catchment might be expected to be more similar to each other than to those from rivers from other catchments. Some degree of similarity might also be expected, however, from sites across any one longitudinal river zone within a biome (e.g. mountain streams in the fynbos biome) as temperature, altitude and habitat availability are known to influence invertebrate community structure (Hynes 1970; Southwood 1977; Minshall 1984; Hawkins *et al.* 1993; D'Angelo *et al.* 1997; Poff 1996; Townsend *et al.* 1997). In the King & Schael (2001) study, however, catchment was found to be more important than river zone in defining the nature of the invertebrate assemblage: samples from different zones of LD rivers within one catchment were more similar than were samples from the same zone across several catchments (Figure 2.1). In three cases, samples from two catchments grouped together (Olifants-Berg, Eerste-Molenaars, and Table Mountain) but the pattern remained clear: samples were grouping by catchments rather than by longitudinal river zone. The only exception to the catchment grouping was the Berg River site (B17), which grouped with the Breede sites. This site is about 1 km upstream from an inter-basin transfer scheme that brings in water from the Breede catchment, and this appears to be influencing community composition in the receiving river. In subsequent chapters of this report the Berg River is grouped with the D rivers.

The objective of the research reported in this chapter was to ascertain whether or not the catchment signatures were artefacts of either the sampling strategy or the process of identification of the invertebrates. The sampling strategy could have biased the results if different kinds of habitats were more common (and therefore more likely to be sampled) in some catchments than others. The identification process could have influenced results because a number of technical staff contributed to the invertebrate identifications.

2.2 The nature of the data sets

A summary of the data-collection methods is given in Table 1.2 and details are in King & Schael (2001). Relevant points are summarised here.

Invertebrates were collected in a stratified random approach from the 18 LD sites as originally described in King & Schael (2001). The bulk of this report recognises 17 LD sites as the Berg site was removed to the D group, but in this chapter the original 18 are used. At each site the sampling points were randomly chosen, whilst ensuring that a wide range of available flow and substrata combinations were represented. Identifications were made by project staff to the lowest practical level for each taxonomic group, with some groups checked by specialist taxonomists. Where technical assistants made preliminary identifications, these were checked, coordinated and standardised to minimise discrepancies within the data. Since sampling was not quantitative, counts could not be treated as invertebrate densities but could be used in semi-quantitative

analyses by converting them to ratings of abundance, these abundances were then used in the analyses as untransformed ratings (Table 2.1). As the sampling effort at each point had been standardised by time the abundance ratings for different sites and habitats could be compared.

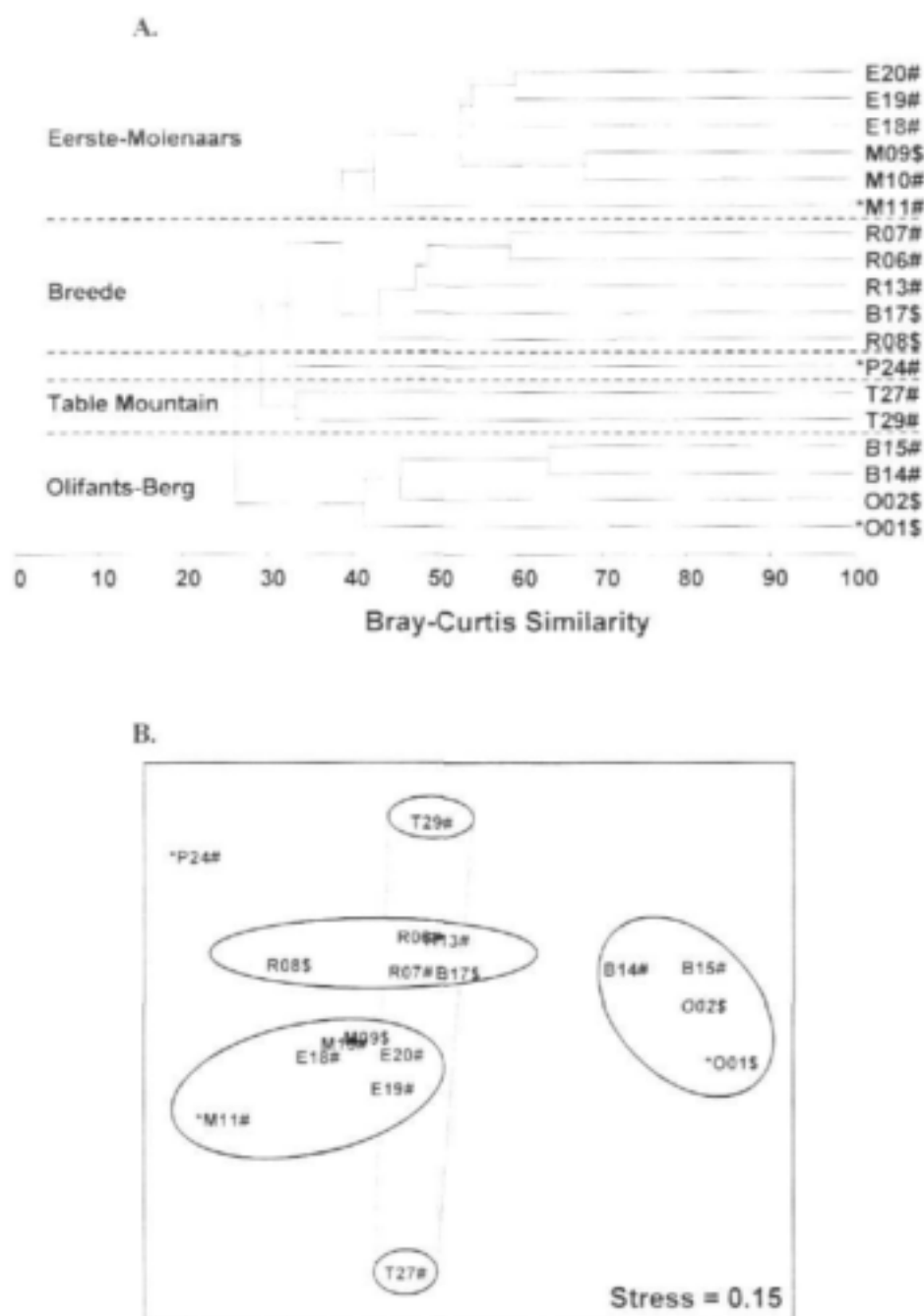


Figure 2.1 A. Dendrogram of the 18 sites (as in King & Schael 2001) on LD rivers, using species-level invertebrate untransformed abundance rating data derived from up to twelve samples from each site. B. 2-d MDS plot, with the main groups delineated in the dendrogram separated by circles. # = site pre-identified as in the mountain zone and \$ as site in the foothill zone, as per Table 1.1. * = site with bedrock as the dominant substratum (modified from Figure 10.4: King & Schael 2001).

Table 2.1 Abundance ratings for the invertebrate taxa. From Table 10.1 in King & Schael (2001).

Rating	Numbers of animals per taxon per site
1	1
2	2 – 6
3	7 – 20
4	21 – 100
5	>100

2.3 Testing for a possible habitat bias

Creating the data sub-sets

A standard set of hydraulic biotopes was not sampled at each of the 18 LD rivers, because the nature of the substratum-flow combinations differed to some extent from site to site. This could have led to bias in the resulting invertebrate data, through sites within any one catchment possibly tending to have the same kind of bed and flows. This first series of analyses, then, was designed to assess if such a bias existed in the data.

Initially, the overall number of samples used to represent each site was reduced, from the original 216 linked sets of invertebrate and hydraulic-habitat data to a standardised sub-set for each site based on defined hydraulic criteria (Table 2.2). Sample points that did not meet these habitat criteria were excluded.

Table 2.2 Criteria for each sub-set of invertebrate data, based on standardised hydraulic criteria. Flow type codes and substrata categories are composites of those defined in Appendix 1. BIG = bedrock and boulder and MED = large and small cobble.

Data Sub-set	Criteria for inclusion of a sampling point
Single Flow Type	RS
Flow Type Group	BPF, SBT, RS, FRF, USW, CAS
Single Flow Substratum	Fast/Big = CAS/BIG and/or BSW/BIG
Flow Substratum Groups	CAS/BIG, RS/BIG, BPF/BIG, RS/MED, SBT/BIG, SBT/MED, FRF/MED
Near-bed Flow	All sample areas with mean near-bed flows of $0.1 - 0.5 \text{ m s}^{-1}$
Froude Number	All sample areas with mean Froude number of $0.1 - 0.5$

The first level of assessment was to identify a Single Flow Type that occurred in each site's data set. The only flow type that qualified was Rippled Surface (RS), which was linked to one to six of the twelve invertebrate samples per site, or 23% of the total number of samples in the data-set (Table 2.3). The low number of samples for this analysis is not the ideal situation for analysis as the inherent variability in benthic samples weakens the power of a statistical analysis. A second approach was therefore adopted, in which samples collected from rare flow types were

eliminated. The combination of each individual rare types comprised < 50% of the total number of samples, leaving the six most common flow-types (Flow Type Group) for inclusion in the analyses (Table 2.2). This approach reduced the overall data set by only 18% (Table 2.3).

Table 2.3 Number of samples, *N*, of a possible 12 per site, meeting criteria for use in each data sub-set listed in Table 2.2.

River #	River	Single Flow-Type N	Flow Type Group N	Single Flow-Substratum Type N	Flow-Substratum Group N	Near-bed Flow N	Froude Number N
1	Jan Dissels	6	10	1	7	4	4
2	Rondegat	1	11	1	6	7	6
6	Steenbok	5	11	2	7	8	6
7	Wolwekloof	3	9	2	7	6	3
8	Wit	1	10	0	6	2	1
9	Molenaars	4	9	1	8	8	8
10	Elands	4	9	2	7	6	5
11	Elandspad	2	7	3	6	1	3
13	Du Toits	3	11	1	6	4	5
14	Bakkerskloof	1	8	2	6	3	2
15	Zachariashoek	3	9	2	4	6	3
17	Berg	3	12	1	6	5	5
18	Eerste 1	2	10	1	7	5	5
19	Langrivier	1	9	2	6	4	5
20	Swartboskloof	4	10	3	8	7	7
24	Dwars	2	12	3	8	3	3
27	Newlands	2	9	2	7	5	4
29	Disa	2	11	1	7	3	4
Total number used		49	177	30	119	87	79
Percent of total possible		23	82	14	55	40	37

The next two data sub-sets were based on flow type/substrata combinations. As there was a mix of alluvial, bedrock, and mixed channels represented in the river sites, substrata were combined into coarser substratum categories than those of Appendix 1.B so that all the sites remained in the analyses. The new substratum categories were: BIG (bedrock and boulder); MED (large and small cobbles); SMALL (large and small gravel); and FINE (sand and silt). As the sampling of hydraulic biotopes had been random at each site, none of these new coarse substratum categories, when linked with a single flow type, were sampled at least once in every site. Cascade (CAS) over BIG substrata scored highest, being sampled at least once in 77% of the sites, but this excluded too many sites for a good comparison with the original data set that had produced the catchment signatures. As the flow-type Broken Standing Waves (BSW) is similar in hydraulic character to CAS, it was added to the CAS/BIG samples to increase the number of samples available for use in this permutation, thereby creating a new category, Fast/BIG, for the Single Flow Substratum analysis (Table 2.2). Similar to the Single Flow Type data sub-set, the number of samples per site was low, and the Wit River site was dropped from the analysis because no

samples meeting the Fast/BIG criterion were taken. This left 14% of the total number of samples collected to be used for the Single Flow Substratum comparative analysis (Table 2.3). The final data sub-set based on visual observations was named Flow Substratum Group. It employed the same strategy used in the Flow Type Group analysis (Table 2.2). Flow Substratum Group consisted of seven commonly sampled flow/substratum combinations, thereby keeping 55% of the total number of available samples (Tables 2.2 and 2.3).

The above data sub-sets were created using flow types, which are a visual classification of flow, and visually-classified substrata. Two final data sub-sets were thus included, based on measured hydraulic comparisons across sites. These were: near-bed velocity, as near-bed flows have been shown to be important to macro-invertebrate distributions (Davis & Barmuta 1989; Young 1992); and the Froude number (Fr), which is a dimensionless number based on mean water column velocity and depth (Table 2.2). Means were calculated for each of these variables from the two to six measurements recorded with each invertebrate sample. The Near-bed velocity class of $0.1 - 0.5 \text{ m s}^{-1}$ was represented in at least one sample from each site (40% of total number of samples), and similarly, the Fr number range of $0.1 - 0.5$ was common to 37% of samples, and so these two classes were used in the ensuing analyses.

Using the data sub-sets to compare invertebrate assemblages from the LD sites

When the sites were compared using the Single Flow Type data sub-set, 40% of the sites showed no catchment trend in their grouping (Figure 2.2) whilst the remainder grouped into three of the four main catchment groups shown in Figure 2.1. Rondegat (O02) grouped with other Olifants catchment sites but the MDS plot showed the groups were not as strong as those of the Eerste-Molenaars and Breede catchment groups (Figure 2.2b).

Repeating the same set of analyses for the Single Flow Substratum data sub-set, a pattern emerged of some splitting of groups and some minor re-alignment of groups of sites with other groups (figure not shown). The overall pattern showed a much stronger catchment signature than the first data sub-set.

The next level of exploration was to use the coarser categories that grouped similar flow types (Flow Type Group) and similar flow type/substrata combinations (Flow Substratum Group) (Table 2.2). This added to the number of samples contributing to the composite species list for each site and increased the power of the overall analysis, but weakened the approach of comparing like samples with like. Samples from rare conditions, such as fast riffle flow over SMALL or smooth boundary turbulent over FINE, were also eliminated. The Flow Type Group sub-set of data produced a pattern very similar to the original one in Figure 2.1 (Figure 2.3), with the exceptions of the Berg River site (B17), which did not group with the Breede sites, and the Table Mountain sites (T27 and T29), which did not form a group. The three remaining catchment groups remained intact, their strength indicated by both the cluster analysis and the MDS plot.

The data sub-set Flow Substratum Group produced the same pattern as the original one in Figure 2.1 (figure not shown), except there was no grouping of the two Table Mountain rivers.

When near-bed velocities and Froude number data sub-sets were analysed the same basic pattern emerged. The three main catchment groups were created by the Near-bed Flow data sub-set, with a few sites not included in their usual or any other group (figure not shown). The same pattern emerged from the Froude number sub-set (Figure 2.4), with the same three main groupings. The Wit River (R08) was represented by only one sample of its twelve, which could account for its separating out so markedly from the other sites.

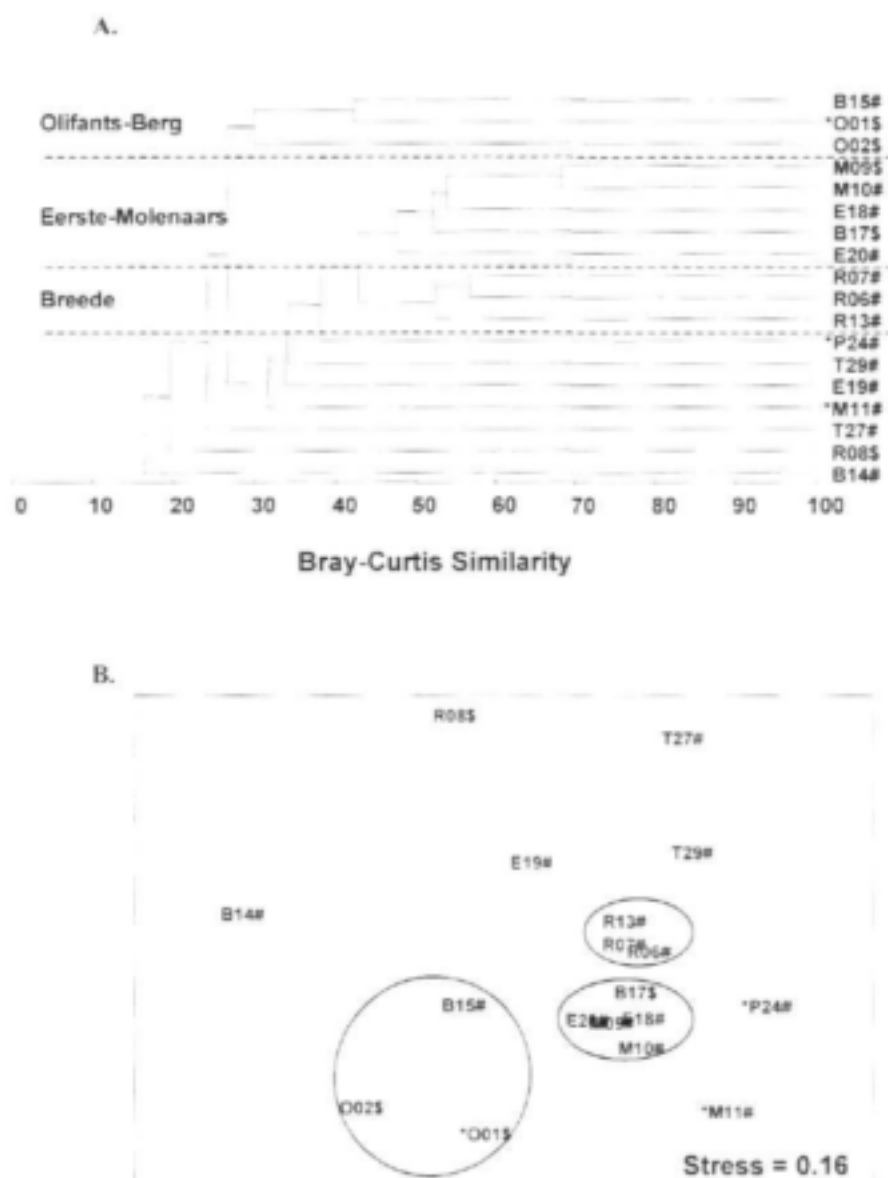


Figure 2.2 A. Dendrogram of the 18 sites on LD rivers, using species-level invertebrate data in the Single Flow Type sub-set. B. 2-d MDS plot, main groups identified in the dendrogram separated by circles. # = pre-identified as a site in the mountain zone and \$ as a site in the foothill zone, as per Table 1.1. * = site with bedrock as the dominant substratum.

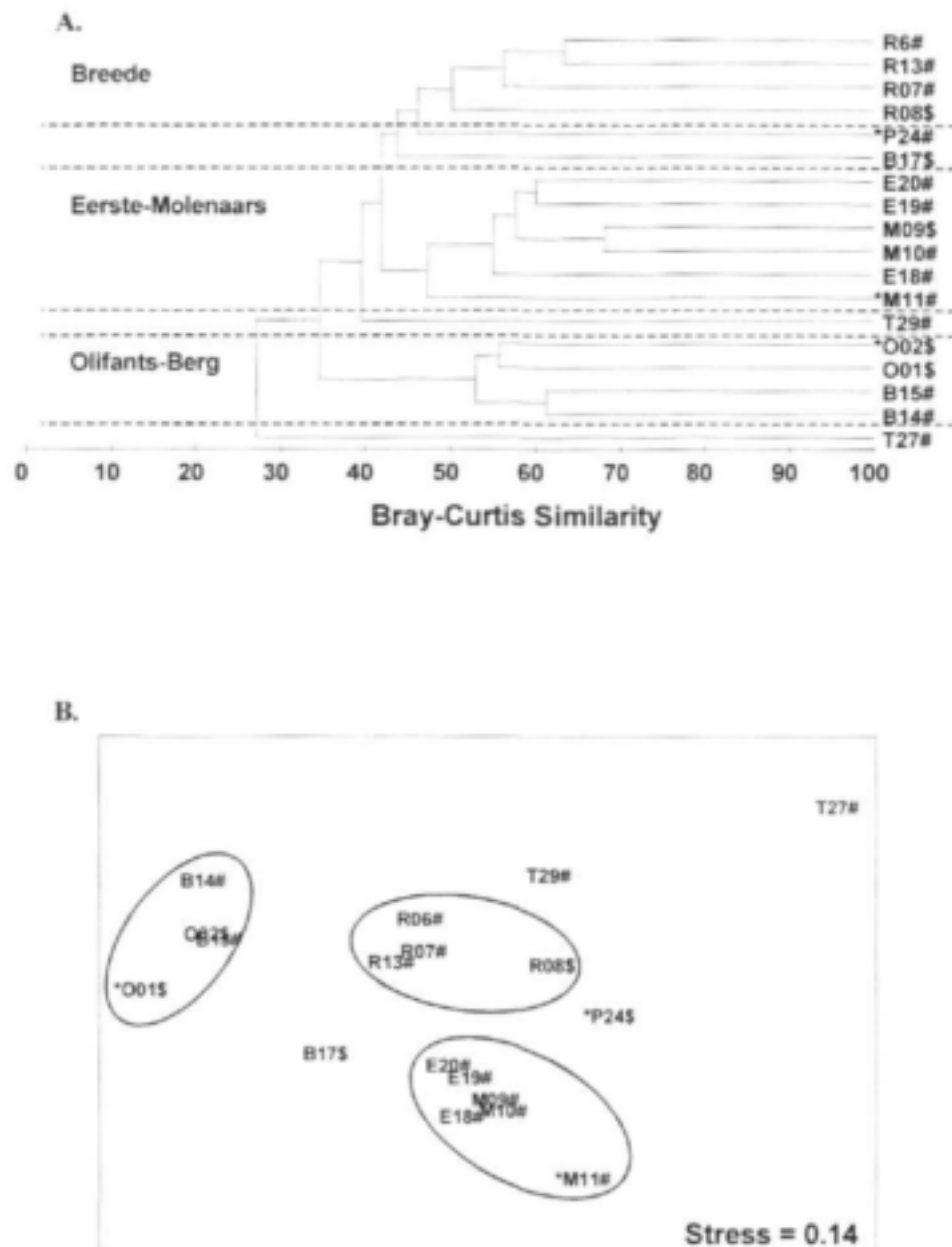


Figure 2.3 A. Dendrogram of the 18 sites on LD rivers, using species-level invertebrate data derived from the Flow Type Group data sub-set. B. 2-d MDS plot, with the main groups identified in the dendrogram separated by circles. # = pre-identified as a site in the mountain zone and \$ as a site in the foothill zone, as per Table 1.1. * = site with bedrock as the dominant substratum.

ANOSIM results testing the hypothesis that the invertebrate data group sites by catchment (as in Table 1.1, not catchment groups) showed the persistence of catchment signatures. All tests were significantly different to random permutations of the data at a $P \leq 0.05$ (Table 2.4). The data sub-sets Flow Substratum Group and Near-bed Flow produced the best match with catchments, with

the Flow Substratum Group being closest to the original ANOSIM of King & Schael (2001) for the species-level ANOSIM test of $R = 0.75$. The Single Flow Type Group had the lowest R -value (and thus produced the weakest catchment pattern) of any of the sub-sets, probably due to the low numbers of samples. Although the the Flow Type Group and Froude Number data sub-sets produced similarity matrices that were strongly similar to the original one, they had lower ANOSIM R -values than the Flow Substratum Group and Near-bed Flow (Table 2.4). This demonstrates that the catchment groups (i.e. Eerste-Molenaars) were actually stronger in those data-sets than single catchments, with the reverse holding true for the Flow Substratum Group and Near-bed Flow data sub-sets.

Table 2.4 Comparison of the similarity matrices produced using the data sub-sets with the original one using ANOSIM. $R = 1$ represents a complete match, and $R = 0$ represents no match to either the original similarity matrix or catchment designation. All P -values were ≤ 0.05 therefore the test data were significantly different from random sample permutations. * = a modified comparison, with the Wit River not represented as there were no samples from this river that met the criterion. FT = Flow Type, FS = Flow Substratum, NB = near-bed, Fr = Froude.

Analysis Type	R-value
Single FT	0.30
Single FS*	0.53
FT Group	0.50
FS Group	0.70
NB Flow	0.69
Fr Number	0.45

In summary, using different permutations of the available physical data, the catchment signature found in King & Schael (2001) persisted. The three main groupings (Breede, Eerste-Molenaars, and Olifants-Berg) occurred in every analysis to at least a basic degree. Sites that moved in and out of groups in the different analyses, such as Elandspad (M11) in the Eerste-Molenaars and Wit (R08) in the Breede, did not have strong links with groups in the initial analysis. The few samples contributing to the overall taxonomic list for the Single Flow Type and Single Flow Substratum Group data sub-sets had a significant effect on the R -values in the ANOSIM analysis. These analyses were too dependent on one or two samples per site being entirely representative of the site, whereas the natural variability of invertebrate species distributions is high (Chutter 1972) and more samples would realistically be needed to adequately represent the sites. Despite this, there was a good relationship between the original similarity matrix and those from the data sub-sets, particularly from the composite sub-sets as these included more samples. The Flow Type Group sub-set produced a similarity matrix that was a very good match with the original one; most probably due to the fact that the overall sample reduction was only 18%. The most evenly distributed and well represented data sub-set was Flow Substratum Group, which retained 55% of the original samples. The data sub-sets of hydraulic measurements showed the same overall pattern, with the three main catchment groups still combined, but with two sites in each analysis represented by two or fewer samples. These poorly represented sites had the most tenuous links with their original groups.

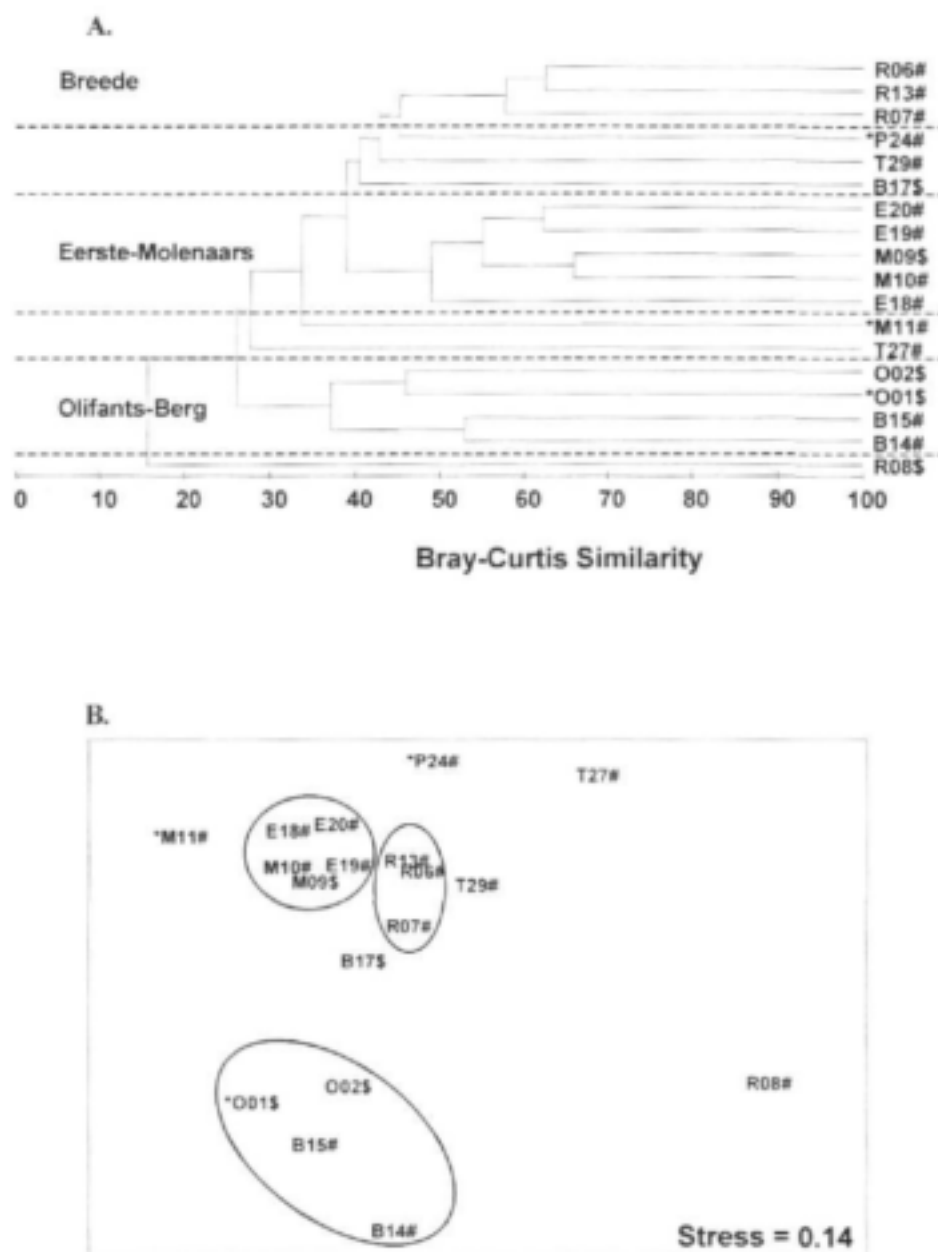


Figure 2.4 A. Dendrogram of the 18 sites on LD rivers, using species-level invertebrate data derived from the Froude number data sub-set. B. 2-d MDS plot, with main groups identified in the dendrogram separated by circles. # = pre-identified as a site in the mountain zone and \$ as a site in the foothill zone, as per Table 1.1. * = site with bedrock as the dominant substratum.

2.4 Testing for a possible taxonomic bias

Creating the data sub-sets

The objective of this second group of analyses was to explore whether the catchment signatures could have been produced through faunal identifications having been undertaken by a series of different people, sometimes with different technicians concentrating on different catchments. In contrast to the last group of analyses, all twelve samples from a site were used, and instead selected taxa were excluded from various analyses.

Initially, the original data set of 372 taxa was used to create data sub-sets of different taxonomic character (Table 2.5). The first sub-set was INSECTS, because the non-insect groups were less likely to have been identified further than family, constituted only 6% of the taxa identified at all sites, and occurred in the lowest numbers. From the INSECT sub-set, the Coleoptera were then removed to produce the NO COLEOPS sub-set, because they represented the taxonomic group of lowest consistency in identification. One technician involved in their identification for some catchments was an expert in that taxonomic group and the others were not and so, although type specimens were compared and identifications reconciled, Coleoptera still represented a possible source of identification bias. The Simuliidae were also removed from the NO COLEOP sub-set because they were not identified to species due to loss of some samples (and the car they were in).

The DEPT sub-set was created because the identification confidence was high and these four groups tend to be important in bioassessments. The following sub-sets in Table 2.5, of single orders or families, were used because they represented varying degrees of identification confidence (high: Ephemeroptera, Diptera, Plecoptera and Trichoptera; low: Coleoptera) and might allow any possible identification bias to be narrowed down to specific orders or families. Very high levels of confidence were awarded to the Baetidae sub-set (all individuals identified to species level by one person) and the Chironomidae sub-set (identified to genus, and to species where possible, by the project team, and every specimen verified by a specialist in this taxonomic group) (Appendix 2). The last data sub-set (DISCRIM) was created from taxa identified by PRIMER as 'top discriminators' between sites within each catchment group (King & Schael 2001). Each catchment group had been compared to the others using the routine SIMPER in PRIMER, producing a list of all taxa that made a large contribution (≥ 2 average dissimilarity to standard deviation ratio given in results of SIMPER) to their dissimilarity. These taxa may be seen as the drivers that separate the sites into catchments.

The DISCRIM data sub-set became the basic taxon list for the second set of taxonomic analyses (Table 2.6), which was designed to ascertain which orders were most influencing the catchment groupings. Initially, orders were eliminated, beginning with the non-insect orders, to produce a sub-set DINSECT. All insect orders except the main ones were then eliminated (MAIN ORDERS), and then each of the main orders in turn to produce six more data sub-sets (Table 2.6). Two non-insect data sub-sets were also created.

DISCRIM was used again to create data sub-sets based on perceived dispersal capabilities. It was hypothesised that those taxa able to disperse well as adults would be least likely to contribute toward catchment signatures, whilst those with no aerial life stage or with poor flying ability would tend to remain within a system and thus contribute strongly to catchment signatures.

Table 2.5 Sub-sets of the original data set for the investigation of possible taxonomic bias, using all 372 taxa.

Taxon Group	Composition of group	No. Taxa
INSECT	Insects only, all non-insect taxa removed	344
NO COLEOPS	Insects, no Simuliidae, no Coleoptera	313
DEPT	Diptera (no Simuliidae), Ephemeroptera, Plecoptera, Trichoptera	232
EPHEM	Ephemeroptera only	48
BAETID	Baetidae (Ephemeroptera) only	21
LEPTO-TELO	Leptophlebiidae and Teloganodidae (Ephemeroptera) only	19
CHIRON	Chironomidae (Diptera) only	67
COLEOP	Coleoptera only	50
ELMID	Elmidae (Coleoptera) only	18
PLECOP	Plecoptera only	10
TRICHOP	Trichoptera only	54
DISCRIM	Top taxa that discriminate between catchment groups	136

Table 2.6 Sub-sets of the original data set, for the investigation of possible taxonomic bias using the top discriminating species (DISCRIM) list.

Taxon Group	Composition of group	No. Taxa
DINSECT	Insects only, all non-insects excluded	124
MAIN ORDERS	Coleoptera, Diptera, Ephemeroptera, Odonata, Plecoptera, Trichoptera	114
DNO COLEOPS	All taxonomic groups except Coleoptera	110
NO DIPT	All taxonomic groups except Diptera	118
NO EPHEM	All taxonomic groups except Ephemeroptera	100
NO ODON	All taxonomic groups except Odonata	127
NO PLECOP	All taxonomic groups except Plecoptera	127
NO TRICHOP	All taxonomic groups except Trichoptera	120
NON-INSECT1	Only non-insect taxonomic groups	13
NON-INSECT2	Non-insect except Cladocera, Copepoda, Ostracoda	10
GOOD	Good dispersers: Odonata and Diptera	46
MEDIUM	Medium dispersers: Ephemeroptera, Plecoptera, Trichoptera	43
BAD	Bad dispersers: Coleoptera, Hemiptera, Non-insects	48
MED+BAD	Medium and bad dispersers	91

Using the data sub-sets to compare invertebrate assemblages from the LD sites

The different taxonomic data sub-sets produced an overwhelmingly similar pattern of catchment groupings to the original data set (Figure 2.1), with just a few already tentatively linked river sites uncoupling from their original groups. Since the dendograms and MDS plots for the data sub-sets are so similar, selected representatives of these analyses are given (Figures 2.5 – 2.8), along with mention of specific characteristics of the other analyses.

The INSECT data sub-set cluster analysis (Figure 2.5a) showed a close similarity to the full data set (Figure 2.1a), with the exception of the two Table Mountain sites, which did not group together, and the Berg River site (B17), which did not group with the Breede sites. The best match in the dendrogram and MDS plot patterns (Figure 2.6) was produced by DISCRIM, which is not unexpected as this sub-set of data was created using the taxa that best discriminated between catchment groups. NO COLEOPS, COLEOPS and DEPT all produced similar patterns to the original data where the catchment groups remained intact, with the Dwars (P24), Berg (B17), Wit (R08) and Elandspad (M11) switching positions and moving in and out of the various groups (figures not shown). In the NO COLEOPS group, the Elandspad (M11) and Dwars (P24) formed their own small group, most probably due their bedrock channel type. Once again, the Table Mountain rivers separated from the three other main groups. The ELMID group showed a weakening of catchment groups, with the Breede sites interspersed among the other groups, the Eerste-Molenaars group losing a few sites, and the Olifants-Berg without one Berg site.

The EPHEM and CHIRON analyses showed greater differences to the original similarity matrix than the above analyses, but the main catchment groups remained intact in the EPHEM analysis, with the Table Mountain rivers grouped (62% similarity) and the two bedrock mountain streams grouped at a 45% similarity (Figure 2.7). The Eerste-Molenaars group included the Berg (B17) and Wit (R08), whereas the Olifants-Berg group and the core Breede group remained the same.

The CHIRON data sub-set produced a different outcome to all the previous ones (Figure 2.8). The catchment groups were not evident, with the exception of the Olifants-Berg group that remained intact but with the addition of two Breede sites (R13 and R06). The only other link to the original groups was tenuous: a Molenaars group was present that included one Eerste (E20) and one Breede site (R07). The remaining sites did not form any groups.

The remaining taxonomic levels, order and family-level groups BAETID, LEPTO-TELO, PLECOP AND TRICHOP, produced catchment groupings on a gradient from that of the EPHEM sub-set to that of the CHIRON sub-set. There were some remnants of catchment groups, but the catchment signatures started to disappear at R-values < 0.6 .

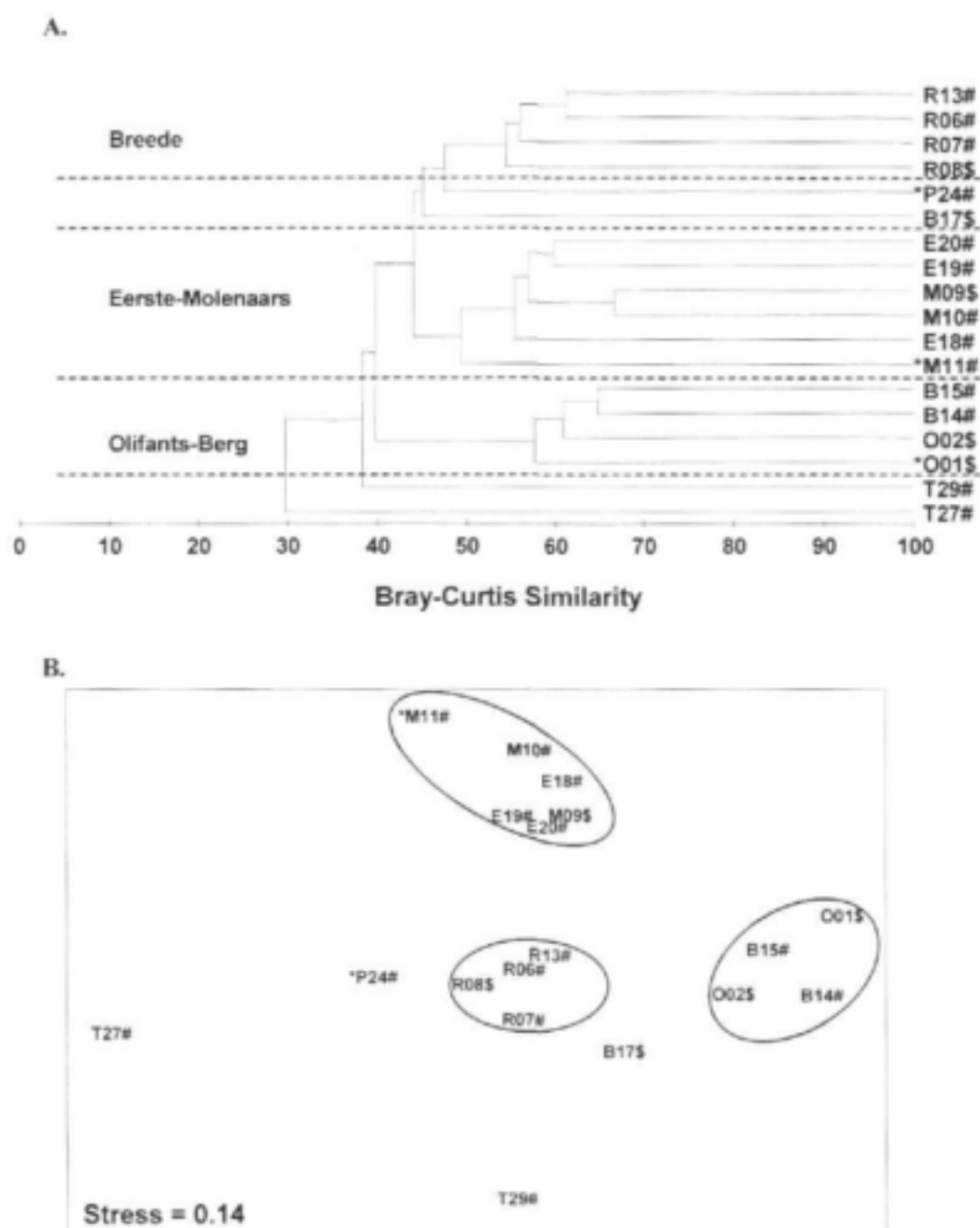


Figure 2.5 A. Dendrogram of the 18 sites on LD rivers, using the INSECT data sub-set derived from the twelve samples at each site. B. 2-d MDS plot, with the main groups identified in the dendrogram separated by circles. # = pre-identified as a site in the mountain zone and \$ as a site in the foothill zone, as per Table 1.1. * = site with bedrock as the dominant substratum.

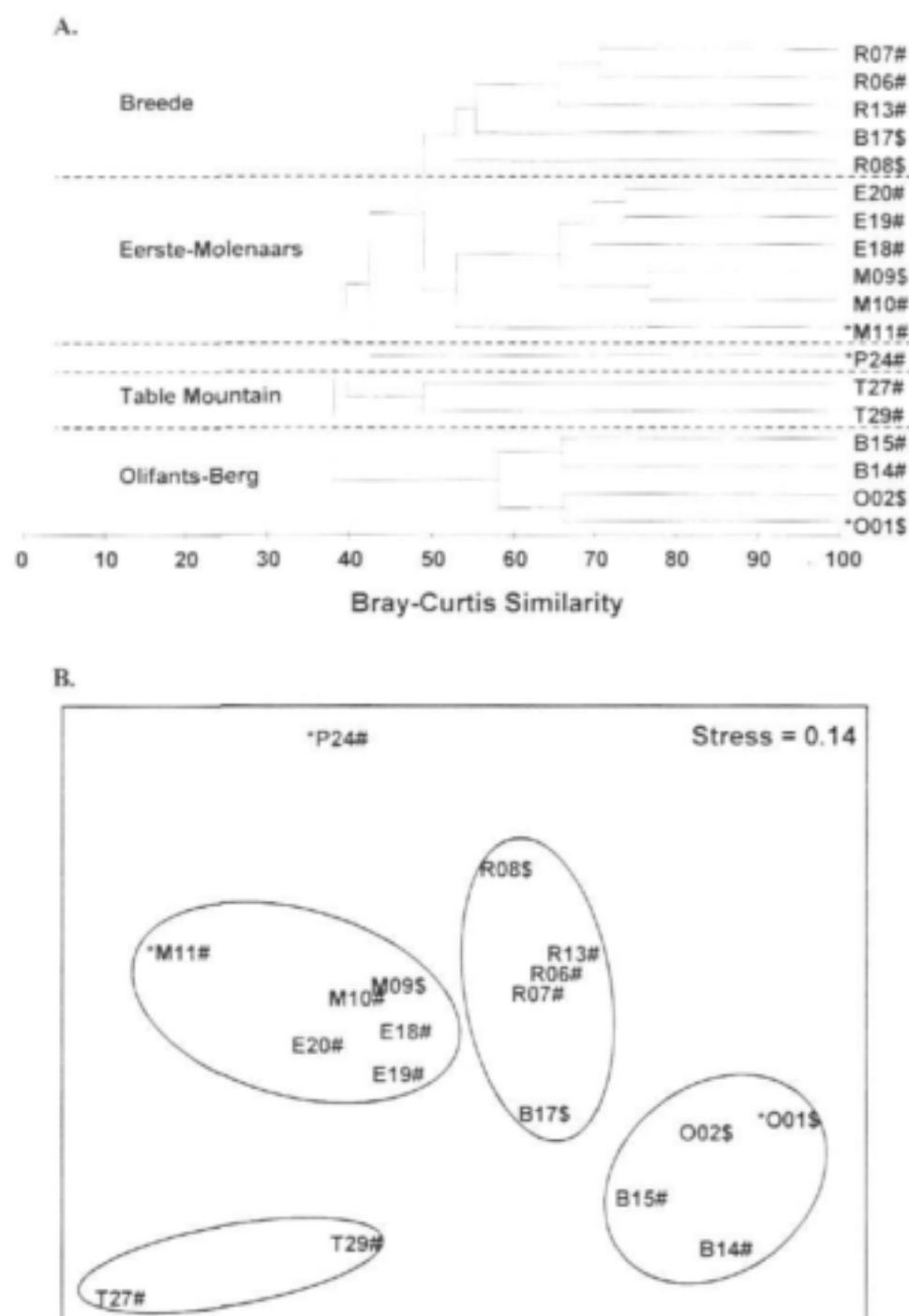


Figure 2.6 A. Dendrogram of the 18 sites on LD rivers, using the top discriminator (DISCRIM) data sub-set derived from the twelve samples at each site. B. 2-d MDS plot, with the main groups identified in the dendrogram separated by circles. # = pre-identified as a site in the mountain zone and \$ as a site in the foothill zone, as per Table 1.1. * = site with bedrock as the dominant substratum.

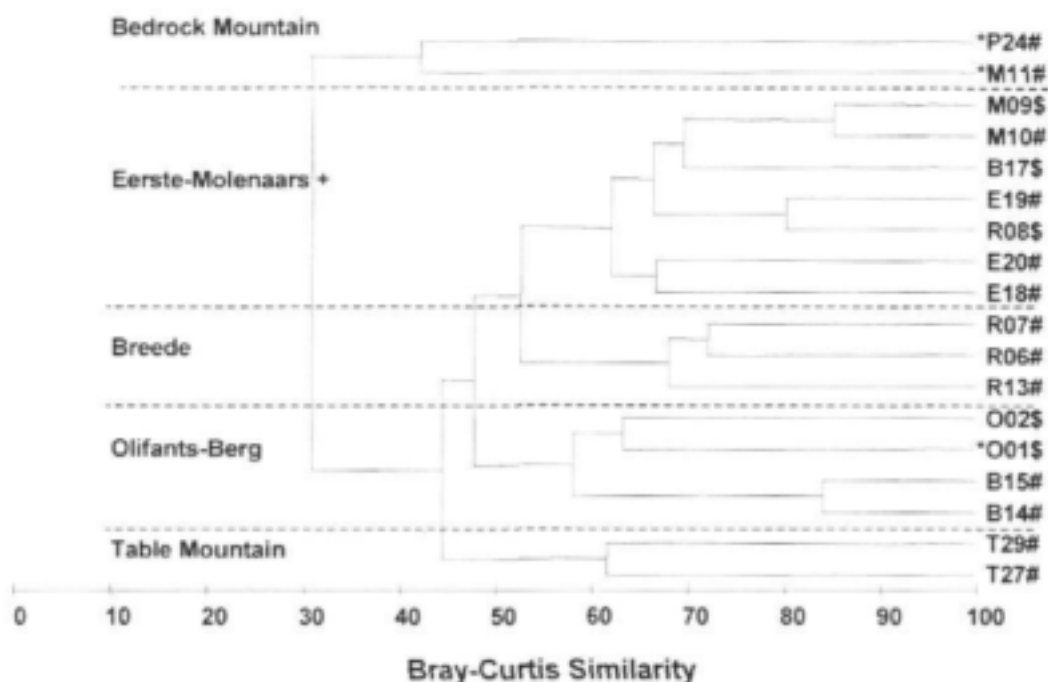


Figure 2.7 Dendrogram of the 18 sites on LD rivers, using the species-level Ephemeroptera (EPHEM) data sub-set. # = pre-identified as a site in the mountain zone and \$ as a site in the foothill zone, as per Table 1.1. * = site with bedrock as the dominant substratum. + denotes original group plus other sites.

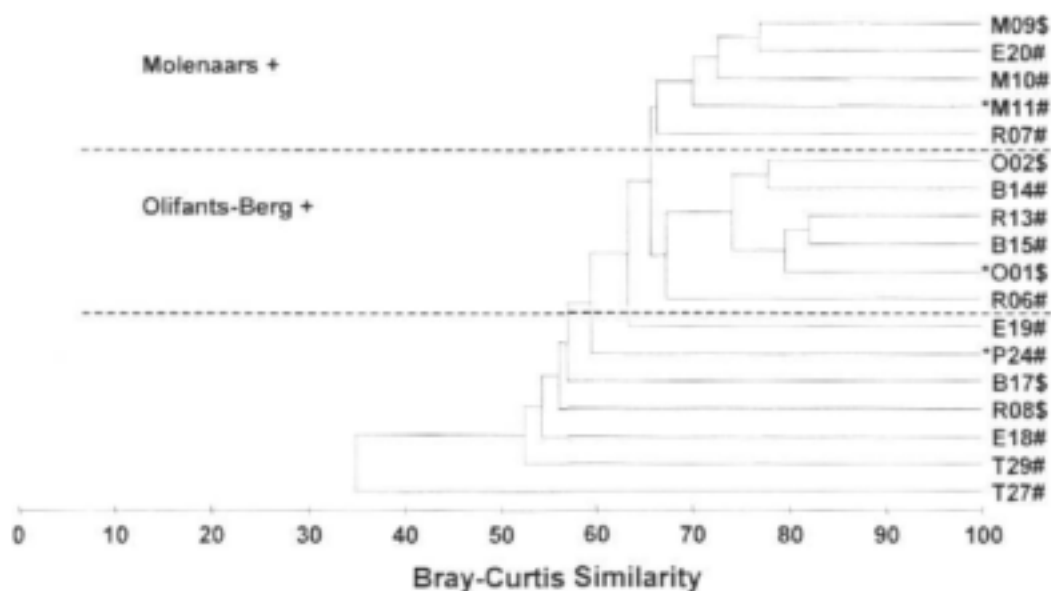


Figure 2.8 Dendrogram of the 18 sites on LD rivers, using the species-level Chironomidae (CHIRON) data sub-set. # = pre-identified as a site in the mountain zone and \$ as a site in the foothill zone, as per Table 1.1. * = site with bedrock as dominant substratum. + denotes original group plus other sites.

