

**ESTABLISHING REFERENCE CONDITIONS FOR BENTHIC
INVERTEBRATE MONITORING IN THE FRASER RIVER CATCHMENT,
BRITISH COLUMBIA, CANADA**

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ABSTRACT

The problem of assessing pollution in the catchment of the Fraser River, British Columbia, Canada, was addressed by using benthic macroinvertebrates to develop a biomonitoring program based on the reference-condition approach to water-quality assessment. The reference condition is represented by groups of minimally disturbed sites organized by selected physical, chemical, and biological characteristics. Potentially impaired sites in the catchment can eventually be compared against the appropriate reference group. Multivariate statistics are used to create the reference groups of macroinvertebrate assemblages, to create the physical-chemical models to predict group membership, and to compare potentially impaired sites with reference groups. Techniques are described for: (1) selecting reference sites; (2) choosing physical, chemical, and biological variables to be measured at each site and the methods of measurement involved; (3) developing the sampling and processing protocols used for benthic macroinvertebrates; (4) creating a family-level predictive model of invertebrate assemblage structure, and testing it with sites exposed to logging, mining, and agricultural disturbances; and (5) choosing appropriate metrics for analysis and interpretation.

Reference and impaired sites were chosen with the aid of local experts, and represented the range of ecoregions and stream orders available in the Fraser River catchment. The chemical, physical, and biological variables measured at each site were mainly obtained from relevant literature and represented four different spatial scales: landscape, site/reach, channel/substrate, and water-column. A pilot calibration study done in a Fraser River tributary revealed that: (1) five replicate samples were optimal in terms of total numbers and numbers in major orders collected, although further examination of multiple replicates revealed that one per site was sufficient; (2) no operator differences existed in the collection of samples in terms of total numbers or numbers in major orders; (3) no differences existed among 1-, 3-, and 5-min collections in terms of total numbers or numbers in major orders, although numbers of taxa

(mainly family) were lower in 1-min samples than the others; and (4) 200- μ m-mesh kick nets retained higher numbers of invertebrates than 400- μ m-mesh nets, although the overall number of taxa was similar. Total numbers of individuals and family counts estimated from 100-, 200-, and 300-organism subsamples using a Marchant box were similar. The subsamples usually had fewer families than whole samples, but the missing families were rare. The protocol eventually used for sampling and processing benthic macroinvertebrates involved collecting a single replicate with a kick net (400- μ m mesh) for 3 min at each site and subsampling the first 200 organisms encountered in a Marchant box. The protocol represented the most efficient, cost-effective way to obtain the macroinvertebrate data needed to develop the reference condition.

A total of 270 sites was sampled, 219 of which were identified as reference sites. The reference sites were used to build a family-level predictive model relating invertebrate assemblage structure to environmental attributes. The reference sites were classified into groups representing similar invertebrate assemblages using cluster analysis. The predictive model was developed using Discriminant Function Analysis along with environmental descriptors. The model predicted 62% of the reference sites to the correct invertebrate group.

The family-level model was then used to assess 21 sites exposed to agriculture, logging, or mining activities. The model was able to discriminate between impaired and unimpaired sites, and identify the degree of impairment based on the extent of modification of the invertebrate assemblage. There was no consistent relationship between apparent physical disturbance at a site and the response of the in-stream invertebrate assemblage. Therefore, use of the family-level model is necessary for an objective assessment of biological stream condition.

Performance of the family-level model was compared to other reference-site models using lower taxonomic levels, and derived biological measures (metrics) rather than assemblage structure. The family-level model proved to be superior and is recommended for assessment of sites in the Fraser River catchment.

Benthic macroinvertebrate collections made at the 219 Fraser River reference sites contained at least 318 taxa belonging to 74 families and 14 orders; their distribution and abundance are presented by subcatchment. Metrics describing 33 genus/species-level and 14 family-level structural and functional aspects of benthic macroinvertebrate assemblages were calculated for each subcatchment. The metrics, which can be divided into descriptors of taxa richness, enumerations, proportions of functional feeding groups, and biotic index values, can serve as the basis for multimetric biomonitoring designs and/or be used in interpretation of the results of multivariate models (described above). Habitat descriptors involving physical, chemical, and other biological (algal) measures are also discussed by subcatchment.

Forty-four metrics were calculated from benthic macroinvertebrates collected at 17 sites in 1994 to determine precision and accuracy of metrics in describing reference- and test-site conditions in the Fraser catchment. Richness measures had the lowest variability in mean values across the five subcatchments examined, and lowest coefficients of variation based on replicate samples collected at a single site within each subcatchment. Most (59.1%) metrics could be calculated at all sites examined in this study, and most (55.3%) correctly indicated impairment when presumed impaired and unimpaired sites were compared. However, incorrect indications of impairment were noted in 40-60% of the metric comparisons made between unimpaired sites located in different ecoregions, between unimpaired sites in different streams of the same ecoregions, and between unimpaired sites in the same stream.

Richness metrics consistently had the lowest error rates of the metrics examined. Incorporation of non-richness metrics into multivariate approaches may increase incorrect indications of impairment (i.e. Type 1 errors). Although we do not recommend the inclusion of metrics in multivariate approaches, we do recommend that multimetric approaches should consider incorporating multivariate analyses for defining reference conditions and assessing impairment of test sites.

This project provides prospective users in the Fraser River catchment with (1) tested sampling protocols, (2) reference conditions, (3) methods and a family-level multivariate model for comparing potentially impaired sites with reference sites, (4) faunal and distributional information, and (5) habitat descriptors. This report may serve as a prototype for future development of regionally based biomonitoring programs.

RÉSUMÉ

Pour aborder le problème de l'évaluation de la pollution dans le bassin versant du Fraser, en Colombie-Britannique, au Canada, nous avons utilisé des macroinvertébrés benthiques afin d'élaborer un programme de biosurveillance basé sur l'approche de la condition de référence pour l'évaluation de la qualité de l'eau. La condition de référence est représentée par des groupes de sites minimalement perturbés organisés selon certaines caractéristiques physiques, chimiques et biologiques. On peut ensuite comparer les sites potentiellement perturbés d'un bassin versant au groupe de référence approprié. L'analyse statistique multidimensionnelle permet de créer les groupes de référence d'assemblages de macroinvertébrés, d'établir les modèles physico-chimiques permettant de prédire l'appartenance à un groupe, et de comparer les sites potentiellement perturbés aux groupes de référence. Nous décrivons des techniques permettant : 1) de choisir les sites de référence; 2) de choisir les variables physiques, chimiques et biologiques à mesurer à chaque site, et les méthodes de mesurage nécessaires; 3) de développer les protocoles d'échantillonnage et de traitement convenant aux macroinvertébrés benthiques; 4) de créer un modèle prédictif basé sur la famille pour la structure des assemblages d'invertébrés, et de le tester sur des sites exposés à des perturbations causées par l'exploitation forestière, l'extraction minière et l'agriculture; et 5) de choisir une métrologie (ensemble de paramètres) appropriée pour l'analyse et l'interprétation.

Les sites de référence et les sites perturbés, qui ont été choisis avec l'aide d'experts de la région, représentaient la gamme d'écorégions et d'ordres de cours d'eau existant dans le bassin versant du Fraser. Les variables chimiques, physiques et biologiques mesurées à chaque site ont été pour l'essentiel tirées de publications pertinentes et représentaient quatre échelles spatiales différentes : paysage, site/tronçon, chenal/substrat, colonne d'eau. Une étude pilote d'étalonnage réalisée dans un affluent du Fraser a révélé que 1) le nombre de cinq

échantillons répétés était optimal pour ce qui est de l'effectif total et du nombre d'individus prélevés dans les principaux ordres, mais un examen approfondi de multiples échantillons répétés a révélé qu'un échantillon par site était suffisant; 2) on ne notait pas de différences liées à l'opérateur dans la collecte des échantillons en ce qui concerne l'effectif total ou le nombre d'individus dans les principaux ordres; 3) il n'existait pas de différences entre les prélèvements de 1, 3 et 5 min en termes d'effectif total ou de nombre d'individus dans les principaux ordres, mais le nombre de taxons (principalement la famille) était plus bas dans les échantillons de 1 min que dans les autres; et 4) le filet troubleau à maille de 200 μm retenait un nombre plus grand d'invertébrés que le filet à maille de 400 μm , même si le nombre total de taxons était semblable. L'effectif total et le nombre d'individus par famille, estimés à partir de sous-échantillons de 100, 200 et 300 organismes à l'aide d'une boîte de Marchant, étaient semblables. Les sous-échantillons présentaient généralement un nombre moins grand de familles que les échantillons entiers, mais rares étaient les familles manquantes. Le protocole finalement mis au point pour échantillonner et traiter les macroinvertébrés benthiques était le suivant : prélèvement d'un seul échantillon répété avec un filet troubleau (maille de 400 μm) pendant 3 min à chaque site, et sous-échantillonnage des 200 premiers organismes trouvés dans une boîte de Marchant. Le protocole représentait la façon la plus efficace et la moins coûteuse pour obtenir les données sur les macroinvertébrés nécessaires pour établir la condition de référence.

Sur le total de 270 sites échantillonnés, 219 ont été identifiés comme sites de référence. Ces sites de référence ont été utilisés pour construire un modèle prédictif basé sur la famille qui relie la structure des assemblages d'invertébrés à des attributs environnementaux. Les sites de référence ont été classés en groupes représentant des assemblages similaires d'invertébrés à l'aide de l'analyse typologique. Le modèle prédictif a été développé à partir d'une analyse discriminante et de descripteurs environnementaux. Le modèle a attribué 62 % des sites de référence au groupe correct d'invertébrés.

Le modèle basé sur la famille a ensuite servi à évaluer 21 sites exposés à des activités d'agriculture, d'exploitation forestière ou d'extraction minière. Il a réussi à faire la distinction entre les sites perturbés et non perturbés, et à identifier le degré de perturbation à partir de l'ampleur de la modification de l'assemblage d'invertébrés. Il n'y avait pas de relation constante entre la perturbation physique apparente d'un site et la réaction de l'assemblage d'invertébrés dans le cours d'eau. L'utilisation du modèle basé sur la famille est donc nécessaire à une évaluation objective de la condition biologique d'un cours d'eau.

Nous avons comparé la performance du modèle basé sur la famille à d'autres modèles de sites de référence basés sur des niveaux taxinomiques inférieurs, et sur des mesures biologiques dérivées (métrologie) plutôt que sur la structure de l'assemblage. Le modèle basé sur la famille s'est révélé supérieur, et nous le recommandons pour l'évaluation des sites dans le bassin du Fraser.

Les échantillons de macroinvertébrés benthiques prélevés aux 219 sites de référence du Fraser contenaient au moins 318 taxons appartenant à 74 familles et 14 ordres; leur répartition et leur abondance sont présentées par sous-bassin. Nous avons établi pour chaque sous-bassin une métrologie décrivant des aspects structurels et fonctionnels des assemblages de macroinvertébrés benthiques (33 au niveau du genre et de l'espèce, et 14 au niveau de la famille). Cette métrologie, que l'on peut répartir en descripteurs de la richesse taxinomique, dénombrements, proportions des groupes trophiques fonctionnels, et valeurs des indices biotiques, peut servir de base à la conception d'opérations de biosurveillance multimétrique et/ou être employée pour l'interprétation des résultats des modèles multidimensionnels (décrits plus haut). Nous analysons aussi, par sous-bassin, les descripteurs de l'habitat faisant appel à des mesures physiques et chimiques et à d'autres paramètres biologiques (algues).

Nous avons calculé 44 paramètres à partir des macroinvertébrés benthiques prélevés à 17 sites en 1994 afin de déterminer la précision et l'exactitude de la métrologie pour la description des conditions des sites de référence et des sites testés du bassin du Fraser. Ce sont les mesures de la richesse taxinomique qui présentaient la plus faible variabilité des valeurs moyennes dans les cinq sous-bassins examinés, et les plus faibles coefficients de variation à partir des échantillons répétés prélevés à un seul site dans chaque sous-bassin. La plupart (59,1 %) des paramètres ont pu être calculés à tous les sites examinés dans notre étude, et la majorité (55,3 %) ont correctement indiqué la perturbation quand on comparait des sites perturbés et non perturbés. Toutefois, on a noté de fausses indications de perturbation dans 40-60 % des comparaisons de mesures faites entre des sites non perturbés situés dans des écorégions différentes, entre des sites non perturbés de cours d'eau différents de la même écorégion, et entre des sites non perturbés d'un même cours d'eau.

Ce sont les mesures de la richesse taxinomique qui présentaient de façon constante le taux d'erreur le plus faible. L'intégration dans les approches multidimensionnelles de paramètres autres que la richesse taxinomique peut accroître les fausses indications de perturbation (erreurs de type I). Alors que nous ne recommandons pas l'inclusion des paramètres dans les approches multidimensionnelles, nous suggérons dans les approches multimétriques d'intégrer des analyses multidimensionnelles pour définir les conditions de référence et évaluer la perturbation des sites étudiés.

Ce projet apporte aux utilisateurs éventuels du bassin versant du Fraser : 1) des protocoles d'échantillonnage vérifiés; 2) des conditions de référence; 3) des méthodes et un modèle multidimensionnel basé sur la famille pour comparer les sites potentiellement perturbés aux sites de référence; 4) de l'information sur la faune et sa distribution; 5) des descripteurs de l'habitat. Notre rapport peut servir de prototype pour l'élaboration future de programmes de biosurveillance à l'échelle régionale.

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1. DEVELOPMENT OF PROTOCOLS FOR ESTABLISHING REFERENCE CONDITIONS IN THE FRASER RIVER CATCHMENT, BRITISH COLUMBIA, CANADA

1.1 Introduction

The Fraser River catchment covers ~230,000 km² or ~25% of B.C., Canada's westernmost province (Fig. 1.1; B.C. Ministry of Environment, Lands and Parks and Environment Canada 1993). The Fraser itself has a mean annual discharge of 3620 m³ • s⁻¹, which makes it the sixth largest river in North America, after the Mississippi (18,400 m³ • s⁻¹), St. Lawrence (10,800), Mackenzie (9910), Columbia (7500), and Yukon (6370) rivers (Dynesius and Nilsson 1994). Approximately 1.7 million people live in the Fraser catchment, ~2/3 of B.C.'s population. Although the Fraser is one of the last unregulated large rivers of North America, urban and industrial pressures pose a severe threat to the health of this ecosystem, a fact that was recognized by the establishment in 1991 of the Fraser River Action Plan (FRAP) by Environment Canada (Environment Canada 1995). The research described in this technical report addresses the assessment of pollution in the Fraser River catchment through the use of benthic macroinvertebrates and the development of a biomonitoring program based on the reference-condition approach to water-quality assessment (Reynoldson et al. 1997b). Benthic macroinvertebrates are the basis for most biomonitoring programs currently in operation worldwide (Rosenberg and Resh 1993b), and the reasons underlying the use of these organisms are compelling (Rosenberg and Resh 1996). Our objective was to provide prospective users in the Fraser River catchment with (1) straightforward sampling protocols, (2) reference-condition baselines, (3) methods for comparing sites suspected of being impacted with the appropriate reference group, and (4) basic faunal information. We also included a toxicity-testing component in response to concerns over potential impacts of chemical contaminants being discharged by pulp mills into the Fraser River.

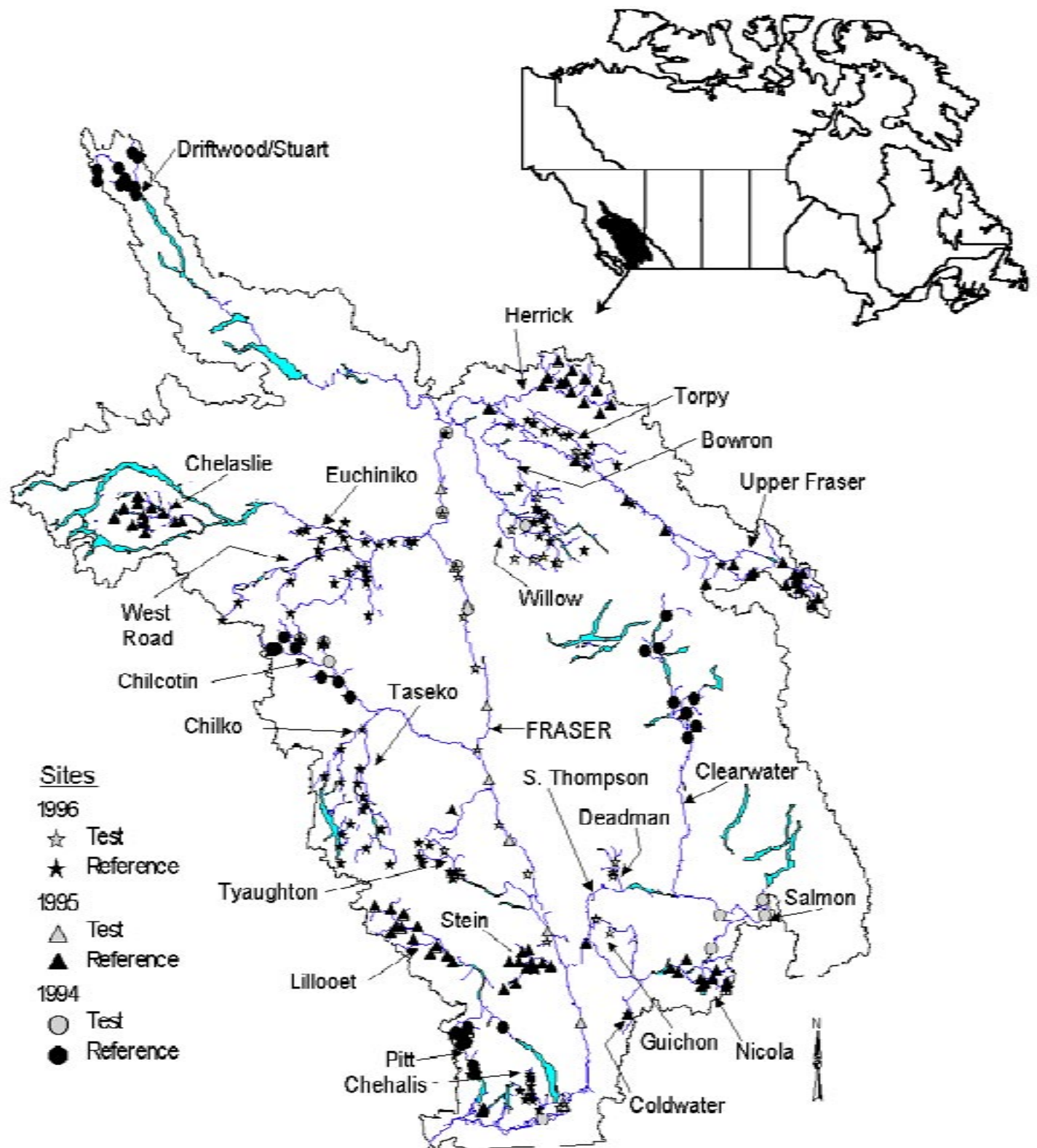


Figure 1.1 The Fraser River catchment, British Columbia, Canada, showing the mainstem river, major tributaries, and sites sampled from 1994-1996. Some symbols may overlap.

This section mainly describes activities and planning conducted in the first year of the study (1994), whereas the following two sections deal with data from all three years of the study (1994-1996). In the first section, we discuss how key elements of regional- or catchment-scale benthic monitoring programs can be tailored to local conditions. We describe specific aspects of the design of the project: site selection; choice of environmental variables; development of sampling methods and protocols; analytical methods; and decisions on the best approaches to take. The design of this project may serve as the basis for future attempts at developing biomonitoring programs that are relevant to a specific region or catchment.

1.1.1 Study area

The Fraser River has a mainstem length of 1375 km (see descriptions in Dorcsey and Griggs 1991). The river rises near Mt. Robson (3956 m elevation) in the Rocky Mountains of eastern B.C. and flows northwest in an “S”-shaped course through the Caribou Mountains of central B.C., then southwest through the Coast Ranges, and into the Pacific Ocean at Vancouver (Fig. 1.1). Mean flow of the river varies from $750 \text{ m}^3 \cdot \text{s}^{-1}$ in winter to $11,500 \text{ m}^3 \cdot \text{s}^{-1}$ in summer (overall range $450\text{-}20,000 \text{ m}^3 \cdot \text{s}^{-1}$).

Rainfall, snowmelt, and glacial melt contribute water to the Fraser River catchment; the contribution of each varies temporally and spatially (see Moore 1991 for details). Precipitation can be as high as the annual mean of 2000 mm in the Coast Ranges to as low as 400-800 mm in the Interior Plateau. Mean temperatures decrease with increases in both elevation and latitude, as does the importance of snow (as precipitation) and the seasonal variation in snowmelt contribution to consequent hydrology.

The Fraser crosses four geological belts (Cameron 1995); a simplified description of the bedrock geology of the basin includes areas of igneous intrusion, volcanic and sedimentary rock, foliated metamorphic rock, folded sedimentary rock, and areas of flat lava and sedimentary rock

(Hall et al. 1991). The great variation in climate, soils, and elevation result in 11 of the 14 biogeoclimatic zones of B.C. being represented in the Fraser catchment; diverse forest types are present but are predominantly subboreal spruce (6.9 million ha), Englemann spruce-subalpine firs (5 million ha), and interior Douglas fir (3.3 million ha) (Moore 1991). Water quality and the effects of land-use activities, waste discharges, agriculture and forestry practices, and mining and pulp mill effluents are presented in Schreier et al. (1991).

Although the Fraser is the sixth largest river in North America (in terms of discharge) and the 28th worldwide in terms of river length, it is the most important salmonid-producing river in the world (Northcote and Burwash 1981; Northcote and Larkin 1989). The fish fauna today contains 53 species but in the past 40 million years the fauna has ranged from being absent to fairly rich (Northcote and Burwash 1991). The river also presents rich waterfowl habitat, containing 21 species (Dorcey 1991).

Of the 40 subcatchments of the Fraser River, 21 were included in our analysis. These 21 subcatchments contained sites that were used to describe reference conditions (sensu Reynoldson et al. 1997b)

1.1.2 The reference-condition approach to biomonitoring

The “reference condition” is defined as “the condition that is representative of a group of minimally disturbed sites organized by selected physical, chemical, and biological characteristics” (Reynoldson et al. 1997b; see also Reynoldson et al. 1995; Wright 1995). Once reference conditions are established, they can be used to assess environmental impacts, conservation status, or biodiversity at any new site. The Fraser is the first major Canadian river to which the reference-condition approach has been applied.

The reference-condition approach can be regarded as an alternative to more traditional control/impact studies for bioassessment. The approach establishes an array of reference sites

(i.e. those areas having no or minimal impact) that characterizes the many potential biological conditions in a region (Reynoldson et al. 1997b).

New sites suspected of being impacted are then compared to an appropriate subset of reference sites. A subset of sites is selected by using models relating conservative physical and chemical variables collected at each site to the benthic assemblage. The creation of reference groups and physical-chemical models to predict group membership, and the comparison of test sites with reference groups are done using multivariate statistics (reviewed by Reynoldson et al. 1997b).

Similar reference-condition approaches have been used in the U.K. for river water-quality assessment (Wright 1995), in Canada to develop sediment guidelines for the Laurentian Great Lakes (Reynoldson et al. 1995), and in the Australian National River Health Program (Parsons and Norris 1996; Simpson and Norris 2000). A different reference-condition approach, one using “multimetrics”, has been developed for water-quality monitoring in the U.S.A. (Plafkin et al. 1989; Barbour et al. 1995, 1996; Resh et al. 1995; USEPA 1998). A previous study using Fraser River data found that the multimetric method was less accurate and precise than the Australian and Canadian reference-condition approaches (Reynoldson et al. 1997b), but further research on this topic is needed (Resh et al. 2000).

1.2 Methods

The following material describes the rationale for: (1) the selection of reference sites; (2) the choice of physical, chemical, and biological variables measured at each site; (3) the sampling protocols used; (4) the toxicity testing program; and (5) quality assurance procedures.

1.2.1 Choice of reference sites

The multivariate methods used to match new sites to a subset of reference sites require a substantial initial investment in effort because sufficient sites must be sampled to characterize

the different conditions in the catchment and the variability associated with these conditions.

No absolute guideline exists for the total number of sites required. Other studies (e.g. Reynoldson et al. 1995; Wright 1995) have indicated that ~250 are required to characterize variability adequately and to build appropriate predictive models, although a minimum of 60-70 sites may be capable of generating a preliminary model (Reynoldson and Wright 2000).

Two stratification methods were used to encompass the range of conditions within the study area: (1) ecoregion, which ensured that climatic and landscape conditions were included in the reference sites selected, and was based on previous studies by Demarchi (1990) and B.C. Ministry of Environment, Lands and Parks (1991); and (2) stream order, which ensured that a range of hydraulic conditions was included in the reference sites selected, and was based on Strahler (1964).

Actual site selection involved two stages. First, a series of workshops with provincial experts served to identify non-, moderately, and heavily impacted subcatchments, and to choose subcatchments that were distributed through as many ecoregions as possible. Reference subcatchments selected for sampling were then outlined on 1:250,000 maps and stream orders were identified using the Strahler (1964) method. Two or three sites were randomly located on each stream order within a subcatchment. A “site” was considered to be a stream reach with a longitudinal distance ~6X its width (Newbury 1984). Only erosional (i.e. riffle/run) reaches were sampled (except for toxicity testing: see below) because they were the dominant habitat type, sampling of other habitat types would have taken more time, and multiple-habitat sampling often provides redundant data (Parsons and Norris 1996). The same maps were subsequently used to locate sites in the field.

Second, field verification, which involved either land-based or aerial (via helicopter) surveys of the area surrounding the site confirmed that sites were not impacted. Occasionally, site locations were moved during the field operation because the original ones were inaccessible or because the identified streams were dry; however, the distribution of sites among stream orders was maintained.

In addition, a small number of impacted catchments was included to verify performance of the reference-site model during its development, and 28 sites along the Fraser River were selected at ~50-km intervals to provide data for analysis of environmental health in the Fraser mainstem. Five, 14, and 17 of these sites were sampled in 1994, 1995, and 1996, respectively.

The large number of reference sites required a sampling program that was staged over three years: ~50 sites were sampled in 1994 and ~100 sites in each of 1995 and 1996. The 1994 sites were sampled by one four-person team, whereas the 1995 and 1996 sites were sampled by two four-person teams. Surveys were completed by helicopter within a 2-week period in autumn to maximize accessibility to streams during the low-flow period; most sites were inaccessible by any other means.

1.2.2 *Choice of environmental variables*

The reference-condition approach requires the preparation of two data matrices for the reference sites. The first constitutes the information on invertebrate assemblage structure (site-by-taxa) that are grouped together by site similarity using multivariate techniques. The second includes environmental information that is used to relate habitat conditions to subsets of sites selected based on similarities in invertebrate assemblages. These habitat data are then used in building the predictive models for matching new sites to the appropriate subset of reference sites. Therefore, the set of environmental variables (physical, chemical, biological) chosen for measurement at each site is critical because some will eventually be used to predict group membership of the benthic macroinvertebrates from each site (e.g. Wright et al. 1984; Reynoldson et al. 1995, 1997b). Because the optimum set of predictor variables cannot be determined *a priori*, it is necessary to select a maximum number of likely variables for measurement.

Previous studies examining the relationship between environmental characteristics and the assemblage structure of benthic invertebrates in lotic systems were canvassed for variables considered most useful (Table 1.1). The list was discussed at an initial workshop and modified as deemed necessary for work on the Fraser River catchment. The final list represented variables at four different spatial scales: (1) landscape variables (e.g. latitude, longitude); (2) site/reach variables (e.g. flow state, canopy coverage); (3) channel/substrate variables (e.g. discharge, substrate composition); and (4) water-column variables (e.g. pH, conductivity) (Table 1.2). This set of common variables was measured at all sites.

Existing protocols developed in other areas or programs were adopted to obtain information on environmental variables, e.g. hydraulic variables from Newbury (1984) and Newbury and Gaboury (1993), riparian vegetation and logging extent from B.C. Ministry of Environment, Lands and Parks and Department of Fisheries and Oceans (1994), canopy coverage from G.A. Lamberti (University of Notre Dame, Notre Dame, IN, personal communication), and substrate analysis from Nielsen et al. (1983). The sampling of benthic algae on rocks for primary production (as measured by chlorophyll *a* concentration) and biomass (as measured by suspended carbon concentration) was a composite of methods described by Lamberti and Resh (1985), Turner et al. (1991), B.C. Ministry of Environment, Lands and Parks and Department of Fisheries and Oceans (1994), M.A. Turner (Freshwater Institute, Winnipeg, MB, personal communication), G.A. Lamberti (personal communication), and M.P. Stainton (Freshwater Institute, Winnipeg, MB, personal communication). Water samples were returned to the National Water Research Institute (NWRI) in Burlington for analysis of total suspended solids (TSS), total phosphorus, nitrate, and major ions (Cancilla 1994; Paquette et al. 1997), as were samples of fine bottom sediments taken for particle-size determination (Duncan and LaHaie 1979). Subsamples of benthic algae for chlorophyll *a* and suspended carbon measurements were returned to the Freshwater Institute for analysis according to Stainton et al. (1977).

Table 1.1. Summary of environmental variables that correlate with benthic invertebrate assemblage structure in lotic systems. + = variable measured; +++ = variable correlated with invertebrate assemblage structure. (Reprinted from Rosenberg et al. 1997b, with permission of the Society of Environmental Toxicology and Chemistry, Pensacola, FL).

Variable	United Kingdom ¹	Pacific Northwest ² (North America)	South Wales ³
Distance from source	+	+++	+++
Slope	+++	+	+++
Latitude		+++	
Altitude	+	+	+++
Discharge category	+++		+
Geology		+++	
Vegetation cover		+++	
Physiography		+	
Land use		+++	
Stream order			+
Mean channel width	+++	+	
Depth category	+		
Substrate heterogeneity	+		
Date	+	+++	
Water width	+	+++	
Water depth	+	+	+++
Surface velocity	+++	+	
Mean substrate	+++	+	+
Dominant particle size	+++		
% macrophyte cover	+++	+	
Overhanging vegetation		+++	
pH	+++	+	+++
Oxygen	+		
Nitrate	+		+++
Chloride	+++		
Phosphate	+++		+
Alkalinity	+++		+++
Conductivity		+++	+++

¹ Wright et al. (1984)

² Corkum and Currie (1987), Corkum (1989)

³ Ormerod and Edwards (1987)

Table 1.2. Environmental variables measured in the Fraser River biomonitoring program. Landscape, site/reach, channel/substrate, and water-column variables were used.

Landscape	Site/reach	Channel/substrate	Water-column
Latitude	Date of sampling	Wetted width	pH
Longitude	Flow state	Mean depth	Dissolved oxygen
Altitude	Macrophyte cover	Maximum depth	Conductivity
Ecoregion	Riparian vegetation ¹	Bankfull width	Temperature
Stream order	Grasses ²	Slope	Total phosphorus
	Shrubs ²	Water velocity (mean and max.)	Nitrate-nitrite and Kjeldahl nitrogen
	Conifers ²	Framework ³	Alkalinity
	Deciduous ²	Matrix ⁴	Total suspended solids
	Canopy cover	Interstitial material (%)	
	Extent of logging in riparian zone	Gravel	
		Sand	
		Silt	
		Clay	
		Embeddedness ⁵	
		Benthic algae biomass	
		Benthic algae chlorophyll <i>a</i>	

¹ Summed score of vegetation categories present: grasses = 1, shrubs = 2, conifers = 3, deciduous = 4

² Scored as present (1) or absent (0)

³ Diameter of dominant substrate (see Section 2 for details)

⁴ Diameter of next dominant substrate (see Section 2 for details)

⁵ Degree of exposure of dominant substrate (see Section 2 for details)

1.2.3 Benthic macroinvertebrates

Benthic invertebrate studies of the Fraser River catchment through mid-1993 have been summarized by Johansen and Reis (1994). However, the studies assembled by these authors have limitations in that: (1) most studies were done in the estuary of the river; (2) most of the studies of the middle Fraser River catchment were annual compliance surveys done by regulatory agencies; (3) data were collected using various methods; and (4) parameters measured and analyzed differed among sites (Johansen and Reis 1994). However, most of these data sets were of very high quality in terms of collection, storage, and analysis. These data coupled with the data collected in our study make an excellent source of background information for future research on the Fraser River catchment. Taxonomic keys that are appropriate for this region are presented in Johansen and Reis (1994).

The collection of benthic macroinvertebrates was the biomonitoring focus of the Fraser River study. Consequently, the choice of sampling gear, methods of processing the samples collected, and the level of taxonomic identification used were important aspects of the program.

1.2.3.1 Kick-net sampler

A triangular kick net (38.5 cm to the side) was chosen over other possibilities because it was inexpensive to construct and easy to transport and use. Simple equipment is also a feature of other large-scale monitoring programs (e.g. Wright et al. 1984; Wright 1995). The sampling method is described by Rosenberg et al. (1997a).

A calibration study was carried out on the Coldwater River, a tributary to the Nicola River (Fraser River catchment), in August of 1994 to determine the following operating characteristics of the kick net: (1) optimal number (1-10) of replicates; (2) optimal sampling time (1, 3, or 5 min); (3) differences among three operators; and (4) differences between two mesh sizes (200 μm and 400 μm).

To determine optimal number of replicates, ten 3-min kick-net samples were taken by the same individual in a riffle of the Coldwater River. The samples were sorted to family level and counted. Cumulative coefficients of variation (CV) were calculated for total numbers of organisms and numbers in four different insect orders (Plecoptera, Ephemeroptera, Trichoptera, and Diptera).

Operator differences were examined by having three individuals each take five 3-min replicates from the same riffle of the Coldwater River. The samples were sorted to family level and counted. Total numbers and numbers in major orders were compared using ANOVA.

The effect of sampling time was examined by one individual taking five replicate samples at each of 1-, 3-, and 5-min intervals from the same riffle of the Coldwater River. The samples were sorted to family level, counted, and expressed as organisms collected per minute of sampling effort. Total numbers and numbers in the major orders for the three time intervals were compared using ANOVA, and replicates were plotted in ordination space using Non-Metric Multidimensional Scaling (Belbin 1991) to reveal similarities and differences among the three time-intervals.

To compare collection efficiency of 200 μm versus 400 μm mesh, one individual collected five 3-min kick-net samples using each mesh size in a riffle of the Coldwater River. Counts were compared using ANOVA.

1.2.3.2 Sample processing

Sample sorting after the 1994 field season was the single factor limiting the timely production of data. Based on sorting three out of five replicates (see Results and discussion) from 22 sites, individual replicates took an average of five days to sort. Therefore, processing all five replicates from 50 sites would take ~5 person years. Clearly, the time required for processing had to be reduced, so the need for replication and the possibility of subsampling were examined.

1.2.3.2.1 Number of replicates re-examined

Cluster analysis (Unweighted Pair Group Mean Average [UPGMA]; Belbin 1993) was used to assess the significance of within-site variation (as indicated by among-replicate variation) compared to among-site variation for the three replicates sorted from the 22 sites.

1.2.3.2.2 Subsampling

The inordinate length of time required to process the 1994 samples led to further searches for cost-saving methods and the eventual adoption of the Marchant (1989) subsampling device and procedure. The subsampler is a box (35 X 25 X 10 cm) divided into 100 equal cells. An unsorted sample is placed into the box, the box is covered and shaken to distribute the sample evenly among the 100 cells, and cells are randomly sampled until a predetermined number of organisms (100, 200, or 300) is collected. The number of organisms in the entire sample is then estimated by extrapolation.

The adequacy of counting 100, 200, or 300 organisms was examined. A fourth replicate from each of four sites (out of the 22 sites for which three replicates had been sorted) was subsampled as described above. All 100 cells were counted for each of the four samples. Cells were then chosen at random until 100 organisms were counted; this was done five times. The same "simulation" was done using counts of 200 and 300 organisms. Counts of total numbers for the entire fourth replicate and estimated from counts of 100, 200, and 300 organisms were then compared to averages obtained from the mean of the previously sorted three replicates. Counts of families for the 100-, 200-, and 300-organism subsamples for the four sites examined were compared using ANOVA followed by Tukey's Multiple Comparison Test. Mean total abundances of the three replicates were compared to estimates generated by each subsample size using ANOVA.

1.2.3.3 Taxonomic level

The use of species-level identifications versus higher taxonomic levels in biomonitoring has been the subject of an ongoing debate (e.g. Resh and McElravy 1993). Of special concern to the Fraser River study is the eventual need by non-specialists to identify macroinvertebrates. Therefore, for the Fraser River material, we identified material to both family level and lowest-possible taxon (mostly genus and species) to enable evaluation of the relative performance of family-level and lower-taxon models in correctly predicting reference sites and in their ability to detect differences between reference and test sites (see Section 2, which only deals with family level).

1.2.3.4 Seasonal and annual variation

Most of the reference sites were visited only once, in autumn, because of the large geographic scale of the study. The autumn period was chosen because it represented a low-water period in the long-term hydrograph of the Fraser River, which was important in terms of accessibility to streams in the catchment.

Because predictive models developed from this reference database could, therefore, be constrained to an annual autumn sampling, we examined the effects of seasonal and annual variability on the accuracy of the predictive models (e.g. Reynoldson et al. 1995; Wright 1995). Seasonal variation was examined by sampling eight sites monthly over a two-year period (Dymond 1998; Reece et al., submitted). Results indicated unpredictable effects of season on the predictive models, so Dymond (1998) recommended that sampling should be restricted to the autumn or done over multiple seasons. Annual variation was examined by resampling 10% of the sites in years 2 and 3 of the study. More details of the study of seasonal and annual variability are presented in Section 2.

1.2.3.5 Toxicity testing

Testing focused on depositional areas of the river because organic contaminants tend to be associated with fine-grained sediments, which are typically found in depositional zones. Five sampling sites were located upstream and downstream of discharges from pulp mills at Prince George and Quesnel in 1994: (1) Fraser (FRA)11 - at Shelley, ~5 km upstream of Prince George; (2) FRA13 - at Woodpecker, ~50 km downstream of Prince George; (3) FRA14 - ~100 km downstream of Prince George and just upstream of Quesnel; (4) FRA16 - ~25 km downstream of Quesnel and subject to municipal effluents as well as discharges from two pulp mills; and (5) FRA28 - at Seabird Island, ~20 km downstream of Hope.

1.2.3.5.1 Methods

Five mini-ponar grab samples of sediment were taken at each site for laboratory testing. Each replicate was placed in a plastic bag and held, unpreserved, at 4°C until tests could be done (maximum storage time was two months).

Four species of benthic invertebrates were used to assess the status of Fraser River sediments: *Chironomus riparius* Meigen (midge larvae), *Hexagenia limbata* Serville (mayfly nymphs), *Hyalella azteca* (Saussure) (freshwater shrimps), and *Tubifex tubifex* (Müller) (freshwater worms). The effects of Fraser River sediment on survival (all four species), growth (*C. riparius*, *H. limbata*, *H. azteca*), and reproduction (*T. tubifex*) were measured in the NWRI laboratory using the procedures described by Borgmann et al. (1989), Reynoldson et al. (1991), Bedard et al. (1992), and Day et al. (1994). Reference data from the Great Lakes were used to establish limits for each of the test endpoints (e.g. *C. riparius* survival and growth) in one of three classes of toxicity: non-toxic, potentially toxic, and toxic (Reynoldson et al. 1997a). Attributes of Fraser River sediments such as particle size and organic matter content were similar to Great Lakes sediments, allowing the use of reference endpoints from the latter.

1.2.3.6 Quality assurance

Reference-condition research on the Fraser River used elements of care that should be characteristic of benthic research programs. These procedures are discussed under four headings: field steps, laboratory steps, data management, and variability of methods.

1.2.3.6.1 Field steps

Data collection is described in Reynoldson et al. (1998). Field crews were trained in a workshop prior to the start of sampling each year. Data collection in the field was regulated by using standard field forms at every site (Appendix 1). These field forms either required collection and entry of physical, chemical, or biological data, or provided checklists to ensure that nothing was omitted.

Most sample containers were labelled on tape applied to the outside so the containers could be reused. Paper labels were also added to the inside of containers holding biological samples. Type of sample, station number, and date of sampling appeared on all labels.

At each site sampled by a four-person team, two persons did the biological sampling and two did the physical and chemical sampling. The partner system provided an element of safety and served as a check to ensure that all samples were taken using proper procedures and that samples were accurately labelled.

1.2.3.6.2 Laboratory steps

All samples were accounted for upon arrival at NWRI or the Freshwater Institute by checking them against the field sheets. Samples were then sent to the appropriate laboratories in either the NWRI (water, sediment, benthic macroinvertebrates) or the Freshwater Institute (benthic algae) (see above).

Benthic macroinvertebrate samples were processed according to the following protocol: (1) the sample was confirmed by checking its internal label; (2) large pieces of debris were removed, washed, and checked for remaining organisms; (3) the sample was rinsed through a 250- μ m sieve and 200 organisms were subsampled by using either the Marchant (1989) method or the Sebastien et al. (1988) method if large quantities of filamentous algae or mosses were present; and (4) the unsorted residue was preserved in 70% ethanol and stored for future reference.

Acceptable sorting efficiency was set at 90%. Initial samples sorted by new staff were resorted to ensure that this level was achieved. Random monthly checks were done on all sorters; recoveries of 95-99% were maintained.

Identifications of macroinvertebrates to lower taxa were done by one person (C. Logan). Identified taxa were preserved separately in a completely labelled one-dram vial. Identifications were recorded on laboratory sheets, which were submitted for data entry (see below). New taxa were submitted to acknowledged experts for verification. Misidentifications were corrected; they were generally <10% (determined by dividing the number of misidentifications by the total number of specimens submitted for verification). Voucher collections of all species are maintained at the NWRI (Environment Canada, 867 Lakeshore Road, Burlington, ON L7R 4A6; contact: T.B. Reynoldson) and the Royal British Columbia Museum (675 Belleville Street, Victoria, B.C. V8V 1X4; contact: J. Cosgrove), and are available for consultation purposes.

1.2.3.6.3 Data management

All Fraser River data are kept in the **Benthic Information system for Reference Conditions** (BIRC, Pascoe and Reynoldson 1998), which uses a relational database design to manage the large volume of information associated with the Fraser River reference-condition models. Relational design manages large volumes of data more efficiently than a simple spreadsheet, minimizes duplication, and permits the rapid recall and manipulation of stored data (Silberschatz et al. 1997).

BIRC uses Microsoft Access™ as its foundation, which maintains data in a series of linked tables; information is stored in a hierarchical format. Primary grouping of information is based on unique study names that are assigned by the user; individual sampling locations within each study are assigned unique identification numbers, and site data are entered into the appropriate table (e.g. benthic taxon counts, water chemistry, etc.). Data hierarchy/relational structure is maintained automatically through the implementation of a graphic user interface (GUI). Based on a series of menus and forms, the GUI also automates data entry, limiting errors normally associated with this process. Calculations such as average number of organisms in replicate samples are done by the system, and acceptable ranges for variables are enforced. A master list of taxon names is also maintained, which accelerates data entry and eliminates errors in spelling; a taxon coding system allows data to be generated at a number of different taxonomic levels.

1.2.3.6.4 Variability of methods

Ten percent of the sites sampled each year were sampled three times (i.e. all measurements of physical and chemical variables and all collections of biological material) to assess replicability of methods. Coefficients of variation were calculated for selected variables and mean CVs were calculated over the three years of the study.

1.3 Results and discussion

1.3.1 *Site selection*

Major subcatchments of the Fraser River from which reference and test sites were chosen and sampled over the three years of the study are listed in Table 1.3, which also lists the ecoregions through which the Fraser River and its tributaries flow. The Fraser mainstem flows through seven ecoregions; individual tributaries flow through a maximum of three ecoregions.

Two-hundred and twenty-two reference sites and 48 test sites were sampled over the three years of the study (Fig. 1.1): 37 reference and nine test sites in 1994, 89 reference and 12 test sites in 1995, and 96 reference and 27 test sites in 1996. Nine sites were resampled each year to measure annual variability, and 21 sites were sampled in triplicate to provide information on intrasite variability of methods.

1.3.2 *Benthic macroinvertebrates*

1.3.2.1 Kick-net calibration

1.3.2.1.1 *Optimal number of replicates*

Cumulative CVs for total numbers, and numbers of Plecoptera, Ephemeroptera, Trichoptera, and Diptera for 10 replicates indicated that CVs for total numbers stabilized at 3-5 replicates; for numbers of Plecoptera, Ephemeroptera, and Trichoptera at 4-5 replicates; and for numbers of Diptera at 3-4 replicates (Fig. 1.2). Consequently, because of the asymptotic trends shown, five replicates were collected during the 1994 pilot study.

1.3.2.1.2 *Operator differences*

No significant differences ($p > 0.05$; ANOVA) existed among the three operators in terms of total numbers or numbers in the four major orders collected (Fig. 1.3). The apparent robustness of the kick-net sampling method was reassuring because there was no difference between inexperienced operator 3 and the other two experienced operators.

Table 1.3. Subjective categorization of impacts in major subcatchments of the Fraser River (N - non-impacted, M - moderately impacted, I - impacted; ecoregions after B.C. Ministry of Environment, Lands and Parks 1991).

Subcatchment	Site code	Ecoregion ¹	Use as reference (R)/ test (T) site		Impact	Year sampled
Fraser headwater tributaries	UFR		R	N		1995
Fraser mainstem	FRA					1994, 1995, 1996
- upstream of McBride		SRMT, WCR	R	N		
- McBride to Prince George		SMRT, FB	R ²	M - logging		
- Prince George to Marguerite		FB	T	I - pulp mills		
- Marguerite to Lytton		FP, ITR	T	M - logging, pulp mills M - agriculture		
- Lytton to Hope		ITR, PR	T	I - agriculture, logging,		
- Hope to Mission		PR, LM	T	urban M - logging		
Torpy	TOR	ECR	R			1996
Bowron	BOW					
- Upper		SRMT	R	N		1996
- Lower		FB, SRMT	T	M - logging		
- Willow	WIL	SRMT	T	I - logging, mining		1994, 1996
McGregor	-	ECR		M - logging		
Herrick	HRK	ECR	R	N		1995
Nechako	-					
- upstream of Vanderhoof		FP		M - agriculture, logging, hydro development		
- downstream of Vanderhoof		FB		M/I - agriculture, logging		
Chelaslie	CLA	FP	R	N		1995
Stuart	STU	OM, FB	R	N		1994
Chilako	-	FB, FP		N		
West Road	WRD	FP	R	N/M - some ranching, fishing camps, tourism N - some ranching		1996
Euchiniko	EUC	FP	R	N/M - logging,		1996
Nazko	-	FP		ranching		

Subcatchment	Site code	Ecoregion ¹	Use as reference (R)/ test (T) site	Impact	Year sampled
Quesnel	-	SRMT, FP, FB		M - logging, mining	
		SRMT		M - mining, logging	
Cariboo	-			M - logging, fishing	
		FP		camps, ranching	
Horsefly	-				
Chilcotin (upstream of Chilcotin Lake)	CHI	FP	R/T	N/M - logging (new), canoeing, ranching	1994
				M - ranching, logging	
Big Creek	-	CR, FP			
				M - old logging, mining	
				M - old logging,	
Taseko	TAS	CR, FP	R ²	rafting, ranching,	1996
				fishing lodges	
Chilko	CKO	CR, FP	R ²	M - old logging,	1996
				ranching	
Chilanko	-	FP			
Bridge	-	ITR		M/I - hydro development	
Tyaughton	TYA	CR, ITR	R/T	N/M - logging	1996
Stein	STN	ITR	R	N	1995
Thompson (downstream of Kamloops)	TOM	T-OP, ITR	R ²	I - agriculture, transport, pulp mills, urban	1995
Bonaparte	-	FP, ITR, T-OP		I - agriculture, logging, urban	
Deadman	DEA	FP, T-OP	T	M - agriculture, logging	1996
Nicda	NIC	T-OP	R ² /T	I - agriculture, logging, urban	1995
Guichon	GUI	T-OP	T	I - mining, agriculture	1996

Subcatchment	Site code	Ecoregion ¹	Use as reference (R)/ test (T) site	Impact	Year sampled
Coldwater	CLD	T-OP, ITR	R ²	M - agriculture, logging	1995, 1996
North Thompson	-	T-OP, CMH		M - logging, urban, agriculture	
Clearwater	CLR	FP, CMH, T-OP	R	N - except lower	1994
South Thompson	-	T-OP, CMH		M/I - agriculture, logging	
Adams	-	CMH, T-OP		N	
Salmon	SAL	T-OP	T	I - agriculture, logging	1994
Harrison/Lillooet	-	PR		M/I - logging, urban	
Lillooet (upstream of Pemberton)	LIL	PR	R ²	M/I - logging	1995
Chehalis	CHH	PR	R ²	I - logging	1996
Pitt (upstream of Pitt Lake)	PIT	PR	R	N/M - logging	1994

¹ SRMT = Southern Rocky Mountain Trench; WCR = Western Continental Ranges; FB = Fraser Basin; FP = Fraser Plateau; ITR = Interior Transition Ranges; PR = Pacific Ranges; LM = Lower Mainland; ECR = Eastern Continental Ranges; OM = Omineca Mountains; CR = Chilcotin Ranges; T-OP = Thompson-Okanagan Plateau; CMH = Columbia Mountains and Highlands

² Sites sampled in undisturbed areas, so reference classification retained

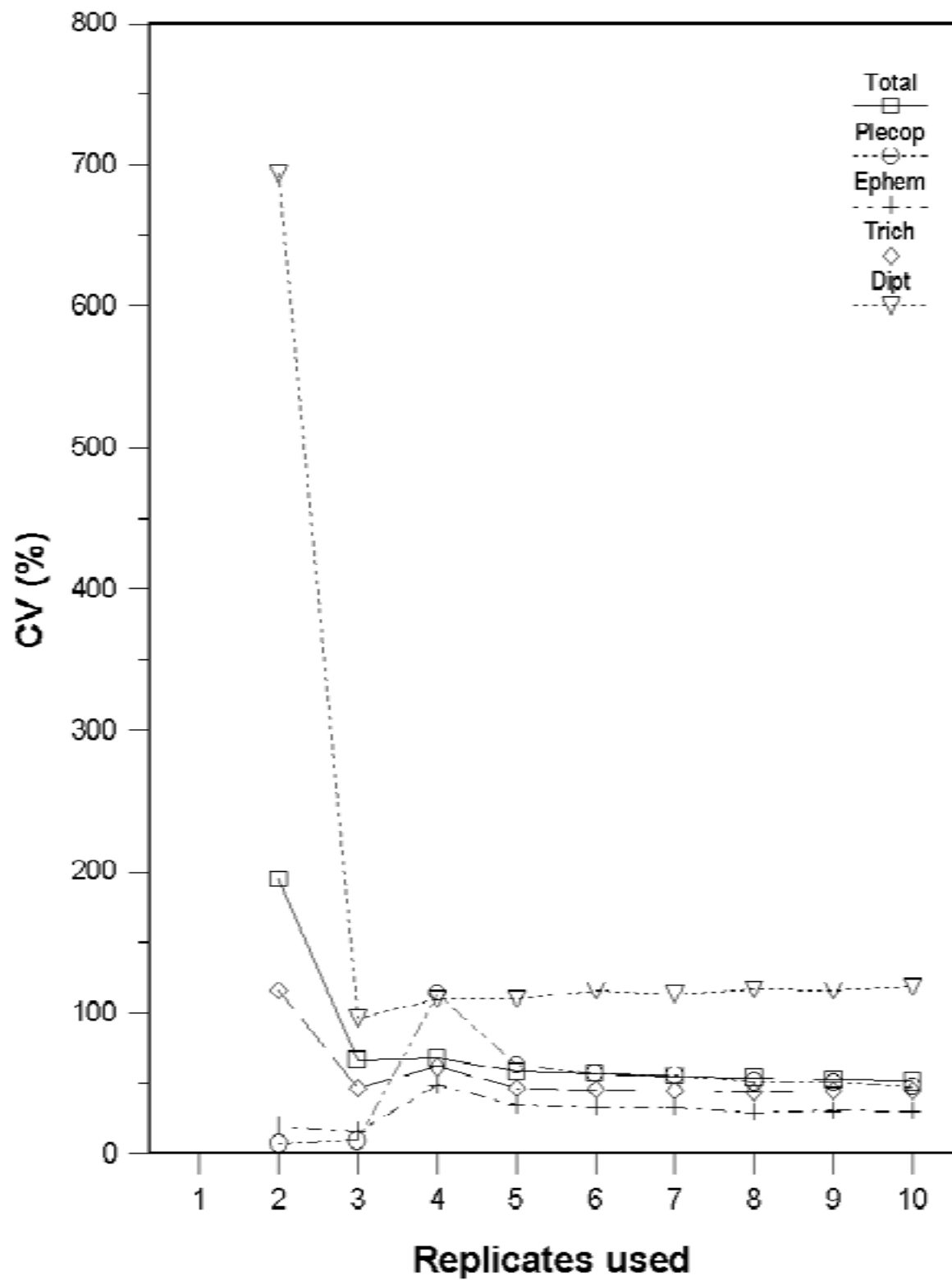


Figure 1.2 Cumulative coefficients of variation (CV) for 10 replicate kick net samples taken in a riffle of the Coldwater River. Replicates were generally pooled in an order that maximized variability (i.e. low, high, low, etc. counts).

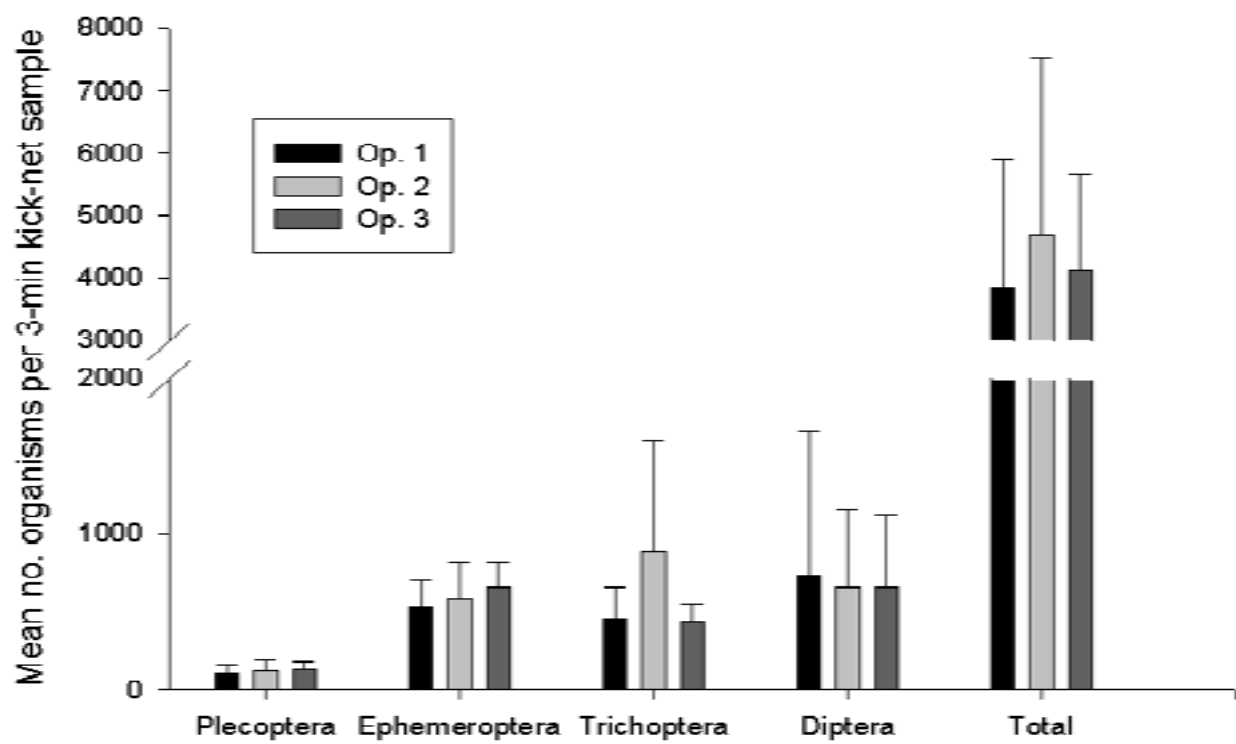


Figure 1.3 Mean numbers (+ 1 SD) of organisms collected in kick-net samples by three different operators (Op.) in a riffle of the Coldwater River.

However, some minor differences were detected for operator 3: out of 10 major taxa (order or class) and 12 families, operator 3 collected significantly ($p < 0.05$) more individuals in four groups (Hydracarina, Chloroperlidae, Tipulidae, Simuliidae) than the other two operators. No differences existed between operators 1 and 2.

1.3.2.1.3 *Sampling time*

No significant differences ($p > 0.05$; ANOVA) existed among the three time-intervals for total numbers or numbers in the major orders, which were all corrected to reflect $\text{no} \cdot \text{min}^{-1}$ (Fig. 1.4A). However, the number of taxa collected in 1-min samples was significantly ($p < 0.05$) lower than in the 3- and 5-min samples. For example, Pteronarcidae, other unidentified Plecoptera, and Athericidae were absent from the 1-min samples. The similarity between 3- and 5-min samples was verified in the plots of replicates in ordination space (Fig. 1.4B). Therefore, 3 min was adopted as the standard collection time.

1.3.2.1.4 *Mesh size*

The 200- μm mesh nets retained significantly higher numbers of invertebrates than the 400- μm mesh nets ($p < 0.05$; ANOVA), especially Ephemeroptera and Trichoptera (Fig. 1.5). Baetidae, Leptoceridae, and Hydroptilidae were the families most responsible for these differences. Other taxa (Platyhelminthes, Hydracarina, and unidentified Diptera) were also collected in significantly ($p < 0.05$) higher numbers in the finer mesh. Despite these individual quantitative differences, the overall number of taxa collected was similar in both mesh sizes ($p > 0.05$). Consequently, we decided to use 400- μm mesh for the remainder of the study for purely practical reasons: the 200- μm -mesh samples took $\sim 8 \text{ d} \cdot \text{replicate}^{-1}$ to process, which precluded the use of this mesh size in a large-scale study.

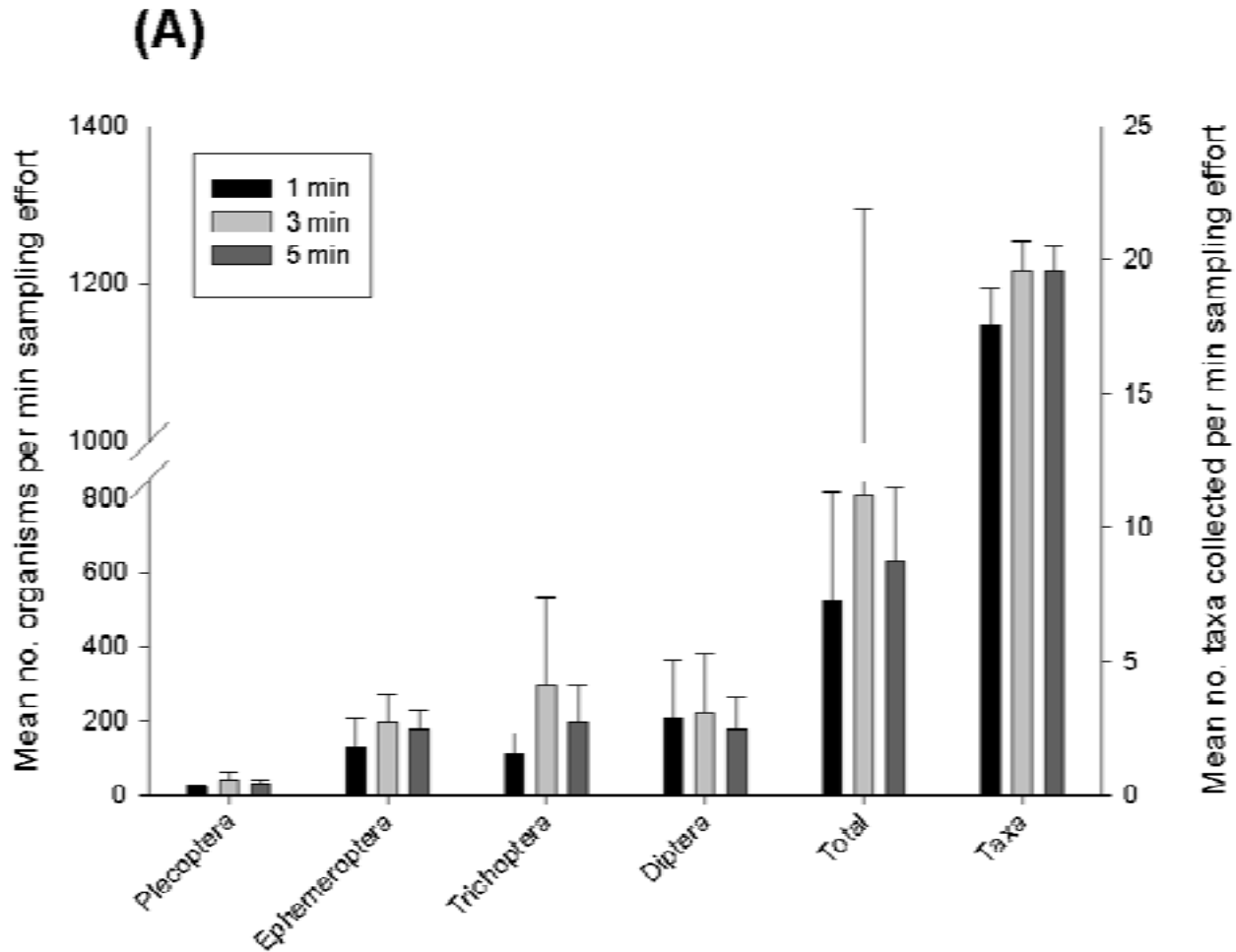
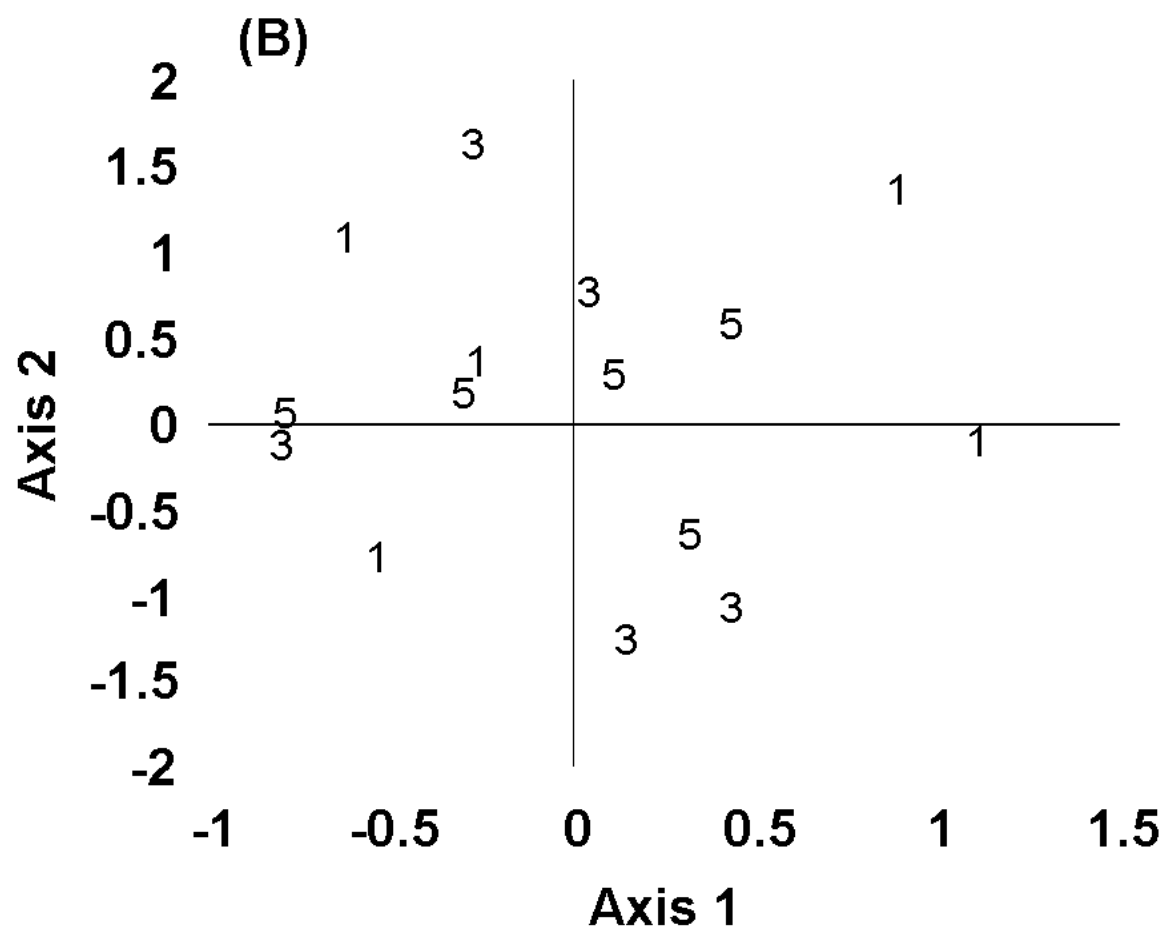


Figure 1.4 (A) Effect of sampling time (1, 3, and 5 min) expressed per unit of time on mean numbers (+1 SD) of organisms and mean numbers (+1 SD) of taxa collected by kick nets from a riffle of the Coldwater River. (B) Comparison of kick-net sampling times (1, 3, and 5 min) examined in ordination space (Non-Metric Multidimensional Scaling).



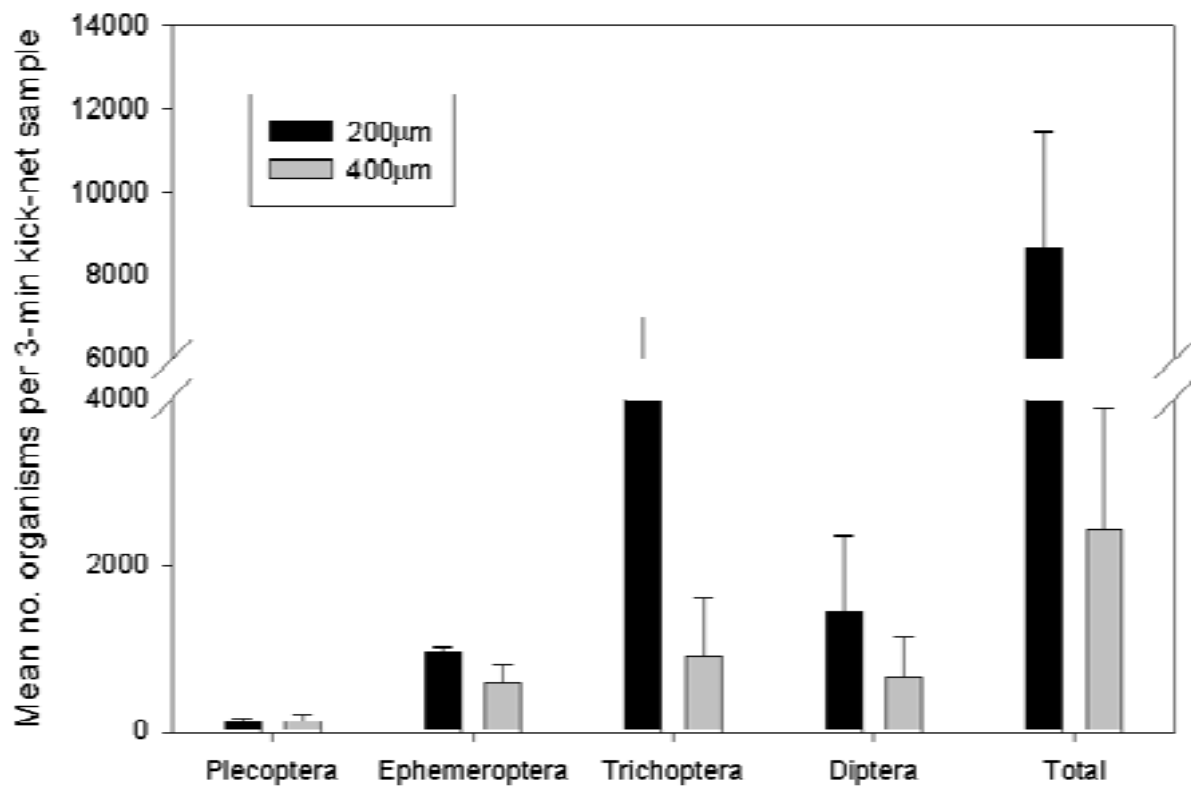


Figure 1.5 Mean numbers (± 1 SD) of organisms collected by two mesh sizes (200 μm , 400 μm) used in kick-net samples taken in a riffle of the Coldwater River.

In summary, based on the 1994 calibration study, it was decided that five replicate kick-net samples would be collected at each site (this number was subsequently changed: see below), the time of collection was generally 3 min, one person took all the kick-net samples to avoid possible operator inconsistency, and 400- μ m mesh was used. In practise, however, a number of modifications were made. For example, 1994 samples were sometimes taken for only 1 min because the net became clogged with organic debris when operated for 3 min; consequently, counts for all samples were standardized to a 3-min unit.

1.3.2.2 Sample processing

1.3.2.2.1 *Number of replicates*

The comparison of within-site to among-site variation (Fig. 1.6) indicated much greater among-site variation than within-site variation. The three replicates from each site grouped together for 21 out of 22 sites; only one replicate from station 1 on the Clearwater River (CLR1) did not group with its mates. Given this result and an emphasis of the study on regional-scale assemblages, we decided that single replicates were adequate for site characterization. Consequently, the protocol for 1995 and 1996 was changed to one 3-min kick-net sample at each site.

1.3.2.2.2 *Subsampling*

Total numbers of individuals estimated from counts of 100, 200, and 300 organisms were similar to each other and to the actual number in the sample (Fig. 1.7). Comparisons of family counts among the 100-, 200-, and 300-organism subsamples for the four sites examined revealed only one significant difference out of 72 possibilities (Site CHI1; ANOVA followed by Tukey's Multiple Comparison Test). Higher variability was obvious in comparing mean total numbers of organisms in three replicates with the mean numbers estimated from the completely sorted fourth replicate and the subsampled counts (Fig. 1.7). However, comparisons between the mean of three replicates and estimates generated by different subsample sizes revealed a significant difference ($p < 0.05$; ANOVA) for only the FRA1 site.

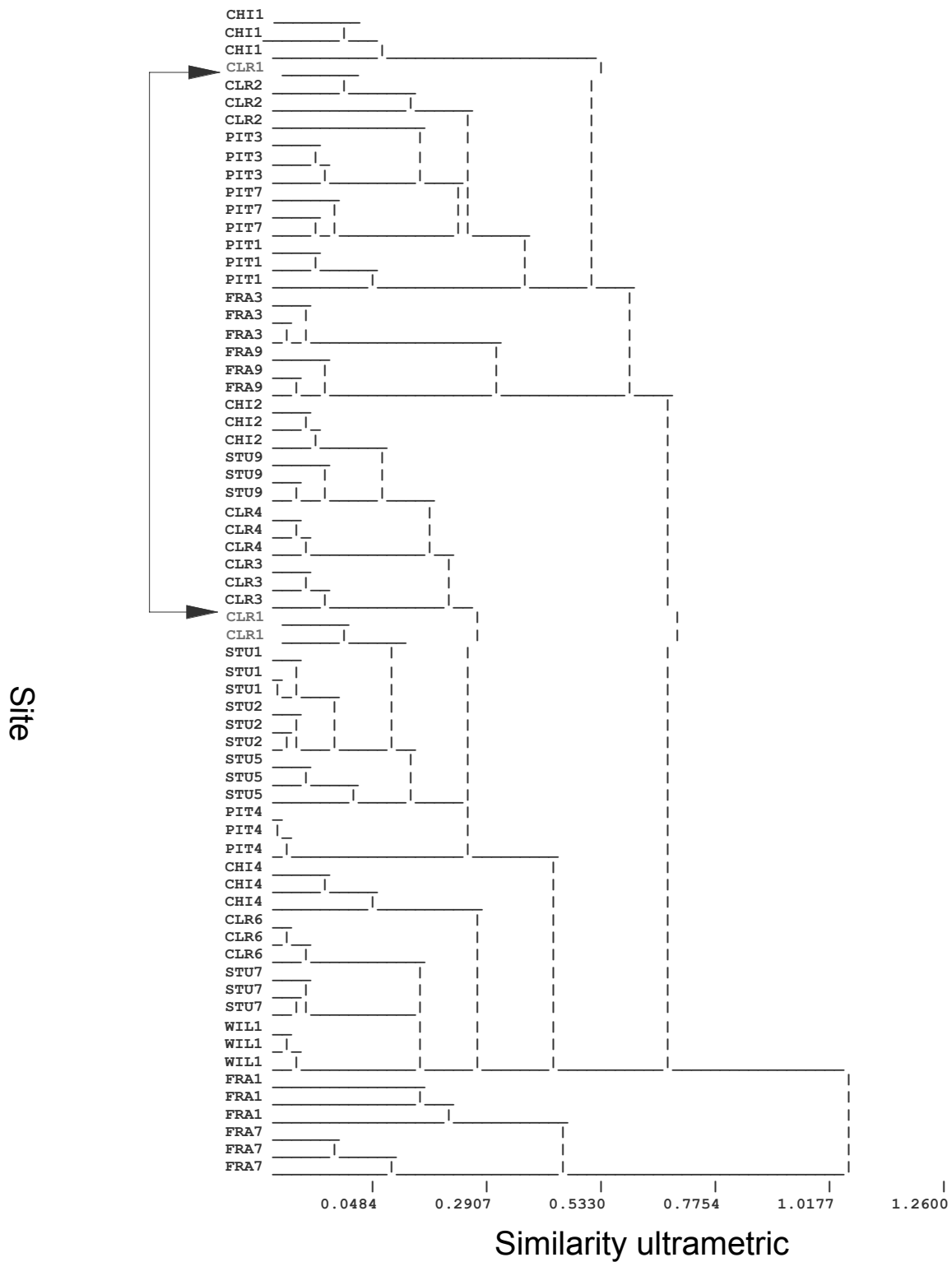


Figure 1.6 Cluster-analysis dendrogram comparing within-site variation (three replicates) to among-site variation (22 sites) for kick-net samples taken from the Fraser River catchment, 1994. Arrows show separation of the Clearwater River station 1 replicates. Site abbreviations appear in Table 1.3

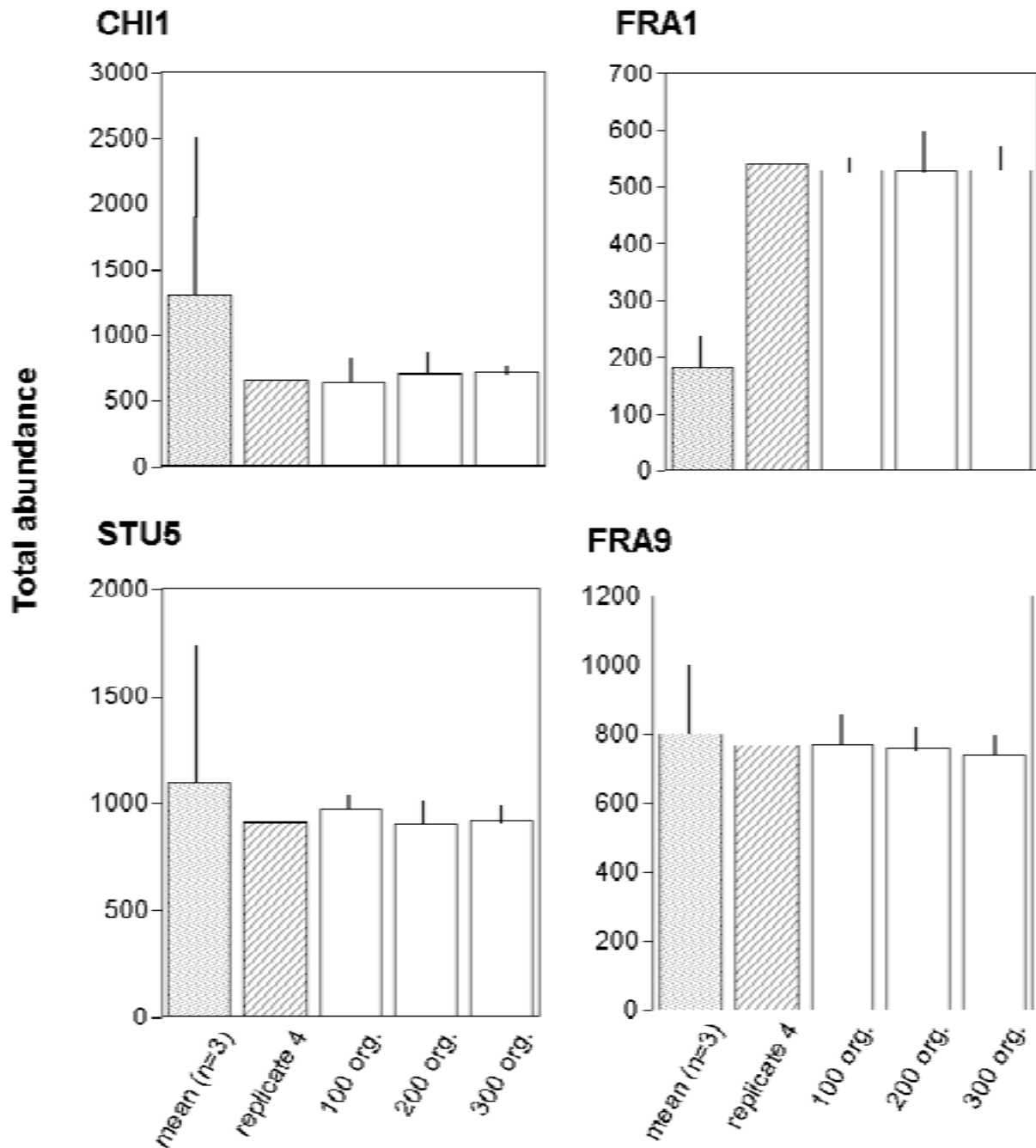


Figure 1.7 Comparison of mean total numbers estimated from three subsample sizes (100, 200, and 300 organisms [org.]) with total numbers of a completely sorted replicate (replicate 4), and mean total numbers of three completely sorted replicates. Kick-net samples came from four sites in the Fraser River catchment (site abbreviations as in Table 1.3). Vertical bars are +1 SD.