Despite the weakening pattern of catchment signatures within the plots, the ANOSIM results showed that all of the taxonomic sub-sets had a significant correlation with catchment (Table 2.7), even though the pattern of catchment or catchment groups was not evident from the cluster and MDS plots. The strength of the relationship was dependant on the taxonomic level or group used, with DISCRIM scoring highest. Not surprisingly, the DISCRIM taxon showed an even stronger correlation with catchment than did the original data set (R-values of 0.81 and 0.75 respectively). Once again the CHIRON group had the weakest relationship to catchment with LEPTO-TELO and the order-level identification also low.

Table 2.7 Analysis of Similarity (ANOSIM) R-values at a $P < 0.05$ level comparing catchment designation to taxonomic level or composition of each site.

Taxon Level	R-value	Taxon Group	R-value	Taxon Group	R-value
Phylum	0.44	INSECT	0.57	CHIRON	0.22
Class	0.51	NO COLEOP	0.57	COLEOP	0.61
Order	0.39	DEPT	0.58	ELMID	0.50
Family	0.45	EPHEM	0.57	PLECOP	0.43
Genus	0.68	BAETID	0.47	TRICHOP	0.58
Species	0.75	LEPTO-TELO	0.32	DISCRIM	0.81

The same set of analyses was completed for the different taxonomic groups derived from the DISCRIM list of species (Table 2.6), using ANOSIM. All but the NON-INSECT1 and NON-INSECT2 groups and GOOD dispersers produced very similar matrices to both the DISCRIM and original data sets. As such, the dendrograms and MDS plots are not shown because they do not differ greatly from Figures 2.1 and 2.2. There was a tendency for sites that are not strongly affiliated within their original groups to leave and either become isolated or join other groups, as was seen in the habitat-standardisation analyses.

The GOOD disperser group and NON-INSECT1 (Figures 2.9 and 2.10) illustrate the weakest demonstrations of catchment patterns. The GOOD dispersers were expected to exhibit a weaker catchment signature, as the taxa within this group are ubiquitously distributed. The GOOD data sub-set produced two broad groups of sites, one consisting of the Eerste-Molenaars with the addition of some Breede and Berg sites, and the other a mix of Olifants-Berg and Breede sites (Figure 2.9). The Table Mountain sites, Palmiet and one Breede site were not part of any group. The NON-INSECT groups were also not expected to show a catchment signature because the level they were identified to was coarse, but there was evidence of catchment groupings in NON-INSECT1 similar to that of the GOOD dispersers (Figure 2.10). There was a Breede group with one Eerste and one Berg site, and then a larger Eerste-Molenaars group with the Table Mountain and Palmiet sites interspersed. The Olifants-Berg group was largely intact, with one site excluded.

The ANOSIM results tests if catchments within the invertebrate data showed similar results as the dendrogram and MDS plots, where the relationship was significant for all tests and ranged in

strength (Table 2.8). All tests had R-values > 0.75 with the exception of GOOD, NON-INSECT1 and NON-INSECT2. The catchment signature still persisted, even if weakly, throughout each taxonomic group.

Table 2.8 Analysis of Similarity (ANOSIM) R-values at a $P < 0.05$ level for each different taxonomic group used in the DISCRIM data set tests.

Taxon Group	R-value	Taxon Group	R-value
MAIN ORDERS	0.80	NO TRICHOP	0.83
DINSECT	0.79	NON-INSECT1	0.39
DNO COLEOPS	0.75	NON-INSECT2	0.38
NO DIPT	0.83	GOOD	0.58
NO EPHEM	0.84	MEDIUM	0.76
NO ODON	0.83	BAD	0.77
NO PLECOPT	0.80	MED+BAD	0.84

Standardisation of the data, and use of taxonomic groups that were confidently identified and verified, has supported the validity of the catchment signatures. The main catchment groups held fast with every analysis except the CHIRON data sub-set, where only the Olifants-Berg group remained strong. The conclusion was reached that the catchment signatures are not an artefact of identification procedures.

2.5 Discussion

Habitat standardisation

Refining data sets by standardising the habitats from which samples were collected demonstrated that catchment signatures were not caused by a bias in sampling strategy.

Although the results of each comparison were not a perfect match to the original data set, they all retained the pattern of three main catchment groups demonstrated in King & Schael (2001). When all sampling points from each site were included the signature was stronger, however, indicating the need for sufficient samples to truly represent the species assemblage at any site. Many studies comparing invertebrate community structure at different scales tend to sample one habitat type consistently, usually a riffle (Hawkins *et al.* 1993; Townsend *et al.* 1997; Feminella 2000; Gerritsen *et al.* 2000; Hawkins & Vinson 2000). These studies then effectively become a comparison between riffle species assemblages across different rivers, regions or landscapes, rather than a comparison of whole-site invertebrate assemblages. Feminella (2000) hypothesised that sampling a wider range of habitat types would actually enhance differences between regions and between different landscapes, a prediction borne out by this study.

In addition to testing possible bias in the sampling strategy, the analyses of standardised habitats highlighted the effect of reduced sample size. The correlation between the results using the data sub-sets and those using the original King & Schael (2001) data set increased with the number of

samples in the sub-sets. The data sub-sets with < 3 samples per site had the weakest comparison with the original matrix, while those with an average of > 7 had the best correlation. There is a known effect of sample size on its representativity of the species assemblage of a site (Feminella 2000; Li *et al.* 2001), which could affect the power of multivariate analyses (Clarke & Warwick 1994). Li *et al.* (2001) found that a minimum of six samples at each site should be taken to decrease the overall variability of a data-set. They also found that four to eight new taxa were added to a species list for a site with each additional sample up to five samples, after which each additional sample increased the number of new taxa by one or two. Results reported here support the need for six or more samples to best represent a site. Regardless of the number of invertebrate samples or habitat types used, however, the pattern of the sites grouping by catchment was still apparent (Table 2.8).

Taxonomic standardisation

Identification of taxa by different technicians did not create the catchment signatures. Sub-sets of taxonomic data were created in this project to limit any possible bias, and each sub-set, with the exception of CHIRON, showed the same result as the original data set of invertebrate assemblages clustering by catchment. CHIRON (Chironomidae) discriminated least between sites, perhaps because of the lack of local endemism of these midges (Harrison 2002). Of the seven major sub-families of chironomids known in southern Africa, only one is endemic to the region (Aphroteniinae) as a Gondwana relic, and the rest are widespread throughout Africa and the world (Harrison 2002). Different chironomid species are quite indicative of different local-scale habitats (i.e. within-site differences), and are probably more usefully used for that purpose than for distinguishing larger-scale landscape features (i.e. between-site differences) as in this project. They were thus probably not a suitable group with which to test the influence of identification bias on catchment signatures.

The level of taxonomic resolution is an important consideration for all studies of biological assemblages. A species-level approach is thought to have the best chance to detect differences among sites for bioassessments and for linking landscape-feature classifications of sites to invertebrate assemblages (Cranston 1990; Resh & McElravy 1993; Feminella 2000; Hawkins & Vinson 2000). Taxonomic resolution at the family level is common in most biomonitoring programmes, however, as it is most cost effective and time efficient (Downes *et al.* 2000; Feminella 2000; Boyero & Bailey 2001; Dickens & Graham 2002). Some studies have found that identifications to family-level have yielded as much information as species-level data (Downes *et al.* 2000). Others have shown that even though the pattern of assemblage distributions was the same at family and species levels, it was stronger and more clearly defined at species level (Feminella 2000). In the King & Schael (2001) study, higher taxonomic data such as for phylum, class and family did not produce obvious catchment signatures. If species-level data had not been available, the signatures would have not been detected from the higher-level analyses. Unlike previous studies, the family-level taxonomic identification did not yield even the second best relationship between taxa and catchment.

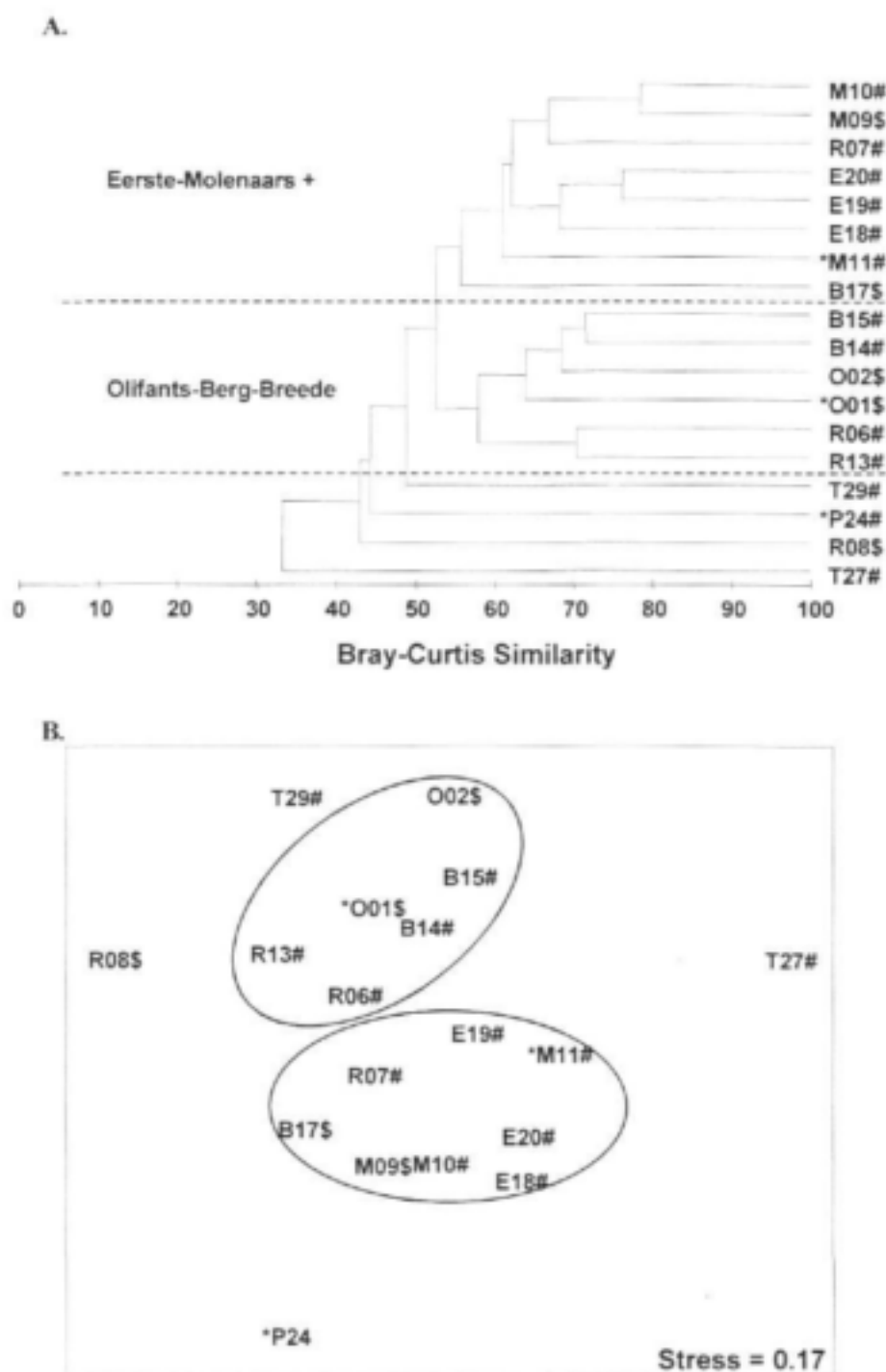


Figure 2.9 A. Dendrogram of the 18 sites on LD rivers, using the good dispersers (GOOD) data sub-set derived from the twelve samples at each site. B. 2-d MDS plot, with the main groups identified in the dendrogram separated by circles. # = pre-identified as a site in the mountain zone and \$ as a site in the foothill zone, as per Table 1.1. * = site with bedrock as the dominant substratum. + denotes original group plus other sites.

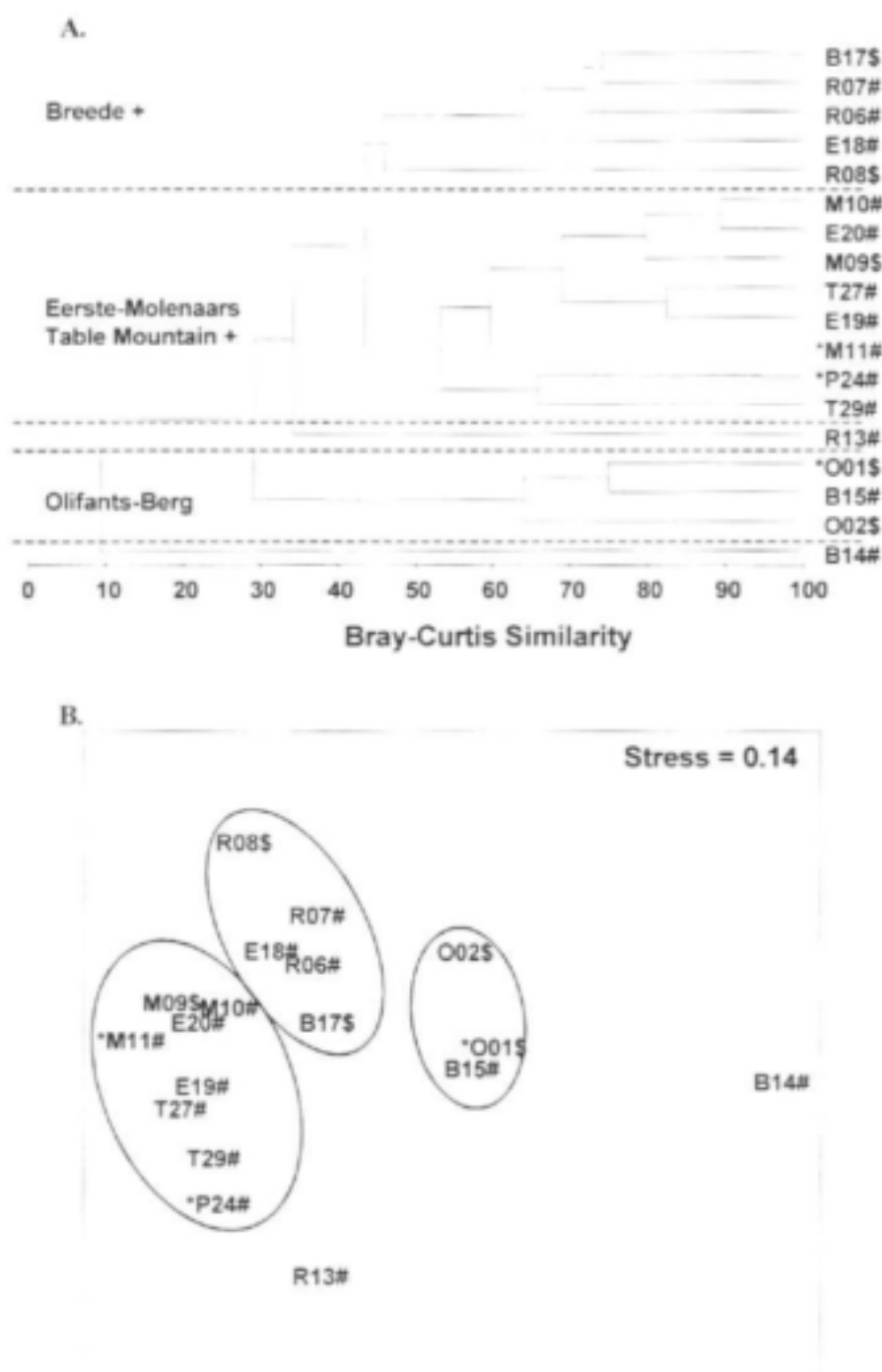


Figure 2.10 A. Dendrogram of the 18 sites on LD rivers, using the NON-INSECT1 data sub-set derived from the twelve samples at each site. B. 2-d MDS plot, with the main groups identified in the dendrogram separated by circles. # = pre-identified as a site in the mountain zone and \$ as a site the foothill zone, as per Table 1.1. * = site with bedrock as the dominant substratum. + denotes original group plus other sites.

There are alternatives to using taxonomic levels to analyse similarities and difference between sites as was done in this project. Richards *et al.* (1997) used species traits or metrics such as diversity rather than species assemblages, abundances and presence/absence data. Life-history traits can be good metrics as they are an adaptive response to environmental conditions and can transcend bioregions, and they are not biogeographically constrained (Richards *et al.* 1997). Species traits or metrics have been used in several studies as surrogates for species to describe how invertebrates can be described in terms of their environment at both large landscape levels (Vannote *et al.* 1980; Statzner *et al.* 1988; Statzner *et al.* 1997; Townsend *et al.* 1997; Li *et al.* 2001; Roy *et al.* 2003) and smaller scales (Gore & Judy 1981; Armitage *et al.* 1995; Downes *et al.* 2000; Lancaster 2000; Weigle 2003; Yuan & Norton 2003). Life-history traits were considered in the project reported here as an alternative analytical approach, as they could avoid the possibility of bias or biogeographic constraints, but there were two problems with this. First, there is insufficient knowledge of life-history and habit traits of South African riverine invertebrates to allow all the animals to be represented accurately. The approach would not necessarily require any less effort in terms of time and costs than identifying taxa to species or morph-species, and might be less accurate due to this poor background knowledge. Second, in a study of only one biogeographical region, differences between sites might not have been sufficiently great for traits or metrics to have distinguished between zones and meso-habitats.

2.6 Conclusion

In their 2001 study King & Schael had selected sites to suit a different research objective and, not expecting a pattern of catchment signatures, had not distributed the sites evenly between catchments. Ideally, for this project on validating catchment signatures, the sites should have been distributed evenly between catchments, and between zones (mountain or foothill) within the catchments (Table 1.1). As an example, the Eerste catchment was represented by mountain sites only, the Olifants catchment was represented only by foothill sites, and the Breede and Berg catchments each had only one foothill site. In multivariate analyses, single sites or unique sites within a sea of similar sites tend to 'float' around and create what could be artificial links with or separations from groups (Clarke & Warwick 1994). If a similar study was to be undertaken in future, it is recommended that all potential sites have zones assigned *a priori* so that there is a balanced number of sites per zone within each catchment of interest. Second, a minimum of three sites per zone per catchment would greatly enhance the strength of the analyses. Finally, standardising a set of habitat types to be sampled within each site, with equal sampling effort, would aid statistical comparison of sites.

The main objective of this chapter was to investigate whether the catchment signatures described by King & Schael (2001) were an artefact of a bias in either the sampling regime or taxonomic identification process. Through all the various permutations of the available data, the catchment signature persisted, independent of taxonomic resolution and despite standardising the invertebrate data by habitat. In the examination of each data sub-set, it was shown that catchment is the landscape feature that can best explain invertebrate distributions. This has been recognised before (Hynes 1970), but the widespread use of catchments or other landscape features as management tools is more recent.

An increasing number of scientists, conservationists and water-resource managers see landscape features as surrogates for biotic attributes of river ecosystems (Hawkins *et al.* 2000; Roux *et al.* 2002), often without knowing the ecological relevance of the features. The results of this study show that catchments are unique entities, which defy easy desktop analysis of physical features to describe biological communities. Wishart *et al.* (2002) also came to this conclusion when examining the genetic structure of both invertebrates and fish in the Western Cape Fynbos bioregion. They identified catchments as the functional unit for conservation of instream biota and biodiversity. The results of King & Schael (2001) and data presented here, combined with the findings of Wishart *et al.* (2002), give further support to the strength of catchment as the important large-scale landscape unit with biological/ecological significance.

3. CATCHMENT CHARACTERISTICS OF INVERTEBRATE SPECIES ASSEMBLAGES

3.1 Introduction

Accepting that catchment and river signatures are not an artefact of the collecting and analytical processes followed (Chapter 2), possible causes for them must be sought within the data set. Three possible causes are:

- unique taxa within each catchment group;
- unique proportions of the same set of taxa within each catchment group;
- unique combinations of taxa within each catchment group.

Each of these possibilities is explored below. To recap, the data set consists of invertebrates collected from Cape mountain streams and foothills during two consecutive summers and identified to species or 'morphological species', with a few Non-Insects distinguished to family level.

3.2 Unique taxa

Two considerations are relevant to this analysis.

First, the analysis is limited to the invertebrate data for the 17 Least-Disturbed (LD) rivers in the King & Schael (2001) data set, as it is from this that the catchment and river signatures emerged. Some taxa shown as unique to one catchment group in this data set are known not to be so – they have been collected in other catchments at other times. This fact does not negate the existence of the signatures, but the details of who contributes what to the signatures could change slightly with analysis of a more comprehensive regional data set such as the distribution records held at the Albany Museum.

Second, fewer LD rivers were sampled in some catchment groups than in others. This occurred because study sites were chosen for another purpose (King & Schael 2001) that did not ensure equal numbers of rivers per catchment. The number of LD rivers per catchment group was:

- Olifants-Berg: $2 + 2 = 4$
- Eerste-Molenaars: $3 + 3 = 6$
- Breede: 4
- Table Mountain: 2
- Palmiet: 1

The term 'catchment group' is used instead of 'catchment', as six catchments grouped into three pairs (Olifants and Berg; Eerste and Molenaars; and Disa + Cecilia (Table Mountain)). Investigations of why they grouped are reported on in Section 3.5.

A composite taxon list for each of the 17 rivers was used to search for the unique taxa, that is, for taxa that occurred in one or more rivers in one catchment group but not in any other catchment group. It is probable that Table Mountain and Palmiet are under-represented in terms of taxa because of the few rivers sampled, and inclusion of more rivers from these areas might have increased the number of taxa recorded for their catchment groups and thus decreased the number of taxa presently shown in the data set as unique to other catchment groups.

Of the 372 taxa recorded in LD rivers, 172 (46%) occurred in only one catchment group (Table 3.1). Diptera, Trichoptera, Ephemeroptera and Other Insects (mostly Hemiptera and Odonata) accounted for most of the single-catchment numbers. The Non-Insect group barely featured, with only eight single-catchment entries. Of these eight, six were worms or planktonic forms. The results were against expectations, as insects had been presumed to be fair to good dispersers and thus were expected to be largely shared across catchments, whilst non-insects were assumed to be poor dispersers and thus more likely to be restricted to a single catchment. The reason for the apparent mobility of the non-insects may be one of identification; many of them were identified to genus or family, and there is a higher likelihood of shared taxa at this level than if the identifications had been to species. This does not explain, however, the few shared taxa among the Insect groups, which is discussed further below.

Table 3.1 Taxa occurring in only one catchment group, and the percentage that this represents of all taxa in their taxon group. Numbers extracted from full taxon list for all LD rivers. OB = Olifants-Berg, EM = Eerste-Molenaars, TM = Table Mountain.

Taxon group	OB	EM	Breede	TM	Palmiet	Total	% not shared
Ephemeroptera	14	9	1	1	2	27	56
Plecoptera	0	1	0	0	0	1	10
Trichoptera	13	16	0	1	1	31	60
Diptera	6	25	10	10	1	52	44
Coleoptera	6	8	1	3	0	18	33
Other Insects	9	10	4	10	2	35	31
Non Insects	3	2	0	3	0	8	14
Total	51	71	16	28	6	172	
Ave. per group	13	12	3	14	6		

In terms of the percentage of taxa in each Insect group that occurred in only one catchment group, the Ephemeroptera (56%) and Trichoptera (60%) scored highest (Table 3.1), indicating the least sharing of taxa between catchments. The Plecoptera had the highest proportion of shared species (90%), although it is difficult to assess how much the figure is influenced by the comparatively few plecopteran taxa. In the opinions of the authors of this report, and of Dr Mike Picker (Plecopteran specialist, Zoology Department, University of Cape Town, pers. comm. May 2004), the Plecoptera are likely to be the poorest of the three orders in terms of dispersal ability, and so their greater level of shared species cannot be explained by better mobility. Compared with the Plecoptera, however, the Ephemeroptera and Trichoptera have few proportions of shared

taxa, and if this is not due to poorer mobility then perhaps it is linked to them being more selective of catchment. This topic is re-visited in Chapter 5.

A further feature of Table 3.1 is the large number of unshared taxa in some catchment groups compared to others. In absolute terms, the Eerste-Molenaars had considerably more unique taxa (71) than any other catchment group. As this number might have been a product of the many rivers sampled in this catchment group, an average number of taxa per river was also calculated for each catchment group (Table 3.1). This left the Eerste-Molenaars, the Olifants-Berg and the Table Mountain catchments groups with roughly equal scores (12-14), whilst the Breede trailed as the catchment with by far the fewest unique taxa (3).

Many of the unique taxa occurred as one to many individuals in only one river. A total of 117 of the 172 unique taxa occurred in this way (Table 3.2) with, for instance, the Ephemeroptera having three taxa recorded as a single individual in a single river and 11 taxa recorded at higher abundances but still in only one river, these taxa would not be present in a SIMPER analysis, for example. These taxa were 6% and 23% respectively of all the ephemeropteran taxa in the data set.

Table 3.2 Number of taxa occurring in only one river, and expressed as the percentage of all taxa in that taxon group.

Taxon group	One river, > 1 individual	%	One river, one individual	%
Ephemeroptera	11	23	3	6
Plecoptera	0	0	0	0
Trichoptera	15	28	6	11
Diptera	23	19	16	13
Coleoptera	4	7	4	7
Other Insects	16	28	14	24
Non Insects	2	7	3	11
Total	71		46	

In order to assess the extent to which these single occurrences could be responsible for the signatures, the analysis was repeated using a Top Discriminator list compiled from the PRIMER catchment dissimilarity runs (Appendix 3 for taxa). This list was compiled from the taxa that contributed the first 25% to the dissimilarity when any two catchment groups were compared, when sorted by Dissimilarity/Standard Deviation, or in other words when ordered in terms of how well they discriminated between the compared groups (Table 3.3). The total number of Top Discriminator taxa was 115.

Only ten of the 113 taxa in the Top Discriminator list were unique to one catchment group. The Ephemeroptera, for instance, fell from 27 unique taxa in the total taxon list (Table 3.1) to only three in the Top Discriminator list (Table 3.3). The Breede catchment had no unique species in the Top Discriminator list.

Table 3.3 Taxa in the Top Discriminator list that occurred in only one catchment. Numbers extracted from Top Discriminator list for all LD rivers. OB = Olifants-Berg, EM = Eerste-Molenaars, TM = Table Mountain.

Taxon group	OB	EM	Breede	TM	Palmiet	Total
Ephemeroptera	1	0	0	0	2	3
Plecoptera	0	1	0	0	0	1
Trichoptera	0	1	0	0	1	2
Diptera	0	0	0	0	0	0
Coleoptera	0	1	0	1	0	2
Other Insects	0	0	0	0	2	2
Non Insects	0	0	0	0	0	0
Total	1	3	0	1	5	10

As a final test, the PRIMER dissimilarity analysis was repeated with all taxa that occurred only once removed. The catchment signatures remained, with only minor changes. The Dwars (P24) joined the Breede group rather than remaining on its own, but all other groups remained as reported in King & Schael 2001 (Figure 3.1).

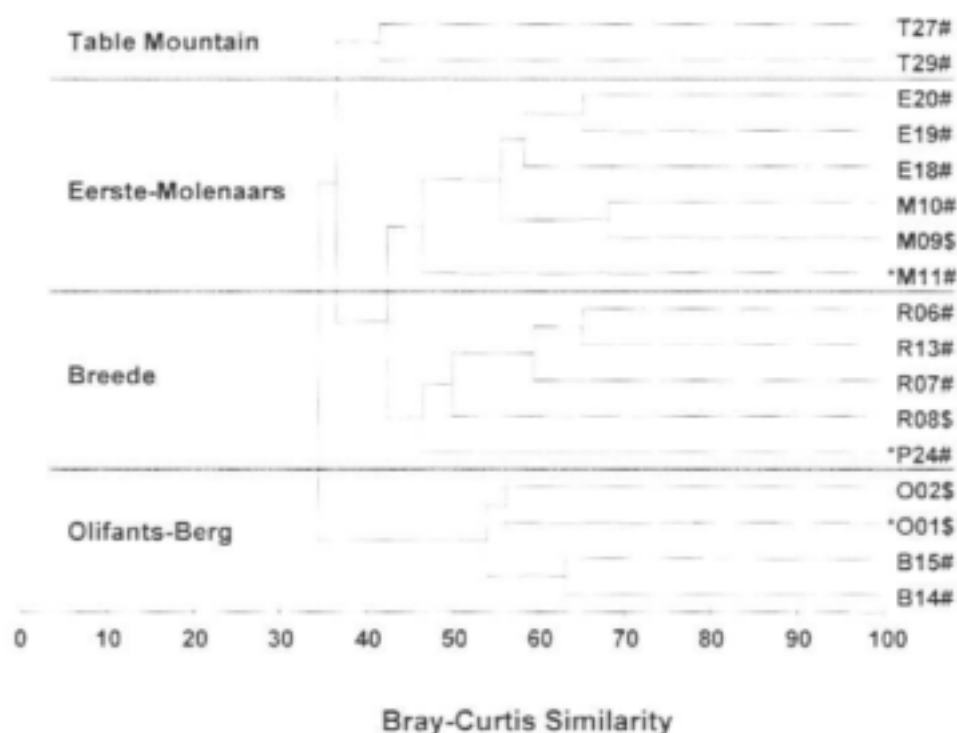


Figure 3.1 Dendrogram (no transform) of the 17 sites on LD rivers, using species-level rated abundance data of invertebrates derived from twelve invertebrate samples at each site. # = pre-identified as biological mountain zone and \$ as a biological foothill zone. An * denotes those streams that have bedrock as their dominant substratum.

In summary, these analyses suggest that unique taxa are not the cause of the catchment or river signatures. The percentage of them represented in the Top Discriminator list is extremely low (8.8%) and one catchment group cannot be distinguished at all in terms of them. Many more unique species with very rare occurrences were in the total list, but their removal from the analysis also did not erase the signatures.

3.3 Unique proportions of the same set of taxa

If the catchment signatures are not due to unique taxa per catchment group, then could they be caused by unique proportions of the various taxa? In the original analyses (King & Schael 2001), the signatures were revealed using untransformed abundance ratings (Table 2.1).

The PRIMER analysis was re-run using Presence/Absence data instead of rated abundances, thereby giving each taxon equal weight. The results were much the same – the catchment signatures remained (Figure 3.2).

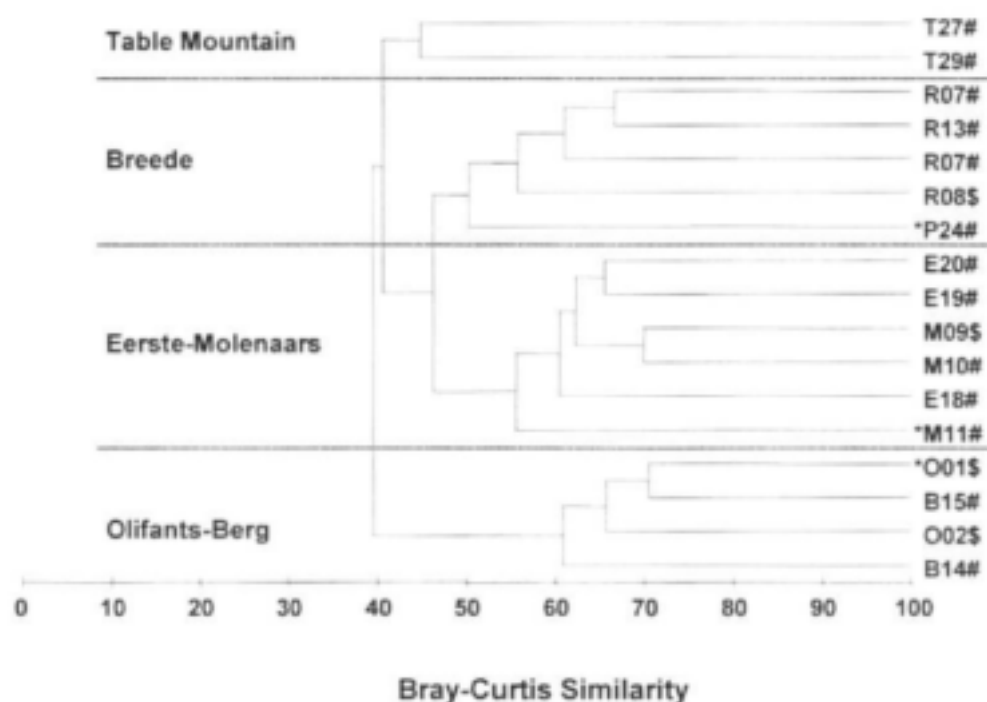


Figure 3.2 Dendrogram (presence/absence) of the 17 sites on LD rivers, using species-level data of invertebrates derived from twelve invertebrate samples at each site. # = pre-identified as biological mountain zone and \$ as a biological foothill zone. An * denotes those streams that have bedrock as their dominant substratum.

In summary, the catchment signatures do not seem to be due to unique proportions of taxa per catchment group.

3.4 Unique combinations of taxa

The remaining possibility is that the signatures were caused by unique combinations of taxa from the same common pool, either further influenced by being in unique proportions (as per Section 3.3), or irrespective of proportions.

The first and overwhelming impression of the pool of taxa collected is the high number involved: 372 taxa in 143 identified genera, 83 families and 25 orders. An initial set of analyses was completed to provide summary statistics that could give some insight to the overall nature of the invertebrate fauna from the sites.

Summary statistics: numbers of taxa and diversity per catchment group

The taxon list for the whole study is dominated by Diptera, which comprised 120 of the 372 taxa (Table 3.4). There is a slight bias in the data because some Non-Insects were not identified to species or morphological species and so this group is probably under-represented. Additionally, the Simuliidae (Diptera) remained at family level identification due to loss of some samples sent to a specialist: the dominance by Diptera would have been even greater with species-level data for the simuliids. Plecoptera are noticeably poorly represented in the assemblage, and are characteristically poor in species and genera in the Western Cape (Stevens & Picker 2003; four genera of six within South Africa known to be specific to the study area and 15 of 31 species). The other main insect groupings have much the same numbers of taxa.

Table 3.4 Number of taxa within each catchment group (and percentage that this represents of all taxa in the taxon group). Data extracted from full taxon list of LD rivers. OB = Olifants-Berg, EM = Eerste-Molenaars, TM = Table Mountain.

Taxon group	Total no. of taxa	OB	EM	Breede	TM	Palmiet
Ephemeroptera	48	30 (63)	29 (60)	21 (44)	9 (18)	8 (17)
Plecoptera	10	6 (60)	9 (90)	6 (60)	5 (50)	2 (20)
Trichoptera	53	26 (49)	33 (62)	9 (17)	6 (11)	9 (17)
Diptera	120	47 (39)	76 (63)	65 (54)	41 (34)	27 (23)
Coleoptera	55	25 (45)	36 (65)	23 (42)	21 (38)	15 (27)
Other Insects	59	23 (39)	22 (37)	29 (49)	6 (10)	9 (15)
Non Insects	27	9 (33)	17 (63)	11 (41)	20 (74)	13 (48)
Total no. of taxa	372	166	222	164	108	83

The three large catchment groups (Olifants-Berg, Eerste-Molenaars, Breede) have roughly comparable numbers of taxa in most groups, with the main exception being the few Trichoptera in the Breede. In almost all comparisons, the Eerste-Molenaars group has more taxa than any other group, whilst the smaller groups (Table Mountain and Palmiet) have the fewest taxa overall. As this trend might be due to the number of rivers sampled in each catchment, the analysis was repeated with the data standardised by dividing them by the number of rivers per group (Table 3.5).

This revealed that the two smaller catchment groups now scored higher than the large groups in almost every category. The Palmiet, in particular, which is represented by just one river, scored very high, with noticeably higher numbers of Trichoptera, Diptera, Coleoptera, Other Insects and Non Insects than any other catchment group. In this analysis, the Eerste-Molenaars rated lower than or equal to most other catchments in most categories, thus suggesting that it is not more diverse.

Table 3.5 Average number of taxa per river, by catchment group. Data extracted from full taxon list of LD rivers. OB = Olifants-Berg, EM = Eerste-Molenaars, TM = Table Mountain.

Taxon group	OB	EM	Breede	TM	Palmiet
Ephemeroptera	7.5	4.8	5.3	4.5	8.0
Plecoptera	1.5	1.5	1.5	2.5	2.0
Trichoptera	6.5	5.5	2.3	3.0	9.0
Diptera	11.8	11.7	16.3	20.5	27.0
Coleoptera	6.3	6.0	5.8	10.5	15.0
Other Insects	5.8	3.7	7.3	3.0	9.0
Non Insects	2.3	2.8	2.8	10.0	13.0

In a last assessment of taxon counts, the three large catchment groups were compared in terms of consistency of occurrence of each taxon. This was done because taxa occurring as a single individual in a single river had been treated in the same way as taxa occurring consistently in several rivers of a catchment group (Table 3.5), and this may have been obscuring strong distribution patterns. For the comparison, the four rivers of the Olifants-Berg group and the four of the Breede group were compared with four randomly picked rivers from the Eerste-Molenaars group (Eerste, Swartboskloof, Elands, Elandspad). A catchment group scored wherever a taxon occurred in at least three of its four rivers. The results were:

- Olifants-Berg 57 taxa in at least three of its four rivers
- Eerste-Molenaars 65 taxa in at least three of its four chosen rivers
- Breede 57 taxa in at least three of its four rivers

This again suggests that the three main catchment groups are much the same in terms of overall diversity, with the Eerste-Molenaars possibly being slightly more diverse.

Species richness and diversity can be expressed in different ways, as described by Clarke & Warwick (1994). One way is by the number of different species/taxa, shown as N_T in Table 3.6. In order to take abundance into account, Marglef's index d can be used, which is the number of species/taxa relative to the total number of individuals within a sample. Pielou's evenness index J' gives a measure of dominance or equity of the abundance of the species or taxa present, as a ratio of observed species diversity to that of the maximum possible diversity expected if all taxa were equally abundant. Where the observed diversity equals the maximum possible the evenness would be 1. The final index used here, the Shannon-Wiener diversity index H' , incorporates both species/taxa richness and evenness into one measure.

The diversity indices calculated for the three main catchment groups, as well as for the modified Eerste-Molenaars group of four selected rivers, produced similar values (Table 3.6). This supports the earlier findings that the three main catchment groups are approximately equal in terms of overall diversity, especially if the number of rivers per catchment group contributing to the indices is equal.

Table 3.6 Diversity indices for the three main catchment groups. N_R = number of rivers used in analysis, N_T = number of taxa (as per Table 3.4), d = Marglef's diversity index, J' = Pielou's evenness index, and $H'(\log_e)$ = Shannon-Wiener diversity index.

Catchment Group	N_R	N_T	Taxa/River	d	J'	$H'(\log_e)$
Olifants-Berg	4	166	41.5	30.75	0.94	4.81
Eerste-Molenaars	6	222	37.0	39.74	0.93	5.02
Eerste-Molenaars2	4	194	48.5	34.84	0.94	4.96
Breede	4	164	41.0	29.90	0.93	4.76

Summary statistics: shared taxa

As with the previous analyses, the counts of taxa shared between catchment groups were probably influenced by the different numbers of rivers sampled in each. Catchments with fewer sampled rivers had fewer chances to score shared taxa. With this in mind, some trends do emerge (Table 3.7). The Non Insects are omitted from this discussion because of the identification of some only to a higher taxonomic level.

The proportions of shared taxa of Ephemeroptera, Plecoptera, Diptera and Coleoptera are approximately the same and relatively high for most comparisons, while there are far fewer shared trichopterans. In any taxon group, the shared proportions tend to be highest between the three large catchment groups, dropping off, for all but the Plecoptera and Coleoptera, between those and the two small catchment groups. This trend could be a reflection of the number of rivers sampled, but there might be some geographical influence also as one of the small catchment groups (Table Mountain) lies outside the mountain range within which the others originate, whilst the other (Palmiet) is at the southern extreme of it. In general the fewest shared taxa are between the two small catchment groups, probably both because of the few rivers involved and because of their geographical isolation. In many respects the single river representing the Palmiet system does exceptionally well, with its proportions of shared species being about the same as for the two-river Table Mountain group.

The general impression from Sections 3.2, 3.4.1 and 3.4.2 is that there are complex mixes of unique and shared species within each catchment group. The assemblages of the catchment groups seem to have much the same general characteristics, with some differences such as few unique taxa and Trichoptera in the Breede system, and a possible higher diversity together with high numbers of Trichoptera in the Palmiet system.

Table 3.7 Shared taxa by catchment group (and percentage that this is of all taxa in each comparison). Data extracted from full taxon list of LD rivers. OB = Olifants-Berg, EM = Eerste-Molenaars, TM = Table Mountain.

Taxon group	Catchment group	EM	Breede	TM	Palmiet
Ephemeroptera					
	OB	15 (34)	14 (38)	7 (21)	4 (12)
	EM	-	22 (71)	8 (29)	6 (19)
	Breede		-	8 (36)	6 (26)
	TM			-	4 (31)
Plecoptera					
	OB	5 (50)	3 (33)	4 (57)	2 (33)
	EM	-	5 (50)	4 (40)	2 (22)
	Breede		-	4 (57)	2 (29)
	TM			-	2 (40)
Trichoptera					
	OB	14 (31)	5 (17)	3 (10)	4 (13)
	EM	-	6 (17)	5 (15)	5 (14)
	Breede		-	1 (7)	8 (80)
	TM			-	1 (7)
Diptera					
	OB	34 (40)	36 (47)	21 (31)	20 (37)
	EM	-	43 (44)	28 (31)	21 (26)
	Breede		-	27 (34)	22 (32)
	TM			-	14 (26)
Coleoptera					
	OB	13 (28)	9 (23)	8 (21)	7 (21)
	EM	-	17 (40)	13 (30)	12 (31)
	Breede		-	12 (38)	12 (46)
	TM			-	7 (24)
Other Insects					
	OB	8 (22)	10 (24)	3 (12)	3 (10)
	EM	-	10 (24)	1 (4)	2 (7)
	Breede		-	2 (6)	6 (19)
	TM			-	1 (7)
Non Insects					
	OB	5 (24)	4 (25)	6 (26)	4 (22)
	EM	-	9 (47)	14 (61)	10 (50)
	Breede		-	9 (41)	7 (41)
	TM			-	11 (50)

Summary statistics: Functional Feeding Groups

A final set of summary data was prepared by allocating each taxon in the full taxon list to a Functional Feeding Group (FFG), and re-running the PRIMER similarity analysis. FFGs were allocated with reference to the following sequence of literature sources and the definitions in

Tables 3.8 and 3.9. Information on list of literature used that occurs higher in the list took precedence over all following sources:

- The Guides to the Freshwater Invertebrates of Southern Africa, volumes 2 – 9. Water Research Commission, Pretoria:
 - Day, J.A., B.A. Stewart, I.J. de Moor and A.E. Louw (eds.). 2000. Crustacea I: Notostraca, Anostraca Conchostraca and Cladocera. Vol. 2. WRC Report No. TT 121/00. 126 p.
 - Day, J.A., I.J. de Moor, B.A. Stewart, and A.E. Louw (eds.). 2001. Crustacea II: Ostracoda, Copepoda and Branchiura. Vol. 3. WRC Report No. TT 148/01. 177 p.
 - Day, J.A., B.A. Stewart, I.J. de Moor and A.E. Louw (eds.). 2002. Crustacea III: Bathynellacea, Amphipoda, Isopoda, Spelaeogriphacea, Tanaidacea, and Decapoda. Vol. 4. WRC Report No. TT 141/01. 141 p.
 - Day, J.A. and I.J. de Moor (eds.). 2002a. Non-Arthropods: The Protozoans, Porifera, Cnidaria, Platyhelminthes, Nemertea, Rotifera, Nematoda, Nematomorpha, Gastrotrichia, Bryozoa, Tardigrada, Polychaeta, Oligochaeta and Hirudinea. Vol. 5. WRC Report No. TT 167/02. 293 p.
 - Day, J.A. and I.J. de Moor (eds.). 2002b. Arachnida and Mollusca: Araneae, Water Mites and Mollusca. Vol. 5. WRC Report No. TT 182/02. 141 p.
 - Day, J.A., A.D. Harrison and I.J. de Moor (eds.). 2002. Diptera. Vol. 9. WRC Report No. TT 201/02. 200 p.
 - de Moor, I.J., J.A. Day and F.C. de Moor (eds.). 2003a. Insecta I: Ephemeroptera, Odonata and Plecoptera. Vol. 7. WRC Report No. TT 207/03. 288 p.
 - de Moor, I.J., J.A. Day and F.C. de Moor (eds.). 2003b. Insecta II: Hemiptera, Megaloptera, Neuroptera, Trichoptera and Lepidoptera. Vol. 8. WRC Report No. TT 214/03. 209 p.
- Appleton, C.C. 1996. Freshwater molluscs of southern Africa. University of Natal Press, Pietermaritzburg. 64 p.
- Chessman, B.C. 1986. Dietary studies of aquatic insects from two Victorian rivers. Australian Journal of Marine and Freshwater Research. 37:129-146.
- Davies, B.R. and J.A. Day. 1998. Keys to the common macroinvertebrate taxa of South African inland waters. In Vanishing Waters. B.R. Davies and J.A. Day (eds). University of Cape Town Press, Cape Town. pp. 418-460.
- Davies, B.R., J.H. O'Keeffe and C.D. Snaddon. 1993. A synthesis of the ecological functioning, conservation and management of South African river ecosystems. Water Research Commission, Pretoria. Report No. TT 62/93. 232 p.
- King, J.M. 1982. An ecological study of the macro-invertebrate fauna of the Eerste River, Western Cape Province, South Africa. PhD thesis, University of Cape Town. 221 p.
- Scott, K.M.F. 1983. On the Hydropsychidae (Trichoptera) of Southern Africa with keys to the African genera of imago, larvae and pupae and species lists. Annals of the Cape Provincial Museums (Natural History). 14(8):299-422.
- Scott, K.M.F. and F.C. de Moor. 1993. Three recently erected Trichoptera families from South Africa, the Hydrosalpingidae, Petrothrincidae and Barbarochthonidae (Integripalpia: Sericostomatoidea). Annals of the Cape Provincial Museums: Natural History. 18(4):293-354.
- Gerber, A. and M.J.M. Gabriel. 2002. Aquatic invertebrates of South African rivers: field guide. Institute for Water Quality Studies, Department of Water Affairs and Forestry. Pretoria. 150p.
- Merrit, R.W. and K.W. Cummins. 1984. An Introduction to the Aquatic Insects of North America. Kendall/Hunt Publishing Company, Dubuque. 722 p.
- Pennak, R.W. 1989. Fresh-water Invertebrates of the United States, Protozoa to Mollusca. Wiley Interscience, New York.

- Thorp, J.H. and A.P. Covich. 1991. Ecology and Classification of North American Freshwater Invertebrates. Academic Press, Inc. London. 911 p.

Table 3.8 Functional Feeding Group (FFG) definitions, modified from the literature listed above. FPOM – fine particulate organic matter. VFPOM = very fine particulate organic matter.

FFG	Feeding Mode	Dominant Food Type
Predator 1	Feeds on animals via active predation.	Micro-organisms – bacteria to zooplankton, zoobenthos, etc.
Predator 2		Insects to small vertebrates
Filter Feeder	Collects small particles of food suspended in the water column.	Range of micro-organisms from bacteria – algae – zooplankton
Deposit Feeder 1	Collector/gatherer of deposited organic material off and within the substratum.	Detritus (VFPOM and FPOM) only
Deposit Feeder 2		Algae and detritus in comparative amounts dependent on availability.
Shredder	Fragments leaves and large pieces of plant material.	Vegetation
Scraper 1	Scrapes thin film of micro-organisms off substrata.	Algae
Scraper 2		Algae and detritus
Grazer 1	Feeds on whole living plants, leaves and stems. Algal mats can be included where scraping is not employed as a mechanism for collection.	Vegetation
Grazer 2		Algae
Omnivore	Feeds on anything and everything available; mainly reserved for scavengers such as crabs.	Everything
DNF	Does not feed; mainly pupal forms of invertebrates that are no longer feeding	Nothing

Table 3.9 Further definition of some of the food types listed in Table 3.8.

Food Type	Definition
Invertebrate	Predominantly macroinvertebrates of > 80µm in size.
Small vertebrate	Tadpoles, small fish
Micro-organisms	Predator terms: microinvertebrates < 80µm in size, zooplankton Filter feeder terms: bacteria, fungi, algae, zooplankton, etc.
Vegetation	Macrophytes, leaves from riparian trees, moss
Algae	Diatoms, epiphytes, epilithon, filamentous algae, etc.
Detritus	Mix of mainly organic and some inorganic particles that are the remains of plant and animal material

Cluster analysis of the rivers, with the invertebrates sorted by FFGs, revealed that the catchment signature had disappeared (Figure 3.3a) – at last!! There was a very high similarity (>80%) in the FFG composition of all the rivers, with two sub-clusters within the main cluster and three outliers. Sub-cluster 1 remained intact in the MDS plot (Figure 3.3b) and contained, with two exceptions, sites with a map gradient of < 0.040. Sub-cluster 2 also retained identity on the MDS plot, and contained sites that had a map gradient of > 0.040. Map gradient alone had a correlation coefficient of $\rho_w = 0.26$ in a BIOENV procedure.

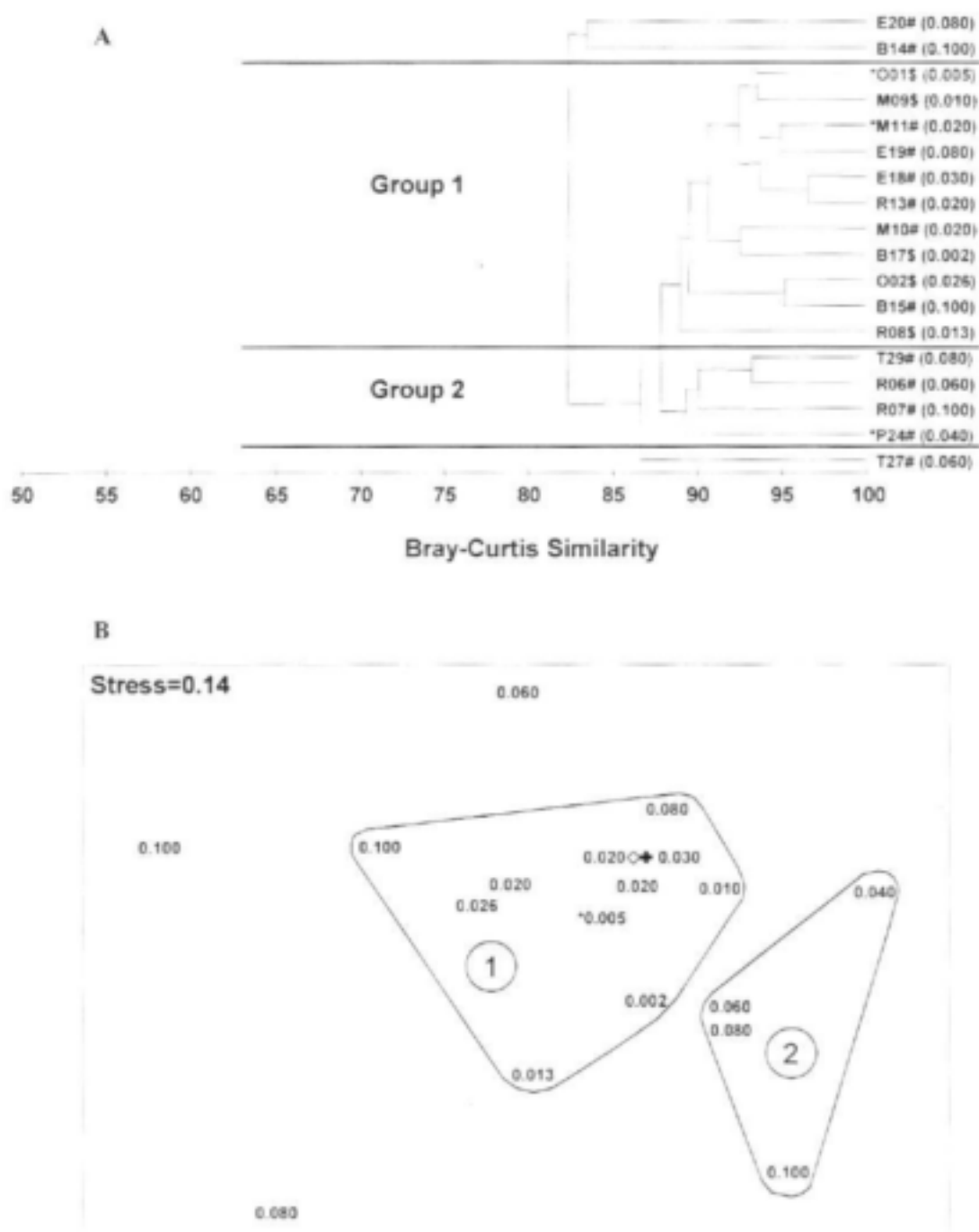


Figure 3.3 A. Dendrogram of invertebrate assemblages from LD rivers when taxa allocated to ten FFGs, map gradient in parentheses after each site code. B. 2-d MDS plot, points represented by map gradient, with main groups identified in the dendrogram separated by circles. Full taxon list used.

Other environmental variables that showed a correlation were site gradient and gravels, and when combined with map gradient, the three variables had a correlation coefficient of $\rho_{\alpha} = 0.41$, which is a much stronger relationship to the FFG distributions than any one of these variables alone (gravels and site gradient each had $\rho_{\alpha} \leq 0.24$ on its own).

The overall impression was that the FFGs were reflecting an imprecise separation of mountain from foothill sites, and thus supporting the distinction of such zones by FFGs as suggested by the River Continuum Concept (Vannote *et al.* 1980). In terms of environmental drivers, map gradients correlated with this division slightly better than did site gradients, suggesting that the overall nature of the river channel and flow at any point may be a more important determinant of trophic functioning than the detailed micro/mesohabitat at that point. Overall, however, all the sites were very similar in terms of FFG composition, suggesting that despite their differences in invertebrate taxa the sites were functioning in much the same way.

While these analyses allow some insight into the nature of the assemblages, they do not explain why the catchment signatures result. To facilitate further investigation, a technique was first developed for graphically summarising and comparing their species assemblages.

Graphic representation of species assemblages

The species assemblages of the three main catchment groups (Olifants-Berg, Eerste-Molenaars, Breede) were summarised by creating curves illustrating the contribution of each taxon group to each assemblage. The curves were created from data on the number of taxa in each taxon group expressed as proportions of all the taxa in that catchment group (Table 3.10).

Table 3.10 The numbers and proportions of taxa present per taxon group in each catchment group. N = number of taxa, OB = Olifants-Berg, EM = Eerste-Molenaars.

Taxon group	OB		EM		Breede	
	N	%	N	%	N	%
Ephemeroptera	12	21.4	12	17.1	8	14.8
Plecoptera	3	5.4	6	8.6	2	3.7
Trichoptera	6	10.7	5	7.1	3	5.6
Diptera	18	32.1	20	28.6	24	44.4
Coleoptera	10	17.9	17	24.3	13	24.1
Non Insects	4	7.1	9	12.9	2	3.7
Other Insects	3	5.4	1	1.4	2	3.7
Total	56	100.0	70	100.0	54	100.0

These values then contributed to cumulative curves compiled by adding each percentage contribution in the order shown in Table 3.10. The shape of each resulting curve is unique for its catchment group (Figure 3.4). Pooling the data by catchment group, the cumulative percentage points were also plotted and a 3rd order polynomial regression fitted (Figure 3.5).

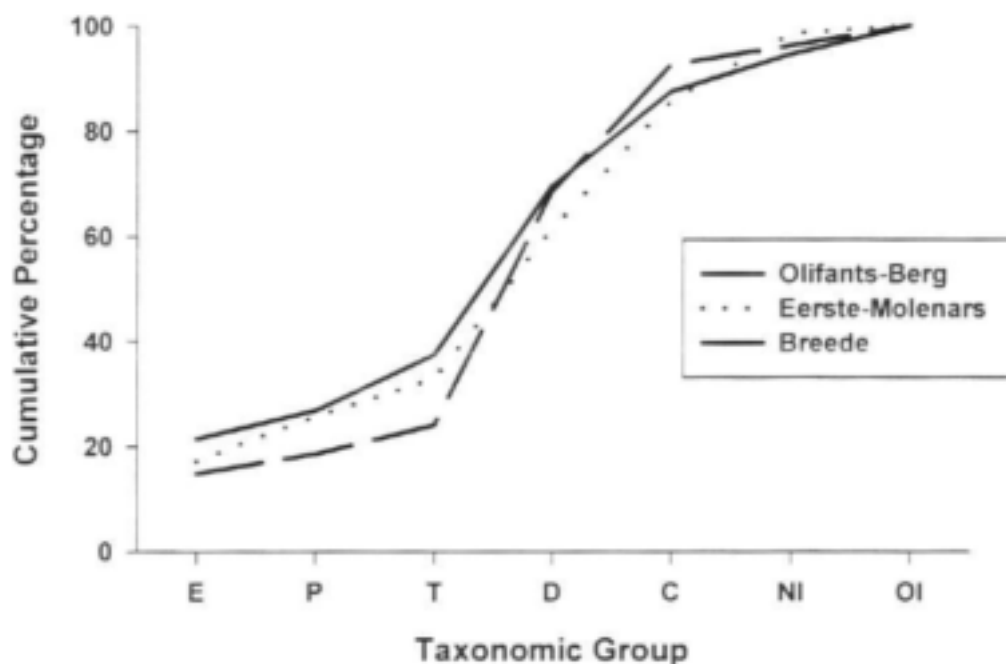


Figure 3.4 Cumulative percentages of taxonomic groups for LD catchment groups. E = Ephemeroptera, P = Plecoptera, T = Trichoptera, D = Diptera, C = Coleoptera, NI = non-insects, OI = other insects.

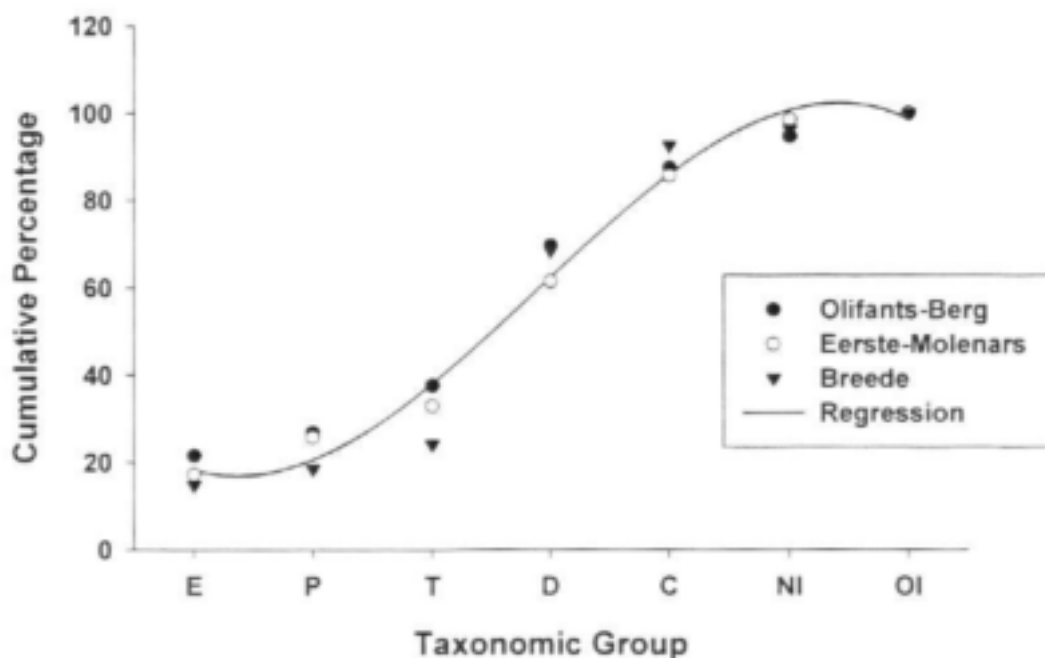


Figure 3.5 A 3rd order polynomial regression analysis of cumulative percentages of taxonomic groups for LD catchment groups. Regression line given for all data points. E = Ephemeroptera, P = Plecoptera, T = Trichoptera, D = Diptera, C = Coleoptera, NI = non-insects, OI = other insects.

These curves support the earlier finding that the overall proportions of different taxon groups in each catchment group are similar. This suggests that the catchment signatures must be caused by the individual mix of species within each taxon group. To explore this further, the PRIMER package was used to analyse between-catchment dissimilarity at the individual taxon level.

Between catchment dissimilarity – characteristics of Top Discriminator list

Again, the first impression is of the large numbers of taxa, in this case required to explain the dissimilarity between catchment groups (Table 3.11). For the larger catchment groups 19-24 taxa are needed to explain 20% dissimilarity and 171-195 taxa for 90% dissimilarity. The marine examples provided in the PRIMER Manual (Clarke & Warwick 1994) show only 1-2 taxa needed for 20% dissimilarity and 10-14 taxa for 90% dissimilarity. With such large numbers in the river analyses, it is very difficult to assess the overall trends in dissimilarity. In an attempt to simplify the task, the Top Discriminators were used as described in Table 3.3 and accompanying text.

Table 3.11 The number of taxa required to explain 20% and 90% of the dissimilarity between catchments. OB = Olifants-Berg, EM = Eerste-Molenaars, TM = Table Mountain.

Catchment groups	Taxa to 20% dissimilarity	Taxa to 90% dissimilarity
OB v EM	24	195
OB v Breede	19	171
OB v TM	20	152
OB v Palmiet	16	128
EM v Breede	22	184
EM v TM	21	170
EM v Palmiet	21	151
Breede v TM	18	144
Breede v Palmiet	13	120
TM v Palmiet	14	106

The proportions of most taxon groups within the Top Discriminator list were similar for all comparisons, with the Plecoptera, Non-Insects and Other Insects possibly being a little less consistent (Table 3.12). The Non-Insects also on average appeared more than twice as often in the Top Discriminator list as their proportion in the total taxa justified, while Other Insects appeared only half as often. This may reflect the generally poor dispersal powers of the Non Insects and good dispersal power of Other Insects such as Odonata. The Trichoptera, Diptera and Coleoptera, which had the highest numbers of taxa in total, appeared in the Top Discriminator list in roughly the same proportions as in the total taxon list. This suggests that there was no major swing in assemblage composition from one catchment group to the other, supporting the findings illustrated by the cumulative curves (Figures 3.4-3.5).

Between catchment dissimilarity – species comparisons

Every analysis to this point has indicated a remarkable consistency in the overall characteristics of the invertebrate assemblages of the LD rivers, and little that reveals why they have individual catchment signatures. As there are no major shifts of taxon groups from catchment to catchment, the cause of the signatures must be the precise mix of species within each taxon group. This is further explored using the Top Discriminator list and the three main catchment groups. In Tables 3.13-3.19, the Top Discriminator taxa are arranged by taxon group, showing those taxa important in distinguishing the Olifants-Berg group from the Eerste-Molenaars (columns 1-2), the Olifants-Berg from the Breede (columns 3-4), or the Eerste-Molenaars from the Breede (columns 5-6). Each entry lies within the catchment group it distinguishes, whilst any occurrence of the same taxon in the other group in the comparison is shown with asterices. For instance, in Table 3.13, *Castanophlebia calida* is a distinguishing taxon for the Breede in its comparison with the Olifants-Berg group, but the latter group also has that species in two of its four rivers (= two asterices).

Table 3.12 Number (and percentage) of taxa in each taxon group that appear in the Top Discriminators in the SIMPER dissimilarity analysis, and the number (and percentage) of each taxon group in the total taxon list. OB = Olifants-Berg, EM = Eerste-Molenaars, TM = Table Mountain, E = Ephemeroptera, P = Plecoptera, T = Trichoptera, D = Diptera, C = Coleoptera, NI = non-insects, OI = other insects.

Catchment groups	E	P	T	D	C	NI	OI
OB v EM	4 (13)	6 (19)	1 (3)	5 (15)	7 (22)	7 (22)	2 (6)
OB v Breede	3 (10)	2 (7)	5 (17)	9 (32)	7 (24)	1 (3)	2 (7)
OB v TM	2 (7)	2 (7)	2 (7)	7 (27)	4 (15)	9 (35)	0 (0)
OB v Palmiet	2 (9)	0 (0)	2 (9)	6 (27)	6 (27)	4 (19)	2 (9)
EM v Breede	3 (9)	3 (9)	3 (9)	11 (35)	7 (22)	4 (13)	1 (3)
EM v TM	4 (14)	2 (7)	4 (14)	9 (32)	5 (18)	3 (11)	1 (4)
EM v Palmiet	2 (6)	0 (0)	4 (14)	9 (31)	3 (10)	4 (14)	7 (25)
Breede v TM	1 (4)	1 (4)	4 (16)	7 (28)	4 (16)	8 (32)	0 (0)
Breede v Palmiet	3 (12)	0 (0)	1 (4)	7 (27)	5 (19)	6 (23)	4 (15)
TM v Palmiet	1 (6)	0 (0)	4 (22)	5 (28)	5 (28)	1 (6)	2 (10)
Average occurrence in TD list	3 (9)	2 (5)	3 (12)	8 (28)	5 (20)	5 (18)	2 (8)
Total (%) of full taxon list	48 (13)	10 (3)	53 (14)	120 (32)	55 (15)	27 (7)	59 (16)

Seven ephemeropteran taxa were involved in ten entries (Table 3.13), with four of these entries involving taxa that were not in the opposing catchment group, and six involving taxa that were (shown in the table by asterices). Two taxa (*C. capensis* and *Aprionyx* spp. early instar) distinguished the Olifants-Berg catchment from both other catchment groups, and one (*Nadinetella crassi*) distinguished the Eerste-Molenaars group from the other two. There were no obvious trends in differences in FFGs.

Table 3.13 Ephemeropteran taxa from the Top Discriminator list that distinguish catchment groups as shown. For further explanation see text. inst = early instar. FFGs represented are: Deposit Feeder 1 and Deposit Feeder 2.

Olifants-Berg	Eerste-Molenaars	Olifants-Berg	Breede	Eerste-Molenaars	Breede
<i>Cheleocloeon excisum</i>	*			<i>Demoreptus capensis</i>	**
<i>Caenis capensis</i>		<i>C. capensis</i>			
<i>Aprionyx</i> spp. inst	*	<i>Aprionyx</i> spp. inst		Leptophlebiidae spp. inst	**
		**	<i>Castanophlebia calida</i>		
	<i>Nadinetella crassi</i>			<i>Nadinetella crassi</i>	**

Six plecopteran taxa were involved in 11 entries (Table 3.14), with seven of these entries involving taxa that were not in the opposing catchment group, and four involving taxa that were. Genera identified to species were late instars with species identification features present. Two taxa (*Aphanicercopsis* spp. and *Desmonemoura* spp.) distinguished the Olifants-Berg catchment from both other catchment groups; one (*Aphanicercella* spp.) distinguished the Olifants-Berg and Breede from the Eerste-Molenaars, and two (*Aphanicercella bicornis* and *Aphanicercella barnardi/scutata*) the Eerste-Molenaars from the two others. There was a clear trend of the Eerste-Molenaars being dominated by shredders and the other two catchment groups by Deposit Feeder 1 (early instars).

Table 3.14 Plecopteran taxa from the Top Discriminator list that distinguish catchment groups as shown. For further explanation see text. *Aphanicercella b/s* = *Aphanicercella barnardi/scutata*. FFGs represented are: Deposit Feeder 1 and Shredder.

Olifants-Berg	Eerste-Molenaars	Olifants-Berg	Breede	Eerste-Molenaars	Breede
	<i>Aphanicercella bicornis</i>			<i>A. bicornis</i>	
	<i>Aphanicercella capensis</i>				
	<i>Aphanicercella b/s</i>			<i>Aphanicercella b/s</i>	
<i>Aphanicercella</i> spp.	***			***	<i>Aphanicercella</i> spp.
<i>Aphanicercopsis</i> spp.		<i>Aphanicercopsis</i> spp.	**		
<i>Desmonemoura</i> spp.	**	<i>Desmonemoura</i> spp.			

Six trichopteran taxa were involved in nine entries (Table 3.15), with five of these entries involving taxa that were not in the opposing catchment group, and four involving taxa that were.

One taxon (*Chimarra* sp. and *Desmonemoura* spp.) distinguished the Olifants-Berg catchment from both other catchment groups; and two (*Parecnomina resima* and *Leptoceridae* spp. early instar) distinguished the Breede from the other two (the first being less abundant in the Breede and the second more abundant). There were no obvious trends in FFGs.

Table 3.15 Trichopteran taxa from the Top Discriminator list that distinguish catchment groups as shown. For further explanation see text. inst = early instar. FFGs represented are: Deposit Feeder 1, Deposit Feeder 2, Filter Feeder, Predator 1 and Scraper 2.

Olifants-Berg	Eerste-Molenaars	Olifants-Berg	Breede	Eerste-Molenaars	Breede
<i>Chimarra</i> sp.	*	<i>Chimarra</i> sp. <i>Parecnomina resima</i> <i>Cheumatopsyche maculata</i> *	Hydropsychidae spp. inst. Leptoceridae spp. inst.	<i>P. resima</i> **** <i>Agapetus</i> sp.	Leptoceridae spp. inst

Eighteen dipteran taxa were involved in 25 entries (Table 3.16), with four of these entries involving taxa that were not in the opposing catchment group, and 21 involving taxa that were. Three taxa (*Atherix* sp. 1 and sp. 2, *Limnophila nox*) distinguished the Breede group, and one (*Polypedium alticola*) distinguished the Eerste-Molenaars. *Cricotopus* sp. 1 and *Rheocricotopus capensis* were least abundant in the Breede. Most of the distinguishing taxa belonged to the FFGs Predator 1 or 2, or Scraper 2.

Table 3.16 Dipteran taxa from the Top Discriminator list that distinguish catchment groups as shown. For further explanation see text. FFGs represented are Predator 1, Predator 2, Deposit Feeder 1, Deposit Feeder 2 and Scraper 2.

Olifants-Berg	Eerste-Molenaars	Olifants-Berg	Breede	Eerste-Molenaars	Breede
<i>Polypedium</i> U sp.	**** <i>Polypedium alticola</i>			**** <i>P. alticola</i> <i>Conchapelopia</i> sp.	<i>Polypedium</i> U sp. *** ****
<i>Procladius</i> sp.	*			<i>Cardiocladius</i> sp.	***
****	<i>Rheocricotopus capensis</i>	<i>R. capensis</i> <i>Cricotopus</i> sp. 1 **** <i>Tanytarsus</i> sp. 1 <i>Tvetenia calvescens</i> <i>Atherix</i> sp. 2 <i>Atherix</i> sp. 3	*** *** ** **** *** ***	<i>Cricotopus</i> sp. 1 * <i>Thienemanniella</i> sp. 1 *** *	*** <i>Stempellina</i> sp. ** <i>Atherix</i> sp. 2 <i>Atherix</i> sp. 3
<i>Hemerodromia</i> sp.	*	** *	<i>Limnophila nox</i> <i>Limnophila</i> sp.	 *	<i>L. nox</i> <i>Chironomidae</i> spp

Fourteen coleopteran taxa were involved in 21 entries (Table 3.17), with 17 of these entries involving taxa that were not in the opposing catchment group, and four involving taxa that were. Four taxa (*Elmidae* sp. 1 adult, *Elpidelmis* sp. 1 adult, *Elpidelmis* sp. A larva, *Helodidae* sp. 5), distinguished the Eerste-Molenaars group, and three (*Elpidelmis* sp. larva, *Peloriolus* sp. adult, *Mesoceration* spp.) the Olifants-Berg. Most of the distinguishing taxa belonged to the FFGs Scraper 1 or 2.

Table 3.17 Coleopteran taxa from the Top Discriminator list that distinguish catchment groups as shown. For further explanation see text. FFGs represented are Scraper 1, Scraper 2 and Grazer 1. Ad = adult, all others are larvae.

Olifants-Berg	Eerste-Molenaars	Olifants-Berg	Breede	Eerste-Molenaars	Breede
				<i>Strina</i> sp. 1 Ad	***
					<i>Dryopidae</i> spp. Ad
	<i>Elmidae</i> sp. 1 Ad			<i>Elmidae</i> sp. 1 Ad	
				<i>Elmidae</i> sp. 1	
	<i>Elpidelmis</i> sp. 1 Ad		<i>Elpidelmis</i> sp. 1 Ad		
	<i>Elpidelmis</i> sp. A		<i>Elpidelmis</i> sp. A		
<i>Elpidelmis</i> spp.	*	<i>Elpidelmis</i> spp.			
<i>Peloriolus</i> spp.		<i>Peloriolus</i> sp.			
Ad		Ad			
		<i>Peloriolus</i> sp. 1			
	<i>Helodidae</i> sp. 5	<i>Hydraena</i> sp. 1		<i>Helodidae</i> sp. 5	
				*	<i>Hydraenidae</i> spp. Ad
<i>Mesoceration</i> spp.	****	<i>Mesoceration</i> spp.			<i>Limnichidae</i> sp.

Three taxa of Other Insects were involved in five entries (Table 3.18), with two of these entries involving taxa that were not in the opposing catchment group, and three involving taxa that were. One taxon (*Aeshna* sp., Odonata) distinguished the Olifants-Berg group and one (*Paragomphus* sp., Odonata) the Breede. All of the distinguishing taxa belonged to the FFG Predator 2.

Table 3.18 Other Insects from the Top Discriminator list that distinguish catchment groups as shown. For further explanation see text. inst = early instar. FFG represented is Predator 2.

Olifants-Berg	Eerste-Molenaars	Olifants-Berg	Breede	Eerste-Molenaars	Breede
*	<i>Corydalidae</i> spp. inst.				
<i>Aeshna</i> sp.		<i>Aeshna</i> sp.	*		
		**	<i>Paragomphus</i> sp.		<i>Paragomphus</i> sp.

The comparisons that highlighted Non-Insects (Table 3.19) are not discussed because most taxa were identified only to family or order level and thus provide too coarse and generalised a picture of differences for this analysis.

Table 3.19 Non Insects from the Top Discriminator list that distinguish catchment groups as shown. For further explanation see text. FFGs represented are Deposit Feeder 1, Predator 1, Predator 2, Scraper 2 and Grazer 2.

Olifants-Berg	Eerste-Molenaars	Olifants-Berg	Breede	Eerste-Molenaars	Breede
	Lumbriculidae spp.				
	Naididae spp.			Naididae spp.	
Oligochaeta spp.		Oligochaeta spp.			
*	Cyclopoida spp.			Cyclopoida spp.	*
	Nematoda spp.				
	Anisakellidae spp.				
	Oribatidae spp.			Oribatidae spp.	
				Chydoridae spp.	

As a whole, the comparisons provide no clear picture of why the catchment signatures form and, apart from the Plecoptera, no clear trend in FFG replacements. Approximately half the Top Discriminators are present not only in the catchment group they distinguish, but also - in lower numbers - in the catchment group they distinguish against, and so the distinctions are ones of abundance as often as of presence and absence. There is no obvious trend in the changes in dominant species per catchment, and no pattern that can be detected within the individual taxa replacements that would allow predictions of what might distinguish an unstudied catchment.

A final investigation of the signatures (Section 3.5) addresses why two of the main catchment groups (Olifants-Berg and Eerste-Molenaars) each consist of two major rivers that are not actually in the same catchment.

3.5 Similarity within catchments groups

The Olifants and Berg Rivers have contiguous catchments on the west coast of the Western Province, and are the only two catchments that drain into the Atlantic Ocean (Figure 1.1). Through all the catchment analyses invertebrate samples from the two rivers in each catchment have remained closely linked. The Eerste is a small catchment draining into False Bay on the south-western coast and the Molenaars a major tributary of the Breede system (Figure 1.1). The two rivers are not geographically contiguous although they do rise in the same mountain range.

PRIMER analyses revealed the following similarity levels between and within catchments:

- Between Olifants-Berg and Eerste-Molenaars 32.33
- Between Olifants-Berg and Breede 36.56
- Between Eerste-Molenaars and Breede 41.33

- Within Eerste-Molenaars 52.00
- Within Olifants-Berg 52.16

- Within Olifants 51.32
- Within Molenaars 52.82
- Within Berg 60.27
- Within Eerste 57.92

- Breede 53.42

Similarity is lowest between the three main catchment groups (32.33–41.33%), appreciably higher within the two multi-catchment groups (52.00–52.16%), and about the same or slightly higher still (51.32–60.27) within the four individual river systems in the two multi-catchment groups. The similarity within the two multi-catchment groups is similar to that within the single-catchment Breede group, indicating why the former have clustered together.

The above findings are well illustrated in the PRIMER dendrograms and MDS plots (e.g. Figure 3.1), but there is no indication of how each taxon group contributes to the pattern. In a final analysis, the percentages of shared taxa between and within catchments were compared with the overall trend shown by the data set (Table 3.20). The mean percent and standard deviation of shared taxa between LD catchments was derived from Table 3.8 (columns 2 and 3). These summary data were compared to the percent of shared taxa within the two multi-catchment groups (columns 4 and 5), between randomly selected individual rivers within the same catchment group (columns 6 and 7) and between randomly selected individual rivers in different catchment groups (columns 8 and 9). In most cases, within-catchment comparisons of shared species (columns 4–7) score higher than the between-catchment comparisons (columns 8 and 9). There are some anomalies, but the overall pattern suggests that all taxonomic groups are contributing in the same way to the similarity and dissimilarity patterns.

The pairing of different catchments within larger multi-catchment groups appears to be caused by more shared species than between catchment groups, with all the major taxon groups involved in much the same way.

Table 3.20 Shared taxa per taxon group, between and within catchments, as a percentage of all taxa within those comparisons. LD rivers only. ** = above mean + SD; * = above mean; # = below mean; ## = below mean – SD.

Taxon group	LD Catchments		OB	EM	Breede	Eerste	Breede	
	Mean % shared taxa	SD	% shared taxa	% shared taxa	% shared taxa	% shared taxa	% shared taxa with Berg	% shared taxa with Olifants
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
Ephemeroptera	32	16	47*	52**	53**	47*	30#	26#
Pleoptera	41	12	67**	60**	33#	71**	25##	50*
Trichoptera	21	22	36*	29*	75**	22*	10#	10#
Diptera	35	7	50**	49**	50**	29#	44**	43**
Coleoptera	30	9	57**	55**	56**	48**	14##	14##
Other Insects	14	8	25**	41**	17*	54**	6#	22*
Non Insects	39	14	67**	52*	67**	14##	18##	11##

3.6 Conclusions

The catchment signatures are not readily explained by the above analyses of invertebrate community structure and can best be summarised as having the following characteristics:

- they are not caused by unique species;
- they are not caused by unique abundances of the taxa present;
- they are not caused by major differences in the proportions of different taxon groups – there is a very high consistency in these proportions from catchment to catchment;
- they are caused by the precise mix of taxa within each taxonomic group;
- the signatures disappear when the invertebrates are represented by FFGs rather than by species names, and another pattern is revealed that suggests invertebrate distributions based on longitudinal river zones.

The mixes of taxa from catchment to catchment are further investigated in Chapter 5.

4. THE EFFECTS OF DISTURBANCE ON CATCHMENT CHARACTERISTICS OF INVERTEBRATE COMMUNITIES

4.1 Introduction

The 17 mountain and foothill LD sites defined reference conditions (King & Schael 2001) for invertebrate community composition (Chapter 3) against which disturbed (D) sites could be compared. Eleven D mountain and foothill sites (Table 1.1) provided the data for investigating the effects of different kinds of human disturbance on the invertebrate communities and catchment signatures. Each site had one main disturbance (Table 4.1):

Table 4.1 The main anthropogenic disturbance at or upstream of each D site.

River	River zone	Disturbance
Palmiet	Mountain	Dams
Window	Mountain	Botanical garden with oak trees and some water abstraction
Cecilia	Mountain	Protected natural area infested with alien grey poplar <i>Populus canescens</i>
Middeldeer	Foothill	Vegetable farming
Noordhoek	Foothill	Bulldozed cobble bed with water diversion
Groot	Foothill	Irrigated vegetable farming
Berg	Foothill	Pine plantations, and inter-basin transfer 1 km downstream
Wemmershoek	Foothill	Dam, with very reduced dry-season flow, and bulldozed cobble bed
Holsloot	Foothill	Dam, with bottom-release of very cold water
Lourens	Foothill	Fruit orchards, vineyards and piggery
Dauidskraal	Foothill	Dam, concrete retaining walls and some sedimentation of bed

Cluster analysis and MDS plots of the invertebrate assemblages of all 28 sites (Figures 4.1 and 4.2) revealed that the D sites reacted to disturbance in four main ways that might reflect increasing levels of impact:

- some sites clustered with other sites from their catchment, suggesting that disturbance had had little impact on invertebrate community structure: e.g. Groot (Olifants catchment) and Window (Table Mountain);
- one site with an inter-basin water transfer about 1 km downstream clustered with the donor system, suggesting a transfer of taxa between catchments: Berg (Berg);
- four sites clustered together in a separate group on the MDS plot, within the circle of LD river catchment clusters, suggesting that they had lost their catchment signatures but were still characteristically Western Cape rivers: Middeldeer and Noordhoek (Olifants), Wemmershoek (Berg) and Palmiet (Palmiet);
- two sites clustered together outside all other groups on the MDS plot, suggesting that they had lost their catchment signatures and, to some extent, their Western Cape characteristics: Holsloot (Breede) and Cecilia (Table Mountain).

In addition, two D sites in small coastal catchments linked with larger catchment groups: Dauidskraal with the Eerste-Molenaars group and Lourens with the Breede group. Geographically, Lourens is nearer to the Eerste and Dauidskraal to the Palmiet and so it is unclear to what extent their grouping indicates a level of disturbance.

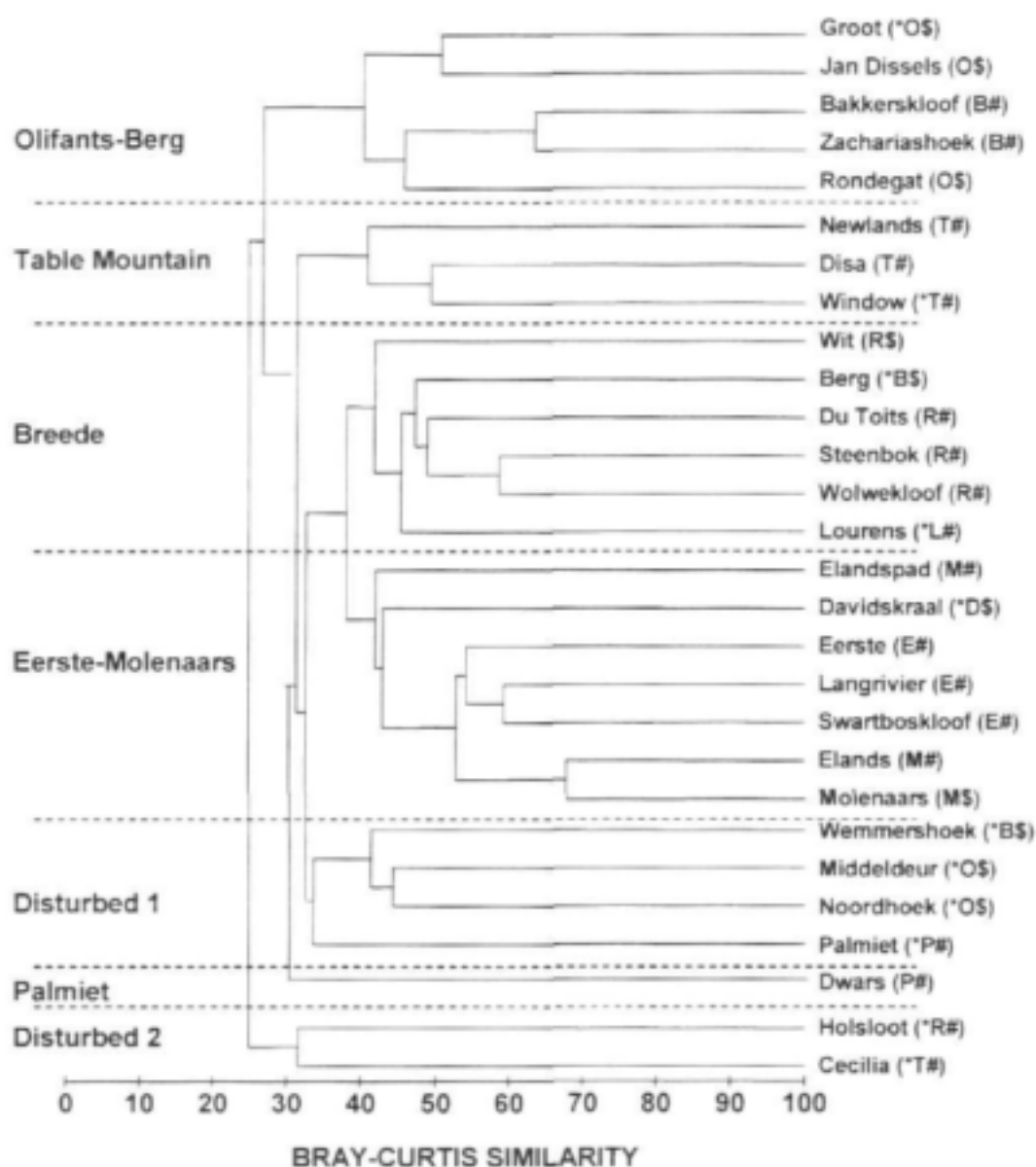


Figure 4.1 Dendrogram of the 17 least-disturbed sites and 11 disturbed sites, using species level data of invertebrates. Modified from King & Schael (2001). River names are given with first letter of the catchment in parentheses. # = predetermined mountain zone and \$ = predetermined foothill zone based on literature; * = disturbed rivers.

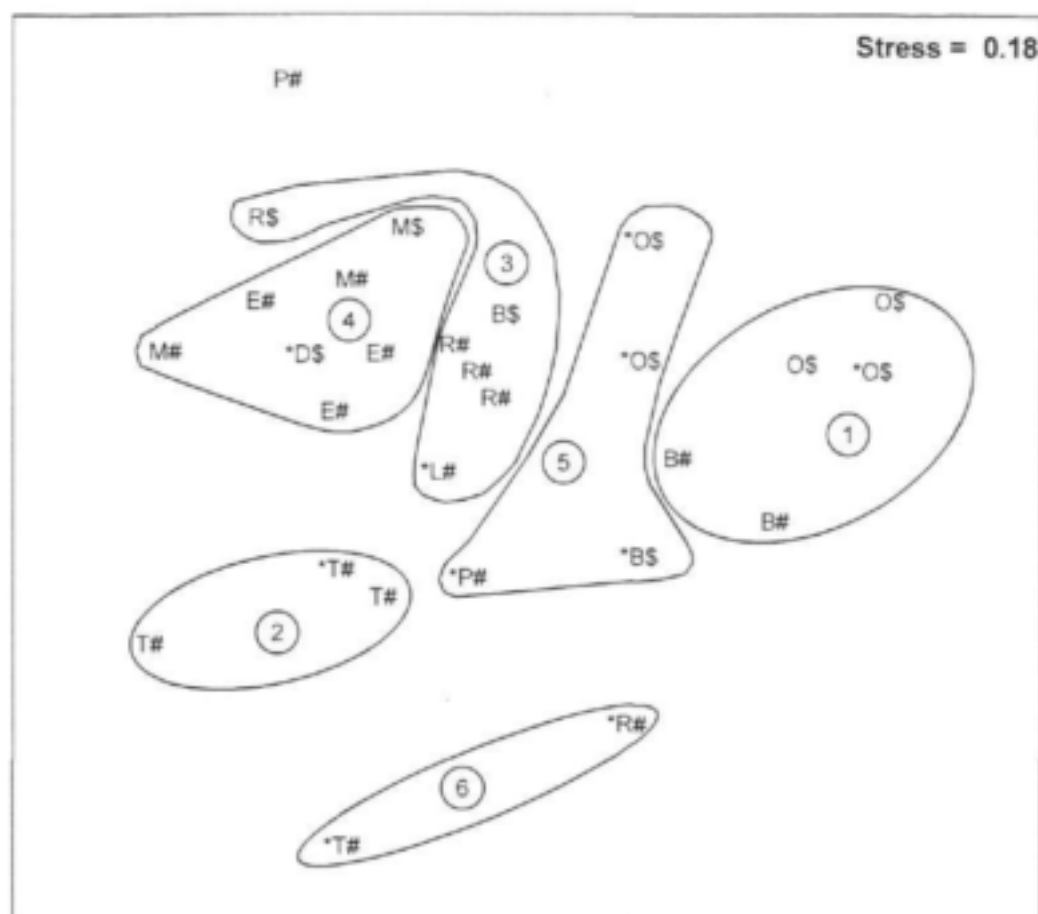


Figure 4.2 Two-dimensional configuration of the 17 LD sites and 11 D sites, using species level data of invertebrates. Modified from King & Schaefer (2001). The groups recognised in Figure 4.1 are shown as different subgroups: 1 = Olifants-Berg; 2 = Table Mountain; 3 = Breede; 4 = Eerste-Molenaars; 5 = Disturbed 1; 6 = Disturbed 2. Each site is referred to by the first letter of its catchment name and zone. # = predetermined mountain zone and \$ = predetermined foothill zone based on literature; * = disturbed rivers.

Five main investigations were completed to ascertain the details of what happened to the invertebrate communities under these disturbances:

- cumulative curves of taxonomic composition per D site were overlayed on the reference condition band for LD rivers (Section 4.2);
- a range of diversity indices was calculated for each D site and compared with the LD ranges (Section 4.3)
- the numbers of shared taxa between each D site and its LD reference condition (Table 3.13) were calculated (Section 4.4);
- abundance ratings for all taxa in all LD and D sites were weighted by SASS values in an attempt to distinguish between invertebrate communities that are more or less sensitive to chemical disturbance (Section 4.5);
- the number of taxa and mean abundance rating of each taxon group in each D site were compared with its LD reference condition, and community shifts analysed (Section 4.6)

4.2 Percentage composition of taxonomic groups for D sites

The calculations of percentage composition of taxonomic groups for the three main LD catchments (Table 3.10) were repeated for all LD and D rivers individually. The results for LD rivers were used to create a reference-condition cumulative curve similar to Figure 3.5. The cumulative curve for each D river was then overlayed on the reference-condition curve (Figure 4.3a-d).

All but one of the regression lines for the D sites were similar to the reference-condition regression provided by the LD sites, the exception being Cecilia. Six of the D sites had one or more individual cumulative percentage values that lay outside the reference-condition line: Wemmershoek, Holsloot and Palmiet (Figure 4.3a), Cecilia and Window (Figure 4.3c) and Lourens (Figure 4.3d). A paired *t*-test was used to test if the cumulative percentage of taxonomic groups for each individual D site was significantly different from that of the overall average of each group for the LD rivers. The means across taxonomic groups for all D sites versus that of the mean of the LD were also tested. The comparison between all D and LD sites showed a significant difference between distributions at $P = 0.016$ ($t = 3.33$, d.f. = 6). Each individual D site comparison, however, showed only three D sites were significantly different from the LD average at a $P < 0.05$ level: Palmiet ($t = 4.2$, d.f. = 6, $P = 0.006$), Wemmershoek ($t = 3.15$, d.f. = 6, $P = 0.020$) and Cecilia ($t = 2.74$, d.f. = 6, $P = 0.034$). Three other D sites were significantly different at a $P < 0.1$ level: Berg ($t = -2.44$, d.f. = 6, $P = 0.051$), Noordhoek ($t = 2.21$, d.f. = 6, $P = 0.069$) and Lourens ($t = 2.05$, d.f. = 6, $P = 0.086$). All other D sites were not significantly different from the LD sites at $P > 0.1$. These results were not as expected from Figure 4.3a-d as, from inspection of the points on the plots (Figure 4.3), Holsloot was expected to be significantly different from the LD sites and Noordhoek was not expected to be significantly different. The test does not indicate where the significance difference lies, but inspection of the individual points on the plots gives an indication of this. The Palmiet (Figure 4.3a), for instance, begins to deviate from the reference condition curve at point 3, indicating proportionally fewer Trichoptera taxa than expected. More Diptera than expected bring the cumulative percentage back to the reference condition, but then fewer than expected Coleoptera and Non-Insects cause a further deviation.

4.3 Diversity indices for D sites

Disturbance can appreciably reduce biological diversity, and so a second analysis focussed on comparing LD and D sites in terms of a range of diversity indices. Combining the taxonomic lists of the D sites with that of the LD sites increased the overall number of taxa from 372 to 460, a 20% increase. As shown for the LD sites, dipterans provided the most taxa, 143 in total of which the D sites provided 23 new taxa. The D sites also added 25 new Trichoptera taxa, but only three Ephemeroptera and two Plecoptera. In terms of the other insect groups, the D sites added 11 Odonata taxa out of a total of 14.

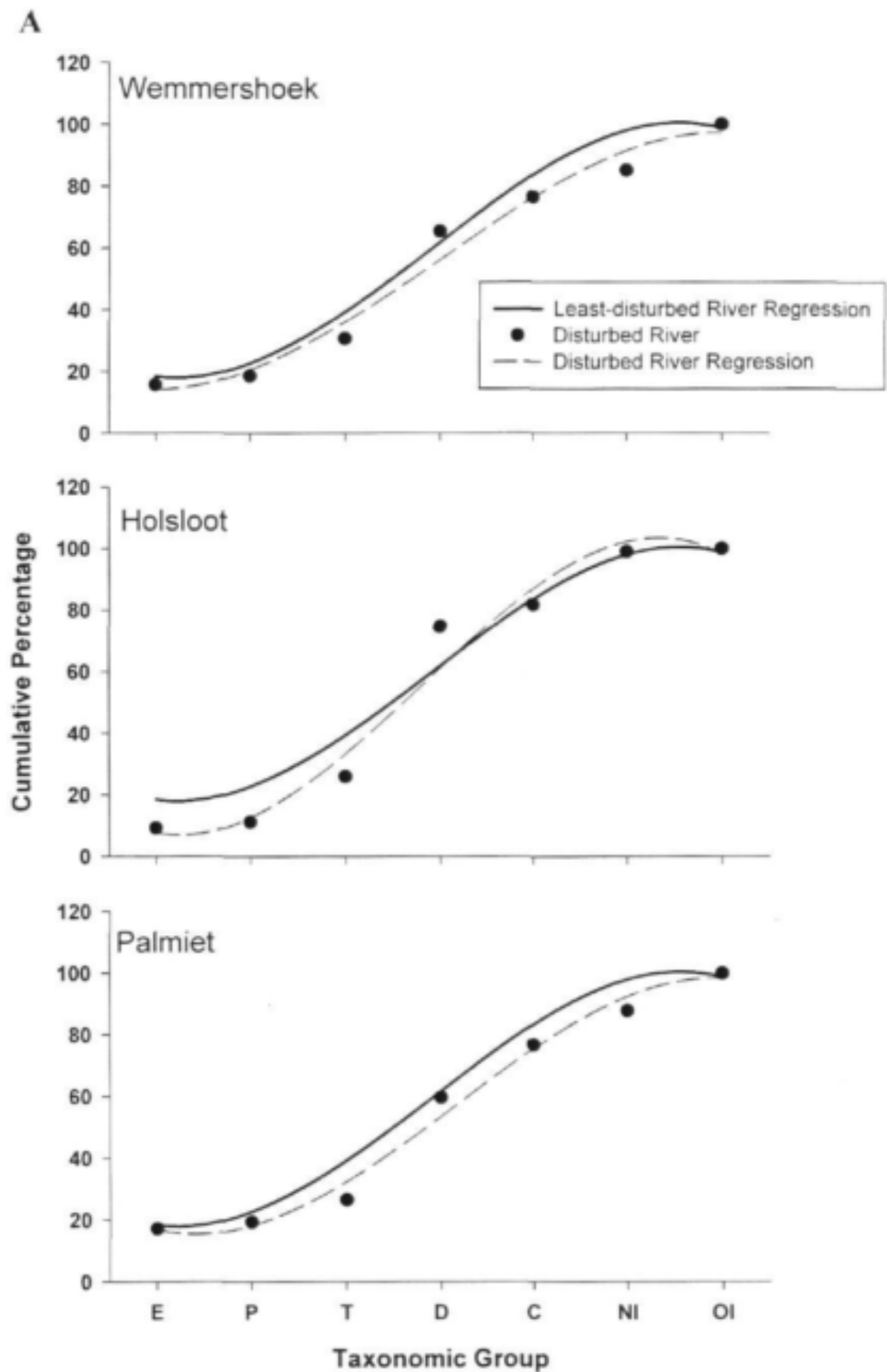


Figure 4.3a-d. Cumulative curves fitted with a 3rd order polynomial regression for each D site compared to the regression of all LD sites. Figures follow on the subsequent four pages.