In terms of taxa richness, the subsamples usually had fewer families than either the completely sorted fourth replicate or the three-replicate set (Table 1.4). However, the missing families consisted of rare organisms (Table 1.5), and the 100-, 200-, and 300-organism subsamples captured all families that represented >5% of the sample. The 100-organism subsample was least accurate for families that represented <5% of the sample; it only captured 88% of families representing 1-5% of the sample and 36% of families representing <1% of the sample. In contrast, the 200- and 300-organism subsamples captured all of the families representing 1-5% of the sample, and 46% (200-organism subsample) and 70% (300-organism subsample) of families representing <1% of the sample. In any event, rare taxa are excluded from pattern analysis because they add noise to the overall assemblage characterization (Faith and Norris 1989) so the loss of such families in the subsampling procedure was not considered to be a major problem. Consequently, the 200-organism subsample was chosen. These subsamples required an average of 4 h to sort and identify compared to 6 h for a 300-organism subsample.

By taking a single sample at each site and subsampling 200 organisms from that sample, an ~30-fold saving in time (cf. ~20-fold for 300 organisms) was achieved compared to sorting and identifying three (out of five) full replicates per site. Hence, a single sample that was eventually subsampled was the approach used for the remainder of the study.

Thus, the macroinvertebrate protocol that resulted from the calibration study on the Coldwater River, sampling during the 1994 field season, and subsequent laboratory analyses can be summarized as follows: (1) one kick-net sample per site; (2) a net mesh of 400 μm ; (3) only erosional areas (riffles) sampled; (4) a 3-min sampling period; (5) a 200-organism subsample taken from each sample; and (6) identification of macroinvertebrates to both family and lowest- possible taxon.

Table 1.4. Number of families of invertebrates in the three-replicate set, the completely sorted fourth replicate, and estimated by subsampling. Site abbreviations as in Table 1.3.

Site	3-replicate set	4th replicate	Subsample (mean \pm 1 SD)		
	(mean \pm 1 SD)	(total)	100	200	300
CHI1	12.7 (0.6)	12	9.2 (1.5)	9.0 (0.9)	10.8 (0.7)
FRA1	6.0 (1.0)	12	6.5 (1.5)	6.7 (0.7)	9.3 (1.2)
FRA9	9.0 (1.0)	10	7.0 (1.5)	7.5 (2.1)	8.7 (1.1)
STU5	17.7 (1.5)	16	11.3 (0.5)	11.0 (1.0)	11.8 (0.8)

Table 1.5. Effects of subsampling on occurrence of families of macroinvertebrates.

Contribution of numbers of organisms in a family to the whole sample (%)	Number of families in each category (4 pooled sites)	% occurrence (± 1 SD) in a subsample (4 pooled sites) ¹		
		Subsample size		
		(No. of organisms)		
		100	200	300
<1	28	36(28)	46(36)	70(28)
1-5	9	88(14)	100(0)	100(0)
5-10	3	100(0)	100(0)	100(0)
>10	10	100(0)	100(0)	100(0)

¹ CHI1, FRA1, FRA9, STU5 (abbreviations as in Table 1.3)

1.3.2.3 Toxicity testing

Tests using the four invertebrate species provided no evidence of sediment-related toxicity attributable to pulp mill discharges for the Fraser River depositional sites sampled. Reduced survival and growth of *H. limbata* occurred at two mainstem sites, FRA11 and FRA13, and reduced growth occurred at FRA28; however, these results were caused by the suboptimal particle size of sediments present in the Fraser River. *Hexagenia* prefer silty substrate; the substrates at the above locations had a high sand content. Enhanced growth in *C. riparius* and *H. azteca*, and enhanced reproduction in *T. tubifex* at FRA14 and FRA16 sites suggested an enrichment effect by pulp mill discharges. Based on the absence of toxic effects, we considered further toxicity testing to be unnecessary, and eliminated this component from the Fraser River study.

1.3.3 Variability of methods

Methods of measuring channel morphology (e.g. bankfull width, channel depth) and discharge had low CVs (~5-10%), whereas measures of substrate composition (~10-87%) and benthic algae (~35%) were more variable (Table 1.6A). Characteristics of the substrate and biomass of benthic algae are naturally patchy, so the high CVs for these variables are not surprising.

All water variables had CVs <25% (Table 1.6B). The lowest CVs in the variability study were obtained for physical measurements such as pH (0.26%) and dissolved oxygen (0.91%). Nutrients and total suspended solids had much higher CVs (~22-24%).

We also checked the variability of the benthic macroinvertebrate collections by calculating CVs for two variables (Table 1.6C). Abundance (number collected per unit time) had a mean CV = 32.30% and number of families had a mean CV = 13.38%. These values are less than typical for macroinvertebrate sampling (e.g. Resh 1979), probably because kick-net sampling integrates habitat patches. The values yield confidence in model calculation using macroinvertebrate data (see Reynoldson et al., submitted).

Table 1.6. Mean coefficients of variation (CV) for selected variables from the Fraser River study (see Table 1.2).

Variable	Average CV (%)	Number of sites
A: Channel		
Bankfull width	8.28	24
Mean depth	4.49	24
Maximum depth	5.56	24
Discharge	9.50	20
Substrate composition:		
% gravel	44.86	14
% sand	10.23	14
% silt/clay	87.32	14
Chlorophyll <i>a</i>	37.51	6
Suspended carbon	35.29	10
B: Water		
pH	0.26	20
Dissolved oxygen	0.91	23
Conductivity	0.87	17
Temperature	0.39	19
Total phosphorus	21.80	24
Nitrate	24.16	24
Alkalinity	5.72	24
Total suspended solids	23.91	24
C: Benthic invertebrate		
Abundance	32.30	21
Number of families	13.38	21

1.4 Summary

The reference-condition approach to water-quality assessment is ideal for large-scale studies, and it is currently being used in this way in the U.K. and Australia (Reynoldson et al. 1997b). In Canada, it has been applied to the Laurentian Great Lakes (Reynoldson et al. 1995) and, now, the Fraser River catchment.

The design of the Fraser River study may serve as a model for other countries (given the size of the Fraser River catchment) or regionally based biomonitoring programs. Essential elements of any program were considered in this section: (1) the choice of reference and impaired sites; (2) environmental variables to be measured at each site; and (3) the development of efficient and cost-effective protocols for sampling and processing benthic macroinvertebrates. Development of family-level reference-condition models for the full complement of reference sites from the Fraser River catchment, the ability of the models to discriminate impaired sites, and seasonal and annual variability are discussed in the next section.

2. DEVELOPMENT OF PREDICTIVE MODELS OF INVERTEBRATE ASSEMBLAGE STRUCTURE

2.1 Introduction

The use of the reference-condition approach in biomonitoring requires the development of a large database of reference sites with information collected on the assemblage of invertebrates present at each site and information on a matching set of habitat descriptors. From this reference database empirical models can be constructed that permit the prediction of the assemblage of invertebrates expected to occur at a site with particular habitat attributes. This approach for describing the expected assemblage of invertebrates at a site was first applied in freshwater systems by Wright et al. (1984). The reliable prediction of the type of

assemblage to be expected at a site using habitat descriptors can serve as a baseline against which a site that is suspected of being exposed to either chemical or physical stress can be assessed. The primary objective of our study was the development of a predictive model for invertebrate assemblages that could be used as the basis of a biomonitoring program for the Fraser River catchment. We used the **BE**nthic **A**ssessment of **S**edimen**T** (BEAST) methods, first described by Reynoldson et al. (1995) for the Laurentian Great Lakes, in fulfilling this objective.

This section describes: (1) the results of sampling invertebrate assemblages and habitats from more than 200 reference sites; (2) the development of a predictive model using the reference condition from the reference-site database at the family taxonomic level; and (3) examples of the assessment of test sites exposed to different stressors.

2.2 Methods

2.2.1 Study area and sampling sites

Details of the study design and methods used in site selection, sampling, and data collection were presented in the previous section. Reference and test sites were chosen with the aid of local experts to represent the diversity of ecoregions and stream orders in the Fraser catchment. A total of 222 reference sites was sampled over the three-year study period, together with 48 test sites, 21 of which were related to specific human activities (agriculture, logging, and mining) and eight sites that were sampled seasonally (Fig. 1.1). Three of the 222 reference sites were excluded from further analyses because they represented a moss-covered habitat and had a unique assemblage of organisms. Additional sampling of sites representing this habitat would allow their inclusion in future models. Therefore, a final set of 219 reference sites was used in the data analyses.

2.2.2 Sampling methods

Benthic invertebrates were sampled at each site by taking a single kick-net sample (400- μ m mesh) of 3-min duration (Section 1). From each sample, using a 100-cell Marchant box (Marchant 1989), a 200-organism subsample was counted and organisms were identified to the lowest possible taxon. The number of cells required to provide a 200-organism subsample was recorded, and the count for a site was adjusted back to a whole-sample estimate to provide the relative abundance at each site. Data were recorded as the number of organisms per 3-min kick sample.

Forty environmental variables were measured at each site (Table 2.1). These variables were selected based on consideration of relevant literature and represented four different categories of variables (landscape, site/reach, channel/substrate and water-column) (Section 1).

2.2.3 Data analysis

Reynoldson et al. (1997b) described the use of reference sites for characterizing the biological conditions of a region, and how test sites are compared to an appropriate subset of the reference sites. Multivariate statistical methods were used for classifying the reference sites, matching test sites with appropriate reference sites, and comparing test sites and reference sites to determine impairment.

2.2.3.1 Assemblage descriptors and taxonomic resolution

The reference-condition approach uses taxonomic counts (e.g. numbers of taxa present, presence or absence of taxa) or a set of derived measures (metrics) to describe the invertebrate assemblage.

Table 2.1. Environmental variables measured in the Fraser River biomonitoring program. The 29 variables used in data analyses are identified (bold), together with their abbreviations and some information on data collection. asl = above sea level.

Environmental variable	Abbreviation	Unit of measurement or no. of categories	Footnote
Landscape			
Latitude	LAT	decimal degrees	1, 2
Longitude	LON	decimal degrees	1, 2
Altitude	ALT	m asl	1, 2
Ecoregion	ECOR	11 categories	1
Stream order	SORD	7 categories	1
Site/reach			
Date of sampling		1-365	
Flow state	FLOW	3 categories	3
Macrophyte cover	MCPHYT	5 categories	4
Grasses	GRASS	2 categories	5
Shrubs	SHRUB	2 categories	5
Conifers	CONIF	2 categories	5
Deciduous	DECID	2 categories	5
Riparian vegetation	RIPAR	1-10	6
Canopy cover		percent	7
Extent of logging in riparian zone		5 categories	4
Channel/substrate			
Wetted width	WIDTH	m	
Mean depth	MNDEP	cm	8
Maximum depth	MXDEP	cm	8
Bankfull width	BNKWI	m	
Slope	SLOPE	m·m ⁻¹	
Mean water velocity	MNVEL	m·s ⁻¹	9
Maximum water velocity	MXVEL	m·s ⁻¹	9
Framework	FWORK	7 categories	10
Matrix	MTRX	7 categories	11
Embeddedness	EMBED	5 categories	12
Interstitial material			
Gravel	GRVL	percent	13
Sand	SAND	percent	13
Silt	SILT	percent	13
Clay	CLAY	percent	13
Benthic algae biomass		mg·L ⁻¹	14
Benthic algae chlorophyll a		mg·L ⁻¹	14
Water-column			
pH	PH		
Dissolved oxygen	DO	mg·L ⁻¹	
Alkalinity	ALK	mg·L ⁻¹	
Conductivity	COND	µS·cm ⁻¹	
Temperature		°C	
Total phosphorus	TP	mg·L ⁻¹	
Nitrate-nitrite	NO3	mg·L ⁻¹	
Total Kjeldahl nitrogen	TKN	mg·L ⁻¹	
Total suspended solids	TSS	mg·L ⁻¹	

1. Obtained from 1:250,000 topographic maps
2. Using on-board GPS
3. Recorded as: 1, riffle/rapids; 2, straight run; 3, pool/back eddy
4. Recorded as: 1, 0%; 2, 0-25%; 3, 25-50%; 4, 50-75%; 5, 75-100%
5. Recorded as present (1) or absent (0)
6. Summed score of 4 vegetation categories present. Grass 1, Shrubs 2, Conifers 3, Deciduous 4
7. Based on visual observation of the site
8. Based on sampling area; in wadeable streams represents the complete channel
9. Based on a minimum of 5 estimates with a flowmeter
10. Dominant particle size in sampling area: 1, <0.2cm; 2, 0.2-0.5 cm; 3, 0.5-2.5 cm; 4, 2.5-5 cm; 5, 5-10 cm; 6, 10-25 cm; 7, >25 cm
11. Material surrounding dominant particles: 1, <0.2cm; 2, 0.2-0.5 cm; 3, 0.5-2.5 cm; 4, 2.5-5 cm; 5, 5-10 cm; 6, 10-25 cm; 7, >25 cm
12. Estimated in sampling area: 1, completely embedded; 2, 75% embedded; 3, 50% embedded; 4, 25% embedded; 5, unembedded
13. From sedigraph particle size analysis (Duncan and LaHaie 1979) of the interstitial material
14. Based on a mean value of a 4-cm diameter sample taken from 3 separate rock surfaces (Section 1)

Multivariate methods for describing and classifying assemblages use either presence/absence of taxa, as in the U.K. (Wright et al. 1984) and Australia (Parsons and Norris 1996; Simpson and Norris 2000), or quantitative abundance counts, as in Canada (Reynoldson et al. 1995, 1997b; Rosenberg et al. 2000) to describe the assemblage. A second approach to using reference conditions is based upon additive indices from a subset of derived measures (e.g. number of taxa, percent Ephemeroptera) and is used widely in the U.S. (Karr 1991; Barbour et al. 1995, 1996). This approach is discussed in detail in the third section of the report.

Reynoldson et al. (submitted) examined the performance and practicality of both raw taxonomic counts at the species, genus, and family levels as well as genus/species and family metrics in predictive models. Reynoldson et al. (submitted) suggested that the family level is the most appropriate for use in the assessment of invertebrate assemblages in the Fraser River catchment, and in this report we have only described the development and application of models using family-level taxonomic counts.

2.2.4 Classification of reference sites

Classification methods were used to describe the biological structure of invertebrate assemblages in the Fraser River catchment. The abundance count for each family from a 3-min kick-net sample was used as a descriptor of the benthic invertebrate assemblage. Faunal data were not transformed because the subsampling procedure provided proportional representation and we wanted to weight numerically dominant taxa. The Bray-Curtis association measure was used as an association metric for the benthic invertebrate counts because it performs consistently well in a variety of tests and simulations using different types of data (Faith et al. 1987; Jackson 1993).

The reference sites were clustered using an agglomerative hierarchical fusion method with Unweighted Pair Group Mean Averages (UPGMA). The appropriate number of groups was selected by examining the group structure and, particularly, the spatial location of the groups in ordination space.

A minimum group size of 10 sites was selected and used as the stopping rule for the classification. Groups formed with fewer than 10 sites were considered to be too small to sufficiently describe normal variability for comparison with test sites.

Ordination was also used to describe and explain the variability observed among the large number of taxa with a reduced number of new variables (ordination axes). A Hybrid Multi-Dimensional Scaling (HMDS) method of ordination was used, i.e. semi-strong-HMDS (Belbin 1991). Multi-dimensional scaling methods can use either metric or non-metric rank-order information. The hybrid technique incorporates both metric and non-metric scaling (Faith et al. 1987). Metric-scaling methods assume that the dissimilarity measure chosen has a linear relationship with ecological distance, whereas non-metric scaling assumes monotonicity and the distances between sample pairs are only maintained in rank order with their dissimilarities. The hybrid method described by Faith et al. (1987) differs from these two approaches in using a prescribed dissimilarity measure that has a robust metric (linear) relationship with distance only over a certain range. A monotonic regression serves as the only direct constraint on larger dissimilarities. This hybrid attribute is of particular value when relating ordination scores to environmental characteristics. All clustering and ordination was done using PATN, a pattern analysis software package developed by CSIRO in Australia (Belbin 1993).

2.2.5 Relationship between faunal and habitat data

Twenty-nine of the 40 environmental variables measured in this study (Table 2.1) were considered for use in predictive models of the biological structure of the data. Variables were excluded from consideration for either of two reasons: (1) they were likely to be influenced by anthropogenic activity (e.g. nutrient enrichment, physical disturbance) because the predictive models are used to establish what assemblage would occur at a test site if it were not affected by human activity; and (2) temporal variability would not be well estimated by a single measurement (e.g. temperature, dissolved oxygen). The variables used were general descriptors of the site, channel, substrate, and water quality (Table 2.1).

Relationship with the biological data was examined in two ways:

- (1) Principal Axis Correlation (procedure PCC in PATN), which determines how well a set of attributes (environmental data) can be fitted to a second set of variables (biota) in ordination space. This is a multiple-linear regression method that takes each environmental attribute and determines the location of the vector with the best fit in ordination space. The variables can be represented as an axis on an ordination plot, and a correlation of the variable with the ordination is provided. A randomization model was used to establish the statistical significance of the correlations.
- (2) Stepwise Discriminant Function Analysis (Procedure STEPDIS in SAS) was used to establish which environmental variables best separate sites into the predefined groups formed by classification of the biological data set. Stepwise selection of variables was used, and the significance level for variable entry and retention was 0.05

2.2.6 Prediction of site groups

An objective of the study was to develop a method for selecting an appropriate subset of the total number of reference sites to be used in assessing any new test site. The subsets of reference sites were established by the grouping of similar sites, as described above.

Discriminant Function Analysis (DFA) was used for predicting the reference group to which a test site was expected to belong. In this method descriptions of the habitat are used to classify sites into the groups formed by the invertebrate data.

PCC and STEPDIS were used to select variables for the discriminant models. Based on these results environmental variables were used in DFA to establish functions for the variables that best separated sites into the predefined biological groups. The SAS version of DFA (Procedure DISCRIM in SAS) was used with raw environmental data to generate discriminant scores and to predict the probability of group membership.

The accuracy of the predictions from the discriminant model was verified by examining how well the reference sites were predicted to the correct group. The predicted groupings and actual groupings were then compared to provide a group and total error rate.

Final selection of the optimal predictor variable data set was done by iteration. Various combinations of predictor variables were selected based on the results of the stepwise DFA and PCC. Sites can be classified into the reference groups formed from the invertebrate fauna, using the predictor variables. The performance of the predicted classification can be compared to the original classification based on the invertebrate fauna in two ways: (1) resubstitution – the entire training data set is used to develop the classification equations; these equations are then used to classify the sites for which they were derived, and (2) cross-validation – the utility of the classification equations is tested for a sample from which they were not derived (Lachenbruch and Mickey 1968). Cross-validation is a more desirable test of the predictions because these equations will be used primarily for assigning new sites. The models are selected by removing each reference site in turn, developing coefficients from all the remaining reference sites, and then classifying the removed site (“jackknifed” classification). The procedure provides a more realistic estimate of the ability of the predictors to discriminate groups. The optimal model was defined as that with the lowest error rate from cross-validation in DFA, with support from resubstitution.

2.2.7 Temporal variation

Much of the effort in model development was directed toward resolution of the effect of spatial variation on the assemblage of invertebrate organisms expected to occur at undisturbed sites. However, the assemblage of organisms found at a site also varies temporally. We examined two aspects of temporal variation: (1) year-to-year, which is unpredictable change influenced by climate, and (2) seasonal, which is the result of changes associated with the life histories of organisms over a season.

Annual variation was examined at 14 sites that were visited in more than one study year. Three sites were sampled in each of the three years, whereas the remaining sites were sampled in two of the three years. The importance of annual variation on the ability to predict invertebrate assemblages was assessed by examining the annual stability of the assemblage sampled at a site and whether or not the predictive model performed as well with sites in multiple sampling years. A site was considered to have a stable assemblage if it appeared in the same faunal group in each sampling year.

Seasonal effects were examined at eight streams (Dymond 1998; Reece et al., submitted). Three interior streams were in the Nicola River catchment (Mellin, Glimpse, and Beak Creeks), three were coastal streams in the Pitt River catchment (Spring Creek, Mayfly Creek, and the North Alouette River), and two were large-river sites (Fraser and Thompson rivers) (Fig. 1.1). The autumn data of these seasonal test sites were included in the reference database, except for the Fraser River and Mellin Creek sites, which were suspected of being impaired. The Mellin site was exposed to cattle grazing and physical disturbance; the Fraser site was downstream of several municipalities and was of unknown status.

The effect of seasonal variation on the applicability of the predictive model and site assessment was determined by treating seasonal sites as test sites. We predicted the expected assemblage and determined how the seasonal assessment varied from the autumn-based assessment. If the assessment of a seasonal sample was the same as that based on an autumn sample, then we concluded that seasonal variation did not affect a test-site assessment using autumn-collected reference data.

2.2.8 *Assessing test sites*

The reference-condition approach assumes that a set of reference sites describes normal or unimpaired conditions, and that the quality of a test site is determined by the degree of similarity between the test site and the reference sites. Reynoldson et al. (1997b) used these approaches for comparing reference and test sites, and determined that the multivariate methods performed best. These methods were used for our analysis of the complete data set.

To assess a test site it is first predicted to belong to one of the reference-site groups formed from the original classification, using the predictive model constructed from DFA. The variation among the reference sites of the group to which the test site is predicted is assumed to encompass the normal range of variation expected at the test site, if it is unimpaired. To determine the similarity between the test site and the appropriate reference sites, both the reference sites and the test sites are ordinated and plotted in ordination space. If the test site falls within the “cloud” of sites representing the reference condition (Fig. 2.1), then it is considered to be equivalent to reference; if it is outside the reference-site cloud it is considered to be different than reference. Construction of probability ellipses around the reference sites defines the bounds of the reference-site cloud, and the degree of difference or similarity between the test site and the reference-site cloud can be quantified (Fig. 2.1). The greater the departure from the reference sites, as measured in ordination space, the greater the difference from the reference condition. However, determining degree of impairment and unacceptable departure from the reference condition are ultimately subjective decisions.

A series of bands, representing grades of biological quality from good to poor, was developed by Wright et al. (1991). Their method provided a simple statement of biological quality, allowing broad comparisons in either space or time that would be useful for management purposes.

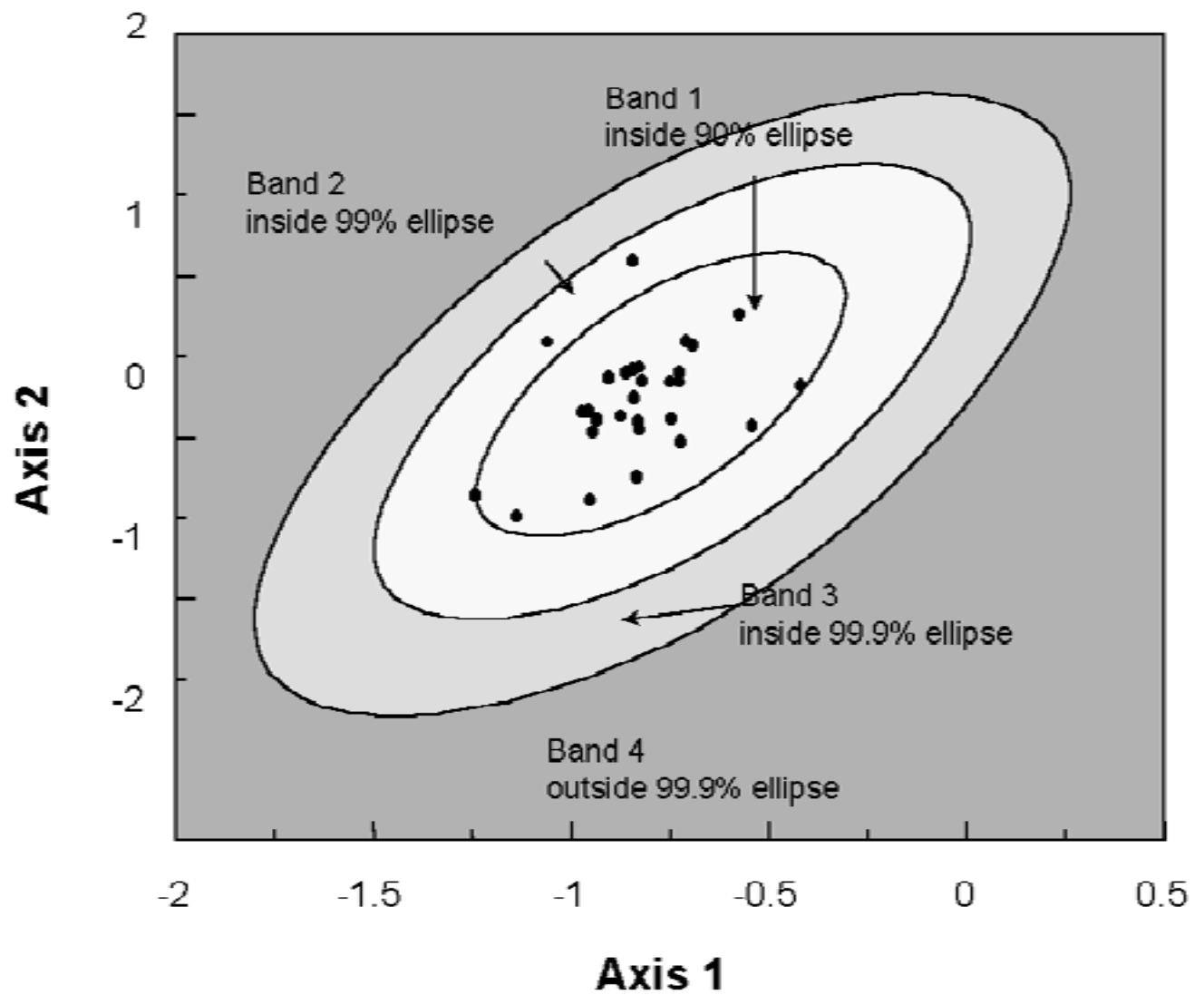


Figure 2.1 Probability ellipses (90, 99, 99.9%) constructed around reference sites to describe four quality bands.

We have established four categories or bands of biological quality based on how similar a test site is to the reference sites. Band 1 is inside the smallest ellipse (90% probability), which would be considered as *equivalent to reference*; Band 2 is between the smallest (90%) and next ellipse (99% probability), which would be considered *possibly different*; Band 3 is between the 99% probability and the largest ellipse (99.9% probability), and would be considered *different*; and Band 4 is outside the 99.9% ellipse where sites would be considered *very different* (Fig. 2.1). If more than two ordination axes were required to describe the variation in the invertebrate matrices, then the worst-case assessment was used to determine the condition at a test site.

The discriminant model was run for each of the 21 test sites, and each test site was compared to the group of reference sites to which it was assigned as having the highest probability of belonging, and to any other group to which it had >25% probability of belonging. A test site was assessed as being equivalent to reference, possibly different, different, or very different by being plotted in ordination space with the reference sites to which it had the greatest probability of belonging, as described above.

2.3 Results and discussion

The reference sites were distributed over 11 ecoregions. The number of sites per ecoregion ranged from three in the Lower Mainland ecoregion to 56 in the Fraser Plateau. Reference sites were located in 21 different subcatchments. Seven stream orders were sampled and the median stream order was 3 (Table 2.2). Sites ranged in altitude from 30 m above sea level (m asl) to a maximum of 2000 m asl, stream width ranged between 0.4-226 m (median 9.8 m), and sampling depth between 5-73.3 cm (median 24.2 cm). The range for other variables is summarized in Table 2.2.

Table 2.2. Range of selected site descriptors for 219 reference sites sampled in the Fraser River catchment. asl = above sea level.

Variable	Minimum	Maximum	Median
Stream order	1	7	3
Altitude (m asl)	30	2000	970
Channel width (m)	0.4	226.8	9.8
Mean depth (cm)	5	73.3	24.2
Mean velocity ($\text{m}\cdot\text{s}^{-1}$)	0.075	1.254	0.406
Alkalinity ($\text{mg}\cdot\text{L}^{-1}$)	0	201	38.1
Total suspended solids ($\text{mg}\cdot\text{L}^{-1}$)	0.4	168.0	7.1
Total phosphorus ($\text{mg}\cdot\text{L}^{-1}$)	0	0.149	0.008
Nitrate-nitrite ($\text{mg}\cdot\text{L}^{-1}$)	0.001	0.334	0.013
pH	5.7	9.3	7.7
Conductivity ($\mu\text{S}\cdot\text{cm}^{-1}$)	4.6	426.0	92.0
Dissolved oxygen ($\text{mg}\cdot\text{L}^{-1}$)	5.0	14.8	11.8
Framework (category Table 2.1)	1.0	8.0	6.0
Matrix (category Table 2.1)	0	8.0	3.0
Embeddedness (category Table 2.1)	1.0	5.0	4.0

2.3.1 *Assemblage composition*

The 219-site reference database included 74 families. A complete taxa list and the data matrices are available (contact T. Tuominen, Pacific and Yukon Region, Environment Canada, Vancouver, B.C.). Only 12 families were common, occurring at >50% of the sites (Table 2.3), and 40 families occurred at <10% of the sites. The most common family was the Chironomidae, which was absent from only two of the 219 sites. Of the 12 most common families, three were Ephemeroptera (mayflies) and five were Plecoptera (stoneflies). These 12 families also represented 81.1% of the total organisms collected.

2.3.2 *Classification of sites*

The assemblages present in the basin were differentiated using cluster analysis. The complete dendrogram is presented in Appendix 2; however, we have also presented a reduced dendrogram showing only 15 groups of sites (Fig. 2.2A). The degree of similarity between the sites is indicated by the scaled association measure shown at the top of each dendrogram. The cluster analysis first separated Groups 3 and 4 from Groups 1 and 2. Based upon a minimum group size of 10 sites, four groups were discriminated (Fig. 2.2A).

Ordination showed that the sites distributed themselves along a dominant axis, and the four groups separated along an axis from the bottom right to top left of the ordination plot (Fig. 2.2 B). This axis was associated with those families most correlated ($r > 0.40$) to the ordination axes (Fig. 2.2C). Groups 3 and 4 had the greatest number of individuals and highest family richness (Table 2.4). Group 1 sites had the third lowest overall abundances and were dominated numerically by the Heptageniidae, Baetidae (both families of Ephemeroptera), and Taeniopterygidae (Plecoptera) (Table 2.4). The Chironomidae (Diptera), Baetidae, Heptageniidae, and Ephemerellidae (Ephemeroptera) were the most widely distributed families. Group 1 streams were intermediate in size (based on stream width), had the highest water velocities recorded, and had low nutrient levels (Table 2.5).

Table 2.3. Percent occurrence and abundance of the 12 most common (occurring at >50% of the sites) families of benthic invertebrates from 219 reference sites in the Fraser River catchment.

Genus	No. sites present	% occurrence	Abundance (avg. no./3-min kick)	% total
Chironomidae	217	99.1	1661.6	26.7
Heptageniidae	210	95.9	992.5	15.4
Baetidae	198	90.4	1118.5	16.4
Ephemerellidae	195	89.0	521.4	7.5
Chloroperlidae	176	80.4	130.0	1.7
Nemouridae	169	77.2	375.8	4.7
Perlodidae	152	69.4	77.6	0.9
Capniidae	149	68.0	316.9	3.5
Tipulidae	130	59.4	68.5	0.7
Empididae	120	54.8	58.5	0.5
Rhyacophilidae	119	54.3	64.2	0.6
Taeniopterygidae	115	52.5	312.6	2.7

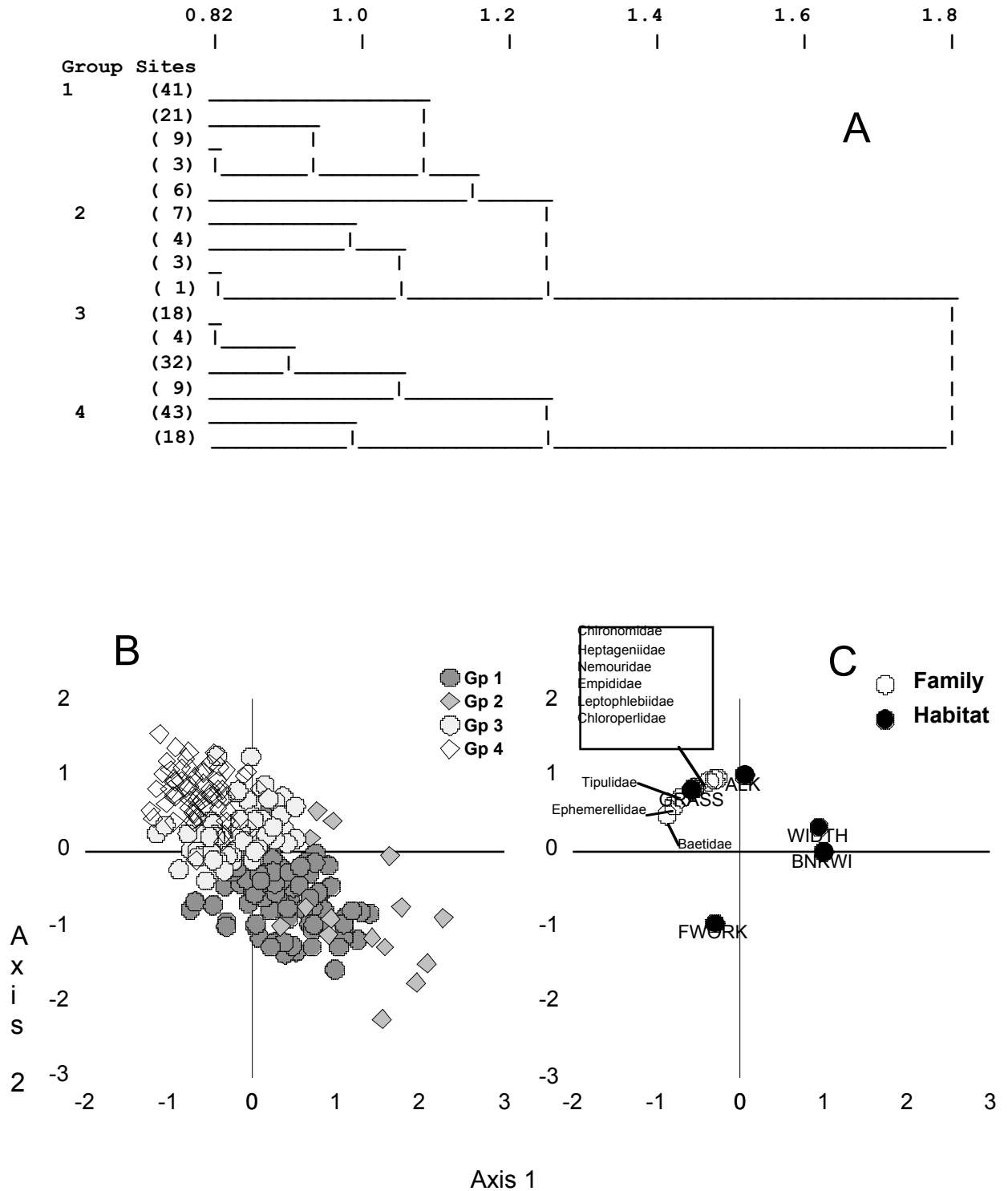


Figure 2.2 Classification (dendrogram: A) and ordination (B, C) of 219 reference sites at the family level for the Fraser River catchment. Fifteen clusters of sites are shown in the dendrogram (number of sites in each cluster is indicated in parentheses). The ordination plots show the individual sites with the four faunal groups indicated (B), and the vectors for selected family and habitat variables to the site ordination (C). Abbreviations as in Table 2.1.

Table 2.4. Richness, total abundance, and abundance and distribution of common (present at >50% of sites) families for four groups of reference sites formed by cluster analysis of 74 families in the Fraser River catchment.

	Group (no. of sites)							
	1 (80)		2 (15)		3 (63)		4 (61)	
	Mean no./3-min kick (SD)	Sites present (%)	Mean no./3-min kick (SD)	Sites present (%)	Mean no./3-min kick (SD)	Sites present (%)	Mean no./3-min kick (SD)	Sites present (%)
No. families	15.4 (4.7)		12.1 (5.3)		16.5 (3.2)		16.5 (3.9)	
No. individuals	1014 (876)		319 (317)		5074 (3424)		15521 (7827)	
Chironomidae	93 (90)	97.5	156 (235)	100.0	835 (506)	100.0	4888 (3625)	100.0
Tipulidae	6 (10)	60.0	2 (6)	46.7	37 (51)	68.3	99 (164)	52.5
Empididae	4 (7)	47.5	3 (5)	53.3	30 (40)	65.1	78 (109)	54.1
Elmidae	7 (24)	18.8	1 (3)	13.3	82 (222)	28.6	469 (776)	63.9
Hydropsychidae	7 (14)	50.0	3 (10)	33.3	116 (309)	52.4	214 (401)	47.5
Rhyacophilidae	13 (34)	65.0	0 (1)	26.7	51 (65)	68.3	55 (115)	32.8
Baetidae	148 (179)	93.8	8 (14)	60.0	872 (950)	88.9	2534 (2581)	95.1
Heptageniidae	203 (222)	96.8	12 (18)	73.3	718 (838)	98.4	2406 (2476)	95.1
Ephemerellidae	85 (106)	93.8	10 (15)	60.0	595 (997)	90.5	939 (1591)	88.5
Ameletidae	12 (35)	46.3	3 (5)	66.7	17 (49)	31.7	36 (80)	31.1
Chloroperlidae	43 (58)	87.5	6 (15)	53.3	112 (173)	84.1	201 (243)	73.8
Perlodidae	21 (28)	83.8	5 (7)	40.0	40 (68)	65.1	124 (174)	62.3
Nemouridae	41 (80)	77.5	13 (28)	60.0	289 (447)	73.0	685 (845)	85.2
Taeniopterygidae	219 (549)	76.3	2 (3)	40.0	108 (244)	42.9	190 (793)	34.4
Capniidae	22 (41)	63.8	61 (79)	66.7	296 (1066)	71.4	424 (648)	70.5

Group 2 sites had the lowest overall abundance and richness (Table 2.4). The sites in Group 2 were dominated numerically by the Chironomidae, which occurred at every site. The Capniidae (Plecoptera), Ameletidae (Ephemeroptera), and Heptageniidae were also widespread, but occurred in low numbers. Group 2 streams were the widest, highest-order, lowest velocity, and had the lowest proportion of grasses in the riparian zone of the four groups (Table 2.5). Group 3 sites had higher abundance and richness than the previous groups, and were dominated numerically by the Chironomidae, Baetidae, and Heptageniidae, which were also the most widely distributed families (Table 2.4). The Ephemerellidae was also widespread, but was less abundant than the other three families. Group 3 streams were the smallest (based on width and stream order) of the four groups and they had higher nutrient levels than Groups 1 and 2 (Table 2.5). Group 4 sites had the highest overall abundance, which was two orders of magnitude greater than Group 2 (Table 2.4). Group 4 sites were dominated numerically by the Chironomidae, followed by the Baetidae and Heptageniidae. All three families were widespread. Elmidae (Coleoptera) were common in this group. The relative proportions of families were similar to Group 3 sites, and Group 4 was discriminated from Group 3 more so on overall abundance than the actual families that occurred. Group 4 streams were small and had lower water velocities than Group 3 streams, but had the highest nutrient levels and proportion of grasses in the riparian zone of all four groups (Table 2.5).

The spatial distribution of the sites in these four groups showed some large-scale geographic patterns (Fig. 2.3). Group 1 sites were mainly located in southwestern streams (e.g. Pitt, Lillooet, and Chehalis) or were tributaries of the upper Fraser (e.g. Torpy). Group 2 sites tended to be associated with large rivers (e.g. mainstem Fraser, Thompson), but also included a few headwater sites (e.g. Chilko, Herrick, and upper Fraser subcatchments). Group 3 sites were more widely distributed; of the 21 subcatchments containing reference sites only four did not include Group 3 sites. Many Group 4 sites were located in the northwestern portion of the Fraser catchment (e.g. West Road, Chelaslie, Euchiniko, and Chilcotin).

Table 2.5. Selected habitat characteristics (mean [SD]) of 219 Fraser River reference sites separated into four groups from cluster analysis of 74 families, and relationship between habitat and invertebrate assemblage matrices at 219 reference sites established using Principle Axis Correlation. Strength of the relationship is indicated by the *r* value. (Variable abbreviations as in Table 2.1.)

Variable	Group				<i>r</i>
	1	2	3	4	
TKN (mg·L ⁻¹)	0.05 (0.04)	0.07 (0.04)	0.13 (0.14)	0.23 (0.17)	0.515
GRASS (% sites with grass)	15	7	48	69	0.506
ALK (mg·L ⁻¹)	29.1 (27.3)	45.6 (30.4)	43.2 (31.1)	62.3 (37.8)	0.413
WIDTH (m)	23 (25)	77 (77)	12 (14)	15 (31)	0.409
FWORK (see Table 2.1)	6.7 (1.3)	5.5 (1.4)	6.1 (1.5)	5.1 (1.9)	0.350
BNKWI (m)	61.1 (60)	126 (108)	27 (25)	30 (60)	0.350
MXVEL (m·s ⁻¹)	0.73 (0.25)	0.51 (0.31)	0.60 (0.23)	0.54 (0.28)	0.325
MNVEL (m·s ⁻¹)	0.52 (0.18)	0.36 (0.25)	0.41 (0.17)	0.38 (0.18)	0.315
MNDEP (cm)	32 (13)	30 (18)	24 (14)	21 (12)	0.314
TP (mg·L ⁻¹)	0.012 (0.013)	0.011 (0.009)	0.020 (0.030)	0.032 (0.037)	0.301
ALT (m asl)	2581 (1543)	3165 (1600)	3612 (1219)	3607 (1160)	0.265
SORD	2.8 (1.1)	3.9 (2.0)	2.6 (1.3)	2.9 (1.7)	0.192

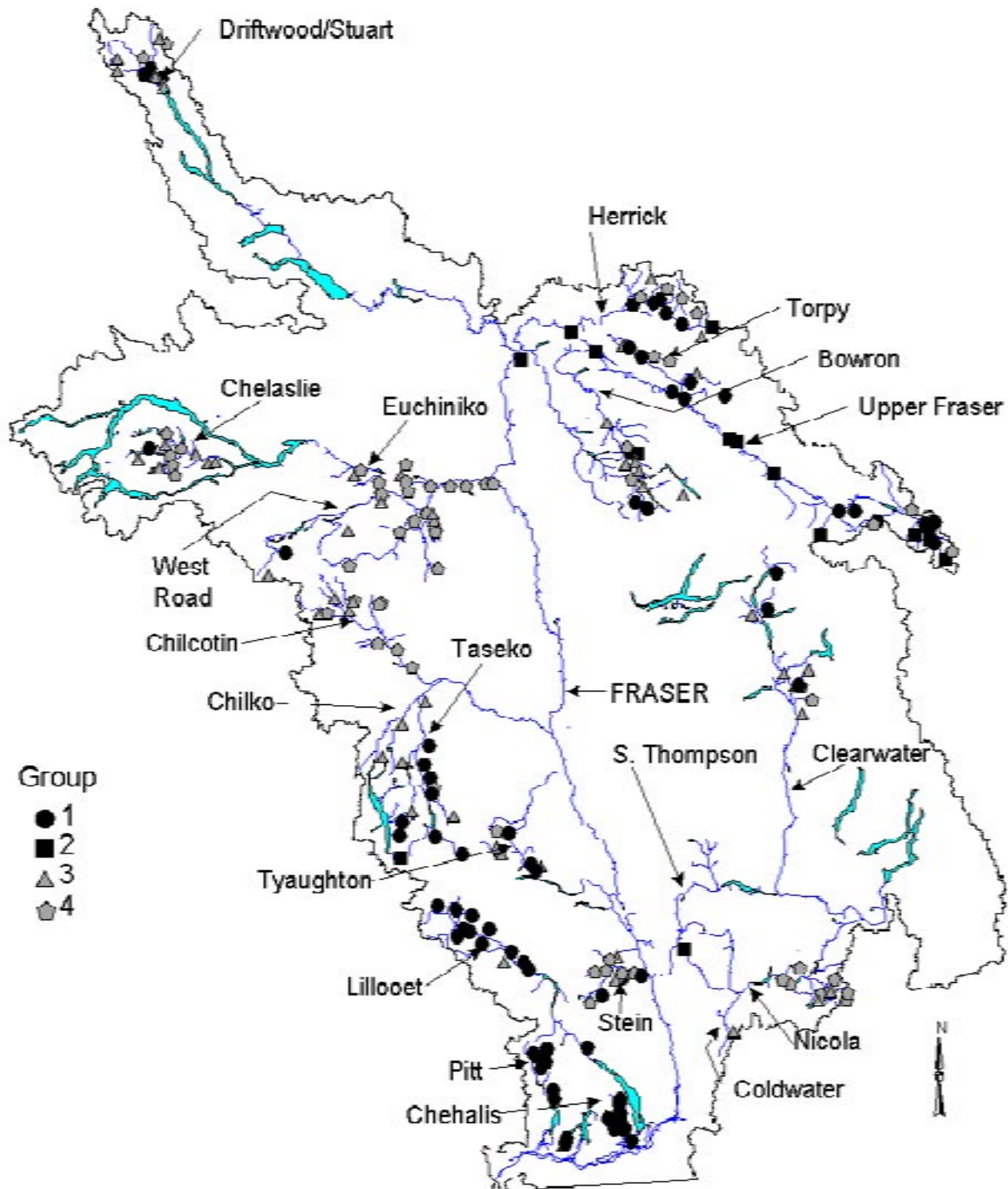


Figure 2.3 Geographic distribution of four groups formed from cluster analysis of invertebrate assemblage data from 219 Fraser River catchment reference sites at the family level.

However, most of the Nicola sites, in the southeastern Fraser catchment, were also in Group 4. It is important to note that some subcatchments included sites from all four groups in close proximity (e.g. Bowron, Herrick), and 12 subcatchments included sites from three or more of the faunal groups.

2.3.3 *Predicting site groups*

Of the 29 variables considered suitable predictors (Table 2.1) the presence of grasses in the riparian zone showed the strongest correlation with the pattern observed in the invertebrate assemblages ($r = 0.506$, Table 2.5). Other environmental variables strongly correlated with the ordination axes of the invertebrate assemblages were: alkalinity, stream width (wetted and bankfull), framework, maximum velocity, and mean velocity. Variables that showed little relationship with the ordination axes from the invertebrate fauna were: occurrence of conifers in the riparian zone, slope, substrate embeddedness, and presence of shrubs.

Stepwise DFA selected eight variables (ecoregion, latitude, grass, width, maximum depth, alkalinity, conductivity, and framework). Using resubstitution, these variables predicted 59% of the sites to the correct group (Table 2.6). Use of all 29 variables in resubstitution predicted 67% of the sites correctly, compared to only 53% for cross-validation. Other models were examined that were based on the stepwise model with variables added, depending on their correlation with the family-level ordination from PAC (Table 2.5). These further models resulted in slight improvements over the stepwise model in resubstitution (Table 2.6). The final model chosen used the variables selected by DFA plus longitude. This model performed similarly to the stepwise model in cross-validation (each 56%), but was superior in resubstitution (62%).

The performance of this optimal model for all sites in both resubstitution and cross-validation modes is summarized in Table 2.7. The model had most difficulty in discriminating between Groups 3 and 4 and 1 and 3.

Table 2.6. Resubstitution (Resub.) and cross-validation (Crval.) performance of various discriminant models in predicting reference sites using variables selected by Stepwise Discriminant Function Analysis, Principal Axis Correlation, and iteration. Final model shown in bold. (Variable abbreviations in Table 2.1.)

Discriminant function model variables		Sites correctly classified				% correct	
Number	Variables included	Group				Resub.	Crval.
		1	2	3	4		
8	ECOR LAT GRASS WIDTH MXDEP ALK COND FWORK ¹	49	7	30	36	59	56
29	ALL	47	9	25	35	67	53
9	ECOR LAT GRASS WIDTH MXDEP ALK COND FWORK EMBED	48	7	29	36	61	55
9	ECOR LAT GRASS WIDTH MXDEP ALK COND FWORK ALT	47	7	28	37	64	54
9	ECOR LAT GRASS WIDTH MXDEP ALK COND FWORK LON	48	8	29	37	62	56
8	ECOR LAT GRASS WIDTH MXDEP ALK COND LON	47	7	26	3	60	53

¹ Stepwise model

Table 2.7. Summary of the performance of a discriminant model using nine variables in predicting 219 reference sites to four groups formed from cluster analysis of family-level data. The number of sites correctly predicted for each group (bold) and the total percentage of correctly predicted reference sites are given.

Resubstitution classification matrix

From Group	To Group				% correct
	1	2	3	4	
1	51	8	17	4	54
2	3	9	2	1	60
3	8	2	34	19	54
4	2	1	17	41	67
Total	64	20	70	65	62

Cross-validation classification matrix

From Group	To Group				% correct
	1	2	3	4	
1	48	8	20	4	60
2	4	8	2	1	53
3	9	2	29	23	46
4	3	2	19	37	61
Total	64	20	70	65	56

There is some biological similarity between Groups 3 and 4 and 1 and 3 because they overlap in ordination space (Fig. 2.2B), which suggests that the assemblages represent a distribution continuum rather than discrete assemblage types.

2.3.4 Temporal variation

2.3.4.1 Annual

Of the three sites sampled over the three study years, two (CHI1, PIT8) were members of the same faunal group in each sampling year, whereas the third (CLR6) was in a different group each year (Table 2.8; see Table 1.3 for site abbreviations). Of the 11 sites sampled in two years all but one (CHI9) were assigned to the same group in both sampling years. This result indicated considerable stability in invertebrate assemblages over the three-year period.

The effect of annual variation on model performance was shown by comparing the accuracy of the predictions at those sites sampled in multiple years versus overall model performance. Twenty of the 31 (64.5%) multi-year samples were predicted to the correct group (Table 2.8), a similar result to the overall performance of the model, which predicted 62% of the sites correctly (Table 2.6). Therefore, the effects of inter-annual variation were no greater than caused by other sources of variability.

2.3.4.2 Seasonal

The interior streams were placed into Groups 3 and 4, the large river sites into Group 2, and the coastal streams into Group 1. Winter, spring, and summer samples from seasonally sampled sites were classified by the predictive model into the same group as the autumn sample (Table 2.9). This result indicated that seasonal variation in the predictor variables did not affect the outcome of faunal group prediction and thus we concluded that the predictive models were robust with regard to seasonal variation.

Table 2.8. Summary of sites sampled in multiple years showing their group membership and the predicted group (in parentheses) based on the optimal discriminant function model. CHI = Chilcotin, CLR = Clearwater, PIT = Pitt, CLD = Coldwater, and FRA = Fraser mainstem.

Site	1994	1995	1996
CHI1	3 (4)	3 (4)	3 (4)
CLR6	4 (4)	3 (1)	1 (1)
PIT8	1 (1)	1 (1)	1 (1)
CHI8		4 (4)	4 (4)
CHI9		4 (3)	3 (4)
CLD1		3 (3)	3 (3)
CLD2		3 (3)	3 (4)
CLD3		3 (4)	3 (3)
CLR4	3 (1)		3 (1)
CLR7	4 (4)	4 (4)	
FRA11	2 (2)		2 (2)
PIT1	1 (1)		1 (1)
PIT2	1 (1)		1 (1)
PIT4	1 (3)	1 (1)	

Table 2.9. Summary of the assessment of seasonal samples from reference (ref) and impaired (test) sites relative to autumn sampling: Band 1 - equivalent to reference, Band 2 - possibly different, Band 3 - different, and Band 4 - very different. Faunal groups (Gp) to which sites were predicted are shown in parentheses. NS = no sample.

	Autumn Band (Gp)		Spring 1995 Band (Gp)		Summer 1995 Band (Gp)		Winter 1995 Band (Gp)		Spring 1996 Band (Gp)		Concordance with autumn prediction (%)	Concordance with autumn assessment (%)
Glimpse (ref)	2	(4)	3	(4)	2	(4)	2	(4)	2	(4)	100	75
Beak (ref)	2	(3)	1	(3)	1	(3)	NS		1	(3)	100	0
Spring (ref)	1	(1)	2	(1)	3	(1)	2	(1)	2	(1)	100	0
Mayfly (ref)	1	(1)	1	(1)	3	(1)	2	(1)	1	(1)	100	50
N. Alouette (ref)	1	(1)	1	(1)	1	(1)	1	(1)	1	(1)	100	100
Thompson (ref)	1	(2)	2	(2)	1	(2)	1	(2)	2	(2)	100	50
Mellin (test)	2	(4)	4	(4)	2	(4)	4	(4)	2	(4)	100	50
Fraser (test)	1	(2)	2	(2)	1	(2)	1	(2)	1	(2)	100	75

The assessments of the seasonal test sites into the four quality bands, based on the location of the seasonal sites in ordination space, are also summarized in Table 2.9. Only one of eight seasonal sites was 100% concordant with the assessment made from an autumn sample (Table 2.9, last column). It was not possible to establish whether the variable assessment of the impaired Mellin site (Table 2.9) as *possibly different* to reference (Band 2) from the autumn, summer, and spring 1996 samples versus *very different* (Band 4) from the spring 1995 and winter samples represented seasonal differences or intermittent stress and recovery. The other possibly impaired site, the Fraser, was 75% concordant.

Assessments of the six reference sites relative to the autumn assessment were less equivocal. These reference sites should always be assessed the same as the autumn sampling, usually equivalent to reference (Band 1), so a different assessment of a site when sampled in a season other than autumn may be attributed to seasonal variability. Only the North Alouette site was assessed as equivalent to reference (Band 1) regardless of the season sampled. The other five sites differed: (1) Glimpse (autumn = Band 2) as Band 3 in spring 1995, (2) Beak (autumn = Band 2) as Band 1 in spring 1995 and 1996 and summer, (3) Spring (autumn = Band 1) as Band 2 in spring 1995 and 1996 and winter, and Band 3 in summer, (4) Mayfly (autumn = Band 1) as Band 3 in summer and Band 2 in winter, and (5) Thompson (autumn = Band 1) as Band 2 in spring 1995 and 1996. What are the chances that these incorrect assignments are a result of normal variation? The expected distribution of these sites is 90% into Band 1, 9% into Band 2, and 0.9% into Band 3. The actual distribution was 48% (11/23 of the seasonal sites) into Band 1, 39% (9/23) into Band 2, and 13% (3/23) into Band 3. This result indicated that seasonal variation affected the assessment of site quality; we would have expected 10% of the sites to be assessed as different to reference, but the figure was far higher. Therefore, we recommend that sampling be limited to the autumn, unless separate seasonal models are created.

2.3.5 Assessment of test sites

The 21 test sites (Table 2.10) were each classified to a reference group using the predictive models, and assessed relative to the appropriate reference-site group. There was no *a priori* way of determining whether or not the test sites were impaired, but each site looked disturbed prior to sampling (Table 2.10).

2.3.5.1 Agriculture

Eight of the test sites were exposed to some degree of agricultural stress (Table 2.10). The Nicola site (NIC5) was assessed as equivalent to reference (Band 1, Fig. 2.4 - Group 4). Of the four sites on the Salmon River (SAL1-4), the most visibly impaired was SAL4, which was assessed to Band 2 (Fig. 2.4 – Group 4). Sites SAL1-3 were assessed as equivalent to reference (Band 1). The number of individuals at SAL4 was considerably higher than at the Group 4 reference sites (Table 2.10 cf. Table 2.4), suggesting enrichment from a horse paddock immediately upstream of the site. The abundance of many families was also different at the SAL4 site compared to Group 4. One site in the Deadman River (DEA1) was assessed as equivalent to reference, whereas the other two sites (DEA1, DEA2) were assessed as possibly different (Table 2.10). (Recall that assessment was based on **worst case** [see section 2.2.8], which may not be illustrated in Fig. 2.4). DEA2 and DEA3 sites had reduced overall abundances, especially of Chironomidae, Baetidae, and Ephemerellidae, compared to Group 4 reference sites (Table 2.10 cf. Table 2.4). In summary, five of the eight agricultural sites showed no evidence of effects on the invertebrate assemblage, and three showed evidence of possible stress. The SAL4 site appeared to be the most impaired; it was beside a horse paddock and had no riparian vegetation.

2.3.5.2 Mining

Four sites were sampled in locations exposed to mining activity. Two sites were located

Table 2.10. Assessment of 21 tests sites exposed to potential disturbance from agriculture, mining, and logging. Sites are assessed as belonging to one of four quality bands relative to reference: Band 1 - equivalent, Band 2 - possibly different, Band 3 - different, and Band 4 - very different. DEA = Deadman, NIC = Nicola, SAL = Salmon, GUI = Guichon, WIL = Willow, BOW = Bowron, TOR = Torpy, and TYA = Tyaughton rivers. trib = tributary. EPT = Ephemeroptera, Plecoptera, and Trichoptera.

Site	DEA1	DEA2	DEA3	NIC5	SAL1	SAL2	SAL3	SAL4	GUI1	GUI3	WIL2	WIL3
Subcatchment	Lower Thompson Deadman River	Lower Thompson Deadman River	Lower Thompson Deadman River	Nicola	South Thompson Salmon River	South Thompson Salmon River	South Thompson Salmon River	South Thompson Salmon River	Nicola	Lower Thompson Jim Black Creek	Willow	Willow
Stream				Mellin Creek					Tailings pond runoff ditch		Willow River	Willow River
Disturbance Site description	Agriculture Farmland and fenced grazing	Agriculture Farmland and fenced grazing	Agriculture No evidence of local impact	Agriculture Open-range grazing, bank instability, recent cattle watering	Agriculture Open-range grazing	Agriculture No grazing, extensive riparian zone	Agriculture Fenced, bank instability and restoration	Agriculture Paddock with grazing horses	Mining Large tailings dam upstream, no riparian vegetation, channelized and culverted	Mining Extensive encrustation on substrate, well-developed riparian vegetation	Mining No visible evidence of damage, 16 km below Jack of Clubs Lake	Mining No visible evidence of damage, 3 km below Jack of Clubs Lake
Classified to Group	4	4	4	4	4	4	4	4	4	4	3	3
Assessment	1	2	2	1	1	1	1	2	4	4	4	2
No. families	16	16	16	17	20	10	15	14	13	18	18	15
Individuals (no./kick)	26800	7133	10700	23600	33300	26100	13425	47400	2344	1393	1171	5400
Chironomidae	2200	1333	600	11700	16500	3750	5100	8100	156	93	71	100
Elmidae	3700	1733	2150	0	2550	1800	2775	10500	11	0	0	0
Baetidae	5300	1100	1000	1100	1800	5850	675	300	378	750	294	1950
Ephemerellidae	6700	333	750	200	150	6600	2475	18300	0	0	94	75
Heptageniidae	2200	867	2700	3700	2250	1650	300	900	0	0	265	22175
Rhyacophilidae	0	0	0	0	0	0	0	0	0	14	12	0
Nemouridae	2500	0	0	700	1050	0	0	0	11	79	41	375

Table 2.10. Cont'd.

Site	BOW13	BOW14	TOR10	TOR11	TYA1	TYA2	TYA5	WIL1	WIL4
Subcatchment	Bowron	Bowron	Upper Fraser	Upper Fraser	Bridge	Bridge	Bridge	Willow	Willow
Stream	Antler Creek (trib)	Haggen Creek	Torpy River	Don Creek	East Liza Creek	Mud Creek (trib)	Tyaughton Creek	Stephanie Creek	Rond Creek (trib)
Disturbance Site description	Logging Logged to stream bank, no riparian vegetation	Logging Old logging to stream bank with natural regrowth	Logging River valley extensively logged, 30-m riparian zone	Logging 10-m buffer strip on one bank, none on other; bank stabilized with old logs	Logging Old logging with natural regrowth, extensive riparian vegetation	Logging Recent logging in area, extensive riparian vegetation, but culverted below site	Logging 5-y-old logging on one bank down to stream, other bank unlogged	Logging Severe clear cutting in surrounding area, but well-developed riparian vegetation	Logging Recent logging in area, 20 m riparian zone on both banks
Classified to Group	3	3	4	4	4	4	4	3	4
Assessment	4	2	2	2	1	2	2	1	3
No. families	16	16	19	14	14	13	19	23	17
Individuals (no./kick)	893	5900	2525	1809	9350	2383	2100	1854	10600
Chironomidae	247	1000	550	45	3450	233	489	436	4150
Elmidae	0	0	0	0	0	0	0	0	200
Baetidae	60	2550	25	655	1250	33	33	536	3400
Ephemerellidae	93	150	938	373	500	200	367	9	500
Heptageniidae	187	425	413	327	1400	650	511	136	350
Rhyacophilidae	47	50	13	46	0	67	44	9	350
Nemouridae	33	475	63	91	700	150	178	173	400

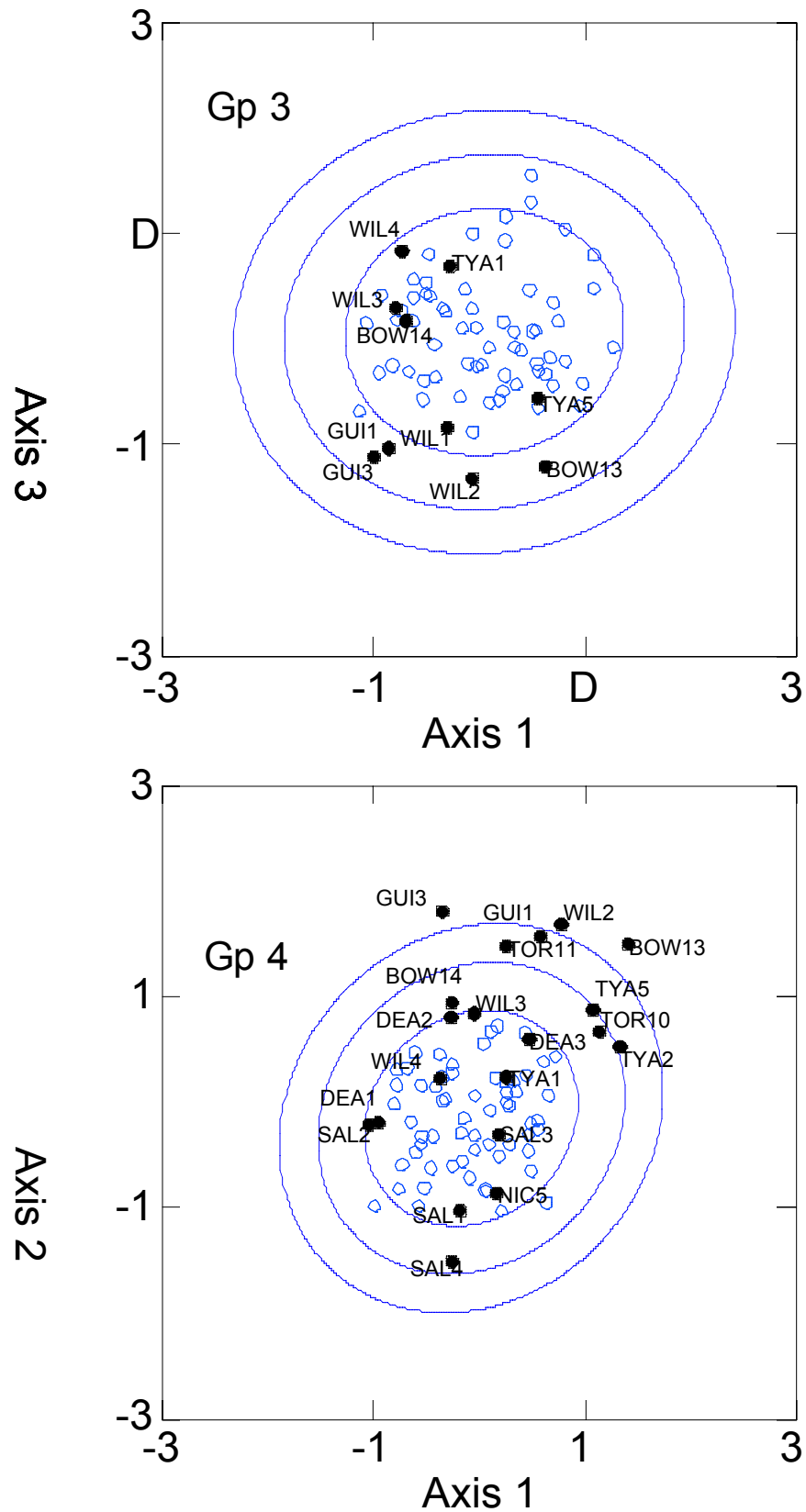


Figure 2.4 Ordination of test sites (solid) with reference sites (open) for selected ordination axes (site abbreviations as in Table 2.10). Only two ordination axes for Groups (Gp) 3 and 4 are shown. Probability ellipses are calculated at the 90, 99, and 99.9% probability levels around reference sites only.

on the Willow River, 3 km (WIL3) and 16 km (WIL 2) downstream of Jack of Clubs Lake. Jack of Clubs Lake has received mine tailings from earlier gold mining activity in the Barkerville area (Mudroch et al. 1993). The potential exposure to leachate from the mine tailings made these suitable test sites. The two Willow River sites had the highest probability of belonging to Group 3; however, both sites may have been members of Group 4 (WIL2, $P = 0.378$ and WIL3, $P = 0.388$). Therefore, both sites were compared to both Group 3 and Group 4.

WIL3, closest to the tailings deposit in Jack of Clubs Lake, was assessed as possibly different to reference when compared to Group 4 (not shown in Fig. 2.4) and equivalent to reference when compared to Group 3 (Fig. 2.4). WIL2 was assigned to Band 4 when compared to the Group 4 reference sites, and to Band 2 when compared to the Group 3 reference sites (Fig. 2.4). Overall abundance and abundance of Chironomidae were markedly lower at the WIL2 site than in Group 4 (Table 2.10 cf. Table 2.4).

The Guichon sites (GUI1 and GUI3) were located in the vicinity of South Forge Mountain. GUI1 was a tailings runoff channel, downstream of the former Bose Lake, which captured runoff from a large tailings dam. GUI3 was approximately 6 km downstream of a large tailings dam in the vicinity of Jim Black Lake; the riparian zone was well vegetated but there was heavy encrustation on the stream bed. The Guichon sites had the highest probability of belonging to Group 4 (Table 2.10), but also had a high probability of belonging to Group 3 (Fig. 2.4).

Both Guichon sites were assessed as belonging to Band 4 in Group 4 (Table 2.10). Overall abundances were markedly lower than in Group 4 reference sites, and no Ephemerellidae or Heptageniidae were collected at either of the Guichon sites (Table 2.10 cf. Table 2.4).

In summary, all four mining sites indicated biological impairment, which was severe at three of the sites. Visual evidence such as mineral encrustation and extensive channelization suggested severe impairment at both Guichon sites, but the two Willow sites looked undisturbed.

2.3.5.3 Logging

Nine sites were sampled in areas where logging was either current or historic. Two sites were assessed as equivalent to reference (Band 1), five sites as possibly different (Band 2), one site as different (Band 3), and one site as very different (Band 4) (Table 2.10). There was little correlation between the visual assessment of the condition of a site and the condition of the invertebrate assemblage. The most visibly modified site was WIL1. The entire catchment had been cleared except for a 3-5 m buffer zone with well-developed riparian vegetation, yet this site was assessed as Band 1 (Table 2.10, Fig. 2.4 - Group 3). The WIL1 site had a high number of families, and the high abundances of Chironomidae, Baetidae, and Heptageniidae characteristic of Group 3 reference sites (Table 2.10 cf. Table 2.4). In contrast, BOW13, which had been logged right down to the stream bank, was assessed to Band 4 (Table 2.10). The BOW13 site had a much-reduced overall abundance, and a much-reduced abundance of three families of Ephemeroptera. BOW14 showed signs of old logging activity and had regrowth of vegetation, but was assessed as belonging to Band 2. This site had similar overall abundance and higher abundance of Baetidae when compared to the Group 3 reference sites. In summary, the sites assigned to Bands 1 and 2 either had a well-developed riparian zone in the midst of extensive logging in the surrounding catchment (WIL1, TYA2), or old logging activities with regrowth (TYA1, BOW14). More severe biological impairment (i.e. assignment to Bands 3 and 4) occurred in recently logged areas (WIL4) or where riparian vegetation was removed (BOW13).

2.4 Summary

This study was designed to provide a system for the assessment of aquatic ecosystem quality for the Fraser River catchment in British Columbia based on the reference-condition approach (Reynoldson et al. 1997b; Rosenberg et al. 2000). The objectives of the study were: (1) to establish a database of reference sites representing undisturbed invertebrate assemblages;

(2) to develop a predictive model that would identify what invertebrate assemblages would be expected to occur at any running-water site in the Fraser catchment based on easily measured habitat attributes; and (3) to test the effects of taxonomic level and seasonal variability on the predictive performance of the models and their ability to assess sites exposed to agricultural, mining, and logging activity.

We have established a reference database of 219 sites. This database contains site-specific information on invertebrates identified to the lowest-possible taxonomic level (either genus or species) and information on 40 habitat descriptors. The data are stored in a Microsoft Access database using the BIRC software (Pascoe and Reynoldson 1998; see Section 1) and are available from the Pacific and Yukon Region of Environment Canada. Data are retrievable from any site or selection of sites at four taxonomic levels (order, family, genus, and sometimes species) with selectable habitat descriptors.

Predictive models were constructed at family, genus, and species levels, using both taxonomic and metric assemblage descriptors (Reynoldson et al., submitted); only family-level data were presented in this report. We recommend the use of the family-level taxonomic model for general application in the Fraser catchment because of best overall performance compared to the other models (Reynoldson et al., submitted). In particular, it has greater ability than the other models to detect differences from the reference condition, it can be used by workers with less taxonomic training and expertise than required for the lower taxonomic models, and it requires fewer calculations than the metric models. Use of the family-level model should be limited to autumn sampling in the Fraser catchment.

An examination of 21 sites exposed to stress from agriculture, mining, and logging showed that the predictive family-level model and in-stream assessments were able to both discriminate between biologically impaired and unimpaired sites, and to designate the degree of impairment of the invertebrate assemblage. There was no consistent relationship between apparent disturbance of the physical habitat and the response of the in-stream invertebrate assemblage.

Therefore, biologically valid measurement is critical for an objective assessment of stream condition.

In conclusion, the classification of reference sites for the Fraser River catchment should provide a valuable tool for broad application in environmental assessment. The software for using the family-level model will soon be available for users. In reality, however, environmental assessment and an adequate description of the response to pollution is almost always a compromise between the scientific ideal and political, financial, and logistic limitations (Warwick 1993). Thus, in the next section we report results that are usable for alternative monitoring approaches that may be selected.

3. MACROINVERTEBRATES COLLECTED FROM REFERENCE SITES OF THE FRASER RIVER CATCHMENT: STRUCTURAL, FUNCTIONAL, AND HABITAT CHARACTERISTICS OF SUBCATCHMENTS, AND METRICS APPLICABLE FOR BIOASSESSMENT

3.1 Introduction

Benthic macroinvertebrates are the basis for most biomonitoring programs currently in use worldwide in both developed (Rosenberg and Resh 1993a) and developing countries (Resh 1995), and the reasons for this choice are clear (Rosenberg and Resh 1996). Through these programs, a great deal of ecological data concerning freshwater biota and habitats are gathered. However, much of this information is not exploited because it is not part of the analytical protocol in place at the time these applied assessments are conducted. However, analytical approaches used in assessments can change over time; data useful for one approach may not be applicable to another, or data not useful for one may be useful for a future approach. For example, in the U.S.A., emphasis has shifted over time from largely qualitative studies (e.g. analysis of faunal components) to quantitative studies (e.g. involving inferential statistics) to a mixture of these approaches (e.g. rapid bioassessment) over the last three decades (Resh and Jackson 1993).