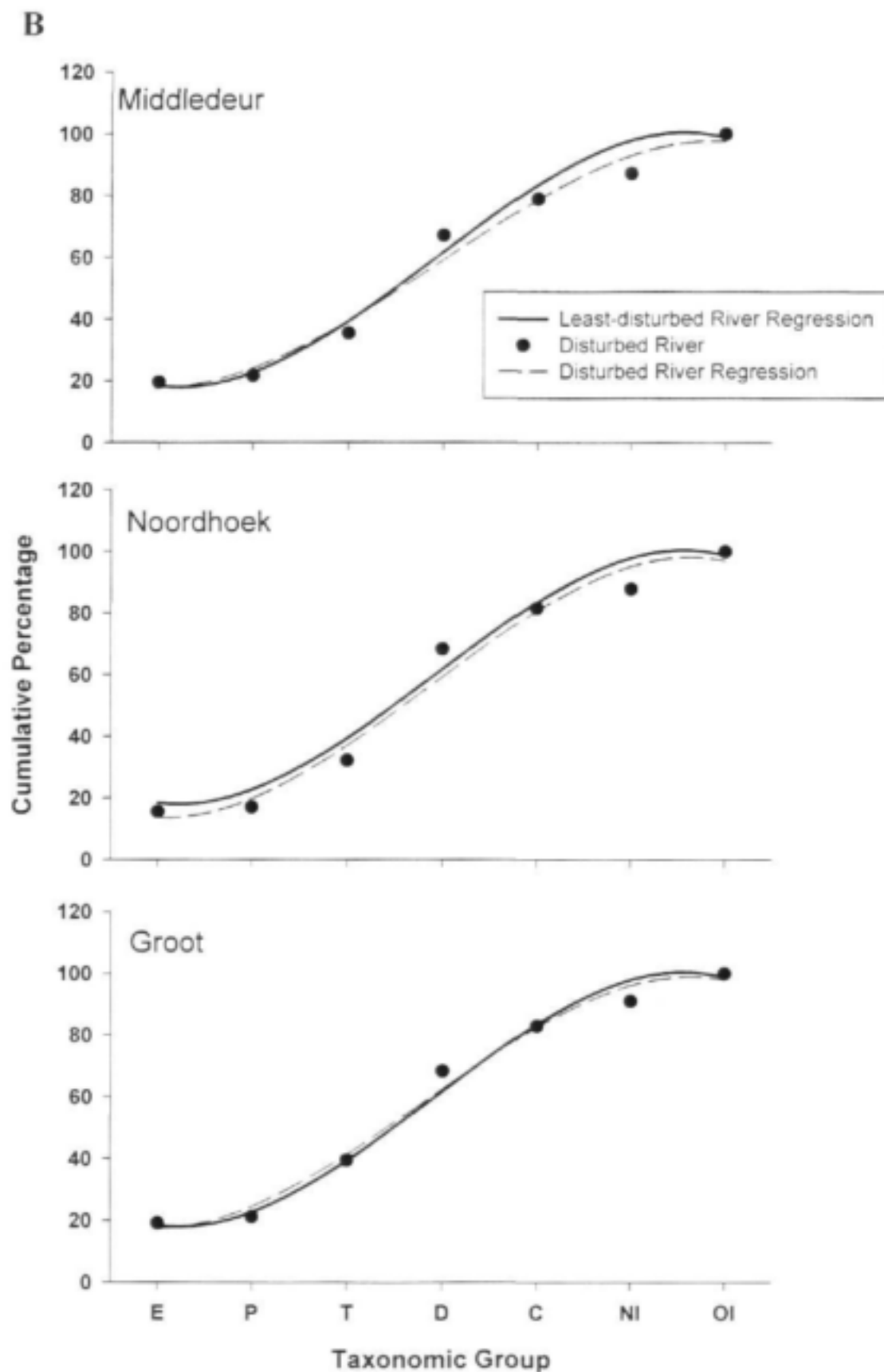


Figure 4.3b

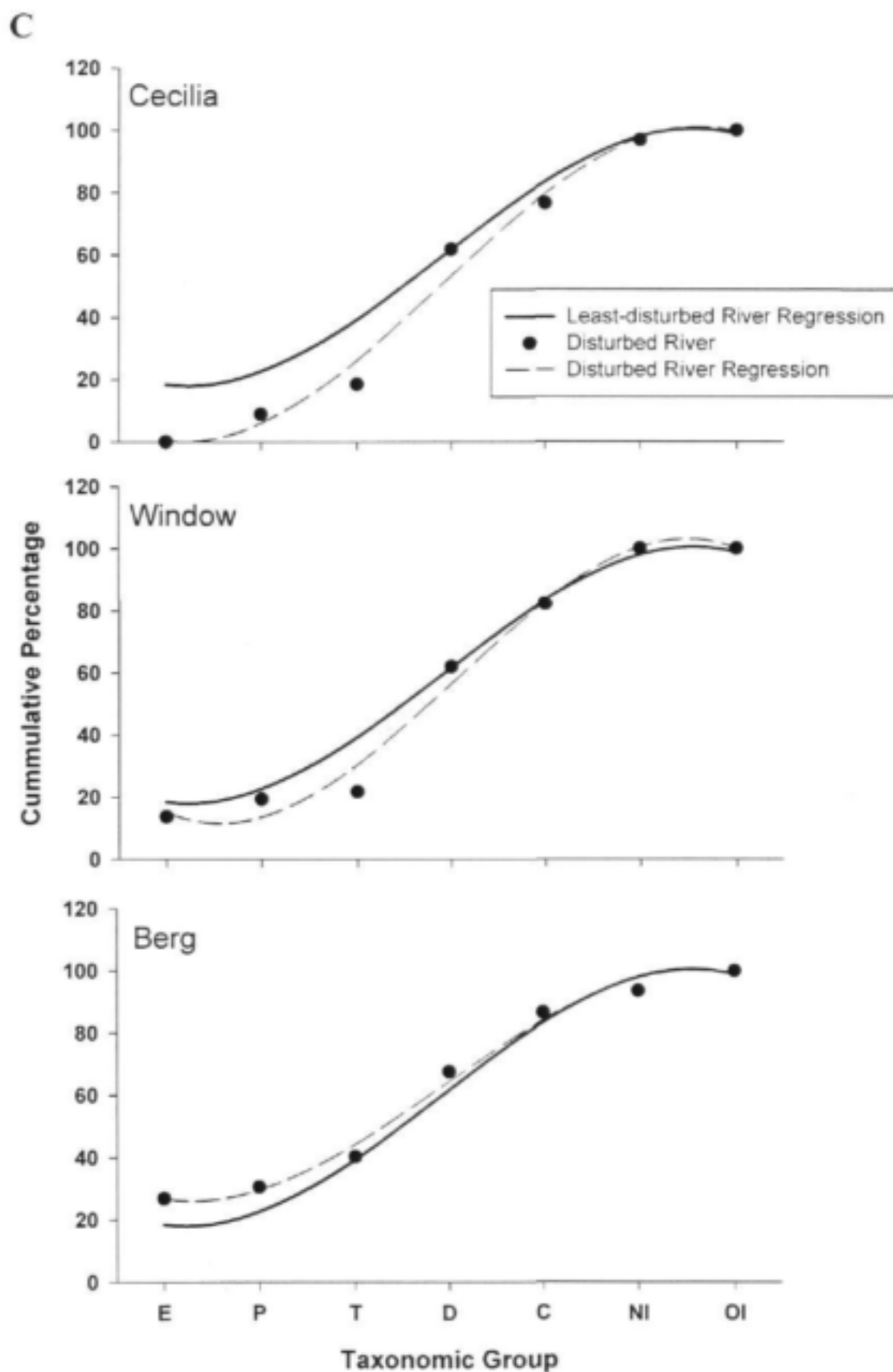


Figure 4.3c

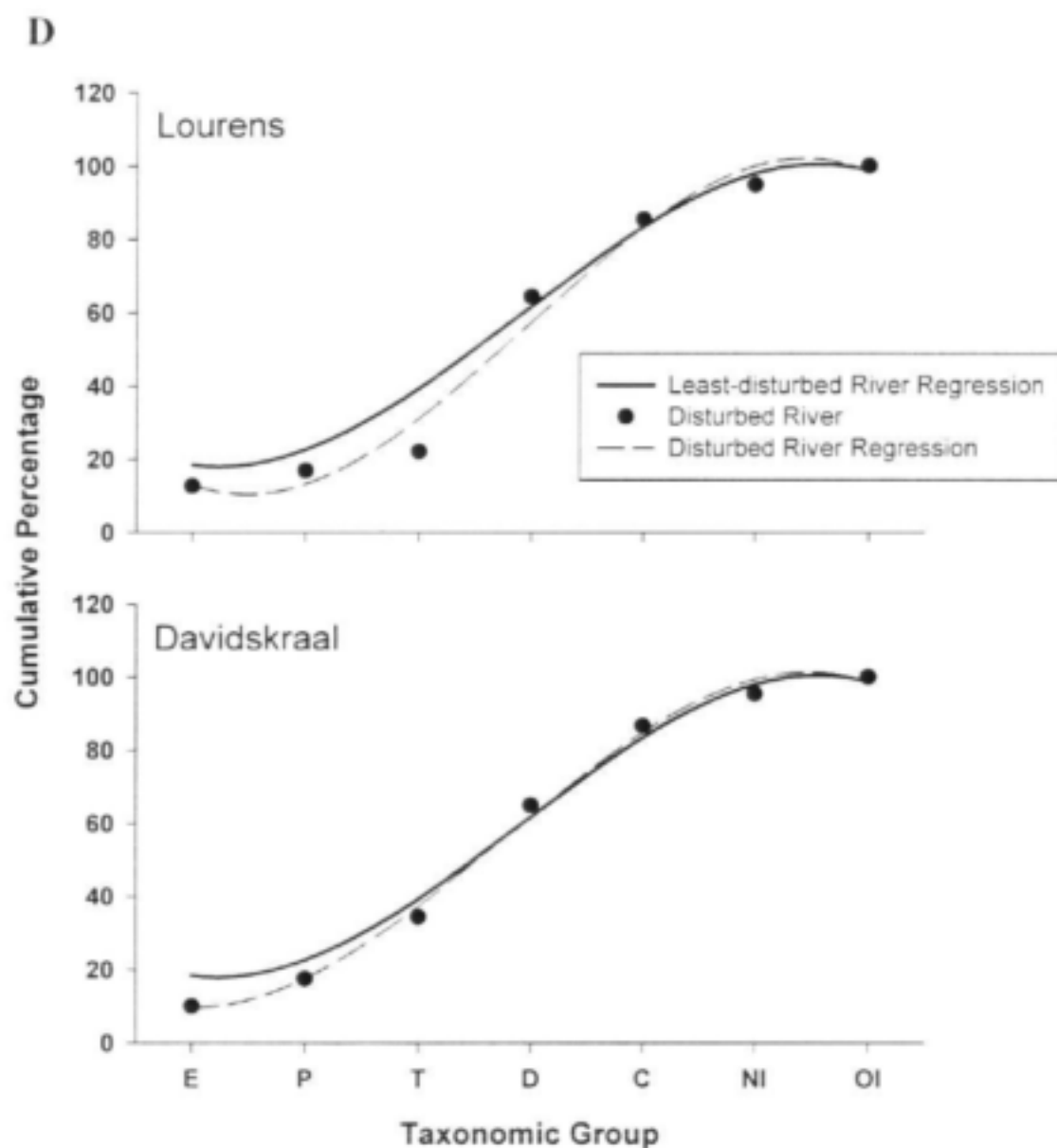


Figure 4.3d

The values for the various indices were compared using a one-way ANOVA, which revealed that none of the D sites were significantly different to the LD rivers at a $P < 0.05$ level. The number of taxa per site ranged from 55 – 119 ($\bar{X} = 88$) for the group of D sites, with Window (six samples) having the fewest taxa and Davidskraal the most. The range for LD sites was 56 – 193 ($\bar{X} = 91$) taxa, with Swartboskloof and Eerste respectively representing the minimum and maximum values. Margalef's diversity index d averaged 21 for D sites and 30 for LD sites. Means of the Shannon-Wiener index H' and Pielou's evenness J' were the same for each group of sites, being 4.3 and 0.98 respectively. In terms of biotic diversity and species richness there were no significant differences between the D and LD sites.

4.4 Shared taxa of D and LD rivers

An analysis of similarity of taxa between sites within any one LD catchment group revealed that generally $\leq 50\%$ of the taxa were shared, with the exception of the Trichoptera and Other Insects (Table 3.20). A comparison of the proportion of shared taxa between a D site and the LD sites within its catchment revealed taxonomic groups with $< 40\%$ of their taxa shared (Table 4.2). A few of the D sites, such as Groot and Window, have several taxonomic groups sharing greater than 50% of their taxa. This stronger similarity is confirmed by their tight grouping within their catchment groups on the MDS plot (Figure 4.1). Overall the results were similar to that of comparing two rivers from different catchments (Table 3.20), with fewer shared taxa overall than within-catchment comparisons.

Table 4.2 Shared taxa per taxon group, between catchment groups and individual D sites, as a percentage of all taxa within those comparisons. LD and D sites data set.

Taxon group	Olifants-Berg					Breede	Table Mountain	
	Middel-deur	Noord-hoek	Groot	Berg	Wemmers-hoek	Holsloot	Window	Cecilia
Ephemeroptera	36	39	29	35	32	29	56	0
Plecoptera	33	33	33	33	33	13	60	29
Trichoptera	15	28	43	13	25	6	14	25
Diptera	33	39	51	31	37	29	35	34
Coleoptera	29	38	54	23	20	15	29	17
Other Insects	18	26	25	11	24	0	0	29
Non Insects	33	23	36	23	27	25	48	48

4.5 SASS-weighted abundance ratings

In order to highlight any potential differences between LD and D sites, the data set was transformed using South African Scoring System (SASS) scores to weight each taxon and its abundance per site. SASS is used to evaluate river sites for water quality through the invertebrates present, with scores allocated to all invertebrate families in relation to their tolerance to a range of water quality variables (Dickens & Graham 2001). In this case, the scores were used to distinguish D sites with suspected water-quality problems from those with physical disturbances, as well as from the LD sites. For each LD and D sites, the abundance rating (Table 2.1) for each taxonomic family was multiplied by its SASS score, and the values combined per taxonomic group. The Non-Insects were not included in this analysis as not all of the taxa have been allocated SASS scores.

An average SASS-weighted abundance rating was calculated for the different taxonomic groups for the LD sites as a whole and compared to those for the D sites (Figure 4.4). A paired t-test was used to assess if the proportions of each taxonomic group in any one D site and the means of all D sites, were significantly different from those of the LD sites. The overall mean comparisons showed that there was a significant difference between D and LD sites at a $P < 0.05$ level.

($T = 2.71$, d.f. = 5, $P = 0.042$) (Table 4.3). When comparing individual D sites to the mean LD values the taxonomic group distributions of only four of the 11 D sites were significantly different. As in Section 4.2, Cecilia and Palmiet were significantly different at a $P < 0.05$ level, with the addition of Window and Holsloot. None of the other river sites were even marginally significantly different.

Table 4.3 Results of paired t-tests comparing the SASS-weighted abundance per taxonomic group of each D site to the mean of the LD sites. T = test statistic, P = significance value. Values in bold are significant at $P < 0.05$, d.f. = 5.

River	T	P	River	T	P
Mean Disturbed Rivers	2.71	0.042	Groot	-1.11	0.317
Berg	-0.42	0.690	Middeldeer	-0.39	0.715
Wemmershoek	-0.33	0.756	Noordhoek	-0.24	0.816
Holsloot	4.19	0.009	Window	3.64	0.015
Davidskraal	-0.73	0.500	Cecilia	2.91	0.033
Lourens	1.01	0.358	Palmiet	3.01	0.030

4.6 Numbers of taxa and mean abundance ratings for D rivers

One possible effect of disturbance is that some taxa might markedly increase in proportion whilst others might be reduced to very low abundances or disappear. To assess if this was happening, the numbers of taxa within a taxonomic group and their average abundance ratings for each D site were compared to the mean, minimum and maximum values for the LD sites (Figures 4.5-4.7). Overall, the D sites were largely within the same range as the LD sites. Within the order Ephemeroptera, all sites were within the LD range except Cecilia, which was the only D or LD site where no Ephemeroptera were collected (Figure 4.5). The maximum expected number of Plecoptera species in this region of the Western Cape is 15 (Stevens & Picker 2003), and therefore the few collected are not surprising, although all sites were within the LD range (Figure 4.5). Holsloot, however, not only had only three plecopteran taxa but their abundances were also well below the minimum value for the LD sites.

Window was the only D site with fewer Trichoptera taxa than the minimum LD site, with Cecilia just above that minimum (Figure 4.6). Trichoptera abundance was also very low in Window, whilst the Lourens site was near the mean in terms of number of taxa but below the LD minimum in terms of abundances (Figure 4.6). Dipterans tend to be robust in terms of water quality and habitat types and often increase in abundance in disturbed rivers. All D sites were well within the LD range for numbers of taxa (Figure 4.6) and several D were above the LD mean in terms of abundances with Middeldeer above the LD maximum. Coleoptera, Other Insects and Non-Insects in D rivers were all within the LD ranges, except for the low values for Other Insects in Window (Figure 4.7).

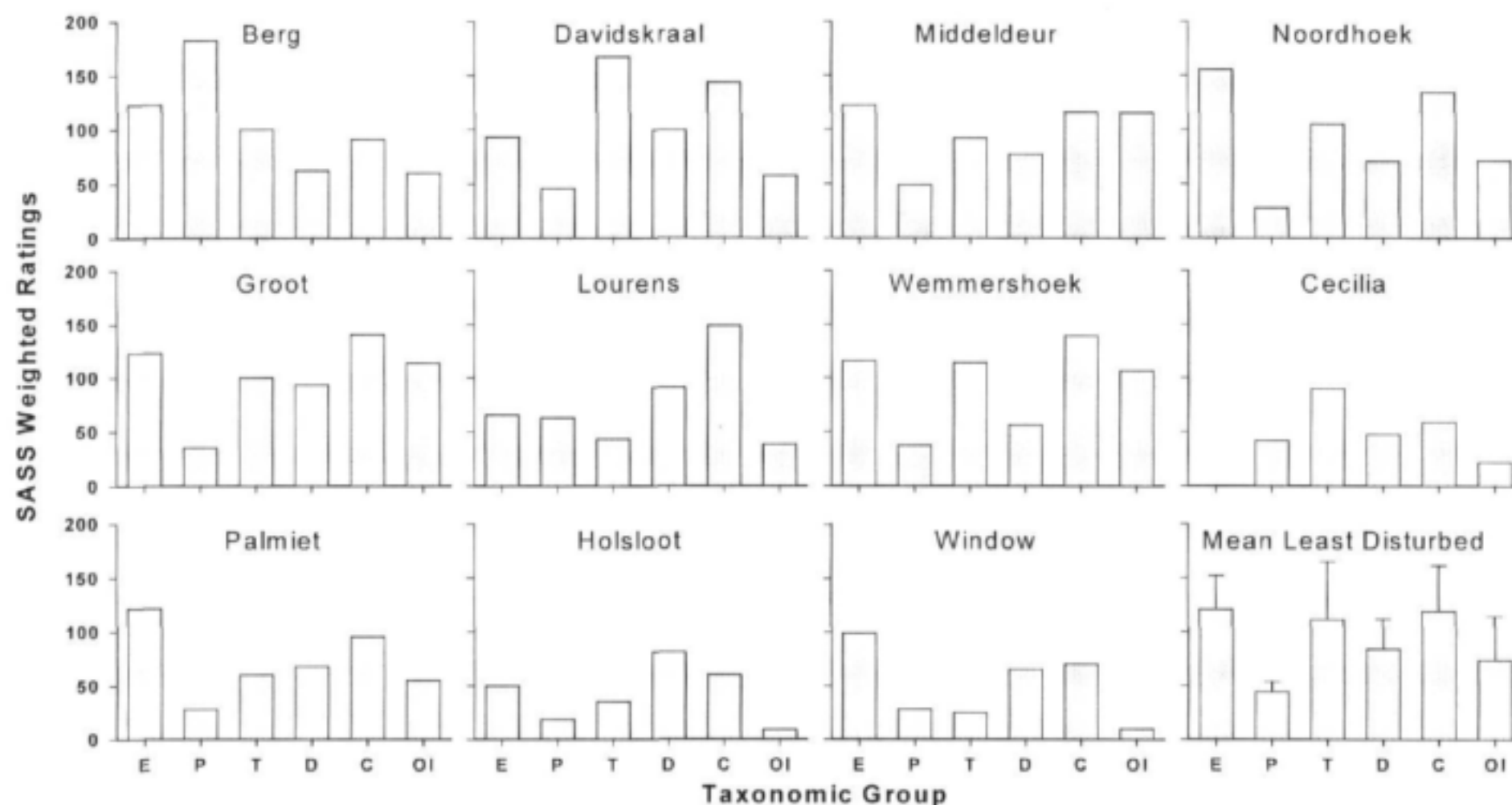


Figure 4.4 SASS-weighted abundance ratings of each taxonomic grouping for the D sites in comparison to the mean ratings for the LD sites. E= Ephemeroptera, P= Plecoptera, T= Trichoptera, D= Diptera, C= Coleoptera, OI= other insects.

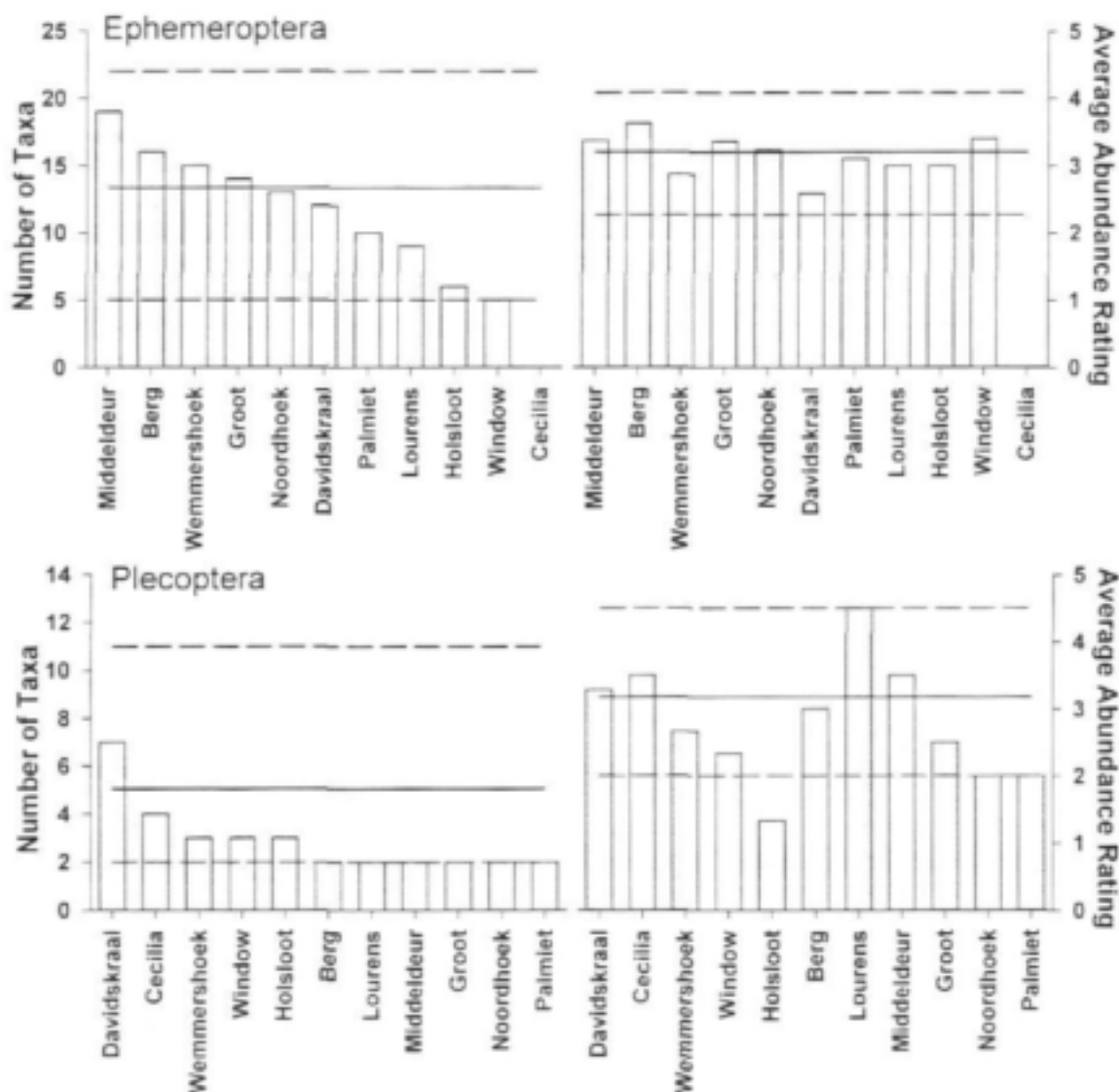


Figure 4.5 Number of taxa (left panel) and average abundance rating (right panel) for the Ephemeroptera and Plecoptera within each D site relative to the mean (solid line), minimum and maximum (dashed lines) of the LD sites. The y-axis for the number of taxa differs from graph to graph. D sites are ranked from highest to lowest numbers per taxonomic group, and so x-axis labels are not in the same sequence for each Order.

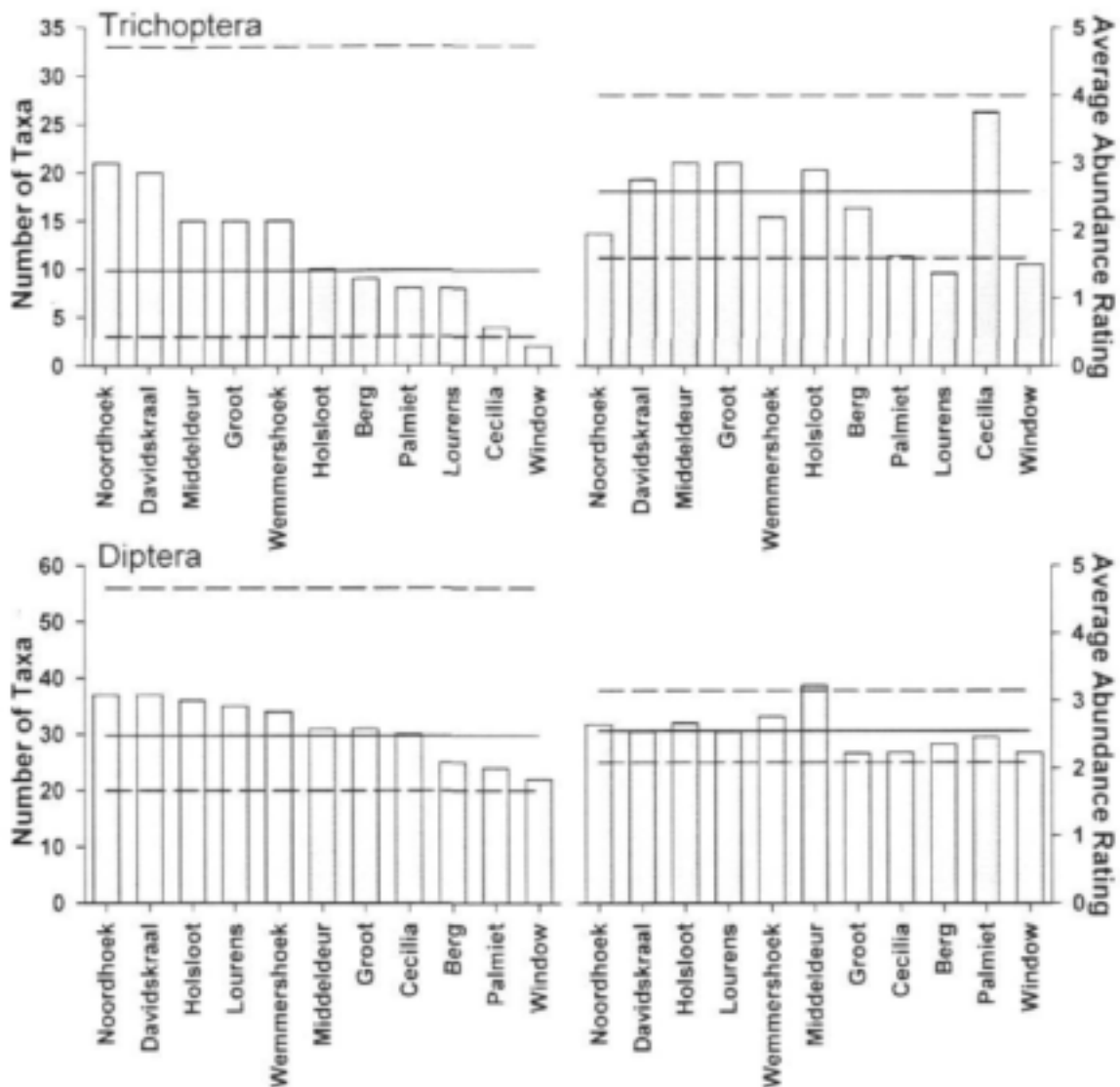


Figure 4.6 Number of taxa (left panel) and average abundance rating (right panel) for the Trichoptera and Diptera within each D site relative to the mean (solid line), minimum and maximum (dashed lines) of the LD sites. The y-axis for the number of taxa differs from graph to graph. D sites are ranked from highest to lowest numbers per taxonomic group, and so x-axis labels are not in the same sequence for each Order.

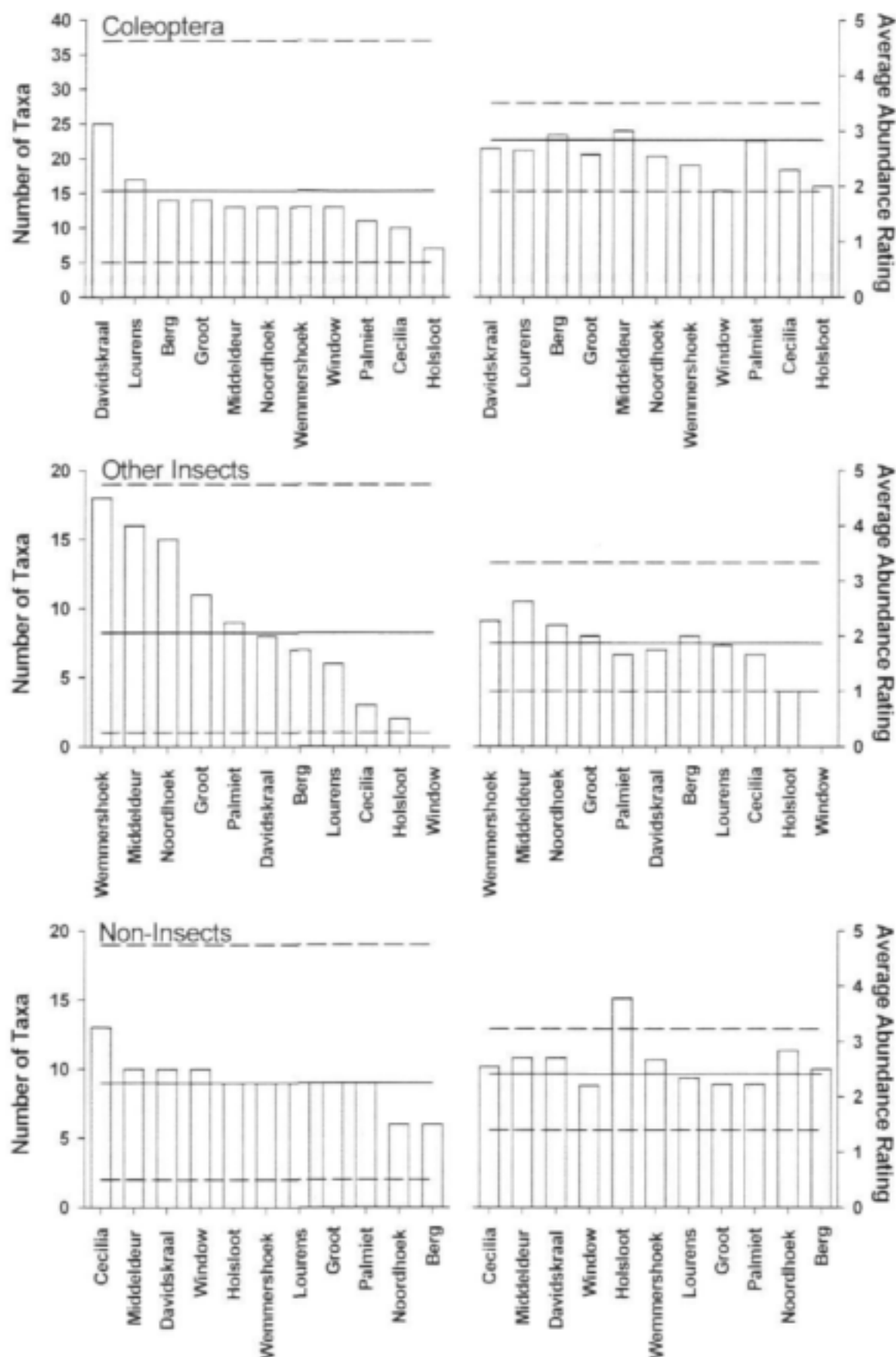


Figure 4.7 Number of taxa (left panel) and average abundance rating (right panel) for the Coleoptera, Other Insects, and Non-Insects within each D site relative to the mean (solid line), minimum and maximum (dashed lines) of the LD sites. The y-axis for the number of taxa differs from graph to graph. D sites are ranked from highest to lowest numbers per taxonomic group, and so x-axis labels are not in the same sequence for each faunal group.

In summary, the comparison revealed no major pattern breaks within taxonomic groups between individual D sites and the LD reference ranges. As some taxonomic groups are universally recognised as tending to be more abundant (Diptera, Oligochaeta) or less abundant (Ephemeroptera, Plecoptera, Trichoptera – EPT) in disturbed rivers, an analysis was done using some summary metrics of the full suite of LD and D sites.

4.7 Summary metrics of LD and D sites

Comparisons between the LD and D sites were made using different taxonomic metrics commonly used in bioassessments to compare reference condition or LD sites to D sites or for comparisons between sites in different regions (Li *et al.* 2001; Roy *et al.* 2003). The metrics investigated were: overall number of taxa; number of families; proportion of Ephemeroptera, Plecoptera and Trichoptera (% EPT); proportion of Diptera; and proportion of worms (Oligochaeta, Nematoda, and similar). Box plots for the grouped LD and grouped D sites illustrate that the means and medians of the numbers of taxa, numbers of families and abundance ratings were almost equal (Figure 4.8). The ranges for number of taxa and number of families, however, were greater for the D sites than for the LD sites. As expected, the mean/median values for the percent of EPT were greater for LD sites than for D sites, and the converse was true for the Diptera and worms. T-test comparisons for all of these metrics, however, revealed no significant difference within any metric at a $P < 0.05$ (Table 4.4).

Table 4.4 T-test comparisons between LD and D sites for different taxonomic metrics. N = 26 for all tests. EPT = Ephemeroptera, Plecoptera and Trichoptera, Worm = Oligochaeta, Nematoda, Nemertea and more.

Taxonomic Metric	T	P
Number of Taxa	0.31	0.76
Number of Families	0.80	0.43
Mean Abundance Rating	0.58	0.57
% EPT	1.15	0.26
% Diptera	-1.18	0.25
% Worms	-1.16	0.26

4.8 Taxonomic audit of presence and absence of discriminator species in LD and D sites

The main difference between LD and D sites appears to be species-level patterns of occurrence and absence that do not change the overall proportions of the major taxon groups. The Berg site, for instance, was recognised as a D site because of its linking with the Breede sites. A major cause of this linkage appeared to be the presence of the ephemeropteran *Labeobaetis* sp. nov.1 in most Breede sites and the Berg site but no other LD sites. Likewise the major difference between the Cecilia and other Table Mountain sites probably lies with its high abundance of the trichopteran *Dyschimus thrymifer* as well as its complete lack of Ephemeroptera.

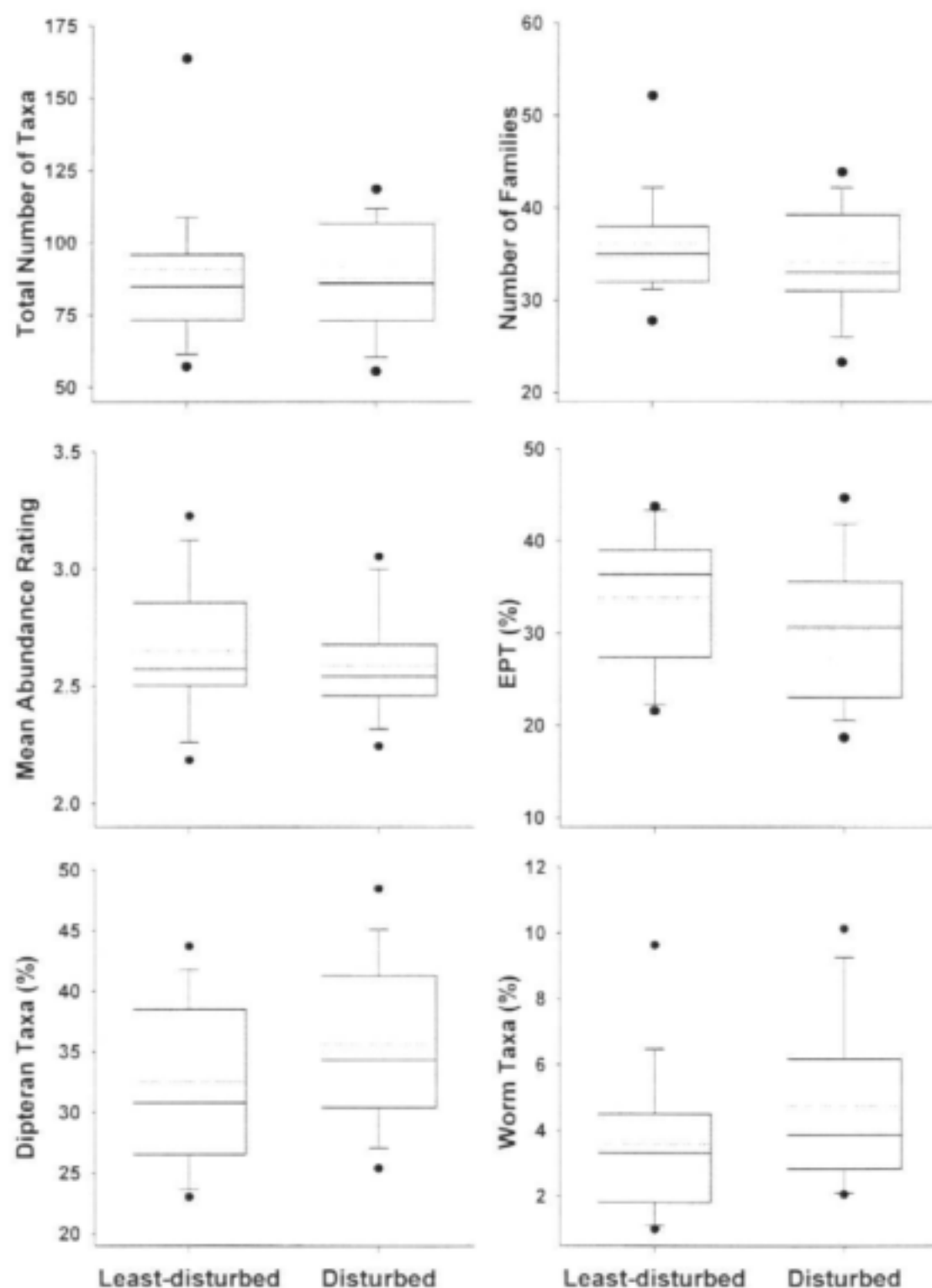


Figure 4.8 Comparison of metrics between LD (n = 17) and D (n = 11) sites. Box and whisker plot: Solid line = median; dotted line = mean; box represents the 75th and 25th percentiles; whiskers = 90th and 10th percentiles; dots = 95th and 5th percentiles.

A final analysis was thus done of the taxa that discriminate between each D site and its LD catchment. Each D site was compared to the catchment that it is geographically located in, with Davidskraal and Lourens removed because they are not within the geographical catchment of any LD sites. The large taxonomic data set of 460 taxa was distilled to a smaller, more manageable list by using the top SIMPER taxa that together contributed 25% to the dissimilarity between a D site and its LD catchment. These taxa were assessed in terms of how strongly they contributed to the difference, and if they only occurred in either the D site or the corresponding LD catchment.

Once all the D and LD comparisons were compiled, taxa that occurred in more than one D site or LD catchment were included in a synthesis of important taxa (Table 4.5). The Non-insects component is not presented in full as the coarse resolution of identification made comparisons meaningless. The table was then used to determine which taxa were present in D sites but no LD sites within the same catchment (denoted P in Table 4.5), or in LD sites but no D sites within the same catchment (denoted C in Table 4.5). A + sign denotes the taxon was found in both D and LD sites within a specified catchment and a - sign that it was found in neither LD or D sites within a specific catchment. A taxon with Ps but no Cs and no + was found in a D site within the specified catchment and never in a LD site and thus, within this data set, was considered to have potential as an indicator of disturbance. Likewise, a taxon with Cs and no Ps and no + was found only in LD sites within a specified catchment and thus, within this data set, was considered to have potential as a disturbance-sensitive taxon. None of the taxa in the table, however, are known from other literature sources as being indicators of disturbance.

There were ten taxa found only in D sites and four only in LD sites, indicated by the bold font in Table 4.5. Within the D sites, the ten taxa consisted of four Trichoptera, three Chironomidae, two Odonata and one Cladocera. These taxa are probably indicative of slower flows or pool-like conditions rather than disturbance *per se*. Even though there were few taxa solely in D or LD sites, there were some subtle trends within mildly disturbed D sites. The Ephemeroptera *Adenophlebia peringueyella* and Coleoptera *Elpidelmis* sp. 1, for instance, were present in LD sites but also in the D-rated Groot site (Table 4.5). The presence of these taxa in the Groot may indicate that its level of disturbance was mild, as suggested by its position in the original MDS plot (Figure 4.2). Similarly, *Lithogloea harrisoni* (Ephemeroptera) was generally found only in LD sites, but also occurred in the Berg, which again may be indicative of the fact that its disturbance was probably related to a transfer of taxa through an inter-basin transfer scheme rather than through disturbance of the physical or chemical habitat (Table 4.1). There were many such subtle taxon shifts that distinguished between D and LD sites, but these were not easy to detect because of two main confounding factors. First, as stated in Chapter 3, many taxa contributed significantly to the dissimilarities between sites and catchment groups (Section 3.4). Second, the disturbances themselves were subtle, resulting in mixes of taxa that are represented in both LD and D sites.

Table 4.5 Taxa that contribute a total of 25% of the difference between a D site and its LD catchment, and appear in more than one D or LD site. C = present in the LD sites only. P = present in the D site only. Hols = Holsloot, Wems = Wemmershoek, Middel = Middleduur. Inst. = early instar, - = absent in both D site and its LD catchment, + = present in both D site and its LD catchment.

Order	Family	Taxon	Hols	Wems	Berg	Groot	Middel	Noord	Window	Cecilia	Palmiet
Ephemeroptera	Baetidae	<i>Cloeodes</i> sp. nov. 1	C	P	P	-	-	P	-	-	-
		<i>Demareptus capensis</i>	+	C	+	C	C	C	-	-	-
		<i>Labiobaetis</i> spp.	C	C	C	+	+	C	-	-	P
		<i>Labiobaetis</i> sp. nov. 2	+	P	-	-	-	-	C	C	+
		<i>Pseudocloeon vicosum</i>	C	+	+	C	+	+	C	C	+
		<i>Afronurus harrisoni</i>	C	P	P	P	-	-	-	-	-
	Heptageniidae	<i>Adenophlebia peringueyella</i>	-	C	C	+	C	C	-	-	-
	Leptophlebiidae	<i>Aprioxyn</i> spp. inst.	-	+	C	C	C	+	-	-	-
		<i>Castanophlebia calida</i>	C	+	+	C	+	C	+	C	C
	Teloganodidae	<i>Ephemereilina barnardi</i>	-	C	C	C	+	C	-	-	P
		<i>Lestageila pericillata</i>	C	+	+	+	C	+	+	C	-
		<i>Lithogloea harrisoni</i>	C	-	P	-	-	-	+	C	-
Plecoptera	Notonemouridae	<i>Aphanicercella</i> spp. inst.	+	C	C	+	C	+	P	P	+
		<i>Aphanicercopsis</i> spp. inst.	C	+	C	C	+	C	-	-	-
		<i>Desmonemoura</i> spp. inst.	-	C	C	+	C	C	-	-	-
Trichoptera	Ecnomidae	<i>Ecnomus</i> spp.	-	-	-	P	P	-	-	-	-
	Hydropsychidae	<i>Cheumatopsyche alfa</i>	-	+	C	B	C	B	-	-	-
		<i>Cheumatopsyche maculata</i>	-	C	C	C	+	C	-	-	P
		<i>Cheumatopsyche</i> spp. inst.	-	+	+	C	+	C	-	-	-
		<i>Cheumatopsyche</i> sp. type 11	-	P	P	-	-	-	-	-	-
		<i>Macrostemum capense</i>	-	-	-	P	P	-	-	-	-
	Leptoceridae	<i>Athripsodes</i> (bergensis group) spp.	P	+	C	+	+	C	+	C	P
		<i>Leptecho</i> sp. F	-	-	-	-	P	P	-	-	P
		<i>Leptecho</i> spp.	-	-	P	-	-	-	C	C	-
		<i>Oecetis</i> sp.	-	+	+	+	C	C	C	C	-
		Leptoceridae spp. inst.	C	C	+	+	C	C	-	-	+
	Petrothrincidae	<i>Petrothrincus circularis</i>	-	C	C	C	C	C	-	-	C
	Philopotamidae	<i>Chimarra</i> sp.	-	C	C	+	+	+	-	-	-
	Sericostomatidae	<i>Petroplax</i> sp.	-	C	C	+	+	+	-	P	-
Diptera	Ceratopogonidae	<i>Atrichopogon</i> sp.	-	C	+	C	C	C	-	-	-

Order	Family	Taxon	Hols	Wems	Berg	Groot	Middel	Noord	Window	Cecilia	Palmiet
Diptera	Ceratopogonidae	<i>Bezzia</i> spp.	+	P	-	-	-	-	C	C	-
	Chironomidae	<i>Cricotopus obscurus</i>	P	P	-	-	P	P	-	-	-
		<i>Cricotopus kisanuensis</i>	+	+	C	C	C	C	C	C	-
		<i>Cricotopus</i> sp. 1	+	C	C	+	C	+	P	P	P
		<i>Cricotopus</i> sp. 5	P	-	-	P	-	-	-	-	P
		<i>Lersia</i> sp.	C	C	C	+	+	+	P	-	+
		<i>Paradoxocladus mengoldi</i>	-	P	-	P	P	P	-	-	-
		<i>Polypedium alticola</i>	+	-	P	-	P	P	-	P	C
		<i>Stempellina</i> sp.	C	+	C	+	+	+	C	+	C
		<i>Tanytarsus</i> sp. 3.	-	P	-	-	P	-	-	-	-
		<i>Thienemannella</i> sp. 1	+	+	+	C	C	+	-	-	-
	Psychodidae	<i>Pericoma</i> sp. 2	P	-	-	-	-	-	C	C	-
	Simuliidae	<i>Simulium medusaeforme</i> pupa	C	-	-	P	P	-	-	-	-
	Tipulidae	<i>Hemerodromia</i> sp.	+	C	+	+	+	C	-	-	C
Coleoptera	Elmidae	<i>Elmidae</i> spp. adult	-	C	C	C	+	+	-	-	-
		<i>Elpidelmis capensis</i> adult	-	C	C	C	C	C	-	-	-
		<i>Elpidelmis</i> sp. 1 adult	C	P	-	+	P	P	C	C	+
		<i>Elpidelmis</i> spp. larva	-	C	C	+	C	C	-	-	-
		<i>Elpidelmis</i> sp. A larva	C	P	P	-	P	P	+	+	-
		<i>Elpidelmis</i> sp. B larva	C	-	-	-	P	-	P	-	P
		<i>Peloniolus</i> sp. 2 adult	C	-	-	-	-	-	P	-	-
	Helodidae	<i>Helodidae</i> sp. 1 larva	+	-	P	-	P	P	C	+	P
		<i>Helodidae</i> sp. 2 larva	C	-	P	-	-	-	+	C	P
		<i>Helodidae</i> sp. 6 larva	C	C	+	+	+	+	C	C	+
		<i>Helodidae</i> sp. 7 larva	-	C	C	+	+	C	C	C	C
	Hydraenidae	<i>Hydraenidae</i> spp. adult	-	C	C	C	C	C	-	-	C
	Hydrophilidae	<i>Hydrophilidae</i> spp. larva	+	P	-	-	-	-	C	C	-
		<i>Hydrophilidae</i> sp. 1 larva	P	-	-	-	-	-	C	C	-
	Limnichidae	<i>Limnichidae</i> sp.	C	+	C	+	C	+	P	-	C
Hemiptera	Velidae	<i>Microvelia</i> sp. adult	-	-	-	-	-	-	C	C	-
Lepidoptera	Pyalidae	<i>Petrophila</i> sp.	C	C	C	+	+	+	C	+	C
Odonata	Aeshnidae	<i>Aeshna</i> sp.	-	+	+	+	C	+	C	C	-
	Cordulidae	<i>Syncordulia</i> sp.	-	+	C	C	C	C	-	-	-
	Gomphidae	<i>Notogomphus</i> sp. 1	C	P	-	-	-	P	-	-	C
		<i>Paragomphus</i> sp. 1	C	P	P	-	-	P	-	-	P
	Libellulidae	<i>Crocothemis</i> sp.	-	-	-	-	P	P	-	-	-

[illegible]

4.9 Conclusions

The overwhelming pattern in all the analyses presented in this chapter, was the lack of significant differences in overall metrics between LD and D sites. The patterns shown between D and LD sites can be summarised by the following points:

- overall, mean LD and mean D sites are statistically significantly different in terms of proportions of taxa within a taxonomic group (Sections 4.2 and 4.5);
- when comparing proportions of taxa for individual D sites to mean LD sites only 3 – 4 D sites differed significantly from the LD sites;
- number of taxa (richness) and abundances did not differ significantly between most D sites and LD sites and diversity indices did not differ at all (Sections 4.3 and 4.6);
- the percentage of shared taxa between D and LD sites within the same catchment was low and dependant on the degree of disturbance, in support of Figures 4.1 and 4.2 (Section 4.4);
- although metrics such as % EPT, mean abundance and number of families, % dipterans and % worms demonstrated small differences between LD than D sites graphically, there was no statistical difference between the two groups (Section 4.6);
- there are subtle mixes of taxa that define differences between D and LD sites (Section 4.7), some of which may be indicators of disturbance, but further research is needed to determine which taxa were simply absent from D sites due to factors other than disturbance.