The biomonitoring program for the Fraser River catchment described in this report was designed to produce a multivariate model (Reynoldson et al. 1995; see Section 2). However, vast amounts of biological and habitat information have been accumulated in the process of obtaining information to develop this model, and these data could be important as new monitoring approaches develop and are selected.

Water-quality monitoring approaches have become closely identified with their countries of origin and development, examples being the Saprobien index with Germany (Cairns and Pratt 1993) and the **River InVertebrate Prediction And Classification System** (RIVPACS) with the U.K. (Wright 1995). The rapid bioassessment protocols developed in the mid-1980s (Plafkin et al. 1989) are most identified with biomonitoring in the U.S.A. The BEAST model, applied here to the Fraser River and applied previously to the Laurentian Great Lakes (Reynoldson et al. 1995), is thus far the approach most uniquely identified with assessment of Canadian fresh waters. In this section of the report, we describe how the rapid assessment approach used throughout the U.S.A. (USEPA 1998) could also be applied to future water quality monitoring programs of the Fraser River.

Rapid bioassessment attempts to provide an integrated assessment of an aquatic resource, comparing habitat (e.g. physical structure, flow regime) and biological measures with empirically defined reference conditions (USEPA 1998). Resh et al. (1995, 2000) have noted that in almost all its permutations (see appendix in Resh and Jackson 1993), rapid bioassessment approaches use techniques that attempt to evaluate assemblages of benthic macroinvertebrates at reduced costs relative to those associated with traditional, more quantitatively rigorous assessments. The effort (and cost) of benthic analysis is reduced with rapid bioassessment because of four specific features. First, a single relatively large sample, covering an area several-fold larger than that in traditional quantitative collections, is taken instead of several replicate samples. Second, a standardized subsampling procedure is used (e.g. the first 100-300 organisms randomly sorted), which both reduces the number of organisms processed and provides a relatively consistent unit of effort for the processing of all samples.

Third, identification is often to family level. Fourth, the results of surveys can be summarized in ways that can be understood by non-specialists, such as managers, other decision makers, and the concerned public. These are also characteristics of the BEAST model described in Section 2.

Rapid bioassessment protocols in the U.S.A. are based on the use of multimetrics. This approach attempts to provide an integrated analysis of the biological communities at a site by calculating various metrics (or measures) representing functional or structural aspects of the community and summing these into a single score. Their use has not been without controversy; for example, potentially important ecological information may be lost by aggregating individual measures into an index (e.g. Suter 1993; Polls 1994). In addition, some metrics are too variable to detect impairment consistently (or may indicate impairment when it does not occur) and are based on subjective criteria (Resh and Jackson 1993; Hannaford and Resh 1995). Supporters, however, have argued that the advantage of a multimetric approach is that it incorporates ecological information on how aquatic organisms feed, reproduce, and exploit their habitats (Fore et al. 1996) into water quality assessments. They suggest that reliance on combinations of multiple measures minimizes the weaknesses of individual metrics (e.g. USEPA 1998). These debates are often “apples and oranges” in content, and the resolution of these differences seems far from over.

The use of the multimetric approach in biological monitoring has expanded greatly in the U.S.A. over the past decade. Currently 47 of the 50 U.S. states use benthic macroinvertebrates as the “target assemblages” (Utah, Nevada, and South Dakota do not, probably because of the intermittency of their wadeable streams); 31 states also use fish and five use periphyton in bioassessments (Barbour et al. 1995; USEPA 1998). State programs in the U.S.A. are usually based on modifications of a national program, developed and promulgated by the U.S. Environmental Protection Agency (Plafkin et al. 1989).

In this section, we present information on benthic macroinvertebrate assemblages and riverine habitats of the Fraser River catchment to fulfill three objectives: (1) to summarize zoogeographical and ecological information on habitats and macroinvertebrate assemblages; (2) to provide other types of information that users of the BEAST model in the Fraser catchment may also consider in their interpretation of results; and (3) to determine which metrics are most appropriate for examining impairment in the Fraser River catchment if a rapid assessment approach to monitoring is selected or if metrics are considered for inclusion in multivariate models. To accomplish objective 3, we examine a range of metrics in two ways: (a) do they detect impairment when impairment occurs, and (b) do they give incorrect indications of impairment when no impairment occurs (Type 1 errors).

3.2 How do multimetric and multivariate approaches differ?

Both approaches involve similar methods for collection of benthic macroinvertebrates. The range of environmental variables used in the multivariate predictive models are not generally measured when multimetric collections are made. Instead, a habitat assessment supplements the biological information collected in the multimetric approach (Plafkin et al. 1989; Hannaford et al. 1997). The two approaches diverge further once samples are collected, sorted, and specimens are identified. In multimetric analysis, sites are grouped *a priori* based on their geophysical attributes, and final classification is based on taxonomic composition. In multivariate approaches, sites are classified into groups using clustering methods based on the similarity of their species composition. In multivariate approaches, selection may be based on the sites in the reference group with which the test site has the highest probability of inclusion using a discriminant model (e.g. the BEAST). Alternatively, the selection may draw on information from several reference groups according to the weighted probabilities with which the test site would be included in those reference groups [e.g. the RIVPACS of the U.K., the **AU**Stralian **RIV**er **A**ssessment **S**cheme (AusRivAS) of Australia].

Finally, test-site assessment in the multimetric approach is based on quartile distributions of additive metrics, whereas in the multivariate approach it may be based on a comparison of the test and reference sites in taxa ordination space, using probability ellipses constructed around reference sites (the BEAST) or a comparison of the taxa observed at the test site and those expected to be at the site, based on weighted probabilities of taxon occurrence (RIVPACS, AusRivAS). The above distinctions are discussed in detail by Reynoldson et al. (1997b).

Reynoldson et al. (1997b) compared two multivariate predictive models (the BEAST and AusRivAS) with a multimetric analysis using family-level data for 60 sites in the Fraser River catchment. The multimetric analysis was done using two groups of metrics. First, a fixed list of metrics modified from Plafkin et al. (1989) was used, which included calculation of the following: (1) number of individuals; (2) number of families; (3) % EPT individuals; (4) % Chironomidae individuals; (5) number of EPT individuals/number of EPT + Chironomidae individuals; (6) number of Hydropsychidae/number of Trichoptera individuals; (7) % dominance of a single taxon; and (8) the Family Biotic Index (Hilsenhoff 1988). Based on input from M.T. Barbour and J. Gerritsen (Tetra Tech Inc., Owings Mills, MD), a second multimetric analysis was carried out in which (1) number of individuals was deleted, and (5) number of EPT individuals/number of EPT + Chironomidae individuals was replaced with number of Baetidae individuals/number of Ephemeroptera individuals. A composite score was then calculated based on the similarity of metrics to the appropriate reference-site classification. Precision (i.e. whether all replicates at a single site were consistently designated as impaired or unimpaired) and accuracy (i.e. designations of unimpaired sites as unimpaired) of multimetric assessments were estimated. The precision and accuracy of the two groups of metrics were then compared within ecoregion, stream order, and biotic classifications.

The results of this comparison indicated that the two multivariate models performed consistently better than either of the fixed metric designs (Multimetric 1 and 2 in Table 3.1). In one comparison of precision, the BEAST performed less well than AusRivAS. However, AusRivAS failed to designate a known impaired site as impaired, which the BEAST designated as impaired.

Although the approach of using a fixed group of metrics was the procedure applied at the time the Reynoldson et al. (1997b) comparison was done, recent guidelines have indicated that choosing specific metrics that are most appropriate for the region under study from a series of available metrics (USEPA 1998) is preferable. Therefore, in the analysis reported here a large range of potentially appropriate metrics was examined for applicability based on accuracy and precision of their performance.

3.3 Study sites and methods

Only reference sites were used in the following analysis, except for the Salmon River. Samples collected during other seasons (Dymond 1998) or as quality control replicates were not included in the results presented here.

3.3.1 Analysis of faunal composition of the Fraser River

Average abundances were determined for all benthic macroinvertebrates collected from the 219 reference sites and are reported according to subcatchment (see Table 1.3). Standard deviations, and ranges for all metrics and for habitat attributes were calculated by subcatchment.

Table 3.1. Precision (A) and accuracy (B) of assessment methods as percentage correct; see Reynoldson et al. (1997b) for additional details. AusRivAS = AUStralian RIVER Assessment Scheme, BEAST = BEnthic Assessment of SedimenT.

	Ecoregion	Stream Order	Biotic grouping
A. Designations of sites as either all impaired or unimpaired			
Multimetric 1	40	80	60
Multimetric 2	60	80	80
BEAST	80	100	80
AusRivAS	100	100	100
B. Designations of unimpaired sites as unimpaired			
Multimetric 1	50	38	75
Multimetric 2	69	38	88
BEAST	100	100	100
AusRivAS	100	100	100

3.3.2 *Analysis of precision and accuracy of metrics*

Metrics were calculated in two ways: (1) at the family level, because this identification level is used in many rapid bioassessment programs and in the BEAST model (Section 2); and (2) at genus/species when possible (but not, for example, with the Family Biotic Index or % Chironomidae), as used in other programs. A total of 44 metrics was examined, including the same nine metrics used by Reynoldson et al. (1997b) in the analysis described in Table 3.1 and an additional 35 metrics chosen from table 7.1 of USEPA (1998). The 44 metrics can be divided into four groups: measures of richness; numbers of individuals (or enumerations); functional-feeding group ratios; and a biotic index. Means, SDs, and ranges for metrics were calculated for the 219 reference sites and reported by subcatchment.

Analysis of metrics for precision and accuracy, and for appropriateness of use in multivariate and multimetric approaches, involved calculation of CVs for sites in six streams (marked with an asterisk in Table 3.2) in the Fraser River catchment. Sites tested included one considered to be impaired (Salmon River site 3, see Table 2.10) and sites considered to be unimpaired. These designations were initially determined by personnel knowledgeable with this area (see Section 1 for a description of the workshops conducted for this purpose), examination of the area around a site (by helicopter), and evidence of physical disturbance at a site.

To determine if impairment could be detected at presumed impaired sites and, conversely, to determine if impairment would be incorrectly indicated (Type I error) at presumed unimpaired sites, we compared: impaired sites with unimpaired sites (Salmon 1 cf. 3, 2 cf. 3); unimpaired sites of the same stream order in different ecoregions (selected because of their geomorphic similarity: Clearwater 6 cf. Stuart 2); unimpaired sites in different streams of the same order in the same ecoregion (without regard to geomorphic similarity: Clearwater 3 cf. 6, Chilcotin 4 cf. 5, 5 cf. 8, Stuart 2 cf. 4, 2 cf. 6); and sites of the same or ± 1 order in the same stream (Pitt 1 cf. 6, 2 cf. 6, 3 cf. 6, 7 cf. 8).

Table 3.2. Description of sampling sites for this analysis. An asterisk indicates sites where replicate samples were collected.

Subcatchment	Site	River	Order	Ecoregion	Impacts
Salmon	1	Salmon	3	Thompson-Okanagan Plateau	None
	2	Salmon	4	Thompson-Okanagan Plateau	None
	3*	Salmon	4	Thompson-Okanagan Plateau	Agriculture, logging
	4	Salmon	4	Thompson-Okanagan Plateau	Agriculture, logging
Chilcotin	4	Cluska	4	Fraser Plateau	None
	5*	Palmer Creek	4	Fraser Plateau	None
	8	Cluska	3	Fraser Plateau	None
Clearwater	3	Hobson Creek	2	Southern Rocky Mountain Trench	None
	6*	Hemp Creek	2	Southern Rocky Mountain Trench	None
Pitt	1	Pitt	2	Pacific Ranges	None
	2	Pitt	2	Pacific Ranges	None
	3	Pitt	3	Pacific Ranges	None
	6*	Pitt	3	Pacific Ranges	None
	7*	Pitt	4	Pacific Ranges	None
	8	Pitt	4	Pacific Ranges	None
Stuart	2*	Condit Creek	2	Omineca Mountains	None
	4	Lion Creek tributary	2	Omineca Mountains	None
	6	Lion Creek	3	Omineca Mountains	None

Statistical analysis of these 12 comparisons involved one-tailed t-tests at $\alpha = 0.05$, as recommended by USEPA (1998). A one-tailed test was used because the metrics change in one direction (e.g. a decrease in number of taxa present with impairment). Because we could categorize the sites as impaired or unimpaired, and we examined metric response individually, a Bonferroni correction was not necessary. This procedure is described in detail in Resh et al. (2000).

3.4 Results and discussion

3.4.1 Overview

The future use of the information collected during this project depends on its availability in both raw (available from Environment Canada) and synthesized forms (as presented in this report). A taxonomic summary of the fauna, and its distribution, abundance, and frequency of occurrence by subcatchment, is presented in Appendix 3. Information on richness, numerically dominant taxa, abundance, and frequency of occurrence by subcatchment is summarized in Table 3.3 for the invertebrate orders collected. Table 3.4 provides the means, SDs, and ranges (minimum to maximum) for a series of descriptive metrics of the structural and functional attributes of the benthic macroinvertebrate assemblage described at species (Table 3.4A) and family (Table 3.4B) taxonomic levels. Table 3.5 provides means, SDs, and ranges for several habitat attributes of the 219 subcatchments. We describe some of the biological, chemical, and physical features of the reference sites in the Fraser River but the information presented in the tables (3.3-3.5) and Appendix 3 goes far beyond the discussion below.

3.4.2 The fauna

Fourteen orders of aquatic invertebrate animals (Table 3.3) were found at the 219 reference sites sampled; taxa present at reference sites are arranged by subcatchment in Appendix 3.

Table 3.3 Summary of taxonomic, distributional, and numerical dominance, arranged by subcatchment.

Order	Number of families in order collected	Number of taxa in order collected	Number of sub-catchments order found in	Most widely distributed taxa and number of sub-catchments found in
Acariformes	8	8	21	<i>Sperchon</i> spp., 21
Amphipoda	3	3	3	<i>Crangonyx richmondensis-occidentalis</i> , 2
Bivalvia	2	6	14	<i>Sphaerium</i> spp., 8
Coelenterata	1	1	3	<i>Hydra</i> polyps, 3
Coleoptera	1	9	15	<i>Heterolimnius</i> spp., 11
Collembola	2	2	2	<i>Semicerura</i> spp., 1 <i>Xamila</i> spp., 1
Diptera	16	136	21	<i>Eukiefferiella behmi</i> group, 21 <i>Tvetenia gavarica</i> group, 21
Ephemeroptera	8	35	21	<i>Rhithrogena</i> spp., 21
Gastropoda	4	5	5	<i>Gyraulus circumstriatus</i> , 2 <i>Valvata humeralis</i> , 2 <i>Valvata sincera</i> , 2
Hirudinea	1	1	1	<i>Piscicola milneri</i> , 1
Megaloptera	1	1	1	<i>Sialis</i> spp., 1
Oligochaeta	4	19	20	<i>Specaria fraseri</i> , 13
Plecoptera	9	29	21	<i>Capnia</i> spp., 19 <i>Isoperla</i> spp., 19 <i>Taeionema</i> spp., 19
Trichoptera	12	62	21	<i>Rhyacophila acropedes</i> group, 17
TOTALS: 14	72	341		

The orders included 72 families and at least 341 taxa (mostly identified to the generic level). The insect order Diptera contained the most families (16) and taxa (136), followed by the Trichoptera (12 families, 62 taxa). Representatives of several orders (Acariformes, Diptera, Ephemeroptera, Plecoptera, and Trichoptera) were found in all 21 subcatchments containing reference sites; other groups were limited to a single subcatchment (Hirudinea and Megaloptera). Some taxa were found in all subcatchments (Eukiefferiella behmi group [Diptera], Tvetenia gavarica [Diptera], Sperchon spp. [Acariformes], Rhithrogena spp. [Ephemeroptera]), and some in many subcatchments (e.g. Capnia spp. and Isoperla spp. [Plecoptera], 19). Densities of individual taxa sometimes exceeded 1000 individuals per 3-min kick sample for some Diptera (e.g. Micropsectra spp., Euchiniko; Tanytarsus spp., Nicola; Polypedilum spp., Euchiniko) and Ephemeroptera (Baetis bicaudatus, Euchiniko; Baetis tricaudatus, Chilcotin, Ephemerella mollita, Euchiniko; Serratella spp., Coldwater; Heptagenia spp., Chilcotin).

3.4.3 Richness metrics

Richness measures are the most commonly used descriptor of benthic macroinvertebrate assemblages (Resh and McElravy 1993). Highest richness values were found in the Chehalis, Chelaslie, Euchiniko, Nicola, Tyaughton, and West Road subcatchments; all means exceeded 30 taxa per site in a 3-min kick sample (Table 3.4). Lowest richness values were found in the Fraser mainstem, and Herrick, Lillooet, Pitt, and upper Fraser subcatchments (all <22 taxa/site/3-min kick sample). However, the number of taxa in individual samples ranged from six to 53. Numbers of EPT taxa were highest in the Chehalis, Nicola, Stein, Stuart, and Tyaughton subcatchments (mean >14), lowest in the Coldwater, Euchiniko, Fraser mainstem, Lillooet, Pitt, Thompson, and upper Fraser subcatchments (<12), and the range for EPT taxa in individual samples was two to 27.

Table 3.4. Mean, standard deviation (SD), and ranges for rapid bioassessment metrics arranged by subcatchment. Metrics were calculated at genus/species (A) and family (B) levels. EPT = Ephemeroptera, Plecoptera, and Trichoptera. See USEPA (1998) for description of how metrics are calculated.

A: Genus/species

Basin		Bowron	Chehalis	Chelaslie	Chilcotin	Chilko	Clearwater	Coldwater	Euchiniko	Fraser	Herrick	Lillooet	Nicola	Pitt	Stein	Stuart	Taseko	Thompson	Torpy	Tyaughton	Upper Fraser	West Road
No. sites		12	9	12	13	8	12	6	8	12	12	12	10	16	12	10	8	1	8	8	12	18
Total no. taxa	Mean	27.8	30.6	30.1	29.8	27.9	27.4	24.0	30.3	21.6	21.5	15.6	30.1	19.8	25.8	27.9	26.8	27.0	22.6	30.1	18.6	31.8
	SD	5.8	10.2	5.2	7.0	5.7	4.8	2.7	12.3	6.1	4.0	6.5	7.7	8.6	3.4	5.8	6.3		3.9	4.8	8.2	8.0
	Min.	20.0	18.0	19.0	17.0	15.0	21.0	20.0	15.0	12.0	16.0	6.0	18.0	10.0	20.0	19.0	15.0	27.0	19.0	24.0	7.0	15.0
	Max.	36.0	48.0	37.0	44.0	32.0	37.0	28.0	53.0	35.0	28.0	28.0	40.0	39.0	32.0	39.0	35.0	27.0	30.0	38.0	31.0	46.0
No. EPT taxa	Mean	13.8	15.4	13.3	13.4	14.0	12.8	11.0	11.1	9.3	12.6	10.2	15.3	11.6	14.1	14.4	14.0	9.0	13.6	18.0	11.4	13.2
	SD	3.7	5.7	4.3	4.3	3.0	4.6	1.1	5.1	4.1	3.3	3.1	3.8	4.0	3.3	3.5	3.9		4.0	3.2	6.4	3.6
	Min.	8.0	9.0	4.0	6.0	11.0	8.0	9.0	5.0	2.0	7.0	6.0	9.0	6.0	7.0	8.0	10.0	9.0	6.0	13.0	3.0	7.0
	Max.	21.0	27.0	21.0	21.0	19.0	21.0	12.0	20.0	14.0	17.0	17.0	22.0	20.0	19.0	20.0	19.0	9.0	18.0	23.0	20.0	21.0
No. Plecoptera	Mean	4.8	4.6	4.2	3.8	5.3	4.3	1.7	3.6	3.8	6.2	4.2	5.5	4.3	5.8	4.3	5.1	1.0	5.0	6.1	4.6	3.8
	SD	2.2	2.2	2.2	1.4	1.8	2.3	1.0	1.5	1.6	2.1	1.1	1.8	1.4	1.7	0.9	1.7		1.6	1.1	2.9	2.0
	Min.	1.0	2.0	1.0	2.0	3.0	1.0	0.0	2.0	2.0	3.0	3.0	2.0	2.0	3.0	3.0	2.0	1.0	2.0	4.0	1.0	1.0
	Max.	8.0	8.0	9.0	6.0	8.0	8.0	3.0	6.0	6.0	9.0	6.0	9.0	7.0	9.0	6.0	7.0	1.0	7.0	8.0	10.0	8.0
No. Ephemeroptera	Mean	5.1	6.3	5.9	4.8	5.6	5.7	5.3	3.9	3.8	4.5	4.1	5.8	5.0	5.3	5.4	5.8	3.0	5.5	6.4	4.3	4.9
	SD	1.8	1.7	1.4	2.2	0.9	1.9	0.5	2.1	1.9	0.7	1.9	2.0	1.5	1.1	2.0	1.5		1.9	1.8	2.4	1.4
	Min.	2.0	5.0	3.0	1.0	4.0	3.0	5.0	1.0	0.0	3.0	0.0	1.0	3.0	4.0	3.0	4.0	3.0	1.0	3.0	1.0	2.0
	Max.	9.0	9.0	8.0	8.0	7.0	9.0	6.0	7.0	6.0	5.0	7.0	8.0	8.0	7.0	9.0	9.0	3.0	7.0	9.0	7.0	7.0
No. Trichoptera	Mean	4.0	4.6	3.3	4.8	3.1	2.9	4.0	3.6	1.8	1.9	1.9	4.0	2.3	3.0	4.7	3.1	5.0	3.1	5.5	2.6	4.4
	SD	1.3	2.7	1.7	2.1	2.0	1.9	0.9	2.2	1.7	1.8	2.1	2.5	2.5	1.7	2.6	1.9		1.6	2.3	2.1	2.4
	Min.	2.0	2.0	0.0	2.0	0.0	1.0	3.0	1.0	0.0	0.0	0.0	1.0	0.0	0.0	2.0	1.0	5.0	1.0	3.0	0.0	0.0
	Max.	6.0	10.0	6.0	8.0	5.0	6.0	5.0	8.0	6.0	6.0	7.0	9.0	9.0	5.0	9.0	6.0	5.0	6.0	9.0	7.0	9.0
No. Diptera	Mean	11.5	11.1	13.8	13.3	11.1	11.7	10.0	15.6	9.6	8.1	4.9	11.4	6.3	10.8	12.3	9.4	15.0	7.3	11.1	5.8	13.8
	SD	4.4	4.9	3.4	3.6	5.2	2.9	3.1	6.1	4.1	2.9	3.8	4.3	4.1	4.3	4.3	2.6		3.3	3.3	1.9	4.4
	Min.	4.0	4.0	10.0	7.0	3.0	6.0	6.0	8.0	3.0	4.0	0.0	7.0	2.0	5.0	7.0	5.0	15.0	4.0	7.0	3.0	4.0
	Max.	18.0	18.0	20.0	18.0	18.0	17.0	13.0	25.0	17.0	14.0	11.0	18.0	15.0	19.0	21.0	14.0	15.0	14.0	18.0	10.0	22.0
No. Chironomidae	Mean	9.6	8.4	11.7	10.5	8.8	9.4	6.3	12.3	7.8	6.6	3.8	8.7	4.8	8.9	10.2	7.9	15.0	5.0	8.1	4.8	11.6
	SD	4.3	3.8	3.3	3.3	4.1	3.3	2.0	5.4	3.9	2.7	3.2	3.9	2.8	4.7	3.8	2.1		2.4	3.2	2.3	4.0
	Min.	2.0	3.0	8.0	3.0	3.0	4.0	4.0	6.0	2.0	3.0	0.0	5.0	2.0	3.0	6.0	4.0	15.0	2.0	5.0	1.0	3.0
	Max.	16.0	14.0	16.0	15.0	15.0	14.0	9.0	21.0	14.0	13.0	9.0	16.0	11.0	18.0	18.0	11.0	15.0	10.0	14.0	9.0	19.0
No. Odonata	Mean	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	SD	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0
	Min.	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Max.	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
No. Coleoptera	Mean	0.8	0.6	0.5	1.0	0.1	0.5	0.0	1.0	0.1	0.0	0.0	1.6	0.3	0.0	0.1	0.3	0.0	0.5	0.0	0.0	1.6
	SD	0.9	0.5	0.7	0.9	0.4	0.7	0.0	0.5	0.3	0.0	0.0	0.8	0.9	0.0	0.3	0.5		0.5	0.0	0.0	0.7
	Min.	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Max.	3.0	1.0	2.0	3.0	1.0	2.0	0.0	2.0	1.0	0.0	0.0	3.0	3.0	0.0	1.0	1.0	0.0	1.0	0.0	0.0	2.0
EPT/Chironomidae+EPT	Mean	0.7	0.8	0.7	0.8	0.8	0.7	0.9	0.6	0.8	0.8	0.7	0.6	0.9	0.8	0.6	0.8	0.3	0.9	0.8	0.8	0.6
	SD	0.2	0.1	0.2	0.1	0.2	0.2	0.0	0.2	0.3	0.3	0.4	0.2	0.1	0.2	0.1	0.1		0.3	0.2	0.2	0.2
	Min.	0.3	0.6	0.3	0.5	0.5	0.4	0.9	0.2	0.1	0.0	0.0	0.3	0.6	0.5	0.4	0.6	0.3	0.2	0.4	0.4	0.3
	Max.	1.0	1.0	0.9	0.9	1.0	0.9	0.9	0.8	1.0	1.0	1.0	0.9	1.0	1.0	0.8	1.0	0.3	1.0	1.0	1.0	1.0
% EPT individuals	Mean	65.0	75.7	61.4	67.6	68.8	62.0	86.4	52.6	68.8	81.4	89.5	57.6	84.2	72.9	56.8	75.6	24.9	81.2	77.9	75.3	56.0
	SD	23.6	17.7	19.4	14.2	19.8	18.0	3.9	19.2	27.4	26.4	9.7	22.4	16.3	18.2	12.9	11.8		26.2	19.1	17.4	19.7
	Min.	33.0	42.4	24.8	38.3	36.9	32.6	81.0	17.8	9.4	4.5	66.4	22.5	53.1	37.2	35.6	53.5	24.9	17.3	37.6	41.7	23.5
	Max.	94.4	97.4	90.0	86.8	96.0	87.7	90.1	78.3	95.8	97.8	100.0	80.2	98.5	94.8	73.6	95.2	24.9	96.2	93.7	94.2	95.2

A: Genus/species

Basin		Bowron	Chehalis	Chelaslie	Chilcotin	Chilko	Clearwater	Coldwater	Euchiniko	Fraser	Herrick	Lillooet	Nicola	Pitt	Stein	Stuart	Taseko	Thompson	Torpy	Tyaughton	Upper Fraser	West Road
No. sites		12	9	12	13	8	12	6	8	12	12	12	10	16	12	10	8	1	8	8	12	18
% Ephemeroptera	Mean	44.6	47.5	41.8	39.5	32.4	43.6	49.7	29.7	29.1	44.5	24.4	27.8	43.9	51.6	30.5	52.4	16.4	62.3	35.4	48.5	36.7
	SD	25.9	11.0	13.4	16.2	13.9	20.5	12.1	17.5	27.9	27.7	17.4	18.3	18.8	18.5	13.4	13.9		26.8	10.2	25.6	15.7
	Min.	10.3	28.8	18.5	13.4	16.1	11.6	29.6	4.7	0.0	2.5	0.0	1.8	12.7	17.6	6.7	34.1	16.4	1.1	18.3	7.8	8.6
	Max.	80.6	64.8	66.7	70.4	54.3	76.4	62.2	53.0	85.8	84.4	67.3	57.2	68.8	78.8	45.5	69.6	16.4	81.7	47.2	85.3	65.1
% Plecoptera	Mean	12.0	18.4	10.5	19.1	30.5	15.2	1.5	17.3	37.8	35.5	60.8	21.0	37.0	18.0	17.7	19.9	1.6	15.4	21.6	20.3	12.1
	SD	9.5	9.7	9.4	20.2	23.1	9.9	1.0	23.1	21.5	20.6	20.5	22.0	21.0	8.4	6.7	15.3		8.5	10.6	20.0	13.8
	Min.	1.0	1.7	0.8	1.4	6.6	2.0	0.0	1.0	3.9	1.5	15.3	2.0	13.4	10.0	4.9	6.8	1.6	2.2	9.6	3.6	1.6
	Max.	31.2	31.9	33.2	59.2	79.9	30.6	2.7	72.3	75.0	70.9	79.3	74.8	83.9	40.5	25.0	44.9	1.6	28.2	35.5	66.0	48.3
% Trichoptera	Mean	8.4	9.9	9.1	9.0	5.9	3.3	35.2	5.5	1.9	1.4	4.2	8.9	3.3	3.4	8.5	3.3	6.9	3.6	20.9	6.4	7.3
	SD	12.4	9.4	12.3	8.2	7.5	2.3	10.4	4.1	1.8	1.8	6.7	8.7	5.9	2.4	6.0	2.4		3.4	20.1	9.0	4.9
	Min.	2.0	1.8	0.0	0.9	0.0	0.3	23.0	1.3	0.0	0.0	0.0	1.2	0.0	0.0	1.9	0.6	6.9	0.5	3.6	0.0	0.0
	Max.	44.1	26.8	42.0	25.4	21.6	7.5	49.5	14.3	5.3	6.3	21.0	29.1	22.8	9.2	22.1	8.5	6.9	9.7	60.7	31.9	18.9
% Chironomidae	Mean	24.8	15.5	28.9	19.5	20.4	29.3	6.9	40.1	22.7	16.8	9.0	30.6	10.7	22.7	38.5	16.7	70.9	12.4	18.7	20.7	31.1
	SD	19.8	11.8	14.7	9.0	12.8	17.6	2.3	18.9	27.2	25.9	8.8	19.8	12.5	15.2	12.8	11.0		22.9	19.6	17.2	20.8
	Min.	3.0	2.5	8.7	8.7	3.0	5.0	5.1	16.6	1.2	1.3	0.0	5.5	0.9	2.4	19.2	4.1	70.9	1.0	3.1	0.4	3.4
	Max.	62.4	33.1	51.8	38.8	42.8	54.7	11.3	77.1	89.3	93.5	30.1	61.6	41.8	51.4	57.8	37.7	70.9	68.6	60.3	57.4	69.0
% Odonata	Mean	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	SD	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0
	Min.	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Max.	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
% Coleoptera	Mean	2.7	0.6	0.4	2.7	0.8	1.2	0.0	2.0	0.1	0.0	0.0	6.0	0.8	0.0	0.4	0.2	0.0	2.6	0.0	0.0	5.1
	SD	4.9	0.9	0.7	4.2	2.4	2.2	0.0	1.4	0.2	0.0	0.0	6.8	2.2	0.0	1.4	0.4		4.7	0.0	0.0	5.2
	Min.	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Max.	14.0	2.6	2.0	15.4	6.8	7.0	0.0	3.9	0.6	0.0	0.0	20.8	8.1	0.0	4.4	1.0	0.0	13.6	0.0	0.0	18.6
% Tanytarsini	Mean	16.1	5.0	8.4	6.8	3.8	13.3	3.6	26.1	2.6	3.0	0.0	8.6	2.6	6.3	27.6	5.9	0.0	1.5	3.9	4.8	13.5
	SD	18.0	6.8	5.4	5.4	5.3	12.2	1.9	17.4	4.2	7.0	0.0	8.1	6.2	7.7	11.5	9.2		1.7	9.2	12.0	15.2
	Min.	0.0	0.0	1.3	0.3	0.0	0.3	2.4	10.8	0.0	0.0	0.0	1.2	0.0	0.0	9.9	0.0	0.0	0.0	0.0	0.0	0.8
	Max.	51.5	20.3	23.3	15.4	15.1	35.3	7.5	60.5	13.6	25.0	0.0	27.0	23.3	25.0	44.4	28.1	0.0	5.1	26.6	41.2	59.3
% Diptera/non-insect	Mean	86.9	83.7	87.3	84.2	76.0	90.8	76.1	95.0	82.5	95.3	87.2	90.2	82.0	94.2	97.4	75.9	94.4	87.7	93.4	85.2	86.9
	SD	17.0	17.6	10.5	13.6	22.4	13.6	17.5	4.8	12.3	6.4	28.7	12.7	20.1	11.7	3.3	24.3		10.1	9.7	18.1	15.5
	Min.	44.3	50.0	69.6	65.3	41.6	50.0	42.6	86.7	64.0	80.0	0.0	68.0	40.0	59.3	91.6	40.0	94.4	71.4	74.4	37.5	35.4
	Max.	100.0	100.0	100.0	100.0	100.0	100.0	89.7	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	94.4	100.0	100.0	100.0	100.0
% Trichoptera as Hydropsychidae	Mean	14.9	7.8	13.3	12.5	12.5	12.3	15.0	20.7	22.2	10.5	1.4	36.4	7.7	12.0	9.1	18.7	69.2	4.4	12.5	20.1	24.7
	SD	20.5	18.8	15.8	17.4	19.6	20.9	12.3	26.2	35.1	17.1	2.7	41.5	16.7	17.9	15.4	23.1		8.7	11.6	30.1	31.2
	Min.	0.0	0.0	0.0	0.0	0.0	0.0	3.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	69.2	0.0	0.0	0.0	0.0
	Max.	60.0	57.1	42.6	58.8	57.1	55.6	36.8	66.7	100.0	50.0	7.1	100.0	64.3	50.0	50.0	66.7	69.2	23.1	30.0	100.0	100.0
% Ephemeroptera as Baetidae	Mean	45.0	31.7	54.9	58.2	23.0	39.9	7.4	51.1	15.5	36.9	18.9	50.0	33.4	33.5	38.0	17.4	38.7	42.3	26.8	46.3	51.8
	SD	23.0	30.6	25.5	21.5	14.6	31.2	4.7	33.7	25.3	24.9	21.4	26.1	20.6	22.9	21.5	14.0		24.1	18.6	39.2	30.5
	Min.	0.0	3.1	5.2	31.3	0.0	0.0	2.8	8.3	0.0	0.0	0.0	2.7	4.7	0.0	0.0	0.0	38.7	0.0	0.0	0.0	2.2
	Max.	71.5	75.4	80.5	100.0	47.5	96.4	15.6	100.0	85.7	77.0	66.9	100.0	72.5	75.4	61.4	35.4	38.7	62.6	59.4	94.9	94.7
Total abundance	Mean	4262.6	579.1	9024.8	12531.9	2332.8	7726.6	6837.8	17090.4	383.3	6645.8	1531.1	10607.2	1343.5	4968.7	3708.2	3796.0	821.7	5357.1	2817.3	2317.6	10407.3
	SD	5024.2	349.6	6306.2	7535.7	1619.6	10446.4	4460.4	11713.6	330.9	7522.4	1476.9	5379.2	2197.7	2896.1	4058.9	7742.4		6239.8	3663.5	3762.8	7585.5
	Min.	460.0	142.0	2110.0	3211.7	208.0	1070.0	1860.0	5140.0	61.0	475.0	226.0	4720.0	148.0	770.4	796.0	147.0	821.7	1150.0	295.0	23.0	2062.5
	Max.	17900.0	1180.0	21900.0	25700.0	4800.0	32502.9	12400.0	36800.0	1105.9	20500.0	4483.3	18626.6	9225.0	9800.0	14625.0	22800.0	821.7	18000.0	11450.0	10850.0	29500.0

A: Genus/species

Basin		Bowron	Chehalis	Chelaslie	Chilcotin	Chilko	Clearwater	Coldwater	Euchiniko	Fraser	Herrick	Lillooet	Nicola	Pitt	Stein	Stuart	Taseko	Thompson	Torpy	Tyaughton	Upper Fraser	West Road
No. sites		12	9	12	13	8	12	6	8	12	12	12	10	16	12	10	8	1	8	8	12	18
No. predators	Mean	312.2	79.4	1260.4	1317.5	291.8	445.8	541.7	1644.2	86.7	438.7	273.0	2586.1	190.7	487.9	386.4	249.2	204.3	342.3	315.1	91.3	1768.8
	SD	280.7	55.5	1012.2	1290.0	323.1	355.5	358.7	1665.5	110.7	388.2	330.7	3237.8	415.9	355.6	277.8	400.8		166.4	239.5	162.0	2084.9
	Min.	84.6	14.0	330.0	116.7	9.0	63.0	140.0	320.0	5.0	2.9	11.5	320.0	4.0	68.2	124.0	16.0	204.3	150.0	23.0	0.0	250.0
	Max.	1100.0	163.6	3700.0	4800.0	1025.0	1093.9	1200.0	5200.0	383.3	1200.0	1220.0	9300.0	1687.5	1100.0	900.0	1200.0	204.3	600.0	700.0	566.7	6700.0
% predators	Mean	10.5	13.3	16.2	9.9	11.5	10.8	9.0	9.2	22.6	10.9	21.1	20.9	11.1	9.8	14.4	11.4	26.6	12.6	14.8	8.0	15.4
	SD	6.2	4.5	9.2	5.6	8.5	6.5	4.0	4.7	16.5	9.2	14.0	17.9	6.6	3.7	5.7	7.1		8.1	8.6	6.3	9.3
	Min.	5.0	6.8	5.1	3.4	4.0	3.4	2.9	4.3	8.3	0.5	1.5	4.7	4.1	4.2	6.3	5.0	26.6	3.1	6.3	0.0	2.6
	Max.	25.3	19.3	38.5	23.2	27.1	24.0	15.3	17.3	64.8	29.0	47.8	55.0	26.3	15.6	22.2	26.5	26.6	27.9	33.0	22.9	33.8
% gatherers	Mean	78.7	74.2	82.9	75.6	77.0	80.9	95.2	88.9	84.0	83.2	80.7	84.6	86.3	83.8	83.9	79.0	74.0	84.9	67.4	78.6	84.6
	SD	10.0	9.1	12.4	13.1	15.5	11.0	2.4	6.9	13.6	14.0	11.7	12.5	7.8	7.5	8.9	10.1		7.6	17.3	18.0	7.4
	Min.	62.3	63.6	59.1	47.1	56.5	65.4	92.9	74.4	54.0	45.4	62.8	56.8	71.8	68.8	66.7	62.7	74.0	77.7	33.9	35.9	70.0
	Max.	93.2	89.0	95.1	89.4	94.9	96.9	98.4	97.0	100.0	97.0	98.5	95.9	95.9	93.7	93.7	91.5	74.0	95.8	86.2	100.0	95.9
% filterers	Mean	11.0	4.9	6.2	6.9	1.0	6.6	4.1	11.8	3.2	0.8	0.0	4.8	1.0	0.3	9.9	1.0	2.8	5.2	0.3	0.0	13.7
	SD	12.9	6.9	5.6	7.2	1.4	7.5	2.1	13.0	3.5	1.7	0.0	7.1	2.7	0.6	9.7	1.9		8.8	0.8	0.1	16.6
	Min.	0.0	0.0	0.0	0.0	0.0	0.0	2.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.8	0.0	0.0	0.0	0.0
	Max.	34.4	20.3	18.5	21.5	4.0	21.2	8.1	38.9	10.9	6.0	0.0	22.5	10.5	2.1	32.9	5.4	2.8	26.4	2.1	0.3	58.8
% gatherer/filterer	Mean	89.7	79.1	89.1	82.5	78.0	87.5	99.3	100.7	87.2	84.0	80.7	89.4	87.3	84.0	93.8	80.0	76.8	90.2	67.7	78.6	98.2
	SD	13.7	15.0	14.9	16.9	15.1	13.1	2.9	14.0	15.4	14.6	11.7	17.4	7.6	7.5	15.5	11.1		13.9	17.6	18.0	18.8
	Min.	76.8	64.7	59.6	47.1	56.5	68.6	95.4	85.8	54.0	45.4	62.8	56.8	72.4	68.8	66.7	62.7	76.8	78.7	33.9	35.9	82.0
	Max.	127.6	109.3	107.4	101.0	95.4	110.2	103.2	129.3	109.1	97.5	98.5	117.6	95.9	93.7	122.4	96.4	76.8	122.2	86.6	100.0	154.0
% scrapers	Mean	53.5	60.4	43.6	54.2	53.1	51.9	23.4	31.0	28.8	71.5	74.3	38.3	75.6	60.3	31.5	63.7	16.4	69.6	56.7	67.2	43.0
	SD	24.7	18.3	16.9	16.4	20.0	16.4	17.3	16.0	24.8	16.6	20.3	15.4	19.2	22.1	14.6	19.6		24.8	17.6	11.9	18.4
	Min.	20.9	33.1	12.3	23.7	32.5	29.5	4.1	9.8	0.6	43.4	38.0	24.3	34.3	27.8	13.3	35.6	16.4	16.4	30.6	49.5	5.9
	Max.	90.3	89.3	66.5	78.2	84.0	78.5	45.9	54.1	70.6	92.2	99.2	73.8	95.5	84.7	58.3	89.8	16.4	94.5	78.6	82.7	71.4
% shredders	Mean	15.0	25.8	19.7	25.5	27.0	16.7	35.9	25.7	34.7	18.7	6.6	24.2	9.6	18.0	22.5	14.4	33.9	6.7	26.2	20.7	18.4
	SD	9.0	8.3	8.2	16.4	23.4	10.5	11.0	21.4	21.5	13.1	7.6	18.1	11.1	10.1	8.5	11.1		7.0	19.1	23.3	8.6
	Min.	3.1	12.7	7.2	12.6	5.3	3.8	21.1	10.5	4.3	1.5	0.4	2.0	0.0	2.9	8.3	1.5	33.9	1.4	5.9	0.0	5.6
	Max.	30.9	37.3	40.1	62.6	72.9	33.7	53.5	73.2	73.0	51.2	27.0	64.0	31.9	33.9	35.3	33.5	33.9	22.6	60.7	73.8	34.7
% dominant taxa	Mean	35.1	35.1	24.4	25.6	29.4	25.8	42.4	31.1	42.2	35.8	49.6	27.1	36.0	31.1	24.5	30.8	30.7	36.6	26.4	38.2	28.7
	SD	13.0	10.7	8.0	9.3	8.6	6.5	6.1	17.7	21.1	12.4	17.1	10.8	17.5	14.2	8.7	7.9		7.8	12.7	14.4	12.8
	Min.	17.4	21.2	13.1	14.4	16.3	16.3	36.3	12.7	17.2	18.8	25.7	14.6	13.4	9.9	13.1	17.1	30.7	23.2	15.2	14.7	15.1
	Max.	57.7	57.1	41.8	41.5	46.2	39.7	49.0	70.6	73.5	58.8	77.3	43.8	75.6	47.5	36.7	44.2	30.7	45.9	55.3	68.2	54.9
% 2 dominant taxa	Mean	49.3	51.1	36.5	43.5	43.6	41.3	66.6	46.4	55.8	55.1	66.7	41.5	54.0	44.5	40.6	49.4	47.6	53.9	40.3	58.3	42.1
	SD	11.8	12.3	13.1	15.0	10.4	9.5	9.3	17.9	16.8	12.2	12.5	11.5	18.5	15.2	11.6	9.8		10.3	12.4	16.4	13.3
	Min.	28.3	33.7	9.1	26.8	31.3	28.0	48.8	21.3	32.0	35.0	46.0	26.2	21.1	19.7	24.1	30.2	47.6	38.6	28.4	26.7	27.3
	Max.	68.0	72.4	56.6	69.2	63.8	60.5	75.5	81.7	79.6	77.6	87.4	57.7	81.0	68.0	58.0	64.6	47.6	66.0	63.8	79.1	75.5
% 5 dominant taxa	Mean	69.2	70.1	61.0	64.2	65.9	63.6	81.3	66.6	77.2	81.1	86.6	62.8	79.2	67.3	62.3	72.5	65.6	77.0	61.7	77.6	63.5
	SD	9.4	10.8	10.6	13.3	11.5	10.2	4.2	15.2	8.6	7.1	9.2	10.9	17.2	15.4	9.2	7.6		11.8	11.7	12.9	12.1
	Min.	53.8	53.2	46.1	47.8	52.2	47.7	74.2	41.3	62.5	71.7	72.3	47.6	40.7	30.3	48.2	61.8	65.6	60.9	47.4	54.3	40.6
	Max.	83.2	86.7	79.0	86.4	85.9	78.5	85.5	92.8	87.7	93.0	99.2	77.5	97.0	86.0	77.2	88.4	65.6	93.3	80.8	92.1	88.4
Genus/species biotic index	Mean	4.1	3.0	4.0	3.9	3.2	3.7	2.3	4.5	3.4	2.7	2.0	3.9	2.5	3.3	3.9	3.3	5.3	3.3	2.5	3.5	4.4
	SD	0.9	1.2	1.0	0.5	1.2	0.8	0.5	0.7	1.3	1.2	0.7	0.9	0.8	1.0	0.8	1.3		0.6	1.1	0.8	0.8
	Min.	2.8	0.8	2.1	3.3	1.7	2.6	1.9	3.7	1.6	1.7	1.0	2.7	1.6	1.8	2.8	0.9	5.3	2.3	1.0	2.4	2.8
	Max.	5.8	4.4	5.8	5.1	5.5	5.2	3.3	5.8	6.0	5.5	3.3	5.3	4.4	5.3	5.1	5.0	5.3	4.3	4.5	4.9	5.6

B: Family

Basin		Bowron	Chehalis	Chelaslie	Chilcotin	Chilko	Clearwater	Coldwater	Euchiniko	Fraser	Herrick	Lillooet	Nicola	Pitt	Stein	Stuart	Taseko	Thompson	Torpy	Tyaughton	Upper Fraser	West Road
No. sites		12	9	12	13	8	12	6	8	12	12	12	10	16	12	10	8	1	8	8	12	18
Total no. taxa	Mean	17.2	18.8	16.2	17.6	16.4	16.7	17.0	17.6	14.8	13.2	10.5	17.4	13.4	14.3	16.1	17.1	12.0	16.4	18.5	12.3	18.0
	SD	3.1	4.1	3.3	3.8	2.8	4.3	1.8	4.5	4.4	2.9	3.8	2.7	4.8	1.7	3.1	3.4		3.5	3.5	5.3	4.6
	Min.	12.0	14.0	8.0	11.0	11.0	12.0	14.0	10.0	7.0	10.0	5.0	12.0	8.0	11.0	11.0	13.0	12.0	11.0	15.0	5.0	11.0
	Max.	23.0	27.0	20.0	23.0	19.0	25.0	19.0	25.0	21.0	19.0	18.0	22.0	24.0	16.0	22.0	22.0	12.0	20.0	25.0	21.0	26.0
No. EPT taxa	Mean	11.1	11.3	10.2	10.7	10.3	10.2	10.0	9.6	8.5	9.7	8.1	11.3	9.4	10.8	11.8	11.1	8.0	11.0	12.8	8.8	10.8
	SD	1.9	3.0	2.6	2.5	2.1	3.3	1.3	2.7	3.3	1.6	2.3	1.9	3.0	1.7	2.1	2.0		2.9	1.3	4.1	2.3
	Min.	8.0	8.0	5.0	6.0	7.0	5.0	8.0	5.0	2.0	7.0	5.0	9.0	7.0	7.0	8.0	9.0	8.0	6.0	11.0	4.0	7.0
	Max.	14.0	17.0	16.0	15.0	13.0	16.0	11.0	13.0	11.0	12.0	13.0	13.0	16.0	13.0	15.0	14.0	8.0	15.0	15.0	15.0	15.0
No. Ephemeroptera	Mean	3.4	4.2	4.0	3.5	3.1	3.7	4.2	3.4	3.1	3.3	2.7	3.9	3.5	3.5	3.6	3.5	3.0	4.1	3.6	3.1	3.6
	SD	0.8	0.7	0.6	0.9	0.6	0.9	0.4	1.2	1.4	0.5	1.4	0.9	0.7	0.7	0.8	0.5		1.2	0.5	1.2	0.7
	Min.	2.0	3.0	3.0	2.0	2.0	2.0	4.0	2.0	0.0	3.0	0.0	2.0	2.0	3.0	2.0	3.0	3.0	2.0	3.0	1.0	2.0
	Max.	5.0	5.0	5.0	5.0	4.0	5.0	5.0	5.0	5.0	4.0	4.0	5.0	5.0	5.0	5.0	4.0	3.0	6.0	4.0	4.0	5.0
No. Trichoptera	Mean	3.7	3.1	2.8	3.5	2.5	2.6	3.8	2.9	1.8	1.7	1.9	2.7	1.9	2.8	3.7	2.6	4.0	2.1	3.9	2.1	3.5
	SD	0.8	1.3	1.4	1.4	1.8	1.8	0.8	1.0	1.1	1.2	1.6	1.3	2.0	1.2	1.4	1.3		1.4	0.8	1.5	1.9
	Min.	3.0	2.0	0.0	1.0	0.0	1.0	3.0	1.0	0.0	0.0	0.0	1.0	0.0	0.0	2.0	1.0	4.0	1.0	3.0	0.0	0.0
	Max.	5.0	6.0	5.0	5.0	5.0	6.0	5.0	4.0	4.0	4.0	5.0	5.0	6.0	4.0	6.0	4.0	4.0	4.0	5.0	5.0	7.0
No. Plecoptera	Mean	4.0	4.0	3.4	3.8	4.6	3.9	2.0	3.4	3.7	4.7	3.5	4.7	4.0	4.5	4.5	5.0	1.0	4.8	5.3	3.7	3.7
	SD	1.7	1.7	1.4	1.1	0.7	1.6	1.3	1.1	1.2	0.9	0.8	1.5	0.9	1.0	0.8	1.3		1.2	0.7	2.1	1.4
	Min.	1.0	2.0	1.0	2.0	4.0	1.0	0.0	2.0	2.0	3.0	2.0	2.0	3.0	3.0	3.0	3.0	1.0	3.0	4.0	1.0	1.0
	Max.	7.0	7.0	7.0	6.0	6.0	6.0	4.0	5.0	5.0	6.0	5.0	7.0	6.0	6.0	5.0	7.0	1.0	6.0	6.0	7.0	6.0
No. Diptera	Mean	2.9	3.3	2.9	3.5	3.3	3.1	4.0	3.9	2.5	2.3	1.8	3.3	2.2	2.5	3.0	2.3	1.0	2.9	4.4	2.0	2.9
	SD	1.1	1.2	1.1	1.4	1.3	1.6	1.7	1.5	0.8	1.0	1.1	1.2	1.3	0.9	0.8	0.7		0.6	1.8	0.7	1.2
	Min.	1.0	1.0	1.0	1.0	1.0	1.0	2.0	1.0	1.0	1.0	0.0	1.0	1.0	1.0	2.0	1.0	1.0	2.0	1.0	1.0	1.0
	Max.	5.0	5.0	5.0	6.0	5.0	5.0	6.0	6.0	4.0	4.0	4.0	5.0	4.0	4.0	4.0	3.0	1.0	4.0	7.0	3.0	5.0
No. Odonata	Mean	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	SD	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0
	Min.	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Max.	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
No. Coleoptera	Mean	0.6	0.6	0.4	0.7	0.1	0.4	0.0	0.9	0.1	0.0	0.0	0.9	0.1	0.0	0.1	0.3	0.0	0.5	0.0	0.0	0.9
	SD	0.5	0.5	0.5	0.5	0.4	0.5	0.0	0.4	0.3	0.0	0.0	0.3	0.3	0.0	0.3	0.5		0.5	0.0	0.0	0.3
	Min.	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Max.	1.0	1.0	1.0	1.0	1.0	1.0	0.0	1.0	1.0	0.0	0.0	1.0	1.0	0.0	1.0	1.0	0.0	1.0	0.0	0.0	1.0
No. predators	Mean	1169.8	148.1	3289.6	3603.5	789.8	3676.1	951.4	7561.7	134.4	1255.7	216.2	5024.4	397.5	1637.7	1936.2	1480.2	660.9	554.0	1323.6	862.0	4039.6
	SD	1328.1	115.8	2494.1	2692.8	610.5	5862.8	578.1	5014.4	174.0	2098.5	198.4	4500.5	1069.3	1448.3	2376.7	3341.8		426.5	2591.4	1590.3	2994.5
	Min.	145.5	16.0	580.0	450.0	73.0	192.0	350.0	2260.0	16.0	87.0	67.0	580.0	8.0	90.9	285.7	36.0	660.9	213.3	39.0	6.0	380.0
	Max.	4100.0	340.0	9400.0	9600.0	1800.0	17478.0	2000.0	13900.0	650.0	7700.0	800.0	13088.9	4387.5	4100.0	8325.0	9700.0	660.9	1475.0	7700.0	4233.3	10100.0
% predators	Mean	30.6	23.7	35.4	26.6	31.5	33.4	14.4	42.3	31.4	23.6	23.5	33.9	19.6	24.8	45.7	24.4	77.9	22.5	29.9	27.9	36.4
	SD	19.8	10.4	11.1	9.3	9.6	16.2	3.3	16.2	22.1	24.2	18.5	21.9	14.9	10.9	10.9	6.8		28.0	17.6	16.8	17.7
	Min.	7.9	8.1	18.9	12.9	17.4	8.3	9.2	19.5	8.7	6.0	3.7	12.3	3.0	9.4	30.5	14.9	77.9	3.2	11.0	8.4	9.6
	Max.	66.8	36.4	56.3	45.3	49.3	53.3	18.4	71.4	87.7	93.5	65.9	66.6	47.7	42.1	60.0	34.3	77.9	88.5	62.1	60.0	68.2
% gatherers	Mean	84.8	91.0	92.0	90.5	88.3	91.2	96.4	95.5	86.6	92.6	85.0	93.9	90.0	94.2	90.3	89.0	94.9	88.7	88.5	90.9	91.8
	SD	11.4	5.0	4.5	6.1	6.1	4.2	2.0	3.0	10.3	5.4	12.2	2.4	7.4	1.2	4.9	5.5		9.3	5.6	6.2	6.3
	Min.	56.8	81.6	83.8	76.3	77.8	81.8	93.7	89.9	59.0	84.7	63.1	90.4	73.9	91.3	82.6	77.0	94.9	74.5	75.2	77.7	72.7
	Max.	97.6	96.4	97.5	96.8	95.5	98.0	99.3	99.6	98.2	98.7	98.9	96.8	99.4	96.4	96.0	92.7	94.9	97.9	91.9	100.0	98.8

B: Family

Basin		Bowron	Chehalis	Chelaslie	Chilcotin	Chilko	Clearwater	Coldwater	Euchiniko	Fraser	Herrick	Lillooet	Nicola	Pitt	Stein	Stuart	Taseko	Thompson	Torpy	Tyaughton	Upper Fraser	West Road
No. sites		12	9	12	13	8	12	6	8	12	12	12	10	16	12	10	8	1	8	8	12	18
% gatherer/filterer	Mean	88.7	92.3	95.6	95.2	88.9	92.7	97.0	97.6	87.5	92.8	85.0	95.9	90.4	94.3	91.3	89.7	96.4	89.6	88.5	91.0	95.2
	SD	10.4	3.7	5.0	4.9	6.6	3.9	2.5	2.5	10.1	5.5	12.2	5.1	6.8	1.1	5.3	5.8		9.6	5.6	6.2	3.3
	Min.	58.3	86.3	85.1	88.0	77.8	88.2	93.7	93.5	60.4	84.7	63.1	90.4	76.6	92.1	84.1	77.0	96.4	74.5	75.2	77.7	86.5
	Max.	97.6	96.5	105.3	105.9	98.0	100.5	101.1	101.3	100.0	98.7	98.9	105.8	99.4	96.4	97.7	94.0	96.4	98.0	91.9	100.0	98.8
% filterers	Mean	3.8	1.3	3.7	4.7	0.6	1.5	0.7	2.1	0.9	0.2	0.0	2.0	0.4	0.1	1.0	0.6	1.5	0.8	0.0	0.0	3.3
	SD	7.1	2.6	3.8	5.3	0.9	2.5	0.6	2.4	1.2	0.5	0.0	3.8	1.1	0.3	1.7	1.0		1.5	0.0	0.1	5.9
	Min.	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0	0.0	0.0
	Max.	24.2	8.0	12.2	14.2	2.5	7.6	1.8	7.2	3.8	1.7	0.0	11.2	4.0	0.8	5.2	2.4	1.5	3.9	0.0	0.2	24.5
% scrapers	Mean	44.8	39.0	40.5	42.1	33.1	40.3	17.1	28.0	24.2	40.2	25.6	44.9	44.4	53.0	33.9	51.5	10.3	62.5	36.4	48.6	38.9
	SD	20.7	16.4	11.7	15.7	15.6	15.5	6.6	15.8	26.9	24.2	18.6	20.9	19.5	14.0	14.9	10.4		24.0	18.8	24.2	15.0
	Min.	17.3	20.5	17.6	16.5	13.3	20.0	9.8	6.2	0.5	2.5	0.4	19.4	17.1	28.8	8.9	37.7	10.3	8.5	20.6	8.7	7.5
	Max.	74.3	63.5	61.2	69.4	54.1	68.1	27.7	51.9	81.4	76.6	50.8	74.6	83.8	76.0	53.4	66.4	10.3	81.9	69.7	84.3	62.1
% shredders	Mean	15.8	20.6	12.5	22.4	26.7	12.4	29.2	19.7	29.9	28.8	48.7	14.8	31.4	15.6	20.0	14.4	1.0	9.4	21.6	19.9	13.4
	SD	10.6	7.3	9.0	17.3	19.2	9.2	11.3	22.3	21.5	19.0	21.5	10.5	20.3	9.0	9.4	11.4		7.4	9.2	20.8	10.7
	Min.	4.4	8.9	0.6	7.0	5.0	0.0	12.9	5.9	4.2	2.5	11.9	2.0	9.6	7.3	5.3	2.5	1.0	2.0	11.3	1.8	0.8
	Max.	40.2	28.9	33.3	58.6	64.7	31.4	43.1	73.5	71.7	62.7	77.3	31.7	75.6	38.7	30.0	37.3	1.0	25.0	33.9	65.0	43.2
Family biotic index	Mean	4.0	3.3	4.1	3.9	3.6	3.9	2.2	4.0	3.2	3.2	2.7	4.0	3.2	3.8	3.9	3.6	5.2	3.5	3.2	3.6	4.1
	SD	0.7	0.9	0.8	0.6	1.2	0.5	0.4	0.9	1.1	0.9	0.4	0.7	0.4	0.4	0.4	0.5		0.7	0.6	0.7	0.5
	Min.	2.9	1.8	2.8	3.0	1.9	3.4	1.8	2.3	2.1	2.0	2.1	3.1	2.3	3.0	3.4	2.9	5.2	2.7	2.3	2.5	2.9
	Max.	5.1	4.3	5.7	4.9	5.6	4.9	3.0	5.2	5.5	5.8	3.4	5.3	4.0	4.9	4.6	4.2	5.2	5.0	4.2	5.0	4.9

Family richness was highest in the Chehalis, Tyaughton, and West Road subcatchments (mean ≥ 8), lowest in the Lillooet, Thompson, and upper Fraser subcatchments (< 12.4), and individual samples ranged from five to 27 families. Numbers of EPT families were highest in the Bowron, Chehalis, Nicola, Stuart, Taseko, and Tyaughton subcatchments (mean > 11), lowest in the Fraser mainstem, and Lillooet, Thompson, and upper Fraser subcatchments (< 9), and individual samples ranged from two to 17 families. Diptera and chironomid taxa richness was highest in the Chelaslie, Chilcotin, Euchiniko, Stuart, Thompson, and West Road subcatchments (> 12 and 10 taxa, respectively). Coefficients of variation were generally low for all these measures of taxa richness ($\sim 20\%$).

3.4.4 Enumeration metrics

Densities, like taxa richness, are common descriptors of macroinvertebrate assemblages. Numbers of individuals in the subcatchments had mean values that covered almost a 50-fold range (383.3 in the Fraser mainstem to 17,090.4 per 3-min kick sample in the Euchiniko), and densities in individual samples covered more than three orders of magnitude (23 in the upper Fraser to 36,800 per 3-min kick sample in the Euchiniko) (Table 3.4). Four subcatchments had mean densities $> 10,000$ per 3-min kick sample (Chilcotin, Euchiniko, Nicola, and West Road), but five had < 2000 (Chehalis, Fraser mainstem, Lillooet, Pitt, and Thompson). EPT individuals exceeded 80% of numbers in the Coldwater, Herrick, Lillooet, Pitt, and Torpy, were $< 25\%$ in the Thompson, and ranged from 4.5 to 100% in individual samples. Chironomidae composed $> 30\%$ of numbers in the Euchiniko, Nicola, Stuart, Thompson (where they were $> 70\%$), and West Road; they were $< 11\%$ in the Coldwater, Lillooet, and Pitt, and ranged from 0 to 77% in individual samples. Coefficients of variation were higher for enumerations than for the richness measures (usually $> 60\%$).

Numerical dominance of sites by a single taxon is an expression of assemblage evenness. In those terms, dominance by a single taxon ranged from 9.9 to 77.3% for individual samples but mean values per subcatchment were generally between 25 to 40%.

When the numerical dominance of the two most common taxa was considered, two subcatchments had means exceeding 66% (Coldwater and Lillooet) and only one was below 40% (Chelaslie). A consideration of five numerical dominants produced seven subcatchments with <65% (Chelaslie, Chilcotin, Clearwater, Nicola, Stuart, Tyaughton, and West Road), but only two that had >80% (Coldwater and Lillooet).

3.4.5 Functional-feeding group metrics

The use of functional-feeding group measures has been largely confined to the U.S.A. and, in particular, to states and agencies using the rapid bioassessment protocols of Plafkin et al. (1989) (Resh and Jackson 1993). However, the use of other types of species traits (e.g. length of life span, number of reproductive cycles) in bioassessment is likely to occur in the future. Several of these functional-feeding group measures are included in Table 3.4. Functional-feeding group metrics assume that invertebrate groups evolved specific feeding mechanisms to capitalize on existing food sources, and that these groups will predominate under certain environmental conditions. For example, scrapers would be present in sunny areas where algae predominate, filterers would be present when suspended organic loads are high, and shredders would predominate in accumulations of leaf packs. Sylvestre (1998) discussed functional feeding groups in the Fraser River studies.

Percentages of different functional-feeding groups varied greatly among subcatchments and had high CVs (often >50% and sometimes >100%). For example, % predators ranged from <1% to >64% in individual samples, and from 8.0 to 26.6% as mean values per subcatchment. Gatherers were generally >80% for subcatchment mean values but % filterers were >10% in only the Bowron and Euchiniko subcatchments. Scrapers had mean values that ranged from 16.4 to 75.6%, whereas shredders only exceeded 35% in the Coldwater subcatchment. Functional-feeding group values at the family level differ from those at lower taxa because numbers of possible groups for assignment increase as taxonomic diversity increases.

3.4.6 *Biotic indices*

The biotic-index approach is the oldest and most widely used approach to water-quality monitoring, and in many parts of Europe is the approach most commonly used (Resh and Jackson 1993). In the biotic index score used here, higher numbers indicate poorer water quality. Mean biotic index values, using species- and generic-level tolerance scores, were <2.6 in the Coldwater, Lillooet, and Tyaughton subcatchments, were >4.0 for the Bowron, Euehiniko, Thompson, and West Road subcatchments, and scores for individual samples ranged from 0.8 to 6.0 (Table 3.4).

Scores were also calculated using family-level tolerances. Mean biotic index values generally ranged from 3 to 4 for most subcatchments but were <2.6 in the Coldwater subcatchment and >4.0 in the Chelaslie, Thompson, and West Road subcatchments. Comparison of species/generic-level and family-level biotic index values indicated that mean values in two subcatchments were unchanged, seven increased (by 0.1-0.5), and 11 decreased (by 0.1-0.7).

3.4.7 *Habitat attributes*

Habitat descriptors included chemical, physical, and biological (algal) measures (Table 3.5). A discussion of selected variables follows.

Alkalinity ranged from 0 to $201 \text{ mg}\cdot\text{L}^{-1}$ in different samples, and was highest in the Chilcotin and Euehiniko subcatchments ($>80 \text{ mg}\cdot\text{L}^{-1}$), and lowest in the Chehalis and Pitt subcatchments ($<7 \text{ mg}\cdot\text{L}^{-1}$). Total suspended solids were highest in the Chilcotin and Stuart subcatchments ($>63 \text{ mg}\cdot\text{L}^{-1}$) and lowest in the Coldwater and Torpy subcatchments ($<2 \text{ mg}\cdot\text{L}^{-1}$). Phosphorus and nitrogen concentrations were usually below detectable levels.

Table 3.5. Mean, standard deviation (SD), and ranges for several habitat attributes of the sampling sites arranged by subcatchment. See Section 1 for description of how habitat attributes were measured.

Basin		Bowron	Chehalis	Chelaslie	Chilcotin	Chilko	Clearwater	Coldwater	Euchiniko	Fraser	Herrick	Lillooet	Nicola	Pitt	Stein	Stuart	Taseko	Thompson	Torpy	Tyaughton	Upper Fraser	West Road
No. sites		12	9	12	13	8	12	6	8	12	12	12	10	16	12	10	8	1	8	8	12	18
Water column:																						
Alkalinity (mg.L ⁻¹)	Mean	45.5	1.7	15.3	84.7	27.2	40.4	58.3	84.3	57.4	58.6	20.3	70.3	6.3	15.4	31.2	30.3	35.4	64.1	72.0	32.6	70.3
	SD	26.3	4.5	6.8	32.8	15.4	25.3	5.5	22.3	18.5	31.0	9.5	49.8	4.8	7.5	16.6	33.3		29.8	20.2	26.5	29.9
	Minimum	0.2	0.2	6.5	33.4	12.2	11.7	52.3	50.4	21.1	0.0	5.2	19.8	0.1	0.0	0.1	9.9	35.4	19.8	41.8	0.1	10.4
	Maximum	83.3	13.7	29.0	154.0	59.5	89.8	63.5	111.0	84.5	96.3	33.9	201.0	15.1	27.5	42.9	112.0	35.4	97.9	104.0	76.6	125.0
Total suspended solids (mg.L ⁻¹)	Mean	14.2	2.3	3.0	75.2	12.9	46.8	1.9	4.9	27.2	8.6	21.4	7.7	24.4	6.6	63.2	18.3	3.1	1.3	10.6	15.2	8.5
	SD	22.4	1.7	1.4	74.4	16.3	50.6	1.0	3.2	36.1	6.0	16.8	4.6	21.7	5.9	18.7	12.1		0.6	7.4	19.0	5.7
	Minimum	1.8	0.4	1.2	3.7	0.9	1.8	1.0	2.0	9.2	2.0	4.3	3.0	0.9	1.1	33.0	4.5	3.1	0.8	1.6	1.1	1.6
	Maximum	79.0	6.3	6.4	168.0	44.3	152.0	3.5	10.6	141.0	20.4	68.0	15.8	61.2	21.1	90.0	36.3	3.1	2.3	23.1	61.1	21.2
Total phosphorus (mg.L ⁻¹)	Mean	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1
	SD	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0
	Minimum	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Maximum	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.1
Nitrate-nitrite (mg.L ⁻¹)	Mean	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.0	0.0	0.1	0.0
	SD	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	0.1	0.1	0.0	0.0		0.0	0.0	0.0	0.0
	Minimum	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0
	Maximum	0.1	0.2	0.0	0.0	0.0	0.1	0.0	0.2	0.1	0.2	0.0	0.3	0.2	0.3	0.0	0.0	0.1	0.1	0.1	0.2	0.0
Total Kjeldahl nitrogen (mg.L ⁻¹)	Mean	0.2	0.0	0.2	0.1	0.0	0.1	0.1	0.4	0.1	0.1	0.0	0.4	0.0	0.1	0.1	0.1	0.1	0.1	0.0	0.0	0.3
	SD	0.1	0.0	0.1	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.1		0.0	0.0	0.0	0.2
	Minimum	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.2	0.0	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.1
	Maximum	0.3	0.1	0.3	0.4	0.2	0.1	0.1	0.7	0.1	0.1	0.1	0.8	0.1	0.1	0.2	0.3	0.1	0.2	0.1	0.1	0.9
pH	Mean	8.1	6.7	7.0	7.7	7.8	7.8	7.9	8.1	8.1	7.7	7.1	7.6	6.9	7.0	7.7	7.7	8.0	8.2	8.1	7.2	8.3
	SD	0.3	0.4	0.2	0.6	0.2	0.5	0.3	0.2	0.5	0.2	0.3	0.6	0.7	0.2	0.2	0.2		0.3	0.2	0.5	0.6
	Minimum	7.5	6.1	6.6	6.5	7.5	6.8	7.6	7.7	7.3	7.2	6.4	6.9	5.7	6.6	7.4	7.4	8.0	7.8	7.7	6.5	7.0
	Maximum	8.6	7.4	7.4	8.4	8.1	8.6	8.2	8.3	8.8	8.2	7.4	8.5	7.7	7.3	7.9	7.9	8.0	8.8	8.3	8.0	9.3
Conductivity (µS.cm ⁻¹)	Mean	91.6	29.5	27.3	140.7	63.3	84.1	166.8	185.4	142.2	145.7	77.2	153.1	23.2	46.2	83.2	74.4	88.0	121.7	244.8	100.7	132.0
	SD	46.0	42.7	12.3	60.3	29.8	46.1	11.9	74.5	32.0	34.5	32.1	85.9	15.7	15.6	15.9	72.5		49.9	98.2	44.3	52.5
	Minimum	21.6	5.0	11.5	41.0	24.9	28.0	155.0	93.0	73.3	86.3	20.0	74.6	4.6	12.8	42.0	22.0	88.0	47.0	113.0	35.0	38.7
	Maximum	163.0	139.0	50.7	253.0	112.2	174.0	182.0	352.0	183.0	191.0	137.2	365.0	60.7	68.0	95.4	251.0	88.0	181.0	426.0	189.0	231.0
Dissolved oxygen (mg.L ⁻¹)	Mean	11.3	10.4	11.2	13.0	12.3	12.3	9.5	10.5	12.3	12.0	11.6	11.3	12.2	12.0	12.3	12.2	10.2	12.1	10.4	11.6	12.0
	SD	1.0	0.3	0.7	1.6	0.4	1.5	0.4	0.5	0.9	0.6	0.7	0.7	2.5	0.4	0.7	0.8		1.1	0.5	0.5	0.9
	Minimum	9.5	9.9	10.1	10.8	11.7	10.1	8.9	9.8	10.8	11.0	10.0	10.2	5.0	11.1	11.2	11.4	10.2	10.6	9.6	10.9	10.4
	Maximum	12.8	10.9	12.2	14.5	12.8	14.3	9.9	11.3	13.8	13.3	12.3	12.1	14.8	12.7	13.3	13.5	10.2	13.9	11.2	12.6	13.2
Temperature (°C)	Mean	6.7	10.1	5.7	3.1	7.5	6.4	11.1	6.6	6.5	5.2	5.8	6.2	6.7	4.6	3.3	7.2	13.7	3.9	5.6	3.6	7.0
	SD	1.2	1.7	2.1	2.0	1.2	3.3	1.8	2.2	1.0	1.3	2.0	2.2	1.9	2.3	1.2	2.6		0.8	1.4	1.8	1.6
	Minimum	5.3	8.1	1.3	0.1	5.5	2.1	9.4	4.0	5.0	2.2	3.5	3.6	3.6	1.0	0.9	2.7	13.7	2.3	2.3	1.6	4.0
	Maximum	8.5	12.5	8.7	6.6	9.4	11.8	13.3	10.1	8.0	7.1	8.3	10.1	9.8	7.3	4.7	9.5	13.7	4.8	6.8	8.2	9.8
Channel/substrate:																						
Benthic algae chlorophyll-a (mg.L ⁻¹)	Mean	2.7	0.8	3.6	4119.9	3.5	1426.5	1.7	4.5	22.2	2.3	2.3	8.3	138.7	1.7	266.8	3.7	10.8	1.9	0.8	1.8	9.9
	SD	3.6	1.6	3.3	7991.7	3.8	2610.3	0.5	4.0	67.2	3.0	1.6	4.6	171.2	2.2	121.4	4.4		1.4	0.8	3.8	7.5
	Minimum	0.3	0.1	0.3	1.6	0.1	0.6	1.3	0.8	0.4	0.4	0.8	2.2	0.1	0.3	55.0	0.1	10.8	0.3	0.4	0.1	0.5
	Maximum	13.0	4.8	10.3	27384.7	9.2	8904.8	2.3	12.5	235.4	9.4	6.3	14.7	606.2	7.9	543.0	13.3	10.8	4.4	2.8	13.2	24.1
Benthic algae biomass (mg.L ⁻¹)	Mean	1.8	0.6	2.4	2608.2	2.3	1073.0	1.1	2.7	17.3	1.7	1.8	6.0	110.7	1.2	162.1	2.2	6.3	1.3	0.6	1.4	4.8
	SD	2.3	1.2	2.1	5484.7	2.6	1577.2	0.4	2.3	52.6	2.8	1.2	3.3	159.7	1.5	82.9	2.3		0.8	0.6	3.1	3.5
	Minimum	0.2	0.0	0.2	1.3	0.1	0.3	0.8	0.5	0.3	0.3	0.6	1.8	0.0	0.2	0.0	0.0	6.3	0.3	0.3	0.0	0.3
	Maximum	8.3	3.6	6.6	19551.7	6.3	4819.2	1.5	7.7	184.2	10.2	4.4	10.1	571.0	5.2	340.0	6.9	6.3	2.6	2.0	10.6	10.6

Basin		Bowron	Chehalis	Chelasie	Chilcotin	Chilko	Clearwater	Coldwater	Euchiniko	Fraser	Herrick	Lillooet	Nicola	Pitt	Stein	Stuart	Taseko	Thompson	Torpy	Tyaughton	Upper Fraser	West Road
No. sites		12	9	12	13	8	12	6	8	12	12	12	10	16	12	10	8	1	8	8	12	18
% gravel	Mean	31.0	46.4	46.7	24.2	14.5	32.0	23.6	28.4	22.1	20.9	11.5	43.4	31.2	14.7	23.6	11.7	0.0	23.8	25.8	16.6	26.3
	SD	15.5	19.4	32.3	11.8	9.6	23.6	10.1	16.0	13.1	15.6	7.6	28.5	26.6	9.3	8.8	10.5		15.6	21.3	15.3	12.1
	Minimum	2.2	30.1	5.1	4.6	0.7	0.0	12.1	8.1	0.0	0.0	0.4	0.0	5.3	0.1	10.0	0.0	0.0	0.0	0.0	0.0	0.0
	Maximum	54.1	79.4	100.0	53.6	27.3	100.0	35.8	51.4	43.0	43.8	25.3	95.9	90.5	34.3	45.3	28.3	0.0	49.9	55.5	45.6	40.9
% sand	Mean	68.9	53.4	52.9	75.6	60.2	59.5	76.4	71.3	73.6	70.7	85.2	46.6	68.1	84.7	76.3	87.6	0.0	75.6	62.7	66.8	69.2
	SD	15.4	19.2	31.9	11.8	37.6	28.4	10.1	16.0	14.6	26.4	5.9	29.1	27.2	9.1	8.8	10.0		16.1	32.2	18.7	15.8
	Minimum	45.9	20.7	0.0	46.2	0.0	0.0	64.1	48.6	50.5	0.0	74.5	0.0	9.5	65.7	54.7	71.0	0.0	49.9	0.0	22.1	20.8
	Maximum	97.8	69.8	91.4	95.4	89.2	84.3	87.9	91.9	100.0	99.5	92.5	84.2	94.6	98.9	90.0	99.3	0.0	100.0	100.0	91.8	94.3
% silt	Mean	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	11.1	3.1
	SD	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	7.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	18.1	13.3
	Minimum	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Maximum	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	27.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	51.6	56.5
% clay	Mean	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	4.3	1.3
	SD	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	8.2	5.4
	Minimum	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Maximum	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	9.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	26.3	22.8
Framework (7 Categories)	Mean	4.9	7.1	6.2	5.2	6.6	5.9	5.3	3.9	5.8	5.1	7.3	6.2	7.0	6.6	5.4	7.3	8.0	5.6	6.8	5.9	5.7
	SD	1.7	0.8	2.6	1.6	0.7	1.9	1.0	2.4	1.1	1.0	1.2	1.4	1.4	1.1	1.6	0.7		1.1	1.2	1.7	1.8
	Minimum	1.0	6.0	1.0	1.0	6.0	1.0	4.0	1.0	4.0	4.0	5.0	4.0	4.0	5.0	2.0	6.0	8.0	4.0	5.0	2.0	1.0
	Maximum	7.0	8.0	8.0	7.0	8.0	8.0	7.0	6.0	8.0	7.0	8.0	8.0	8.0	8.0	7.0	8.0	8.0	7.0	8.0	7.0	8.0
Matrix (7 Categories)	Mean	2.8	4.7	3.7	3.1	2.4	3.7	3.7	2.1	1.8	2.6	3.0	2.3	4.0	2.4	2.9	2.8	6.0	3.3	4.3	2.9	2.7
	SD	1.3	0.5	1.1	1.6	0.7	1.5	1.0	1.9	0.9	0.7	1.1	0.7	1.8	0.8	1.0	1.0		0.9	0.7	1.3	1.6
	Minimum	0.0	4.0	1.0	0.0	2.0	2.0	2.0	0.0	1.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	6.0	2.0	4.0	2.0	0.0
	Maximum	5.0	5.0	5.0	6.0	4.0	6.0	5.0	4.0	4.0	4.0	5.0	4.0	8.0	4.0	5.0	4.0	6.0	4.0	6.0	6.0	6.0
Embeddedness (5 Categories)	Mean	3.5	4.8	4.3	4.3	2.9	4.0	3.3	3.1	3.4	3.8	3.9	4.1	3.8	4.4	3.0		4.0	4.0	4.0	3.6	3.8
	SD	1.5	0.4	0.8	1.1	0.6	1.2	0.5	1.9	0.7	0.8	0.8	0.7	1.0	1.3	0.8	0.9		0.8	0.9	1.1	1.4
	Minimum	1.0	4.0	3.0	1.0	2.0	2.0	3.0	1.0	2.0	2.0	3.0	3.0	2.0	2.0	3.0	2.0	4.0	3.0	3.0	1.0	1.0
	Maximum	5.0	5.0	5.0	5.0	4.0	5.0	4.0	5.0	4.0	4.0	5.0	5.0	5.0	5.0	4.0		4.0	5.0	5.0	5.0	5.0

pH ranged in samples from 5.7 to 9.3. Conductivity exceeded $150 \mu\text{S}\cdot\text{cm}^{-1}$ in the Coldwater, Euchiniko, Nicola, and Tyaughton subcatchments, but was $<30 \mu\text{S}\cdot\text{cm}^{-1}$ in the Chehalis, Chelaslie, and Pitt subcatchments. Mean values of dissolved oxygen ranged from 5.0 to $14.8 \text{ mg}\cdot\text{L}^{-1}$, and water temperature ranged from 3.1 to 11.1°C .