Even though there were indications of physical disturbance in most D sites, these did not translate into measurable changes within the invertebrate species assemblages sampled.

5. THE UNDERLYING ENVIRONMENTAL CAUSES OF CATCHMENT SIGNATURES

5.1 Introduction

The investigations into catchment and river signatures in Chapters 2-4 revealed that they are a result of changes in invertebrate communities at the species level. This is the proximate cause of the signatures, which will have been driven by underlying, environmental differences within the rivers/catchments. In this Chapter some possible candidates for these environmental drivers are investigated.

5.2 Water chemistry

The original research upon which this project was based (King & Schael 2001) focussed on physical-biological links, and did not include a comprehensive investigation of water quality. Spot measurements of water temperature, pH, colour and conductivity were made in the field at one point per site. Of these, only conductivity showed any correlation with the catchment grouping of invertebrates, and this was very weak.

There may have been fundamental differences in water chemistry between the catchments that would not have been revealed by this limited chemical analysis. Department of Water Affairs (DWAF) gauging-weir data of water quality were thus analysed for any insights they may provide on catchment signatures. DWAF data from the summer months (December to March) were selected from gauging stations nearest to LD sites or, for rivers where no stations existed, from stations considered representative of those catchments (Table 5.1). Water chemistry records were used to characterise the catchments, and were analysed for their individual patterns, not in conjunction with the invertebrate data. Records were of variable length from one year to 40 or more, but no relevant records were found for the Table Mountain or Davidskraal sites. Using only those water-chemistry variables that were available for all the selected stations (Table 5.2), one mean value was calculated for each station from all the available years of data. The PRIMER packages CLUSTER and MDS were then used to analyse the pattern of station distributions based on their available water chemistry.

If regional water chemistry was playing a significant role in the appearance of catchment signatures, hierarchical clustering of the water-chemistry stations should be similar to that of the invertebrates (Figures 3.1, 3.2 and 4.1). The clustering of stations by water-chemistry values, however, was quite different from that of the invertebrates (Figure 5.1). There were two main groups of stations, dividing at the 63% similarity level. The first group consisted of stations from all of the catchments studied except the Berg and Molenaars. The second group has at least one station from each studied catchment except the Lourens, and divided into three sub-groups: Eerste, Palmiet and Breede (2a), Olifants (2b) and Berg, Molenaars and Breede (2c) (Figure 5.1). The locations of the stations in the first cluster group were from areas with probable farming impacts (groups 1b and 1c), and a combination of dam and farming impacts (group 1a), whilst the

group 2 stations were in relatively less impacted areas. Each main group had one Breede site that did not join with any of the sub-groups (Figure 5.1).

Table 5.1 DWAF water-chemistry data used for regional summer water-chemistry analysis, and the number of years of data captured for each. Sampling intervals varied from biweekly to seasonally. n = number of samples.

Code	DWAF weir	Location	Record Period	n
O1	E1H006Q01	Jan Dissels River at Clanwilliam commonage	1978-89, 1997-04	108
O2	E1H007Q01	Bulshoek dam on Olifants River: left canal	1983-89, 1998-01	35
O3	E1H013Q01	Olifants River at Citrusdal	1995-99	15
O4	E2H007Q01	Leeu River	1977-04	141
R1	H1H007Q01	Wit River at Drosterskloof	1979-04	380
R2	H1H009Q01	Holsloot River at Boontjies River	1996-99	14
R3	H1H012Q01	Holsloot River at Daschbosch River	1981-86, 2000-03	85
R4	H1H015Q01	Breede River at die Nekies (under Brandvlei)	1973-81, 1986-04	234
R5	H1R002Q01	Stettynskloof dam on Holsloot river: near dam wall	1972-99	20
M1	H1H017Q01	At Hawequas Forest Reserve on Elands River	1971-92	241
M2	H1H018Q01	Molenaars River at Hawequas Forest Reserve	1971-04	375
B1	G1H071Q01	Wemmershoek dam on river: pipeline from D	1987-88, 1992	4
B2	G1R002Q01	Wemmershoek dam on river: near dam wall	1971-77, 1985-99	130
E1	G2H002Q01	Jonkershoek on Bosboukloof	1981-90	31
E2	G2H007Q01	Langrivier at Jonkershoek	1982-90	31
E3	G2H008Q01	Jonkershoek (Eerste) river Jonkershoek /Kleinplas	1977-93	144
E4	G2H009Q01	Lambrechtsbos spruit at Jonkershoek	1983-90	26
E5	G2H028Q01	Swartboskloof spruit at Jonkershoek	1985-90	22
L1	G2H016Q01	Lourens River at Somerset West	1978-91	88
P1	G4H005Q01	Palmiet River at Van Aries Kraal/Applethwaite	1978-04	125
P2	G4H007Q01	Palmiet River at Farm 562- Welgemoed/Kleinmond	1978-04	381
P3	G4H029Q01	Kogelberg Dam on Palmiet River: down stream weir	1988-04	130
P4	G4R002Q01	Eikenhof Dam on Palmiet River: near dam wall	1982-03	66
P5	G4R005Q01	Arieskraal Dam on Palmiet River: near dam wall	1982	6
P6	G4R006Q01	Kogelberg Dam on Palmiet River: near dam wall	1995-03	13

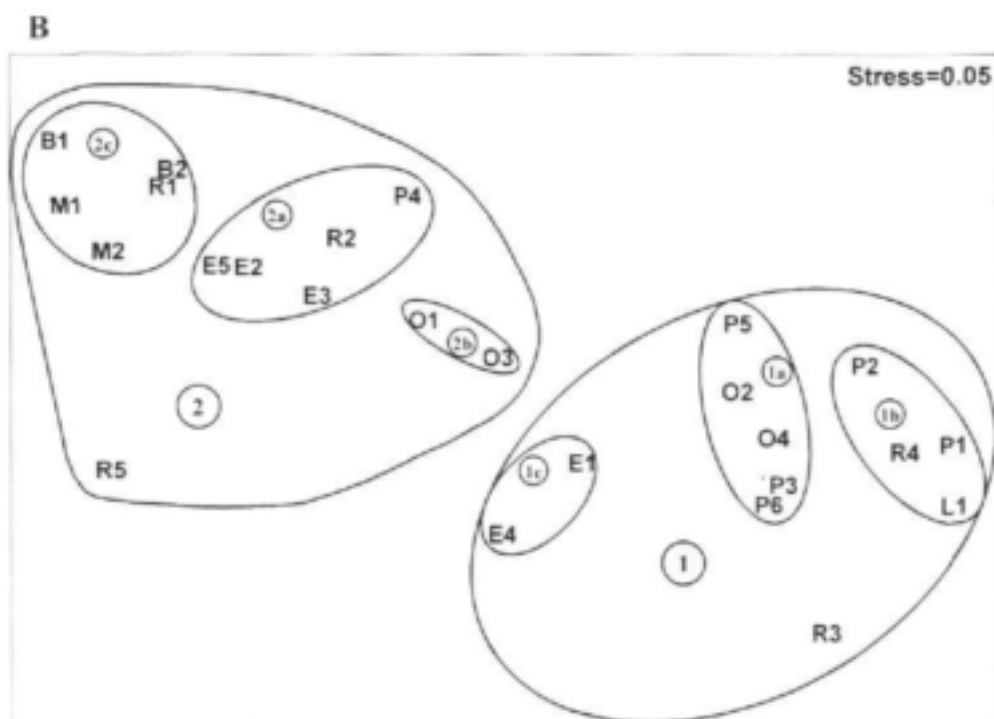
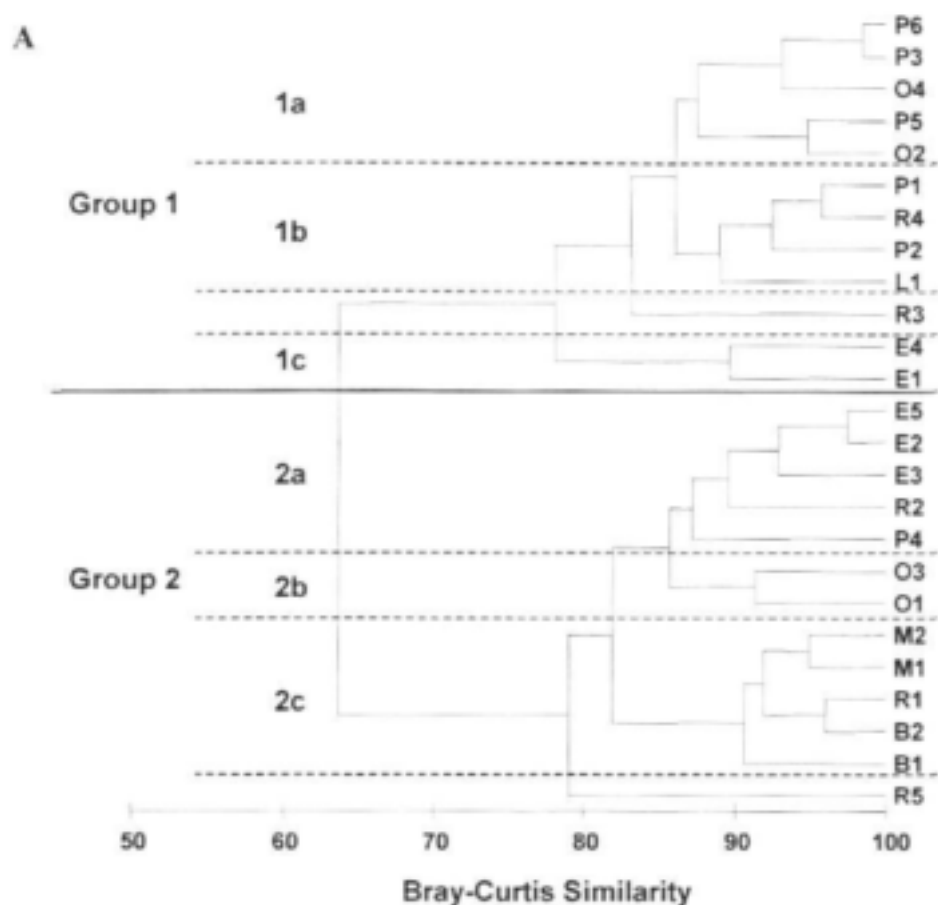


Figure 5.1 A. Dendrogram of water chemistry stations. B. 2-d MDS plot, with the main groups identified in the dendrogram separated by circles.

A series of t-tests comparing each water chemistry variable within each of the cluster groups showed that the values of pH, TAL, COND, Na^+ , Mg^{+2} , SO_4^{-2} , Cl^- and K^+ were all significantly greater for group 1 stations than for group 2 (Table 5.3). The main nutrient levels affecting primary production - nitrogen and phosphorus - were not significantly different between the groups. Since there was such an obvious split between groups, a separate analysis of the least disturbed group (group 2) was done to search for possible catchment-signature patterns (Figure 5.2).

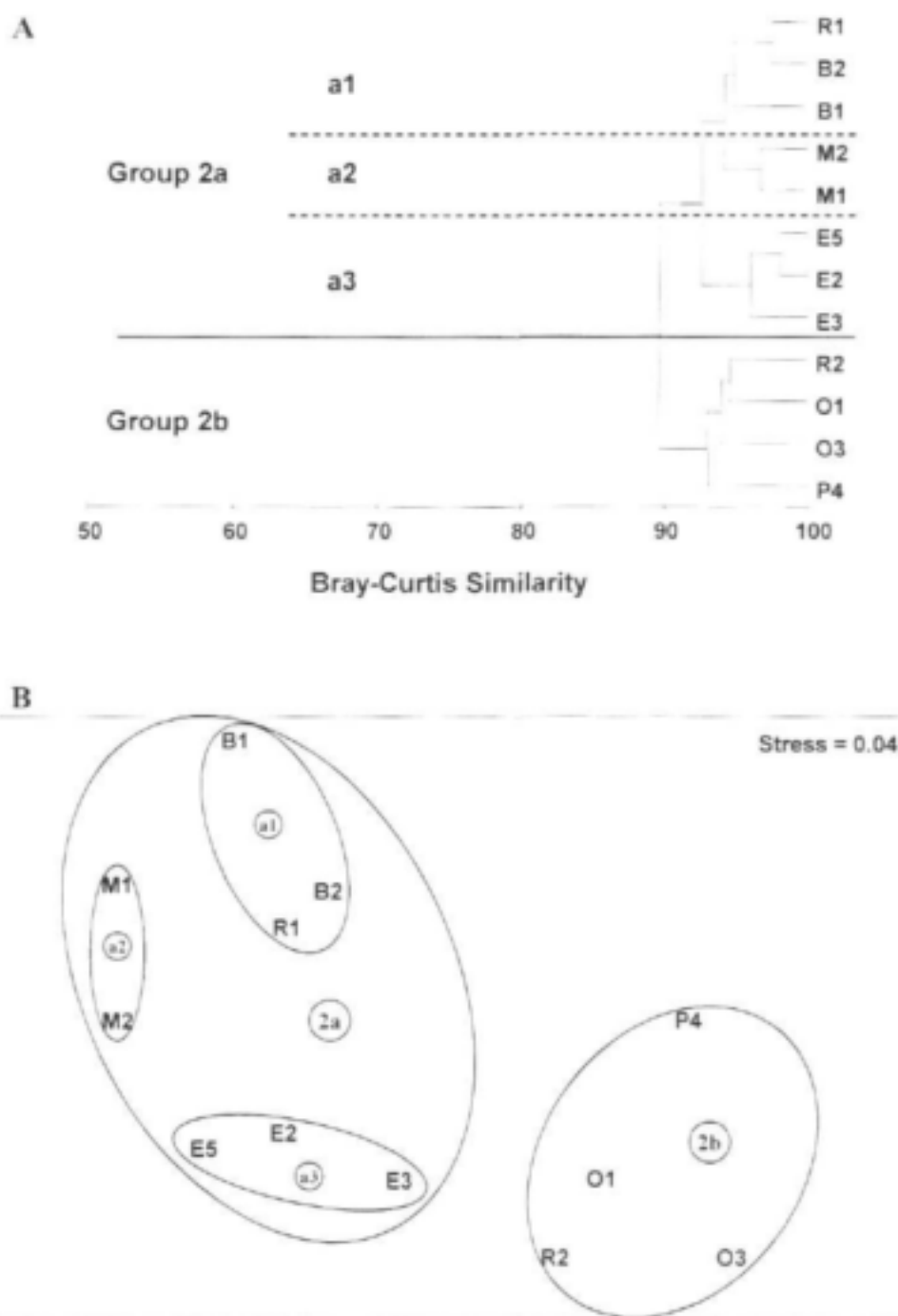


Figure 5.2 A. Dendrogram of group 2 water chemistry stations from Figure 5.1. B. 2-d MDS plot, with the main groups identified in the dendrogram separated by circles.

Table 5.2 DWAF water-chemistry variables used in the catchment analyses.

Variable	Abbreviation	Units
pH	pH	pH units
Total Alkalinity	TAL	mg L ⁻¹
Conductivity	COND	mS m ⁻¹
Nitrate + Nitrite	NO ₂ ⁻ + NO ₃ ⁻ -N	mg L ⁻¹
Ammonium	NH ₄ ⁺ -N	mg L ⁻¹
Orthophosphate	PO ₄ ⁻³ -P	mg L ⁻¹
Sulphate	SO ₄ ⁻² -S	mg L ⁻¹
Sodium	Na ⁺	mg L ⁻¹
Magnesium	Mg ⁺²	mg L ⁻¹
Silica	Si	mg L ⁻¹
Chloride	Cl ⁻	mg L ⁻¹
Potassium	K ⁺	mg L ⁻¹

Table 5.3 Results of t-test comparison of cluster groups 1 and 2 from Figure 5.1 to ascertain significant differences in water chemistry. Degrees of freedom = 23; t = t-test statistic; P = significance value; statistically significant P-values < 0.05 are in bold.

Variable	t	P
pH	-2.76	0.011
TAL	-3.98	≤ 0.001
COND	-3.95	≤ 0.001
NO ₂ ⁻ + NO ₃ ⁻ -N	-0.29	0.773
NH ₄ ⁺ -N	-0.54	0.592
PO ₄ ⁻³ -P	0.67	0.512
SO ₄ ⁻² -S	-2.80	0.010
Na ⁺	-5.90	≤ 0.001
Mg ⁺²	-4.70	≤ 0.001
Si	0.20	0.842
Cl ⁻	-6.28	≤ 0.001
K ⁺	-3.12	0.005

The level of similarity between the group 2 stations sites was high, with a split into two main groups at 89% similarity (Figure 5.2). Group 2a comprised the Eerste, Molenaars, Berg and one Breede stations, and group 2 the Olifants, Palmiet and remaining Breede station. Within group 2a, there is a split into Berg-Breede, Molenaars and Eerste sub-groups. This is along catchment lines to some extent, but the invertebrate clustering of the Eerste with the Molenaars and the Olifants with the Berg is not evident in these water-chemistry clusters. Water chemistry thus does not appear to be a major driver of the catchment signatures.

5.3 Alien and indigenous fishes

The Western Cape has a low biodiversity of indigenous freshwater fishes, with 18 main species, 50% of which are endemic and 14 that are threatened or endangered (Impson *et al.* 2000). The Olifants catchment is considered a fish endemic hotspot with eight species endemic to the area and threatened with extinction (Impson *et al.* 2000). One of the major threats to the indigenous fish population is posed by introduced alien fishes. Aliens such as smallmouth bass (*Micropterus dolomieu*) and rainbow trout (*Oncorhynchus mykiss*) are voracious predators of the indigenous fish population, and their early life stages are competitors for food sources such as invertebrates. Different combinations of indigenous and alien fish populations may be resulting in invertebrate communities with varying levels of impact from catchment to catchment. A list of rivers that are known to have alien fish was compiled (Table 5.4), together with the species present.

A BIOENV analysis was done, incorporating all 28 sites, to assess possible linkages between fish communities and catchment signatures. A standard set of environmental variables as per King & Schael (2001), namely -chemical (conductivity, pH, colour), substratum (percent composition of bedrock, boulder, cobbles and gravels), vegetation (percent cover of moss, algae, emergent macrophytes, *Scirpus* (a submergent macrophyte)) and topography (altitude, site slope, map slope), was supplemented with information on the fish. Native and alien fish were entered separately, indicating in each case the number of species present.

Table 5.4 River systems from Table 1.1 known to harbour alien fish. SMB = smallmouth bass (*Micropterus dolomieu*), BGS = bluegill sunfish (*Lepomis macrochirus*), BT = banded tilapia (*Tilapia sparmanii*), RT = rainbow trout (*Oncorhynchus mykiss*). Dean Impson, Cape Nature, pers. comm. and Impson *et al.* 2000. An asterix denotes that these aliens may not be resident, but present during high flows.

River #	River name	Alien fish present
1	Jan Dissels	SMB & BGS
3	Noordhoek	BT
5	Grootrivier	SMB & BGS
9	Molenaars	RT & SMB
10	Elands	RT
11	Elandspad	RT
12	Holsloot	RT & SMB
16	Wemmershoek	RT, SMB & BGS
17	Berg	RT & SMB
18	Eerste	RT
19	Lang*	RT
20	Swartboskloof*	RT
22	Lourens	RT

The results show which environmental variable or combination of variables best matches the invertebrate ordination of sites, that is, the set of environmental variables that best explains the biotic structure of the sites. A Spearman weighted correlation coefficient (ρ_s) is generated, with a correlation coefficient of 1.000 indicating a perfect match between the environmental and biotic

matrices. The analysis was done twice, first using the 17 LD sites and then using all 28 sites. The addition of fish to the BIOENV analysis did alter the original result reported King & Schael (2001) (Tables 5.5 and 5.6).

In the analysis using the 17 LD sites, the suite of environmental variables that best matched the invertebrate matrix was the combination of conductivity, gravels, cobbles, indigenous fish and moss cover ($\rho_w = 0.542$, Table 5.5). The original BIOENV results in King & Schael (2001) also used five variables to best explain the pattern, but the correlation coefficient was slightly weaker ($\rho_w = 0.491$) and included a different mix of variables, namely, cobbles, gravels, boulder, altitude and conductivity. Inclusion of the fish made the correlation stronger and other variables become less important. In both the original analysis in King & Schael (2001), and in this one, the highest scoring single variable was *Scirpus* (Table 5.5), but as this drops out when other variables are introduced, it is most likely also related to those physical variables.

The best combination of variables to match all river sites was indigenous fish and site slope ($\rho_w = 0.332$, Table 5.6), a weaker correlation coefficient compared to the original $\rho_w = 0.381$ (King & Schael 2001). The latter was created with eight different variables: algae, conductivity, macrophytes, site slope, altitude, boulder, cobbles and *Scirpus*, whilst the best correlation coefficient with only two variables, conductivity and macrophytes, was $\rho_w = 0.309$. Interestingly, indigenous fish emerged as the best single variable, and alien fish also appeared in the group of the best three variables, together with indigenous fish and site slope (Table 5.6).

Table 5.5 Variables used and coefficients derived from the BIOENV matching exercise of biotic and abiotic similarity matrices of the 17 LD rivers. The best overall match is indicted in bold font.

Number of variables	Best variable combinations	ρ_w	Rank
1	<i>Scirpus</i>	0.368	5
2	Conductivity and gravels	0.446	4
3	Conductivity, gravels, and cobbles	0.537	3
4	Conductivity, gravels, cobbles, and indigenous fish	0.539	2
5	Conductivity, gravels, cobbles, indigenous fish, and moss	0.542	1

Table 5.6 Variables used and coefficients derived from the BIOENV matching exercise of biotic and abiotic similarity matrices of all 28 sampled river sites. The best overall match is indicted in bold font.

Number of variables	Best variable combinations	ρ_w	Rank
1	Indigenous fish	0.299	5
2	Indigenous fish and site slope	0.332	1
3	Indigenous fish, site slope, and alien fish	0.305	2
4	Algae, conductivity, colour, and boulder	0.301	4
5	Indigenous fish, algae, conductivity, colour, and boulder	0.302	3

In summary, the presence and numbers of indigenous and alien fish taxa may play a role in catchment signatures but the uncertainty is high and needs research on fish-invertebrate relationships. It seems probable that different kinds of fish communities do affect the structure of invertebrate communities, probably acting as one of several environmental drivers rather than the primary one.

5.4 Geographical context

In the original project (King & Schael 2001) the invertebrates have been identified by catchment group because that is the pattern of clustering indicated by the classification dendrogram (Figure 4.1) and the MDS plot (Figure 4.2). Another possible insight on the catchment signatures can be gained if the groups on the MDS plot are delineated by geographical catchment and not by the dendrogram clusters. The catchments stretch from the Olifants in the north, to Davidskraal and the Palmiet in the south, and to the Table Mountain group in the south-west (Figure 5.3). The MDS plot can be orientated to coincide with this geographical layout (Figure 5.4), and then new lines drawn around the sites that are located within each individual catchment. The fact that the MDS plot can be orientated successfully in this way suggests that the catchment signatures may at least partly be attributable to biogeographical distribution patterns. In other words, knowing that the signatures are caused by species replacing species within each major taxonomic group (Chapter 3), could these replacements be a result of some species reaching the edge of their distributional ranges and being replaced by others?

To investigate this, individual distribution maps were drawn up for all the top discriminator taxa in Tables 3.13, 3.14, 3.15 and 3.17 (Figure 5.5a-e). A few taxa occurred mostly in the Olifants catchment in the north with very limited occurrence elsewhere (designated RN on the maps). Some were found only in the southern clump of catchments (designated RS), whilst others were widespread and common (W) or widespread but very patchily distributed (S). A few of the taxa were widespread but never collected on Table Mountain (W-TM).



Figure 5.3 Map of quaternary catchments containing sample sites. Shading indicates main catchment groups. Molenaars is a sub-catchment of the Breede. Site numbers as per Table 1.1.

Many of the taxa used in this project are known to occur outside the areas listed. The distribution maps in Figure 5.5 are thus far from complete, and interpretation of them should be done with caution. It can be said, however, that there does not appear to be a simple shift of species from north to south. Several different kinds of distributions appear to be present, perhaps reflecting biogeographical histories such as river capture and changing climate, as well as physical and physiological abilities to cope with different environments. The catchment signatures do not appear to be caused by a drift from species to species across the landscape.

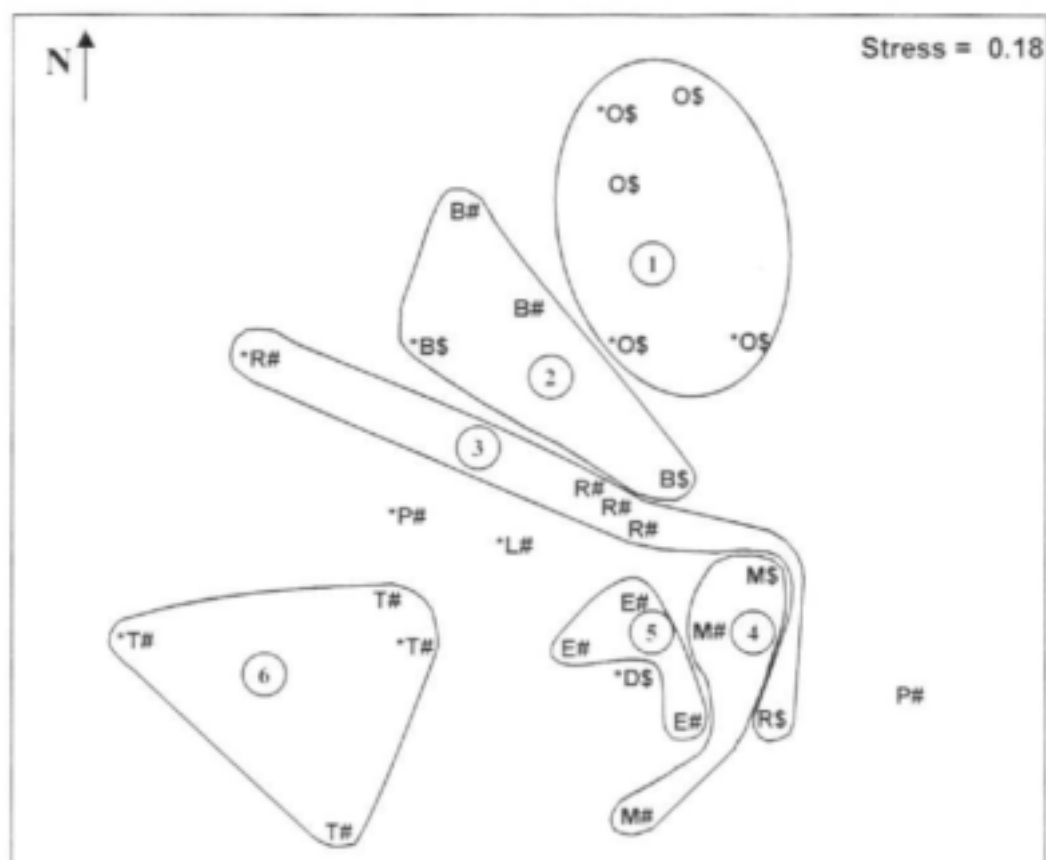


Figure 5.4 Two-dimensional MDS configuration of the 17 LD sites and 11 D sites, using species level data of invertebrates and rotated to positions which approximate the geographical positions of the catchments. Modified from Figure 4.2: 1 = Olifants; 2 = Berg; 3 = Breede; 4 = Molenaars; 5 = Eerste; 6 = Table Mountain; Palmiet, Lourens and Davidskraal lie outside these groups. Each site is designated by the first letter of its catchment name and by zone. # = predetermined mountain zone and \$ = predetermined foothill zone (King & Schael 2001); * = disturbed rivers.

Figure 5.5 Distributional maps for top discriminator taxa listed in Tables 3.14, 3.15, 3.16 and 3.18, by quaternary sub-catchment, a) Ephemeroptera, b) Plecoptera c) Trichoptera, d) and e) Coleoptera. Dark shading indicates a study catchment where a species was collected; light shading indicates a study catchment where the species was not collected. RN = restricted to the north; RS = restricted to the south; W = widespread; W-TM = widespread but absent from Table Mountain; S = scattered. Figures on the subsequent five pages.

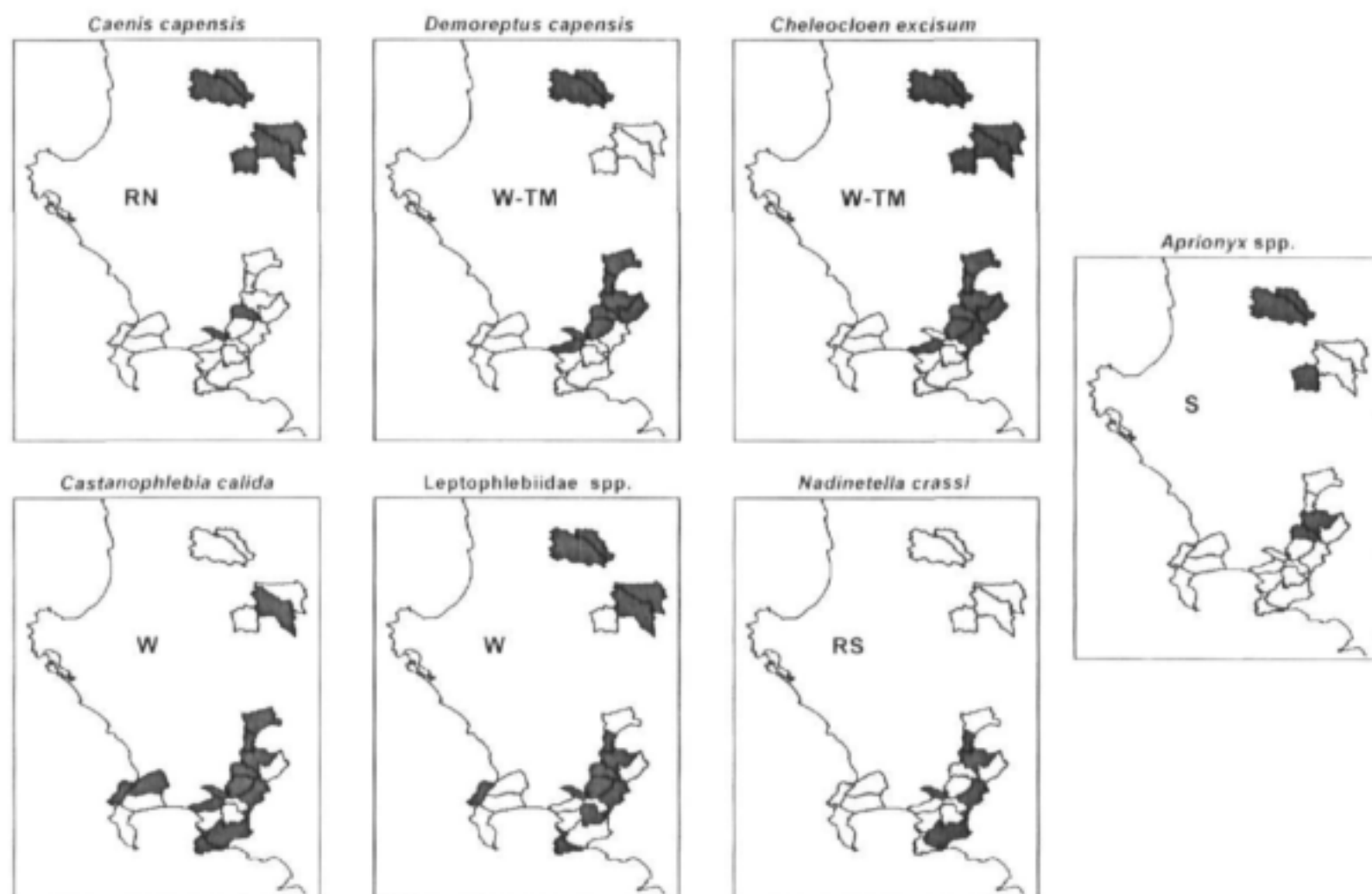


Figure 5.5a

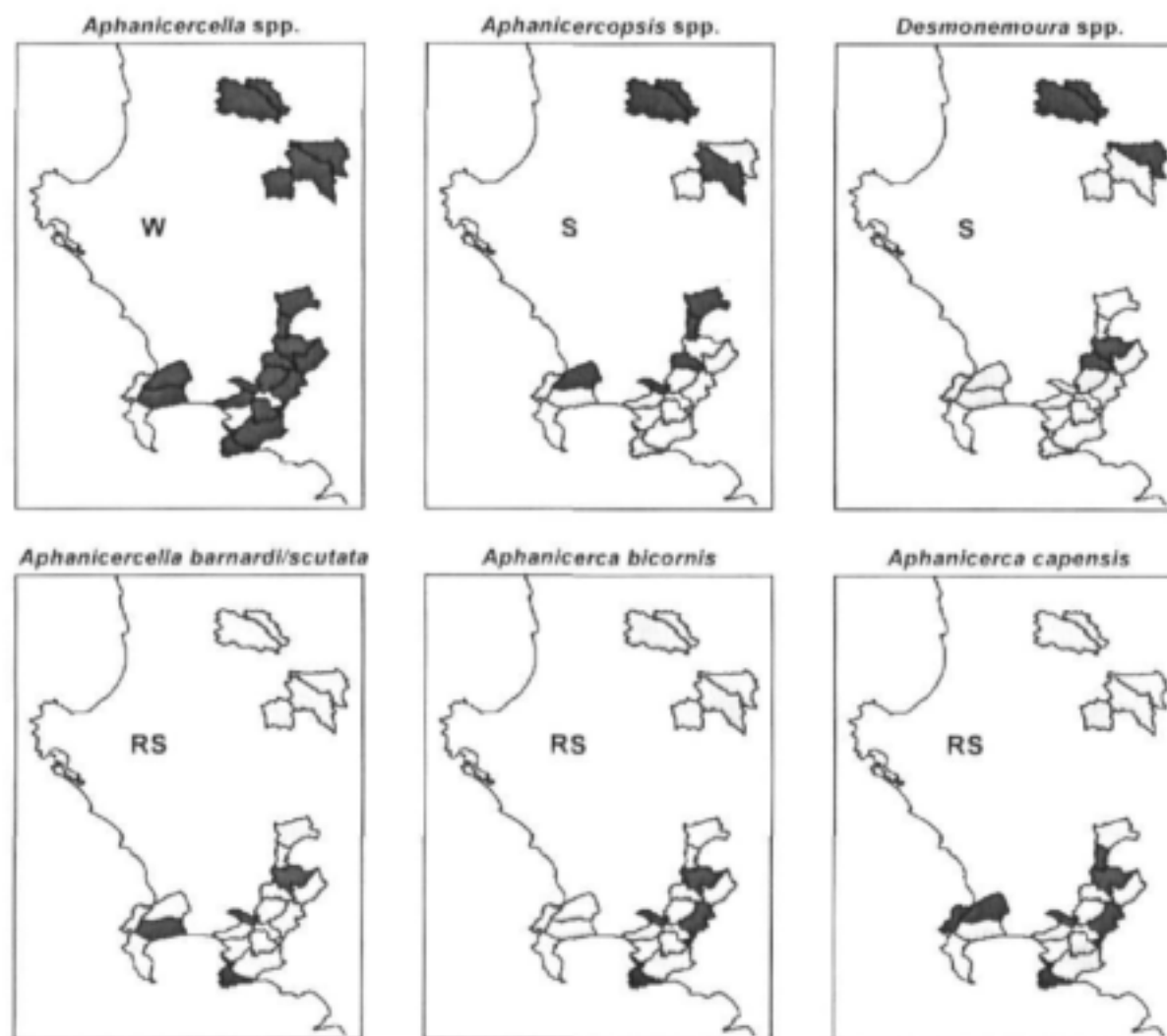


Figure 5.5b

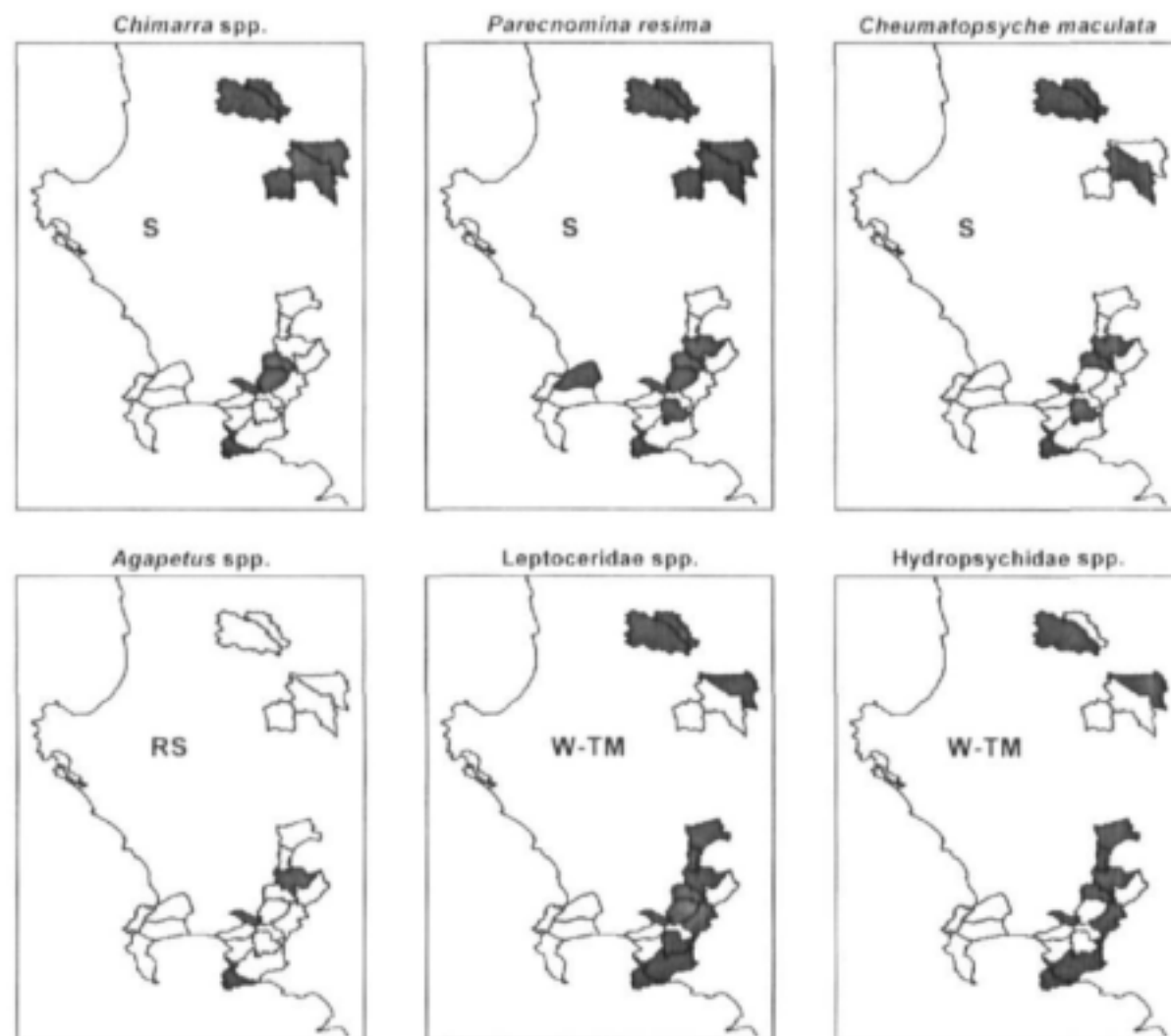


Figure 5.5c

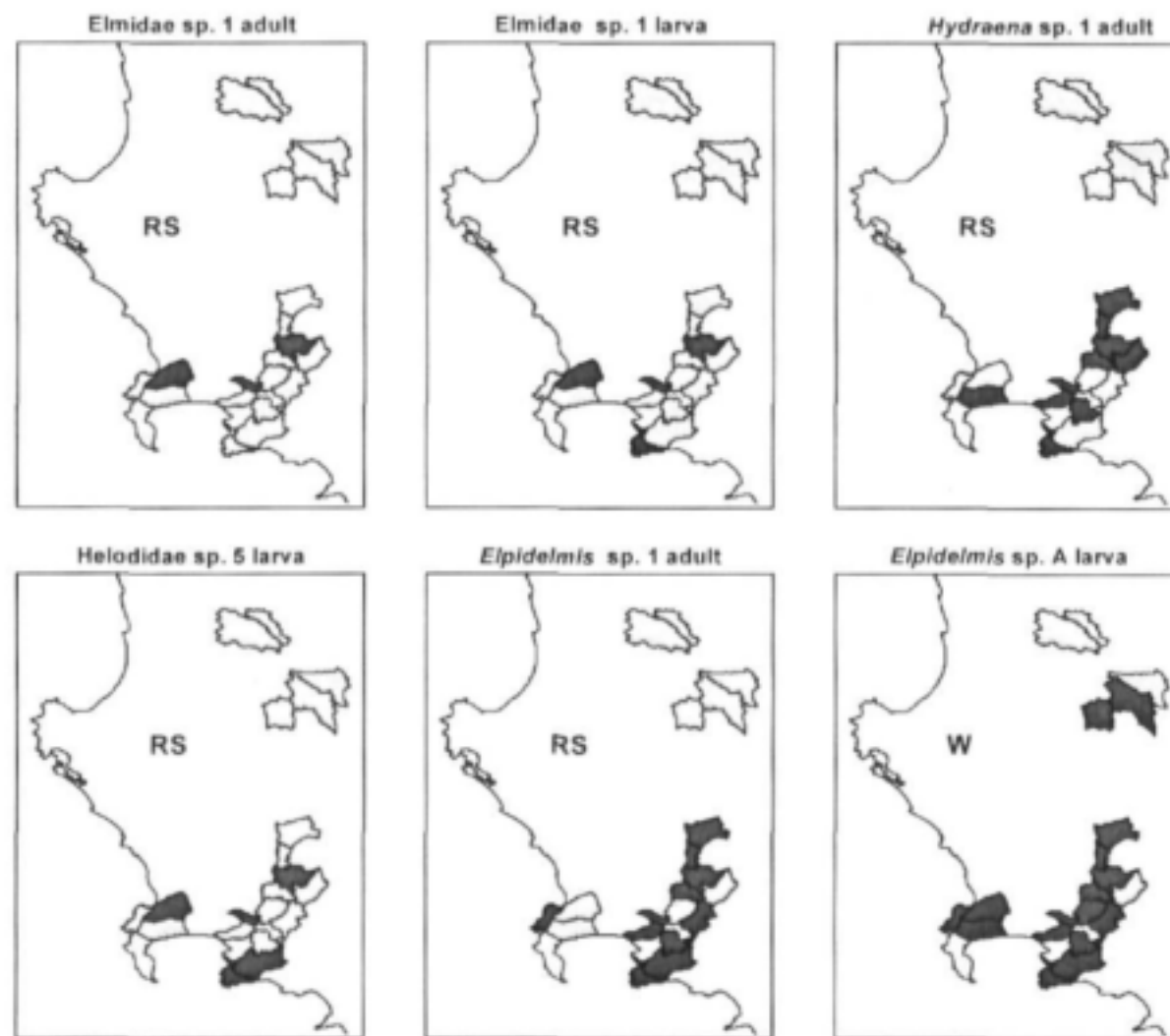
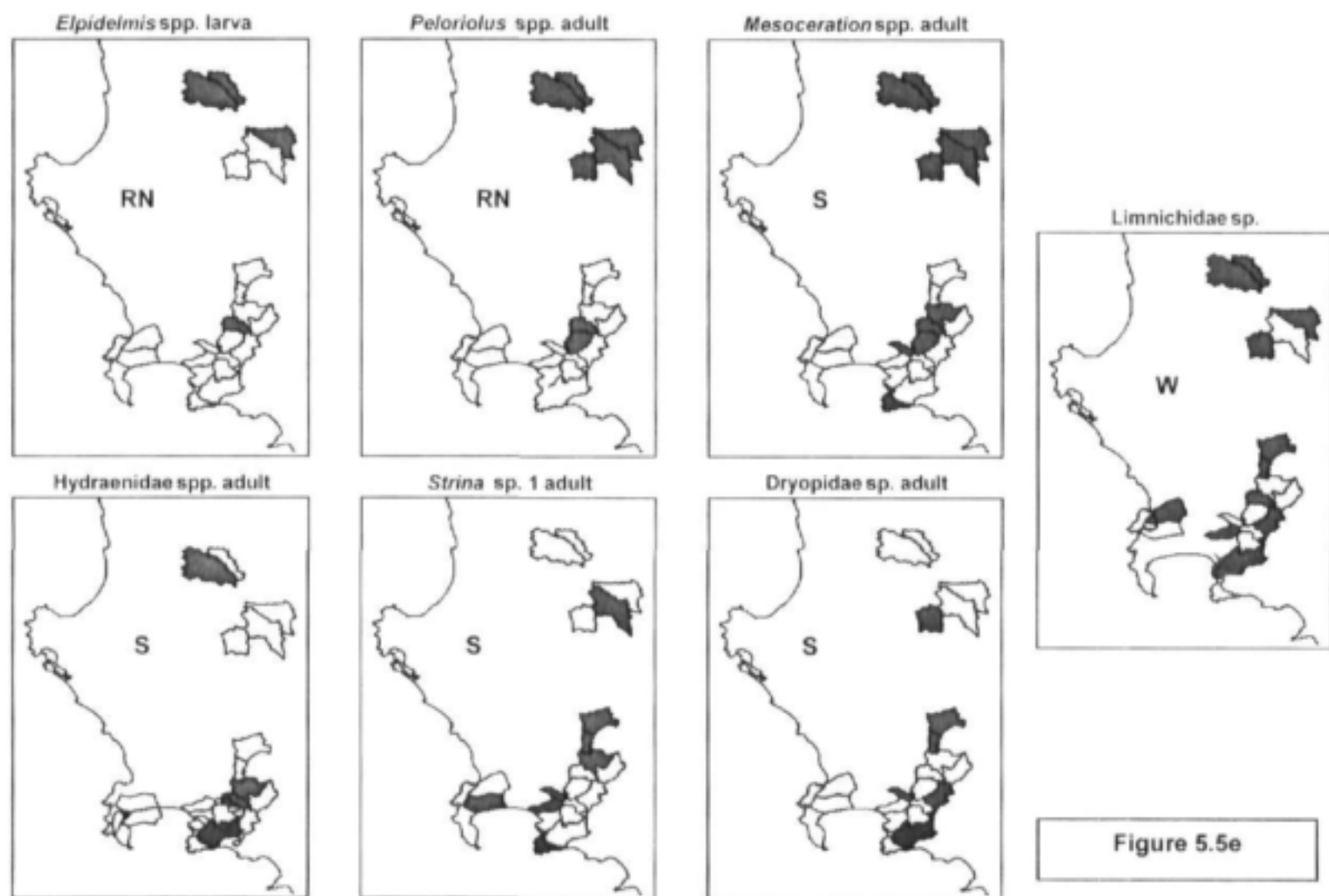


Figure 5.5d



5.5 Paleogeography: links to the past

Invertebrate samples from the Berg and Olifants Rivers clumped together through all the analyses reported in this project, except the one on Functional Feeding Groups. This persistent grouping could not be due to geographical contiguity, as the Breede headwaters lie between the Olifants and Berg headwaters. The Olifants and Berg are the only rivers in the study draining to the Atlantic Ocean, with all the others draining to the Indian Ocean. Part of the geographical history of the Western Cape is that the Berg and Olifants Rivers may have shared a common estuary during the Oligocene epoch in the Cenozoic era (Hendey 1983). Is it possible that their invertebrate communities are similar because of this - a phenomenon that, if their mountain-stream species did not distribute widely over the mountains and into the Breede headwaters, would presumably have required them to distribute down the complete length of one of the rivers and up the complete length of the other?