Chlorophyll *a* mean values from benthic algae measurements ranged from $0.8 \text{ mg}\cdot\text{L}^{-1}$ (Chehalis and Tyaughton subcatchments) to $>1400 \text{ mg}\cdot\text{L}^{-1}$ (Chilcotin and Clearwater subcatchments) and benthic algal biomass followed the same pattern. However, CVs were usually $>100\%$. In terms of major substrate characteristics, the dominant material (framework) across subcatchments ranged from category 1 (organic cover) to category 8 ($>25 \text{ cm}$) (see Table 2.1), and the mean values ranged from category 3.9 (0.2-2.5 cm) to category 7.3 (10-25 cm). The surrounding material (matrix) across subcatchments ranged from mean values of category 1.8 (organic cover-0.2 cm) to category 6 (5-10 cm). In terms of interstitial substrate characteristics, sand predominated at all sites (mean $>50\%$), and silt and clay exceeded mean values of 2% in only the Chilko and Lillooet subcatchments.

3.4.8 *Precision and accuracy of metrics*

The first analysis examined the variability of 44 metrics. Mean values and CVs for all metrics varied greatly, sometimes by over an order of magnitude at the six sites in different basins (Table 3.6).

Richness measures showed low variability in terms of either mean values or CVs (Table 3.6). Mean values ranged over less than a two-fold difference among sites for: number of families; number of EPT taxa and families; number of Ephemeroptera families; number of Plecoptera taxa; number of Diptera families; the ratio of EPT individuals to EPT and Chironomidae individuals; the contribution of the five dominant taxa; and the % gatherer taxa and families (Table 3.6).

Table 3.6. Mean metric values/coefficients of variation (%) for selected metrics at six sites (see Table 3.2 for descriptions) for which sample replicates were collected. Metrics marked* are those typically used in the fixed-metric approach of Plafkin et al. (1989). For a complete description of metric calculation see USEPA (1998, table 7.2). A dash indicates that the metric could not be calculated at that site. CHI = Chilcotin, CLR = Clearwater, PIT = Pitt, SAL = Salmon, STU = Stuart rivers. Family values may be higher than taxa values because some smaller specimens could only be identified to family.

Metrics	CHI5	CLR6	PIT6	PIT7	SAL3	STU2
RICHNESS	(n = 5)	(n = 5)	(n = 3)	(n = 5)	(n = 3)	(n = 5)
Total number of taxa	27.6/11.0	28.4/6.9	12.0/25.0	19.8/8.3	26.0/6.7	21.0/21.6
*Total number of families	20.0/8.7	16.4/14.0	10.3/14.8	14.2/12.7	14.7/10.4	13.2/12.4
No. EPT taxa	9.6/16.3	15.4/14.2	9.0/15.1	7.5/11.1	8.7/8.7	14.4/19.4
No. EPT families	9.6/11.9	11.2/9.8	7.7/15.1	8.6/13.3	7.7/19.9	10.2/16.1
No. Ephemeroptera taxa	3.0/62.4	5.2/21.1	3.0/0	6.2/13.5	1.3/43.3	5.6/24.0
No. Ephemeroptera families	4.0/0	4.4/12.5	4.0/0	3.0/0	3.7/15.8	4.0/17.7
No. Trichoptera taxa	3.6/15.2	2.8/46.6	2.0/0	1.3/43.3	3.3/17.3	1.6/55.9
No. Trichoptera families	3.2/14.0	2.6/43.9	2.0/0	1.3/43.3	3.0/33.3	1.4/39.1
No. Plecoptera taxa	6.0/0	7.4/12.1	4.0/0	4.0/0	4.0/0	7.2/15.2
No. Plecoptera families	2.4/47.5	4.2/20.0	3.0/0	4.6/9.3	1.0/0	4.8/17.4
No. Diptera taxa	8.8/23.3	13.6/13.9	5.3/39.0	9.2/11.9	14.3/10.7	7.2/26.7
No. Diptera families	3.6/34.3	3.2/26.2	2.0/0	3.2/13.1	3.3/34.7	2.4/22.8
No. Chironomidae taxa	5.6/32.4	11.6/13.1	3.3/62.5	6.2/17.9	11.3/18.4	5.8/37.4
No. Odonata taxa	-	-	-	-	-	-
No. Odonata families	-	-	-	-	-	-
No. Coleoptera taxa	2.4/22.8	-	-	-	1.0/0	-
No. Coleoptera families	1.0/0	-	-	-	1.0/0	-
NUMBER OF INDIVIDUALS						
*No. EPT individuals/ no. Chironomidae + EPT individuals	0.6/22.0	0.5/13.1	1.0/2.1	0.6/2.0	0.6/23.3	0.7/12.6
*% EPT individuals	45.4/22.2	46.5/12.8	94.1/2.9	81.4/3.0	49.6/32.8	66.7/12.8
% Ephemeroptera	36.3/19.5	26.1/23.0	56.6/12.4	28.7/8.5	27.6/20.8	55.4/10.4
% Plecoptera	4.0/50.0	17.7/6.5	35.9/24.5	52.2/24.5	6.1/102.3	10.2/23.4
% Trichoptera	5.1/34.2	2.7/28.1	1.6/0	0.6/34.6	16.1/72.9	1.1/49.8
*% Chironomidae	25.9/38.2	49.4/12.9	2.1/91.7	11.7/13.0	31.7/25.5	32.1/26.1
% Coleoptera	2.4/31.6	-	-	-	1.0/108.7	-

Table 3.6. Cont'd.

Metrics	CHI5	CLR6	PIT6	PIT7	SAL3	STU2
% Odonata	-	-	-	-	-	-
% Tribe Tanytarsini	19.3/37.9	17.0/48.2	-	0.8/47.1	18.1/31.6	26.7/30.8
% Diptera and non-insects	46.3/18.8	56.2/10.8	7.5/47.6	19.1/13.1	57.0/15.7	34.4/23.3
*% dominant taxon	17.9/22.6	17.5/29.2	39.3/6.2	36.7/2.6	21.6/17.6	32.7/8.7
% 2 dominant taxa	30.5/12.0	30.6/19.9	64.7/6.4	54.7/7.2	37.6/14.4	55.1/7.0
% contribution of 5	57.3/5.3	56.4/8.0	92.5/6.1	73.2/2.1	65.2/5.1	79.0/4.2
Dominant taxa						
*% of Trichoptera that are Hydropsychidae	53.3/40.1	20.0/0	-	75.0/47.1	52.2/25.3	88.9/21.7
*% of Ephemeroptera that are Baetidae	38.0/42.7	31.3/9.6	59.0/14.6	61.5/14.0	16.2/57.4	48.2/15.4
* Total abundance	11,191.6/ 23.3	12,904.2/ 20.5	324.3/ 41.0	414.6/ 44.0	4325.0/ 19.1	4216.4/ 23.3
FUNCTIONAL FEEDING						
MEASURES						
% gatherers	53.6/8.6	76.4/3.3	89.1/0.6	79.0/2.3	45.6/10.8	86.1/3.4
% gatherer families	37.9/9.9	51.8/13.7	51.9/6.2	42.1/5.2	48.1/10.8	48.0/15.7
% filterers	21.7/34.2	8.3/74.1	-	1.9/60.0	10.0/63.8	-
% filterer families	19.2/17.2	10.9/18.2	-	8.4/28.9	11.2/27.2	-
% predators	3.3/43.7	3.8/42.2	8.7/8.7	11.7/9.8	10.9/50.7	5.8/24.8
% predator families	17.7/37.0	16.4/53.4	39.3/14.2	24.7/38.9	21.0/42.6	30.9/28.9
% scrapers	18.3/18.4	16.1/38.1	54.4/16.9	55.3/6.0	7.8/120.8	23.6/113.5
% scaper families	18.0/12.5	24.9/37.4	42.0/5.3	21.4/12.8	18.0/13.2	26.8/23.6
% shredders	3.9/38.9	21.7/30.1	-	4.2/31.0	30.1/49.8	5.9/41.7
% shredder families	11.1/37.4	30.2/30.4	-	17.1/24.1	20.6/10.8	21.2/11.8
Biotic indices						
Family Biotic Index	3.3/11.1	2.9/8.9	2.2/7.9	1.6/11.8	3.0/16.3	3.0/16.9
Species/Genus Biotic Index	4.5/8.4	4.8/8.3	2.6/11.4	3.2/3.8	3.7/16.5	4.8/5.6

Coefficients of variation showed the lowest range for number of families (8.7-14.8%) and the highest range for % Chironomidae individuals (12.9-91.7%). Lowest CVs were for number of taxa ($\leq 25.0\%$ at all six sites) and families ($\leq 14.8\%$); number of EPT taxa ($\leq 19.4\%$) and EPT families ($\leq 19.9\%$); number of Ephemeroptera families ($\leq 17.7\%$); number of Plecoptera taxa ($\leq 15.2\%$); % Ephemeroptera ($\leq 23.0\%$), two dominant taxa (19.9%); five dominant taxa ($\leq 8.0\%$); % gatherer taxa ($\leq 10.8\%$) and families ($\leq 15.7\%$); and the Family Biotic Index ($\leq 16.9\%$).

In the second analysis, 12 among-site comparisons were made for the detection of impairment. In terms of how often metrics were calculable (i.e. the information required was available from collections at a site; e.g. number of Trichoptera taxa would require that Trichoptera occurred at a site), six of 17 richness metrics, 12 of 16 enumerations, seven of 10 functional-feeding group metrics, and the Family Biotic Index could be calculated in the 12 comparisons (Table 3.7).

With regard to correct indications of impairment (i.e. impairment was noted when it occurred; e.g. Salmon River 1 and 2 cf. 3 comparisons), six of 12 richness metrics, 10 of 15 enumeration metrics, five of 10 functional-feeding group metrics, but not the Family Biotic Index, had t values higher than expected at $p = 0.05$ (Table 3.7).

Incorrect designations of impairment when a site was not impaired were as follows. For unimpaired streams in different ecoregions, errors were found for three of 15 richness metrics that were calculable, for 10 of 13 enumerations, and for six of 10 functional-feeding groups metrics. In different rivers of the same ecoregion, errors were found for 35 of 65 richness comparisons, for 49 of 71 enumerations, for 24 of 44 functional-feeding group metrics, and for three of five biotic index comparisons. Unimpaired sites in the same river had the lowest errors, with errors in richness being five of 32, enumerations 21 of 47, functional-feeding groups 17 of 28, and biotic index two of four (Table 3.7).

Table 3.7. Summary of one-tailed t-test evaluations ($p = 0.05$) comparing metrics in terms of: (a) how often data were available for a statistical comparison; (b) correct indications of impact ($n = 2$); and incorrect indications of impact in terms of site comparisons in different rivers in (c) different ($n = 1$) ecoregions or (d) the same ecoregion ($n = 5$), or (e) different sites in the same river ($n = 4$). See sampling methods for sites involved in comparisons.

Metric	(a) Metric calculable at how many of 12 sites?	(b) Did metric indicate impairment?	Did metric incorrectly indicate impairment when sites were compared in:		
			(c) different ecoregions?	(d) different rivers?	(e) same rivers?
Richness					
Total number of taxa	12	Yes	Yes	Yes (2/5)	Yes (1/4)
Total number of families	12	Yes	No	Yes (4/5)	No (0/4)
No. EPT taxa	12	Yes	No	Yes (1/5)	No (0/4)
No. EPT families	12	Yes	No	Yes (2/5)	No (0/4)
No. Ephemeroptera taxa	9	Yes	No	Yes (1/5)	No (0/1)
No. Ephemeroptera families	9	No	No	Yes (1/3)	-
No. Trichoptera taxa	9	Yes	No	Yes (4/5)	Yes (1/1)
No. Trichoptera families	12	No	No	Yes (4/5)	Yes (1/4)
No. Plecoptera taxa	6	No	No	No (0/3)	-
No. Plecoptera families	7	-	No	Yes (1/5)	No (0/1)
No. Diptera taxa	12	No	Yes	Yes (4/5)	Yes (1/4)
No. Diptera families	12	No	No	Yes (3/5)	No (0/1)
No. Chironomidae taxa	12	No	Yes	Yes (4/5)	Yes (1/4)
No. Odonata taxa	0	-	-	-	-
No. Odonata families	0	-	-	-	-
No. Coleoptera taxa	3	-	No	Yes (2/2)	-
No. Coleoptera families	3	-	No	Yes (2/2)	-
Number of Individuals					
No. EPT individuals/ no. Chironomidae + EPT individuals	12	No	Yes	Yes (3/5)	Yes (1/4)
% EPT individuals	12	No	Yes	Yes (3/5)	Yes (1/4)
% Ephemeroptera	12	Yes	Yes	Yes (4/5)	Yes (1/4)
% Plecoptera	12	No	No	Yes (3/5)	Yes 3/4
% Trichoptera	9	No	No	Yes (3/5)	Yes (1/1)

Metric	(a) Metric calculable at how many of 12 sites?	(b) Did metric indicate impairment?	Did metric incorrectly indicate impairment when sites were compared in:		
			(c) different ecoregions?	(d) different rivers?	(e) same rivers?
% Chironomidae	12	Yes	Yes	Yes (3/5)	Yes (1/4)
% Coleoptera	4	No	-	Yes (2/2)	-
% Odonata	0	-	-	-	-
% Tribe Tanytarsini	9	Yes	No	Yes (3/5)	Yes (1/1)
% Diptera and non-insects	12	Yes	Yes	Yes (4/5)	Yes (1/4)
% dominant taxon	12	Yes	Yes	Yes (4/5)	Yes (3/4)
% 2 dominant taxa	12	Yes	Yes	Yes (4/5)	Yes (2/4)
% contribution of 5 dominant taxa	12	Yes	Yes	Yes (3/5)	Yes (1/4)
% of Trichoptera that are Hydropsychidae	7	Yes	-	Yes (4/4)	Yes (1/1)
% of Ephemeroptera that are Baetidae	12	Yes	Yes	Yes (2/5)	Yes (2/4)
Total abundance	12	Yes	Yes	Yes (4/5)	Yes (2/4)
<i>Functional feeding measures</i>					
% gatherers	12	Yes	Yes	Yes (4/5)	Yes (2/4)
% gatherer families	12	Yes	Yes	Yes (3/5)	Yes (3/4)
% filterers	7	No	No	Yes (2/3)	No (0/1)
% filterer families	7	Yes	Yes	Yes (2/3)	No (0/1)
% predators	12	No	No	Yes (3/5)	Yes (2/4)
% predator families	12	No	No	No (0/5)	Yes (2/4)
% scrapers	12	Yes	No	Yes (5/5)	Yes (4/4)
% scraper families	12	No	Yes	Yes (3/3)	Yes (4/4)
% shredders	12	No	Yes	Yes (1/5)	No (0/1)
% shredder families	12	Yes	Yes	Yes (3/5)	No (0/1)
<i>Biotic Indices</i>					
Family Biotic Index	12	No	No	Yes (3/5)	Yes (2/4)
Species/Genus Biotic Index	12	No	No	Yes (4/5)	Yes (2/4)

Combining error rates across different scales (different ecoregions, different rivers, sites in the same river) by summing the last three columns in Table 3.7 indicated that the best-performing metrics were all richness metrics: number of taxa (only four errors in 10 comparisons); families (four of 10); EPT taxa (one of 10) and families (two of 10); Ephemeroptera taxa (one of seven) and families (one of four); and Plecoptera taxa (zero of four) and families (one of seven).

Lowest error rates occurred when unimpaired sites in the same rivers were compared, and this result was especially evident for richness metrics. Fewer incorrect designations occurred (although only one site comparison was used) when sites in different ecoregions (located several hundred km apart) were picked because of physical habitat similarities, than when streams in the same ecoregion were compared (Table 3.7).

3.4.9 Choice of metrics for biomonitoring of the Fraser River

This analysis of metrics calculated from macroinvertebrate collections from the Fraser River clearly showed that: (1) richness metrics were the most useful of all the types of metrics tested in terms of ability to indicate impairment when impairment occurred, and not to indicate impairment when impairment did not occur; (2) the fixed metric approach of Plafkin et al. (1989) that attempts to include a variety of structural and functional measures of benthic invertebrate assemblages (i.e. those marked by an asterisk in Table 3.6) would not be significantly improved by substitution of other metrics (i.e. those without an asterisk in Table 3.6) because it is mainly the richness metrics that performed well; (3) there were more classification errors (i.e. incorrect indications of impairment) with the multimetric approach when sites in different rivers were compared than when sites in the same river were compared, and that two sites in different ecoregions selected because of geomorphic similarity may have fewer classification errors than sites in the same river or ecoregion.

The high variation in mean values for the six sites in Table 3.6 indicated that rather than having geographically broad-based thresholds reflecting unimpaired conditions, local thresholds

must be established. Given that these streams have different underlying geology, nutrient bases, geomorphology, etc., the variability observed in mean values of benthic macroinvertebrate metrics between subcatchments is not unexpected; consequently, even for metrics that have high CVs, finding statistically significant differences in the absence of impairment is not surprising. Other studies have examined the appropriateness of benthic macroinvertebrate metrics for different regions, and their results indicated that some metrics could be used successfully in different regions (Table 3.8) but most could not. Although these studies examined a range of metrics, it is important to note that only the richness measures seem to be reported as consistently useful across studies.

3.5 Summary

How can the evaluation of individual metrics be related to the BEAST model (Section 2) and future biological monitoring of the Fraser River? Water quality monitoring agencies worldwide are considering using multivariate models as the basis for monitoring programs. Although reliance on the use of a few fixed metrics (e.g. % EPT) may be appropriate for developing countries (Resh 1995; Sivaramakrishnan et al. 1996), U.S.A. regulatory agencies are now selecting metrics that are appropriate for specific regions (USEPA 1998). Reynoldson et al. (1997b) recommended that a safe, cost-effective strategy for agencies that are currently using the multimetric approach may be to (1) supplement the multimetric biological collections, which are fundamentally the same as those used for multivariate approaches, with similar environmental measurements required for multivariate analyses, and (2) do multimetric and multivariate analysis simultaneously and base the ultimate decision of site impairment on analysis and interpretation of both approaches. Our recommendation is the same if multimetric approaches are considered for use in the Fraser River catchment.

Table 3.8. Benthic macroinvertebrate metrics found to be useful in previous analyses: Kerans et al. (1992) determined success of a metric if no differences or consistent differences were found between sampling devices used, riffles and pools, or year-to-year differences; Barbour et al. (1992) used ability to distinguish classes (montane versus valley/plains); Resh and Jackson (1993) used low variability between sites and years, and consistent patterns of difference between impacted and unimpacted sites; Kerans and Karr (1994) used concordance with water quality and fish assemblage analyses and variability across habitats and ecoregions; and Fore et al. (1996) distinguished disturbed sites from minimally disturbed sites. EPT = Ephemeroptera, Plecoptera, and Trichoptera.

Kerans et al. (1992) (18 metrics)	Barbour et al. (1992) (17 metrics)	Resh and Jackson (1993) (20 metrics)	Kerans and Karr (1994) (18 metrics)	Fore et al. (1996) (30 metrics)
Plecoptera richness Intolerant snail and mussel richness % individuals in 2 numerically dominant taxa % omnivores % gatherers % grazers % predators % filterers % shredders % Chironomidae	Number of taxa EPT richness Pinkham-Pearson Index Quantitative similarity index Biotic index % dominant taxa Dominants in common for 5 most abundant taxa Ratio of Hydropsychidae to total Trichoptera individuals % scrapers % shredders Quantitative similarity index for functional-feeding groups	Number of taxa Number of EPT taxa Number of families Margalef's Index Family Biotic Index % scrapers	Taxa richness Intolerant snail and mussel richness Ephemeroptera richness Trichoptera richness Plecoptera richness % <i>Corbicula</i> % oligochaetes % omnivores % filterers % grazers % predators % individuals in 2 numerically dominant taxa Total abundance	Taxa richness Ephemeroptera richness Plecoptera richness <i>Pteronarcys</i> richness Trichoptera richness Intolerant taxa richness Sediment-intolerant taxa richness Sediment-tolerant taxa richness % tolerant species % sediment-tolerant species % dominance of 3 most abundant taxa

Multivariate approaches develop predictive models using abundance (the BEAST), or presence/absence (RIVPACS, AusRivAS) of taxa as the basis for predictions of faunal occurrence in test sites. It is apparent that a trend in the future development and expansion of multivariate models will likely include non-richness metrics that reflect other structural and functional aspects of benthic macroinvertebrate assemblages (e.g. Simpson and Norris 2000). However, the analysis performed in this study showed that richness metrics were most accurate in detecting impairment and avoiding classification errors; it should be expected that predictive, multivariate models incorporating non-richness measures will also produce higher misclassification rates. Using Fraser River data, a comparison of the BEAST and AusRivAS (Reynoldson et al. 1997b) indicated that although presence-absence data alone had lower rates of classification errors, inclusion of abundance (as in the BEAST) may make the model more sensitive in detecting impairment. This suggestion needs further testing; however, it does underscore the potential problems of increased misclassification but also the benefits of increased sensitivity from including non-richness metrics.

Why did richness measures work better than the other metrics examined in the limited data set presented in this section? The success of using presence-absence information suggests that with impairment, taxa abundance is not just reduced but, rather, taxa are eliminated. Furthermore, changes in density can result from either impairment- or nonimpairment-related sources. Problems with functional feeding-group designations and biotic indices may involve issues of methods, i.e. the need for correct designation of feeding groups (or the concept itself), and correct designations of individual-taxa tolerances, respectively. The above questions require far more experimental study.

As stated in the Introduction to this section, future analysis trends may continue along present lines (e.g. multivariate approaches such as the BEAST model), rely on conventional approaches (e.g. multimetric analysis), or enter into new, unanticipated realms (e.g. Resh et al. 1996). The raw data and summarized data (as metrics) presented in this section, and the other sections of the report are designed to provide both immediate programs for biomonitoring, and

the flexibility to follow new and promising biomonitoring trends. These results also suggest an array of future research possibilities to further enhance biomonitoring in the Fraser River catchment (e.g. Dymond 1998; Reece and Richardson 1998).

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Appendix 1. Standard field forms used at sites in the Fraser River study.

I: General & Biological Sections

A. General Information

River: _____
(Geographical description)

Station Number: _____

Team: _____

Latitude: _____ Longitude: _____ Altitude: _____

Sampling Date(D.M.Y) ____ / ____ / ____ QA/QC site (circle one): Yes No

B. Reach Characteristics

1. **Stream Order:**

2. **Flow State(Circle one):**

rifle/rapids

straight run

pool/back eddy

3. **Canopy Coverage (Approx. %):**

4. **Macrophyte Coverage (circle one):**

0%

0-25%

25-50%

50-75%

75-100%

5. **Riparian Zone Score (circle those present):**

grasses - 1

shrubs - 2

deciduous trees - 3

coniferous trees - 4

6. **Extent of Logging in riparian zone (circle one):**

0%

0-25%

25-50%

50-75%

75-100%

C. Sample Site Characteristics

1. **Flow State (circle one):**

slow-subcritical

rapid-accelerating

supercritical-shooting

hydraulic jump area

2. **Benthic Invertebrate Samples**

Sample No.	1	2	3	4	5
Operator					
Sampling time (mins)					
Bags/ sample					
Depth (cms)					

D. Photographs:

a) Station Sheet: __ Site: Upstream ____ Downstream ____ Across Aerial ____

b) Substrate (0.09 m² grid): Dry (exposed bar) ____ Aquatic ____

E. Water/Substrate Samples:

TSS(2L) ____ total P ____ Nitrate ____ Major Ions ____

II: Physical/Chemical Section

Station No. _____ Team: _____

A. Field Measurements:

Temp. _____ pH _____ Cond. _____ DO __ = _____ %

B. Channel Measurements:

1. Channel Slope (m): Horizontal Dist. _____ Vertical Dist. _____

2. Bankfull measures:

LOC	A	B	C	D	E	F	G	H	I	J
Horiz. Dist										
Vert Dist										

3. Stream Cross-Section and Flow:

Total Stream Width: _____ (m) Meter No: _____

DIST. (M)							
Depth (cm)							
Revs. *	40	40	40	40	40	40	40
Time (sec)							

* indicates counts other than 40 revs

C. Substrate measures:

Weight of equipment: _____

	Substrate with armour layer	Substrate without armour layer
1. Total weight - Equipment wt = Framework + matrix		
2. Weight after sieving - Equipment wt = Framework		
3. Sum of 1-2 = Matrix		

Station Number: _____

Team: _____

D. Typical Substrate Composition at Sample Sites:

Values for particle sizes and embeddedness used to calculate substrate score.

PARTICLE TYPE/SIZE		EMBEDDEDNESS	
Category	Score	Category	Score
organic cover (>50% of surface)	1	Completely embedded	1
<0.1-0.2 cm	2	3/4 embedded	2
0.2-0.5 cm	3	1/2 embedded	3
0.5-2.5 cm	4	1/4 embedded	4
2.5-5 cm	5	unembedded	5
5-10 cm	6		
10-25 cm	7		
> 25 cm	8		

Substrate Score (See above table)

i) Particle Type or Size

1. Size of predominant particle _____
2. size of 2nd most predominant particle _____
3. size of material surrounding 1 & 2 _____

ii) Embeddedness _____

Total _____

E. Periphyton Samples:

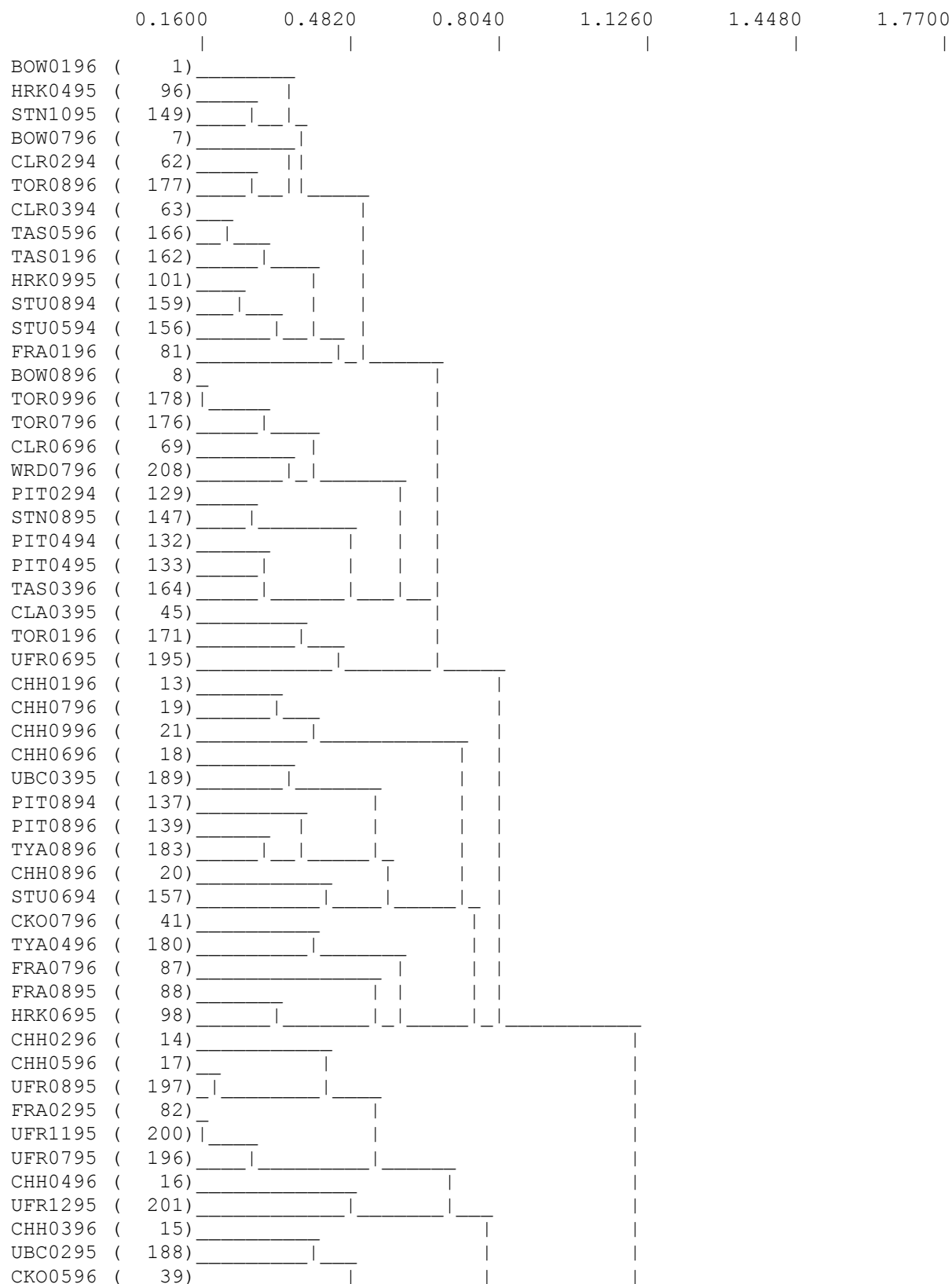
Rock Dimensions (cm)

Rock No.	Length	Width	Depth
1			
2			
3			
4			
5			
6			
7			
8			
9			

F. Leaf-Pack Samples

(circle one): Yes No

Appendix 2. Dendrogram of 219 reference sites from the Fraser River catchment, sampled from 1994 to 1996. Identifications used for the dendrogram were at the family level (74 families included).



[illegible]

WRD0196	(202)	_____		_____		_____		_____			
CLR0695	(68)	_____		_____		_____		_____			
HRK0795	(99)	_____		_____		_____		_____			
TOR0696	(175)	_____		_____		_____		_____			
CHI0194	(22)	_____		_____		_____		_____			
CHI0195	(23)	_____		_____		_____		_____			
CHI0196	(24)	_____		_____		_____		_____			
EUC0396	(75)	_____		_____		_____		_____			
BOW0396	(3)	_____		_____		_____		_____			
TOR0396	(172)	_____		_____		_____		_____			
BOW1096	(10)	_____		_____		_____		_____			
STU1094	(161)	_____		_____		_____		_____			
STU0194	(152)	_____		_____		_____		_____			
CHI0394	(26)	_____		_____		_____		_____			
STU0294	(153)	_____		_____		_____		_____			
CLR0594	(66)	_____		_____		_____		_____			
CLA1295	(54)	_____		_____		_____		_____			
CLA0295	(44)	_____		_____		_____		_____			
STN0295	(141)	_____		_____		_____		_____			
CLR0194	(61)	_____		_____		_____		_____			
CKO0196	(35)	_____		_____		_____		_____			
CKO0296	(36)	_____		_____		_____		_____			
CKO0396	(37)	_____		_____		_____		_____			
STU0994	(160)	_____		_____		_____		_____			
WRD1896	(219)	_____		_____		_____		_____			
CKO0496	(38)	_____		_____		_____		_____			
BOW0496	(4)	_____		_____		_____		_____			
TYA0996	(184)	_____		_____		_____		_____			
TYA0796	(182)	_____		_____		_____		_____			
HRK0395	(95)	_____		_____		_____		_____			
BOW1196	(11)	_____		_____		_____		_____			
CLR0494	(64)	_____		_____		_____		_____			
CKO0896	(42)	_____		_____		_____		_____			
TAS0696	(167)	_____		_____		_____		_____			
STU0494	(155)	_____		_____		_____		_____			
CLR0496	(65)	_____		_____		_____		_____			
CLR0894	(72)	_____		_____		_____		_____			
WRD1796	(218)	_____		_____		_____		_____			
LIL0295	(106)	_____		_____		_____		_____			
TYA0696	(181)	_____		_____		_____		_____			
CLA0795	(49)	_____		_____		_____		_____			
CLD0395	(59)	_____		_____		_____		_____			
CLD0395	(60)	_____		_____		_____		_____			
UBC0195	(187)	_____		_____		_____		_____			
WRD0896	(209)	_____		_____		_____		_____			
CLD0195	(55)	_____		_____		_____		_____			
CLD0196	(56)	_____		_____		_____		_____			
CLD0296	(57)	_____		_____		_____		_____			
CLD0296	(58)	_____		_____		_____		_____			
BOW0696	(6)	_____		_____		_____		_____			
WRD1096	(211)	_____		_____		_____		_____			
CHI0594	(27)	_____		_____		_____		_____			
CHI0294	(25)	_____		_____		_____		_____			
CLA0195	(43)	_____		_____		_____		_____			
WRD0696	(207)	_____		_____		_____		_____			
WRD1496	(215)	_____		_____		_____		_____			
CHI0794	(29)	_____		_____		_____		_____			

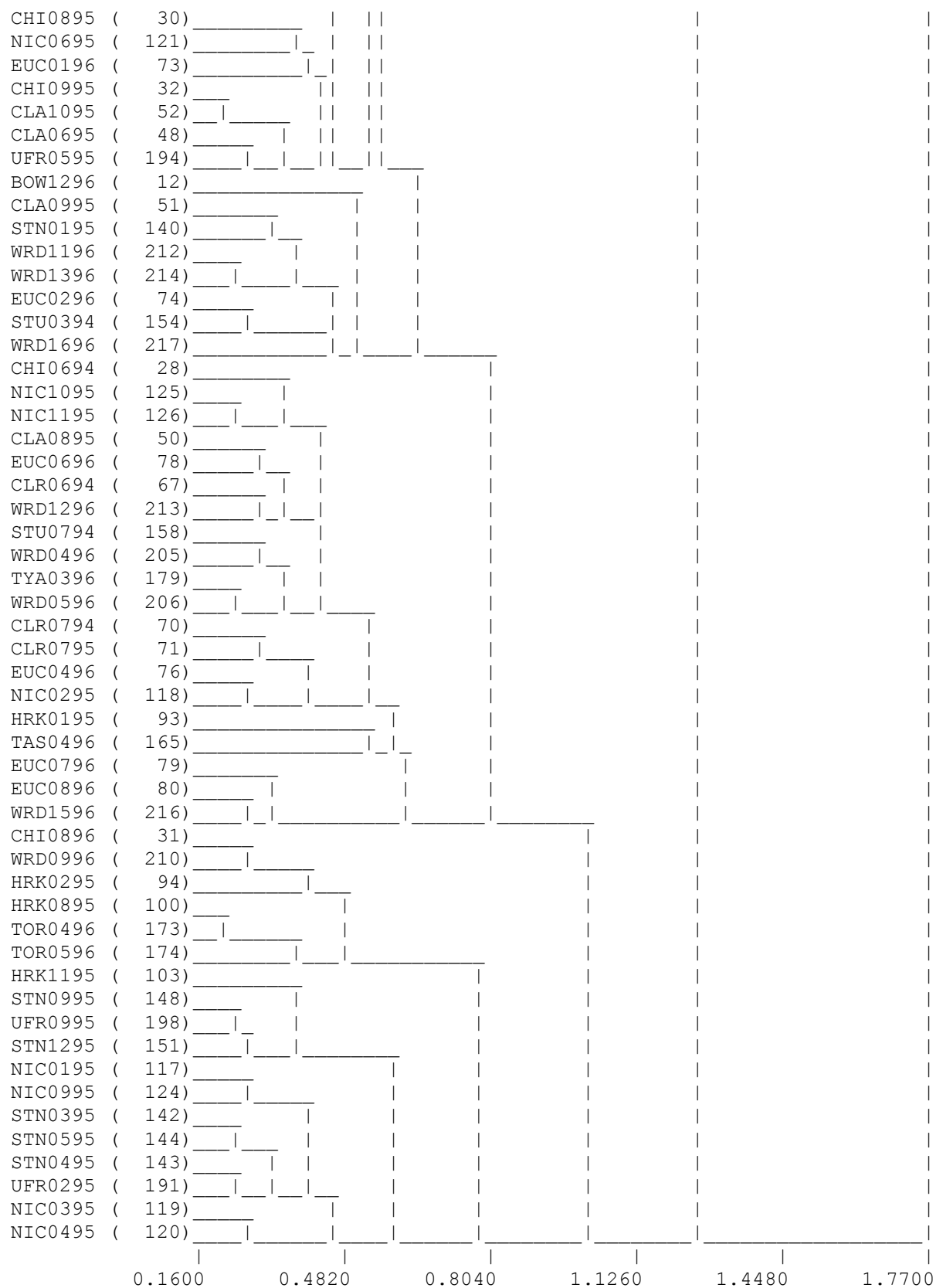


Table 3.4. Mean, standard deviation (SD), and ranges for rapid bioassessment metrics arranged by subcatchment. Metrics were calculated at genus/species (Table 3.4A) and family (Table 3.4B) levels. EPT = Ephemeroptera, Plecoptera, and Trichoptera. See USEPA (1998) for description of how metrics were calculated.