Past geographical isolation may be the cause of the Table Mountain streams grouping together, although they are in different catchments. Table Mountain has at times been an isolated island off the coast of South Africa, with its last re-connection to mainland Africa being at the end of the Pleistocene about 150 000 mya (Walker 1952; Deacon *et al.* 1983).

These two examples trigger the question of how long a river might maintain a catchment signature based on ancient land and drainage connections. One investigation that might shed light on this is of the Klein Berg River, which used to be a headwater of the Breede system (Prof de Wit, Geological Sciences, University of Cape Town, pers. comm.). Macro-invertebrates from the Klein Berg headwaters may have retained their Breede identity or assumed a Berg identity, and calculating the time when the river was captured by the Berg would give some idea of the times over which catchment signatures could persist among invertebrate communities.

5.6 Conclusion

None of the analyses reported here provide clear proof of a single environmental driver for the catchment signatures. Rather, the signatures most probably are the result of complex interactions of many variables over millions of years.

6. EFFECT OF SAMPLING POINT HYDRAULICS ON THE OUTCOME OF SASS SCORES

6.1 Introduction

The South African Scoring System (SASS) is a tool used in the rapid bioassessment of water quality in South African rivers. It uses benthic macroinvertebrate communities to indicate a level of biotic integrity or system health (Dickens & Graham 2002). It was first developed by Chutter (1972) and further refined for ease of use for local and national regulatory authorities (Chutter 1994; Chutter 1998). SASS was based on similar biotic indices developed in other parts of the world, such as RIVPACS in the United Kingdom (Wright *et al.* 1984) and AusRivAS in Australia (Smith *et al.* 1999). The focus of all of these indices was the use of invertebrates as indicators of the chemical aspects of water quality, with stream morphology and availability of habitat as only cursory elements of the indices.

Despite the lack of integration of habitat in these early bioassessment indices, it is widely recognised that differences in habitat do result in differences in species composition (Southwood 1977; Minshall 1984; Poff & Ward 1990; Palmer *et al.* 1991; Statzner *et al.* 1997), which could then affect the outcome of a bioassessment (Chessman 1995; Dallas 2001). The research conducted by Chutter (1998) and Dallas (1997 and 2001) into integrating habitat into SASS assessments has made the system much more robust. Dallas (2001) in particular has done extensive work to enhance understanding of the effects of different habitats on SASS scores.

The essence of the SASS system as it stands now (SASS: Chutter 1998; SASS5 Dickens & Graham 2002) is the field identification of aquatic invertebrates to the family level. Each family has a designated score that reflects its tolerance to chemical pollution. The invertebrate samples are collected in a number of different physical conditions – here called SASS biotopes – and three main metrics are calculated for each SASS biotope and for all SASS biotopes in combination. The combined score for all SASS biotopes is used to compare rivers across the landscape. The metrics are SASS score, number of taxa (families), and the Average Score per Taxon (ASPT). These provide different perspectives on the data. The SASS score indicates the sum of the taxon scores for taxa present at a site, with taxa that are sensitive to pollution being accorded higher scores than those that have a higher tolerance. A high SASS score would therefore indicate the presence of sensitive taxa and thus low levels of chemical pollution (Chutter 1995; Dallas *et al.* 1998). The ASPT is the SASS score divided by the number of taxa used to create the score and is the most stable of the two measures as it is least affected by biotope availability as sensitive and hardy species will be absent equally (Dallas 1997; Chutter 1998; Dickens & Graham 2002). The ASPT is also less affected by an increase in sampling effort than is the SASS score (Dickens & Graham 2002). As an example, the SASS score for an unpolluted headwater stream in the Western Cape is ≥ 140 and $ASPT \geq 7.5$ and a score and ASPT for a lowland stream is ≥ 50 and ≥ 5.0 respectively (Dallas *et al.* 1998). These two biological zones have naturally different SASS values because there are more pollution-tolerant taxa in the downstream reaches.

The data set used in the project reported here was not collected with SASS in mind or using the SASS method but it does contain comprehensive details of the species present in a range of physical conditions in Western Cape rivers. Because many samples were collected from many sites, these data have the potential to provide some insight into whether or not various permutations of sampling points within a site would produce differences in SASS scores. The objective of this chapter is thus to assess how different combinations of physical conditions could effect the resulting SASS score.

6.2 Development and analyses of SASS metrics

A summary of the sampling design, and enumeration and identification of the invertebrates, is reported in Table 1.2 and details are in King & Schael (2001). Basic points regarding the research reported here are summarised this section.

Each invertebrate sample was reduced to family-level data and the relevant SASS score was assigned to each family as prescribed by Dickens & Graham (2002). Each sample (6-12 per site) also had data on its flow and substratum conditions (King & Schael 2001). The samples were then combined into larger groups in three ways. They were grouped according to SASS4 biotopes (SIC, SOOC, VEG, GSM), to SASS5 biotopes (S, VEG, GSM) and to Schael's (in prep.) flow-substratum (FS) biotopes (Table 6.1). The SASS metrics were then calculated per site and per SASS or FS biotope. These metrics are not true SASS ones as the invertebrates were not collected and identified in the prescribed SASS way – finer net-mesh than the standard 1.0 mm SASS net was used, and the animals were identified to species by microscope rather than in the field by eye. Taxa that could have been missed in the field were thus probably captured, and mis-identification at the family level was less likely. The metrics may still serve a useful purpose, however, allowing samples to be mixed and matched in various ways (Table 6.1) and the resulting scores to be compared in the search for the influence of physical habitat. Because they are not true SASS metrics, they are shown in this report in italics, as *SASS metrics*.

For each LD and D site, the total *SASS Score*, *number of taxa* and *average score per taxon (ASPT)* were calculated using SASS4, SASS5 and FS biotopes. These metrics were the source data for all the analyses reported in section 6.3.

First, an analysis of variance (ANOVA) was used to determine if LD and D sites had significantly different *SASS Scores*. A series of one-way ANOVAs was then used to compare *SASS Score* and *number of taxa* between biotopes. If the general ANOVA model showed significant difference between biotopes, a Tukey's multiple pair-wise comparison test was then used to determine which biotopes were significantly different. The results of the Tukey's test are illustrated on the figures comparing biotopes, where those biotopes that are represented by the same lower case letter, e.g. 'a', were not significantly different from one another. The *ASPT* data violated the assumption of a normal distribution of data, therefore an ANOVA could not be used. A Kruskal-Wallis ANOVA on ranked data was then used to test if there was a significant difference between biotopes in terms of *ASPT*. To compare each biotope group type for the

ASPT data the Dunn's pair-wise comparison procedure for ranked data was used, instead of the Tukey's test used in the ANOVA procedure for the other variables.

Table 6.1 **Biotopes to which invertebrate samples were assigned.** Each sample from each site was assigned to one biotope in each of the three biotope columns. Details of SASS biotopes are in Dickens & Graham (2002) and Dallas (2001); and of FS biotopes in King & Schael (2001) and Schael (in prep.)

SASS4		SASS5		FS		
Code	Description	Code	Description	Code	Flow description	Substratum description
SIC	Stones (> 2 cm) and bedrock in current	S	SIC + SOOC as in SASS4	FB	Fast currents such as FF, CAS, CH, BSW, USW and FRF, as defined in Appendix 1	Bedrock and boulder, > 25 cm as per Appendix 1
SOOC	Stones (> 2 cm) and bedrock out of any perceptible current	VEG	As in SASS4	FC	As for FB	Large and small cobble, 6 – 25 cm, as per Appendix 1.
VEG	Emergent and submergent vegetation in and out of current	GSM	As in SASS4	FO	As for FB	All substrata < 6 cm, such as gravels, sand and much, as per Appendix 1
GSM	Gravel, sand and mud (≤ 2 cm) in a variety of currents			MB	Moderate currents such as RS and SBT, as defined in Appendix 1	As in FB
				MC	As in MB	As in FC
				MO	As in MB	As in FO
				SL	Slow currents such as BPF and NF as defined in Appendix 1.	All substratum types.

6.3 The effect of biotope on SASS Scores

The samples collected were not apportioned equally by biotope as prescribed by SASS (Figure 6.1).

Of the three SASS5 categories, 81% of samples taken were from the stones (S) category with 17 and 2% from gravel, sand and mud (GSM) and emergent and submergent vegetation (VEG) respectively (Figure 6.1a). Only four samples of 328 fitted the VEG biotope description, mainly because aquatic and marginal vegetation is rare in Western Cape headwater streams.

When the samples allocated to the S biotope of SASS5 were re-allocated to the two separate stony biotopes of SASS4 (SIC – stones in current - and SOOC – stones out of current), most (65%) went to the SIC biotope (Figure 1b) indicating the fast-flowing, cobble nature of the streams. The samples allocated to GSM and VEG biotopes remain the same in SASS4 and SASS5 (Figure 6.1a).

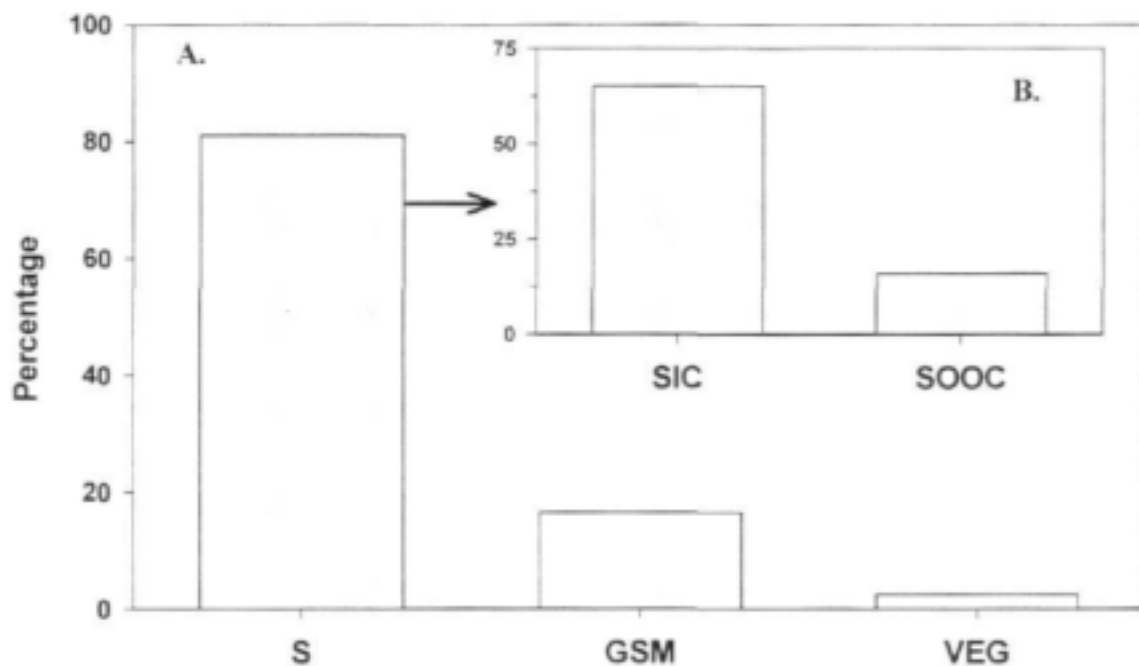


Figure 6.1 Proportion of invertebrate samples allocated to SASS biotopes for, a) SASS5, and b) the individual SASS4 components of stones (S) inset. Codes as per Table 6.1. The scale in b) is not equivalent to that in a).

When the samples were allocated to FS biotopes the proportions were more even (Figure 6.2a). The initial allocation was by flow: fast (F), moderate (M) or slow (SL). F and M held approximately equal numbers of samples (38 and 40% respectively), with fewer samples representing SL (22%). With the substratum component added, most samples from F flows were allocated to bedrock and boulder (Figure 6.2b), and about the same number of samples from M flows went to boulders/bedrock or to cobble (Figure 6.2c).

Few samples came from other substrata. Representing essentially the same set of samples as GSM does in Figure 6.1a, the samples were allocated between the FO (<5%), MO (<10%) and SL biotopes (Table 6.1).

The *SASS Score*, *number of taxa* and *ASPT* do not differ markedly between SASS4 and SASS5, and so all results from hereon refer to SASS5. *SASS Scores* were high for all sites (Table 6.2), indicating that the water quality of each site, in terms of the Dallas (1997), Dallas *et al.* (1998) and DWAF (1999) assessment categories, would be considered excellent (A-category, >140).

The only exception was the Holsloot which, with a score of 134, would be considered very good (B-category, 121-140). The *ASPT* values are also within the A category of >7, with the exception of Holsloot, which is once again in the B category. A one-way ANOVA comparison of *SASS Scores*, *number of taxa* and *ASPT* between LD and D sites confirmed that there was no significant difference between the two kinds of sites (Score: $F_{1,26} = 0.016$, $P = 0.899$; No. Taxa: $F_{1,26} = 0.017$, $P = 0.898$; ASPT: $F_{1,26} = 0.00025$, $P = 0.988$). All subsequent statistical tests then combined LD and D sites into one data set to evaluate the effects of different biotopes on *SASS metrics* compared to the sites totals.

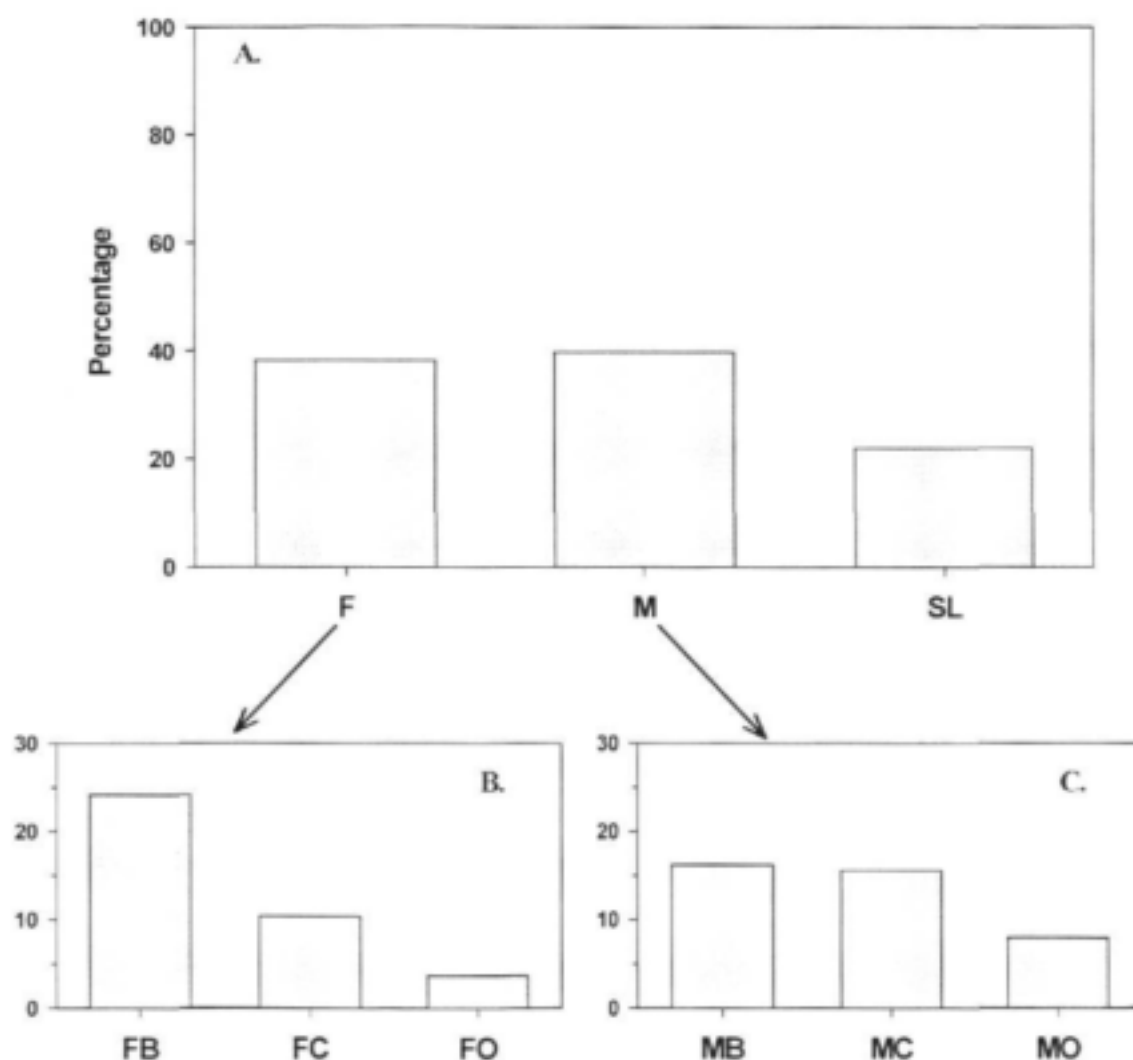


Figure 6.2 Proportion of all samples that were within a) each individual hydraulic biotope of fast (F), moderate (M) and slow (SL) current, and the individual flow-substratum components of, b) the fast current, and c) moderate current by substratum type. Codes as per Table 6.1. Note that the scales of b) and c) are not equivalent to that of a).

SASS biotope metrics

Data from all sites were pooled by biotope (Table 6.1) and the *SASS metrics* illustrated as box plots (Figures 2.3 and 2.4). Differences were evident between the metrics for individual biotopes and between these and the metrics for all biotopes combined (T). A one-way ANOVA comparing SASS5 with SASS4 biotopes, essentially a comparison between S on the one hand and SIC and SOOC on the other, showed an overall significant difference in terms of *SASS Score* ($F_{5,134} = 27.34$, $P < 0.001$). The Tukey's test, represented by the lower case letters on each figure, where those biotopes with the same letter were not significantly different from one another, showed that the *SASS Score* for T was not significantly different from those for either S or SIC at a $P < 0.05$ level (Figure 6.3a). *SASS Scores* for GSM and SOOC were not significantly different, but both were significantly different from those for T, S and SIC ($P < 0.05$). The under-represented VEG biotope had a large range of *SASS Scores*, and was only significantly different from T ($P < 0.05$).

Table 6.2 *SASS5 Score, number of taxa and average score per taxon (ASPT) for each site, following the protocol of Dickens & Graham (2002). (D) = disturbed as in Chapter 4.*

River #	River Name	Score	Taxa	ASPT
1	Jan Dissels	281	36	7.8
2	Rondegat	244	32	7.6
3	Noordhoek (D)	255	33	7.7
4	Middleduer (D)	238	31	7.7
5	Groot (D)	275	37	7.4
6	Steenbok	223	30	7.4
7	Wolvekloof	228	30	7.6
8	Wit	247	31	8.0
9	Molenaars	236	30	7.9
10	Elands	271	35	7.7
11	Elandspad	207	27	7.7
12	Holsloot (D)	134	20	6.7
13	DuToits	219	30	7.3
14	Bakkerskloof	215	29	7.4
15	Zachariashoek	231	32	7.2
16	Wemmershoek (D)	275	38	7.2
17	Berg (D)	221	28	7.9
18	Eerste	345	43	8.0
19	Langrivier	214	28	7.6
20	Swartboskloof	159	20	8.0
22	Lourens (D)	286	36	7.9
23	Palmiet (D)	255	30	8.5
24	Dwars	152	20	7.6
25	Davidskraal (D)	213	28	7.6
26	Window (D)	178	23	7.7
27	Newlands	216	28	7.7
28	Cecilia (D)	141	17	8.3
29	Disa	185	24	7.7

The same pattern of a significant difference between biotopes was shown by the *number of taxa* ($F_{5,134} = 27.82$, $P < 0.001$) and the Tukey's test also showed the same pattern of significant differences between biotopes (Figure 6.3a&b).

The *ASPT* was not significantly different between biotopes, and means ranged between 6.8 and 8 (Table 6.2, Figure 6.3c). Similar to the *SASS score* and *number of taxa*, the *ASPT* overall Kruskal-Wallis ANOVA on ranks showed that there was a significant difference between groups ($H = 13.5$, $df = 5$, $P = 0.019$). Unlike the other two metrics, however, the pair-wise comparison test (Dunn's) did not reveal any significant differences in *ASPT* between each of the biotopes or between them and T, with P -values > 0.05 , hence there are no lower case letters on Figure 6.3c as all biotopes and T were designated the same.

FS biotope metrics

There were no large differences in *SASS metrics* between the FS biotopes, but there was a significant difference between individual FS biotopes and T (Figure 6.4). Overall, *SASS Scores* differed significantly between biotopes ($F_{7,163} = 16.84$, $P < 0.001$), but only T differed significantly from all the individual FS biotopes (Tukey's $P < 0.05$; Figure 6.4a). The same pattern was shown in *number of taxa* ($F_{7,163} = 17.65$, $P < 0.001$, Figure 6.4b). Again the Kruskal-Wallis ANOVA on ranks showed an overall significant difference in the *ASPT* between biotopes ($H = 19.58$, $df = 7$, $P = 0.007$). The Dunn's pair-wise comparisons did not show significant differences between biotopes at $P < 0.05$, however. *ASPT* was very stable across all biotope combinations in comparison to *SASS Score* and *number of taxa* (Figures 2.3 and 2.4).

SASS metrics by biotope

The mean, standard deviation (SD) and coefficient of variation percentage (CV%) of each *SASS metric*, across biotopes, demonstrated that *ASPT* is the least variable and most consistent across biotopes (Table 6.3). In terms of river assessment category (Dallas *et al.* 1998 and DWAF 1999), the *ASPT* of any one biotope, if that were the only one sampled, would put, on average, all of our sites into an A category (Table 6.3). The exception was the SL biotope, which marginally missed that category and, if sampled alone, would have placed most of our sites, on average, in the B category.

The *SASS Score* showed much greater variability between biotopes (Table 6.3). The *SASS Scores* for T, and the S, VEG, SIC, and FC biotopes, if sampled individually to represent a site, would put that site within category A, the FB, FO, MB and MC biotopes in category B, and the GSM, SOOC, MO and SL would be in category C (101 – 120), on average. There was high variance within each biotope, suggested by the high CV% and large range (Figures 2.3 and 2.4) within VEG, GSM, MB, MO, MC, SOOC and SL. These biotopes would not necessarily be good representatives of a particular site, as they could over or under-estimate *SASS Scores*.

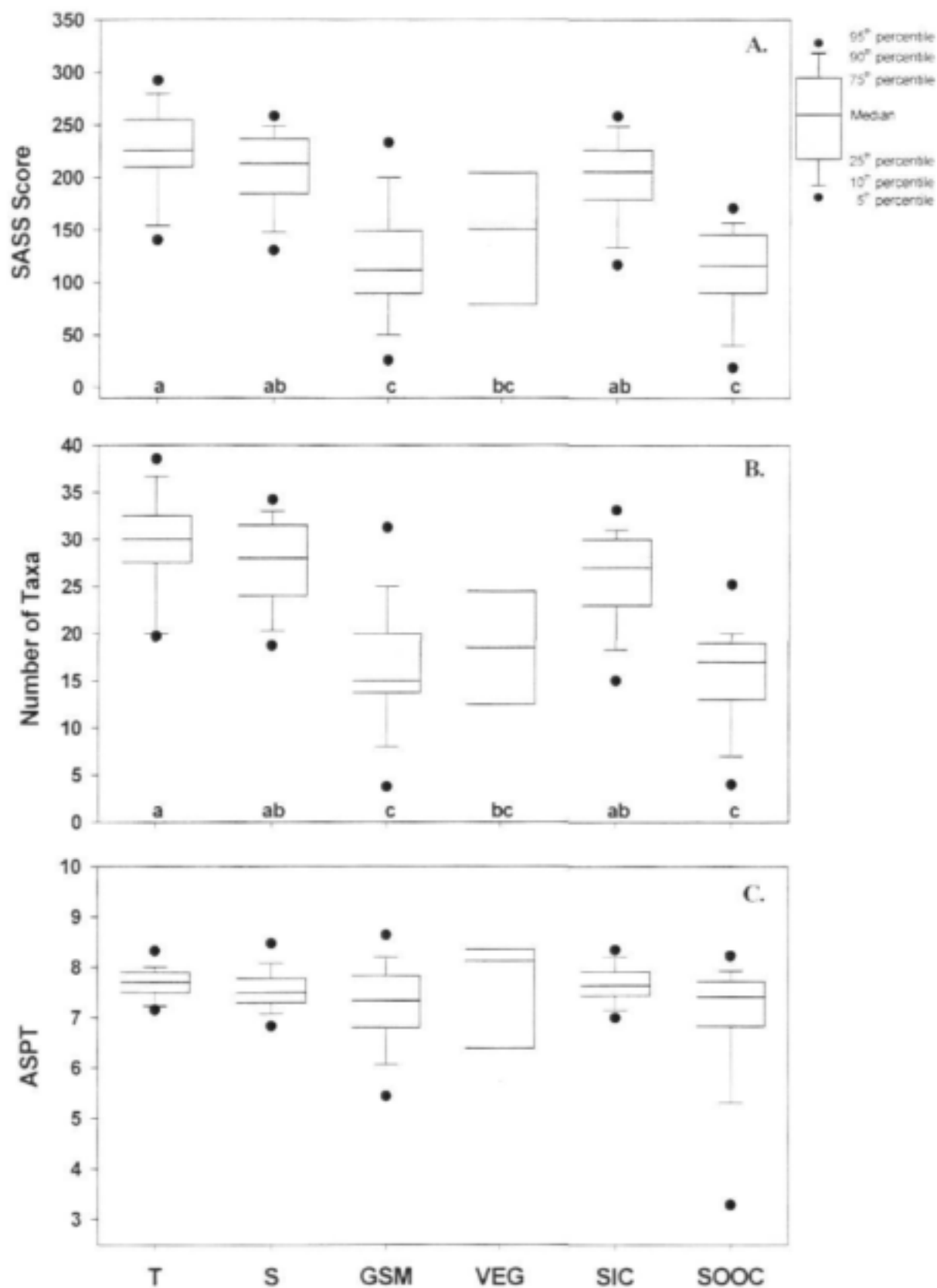


Figure 6.3 a) SASS Score, b) number of taxa and c) ASPT for all SASS5 biotopes combined (T) and for each SASS4 and SASS5 biotope. Codes as in Table 6.1. Same lower-case letter for each biotope denotes no significant difference between comparisons using Tukey's test at $P < 0.05$. ASPT had no significant differences between groups.

The strongest differences in *SASS Scores*, *number of taxa* and *ASPT* were between the SASS5 biotopes (Figure 6.3 and Table 6.3). SIC (a SASS4 biotope) had very similar *SASS Scores* to S (SASS5 biotopes), and SOOC similar ones to GSM. The FS biotopes did not show strong differences for any of the *SASS metrics*, and are therefore not considered further.

To determine which of the family-level taxa contributed to the differences between the SASS5 biotopes (S, GSM and VEG), the proportion of the samples from each biotope in which each taxon occurred was calculated (Table 6.4). Several taxa occurred in consistently high proportions in all three SASS5 biotopes, such as the Notonemouridae, Chironomidae and Elmidae/Dyropidae. Others were dominant within the S biotope such as the Blephariceridae, Ceratopogonidae, Veliidae/Mesovellidae, and Ecnomidae. Taxa that co-occurred in GSM and in S and/or VEG were present in equal or lower proportions of the GSM samples. VEG was under-represented in the data set due to its rarity in the study streams and, possibly for this reason, had relatively few taxa though some, e.g. Notonectidae, Naucoridae, Coenagrionidae and Pyralidae, were present in the that biotope in higher percentages than in others.

Table 6.3 The number of sites (N), mean, standard deviation (SD) and coefficient of variation percentage (CV%) for *SASS Score*, *number of taxa* and *ASPT* for each biotope. Codes as per Table 6.1, TOTAL = all biotopes combined. An "A" category has a score of > 140 and ASPT of > 7, a "B" category has a score ranging from 121 – 140 and ASPT from 6 – 7 and a "C" category has a score range from 101 – 120 and ASPT from 5 – 6 (DWAF 1999).

Code	N	Score			Number of Taxa			ASPT		
		Mean	SD	CV%	Mean	SD	CV%	Mean	SD	CV%
TOTAL	28	226.6	47.5	21	29.5	6.0	20	7.7	0.4	5
S	28	205.9	40.9	20	27.3	4.9	18	7.5	0.5	6
GSM	24	118.2	55.9	47	16.1	6.9	43	7.2	0.9	13
VEG	4	141.8	73.9	52	18.5	7.0	38	7.4	1.8	24
SIC	28	200.0	41.9	21	26.0	5.0	19	7.7	0.4	6
SOOC	26	112.4	47.4	42	15.7	5.8	37	7.0	1.3	19
FB	27	134.6	42.9	32	18.2	2.5	14	7.7	0.7	9
FC	17	143.6	24.4	17	17.2	4.8	28	7.9	0.6	8
FO	9	135.3	34.5	26	17.7	4.3	24	7.6	0.5	7
MB	23	126.6	58.9	47	16.1	7.5	46	8.0	1.0	13
MC	24	131.5	54.5	41	17.4	6.9	39	7.5	0.7	10
MO	16	109.8	48.5	44	14.9	5.5	37	7.1	0.9	13
SL	27	107.3	43.4	40	15.2	5.6	37	6.9	1.5	22

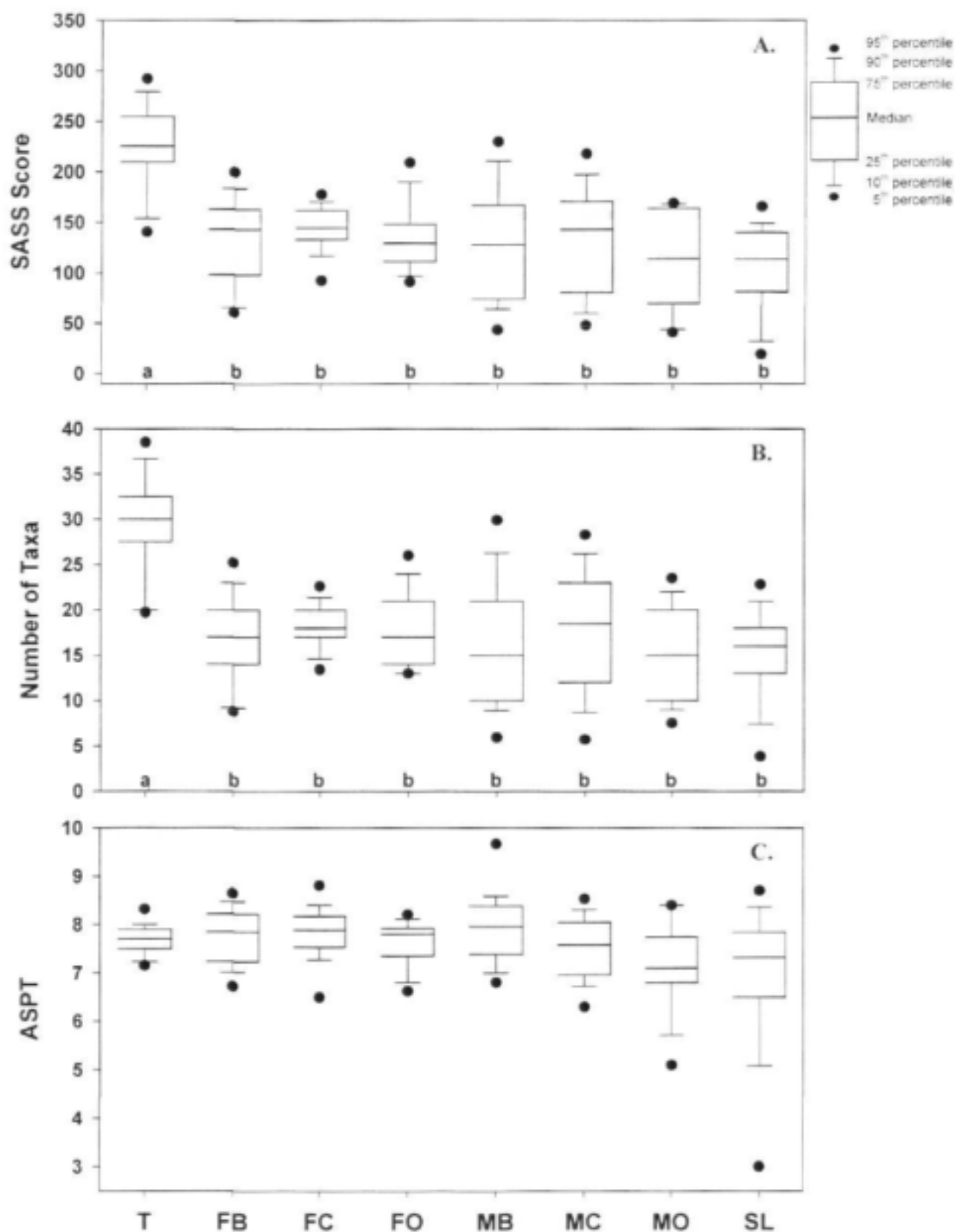


Figure 6.4 a) SASS Score, b) number of taxa and c) ASPT for all SASS5 biotopes combined (T) and for each FS biotope. Codes as in Table 6.1. Same lower-case letter for each biotope denotes no significant difference between comparisons using Tukey's test at $P < 0.05$. ASPT had no significant differences between groups.

Comparing the values shown for each biotope with those for the biotopes combined revealed that overall S contributed most to the total (Table 6.4). This further supported the results reported earlier that *SASS Scores*, *number of taxa* and *ASPT* did not differ statistically between T and S. A Kruskal-Wallis ANOVA showed the taxon composition of each SASS5 biotope was significantly different ($H = 12.5$, $df = 2$, $P = 0.002$), where S and GSM, and S and VEG were significantly different from one another (Dunn's test, $P < 0.05$) and GSM and VEG not significantly different ($P > 0.05$).

Table 6.4 Percentage of each SASS5 biotope that contained the listed family-level taxa. SASS5 biotopes: stones (S), gravel-sand-mud (GSM) and emergent and submergent vegetation (VEG) and for all combined (Total). Definitions of categories as per Table 6.1.

Order	Taxon	S	GSM	VEG	Total
	<i>Number of samples:</i>	<i>27</i>	<i>24</i>	<i>4</i>	<i>55</i>
Acarina	Hydracarina	89	63	75	78
Annelida	Oligochaeta	86	83	50	84
Coleoptera	Dytiscidae	32	13	0	22
	Elmidae/Dyopidae	93	79	75	87
	Gyrinidae	43	21	50	35
	Helodidae	86	75	100	84
	Hydraenidae	82	42	50	64
	Hydrophilidae	25	8	25	18
	Limnichidae	43	21	25	33
	Amphipoda	43	33	50	40
Crustacea	Potamonautidae	43	17	25	31
Diptera	Athericidae	68	42	25	55
	Blephariceridae	21	0	0	11
	Ceratopogonidae	82	58	25	69
	Chironomidae	93	96	100	96
	Culicidae	21	4	25	15
	Dixidae	18	13	25	16
	Empididae	75	25	25	51
	Ephydriidae	4	0	0	2
	Muscidae	4	0	0	2
	Psychodidae	18	13	0	15
	Simuliidae	89	71	75	82
	Tabanidae	14	0	0	7
	Tipulidae	82	46	25	64
	Baetidae 1 type	7	21	0	13
	Baetidae 2 types	7	25	25	16
Ephemeroptera	Baetidae 3+ types	82	42	75	65
	Caenidae	39	21	25	31
	Heptageniidae	29	13	0	20
	Leptophlebiidae	89	63	25	75
	Teloganodidae	82	63	50	73
	Ancylidae	0	4	0	2
Gastropoda					
Hemiptera	Naucoridae	25	13	50	22

Order	Taxon	S	GSM	VEG	Total
Hemiptera	Notonectidae	7	0	25	5
	Veliidae/Mesoveliidae	50	29	0	38
Lepidoptera	Pyralidae	39	13	75	31
Megaloptera	Corydalidae	68	21	0	44
	Sialidae	7	0	0	4
Odonata	Aeshnidae	43	4	25	25
	Chlorolestidae	18	0	0	9
	Coenagrionidae	29	17	75	27
	Corduliidae	25	8	0	16
	Gomphidae	50	25	50	40
	Lestidae	4	0	0	2
	Libellulidae	36	21	25	29
	Platycnemidae	18	4	0	11
	Prototoneuridae	0	4	0	2
Pelecypoda	Corbiculidae	4	4	0	4
Plecoptera	Notonemouridae	96	83	75	91
Trichoptera	Barbarochthonidae	25	4	50	18
	Ecnomidae	68	33	0	49
	Glossosomatidae	21	17	0	18
	Hydropsychidae 1 type	21	33	25	27
	Hydropsychidae 2 types	32	8	25	22
	Hydropsychidae 3+ types	25	4	0	15
	Hydroptilidae	54	25	25	40
	Leptoceridae	93	58	100	80
	Petrothrincidae	32	29	50	33
	Philopotamidae	61	13	50	40
	Pisuliidae	4	4	0	4
Trichoptera	Polycentropodidae	4	0	0	2
	Sericostomatidae	21	17	25	20
Turbellaria	Planariidae	50	21	25	36

6.4 Conclusions

The research reported here indicates that there were differences in *SASS metrics* between the SASS5 and SASS4 biotopes, but not between the FS biotopes. Overall, *SASS Score* and *ASPT* were high for the combined biotopes and for each individual biotope, and placed the sites studied in good to excellent health categories in terms of water quality, irrespective of the degree of physical perturbation. As an example of the anomaly in these results, the study site Wemmershoek in the Berg catchment was downstream of a major dam, and the river bed had been bulldozed to the point where its natural geomorphological character was lost (King & Schael 2001). Despite this, the site had a *SASS Score* of 275 and *ASPT* of 7.2 (Table 6.2), which places it in an A river-health category. Approximately 78% of the study sites had scores >200, which is well above the >140 level set by Dallas *et al.* (1998) for a site in excellent condition in Western Cape mountain streams. It should be remembered that the *SASS metrics* reported in this chapter are most likely inflated due to the laboratory identification of the invertebrates, and would probably have been lower to some unknown extent if based on field identifications, but

probably not to the extent that they would have resulted in the sites being downgraded to category B or lower. Thus, interpretations of river health based on SASS scores should be made with caution and with an understanding that this coarse metric cannot detect many kinds of river degradation.

Even though there were unequal samples of the different biotopes in SASS5, it did not seem to have a negative effect on scores. The additional availability and/or effort within the S (SIC and SOOC) biotope may have also inflated the results because of the tendency to have more taxa and diversity of taxa within SIC and SOOC than GSM or VEG (Pridmore & Roper 1985; Dallas 2001). This skewness may be especially true in summer, or a low flow season, as there are more S biotope types available for sampling than during other sampling periods (Dallas 2001), and these data were collected during the summer. Overall, however, results of the between SASS5/4 biotope comparisons were much the same as that of Dallas (2001) and fairly similar to Dickens & Graham (2002). Dallas (2001) is a comprehensive study that compares biotopes between regions, within regions and within sites, with specific SASS4 sampling methodology in place, and should be consulted for further information.

Our study showed little impact of biotope choice overall on *SASS scores*, *number of taxa* and *ASPT* representing water quality health of a river site. In other words the SASS score will be roughly the same no matter which biotopes the samples are collected from. This study also demonstrates that a SASS score cannot detect physical degradation of a river, and indeed was not designed to do so. Therefore, researchers should avoid the temptation to use SASS as an index of river health in terms of physical disturbance.

7. DATABASE AND QUERY CENTRE FOR LINKED PHYSICAL AND MACROINVERTEBRATE DATA

7.1 Introduction

The database of invertebrate taxa, arranged by Western Cape river, site and hydraulic biotope, was created in WRC project K5/754 (Chapter 9: King & Schael 2001). The database has now been further developed, as reported in this chapter. The database is in Microsoft (MS) Access version 2000 (9.0.2720), upgraded from the previous MS Access version 95. The structure of the database (Section 7.2) and the data-entry facility (Section 7.3) require MS Access 2000 to run. The query centre is a stand-alone product, however, compiled in Visual Basic, and does not require MS Access and would not be prone to problems with different versions of the programme.

The database was designed for two primary reasons. First, a facility was needed to efficiently store and access all data generated in the original project, especially the descriptive data. Second, so much physical-biological linked data were collected within the project that the opportunity was created to initiate a potential national database along the same lines as the chemical-biological one created by Dallas *et al.* 1998 and Dallas & Janssens (1998). This would enable others collecting similar data to contribute to and access the database for future national studies. Although the database for this project cannot be linked directly into the Biobase, SASS and River Health Programme databases developed by Dallas *et al.* (1998), Dallas & Janssens (1998) and Fowler *et al.* (2000) respectively it can be viewed as a companion to these. As these previous databases were designed primarily for linked chemistry and invertebrate data, modifications were made to this database so as to house data on physical variables. Although the bulk of the present data refer to once-off visits to river sites, the database has the flexibility for adding additional sampling dates and sites. The database has already been used for the macro-invertebrate chapter of the Olifants-Doring environmental water requirements study, where 308 data points were provided on Ephemeropteran-flow links, 28 on Trichoptera flow links, 205 on Diptera flow links, 369 on Coleoptera flow links and 22 on Megaloptera flow links (Ractliffe & Dallas 2004).

7.2 Installation

Installation of the database requires a computer with a CD-ROM drive and Windows 98 version or higher. The database and query centre have been tested and will run on the following versions of the Windows operating system: 98, ME, 2000, XP, XP professional. MS Access 2000 is only required to add data to the database via the front-end forms. The query centre, however, does not need that program and can access the data and run on any Windows machine. Installation of the program and associated files is automated after insertion of the CD. It will first install the "Install Shield" program, which may take a minute or two on older computers with processors of Pentium 2 or lower.

- Once "Install Shield Wizard" has installed, a screen with the general database information will appear. Click the "next" button.
 - A standard license agreement will appear. Click the "accept" option and then "next".

- The next screen to appear requires details of name and organisation. Enter these and click "next", where a summary of the installation information will appear.
 - Check that the information provided is correct, then click "next", or click "back" to make an amendment".
 - After the "next" button, the program will install.

After successful installation the following files will be present in a directory created on the hard drive called "uctdata" (C:/uctdata): flowdat.mdb (5.5MB) the actual data, and flowprog2k.mdb (1.8MB) the front-end data entry forms. The *.mdb files are needed for the query centre to operate, as it accesses the data from those files. The installation program will also create a folder within the "Program Files" directory on the computer, called "UCT Query Centre", and an icon within the "start" menu on the Windows tool bar. To access the query centre click that button. To add new data, MS Access must be activated and the file flowprog2k.mdb file opened.

Once installation has been completed once, insertion of the CD a second time will produce a different initial screen with options to "modify", "repair" or "remove" the database program. Each option is explained in the accompanying text. To uninstall the program and all of its components, click "remove".

7.3 Structure

The database consists of interconnected tables, with each table housing a specific set of interrelated data. Each of these tables connects to at least one, if not many, other tables within the database structure. Some variables, such as site code or site name, carry over from one data set to others, thus connecting different types of data. The "Site" table forms the root of the database (Figure 7.1a&b). This table contains relatively constant information on study site, such as river name, site code, altitude, longitude and latitude, access details and stream order. This central table links, for example, to the "Site Visit" table, which lists the dates on which each site was visited, or to the "Site Visit Transect" table, which details all the channel cross-section data.

Data tables are often supported by what are referred to as look-up tables (Appendix 4.J). These tables are created to support and streamline data entry. Terms that are often used when entering data can be put into these tables and accessed. Each look-up table generally only connects with one type of data table. For instance, there is a look-up table for types of valley floor, which is one of the variables entered into the "Site" table of general descriptors. This look-up table contains the different types of geomorphologically defined valley floors common in the Western Cape: erosional bench, flood plain, pediment, terrace, valley side bench, valley floor absent. Regions with different types of valley floors would need to add new terms to this table as described below in Section 7.4. A user would not be directly aware of the look-up tables, as they provide the drop-down lists of terms when entering data.

7.4 Data entry

For ease of data entry, a form-style interface was designed for operation in MS Access 2000. An initial form with a series of icons appears on the start-up form in MS Access, from which the user chooses the type of data that will be entered. Currently a "Sites" option takes the user into the entered list of rivers and sample dates and gives the user the option to add another river, site or sampling date. From that screen, a series of tabbed forms allow for the addition of various site descriptors (for new sites) and other general information. Alternatively, menu/buttons allow data to be entered on, for instance, invertebrates or local hydraulics.

The next three options on the main interface refer to tables that aid in general data entry. These options are "Picklist", "Taxonomy-Invertebrates", and "Taxonomy-Riparian Veg" (riparian vegetation). The "Picklist" option is used to add information to the look-up tables, which are tables of lists of terms commonly used in the data-entry process, as mentioned above. For example, if a new morphological unit (MU) is added to the general terminology, it can be entered into the look-up table for MUs. Terms that are not in the look-up table cannot be added into the database linked to a site until they are inputted into the look-up table that the data table links to. The "Taxonomy-Invertebrates" interface is much the same as the "Picklist" one, but at a larger and more complex scale. All possible faunal taxa must be entered into "Taxonomy-Invertebrates", and floral taxa must be entered into "Taxonomy-Riparian Veg" before they can be entered into the database linked to sites. This is the heart of the biological component of the database, and its most complex part. The very large look-up tables contain their own series of supporting look-up tables, and any mistakes made in creation of this component transfer through the entire database. On the positive side, corrections of mistakes in one area are automatically carried through all interconnected data.

7.5 Using the Database Query Centre

The Query Centre for the database was designed to facilitate access to any required type of data and its linked data. One of the major strengths of a database is the facility it provides to manipulate data so that specific sets can be chosen. The Query Centre is not fully automated, as there are hundreds of possible requirements for linked data. However, there is sufficient structure to answer such queries as "all the flow types in which *Baetis* sp. X has been found". A more experienced user of MS Access will be able to design specific queries within that structure tailored to their requirements. Data can also be out-put in their entirety from the Query Centre and imported into a spreadsheet and manipulated there. The individual queries can also be refined in a spreadsheet.

The drop-down menu bar on the query centre similar to all MS Windows applications, each category can be clicked on and a list of choices are given. The first menu item is "query" which consists of a series of eight automated queries designed to access various components of the database that it was perceived a general user might use. Each of these is discussed in more detail below. The second item - "front end" - has two options. The first - "about the front end" - provides user information about the MS Access part of the database, such as where the program file is located and how to access it. The second - "remove all the front end database records" - removes all of the data held in the database, but

leaves the entire structure intact. It is designed for users who wish to populate the database with only their own records. Once the user has confirmed the deletion process, all the records are permanently deleted and the only way to restore them is to reinstall the program as stated above. The third menu item is "window", which is the standard Windows operating system function to toggle between multiple open frames. The last item is "help", which gives contact details for users experiencing problems with the database.

All of the queries have the option to export all data within that query field (click the "export all data" button), or a subset of data at the user's request ("run query" button can be clicked, criteria must be selected or an error will be returned). Data from queries are exported as *.CSV (comma separated values) files which can then be imported into a spreadsheet or word processing program of the user's choice. Upon running a query the user will automatically be given an output file name and location, which can be amended to a new name and location at the prompt. Once the data have been compiled and saved the file will be accessible via the user's spreadsheet or word processing program, and then another query can be made. Each output table has a set of headings; explanations of these are given in Appendix 4, and further detailed in King & Schael (2001).

7.6 Automated queries

Each sampled site has a unique site code assigned to it when first entered into the database. The codes used in this project reflect the catchment each site is in (first two letters), its river (next two letters) and its longitudinal biological zone (mountain = MT and foothill = FH) (last two letters) (Table 7.1). If there were more than one site on a river a number was added to the end of the alphabetic code. This code is a standard query criterion as well as output for all automated queries. New sites added could have their own coding system, with the new river name and catchment added to the "River" table.

The first automated query in the drop down list is "Extended Site Details", which outputs information on individual sites or all sites in terms of general physical characteristics of the site and catchment, gathered from 1:50 000 maps and site visits (Appendix 4.A). Along with the ability to obtain information on one site or a sub-set of sites, the user can also query for sites with specific characteristics. The query fields are: lateral mobility, channel pattern, bed condition, upstream impacts, upstream land use, channel type, erosion-bank side and erosion type. For instance, a user may wish to assess the data for all sites with a low sinuosity channel pattern and bedrock bed condition. That specific query would return all of the detailed information (Appendix 4.A) for the Palmiet and Middeldeur sites in a *.CSV file. Because data categories such as land use, erosion, and bank have more than one possible entry, information will be repeated for each site with each additional piece of information, which can make the file quite large. Querying one of the fields with multiple entries, such as a specific land use, will decrease the incidence of multiple entries. Extending the example above, if arable land was also selected as a criterion, Palmiet and Middeldeur would still be returned but the number of records returned would decrease from 880 to 368. Thus, as the number of criteria increase and become more specific the number of records returned decreases.

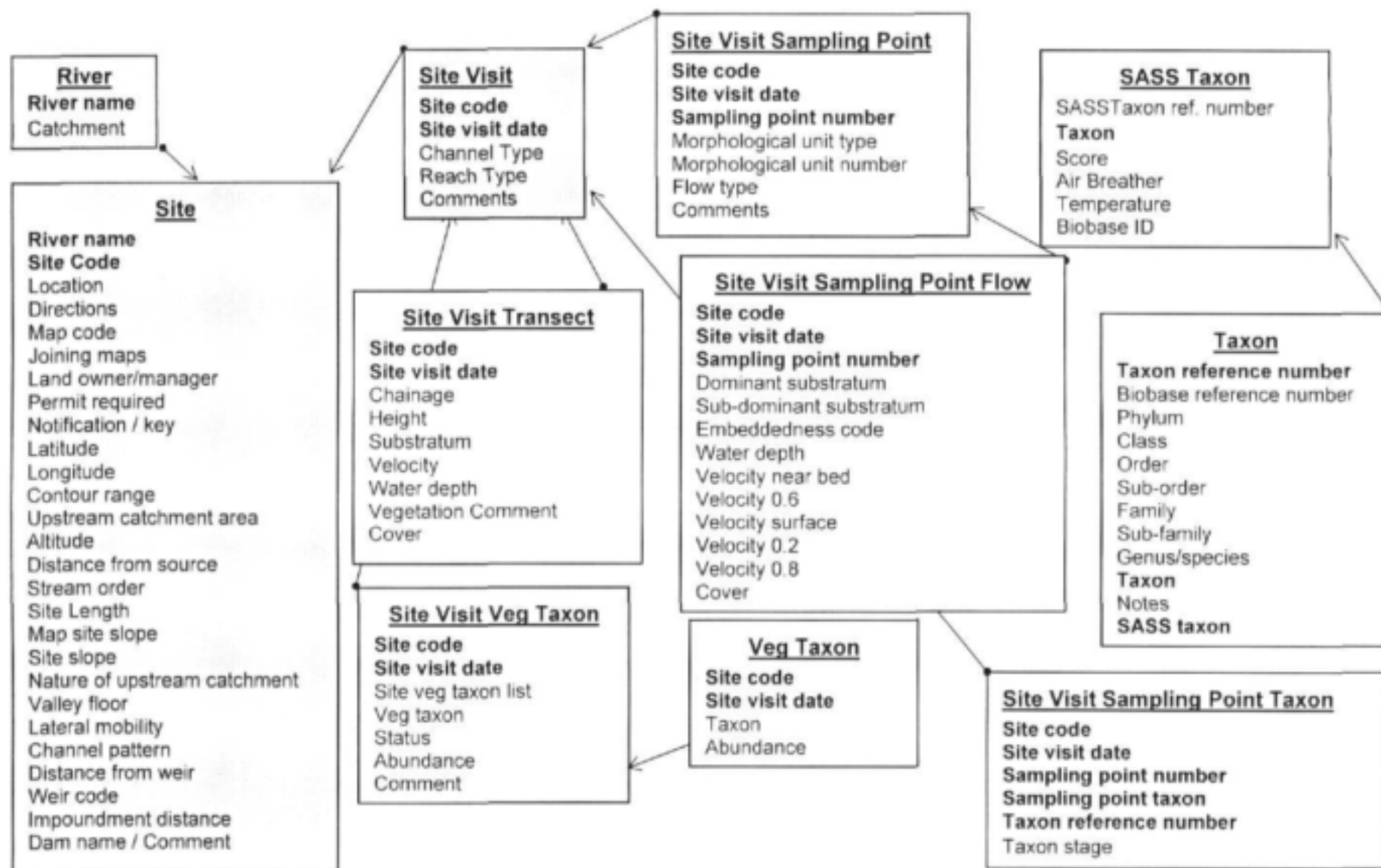


Figure 7.1a Schematic of the database data table structure modified from King & Schael (2001). Each table contains different types of data, which link to other data tables. The bold print indicates linked variables; arrows from each box show connectivity. The "look-up" tables are not included in this schematic because of the complexity. Shaded boxes are repeated in Figure 7.1b to continue linkages.

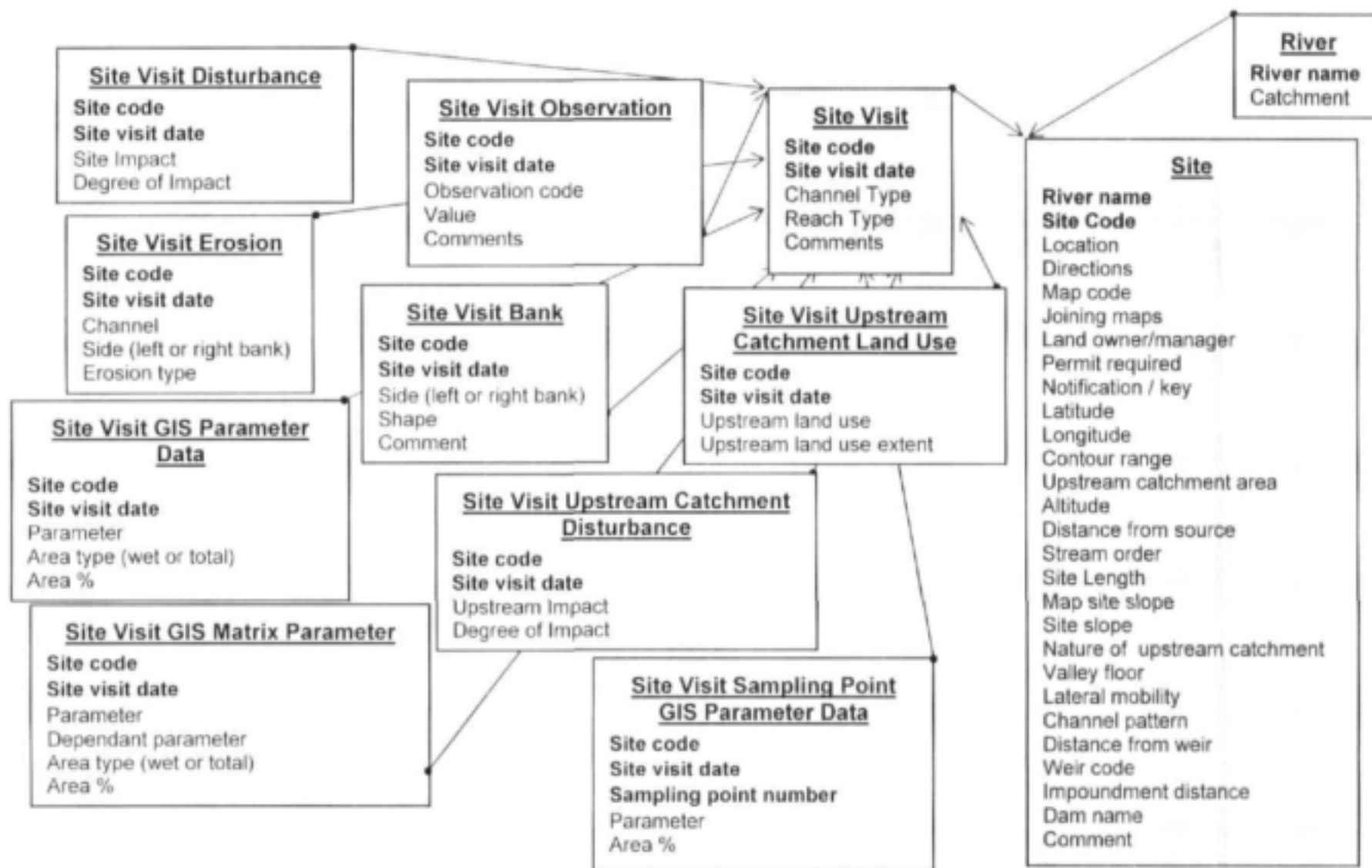


Figure 7.1b As in Figure 7.1a. Shaded boxes were presented in Figure 7.1a and shown here to continue the table linkages.

Table 7.1 Site codes for each river sampled as they appear in the database, with river and catchment listed. Note Eerste River site 1 was sampled for two different purposes (King & Schael 2001), therefore there are two codes in the database for that site.

River Name	Catchment	Site Code
Jan Dissels	Olifants	OLJDFH
Rondegat	Olifants	OLROFH
Noordhoek	Olifants	OLNOFH
Middeldeer	Olifants	OLMIFH
Grootrivier	Olifants	OLGRFH
Steenbok	Breede	BRSTMT
Wolwekloof	Breede	BRWOMT
Wit	Breede	BRWIMT
Molenaars	Molenaars	MOMOFH
Elands	Molenaars	MOELMT
Elandspad	Molenaars	MOEPMT
Holsloot	Breede	BRHOFH
Du Toits	Breede	BRDTMT
Bakkerskloof	Berg	BEBAMT
Zachariashoek	Berg	BEZAMT
Wemmershoek	Berg	BEWEFH
Berg	Berg	BEBEFH
Eerste 1	Eerste	EEJKMT
Eerste 1	Eerste	EEJKMT1
Langrivier	Eerste	EELRMT
Swartboskloof	Eerste	EESWMT
Eerste 2	Eerste	EEJKMT2
Lourens	Lourens	LOLOFH
Palmiet	Palmiet	PAPAMT
Dwars	Palmiet	PADWMT
Davidskraal	Davidskraal	DKDKFH
Window	Liesbeek	LIWIMT
Newlands	Liesbeek	LINLMT
Cecilia Ravine	Sand	SACRMT
Disa	Disa	DIDIMT

The second automated query - "Flow Data-Taxon" - concerns invertebrates and their associated measured hydraulic variables. There are a number of query options available, from searching for all of the taxa recorded in a particular morphological unit (defined in King & Schael 2001) or flow type (Appendix 1.A), to a range of depths, or near-bed or 0.6-depth velocities of the user's choosing. The data output for this query is listed in Appendix 4.B. In order to avoid the problem of multiple entries per record, the depths and velocities returned in the output are averages of the 2 – 6 points collected within each invertebrate sampling area (coded as MI, or macroinvertebrate sample point number). If each measured hydraulic variable was included in the output each taxon would be repeated 2 – 6 times, making the data table extremely large and difficult to manage. If the full set of information is required, a separate query can be run on a particular site and MI within that site for the raw data in the "Flow Data-No Taxon" automated query function.

A query could be run to find all taxa in those sites that are in a bedrock pool MU. Alternatively, a range of depths could be selected to find which taxa occurred within that range. A list of taxa and their related details would be returned.

The "Flow Data-No Taxon", the third query on the list, can be used to retrieve the substrata, depth, and flow measurements linked to each site and MI (Appendix 4.C). MU, flow-type or a specified range of depths, near-bed and 0.6-depth velocities are categories that can be chosen to query the data. The data table report will return measurements recorded for every point within an MI (i.e. the 2 – 6 measurements per MI) and all related data. If the user wanted to know the range of depths and velocities measured in the MU pool, for instance, all records with pool entered would be returned with their allied details.

Site level observations and measurements of water chemistry were recorded in a table called "Site Visit Observations" (Figure 7.1), which provides data on such categories as algal cover, moss cover, overhead riparian cover, discharge, pH, conductivity and temperature. These data can be accessed using the "Observations" query menu item. The output data table lists each biological and physico-chemical observation recorded (Appendix 4.D) for each site and can only be queried by site.

The next two automated queries - "Parameter Coverage" and "Parameter Matrix" - relate to GIS outputs from the digitised site flow, substrata and MU maps (Appendices 4.E and 4.F). The term parameter refers to flow-types, substrata and MUs as different mapped GIS covers with aerial extents. The percentage area covered is provided for each type of flow, substrata or MU within a site, as mapped on the day of sampling. There are three types of aerial coverage within the site, the parts of the river channel that are "wet", "dry" and the "total" or entire site. Each substratum and MU has two entries for its percent composition within the site, a "total" or site-level cover and the parts that are considered within the wetted channel or "wet". For obvious reasons the flow-types are only reported as a percentage of the "wet" area of the site. Each entry has an explanation of how the percentages were calculated for each parameter. This section of the database can be queried by site and/or by parameter type.

The "Parameter Matrix" is an extension of the "Parameter Coverage", in that it represents the area covered by the intersection of two parameter covers, i.e. flow-types and substrata. For ease of data entry, each intersection was entered as a "parameter" and a "dependant parameter", therefore if the user were interested in what percent of the site was composed of B substratum and a RS flow-type, the parameter would be B and the dependant parameter would be RS. Substratum is always a main parameter and flow-type is always a dependant parameter. MU is a dependant parameter with substratum and a main parameter with flow-type. These data can be queried by specific parameter intersections or by site.

The last three automated queries are based on site level information on the channel and discharge transect ("Site Transect Data"), invertebrates collected irrespective of the flow linkage ("Taxonomy Details") and any information collected on the surrounding riparian vegetation ("Vegetation"). Information on channel shape and discharge can be queried from the "Site

Transect Data" query, and be queried by site, or by specific channel features (Appendix 4.G). The location of specific taxa can be queried at any taxonomic level using the "Taxonomy Detail" query, as well as the raw data from a particular site or group of sites (Appendix 4.H). Finally, a search for specific vegetation taxa can also be done, which yields data on their relative abundance per site, if this has been recorded (Appendix 4.I).

The queries outlined above do not allow for further data manipulation within the query centre beyond that which is in the various criteria selection lists. Further manipulation of the data in a spreadsheet might be needed to address additional questions. For more complex queries, an experienced database user can use the MS Access interface and design their own query. It is felt that the automated queries provided will address most users' needs, however.

8. WORKSHOP: RIVER AND CATCHMENT SIGNATURES: WHAT ARE THEY AND ARE THERE MANAGEMENT IMPLICATIONS?

A workshop was held on 28 February 2005 entitled: *Western Cape river and catchment signatures: what are they and are there management implications?* This was a one-day exploratory workshop, involving primarily river scientists and some representatives from the management arena. There were eight presenters and a further ten non-presenting participants, with Dr JM King as the moderator (Table 8.1). The morning session was restricted to presentations of invertebrate, fish and riparian vegetation data that demonstrated catchment or river signatures as well as the use of landscape features to represent biodiversity. The afternoon session formed the interactive discussion part of the workshop where the likely causes of these signatures were discussed. The implications for management of rivers were considered and finally a recommended way forward defined.

8.1 Summary of presentations

Each presenter provided a summary of their presentation, as follows (contributions may have been edited by project staff).

Table 8.1 List of presenters and participants

Participant	Affiliation	Presentation
Jackie King	Freshwater Research Unit, UCT	Opening and moderator
Denise Schael	Freshwater Research Unit, UCT	Catchment and river signatures of macroinvertebrates of the Western Cape
Roger Bills*	SAIAB, Rhodes University	The contribution of the Albany Museum's Makana Biodiversity Centre to understanding aquatic invertebrate and fish biodiversity, and to identifying unique river signatures
Roger Bills and Dean Impson**	SAIAB, Rhodes University and CapeNature, Stellenbosch	Fish diversity and river signatures
Charlie Boucher	Botany Department, University of Stellenbosch	Botanical examples of river and catchment signatures from the Western Cape
Karl Reinecke	Freshwater Research Unit, UCT	River signatures in indigenous riparian vegetation
Barrie Low	Coastec, Cape Town	Floristics of Western Cape riverine systems: patterns and pointers
Jeanne Nel	CSIR, Stellenbosch	Developing physical signatures for biodiversity
Steve Mitchell	Water Research Commission, Pretoria	
Neels Kleynhans	DWAF, Pretoria	
Uschi Pond	Coastec, Cape Town	
Darragh Woodford	Freshwater Research Unit, UCT	

Participant	Affiliation	Presentation
Geordie Ractliffe	Freshwater Research Unit, UCT	
Justine Ewart-Smith	Freshwater Research Unit, UCT	
Candace Hill	Freshwater Research Unit, UCT	
Sandile Koni	Freshwater Research Unit, UCT	
Dean Ollis	Freshwater Research Unit, UCT	
Steven Lowe	Freshwater Research Unit, UCT	

* presentation on behalf of Albany Museum Staff (Ferdie de Moor, Helen Barber-James and Jim Cambray).

** presentation representing both Dean Impson and Roger Bills.

8.1.1 *The contribution of the Albany Museum's Makana Biodiversity Centre to understanding aquatic invertebrate and fish biodiversity, and to identifying unique river signatures – Ferdie de Moor, Helen Barber-James & Jim Cambray, Albany Museum, Grahamstown.*

1. A "bottom-up" approach is used and aquatic ecosystems are carefully examined to identify the diversity of biotopes that support aquatic macroinvertebrates. The basic SASS5 type of surveying has a strict protocol and follows a "top-down" approach to sampling, being rigid in selection of biotopes and sampling effort. This could lead to rare and specialised taxa that would contribute a unique "river signature" being missed.
2. Kinds of data collected: focussed sampling, covering the full diversity of aquatic biotopes and efforts to capture all stages of the life cycle of aquatic insects. A range of aquatic biotopes such as riffles, pools, vegetation in and out of current, sediments and trickling hygropetric seeps are all searched for aquatic biota. Basic bio-physical information is recorded: temperature, pH, conductivity, total dissolved solids, flow.
3. A diversity of techniques are used, preferable over a range of seasons and covering wet and dry hydrological cycles, to capture the largest diversity of species covering all their life-cycle stages. Different mesh sizes and sizes of nets and kick screens ensure a large coverage of potential habitats and species. Various techniques are also used to capture adult insects: drift nets, light traps, malaise traps, emergence traps and hand nets to collect nymphal, larval, pupal and adult stages of aquatic insects.
4. In the laboratory, selected taxa are identified to "species" level and relative abundances are calculated for each site and biotope surveyed. Data are recorded in hand-written catalogues and transferred to an electronic database.
5. Species collected are identified on morphological features, which along with morphometric measurements are used to identify taxa. For species identification, detailed features in the adult stages are often needed. Microscope preparations are needed to identify species.
6. Although not specifically collected to identify river signatures, data collected over many years show a distinct distribution pattern of aquatic invertebrates along a river, associated with particular biotopes. These in turn are related to the zone of the river concerned, so a headwater section has a fauna distinct from a section further downstream. The organisms found in a particular stream are also strongly influenced by the geology, water chemistry

and temperature, so similar streams in different parts of the country will have different species composition and hence a different signature based on species present. The closely approximated Mkomazi and Mooi Rivers in KwaZulu-Natal serve to illustrate that similar rivers can have different biota.

7. Between 1953 – 1998 a total of 296 and 264 taxa were identified from the Mkomazi and Mooi Rivers respectively. Of those, 14% were unique to Mkomazi and 19% to the Mooi. When examining species composition within the Ephemeroptera, Trichoptera and Simuliidae (Diptera), there were large numbers of unique species recorded in each system. In the Mkomazi 18%, 46% and 25% taxa were unique to the Ephemeroptera, Trichoptera and Simuliidae respectively. Within the Mooi River there was a higher percentage of unique taxa, at 38%, 48% and 20% for the Ephemeroptera, Trichoptera and Simuliidae respectively.
8. Distributions of, for example, Ephemeroptera and Simuliidae along the Mkomazi and Mooi Rivers produce distinct zones based on river species assemblages, as does the filter-feeding Trichoptera family, Hydropsychidae.
9. Sometimes, a species varies in appearance not only between rivers but within a site, which can lead to erroneous assumptions on species diversity. For example, there was great variation in the appearance of the baetid, *Cheleocloeon excisum* from one site. Another baetid, *Pseudocloeon glaucum*, is also well known to vary in this way.
10. Both individual species and community structure or assemblages of invertebrate species clearly show differences between and along individual rivers systems. Much more data are needed both within a single river system over a number of years and also between closely approximated river systems before any sound conclusions on the nature and significance of river signatures can be made. In more perennial river systems the community structure of species appears to be more stable from year to year, whereas assemblages in less perennial systems appear to show a larger fluctuation of species over time and thus are predictably poorer in providing strong river signatures.
11. Alien fish are affecting any existing river signatures, as are inter-basin transfers of water, having an homogenising effect on species assemblages of fish.
12. Conclusions:
 - a. Aquatic macroinvertebrate assemblages, when identified to species level, clearly distinguish between rivers catchments provided the rivers are not too disturbed.
 - b. Many abiotic factors, possibly also producing distinct river/catchment signatures of their own, help to shape the environment that is colonised by different suites of species. These suites of species over time represent the biotic river signature.
 - c. Many more invertebrate data, both on different rivers systems and over longer time periods, need to be gathered to enhance our understanding of the nature, persistence and importance of biotic river/catchment signatures.
 - d. Not only morphological species data but also molecular biological information can be used to assess the uniqueness of various river systems.
 - e. River/catchment signatures are a potentially fruitful avenue of research, facilitating investigation of processes or concepts such as colonisation, competition, species redundancy and abiotic drivers of community structure. If further species information, such as life-history data, distribution ranges and

conservation status, can be added this would further enhance understanding of the nature and causes of the signatures.

f. Alien fish species are possibly eradicating biotic river signatures.

13. Acknowledgement and thanks to Roger Bills for delivering the presentation at the workshop.

8.1.2 Fish diversity and river signatures – Roger Bills¹ and Dean Impson², ¹SAIAB, Grahamstown and ²CapeNature, Stellenbosch.

This talk will cover two aspects - 1) the kind of data available within SAIAB and the sorts of analyses SAIAB is involved with, and 2) the diversity of fishes within the Western Cape, which may be relevant to river signatures.

SAIAB, its fish collections and data analysis

1. Title slide. Thanks also to Ernst Swartz & Paulette Bloomer's UP group for data/slides.
- 2-3. SAIAB is a fish museum and most of the people making collections of fishes are systematists. As such, the data associated with the fishes within the collection are orientated towards our interest in the fish and not necessarily the environment. Only basic environmental data are recorded as a general rule e.g. temperature, conductivity, and descriptive notes on where the fish occurred and anything noteworthy about the fish's condition. In turn, much of this information may not be recorded in our databases and may simply remain in original field notes, which may or may not be archived depending on the researchers at the time of accessioning.
4. Many of the data associated with samples are generated within SAIAB using various methods. Basic information includes numbers and size ranges. Depending on research projects it can extend into biological analyses of diet, age and growth, breeding states, and morphological and molecular studies examining geographical variation. The latter is most relevant to river signatures.
5. Mapping of distributions is an essential first step and all data are linked to geographical coordinates. Examples of individual species, overall biodiversity, and endangered species distributions for Swaziland are shown. This was later compared to formally conserved areas within Swaziland and recommendations for increasing levels of protection for non-conserved areas were given.
6. Investigating morphological variation within a species across its distribution range, and differences between closely related species, involves detailed morphological measurements, which are usually analysed using Principal Component Analysis.
7. Genetic analyses are conducted on specimens by various collaborators. Much of this work is associated with understanding fine-scale geographical variation and so is appropriate to the issue of river signatures.

Cape Floristic Region fish diversity

8. Fishes of the CFR. At the present moment recognised species diversity in the CFR is relatively low although endemism is high. However, morphological and genetic diversity within the CFR's fishes is much more complex and does lend itself to use in river signature work. Two detailed examples for *Pseudobarbus* minnows and *Galaxias zebratus* are given.
9. *Pseudobarbus* diversity (slide provided by Ernst Swartz). Although six species are described from the CFR, at least 13 lineages have been identified on the basis of morphology and genetics. Possibly a few more are still to be identified. Much of the diversity within this group is in the southern part of the CFR.
10. *Galaxias zebratus* diversity (slide provided by Ernst Swartz). Only a single species is presently formally recognised in southern Africa although our present samples suggest there is the same level of diversity as in *Pseudobarbus*. However, sampling for *Galaxias* is difficult and targeted surveys will probably reveal many more populations. So far the pattern of distribution of 'morphs' does not follow that for *Pseudobarbus*. There is greater *Galaxias* diversity in the south-western streams of the CFR compared to *Pseudobarbus*, which shows greater diversity in the southern central streams.
11. Four examples of different *Galaxias* morphs from tributary streams in the Cedarberg mountains show some of the morphological diversity.
12. Genetic variation amongst *Pseudobarbus*, *Galaxias* and *Sandelia* is roughly similar.
13. Jan Dissels River - *Austroglanis gilli*. Within-species changes occur down single river systems. An example of the Jan Dissels River near Clanwilliam is used. Here the Clanwilliam rock catfish occurs in approximately 15 km of the river in physically pristine habitat. There are two distinct colour morphs (unspotted and heavily spotted forms), which occur in different proportions down the catchment. We examined this using morphology, mtDNA and allozymes and this work is still in progress. Heavily spotted forms are most frequent in the upper reaches and disappear at the lowest sites.
14. Jan Dissels transect. Mitochondrial DNA analyses indicated different alleles at sites down the river. Allozymes revealed varying frequencies of alleles between sampled fish down the river. Indications are that this species does not move up and down the river to any great extent and that there is genetic structuring down the system.
15. Jan Dissels - alien fish impact on signatures. The impacts of alien fish on native fish species are well known. Eradication of indigenous species either through direct predation or competition results in the loss of populations of indigenous fishes and thus natural river signatures. The Jan Dissels is an example of this: two species (*L. capensis* & *P. phlegethon*) are extinct from the system, almost certainly due to the presence of smallmouth bass (*M. dolomieu*). Smallmouth bass occupy approximately 90% of the mainstream Jan Dissels system and indigenous species excepting *Austroglanis* are restricted to side streams or the final upper reaches of the stream where bass have not yet invaded.
16. The larger scale impact of alien fishes can perhaps be understood if their wider distribution within the CFR is seen. Alien fish distributions in the Western Cape: three species are shown. These are small-mouth bass (*Micropterus dolomieu*), rainbow trout (*Oncorhynchus mykiss*) and carp (*Cyprinus carpio*).

17. Fish signatures? There are undescribed species, some taxa occur in sympatry with close relatives, there is geographical variation across and down river catchments. Genetic diversity in the three groups examined (*Pseudobarbus*, *Galaxias* & *Sandelia*) appear similar despite varied morphology, although their patterns of distribution are not the same. Freshwater fishes in the CFR can thus provide good signatures for catchments if diversity below species levels is examined using a mixture of morphological and genetic methods. 18. Catchment management implications.
 - Avoid indigenous fish movements through IBTs and fisheries operations
 - Avoid alien fish introductions Maintain processes giving rise to variation over substantial lengths of river
19. What's needed to better identify and describe river signatures
 - Shared sites for several disciplines
 - Invertebrate, fish and frog collections
 - Deposit samples in museums
 - All species/populations, all systems
 - Samples - 5-20, range of sizes
 - Formalised specimens and tissues
 - Live colour photos

8.1.3 Botanical Examples of River and Catchment Signatures from the Western Cape - Charlie Boucher, University of Stellenbosch

The question is raised as to whether there is similarity between the Cape Flora and Riparian Phytogeographical Centers (Goldblatt & Manning 2000) in the Cape Floral Kingdom? The following are examples of species with different distribution ranges that could correlate to centers at different levels: *Canthium inerme* (Cape Peninsula-Zimbabwe); *Diospyros whyteana* (Tulbagh-Cape Peninsula-Mapumalanga); *Sideroxylon inerme* (Cape Peninsula-Tropical Africa); *Erica caffra* and *Prionium serratum* (Cape and Natal Group Sandstones); *Brabejum stellatifolium* (Gifberg-Gouritz River); *Penaca encorum* (Kogelberg-Port Elizabeth); *Ischyrolepis subverticillata* (Bainskloof-Riviersonderend); *Cryptocarya angustifolia* (Gifberg-Swellendam) and *Ixianthes retzioides* (Cederberg-Porterville). Each of the above species relate to phytogeographical centers recognised in the Cape Floral Kingdom. This suggests that there is a correlation between the riparian flora signatures and the fynbos flora at a national level.

The number of non-riparian vegetation types centred around the Western Cape suggests that the riparian vegetation should show similar diversity. An analysis of the vegetation of the high-altitude marshes associated with rivers of the Hottentots Holland Mountains (Sieben *et al.* 2004) identified five different Mire (= Fen) communities found in wet, swampy habitats that are characterized by organic-rich, peaty soils and are fed by minerotrophic water (water percolated through mineral substrata). They are dominated by low-growing, mat-forming Restionaceae such as *Anthochortus crinalis*. This excludes the ombrotrophic (rain-fed) bogs at high altitude on steep south-facing slopes with ericaceous vegetation. They describe another four communities, called Restio Marshlands, which occur in the better-drained surrounds of mires with minerotrophic soils relatively low in peat. This vegetation is dominated by tussock-forming Restionaceae, eg. *Restio subtilis* and emergent *Chondropetalum mucronatum*.

They found the major factors influencing the riparian vegetation to be the following environmental gradients (in order of magnitude from high to low):

1. Geological gradient (patchy effect)
2. Climatic gradient
3. Altitudinal gradient (Longitudinal axis of river – stream power effects on rooting strategies)
4. Lateral gradient (Inundation degree – aerobic / anaerobic effects on rooting strategies)

The abiotic signature of each river draining the Hottentots Holland Mountains is determined by each of the above gradients. Every catchment is a unique habitat supporting its own mix of species, possibly including endemic ones? The local geomorphology determines the stream power and the degree of inundation, which is a major determinant of the species assemblage present. The highest similarity between rivers, based on the Jaccard Similarity Index, using species content, is found between the Palmiet and Riviersonderend River catchments (black water rivers), although the Similarity Index is quite low (44%). The Eerste and Berg Rivers had a 40% similarity. The Lourens was very different from the others with a 27% similarity. The low similarity levels are attributed to the large number of species recorded in a single sample.

Examination of the soil associated with indigenous vegetation and with alien stands along the Wit, Molenaars and Hol Rivers (Breede River tributaries) indicated distinctive patterns in each tributary based on soil texture, soil pH, resistance, organic content and changes coupled to soil depth and distance from the main stream.

It is concluded that there are general principles that can be applied to distinguish between Western Cape rivers, based on differences in:

- the ratios of geological substrata;
- basic climatic areas that have different suites of species;
- fire or its absence affecting species composition;
- anthropogenic history influencing the different suite of alien species present;
- alien-vegetation management that alters the substrata.

Natural catchment and river signatures will not be dependent on the last two, but natural biogeographical colonisations/extinctions could be part of what creates the signatures.

We need to separate the general (e.g. widely distributed species or alien invasive species) from the key (endemic or local species responses) biotic indicators in each river system and monitor both elements to understand and interpret river signatures and responses to perturbations. Each river requires unique management procedures varied within a broad general sub-regional framework. The key indicator species are studied and their responses to environmental cues are used to manage a particular river.

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8.1.4 River signatures from riparian vegetation in south-western Cape Rivers – Karl Reinecke, Freshwater Research Unit, University of Cape Town.

Research project: The nature and rehabilitation of alien invaded riparian zones
Research organisation: Freshwater Research Unit, University of Cape Town
Researchers: Dr Jackie King, Mr Karl Reinecke
Scientific Advisor: Dr Patricia Holmes
Project funding: The Water Research Commission and Working for Water campaign
Project duration: April 2003 to April 2006

The project is investigating the impact of woody alien invasive species on indigenous riparian vegetation and monitoring the path of recovery following the clearing of alien species from riparian areas.

Data have been collected from either indigenous, alien invaded or cleared and recovering study sites from the Breede, Olifants and Berg River systems, and some coastal rivers that drain into the Atlantic Ocean near Cape Town.

Vegetation data were collected in Whittaker plots, (a larger plot broken into smaller equal size sub-units), with the width of the larger plot varying from river to river according to the width of the riparian zone. Every plant from every quadrat was recorded and identified to species where possible. Morph species were used in the absence of a positive species identification.

Thus far, CLUSTER and ORDINATION analyses have been performed on presence/absence data of species (or morph species) grouped into growth forms (tree, shrub, fern etc.). Later analyses will use % cover of species (or morph species). Samples that grouped with >50% similarity were considered to be assemblages. Preliminary results from four indigenous study sites revealed the presence of catchment and/or river signatures. These sites were one on the Molenaars, two on the Eerste and one on the Disa Rivers.

The sampled quadrats (many per river and site), based on growth-form data, first separated by catchment. The next level of separation was into two main assemblage types. These were a tree/shrub assemblage type and a Restionaceae/grass assemblage type. The two sites on the Eerste River separated from one another within their assemblage type groups.

These results suggest that species of riparian vegetation demonstrate catchment and river signatures based on differences in growth form.

We expect even stronger signatures to emerge when species-level data are analysed. There is also a suggestion that site-specific signatures may occur.

Signatures are attributed by us to result from a combination of the catchment's history through geological time that produces certain drainage basin characteristics upon which local riverine processes (e.g. floods and sediment transport), and organism-specific mechanisms of extinction and modes of dispersal.

8.1.5 Floristics of Western Cape riverine systems: patterns and pointers – Barrie Low, Coastec, Cape Town.

The River Dancers, an informal conservation group, is studying ten major Western Cape rivers. Aims of the study include providing an account of the flora and vegetation of major Western Cape rivers, and promoting the value, understanding and conservation of these systems.

Data from these as well as several lowlands systems sampled in independent studies were entered into Coastec's SaSFlora database for the Cape & Karoo floras. A contextual analysis of riverine floras and their respective sections was undertaken using PRIMER (cluster and MDS analysis). In addition certain river-plot data were analysed to determine whether there was any patterning in vegetation.

Key findings were the following:

- Lowland and montane systems have distinctly different floras
- Montane systems show a clear gradation in floristic composition from perennial rivers in the south (Limietberg – Elandspad; Witels – Hex River Mountains; Twenty Four Rivers – Groot Winterhoek; Berg, Eerste, Lourens – Hottentots Holland) to more seasonal systems in the north (Matjies, Doring). The Thee (Kouebokkeveld) represents a roughly transitional system, with elements of both northern and southern rivers. The Palmiet is also a very different system, despite its being a wet southern river.
- River stretches, too, possess distinctive floras, with a general change in flora from source to end.
- Lowland systems show major differences between north and south with the Sandveld, West Coast and Cape Flats indicating distinct floristic patterns.
- Riverine versus wetland character also varies with system with the wetter, more perennial rivers dominated by species with riverine and riverine-wetland habitat preferences; correspondingly, the more seasonal montane rivers and the lowland systems (in reality "longitudinal wetlands") in particular display greater wetland characteristics.

- The vegetation analysis indicates there is also variation in riverine versus wetland character as one moves from river source to end, with altitude and substratum playing key roles. The ratio of sand to rock plays a key role in species distribution.
- Finally, where alteration to water quality and amount leads to increased salinity and draw-down of the water table, major shifts in plant species composition occur, coupled with a reduction in species diversity.

Conclusions

- There are clear distinctions amongst riverine floras of the Western Cape mountains and lowlands.
- Differences are driven *inter alia* by landscape, substratum and altitude, as well as by geographic position.
- Impacts through abstraction can cause major shifts in the nature and diversity of riverine floras. Here the northern Sandveld is a classic example.
- Knowledge of river floristics is crucial to protection of these systems, both in terms of conservation prioritisation as well as in monitoring changes brought upon by manipulation.

8.1.6 Developing physical signatures for biodiversity – Jeanne Nel, CSIR, Stellenbosch

Introduction

The physical signatures presented here were developed with the express purpose of serving as biodiversity surrogates for systematic conservation planning of freshwater biodiversity in South Africa (see www.csir.co.za/rivercons/index.html). This is a joint initiative underway between the Department of Water Affairs and Forestry (DWAF), CSIR and the Water Research Commission (WRC), whose broad objectives are as follows.

- In collaboration with DWAF (as national custodians of water resources) and DEAT (as national custodians of biodiversity), develop inter-departmental policy to supplement existing legislation (such as the National Water Act and National Biodiversity Act) and make conservation of freshwater biodiversity operationally feasible. This policy will include an explicit and quantitative goal for conservation of aquatic ecosystems at a national level.
- Develop methods and data layers for the spatial representation of both biodiversity pattern (so that a sample of all biodiversity can be conserved) and ecosystem processes (so that the processes that sustain biodiversity can be conserved). This needs to be done at scales that are appropriate to national and sub-national level biodiversity planning.
- Develop and test a planning framework for generating spatial options to satisfy explicit and quantitative conservation targets.
- Develop conservation plans and implementation strategies to facilitate the mainstreaming of river conservation at sub-national levels (Water Management Areas) across South Africa.

River heterogeneity signatures for representing biodiversity pattern

Spatial conservation planning relies on identification of biodiversity surrogates to spatially represent biodiversity. For biodiversity pattern, these surrogates may be habitats, communities, taxonomic groups or species. Historically, biodiversity assessments have most commonly focused on species, often charismatic ones that catch people's imaginations, such as large mammals. However, unless species datasets are comprehensive, they should be used with caution in biodiversity planning because they can lead to bias in selecting only the areas which happen to have species data, ignoring potentially important areas where there are data gaps. For this reason, conservation planning has moved away from using species as their primary biodiversity pattern layer, and have started to focus on surrogates that use physical variables (such as climate, flow, geomorphology) to predict species distributions. These physically-defined surrogates are deemed preferable for conservation planning as they provide an effective and relatively inexpensive method of sampling biodiversity across the entire region in a consistent manner. Comprehensive species datasets (e.g. large mammal species; fish species), are then used to supplement the physically-defined biodiversity surrogates.

The national conservation planning initiative for freshwater biodiversity has therefore developed river heterogeneity signatures as the physically-defined surrogates to depict river biodiversity pattern consistently across the entire country. Heterogeneity is the ultimate source of biodiversity (Pickett *et al.* 1997), particularly in naturally disturbed and highly dynamic ecosystems such as rivers. Characterising this heterogeneity in time and space is key to predicting pattern and distribution of riverine biota (Du Toit *et al.* 2003, Montgomery 1999, Berman 2002), and can therefore be used as a basis for developing physically-defined biodiversity pattern surrogates for river ecosystems. Heterogeneity within South African rivers is created primarily through physical processes, the main determinants being *water* acting as system driver on *sediment* as the material within the constraints of the *geomorphological* template (Dollar *et al.* in press). These three variables interact over time and space to drive system heterogeneity and hence biotic pattern and distribution. A hierarchical framework is currently being developed (Dollar *et al.* in press) to characterise South African rivers using these three physical descriptors:

- geomorphological template (Level 1 descriptor);
- hydrology (Level 2 descriptor); and
- sediment (Level 3 descriptor).

The framework makes explicit the physical processes driving river structure and resource dynamics, and includes reference to disturbance and recovery processes. This enables us to distinguish components of rivers which, under natural conditions, share the same biological response potential and associated biodiversity. These components, or "river heterogeneity signatures", can therefore be used as surrogates for predicting river biodiversity.

At the broadest level, rivers can be classified across the landscape according to geomorphology (Level 1) and hydrology (Level 2). Rivers have been classified according to these two levels across South Africa in a recent national assessment of rivers (Nel *et al.* 2004), in which geomorphic provinces represented the geomorphological descriptor, and the hydrological index,

which characterizes flow variability (Hannart and Hughes 2003), represented the hydrological descriptor. At a finer, sub-national scale it is appropriate to supplement these broad landscape-level descriptors of geomorphology and hydrology with a characterisation of geomorphologic zones at the level of individual rivers and streams (Rowntree and Wadeson 1999). This geomorphological zonation serves as a surrogate for characterising the ability of a river reach to store or transport sediment, each zone representing a different physical template available for biotic habitation. Using this river-level descriptor in conjunction with the landscape-level characterisation of geomorphology and flow provides a surrogate of the types of natural habitat expected within the river reach, which in turn serves as a good surrogate for biodiversity pattern within river ecosystems.

Conclusions

- Future assessments should attempt to supplement the river heterogeneity signatures with aquatic species datasets which have been relatively comprehensively surveyed across the country.
- It is important to note that these three levels of signature are combined and that conservation planning strives to achieve representation of unique combinations of all these signatures. Thus, it is not only the geomorphological zonation that is targeted, but also the pattern across large areas of the landscape, which includes entire drainage basins. Thus, should the current findings be true - that every catchment is different (but functioning in a possibly similar way) - then the conservation plan would in any case be striving to select for representation across different catchments as well as within geomorphological zones.
- This presentation should be viewed as work-in-progress, which will be refined as the DWAF-CSIR-WRC initiative proceeds. It is through interaction at workshops such as this that the refinements will be achieved.

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8.2 Discussion Session: *Accident of design: what causes the signatures? Are they unique to the Western Cape?*

The afternoon session began with all the presenters being asked to create a definition of a catchment or river signature based on the presentations they had heard and on their own presentations (Table 8.2). A pattern in the definitions was noted by Jackie King that ranged from a focus on biotic attributes (invertebrate and fish specialists) through a combination of biotic and physical attributes (vegetation specialists), or on just physical patterns (biodiversity conservation specialist), depending on the discipline concerned and the goal of each researcher.

Table 8.2 Definition of a catchment or river signature.

Presenter(s)	Definition
Denise Schael and Jackie King	A unique invertebrate species assemblage that distinguishes a river or catchment from others (40% dissimilarity).
Roger Bills and Dean Impson	Unique species/populations or species compositions identifying a river or groups of rivers from others.
Barrie Low	A unique set of attributes that characterise a section of a river as being different from another.
Charlie Boucher	As for B. Low, unique set = finger print/species ratios; attributes: physical and biotic.
Jeanne Nel	Pieces of a river that share the same response potential and hold the potential of sharing similar biodiversity – they are dependant on spatial and temporal scales.

There was lively discussion on the possible causes of the signatures, but no definitive answer that catered for all disciplines. The link between local geology and biotic patterns was clearer in the vegetation studies than it was for either the invertebrates or the fish. Regional geology does play a role in invertebrate and fish distributions, but the local coupling at a medium or fine scale is less obvious.

Several conclusions came from these discussions. First, it was suggested that a shared set of study rivers (site length dependant on discipline) be chosen in one or two regions of the country and invertebrate, fish and riparian vegetation data be collected together, in multiple seasons and across years to better determine if catchment or river signatures occur and at what level or scale the different disciplines reveal the signatures. Another common suggestion was to assess if archived records of invertebrate and fish species distribution records for one or more regions in the country would show the catchment or river signature patterns reported in King and Schael (2001). It was suggested that to do this for Western Cape fish, the data would have to be analysed at a genetic population level due to the low diversity of indigenous fishes. Data from the Limpopo or Mpumalanga regions, however, had good potential for assessing signatures at the

species level as there is a wide variety of native species in those regions and data could easily be accessed via SAIAB.

Although there was common agreement that catchment and river signatures do exist, there was no clear conclusion on what caused them.

8.3 Discussion Session: *Are there management implications?*

The consensus was, especially from the management representatives, that the signatures do have implications for management, especially in the Reserve Determination process within South Africa's current water law. Water developments should proceed with great caution as each catchment appears to be unique and it is presently not clear what this might be indicating about catchment and river functioning.

Managers need further clarity on the validity of the signatures across disciplines; on whether the signatures exist in other parts of the country outside the Western Cape, and within lower rivers; and what the implications of the signatures are for catchment management. It was pointed out that although the genetic population level of species distributions is very interesting and important in a scientific context; managers are more likely to respond to species patterns than genetic patterns.

It was suggested that river classification should be based on an ecoregion and then catchment level approach, with river longitudinal zones being incorporated after catchment (at the moment catchment is essentially ignored). A proportion of whole rivers within each catchment should be set aside as 'untouchable' to be saved in terms of their biodiversity and uniqueness.

It was also mentioned that catchment and river signatures should play an important role in the RDM (Resource Directed Measures) designation of a river's target ecological management class (EMC). Rivers with a low EMC could have this enhanced by being shown, through the signatures analysis, to be of a very rare kind.

8.4 Summary of the importance of catchment and river signatures.

- River and catchment signatures are important in terms of demonstrating the biodiversity of different systems.
- The significance of the high level of catchment and river differences (compared to, say, longitudinal geomorphological zone) should feed into the classification process for rivers.
- Integration of investigations of this phenomenon should occur across disciplines. This could be done by via a collaborative proposal that used both historical and new field data for a series of common field sites.
- Conservation targets need to be addressed per catchment, on which parts will be conserved in terms of their natural biotic signatures and thus biodiversity.
- More data are needed on middle and lower reaches of rivers to further support or give proof of signatures through the entire river, source to sea.

- More data are needed to assess if the catchment and river signatures exist in parts of the country outside the Western Cape.

9. CONCLUSIONS AND RECOMMENDATIONS

9.1 Conclusions

River and catchment signatures are real. As shown in this project, they are biotic fingerprints of upper rivers and catchments in the Western Cape, distinguishing each from the others. So far, they have been detected or suspected at several levels of definition of organisms: at species level in aquatic invertebrate data; at growth-form level in data on riparian vegetation; and probably at genetic levels in fish data. There is no reason to believe they do not exist in other parts of South Africa and, indeed, elsewhere although this remains to be shown. Lower rivers may also have biotic signatures, but as most lower rivers are considerably degraded the data of natural conditions needed to detect the signatures may be largely missing. The biotic signatures can best be detected if species or finer-level data are compared across the same longitudinal zones of many similar rivers within several catchments of one bioregion.

In this Western Cape study, the signatures were not caused by unique species per catchment or river, or by unique abundances of the taxa present, or by differences in the proportions of different taxon groups. They were caused by differences in the mix of taxa *within each major taxon group*. Thus, for instance, despite shifts in the mix of species of Ephemeroptera present from river to river, the percentage of taxa that were Ephemeroptera remained approximately the same. Only in the most extreme cases of disturbance studied did the proportions of taxa per major group start to break down. This suggests to us that such a well-known measure of river health as the %EPT (percentage of taxa in the invertebrate sample that belong to the Ephemeroptera, Plecoptera and Trichoptera) only shows a decline in value when river disturbance is quite advanced. At much lower levels of disturbance, the EPT percentage may indicate an undisturbed river but our data show that the disturbance is already being felt within the ecosystem: the mix of taxa is changing and the biotic signature is starting to be eradicated.

We now know something about what the signatures are and are not, but still have very little understanding of how they arise and what their significance is. The signatures do not appear to be strongly correlated with water chemistry, the presence or absence of native or alien fish, systematic biogeographic species changes across the region or paleogeographic influences, although all of these seem to play some role. Rather the signatures are probably the result of complex interactions of the above and other variables over many millions of years.

Does this mean that the mix of species that makes up each signature occurs by accident or design? Do the species naturally occurring in each river represent the most efficient (in terms of resource use), and possibly the only, mix of species possible for that particular environment or could other species in the regional pool move in with no change to ecosystem functioning? Are the signatures reflecting fundamental differences in the functioning of each river ecosystem (and thus its catchment) or are all similar river zones functioning in much the same way (as suggested by the Functional Feeding Group analysis in Section 3.4) even though they have a different mix

of species? These questions remain unanswered, to a large degree because we do not have sufficient understanding of the biology and habitat requirements of riverine species to attempt further interpretation of the signatures data set. Some additional insights have emerged however.

- Perennial rivers have more stable aquatic communities than non-perennial ones (de Moor, Barber-James and Cambray, pers comm, Chapter 8) and therefore may be expected to have much clearer signatures. This would make them more amenable to assessment of whether or not human disturbance is affecting them.
- Alien fauna and flora appear to be breaking down the biotic signatures, homogenising at least fish and plant communities (see Chapter 8) and presumably reducing biodiversity.
- Rivers appear to have abiotic signatures too: their complex mix of geomorphological, hydrological, chemical and thermal attributes may be of use to distinguish them from each other. The question of whether or not these abiotic signatures are good surrogates for the biotic ones lies at the heart of the conservation planning of freshwater biodiversity outlined in Chapter 8 (see presentation by Nel).

The main management implications of river and catchment signatures are as follows.

- It can no longer be assumed that all rivers within an ecoregion are much the same and thus that a random selection of them can be sacrificed to development with no implications for biodiversity. Biodiversity could be being reduced at the community/landscape level through catchments not being recognised as unique entities.
- The signatures can be used to detect very early levels of degradation of sensitive or important river systems.
- With further data collection, the signatures can be used to grade and compare different kinds of disturbance on a scale from negligible impact to very severe impact.
- More than one river within each catchment needs to be conserved at a very low level of disturbance so that further research on signatures and its links to biodiversity has access to replicate study sites per catchment.

9.2 Recommendations

- The catchment should be high in the hierarchical levels of river classification for biodiversity management – higher than longitudinal zone – because rivers within one bioregion or ecoregion are not all the same. Individual catchments within any one ecoregion, bioregion, geomorphological region or hydrological region (whichever is being used to partition the country) need to be adequately represented in any system of conserved rivers.
- There should be more than one completely undisturbed river in each catchment so that biodiversity is conserved at the community/landscape level and so that future research on signatures and its links to biodiversity has access to replicate sites per catchment.
- Historical records of biotic distributions (such as those at the Albany Museum) should be used to confirm that river and catchment signatures exist in other parts of the country.
- The validity of signatures across disciplines should be researched through a multidisciplinary research programme using shared study sites. This would strengthen understanding of their nature and possibly their causes.

- Full understanding of why catchments and rivers are biologically distinct will not be possible without a deeper understanding of the biology of riverine species. Such research should become an essential component of all relevant research and consultancy work at an appropriate level of commitment.

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APPENDIX 1

Appendix 1.A Categories of visually distinct flow types. After Rowntree 1996; Padmore *et al.* 1996; Newson *et al.* 1998; From King & Schael (2001).

Flow Type	Definition
Free falling (FF)	Water falls vertically without obstruction
Cascade (CAS)	Water tumbling down a stepped series of boulders, large cobble or bedrock
Boil (BOIL)	Water forming bubbles, as in rapidly boiling water; usually below a waterfall or strong chute
Chute (CH)	Water forced between two rocks, usually large cobble or boulders; flowing fast with the fall too low to be considered free falling.
Stream (STR)	Water flowing rapidly in a smooth sheet of water; similar to a chute but not forced between two bed elements
Broken standing waves (BSW)	Standing waves present which break at the crest (white water)
Undular standing waves (USW)	Standing waves form at the surface but there is no broken water
Fast riffle flow (FRF)	Very shallow, fast, flickering flow, still covering most of the substrata
Rippled surface (RS)	The water surface has regular smooth disturbances which form low transverse ripples across the direction of flow
Slow riffle flow (SRF)	Very shallow, slower, flickering flow, still covering most of the substrata
Smooth boundary turbulent (SBT)	The water surface remains smooth; medium to slow streaming flow takes place throughout the water profile; turbulence can be seen as the upward movement of fine suspended particles
Trickle (TR)	Small, slow, shallow flow; when occurring with small or large cobbles, flow is between bed elements with few if any submerged
Barely perceptible flow (BPF)	Smooth surface flow; only perceptible through the movement of floating objects
No flow (NF)	No water movement

Appendix 1.B Categories of substrata. From King & Schael (2001).

Category	Size Range (mm)	Guide Line	φ
Silt (SI)	< 0.063	Fines and mud	6.5
Sand (SA)	0.063 - 2	Coarse grit	2.0
Small Gravel (SG)	2 - 16	finger nail	-2.0
Large Gravel (LG)	16 - 64	middle joint of finger length of small finger	-4.5
Small Cobble (SC)	64 - 128	wrist to halfway along finger	-6.5
Large Cobble (LC)	128 - 256	inside elbow to wrist	-7.5
Boulder (B)	> 256	armpit to wrists ground to waist length of tall person > length of tall person	-9.0
Bedrock (BR)		slabs of rock	-9.5

APPENDIX 2

Appendix 2 Level of taxonomic identification in the laboratory for various orders and families. Specialists that will be confirming identifications or identifying to finer taxonomic level are listed by their specialised group. Note that some specialists will focus on a particular family of animals whereas others will focus on an entire order. From King & Schael 2001.

ORDER	FAMILY	LEVEL	SPECIALIST
ACARINA		Family / morph type	
AMPHIPODA		Family / genus, species	
ANOMOPODA		Family / morph type	
COLEOPTERA	Dryopidae	Family / genus, species / morph type	
	Dytiscidae	Family / morph type	
	Elmidae	Family / genus, species / morph type	
	Gyrinidae	Family / genus, species / morph type	
	Helodidae	Family / morph type	
	Hydraenidae	Family / genus, species / morph type	
	Hydrophilidae	Family / genus, species / morph type	
	Limnichidae	Family / morph type	
	Noteridae	Family / morph type	
	Torridincolidae	Family / morph type	
CYCLOPOIDA		Order	
DECAPODA		Family / genus	
DIPTERA	Athericidae	Family / genus / morph type	
	Blephariceridae	Family / genus, species / morph type	
	Ceratopogonidae	Family / subfamily / genus, species	Prof. Arthur Harrison
	Chironomidae	Sub-family / genus, species	
	Culicidae	Family / genus / morph type	
	Dixidae	Family / morph type	
	Empididae	Family / genus / morph type	
	Psychodidae	Family / genus / morph type	
	Simuliidae	Family / genus, species	Dr. Ferdy de Moor, in part
	Tipulidae	Family / genus / morph type	
	Tabanidae	Family / morph type	
EPHEMEROPTERA			Mrs. Helen Barber-James, type specimens
	Baetidae	Family / genus, species / morph types	Mr. Bruce Paxton
	Caenidae	Family / genus, species	
	Ephemerellidae	Family / genus, species	
	Heptageniidae	Family / genus, species	
	Leptophlebiidae	Family / genus, species	
	Tricorythidae	Family / genus, species	
HEMIPTERA			Mr. Patrick Reavell, type specimens
	Corixidae	Family / genus, species / morph type	
	Gerridae	Family / morph type	
	Mesoveliidae	Family / genus, species / morph type	
	Notonectidae	Family / genus, species / morph type	
	Pleidae	Family / morph type	
	Veliidae	Family / genus, species / morph type	
LEPIDOPTERA	Pyalidae	Family / genus	
MEGALOPTERA	Corydalidae	Family / genus, species	
LEPIDOPTERA	Pyalidae	Family / genus	
NEMATODA (phylum)		Phylum	
NEMATOMORPHA (phylum)		Phylum	

ORDER	FAMILY	LEVEL	SPECIALIST
ODONATA: Anisoptera	Aeshnidae	Family / genus / morph type	
	Corduliidae	Family / genus / morph type	
	Gomphidae	Family / genus / morph type	
	Libellulidae	Family / genus / morph type	
ODONATA: Zygoptera	Chlorolestidae	Family / genus / morph type	
	Coenagrionidae	Family / genus / morph type	
	Protoneuridae	Family / morph type	
OLIGOCHAETA	Lumbriculidae	Family	
	Enchytraeidae	Family	
	Naididae	Family / genus	
PLECOPTERA	Notonemouridae	Family / genus, species	
PODOCOPIDA		Order	
TRICHOPTERA			Dr. Ferdy de Moor, in part
	Barbarochthonidae	Family / genus, species	
	Calamoceratidae	Family / morph type	
	Ecnomidae	Family / genus / morph type	
	Glossosomatidae	Family / genus / morph type	
	Goeridae	Family / genus, species	
	Hydropsychidae	Family / genus, species	
	Hydroptilidae	Family / genus, species / morph type	
	Hydrosalpingidae	Family / genus, species	
	Leptoceridae	Family / tribe / genus / morph type	
	Petrothrincidae	Family / genus, species	
	Philopotamidae	Family / genus / morph type	
	Polycentropodidae	Family / morph type	
	Sericostomatidae	Family / genus / morph type	
TURBELLARIA	Planaria	Family / genus	

APPENDIX 3

Appendix 3 List of taxa that represent the best discriminators between catchment groups. Numbers represent abundance ranking, 1 – 5, and the * denotes absence of that taxon. Site codes use the site number from Table 1.1 and catchment code (O = Olifants, B = Berg, E = Eerste, M = Molenaars, R = Breede, T = Table Mountain, P = Palmiet).

Order	Family	Taxon	O01	O02	B14	B15	E18	E19	E20	M09	M10	M11
Acariformes	Anisitselidae	Anisitselidae spp.	*	*	*	*	4	2	2	3	2	*
	Arrenuridae	Arrenuridae spp.	*	*	*	*	3	*	1	2	1	*
	Hydrachnellae	Hydrachnellae spp.	4	5	*	4	5	3	4	4	4	3
	Oribatidae	Oribatidae spp.	*	*	*	*	1	2	2	*	2	2
	Oxidae	Oxidae spp.	*	*	*	*	*	*	*	*	*	*
Amphipoda	Paramelitidae	<i>Paramelita</i> sp.	5	*	*	2	*	*	1	*	*	*
		<i>Paramelita nigroculus</i>	*	*	*	*	*	*	*	*	*	*
Cladocera	Chydoridae	Chydoridae spp.	*	*	*	*	1	3	2	3	2	*
Coleoptera	Dryopidae	Dryopidae spp. Adult	*	*	*	*	*	*	*	*	*	*
		<i>Strina</i> sp. 1 adult	*	*	*	*	1	*	1	4	4	4
	Elmidae	Elmidae sp. 1 adult	*	*	*	*	3	*	2	3	3	4
		Elmidae spp. Adult	5	3	*	*	*	*	*	2	*	*
		Elmidae spp. Larva	3	*	*	2	2	2	1	4	4	3
		<i>Elpidelmis</i> sp. 1 adult	*	*	*	*	4	1	2	4	3	1
		<i>Elpidelmis</i> sp. 2 adult	*	*	*	*	*	1	*	2	2	3
		<i>Elpidelmis</i> sp. A larva	*	*	*	*	4	2	3	4	4	3
		<i>Elpidelmis</i> sp. Larva	5	4	3	4	1	*	*	*	*	*
		<i>Peloniolus</i> sp. 1	*	*	*	*	3	1	1	*	3	4
		<i>Peloniolus</i> sp. 2	*	*	*	*	4	2	*	*	4	2
		<i>Peloniolus</i> sp. Adult	2	4	2	4	*	*	*	*	*	*
		<i>Peloniolus</i> sp. Larva	4	4	3	3	4	4	1	3	3	2
		<i>Peloniolus</i> sp. nov.	2	3	*	*	*	*	*	*	*	*
	Gyrinidae	Gyrinidae spp. adult	2	1	*	1	*	*	*	*	*	*
		Gyrinidae spp. larva	1	*	*	2	1	2	1	1	2	*
	Helodidae	Helodidae sp. 1	4	*	2	4	5	5	3	4	3	2
		Helodidae sp. 4	*	3	*	*	*	*	*	*	*	*
		Helodidae sp. 5	*	*	*	*	5	4	4	3	2	4
		Helodidae sp. 6	5	4	2	*	4	3	3	4	1	*

Order	Family	Taxon	O01	O02	B14	B15	E18	E19	E20	M09	M10	M11
Coleoptera	Helodidae	Helodidae sp. 7	3	1	2	*	2	*	*	*	*	4
		Helodidae spp. Adult	*	*	*	*	*	*	1	3	*	*
	Hydraenidae	Hydraenidae spp. Adult	*	4	2	3	*	*	*	1	*	*
	Hydraenidae	Mesoceration spp.	3	5	2	4	2	1	*	2	1	*
Coleoptera	Limnichidae	Limnichidae sp.	2	4	*	*	*	*	*	*	*	*
	Torridincolidae	Torridincolidae sp.	*	*	*	*	*	1	*	*	*	*
Copepoda	Copepoda	Cyclopoida spp.	*	*	1	*	*	2	2	2	2	2
Decapoda	Potamonautidae	Potamonautes sp. Adult	2	1	*	2	*	*	1	*	2	*
		Potamonautes sp. Juvenile	3	1	*	2	*	*	*	*	*	*
Diptera	Athericidae	Atherix sp. 2	*	*	*	*	1	*	*	3	3	*
		Atherix sp. 4	*	4	*	*	*	*	*	3	*	*
	Blephariceridae	Elporia capensis larva	*	*	*	*	2	5	4	1	1	*
	Ceratopogonidae	Atrichopogon sp.	*	1	2	2	*	1	*	*	1	*
	Chironomidae	Forcipomyia sp. 1	*	*	*	*	1	2	2	*	*	*
		Aphroterbia tsitsikamiae	*	*	*	*	*	*	*	*	*	1
		Cardiocladius sp.	3	2	*	2	3	4	4	2	3	*
		Cladotanytarsus sp.	*	1	*	*	*	*	*	*	*	*
		Conchapelopia sp. 1	3	4	2	2	3	4	3	4	3	3
		Corynoneura sp. 1	2	2	2	4	3	5	4	3	4	4
		Cricotopus sp. 1	3	2	2	3	2	4	3	*	1	2
		Larsia sp.	2	3	4	3	*	4	3	2	1	2
		Nilotanytus sp. 1	2	*	*	*	2	*	1	4	4	3
		Nilotanytus sp. 2	*	*	*	*	*	*	*	*	*	*
		Notocladius capicola	2	4	3	2	4	3	5	2	4	1
		Parakiefferelia biloba	*	*	*	*	*	*	*	*	*	*
		Paramerina sp.	1	2	1	3	*	3	2	4	4	3
		Parametriocnemus scotti	*	2	2	*	2	3	2	*	*	2
		Polypedium alticola	*	*	*	*	3	4	3	5	3	2
		Polypedium sp.	*	1	*	1	*	*	2	2	*	*
		Polypedium U sp.	4	4	3	3	*	4	1	2	2	*
		Procladius sp.	4	2	3	3	1	*	*	*	*	*
		Pseudosmittia sp.	*	*	*	*	*	*	*	*	*	*
		Rheocricotopus capensis	2	3	3	3	4	5	5	4	4	4
		Stempellina sp.	2	*	*	1	1	*	*	*	*	*
		Tanytarsus sp. 1	3	3	2	2	*	2	3	1	*	2
		Tanytarsus sp. 2	*	*	*	*	*	*	2	*	*	*

Order	Family	Taxon	O01	O02	B14	B15	E18	E19	E20	M09	M10	M11
Diptera	Chironomidae	<i>Thienemanniella</i> sp. 1	2	1	1	3	3	3	4	3	4	4
		<i>Tvetenia calvescens</i>	2	2	3	2	4	3	4	3	3	2
	Empididae	Empididae spp.	1	*	*	1	*	*	3	*	2	1
		<i>Hemerodromia</i> sp.	1	2	1	3	*	2	*	*	*	*
	Simuliidae	<i>Simulium nevermania</i>	*	*	*	*	2	3	2	*	*	*
	Tipulidae	<i>Antocha</i> spp.	4	1	*	*	*	*	*	*	*	*
		<i>Limnophila nox</i>	*	*	2	1	*	*	*	*	*	*
		<i>Limnophila</i> sp.	*	1	*	*	2	2	4	*	1	*
	Ephemeroptera	<i>Afroptium sudafricanum</i>	5	4	*	*	*	*	3	4	4	2
		<i>Baetis harrisoni</i>	3	5	2	1	5	5	5	5	5	*
		<i>Bugillesia</i> sp. nov.	2	1	*	*	*	*	*	*	*	*
		<i>Cheleocloeon excisum</i>	4	3	2	3	*	*	*	2	*	*
		<i>Cloeodes</i> sp. nov. 1	*	*	*	*	*	1	*	5	5	3
		<i>Demoreptus capensis</i>	1	5	1	5	4	5	5	5	5	*
		<i>Demoulinia crassi</i>	*	*	*	*	*	*	*	*	*	*
		<i>Labiobaetis</i> sp. nov. 2	*	*	*	*	*	*	*	*	*	4
		<i>Pseudocloeon vinosum</i>	5	1	*	2	*	*	*	*	1	*
	Leptophlebiidae	<i>Adenophlebia peringueyella</i>	4	2	*	*	*	*	*	*	*	*
		<i>Aprionyx peterseni</i>	3	3	*	1	5	4	4	4	4	*
		<i>Aprionyx</i> spp. early instar	1	1	2	2	*	*	*	3	*	*
		<i>Aprionyx tabularis</i>	*	*	*	*	*	*	*	1	2	2
		<i>Castanophlebia calida</i>	*	*	2	3	5	5	3	1	2	*
		Leptophlebiidae spp. early instar	1	2	4	4	3	3	2	4	5	1
	Teloganodidae	Ephemerellidae sp. 1	*	*	*	*	*	*	*	*	*	*
		<i>Lestagella pericillata</i>	*	3	3	4	4	3	*	5	5	*
		<i>Nadinetella crassi</i>	*	*	*	*	3	*	2	2	3	4
Hemiptera	Naucoridae	<i>Laccocoris spurcus</i> adult	*	*	*	*	*	*	*	*	*	*
		<i>Laccocoris spurcus</i> nymph	*	*	*	*	*	*	*	*	*	*
Isopoda	Janinidae	<i>Protojanira prenticei</i>	*	*	*	*	*	*	*	*	*	*
Lepidoptera	Pyrilidae	<i>Petrophila</i> sp.	4	1	3	*	*	*	*	*	*	4
Megaloptera	Corydalidae	Corydalidae spp. early instar	1	*	*	*	2	2	2	1	1	2
Nematoda	Unspecified	Nematoda spp.	*	*	*	*	2	1	1	1	1	1
Odonata	Aeshnidae	<i>Aeshna</i> spp.	2	2	*	2	*	*	*	*	*	*
	Coenagrionidae	Coenagrionidae spp.	*	*	*	1	*	*	*	*	*	*
		<i>Enallagma</i> sp. 1	*	*	*	*	*	*	*	*	*	*
		<i>Pseudagrion</i> sp. 2	*	*	*	*	*	*	*	*	*	*

Order	Family	Taxon	O01	O02	B14	B15	E18	E19	E20	M09	M10	M11
Odonata	Cordulidae	<i>Macromia</i> sp.	*	*	*	*	*	*	*	*	*	*
	Gomphidae	Gomphidae spp.	*	1	*	1	*	*	2	*	1	*
		<i>Notogomphus</i> sp. 1	*	*	*	*	*	*	*	*	*	*
	Libellulidae	<i>Paragomphus</i> sp.	3	1	*	*	*	*	*	*	*	*
		<i>Orthetrum</i> sp.	3	2	*	*	*	*	*	*	*	*
Oligochaeta	Lumbriculidae	Lumbriculidae spp.	*	*	*	*	2	3	2	2	2	*
	Naididae	Naididae spp.	*	*	*	*	*	3	4	4	4	2
		<i>Nais</i> sp.	*	*	*	2	*	4	*	*	*	*
	Unspecified	Oligochaeta spp.	2	2	3	4	*	*	*	*	*	*
Ostracoda	Unspecified	Ostracoda spp.	*	*	*	*	*	*	2	*	*	*
Plecoptera	Notonemouridae	<i>Aphanicercia bicornis</i>	*	*	*	*	4	4	5	4	3	2
		<i>Aphanicercia capensis</i>	*	*	*	*	5	5	5	4	3	3
		<i>Aphanicercia lyrata</i>	*	*	*	*	2	*	*	3	1	2
		<i>Aphanicercia</i> spp.	*	2	*	3	3	4	4	2	3	4
		<i>Aphanicercella barnardi/scutata</i>	*	*	*	*	4	4	3	3	3	4
		<i>Aphanicercella</i> spp.	3	4	4	4	*	2	*	1	*	3
		<i>Aphanicercopsis</i> spp.	4	4	3	5	*	*	*	*	*	*
		<i>Desmonemoura pulchellum</i>	*	2	*	*	*	*	*	2	3	5
		<i>Desmonemoura</i> spp.	2	2	4	4	*	*	*	*	2	1
		<i>Barbarochthon brunneum</i>	3	*	*	*	*	*	*	*	2	4
		Ecnomidae spp.	*	*	*	*	*	*	*	*	*	*
		<i>Parecnomina resima</i>	2	3	3	1	2	2	1	3	2	*
Trichoptera	Glossosomatidae	<i>Agapetus</i> sp.	*	*	*	*	3	4	3	3	1	*
	Hydropsychidae	<i>Cheumatopsyche afra</i>	3	4	*	*	*	*	*	*	*	*
		<i>Cheumatopsyche maculata</i>	3	3	4	4	2	*	3	2	*	*
		Hydropsychidae spp. larva	*	*	2	*	*	2	3	4	3	2
	Leptoceridae	<i>Athripsodes</i> (bergensis group) sp.	5	2	*	2	1	*	*	*	*	3
		<i>Leptecho scirpi</i>	*	*	*	*	*	*	*	*	*	*
		<i>Leptecho</i> sp.	*	*	*	*	2	*	2	*	2	5
		Leptoceridae spp. early instar	3	1	*	2	*	2	1	2	*	1
	Petrothrincidae	<i>Petrothrincus circularis</i>	2	*	2	3	3	3	*	*	*	2
		<i>Petrothrincus</i> sp.	*	*	*	*	*	*	*	*	*	*
	Philopotamidae	<i>Chimarra</i> sp.	3	1	2	1	*	*	1	*	*	*
		Philopotamidae early instar	*	*	*	*	*	*	*	5	*	2
	Sericostomatidae	Sericostomatidae early instar	*	*	*	*	*	*	*	*	*	*
Tricladida	Planariidae	<i>Dugesia</i> sp.	*	*	*	*	*	2	1	2	*	2

Order	Family	Taxon	R06	R07	R08	R13	B17	T27	T29	P24
Acariformes	Anisitsellidae	Anisitsellidae spp.	4	2	*	1	2	*	*	4
	Arrenuridae	Arrenuridae spp.	*	*	*	*	2	*	2	3
	Hydrachnellae	Hydrachnellae spp.	4	4	4	2	4	2	3	4
	Oribatidae	Oribatidae spp.	*	*	*	*	*	2	4	3
	Oxidae	Oxidae spp.	*	*	1	*	*	*	*	2
Amphipoda	Paramelitidae	<i>Paramelita</i> sp.	*	*	*	*	*	*	4	5
		<i>Paramelita nigrocufus</i>	2	*	*	*	*	5	*	4
Cladocera	Chydoridae	Chydoridae spp.	*	*	*	*	*	3	3	*
Coleoptera	Dryopidae	Dryopidae spp. Adult	4	4	*	2	*	*	*	4
		<i>Strina</i> sp. 1 adult	3	5	2	*	*	*	*	*
	Elmidae	Elmidae sp. 1 adult	*	*	*	*	*	2	*	*
		Elmidae spp. Adult	*	*	*	*	*	*	*	*
		Elmidae spp. Larva	*	*	*	*	*	*	*	3
		<i>Elpodeims</i> sp. 1 adult	4	4	4	4	*	*	3	5
		<i>Elpodeims</i> sp. 2 adult	*	*	*	*	*	*	*	*
		<i>Elpodeims</i> sp. A larva	5	4	5	4	4	5	5	5
		<i>Elpodeims</i> sp. Larva	*	*	*	*	*	*	*	*
		<i>Peloriolus</i> sp. 1	3	5	4	2	4	*	4	4
		<i>Peloriolus</i> sp. 2	5	*	2	3	*	*	*	4
		<i>Peloriolus</i> sp. Adult	*	*	*	*	3	*	*	*
		<i>Peloriolus</i> sp. Larva	4	4	4	4	4	*	2	*
		<i>Peloriolus</i> sp. nov.	*	*	*	*	*	*	*	*
	Gyrinidae	Gyrinidae spp. adult	*	*	*	1	*	*	*	1
		Gyrinidae spp. larva	2	*	*	2	*	*	*	2
	Helodidae	Helodidae sp. 1	*	4	3	2	4	*	4	*
		Helodidae sp. 4	*	*	*	*	1	2	3	*
		Helodidae sp. 5	*	*	*	*	*	*	*	5
		Helodidae sp. 6	5	4	*	4	4	*	4	5
		Helodidae sp. 7	2	*	*	*	*	*	*	5
		Helodidae spp. Adult	*	*	*	*	3	1	*	1
	Hydraenidae	Hydraenidae spp. Adult	4	*	3	4	*	*	1	2
		<i>Mesoceration</i> spp.	*	*	*	*	4	*	*	*
	Limnichidae	Limnichidae sp.	4	3	2	4	*	*	*	4
	Torridincolidae	Torridincolidae sp.	2	*	*	*	*	2	*	2
Copepoda	Copepoda	Cyclopoida spp.	*	*	3	*	*	2	3	3

Order	Family	Taxon	R06	R07	R08	R13	B17	T27	T29	P24
Decapoda	Potamonautidae	<i>Potamonautes</i> sp. Adult	*	2	*	*	2	1	*	*
		<i>Potamonautes</i> sp. Juvenile	*	*	*	*	*	1	*	*
Diptera	Athericidae	<i>Atherix</i> sp. 2	2	3	2	3	1	1	*	4
		<i>Atherix</i> sp. 4	2	*	1	5	4	*	1	3
	Blephariceridae	<i>Elporia capensis</i> larva	*	*	*	*	*	*	*	*
	Ceratopogonidae	<i>Atrichopogon</i> sp.	2	*	*	*	1	*	*	*
		<i>Forcipomyia</i> sp. 1	*	*	*	1	2	*	*	*
	Chironomidae	<i>Aphrotenia tsitsikamae</i>	*	*	*	*	*	*	*	4
		<i>Cardiocladius</i> sp.	*	5	2	1	2	*	*	*
		<i>Gledotanytarsus</i> sp.	*	2	*	*	*	*	*	1
		<i>Conchapelopia</i> sp. 1	5	5	2	3	3	*	4	4
		<i>Corynoneura</i> sp. 1	3	2	*	2	2	4	4	4
		<i>Cricotopus</i> sp. 1	4	4	*	4	*	4	*	*
		<i>Larsia</i> sp.	4	4	3	2	*	5	*	4
		<i>Nilotanytus</i> sp. 1	*	2	*	*	*	*	*	3
		<i>Nilotanytus</i> sp. 2	1	*	*	*	*	*	*	3
		<i>Notocladius capicola</i>	5	5	2	3	4	*	*	3
		<i>Parakiefferiella bioba</i>	*	*	*	*	*	1	*	3
		<i>Paramerina</i> sp.	4	4	4	3	4	*	4	5
		<i>Parametriocnemus scotti</i>	2	*	*	*	*	4	4	*
		<i>Polypedilum alticola</i>	2	4	1	*	4	*	*	4
		<i>Polypedilum</i> sp.	*	*	*	1	*	*	*	1
		<i>Polypedilum</i> U sp.	4	4	2	5	*	*	5	*
		<i>Procladius</i> sp.	2	*	3	1	*	*	*	*
		<i>Pseudosmittia</i> sp.	*	*	2	*	*	*	*	3
		<i>Rheocricotopus capensis</i>	4	4	*	4	2	4	3	2
		<i>Stempellina</i> sp.	4	2	1	4	*	*	5	3
		<i>Tanytarsus</i> sp. 1	4	*	*	2	2	1	*	2
		<i>Tanytarsus</i> sp. 2	*	*	*	*	*	*	*	2
		<i>Thienemannella</i> sp. 1	1	3	*	*	2	*	1	3
		<i>Tsetenia calvenscens</i>	4	4	1	1	3	*	4	4
	Empididae	<i>Empididae</i> spp.	*	*	*	*	*	*	*	1
		<i>Hemerodromia</i> sp.	2	1	1	*	2	1	2	3
	Simuliidae	<i>Simulium nevermania</i>	*	*	*	*	*	2	*	*
	Tipulidae	<i>Antocha</i> spp.	*	*	*	*	*	*	*	2
		<i>Limnophila nox</i>	3	2	2	2	2	*	*	4

Order	Family	Taxon	R06	R07	R08	R13	B17	T27	T29	P24
Diptera	Tipulidae	<i>Limnophila</i> sp.	2	*	2	2	*	*	1	*
Ephemeroptera	Baetidae	<i>Afropium sudafricanum</i>	*	3	*	*	2	*	*	1
		<i>Baetis harrisoni</i>	5	5	4	5	5	5	2	*
		<i>Bugillesia</i> sp. nov.	*	*	*	*	*	*	*	*
		<i>Cheleocloeon excisum</i>	2	4	*	4	2	*	*	*
		<i>Cloeodes</i> sp. nov. 1	*	*	4	*	3	*	*	*
		<i>Demoreptus capensis</i>	2	*	4	*	5	*	*	*
		<i>Demoulinia crassi</i>	*	*	*	*	*	*	*	1
		<i>Labobaetis</i> sp. nov. 2	*	*	*	1	*	*	4	5
		<i>Pseudocloeon vinosum</i>	4	4	*	*	3	*	3	1
	Leptophlebiidae	<i>Adenophlebia peringueyella</i>	*	*	*	*	*	*	*	*
		<i>Aprioryx peterseni</i>	3	4	5	4	5	*	*	*
		<i>Aprioryx</i> spp. early instar	*	*	*	*	*	*	*	*
		<i>Aprioryx tabularis</i>	*	*	*	*	*	*	*	*
		<i>Castanophlebia calida</i>	3	4	5	4	3	5	3	4
		Leptophlebiidae spp. early instar	*	*	3	2	4	*	1	*
	Teloganodidae	Ephemerellidae sp. 1	*	*	*	*	*	*	*	4
		<i>Lestagella penicillata</i>	3	5	2	3	4	2	5	*
		<i>Nadinetella crassi</i>	*	*	3	1	*	*	*	3
Hemiptera	Naucoridae	<i>Laccocoris sparcus</i> adult	*	*	1	2	*	*	*	2
		<i>Laccocoris sparcus</i> nymph	*	*	2	2	*	*	*	2
Isopoda	Janiridae	<i>Protojanira prenticei</i>	*	*	*	*	*	*	2	5
Lepidoptera	Pyridae	<i>Petrophila</i> sp.	*	4	*	*	*	*	2	5
Megaloptera	Corydalidae	Corydalidae spp. early instar	3	*	1	2	*	*	*	*
Nematoda	Unspecified	Nematoda spp.	1	1	*	2	*	1	4	2
Odonata	Aeshnidae	<i>Aeshna</i> spp.	*	*	*	1	2	*	2	*
	Coenagrionidae	Coenagrionidae spp.	*	*	*	*	*	*	*	4
		<i>Enallagma</i> sp. 1	*	*	*	*	*	*	*	2
		<i>Pseudagrion</i> sp. 2	*	*	*	*	*	*	*	4
	Corduliidae	<i>Macromia</i> sp.	*	2	*	*	*	*	*	1
	Gomphidae	Gomphidae spp.	2	*	*	*	*	*	*	2
		<i>Notogomphus</i> sp. 1	3	*	*	4	*	*	*	3
		<i>Paragomphus</i> sp.	2	2	*	2	*	*	*	*
	Libellulidae	<i>Orthetrum</i> sp.	*	*	*	*	*	*	*	*
Oligochaeta	Lumbriculidae	Lumbriculidae spp.	2	3	3	*	2	2	2	*
	Naididae	Naididae spp.	*	*	*	*	*	3	2	3

Order	Family	Taxon	R06	R07	R08	R13	B17	T27	T29	P24
Oligochaeta	Naididae	<i>Nais</i> sp.	2	*	*	5	3	4	4	5
	Unspecified	Oligochaeta spp.	*	*	*	*	*	*	2	*
Ostracoda	Unspecified	Ostracoda spp.	*	*	2	*	*	3	2	*
Plecoptera	Notonemouridae	<i>Aphanicercera bicornis</i>	*	*	*	4	*	*	*	*
		<i>Aphanicercera capensis</i>	*	*	4	3	*	4	1	*
		<i>Aphanicercera lyrata</i>	*	*	*	2	*	*	*	*
		<i>Aphanicercera</i> spp.	4	5	2	3	4	2	3	5
		<i>Aphanicercella bamardi/scutata</i>	*	*	*	*	*	*	*	*
		<i>Aphanicercella</i> spp.	4	4	4	4	4	3	*	4
		<i>Aphanicercopsis</i> spp.	1	4	*	*	*	2	*	*
		<i>Desmonemoura pulchellum</i>	*	*	*	*	*	*	*	*
		<i>Desmonemoura</i> spp.	*	*	*	*	*	*	*	*
		<i>Barbarochthon brunneum</i>	*	*	4	*	*	*	1	4
		<i>Ecnomidae</i> spp.	*	*	3	*	*	*	*	3
		<i>Parecnomina resima</i>	*	*	*	*	3	*	*	*
		<i>Agapetus</i> sp.	*	*	*	*	*	*	*	*
		<i>Cheumatopsyche afra</i>	*	*	*	*	*	*	*	*
Trichoptera	Hydropsychidae	<i>Cheumatopsyche maculata</i>	*	*	*	*	*	*	*	*
		<i>Hydropsychidae</i> spp. larva	2	3	2	3	*	*	*	4
	Leptoceridae	<i>Atopsyche</i> (bergensis group) sp.	*	*	*	*	*	5	5	*
		<i>Lepteco scirpi</i>	*	*	*	*	*	*	*	5
		<i>Lepteco</i> sp.	*	*	*	*	2	2	2	*
		<i>Leptoceridae</i> spp. early instar	5	5	2	4	1	*	*	5
	Petrothrincidae	<i>Petrothrincus circularis</i>	*	*	2	*	*	*	*	3
		<i>Petrothrincus</i> sp.	*	*	1	*	*	*	*	2
	Philopotamidae	<i>Chimarra</i> sp.	*	*	*	*	*	*	*	*
		<i>Philopotamidae</i> early instar	3	*	4	*	*	*	*	3
	Sericostomatidae	<i>Sericostomatidae</i> early instar	*	*	1	*	*	*	*	2
	Tricladida	<i>Dugesia</i> sp.	*	*	*	*	*	2	2	4

APPENDIX 4

The following tables are explanations of the column headings for each of the data output tables from the database discussed in Chapter 7. Further explanations can be sought from King & Schael (2001).

Appendix 4.A Data output from the "extended site detail" query.

Column Headings	Explanation
SiteCode	The code given to each individual site
SiteVisit	Date or dates the site was visited
River	Name of the river for that site
Location	Description of location of the site
LatitudeDegree	Latitude in degrees
LatitudeMinute	Latitude in minutes
LatitudeSecond	Latitude in seconds
LatitudeC	Latitude in map units
LongitudeDegree	Longitude in degrees
LongitudeMinute	Longitude in minutes
LongitudeSecond	Longitude in seconds
LongitudeC	Longitude in map units
ContourRangeFrom	Contour range upper bracket
ContourRangeTo	Contour range lower bracket
UpstreamCatchmentArea	Upstream catchment area, if known
Altitude	Altitude of site
SourceDistance	Distance of site from river's source
MapSlope	Site slope as calculated between contours of 1:50 000 map
SiteSlope	Site slope as measured in the field
DistFromUpstrGWeir	If there is a gauging weir upstream of site, the distance the site is from that weir
WeirCode	If there is a gauging weir, the DWAF weir number
Order	Stream order using Strahler's method
AnnualDischarge	Annual discharge of river to that site if known
MapCode	The 1:50 000 map used to locate site
JoiningMaps	Any joining 1:50 000 maps that may have the catchment that the site is located in
LandOwnerDetail	Telephone number and other details of the land owner/s where the site is located
Notify	Do you need to notify a land owner prior to starting work, yes or no
PermitRequired	Do you need a permit to work on a site, yes or no
PermitAcquired	Notice if a permit was obtained
ValidityofPermit	How long the permit obtained is valid
Key	Notice if a key to a gate on the property is needed for access
KeyAvailability	Details on procedure to get a key
Impoundment	Is there a dam located upstream of site, yes or no
UpstreamDamDist	Distance the site is located from dam
UpstreamDamName	Name/s of dam or dams located upstream of site
UpstreamCatchmentNature	General description of upstream catchment area based on maps and verified in the field
ValleyFloor	Description of the river valley based on map and verified in the field
LateralMobility	Lateral mobility of a river channel based on map and verified in the field
ChannelPattern	Pattern of the river channel in area of the site based on map and verified in the field
SiteLength	Length of the site worked on, and mapped
ChannelType	Geomorphological channel type, bedrock or alluvial
ReachType	Geomorphological reach type
BedCondition	The general condition of the bed material at the site
UpstreamImpact	Description of each possible impact on site from upstream
UpstreamImpactDegree	Indication of the degree of each known impact
UpstreamLandUse	General description of land use upstream of site
UpstreamLandUseExtent	The extent of each of the known land uses upstream of site
Channel	Active or macro channel referring to erosion descriptions
ErosionType	The type of erosion occurring in the active and/or macro channel, i.e. subaerial or active basal
Erosion	Rating of the degree of erosion occurring 1-5
Side	Left or Right bank being described
BankShape	Shape of each bank, i.e. concave, convex
SiteImpact	Specific types of bank erosion, i.e. gully or surface erosion

Appendix 4.B Data output from the "flow data-taxon" query.

Column Headings	Explanation
SiteCode	The code given to each individual site
SiteVisit	Date or dates the site was visited
MI	Sampling area number where invertebrates and flow data were collected from within a site
MorphUnit	Morphological unit where a sampling area was located
FlowType	The visual flow type recorded for each sampling area, i.e. rippled surface (RS)
Taxon1	Database record number for each taxon
TaxonStage	Developmental stage the taxon was in
TaxonCount	The number of that taxon that was present in a sample
Taxon2	The name of that taxon
Family	The taxonomic family that taxon belongs to
AvgWaterDepth	Mean depth (cm) taken from 2 - 6 depth measurements in a sampling area that the taxon was found in
AvgVelocityNearBed	Mean of 2 - 6 velocity (m s ⁻¹) measurements in a sampling area taken near-bed (NB) that the taxon was found in
AvgVelocitySix-tenths	Mean of 2 - 6 velocity (m s ⁻¹) measurements in a sampling area taken 0.6 depth that the taxon was found in
AvgVelocitySurface	Mean of 2 - 6 velocity (m s ⁻¹) measurements in a sampling area taken near the water's surface that the taxon was found in (rarely recorded)
AvgVelocityTwo-tenths	Mean of 2 - 6 velocity (m s ⁻¹) measurements in a sampling area taken 0.2 depth that the taxon was found in (rarely recorded)
AvgVelocityEight-tenths	Mean of 2 - 6 velocity (m s ⁻¹) measurements in a sampling area taken 0.8 depth that the taxon was found in (rarely recorded)
AvgEmbeddednessCode	Mean of embeddedness rating where 0 = no embeddedness and 5 = imbricated bed

Appendix 4.C Data output from the "flow data-no taxon" query.

Column Headings	Explanation
SiteCode	The code given to each individual site
SiteVisit	Date or dates the site was visited
MI	Sampling area number where invertebrates and flow data were collected from within a site
DominantSubstratum	The dominant substrata recorded within a sampling area, i.e. boulder (B)
SubDominantSubstratum	The sub-dominant substrata recorded within a sampling area, i.e. large cobble (LC)
EmbeddednessCode	The degree of embeddedness of substrata within a sampling area
WaterDepth	Depth (cm) of the water at each point (2-6) within a sampling area
VelocityNearBed	The near-bed velocity (m s ⁻¹) recorded at each point (2-6) within a sampling area
VelocitySix-tenths	The 0.6 velocity (m s ⁻¹) recorded at each point (2-6) within a sampling area
VelocitySurface	The surface velocity (m s ⁻¹) recorded at each point (2-6) within a sampling area (rarely recorded)
VelocityTwo-tenths	The 0.2 velocity (m s ⁻¹) recorded at each point (2-6) within a sampling area (rarely recorded)
VelocityEight-tenths	The 0.8 velocity (m s ⁻¹) recorded at each point (2-6) within a sampling area (rarely recorded)
MorphUnit	Morphological unit where a sampling area was located
FlowType	The visual flow type recorded for each sampling area, i.e. rippled surface (RS)

Appendix 4.D Data output from the "observations" query.

Column Headings	Explanation
SiteCode	The code given to each individual site
SiteVisit	Date or dates the site was visited
ObservationCategory	Biological (BioObs) or Chemical (ChemObs) type of recorded data
Value	The percent cover or measurement value of the observation
Comment	general comments
ObservationCode	The type of observation and units the value is in, i.e. Moss cover in percent, or site discharge in $\text{m}^3 \text{s}^{-1}$ or conductivity in $\mu\text{S cm}^{-1}$

Appendix 4.E Data output from the "parameter coverage" query.

Column Headings	Explanation
SiteCode	The code given to each individual site
SiteVisit	Date or dates the site was visited
AreaIndicator	Total site area mapped or only wetted area of site
Parameter	The code for a flow type, substratum type or morphological unit type
ParamType	Indication of whether the parameter area is a flow type, substratum type or morphological unit type
Area	The percent of the site area that the individual parameter covers
Comment	An explanation of how the area for that parameter was calculated from the GIS mapped site data output

Appendix 4.F Data output from the "parameter matrix" query.

Column Headings	Explanation
SiteCode	The code given to each individual site
SiteVisit	Date or dates the site was visited
Parameter	The code for a flow type, substratum type or morphological unit type
DependentParameter	The code for a flow type, substratum type or morphological unit type overlaid with the above
Areastatus	
Area	The percent of the site area that the two overlapping parameter cover within the site
Comment	An explanation of how the area for the overlapping parameters were calculated from the GIS mapped site data output

Appendix 4.G Data output from the "site transect data" query.

Column Headings	Explanation
SiteCode	The code given to each individual site
SiteVisit	Date or dates the site was visited
ChannelType	Geomorphological channel type, bedrock or alluvial
ReachType	Geomorphological reach type
BedCondition	The general condition of the bed material at the site
Distance	The distance at each point along the transect, the first measurement is zero, and the subsequent distances are measured and recorded
Height	The height of the tape measured at each point across the active river channel from bank to bank
Substrate	The type of substratum at each point along the transect
Velocity	The 0.6 velocity (m s^{-1}) recorded at each point along the transect
WaterDepth	The depth of the water (cm) recorded at each point along the transect
VegetationCategory	A general description of the vegetation recorded along the transect, i.e. riparian, grass, instream

Appendix 4.H Data output from the "taxonomy details" query.

Column Headings	Explanation
SiteCode	The code given to each individual site
SiteVisit	Date or dates the site was visited
Mi	Sampling area number where invertebrates and flow data were collected from within a site
Taxon1	Database record number for each taxon
Taxon2	The name of that taxon
BioBaseTaxon	The record number given to this taxon in the BioBase database
Phylum	The taxonomic phylum that taxon belongs to
Class	The taxonomic class that taxon belongs to
Order	The taxonomic order that taxon belongs to
SubOrder	The taxonomic sub-order that taxon belongs to
Family	The taxonomic family that taxon belongs to
SubFamily	The taxonomic sub-family that taxon belongs to
GenusSpecies	The genus and species of that taxon if known
Indigenous	
TaxonStage	Developmental stage the taxon was in
TaxonCount	The number of that taxon that was present in a sample
AirBreather	Indication if the taxon is an air breather or not
Score	SASS4 sensitivity to water quality variables score (has not been amended for SASS5)
Group	SASS4 family groups

Appendix 4.I Data output from the "vegetation" query.

Column Headings	Explanation
SiteCode	The code given to each individual site
SiteVisit	Date or dates the site was visited
VegTaxon	Database record number for each vegetation taxon
Taxon	The name of that taxon
Phylum	The taxonomic phylum that taxon belongs to
Class	The taxonomic class that taxon belongs to
Family	The taxonomic family that taxon belongs to
GenusSpecies	The genus and species of that taxon if known
Status	Indication if the taxon is indigenous or alien to the area
Abundance	The estimated percent coverage of that taxon within the site

Appendix 4.J List of "Look-up" tables within the database.

Look-up Table	Explanation
Phylum	The list of possible taxonomic phyla
Class	The list of possible taxonomic classes
Order	The list of possible taxonomic orders
Order Sub	The list of possible taxonomic sub-orders
Family	The list of possible taxonomic families
Family Sub	The list of possible taxonomic sub-families
GenusSpecies	The list of possible genus and species
Taxon Stage	The stage, adult, larva, nymph, juvenile or early instar a taxon is in
Bed Condition	Whether the stream bed is armoured, loose, imbricated or bedrock
Erosion	Bank erosion categories, 1 = 0 - 10%, 2 = 10 - 30%, 3 = 30 - 60%, 4 = >60%
Erosion Type	Active basal or subaerial erosion types
Lateral Mobility	Channel mobility categories, 1 = confined, 2 = mod. confined, 3 = non-confined, 4 = entrenched
Valley Floor	Valley floor types, erosional bench, flood plain, pediment, side bench and absent
Site Impact	Possible impacts on study site ranging from dams and weirs to orchards and alien vegetation
Upstream impact	Impacts within the catchment upstream of the site, a range of possibilities
Upstream impact degree	The degree to which the impacts effect the study site, rated as 0 = none, 1 = low, 2 = mod., 3 = high
Upstream land use	General land use upstream of site such as urban, orchards, forestry
Upstream land use extent	The extent the land use is in the upstream catchment, 0 = none, 1 = local, 2 = frequent, 3 = wide
Transect Substrata	Codes for substratum recorded on the discharge and channel shape transects
Vegetation Category	General vegetation types recorded along channel transect, riparian, terrestrial, instream
Map	Land Affairs map details listing map code and scale (1:50 000) and name
Parameters	GIS map data, substrata, flow type and morphological unit codes
Parameter Effective Area	GIS map data indicating if the proportion of substrata or morphological unit represents wetted or total mapped area

Other related WRC reports available:

Assessing the ecological relevance of a spatially-nested geomorphological hierarchy for river management

JM King & DM Schael

The research focused on a site in each of 28 headwater streams in the Western Cape. These were all in the mountain and foothill zones of perennial rivers, in order to standardise study sites as much as possible. Sites were designated "mountain" or "foothill" based on prior biological knowledge of which they were likely to be. All fieldwork was done during summer low flows, when flow and other physical conditions are most stable and the rivers most comparable in hydraulic terms. Eighteen of the rivers had minimal disturbance, and were used to detect underlying trends in physical-biotic links. The remaining ten had specific disturbances, and were used to assess how disturbance affected the trends.

At each of the sites, up to 12 biological samples were collected from the widest possible range of physical conditions, and these conditions were measured in detail. The sites, which ranged from 30-100 m in length, were mapped using eight categories of substrata and 14 categories of flow type, and the location of every biological sample shown (Tables E1 and E2). Aquatic invertebrates were used to provide the biological input to the study, as different species are known to seek different kinds of flow or substrata and by this selectivity should illustrate clear physical-biotic links.

The sampling programme as a whole was designed to assess the ecological relevance of all levels of the hierarchy.

Report Number: 754/1/01

ISBN No: 1 86845 818 0

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