No. sites					Bowron 12 Sites present		Chehalis 9 Sites present		Chelaslie 12 Sites present		Chilcotin 13 Sites present	
Order	Family	Species	F-Tol.	S-Tol.	Mean		Mean		Mean		Mean	
Acariformes	Acariformes family*	Unknown Acariformes*					2	1.0	4	11.9		
	Anisitsiellidae	Unknown Anisitsiellinae*	4						2	4.9		
	Aturidae	Unknown Axonopsinae*	4									
	Hydryphantidae	Protzia spp	4	5								
		Wandesia spp	4	5								
	Lebertidae	Lebertia spp	4	2	2	2.3	4	10.2	2	2.9	6	61.2
	Limnesiidae	Limnesia spp	4	5	1	1.1	2	0.3			3	26.9
		Unknown Tyrrellinae*	4									
	Sperchontidae	Sperchon spp	4	4	3	3.6	2	1.6	5	26.4	4	65.9
	Stygothrombidiidae	Stygothrombium spp		5	1	0.6						
	Torrenticolidae	Testudacarus spp	4	5			2	0.8	2	15.0	2	45.7
		Torrenticola spp	4	5			1	0.3	5	54.8	2	20.3
Amphipoda	Crangonyctidae	Crangonyx richmodensis-occidentalis	5	5							2	10.0
	Gammaridae	Gammarus lacustris	4	6							1	9.2
	Talitridae	Hyaella azteca	8	8								
Bivalvia	Margaritiferidae	Margaritifera falcata		5								
	Sphaeriidae	Pisidium casertanum	8	7	5	384.3	1	0.1			5	339.4
		Pisidium nitidum	8	7								
		Pisidium spp	8	7							1	26.4
		Sphaerium spp	8	7	1	3.3						
		Sphaerium striatum	8	7					6	216.3		
		Unknown Sphaeriidae*	8									
Cladocera	Cladocera family*	Unknown Cladocera*					1	0.1				
	Daphniidae	Unknown Daphniidae*							1	14.1		
Coelentrata	Hydridae	Hydra polyps	5	5	1	0.6			3	54.2		
Coleoptera	Elmidae	Cleptelmis ornata	4	4								
		Heterolimnius corpulentus	4	4	2	213.3			1	11.1	1	8.8
		Heterolimnius spp	4	4	2	2.7			3	19.4	3	69.5
		Lara spp	4	4								
		Narpus concolor	4	4	2	0.8						
		Optioservus quadrimaculatus	4	4							1	7.7
		Optioservus spp	4	4	3	22.3	1	0.1	1	8.3	5	329.2
		Zaitzevia parvula	4	4			1	2.5			1	8.8
		Zaitzevia spp	4	4	1	0.2	3	2.8	1	1.2	2	25.0
Collembola	Hypogastruridae	Unknown Hypogastruridae*	5		2	3.9	3	0.4				
		Xenylla spp	5	5			1	0.1				
	Isotomidae	Semicerura spp	5	5							1	3.8
Copepoda	Copepoda family*	Unknown Copepoda*			1	0.2			2	5.6	3	17.0
Diptera	Athericidae	Atherix pachypus	2	4			1	0.3			1	5.8
	Blephariceridae	Bibiocephala grandis	0	0								
	Ceratopogonidae	Atrichopogon spp	6	6							1	7.7
		Bezzia/Palpomyia spp	6	6	1	3.3	4	2.3	2	6.4		
		Culicoides spp	6	6								
		Forcipomyia spp	6	6								
		Monohelea spp	6	6					1	2.5		
		Probezzia spp	6	6								
		Stilobezzia spp	6	6								
		Unknown Ceratopogonidae*	6									
	Chironomidae	Ablabesmyia spp	6	8							1	2.6
		Brillia flavifrons	6	5	1	1.7						
		Brillia retifinis	6	5	3	21.5	6	8.9			1	7.7
		Brillia spp	6	5					3	40.3	2	9.6
		Cardiocladius spp	6	5								
		Chaetocladius spp	6	6								
		Chaetocladius vitillinus group	6	6	2	9.2						
		Chironomus spp	6	10								
		Cladotanytarsus spp	6	7	7	161.2	3	1.8	3	79.2	1	255.4
		Corynoneura spp	6	7	1	0.2	1	0.1	3	25.2	2	11.5
		Cricotopus spp	6	7								
		Cricotopus(Cricotopus) bicintus group	6	7					7	183.4	1	3.8
		Cricotopus(Cricotopus) cylindraceus group	6	7					2	36.5		
		Cricotopus(Cricotopus) festivellus group	6	7							1	1.5

+ - not identified to Genus/Species level.

* - not identified to Family level.

No. sites					Bowron		Chehalis		Chelaslie		Chilcotin	
			F-Tol.	S-Tol.	12 Sites	Mean	9 Sites	Mean	12 Sites	Mean	13 Sites	Mean
Order	Family	Species			present		present		present		present	
		Cricotopus(Cricotopus) fuscus group	6	7							1	1.4
		Cricotopus(Cricotopus) spp	6	7								
		Cricotopus(Cricotopus) tremulus group	6	7	4	13.7	2	4.3				
		Cricotopus(Cricotopus) trifasciatus group	6	7								
		Cricotopus(Isocladus) laricomalis group	6	7					2	34.1		
		Cricotopus(Isocladus) obnixus group	6	7								
		Cricotopus(Isocladus) spp	6	7					1	2.1	2	11.6
		Cricotopus(Nostocoladus) spp	6	7					2	10.7		
		Cryptochironomus spp	6	8	1	0.4						
		Diamesa spp	6	5	1	1.7					2	13.5
		Diplociadus spp	6	6								
		Endochironomus spp	6	10							1	2.3
		Eukiefferiella brehmi group	6	8	8	24.5	2	0.3	8	52.3	6	117.2
		Eukiefferiella brevicar group	6	8			1	0.1			1	4.1
		Eukiefferiella claripennis group	6	8								
		Eukiefferiella devonica group	6	8			1	0.1	3	121.3	6	96.6
		Eukiefferiella gracei group	6	8			4	2.1	4	20.1	3	28.2
		Eukiefferiella rectangularis group	6	8			4	2.2				
		Eukiefferiella similis group	6	8	1	1.2					1	3.1
		Eukiefferiella spp	6	8								
		Euryhopsis spp	6	5								
		Heleniella spp	6	5								
		Heterotanytarus spp	6	5								
		Heterotrissocladus changi	6	0							1	1.5
		Heterotrissocladus spp	6	0								
		Hydrobaenus spp	6	8								
		Krenosmittia spp	6	5			1	0.1				
		Larsia spp	6	6								
		Lopesocladus(Cordiella) hyporheicus	6	6							1	7.7
		Metriocnemus spp	6	6			1	0.1				
		Micropectra spp	6	7	11	270.7	3	0.9	10	406.6	12	496.3
		Microtendipes spp	6	6	1	1.0					1	30.8
		Monodiamesia spp	6	7								
		Nanocladus (Nanocladus) distinctus	6	3								
		Nanocladus (Plecopteracalathus) branchicolus	6	3								
		Nanocladus(Nanocladus) balticus	6	3								
		Nanocladus(Nanocladus) parvulus group	6	3								
		Nanocladus(Plecopteracalathus)	6	3					5	121.7	1	5.8
		Nilotanytus frimbriatus	6	6					4	46.2		
		Odontomesa spp	6	4								
		Orthocladus spp	6	6								
		Orthocladus(Eudactylocladus) spp	6	6	2	10.4			1	4.2	10	302.5
		Orthocladus(Euorthocladus) spp	6	6	3	16.0	1	2.0	2	15.3	2	41.5
		Orthocladus(Orthocladus) doreus	6	6	4	33.8			3	36.3	2	16.9
		Orthocladus(Orthocladus) nigratus	6	6							3	13.2
		Orthocladus(Orthocladus) obumbratus	6	6	3	6.4			4	15.8	2	10.3
		Orthocladus(Orthocladus) spp	6	6							2	5.2
		Pagastia spp	6	1	6	74.6	1	0.1	5	43.2	5	56.5
		Parachironomus arcuatus group	6	10	3	5.6						
		Parachironomus frequens group	6	10			3	2.2			1	7.7
		Paracladopelma camptolabis group	6	7	1	0.4						
		Paracladopelma spp	6	7								
		Paracladopelma winnelli	6	7								
		Paracricotopus spp	6	6								
		Parakiefferiella spp	6	4	2	8.5	1	0.1	2	8.2	4	45.6
		Paramerina spp	6	6								
		Parametriocnemus spp	6	5							7	46.8
		Paraphaenocladus spp	6	4	2	3.8	1	0.9	4	28.8	3	17.3
		Parapsectra spp	6	5								
		Paratanytarus spp	6	6								
		Paratendipes spp	6	8							1	7.7
		Paratrachocladus spp	6	6	1	16.7	6	4.3	4	75.0	3	24.4
		Parorthocladus spp	6	6	1	0.4	3	0.8				
		Phaenopsectra spp	6	7			1	0.1			1	2.6

No. sites					Bowron		Chehalis		Chelasia		Chilcotin	
			F-Tol	S-Tol	12 Sites present	Mean	9 Sites present	Mean	12 Sites present	Mean	13 Sites present	Mean
Order	Family	Species										
		Polypedium spp	6	6	7	30.4	7	14.4	9	446.0	7	295.8
		Potthastia gaedi group	6	2							2	50.0
		Potthastia longimana group	6	2	2	21.5	1	1.1			1	7.7
		Procladius(Holotanypus) spp	6	9								
		Prodiamesia spp	6	3								
		Pseudodiamesa spp	6	6							2	13.5
		Pseudorthocladus spp	6	0	2	3.3						
		Psilometriocnemus	6	5								
		Rheocricotopus(Rheocricotopus) eminellus	6	6	3	8.5	3	0.6	5	47.6	2	13.5
		Rheocricotopus(Rheocricotopus) pauriseta	6	6							2	27.0
		Rheosmittia spp	6	6	3	9.6						
		Rheotanytarsus spp	6	6	3	15.5	2	0.5	6	36.6	3	64.2
		Saetheria tylus	6	4								
		Stempellina bausei group	6	2							1	7.7
		Stempellina spp	6	2	2	5.4					1	5.8
		Stempellinella spp	6	4	5	60.2			4	65.3	2	37.5
		Stictochironomus spp	6	9								
		Stilocladus spp	6	6			1	0.7				
		Subletia coffmani	6	4	4	51.6			3	27.4	1	7.7
		Symposiocladius lignicola	6	5			1	0.1			1	1.5
		Syndiamesa spp	6	6					1	4.2		
		Synorthocladus semivirens	6	2					1	0.8		
		Tanytarsus spp	6	6	5	24.7	6	42.1	4	212.5	6	260.5
		Thienemanniella spp	6	6	1	1.0	1	0.5	4	11.8	1	5.8
		Thienemannimyia group	6	6					8	63.0	3	26.8
		Tribelos spp	6	5								
		Tvetenia bavarica group	6	5	5	16.0	4	2.5	9	254.2	6	59.0
		Tvetenia discoloripes group	6	5	2	13.1			2	45.8	1	23.1
		Unknown Chironominae ⁺	6									
		Unknown Diamesinae ⁺	6									
		Unknown Orthoclaudiinae ⁺	6		2	2.7	1	0.1			4	20.8
		Unknown Tanyptodinae ⁺	6									
		Zavrelimyia spp	6	8	2	8.5	4	1.8	2	45.1		
	Deuterophlebiidae	Deuterophlebia coloradensis	0	0								
	Dixidae	Dixa spp	2	2								
	Empididae	Chellifera spp	6	6	5	9.4	2	1.0	3	13.9	6	79.2
		Clinocera spp	6	6	3	10.0			2	9.5	1	2.6
		Oreogeton spp	6	6			4	2.6	5	36.3		
	Muscidae	Unknown Muscidae ⁺	6		2	1.3	1	1.1	1	2.8		
	Pelicerhynchidae	Glutops spp	3	3								
	Psychodidae	Maruina spp	10	2			1	0.3				
		Pericoma/Thelmatoscopus spp	10	4	2	8.5			2	87.5	7	127.2
	Simuliidae	Prosimulium spp	6	3	3	4.2					2	7.8
		Simulium spp	6	6	1	0.8	3	2.8	2	37.5	7	173.9
	Stratiomyidae	Caloparyphus spp	8	8								
	Tabanidae	Unknown Tabanidae ⁺	6									
	Tanyderidae	Protanyderus margarita	5	5			1	0.3				
	Thaumaleidae	Thaumalea spp	5	5								
	Tipulidae	Antocha monticola	3	3			3	2.2	3	20.6	3	70.0
		Dicranota spp	3	3	1	2.1	3	1.6	3	18.1	5	50.5
		Gonomyodes spp	3	5								
		Hexatoma spp	3	2	7	11.5	2	1.6	2	6.9	3	24.6
		Pseudolimnophila spp	3	5							1	14.4
		Rhabdomastix spp	3	3					1	1.4		
		Tipula spp	3	4								
Ephemeroptera	Ameletidae	Ameletus spp	0	0	4	8.4	8	17.6	5	38.5		
	Ametropodidae	Ametropus ammophilus	11	11								
	Baetidae	Acentrella insignificans	4	4			1	0.1				
		Acentrella macdunnoughi	4	4								
		Baetis bicaudatus	4	5	7	653.4	4	31.5	7	646.1	3	540.6
		Baetis spp	4	5					1	190.6		
		Baetis tricaudatus	4	5	5	163.3	5	24.8	5	690.9	11	1796.5
		Centropilum spp	4	2					2	156.9		

+ - not identified to Genus/Species level.

* - not identified to Family level.

No. sites					Bowron		Chehalis		Chelashie		Chilcotin	
			F-Tot.	S-Tot.	12 Sites	Mean	9 Sites	Mean	12 Sites	Mean	13 Sites	Mean
Order	Family	Species			present		present		present		present	
		Dipheter hageni	4	5	2	51.0	1	0.2	5	190.1	7	229.3
		Fallceon quilleri	4	5			2	3.0	1	12.5		
		Unknown Baetidae*	4						1	247.1		
	Ephemereillidae	Caudatella heterocaudata heterocaudata	1	1							2	18.3
		Caudatella hystrix	1	1							1	3.8
		Caudatella spp	1	1								
		Drunella doddsi	1	0	7	45.2	4	6.4	6	55.6	1	1.4
		Drunella grandis ingens	1	0							1	211.4
		Drunella spinifera	1	0	1	0.6	1	0.3			2	6.7
		Ephemerella inermis	1	1	3	14.4						
		Ephemerella infrequens	1	1	5	168.2					6	146.6
		Ephemerella mollita	1	1								
		Ephemerella spp	1	1	4	118.2	7	102.0				
		Serratella spp	1	2					9	488.7	1	4.6
		Serratella tibialis	1	2					1	41.7	2	30.8
		Unknown Ephemerellidae*	1									
	Ephemeridae	Ephemerella spp	4	4								
	Heptageniidae	Cinygma spp	4	2								
		Cinygmula spp	4	4	1	1.7	6	26.3				
		Epeorus deceptivus	4	0	2	2.7	1	0.1				
		Epeorus grandis	4	0					2	6.3		
		Epeorus longimanus	4	0	1	14.6	3	3.9				
		Epeorus spp	4	0	1	0.8	2	3.5	5	78.2	4	205.8
		Heptagenia spp	4	3	6	323.7	1	0.1			3	1097.4
		Leucrocuta spp	4	1	2	11.0			8	737.5	7	559.1
		Rhithrogena spp	4	0	8	136.9	8	26.8	6	131.7	3	41.3
		Stenonema spp	4	5								
		Unknown Heptageniidae*	4		3	44.3	1	10.6	2	43.3	3	98.6
	Leptohyphidae	Tricorythodes minutes	4	4							1	53.8
	Leptophlebiidae	Paraleptophlebia spp	2	4	2	25.4	3	4.3	8	311.8	8	304.3
Gastropoda	Lymnaeidae	Unknown Lymnaeidae*	8									
	Physidae	Physella spp	8	8								
	Planorbidae	Gyraulus circumstriatus	5	5								
		Menetus opercularis	5	5								
	Valvatidae	Valvata humeralis	5	5	1	0.6						
		Valvata sincera	5	5								
Hirudinea	Piscicolidae	Piscicola milneri		6			1	1.1				
Megaloptera	Sialidae	Sialis spp	4	4	1	8.3						
Nematoda	Nematoda family*	Unknown Nematoda*			6	16.4			1	6.3	2	8.1
Oligochaeta	Enchytraeidae	Unknown Enchytraeidae*			6	8.6	4	3.1	2	11.7	5	25.1
	Lumbriculidae	Ecilipidrilus spp	7	7								
		Kincaldiana hexatheca	7	7								
		Lumbriculus spp	7	7			6	32.1				
		Lumbriculus variegatus	7	7								
		Rhynchelmis spp	7	7			2	1.0				
		Unknown Lumbriculidae*	7		2	1.2						
	Naididae	Chaetogaster diaphanus	8	8					2	6.5		
		Dero digitata	8	8			1	0.2				
		Nais alpina	8	8	2	45.6	3	1.1	2	107.5		
		Nais behningi	8	8							1	200.0
		Nais simplex	8	8								
		Nais variabilis	8	8	2	3.0	1	0.5				
		Pristina aequiseta	8	8								
		Pristinella jenkiniae	8	8			2	1.6				
		Specaria fraseri	8	8			2	1.1	2	15.8		
		Specaria hellei	8	8								
		Specaria josinae	8	8								
		Uncinails uncinata	8	8								
	Tubificidae	Immatures with hair chaetae		10			1	0.1			2	9.0
		Immatures without hair chaetae		10	1	25.0					2	2.9
		Limnodrilus profundicola		9								
		Limnodrilus udekemianus		9								
Ostracoda	Ostracoda family*	Unknown Ostracoda*			5	56.0	1	0.3			7	110.7

+ - not identified to Genus/Species level.

* - not identified to Family level.

No. sites					Bowron		Chehalis		Chelashie		Chilcotin	
			F-Tol.	S-Tol.	12 Sites present	Mean	9 Sites present	Mean	12 Sites present	Mean	13 Sites present	Mean
Order	Family	Species										
Platyhelminthes - Turbellaria	Platyhelminthes - Turbellaria family*	Unknown Platyhelminthes - Turbellaria*			3	11.7	2	0.3			6	63.8
Plecoptera	Capniidae	Capnia spp	1	3	11	81.9	3	0.6	4	48.4	11	321.8
		Unknown Capniidae*	1									
	Chloroperlidae	Haploperla brevis	1	0	8	33.3	1	0.6				
		Plumipera diversa	1	0								
		Suwallia spp	1	0								
		Sweltsa spp	1	1	11	53.5	7	27.2	9	147.1	9	177.5
		Unknown Chloroperlidae*	1								1	61.5
	Leuctridae	Paraleuctra spp	0	3	4	29.5	4	2.8	3	27.1	2	7.1
		Unknown Leuctridae*	0									
	Nemouridae	Podmosta spp	2	2								
		Unknown Nemouridae*	2									
		Visoka cataractae	2	0	1	2.1	2	1.2	2	5.0		
		Zapada cinctipes	2	2	5	31.2	8	38.0	8	182.3	10	701.4
		Zapada columbiana	2	2	5	61.8	2	2.1	3	39.2	2	189.7
		Zapada oregonensis	2	2					1	29.2		
		Zapada spp	2	2	1	6.0			3	82.9	2	33.0
	Peltoperlidae	Yoraperla mariana	0	1								
	Perlidae	Calineuria californica	1	2	1	6.7	4	2.6	2	9.7	1	17.3
		Claassenia sabulosa	1	3			2	2.6				
		Hesperoperla pacifica	1	2			1	0.1	4	25.6	2	5.2
	Perlodidae	Cultus spp	2	2							2	7.1
		Isogenoides spp	2	2								
		Isoperla spp	2	2			2	2.7	7	44.9	3	20.6
		Megarcys spp	2	2	4	6.0						
		Perlinoes aureus	2	2								
		Rickera sorpta	2	2							1	20.8
		Setvena bradleyi	2	2								
		Setvena spp	2	2								
		Skwala spp	2	2	2	0.8	1	1.5			1	15.4
		Unknown Perlodidae*	2		1	5.0					5	42.7
	Pteronarcyidae	Pteronarcella regularis	0	0								
		Pteronarcys californica	0	0							1	7.7
		Pteronarcys spp	0	0								
	Taeniopterygidae	Taenionema spp	2	2	4	23.6	4	1.7	4	31.9	2	18.8
Porifera	Spongillidae	Unknown Spongillidae*										
Trichoptera	Apataniidae	Allomyia spp	4	3								
		Apatania spp	4	1								
		Apatania zonella	4	1			1	0.2	2	9.5		
		Pedomoecus sierra	4	0							1	1.4
	Brachycentridae	Amiocentrus aspilus	1	3			1	0.5				
		Brachycentrus americanus	1	1	2	9.1			2	55.6	4	71.2
		Brachycentrus occidentalis	1	1			1	0.1	1	2.4		
		Micrasema bactro	1	1			1	0.3	4	58.3	7	106.5
		Micrasema spp	1	1	1	1.7	5	9.0			1	30.8
	Glossosomatidae	Anagapetus spp	0	0	1	0.8			1	4.2		
		Glossosoma spp	0	1	4	7.0	1	6.1			2	12.9
		Protoptila spp	0	1							1	76.9
	Hydropsychidae	Arctopsyche grandis	4	1	2	3.3	2	1.1	2	6.9		
		Cheumatopsyche spp	4	5							1	15.4
		Diplectrona spp	4	4								
		Hydropsyche alhedra	4	4								
		Hydropsyche ambilis	4	4					1	13.9	2	80.8
		Hydropsyche morosa	4	4					1	11.1	2	69.2
		Hydropsyche slossanae	4	4	1	0.6	1	0.5			1	35.2
		Hydropsyche spp	4	4					4	234.7	4	75.0
		Hydropsyche tana	4	4	3	17.9	2	1.3				
		Parapsyche almota	4	2								
		Parapsyche elsis	4	2			2	0.6			1	5.8
		Parapsyche spp	4	2	2	7.1						
	Hydroptilidae	Hydroptila spp	4	6	7	380.5					7	183.7
		Leucotrichia pictipes	4	6								
		Oxyethira spp	4	3								

+ - not identified to Genus/Species level.

* - not identified to Family level.

No. sites					Bowron		Chehalis		Chelaslie		Chilcotin	
			F-Tol.	S-Tol.	12		9		12		13	
Order	Family	Species			Sites	Mean	Sites	Mean	Sites	Mean	Sites	Mean
					present		present		present		present	
		Stactobiella spp	4	4	1	0.6	1	0.1	2	12.5		
		Unknown Hydroptilidae ⁺	4									
	Lepidostomatidae	Lepidostoma astaneum group	1	1			1	12.2	3	21.0	3	354.0
		Lepidostoma cinereum	1	1	1	0.2	1	1.1			4	25.7
		Lepidostoma pluviale group	1	1			1	1.1			2	12.9
		Lepidostoma spp	1	1	5	9.5	5	36.7	5	649.4	3	47.4
		Lepidostoma unicolor	1	1								
	Leptoceridae	Ceraclea spp	4	3					1	8.3		
		Oecetis avara	4	8								
		Oecetis disjuncta	4	8							2	48.1
	Limnephilidae	Chyranda centralis	4	1			1	0.1				
		Clostoea disjuncta	4	4			1	0.1				
		Ecclisocosmoecus scylla	4	0			1	0.3				
		Ecclisomyia spp	4	2	1	1.0	2	1.5	3	5.7		
		Grammotaulius spp	4	4	1	8.3						
		Hesperophylax spp	4	3								
		Limnephilus spp	4	3							1	4.6
		Psychoglypha spp	4	0	1	1.0	2	1.2			1	1.3
		Unknown Limnephilidae ⁺	4		3	3.7	1	0.8				
	Philopotamidae	Wormaldia spp	3	3			1	0.1				
	Polycentropodidae	Polycentropus spp	6	6								
	Rhyacophilidae	Rhyacophila acropedes group	0	0	4	9.1	2	0.4	1	8.3	1	1.5
		Rhyacophila alberta group	0	0					1	0.8		
		Rhyacophila angelita group	0	0	4	8.6	1	0.1			1	2.7
		Rhyacophila arnaudi	0	0	2	1.7						
		Rhyacophila betteni group	0	0			1	0.1	2	7.9		
		Rhyacophila blarina	0	0								
		Rhyacophila grandis	0	0								
		Rhyacophila narvae	0	0	3	18.5			1	2.8	4	22.2
		Rhyacophila rotunda group	0	0								
		Rhyacophila spp	0	0							3	7.3
		Rhyacophila vagrita	0	0	2	4.7	3	0.4			2	3.6
		Rhyacophila valuma	0	0								
		Rhyacophila velora	0	0								
		Rhyacophila verrula	0	0								
		Rhyacophila vocala	0	0							1	1.4
	Uenoidae	Neothremma spp	4	0					2	14.2		
		Oligophlebodes spp	4	0								

No. sites					Chilko		Cleanwater		Coldwater		Euchiniko		Fraser	
			F-Tol.	S-Tol.	8 Sites present	Mean	12 Sites present	Mean	6 Sites present	Mean	8 Sites present	Mean	12 Sites present	Mean
Acariformes	Acariformes family*	Unknown Acariformes*					1	34.0						
	Anisitsiellidae	Unknown Anisitsiellinae*	4								1	2.5	1	0.1
	Aturidae	Unknown Axonopsinae*	4											
	Hydryphantidae	Protzia spp	4	5			1	5.6	1	8.3				
		Wandesia spp	4	5										
	Lebertiidae	Lebertia spp	4	2	4	12.9	6	56.3	5	28.6	4	95.0	7	1.8
	Limnesiidae	Limnesia spp	4	5	2	6.7	1	1.4	1	1.7			5	1.2
		Unknown Tyrrelliinae*	4		1	0.3							4	6.1
	Sperchontidae	Sperchon spp	4	4	4	12.7	3	17.6	2	10.0	2	25.0	5	2.0
	Stygothrombididae	Stygothrombium spp		5					1	3.3				
	Torrenticolidae	Testudacarus spp	4	5	1	3.1	4	61.5	1	2.8	3	19.2		
		Torrenticola spp	4	5	1	3.1	3	5.5	1	8.3	1	12.5		
Amphipoda	Crangonyctidae	Crangonyx richmodensis-occidentalis	5	5										
	Gammaridae	Gammarus lacustris	4	6										
	Talitridae	Hyaella azteca	8	8							2	50.0		
Bivalvia	Margaritiferidae	Margaritifera falcata		5							1	12.5		
	Sphaeriidae	Pisidium casertanum	8	7	2	2.5	1	22.7						
		Pisidium nitidum	8	7										
		Pisidium spp	8	7			1	76.7					1	0.1
		Sphaerium spp	8	7			1	4.2			1	12.5		
		Sphaerium striatum	8	7							3	152.5		
		Unknown Sphaeriidae*	8				1	1.9						
Cladocera	Cladocera family*	Unknown Cladocera*											1	0.1
	Daphniidae	Unknown Daphniidae*												
Coelentrata	Hydriidae	Hydra polyops	5	5			2	10.6						
Coleoptera	Elmidae	Cleptelmis ornata	4	4			1	12.8						
		Heterolimnius corpulentus	4	4	1	40.6	1	5.6			1	15.0		
		Heterolimnius spp	4	4			2	4.4			4	129.2	1	0.1
		Lara spp	4	4										
		Narpus concolor	4	4										
		Optioservus quadrimaculatus	4	4							1	112.5		
		Optioservus spp	4	4							1	75.0		
		Zaitzevia parvula	4	4										
		Zaitzevia spp	4	4			2	152.8			1	10.0		
Collembola	Hypogastruridae	Unknown Hypogastruridae*	5		1	0.1								
		Xenylla spp	5	5										
	Isotomidae	Semicerura spp	5	5										
Copepoda	Copepoda family*	Unknown Copepoda*			1	15.6	1	11.3			4	212.5	3	3.1
Diptera	Athericidae	Atherix pachypus	2	4			1	1.4	3	38.3				
	Blephariceridae	Bibiocephala grandis	0	0										
	Ceratopogonidae	Atrichopogon spp	6	6										
		Bezzia/Palpomyia spp	6	6			2	3.0	1	6.7				
		Culicoides spp	6	6							1	4.2		
		Forcipomyia spp	6	6	1	0.1								
		Monohelea spp	6	6					2	12.5				
		Probezzia spp	6	6					2	6.1	1	12.5		
		Stilobezzia spp	6	6					2	18.3	1	12.5		
		Unknown Ceratopogonidae*	6											
	Chironomidae	Ablabesmyia spp	6	8										
		Brillia flavifrons	6	5							1	8.3		
		Brillia retifinis	6	5	8	102.6			1	3.3	4	80.0	3	0.6
		Brillia spp	6	5			5	26.4	1	8.3			1	0.2
		Cardiocladius spp	6	5										
		Chaetocladius spp	6	6	1	1.6								
		Chaetocladius vitillinus group	6	6										
		Chironomus spp	6	10									2	1.0
		Cladotanytarsus spp	6	7	1	1.8	5	18.2	6	152.2	2	25.0	5	6.1
		Corynoneura spp	6	7			2	1.8			1	6.3		
		Cricotopus spp	6	7							1	17.5		
		Cricotopus(Cricotopus) bicintus group	6	7			2	231.7	3	66.7			1	2.3
		Cricotopus(Cricotopus) cylindraceus group	6	7										
		Cricotopus(Cricotopus) festivellus group	6	7										

+ - not identified to Genus/Species level.

* - not identified to Family level.

No. sites					Chilko		Clearwater		Coldwater		Euchiniko		Fraser	
			F-Tol.	S-Tol.	8 Sites	Mean	12 Sites	Mean	6 Sites	Mean	8 Sites	Mean	12 Sites	Mean
Order	Family	Species			present		present		present		present		present	
		Cricotopus(Cricotopus) fuscus group	6	7							2	50.0	2	0.5
		Cricotopus(Cricotopus) spp	6	7			1	45.4			1	25.0		
		Cricotopus(Cricotopus) tremulus group	6	7	1	0.5			1	10.0	2	125.0	1	0.2
		Cricotopus(Cricotopus) trifasciatus group	6	7										
		Cricotopus(Isocladus) laricomalis group	6	7							1	50.0		
		Cricotopus(Isocladus) obnixus group	6	7										
		Cricotopus(Isocladus) spp	6	7	1	3.1	1	90.8	1	8.3	1	25.0	1	0.1
		Cricotopus(Nostocoladius) spp	6	7										
		Cryptochironomus spp	6	8										
		Diamesa spp	6	5	4	22.2					2	31.3	1	0.3
		Diplociadus spp	6	6										
		Endochironomus spp	6	10									1	0.3
		Eukiefferiella brehmi group	6	8	5	74.0	5	73.0	3	27.8	5	88.8	2	0.9
		Eukiefferiella brevicar group	6	8										
		Eukiefferiella claripennis group	6	8										
		Eukiefferiella devonica group	6	8	2	8.0	2	35.7	1	8.3	1	37.5		
		Eukiefferiella gracei group	6	8	2	5.7	3	11.5						
		Eukiefferiella rectangularis group	6	8										
		Eukiefferiella similis group	6	8			1	79.4						
		Eukiefferiella spp	6	8									1	0.2
		Euryhopsis spp	6	5	1	0.1								
		Heleniella spp	6	5										
		Heterotanytarsus spp	6	5										
		Heterotrissocladus changi	6	0									2	0.3
		Heterotrissocladus spp	6	0			1	0.5						
		Hydrobaenus spp	6	8										
		Krenosmittia spp	6	5										
		Larsia spp	6	6										
		Lopesocladus(Cordiella) hyporheicus	6	6										
		Metriocnemus spp	6	6										
		Micropsectra spp	6	7	5	122.5	9	766.4	1	8.3	8	2040.8	4	2.0
		Microtendipes spp	6	6			5	48.9			3	70.8		
		Monodiamesia spp	6	7			1	0.3					7	2.6
		Nanocladus (Nanocladus) distinctus	6	3			1	0.8						
		Nanocladus (Plecopteracalathus) branchicolus	6	3							1	12.5		
		Nanocladus(Nanocladus) balticus	6	3							1	12.5		
		Nanocladus(Nanocladus) parvulus group	6	3									1	0.1
		Nanocladus(Plecopteracalathus)	6	3			2	69.5					1	1.9
		Nilotanytus frimbriatus	6	6										
		Odontomesa spp	6	4									1	0.5
		Orthocladus spp	6	6									1	0.3
		Orthocladus(Eudactylociadus) spp	6	6							3	154.2		
		Orthocladus(Euorthocladus) spp	6	6	3	22.3	3	15.3	1	6.7	1	50.0	1	0.1
		Orthocladus(Orthocladus) doreus	6	6	2	2.2	1	147.5	1	6.7			2	0.6
		Orthocladus(Orthocladus) nigratus	6	6										
		Orthocladus(Orthocladus) obumbratus	6	6	2	5.7	1	4.5			3	109.2	5	6.9
		Orthocladus(Orthocladus) spp	6	6			2	9.8			1	12.5	1	0.5
		Pagastia spp	6	1	2	18.5	3	26.7			3	34.2	1	0.3
		Parachironomus arcuatus group	6	10							1	12.5		
		Parachironomus frequens group	6	10	1	1.6					1	137.5	2	0.2
		Paracladopelma camptolabis group	6	7										
		Paracladopelma spp	6	7			1	0.5						
		Paracladopelma winnelli	6	7									4	2.5
		Paracricotopus spp	6	6									2	0.2
		Parakiefferiella spp	6	4	2	3.9	2	3.6			2	17.5	4	4.5
		Paramerina spp	6	6							1	12.5		
		Parametriocnemus spp	6	5	1	0.4	2	8.3			1	100.0		
		Paraphaenocladus spp	6	4	4	11.6	2	2.9			3	30.8	6	5.2
		Parapsectra spp	6	5										
		Paratanytarsus spp	6	6			1	0.8						
		Paratendipes spp	6	8							1	312.5		
		Paratrachocladus spp	6	6	4	21.1	5	666.9	4	22.8	1	62.5	2	0.2
		Parorthocladus spp	6	6										
		Phaenopsectra spp	6	7										

No. sites					Chiiko										
					8										
					Sites										
					present										
Order	Family	Species	F-Tol.	S-Tol.	Mean	Mean	Sites present	Mean	Sites present	Mean	Sites present	Mean	Sites present	Mean	Sites present
		Polypedilum spp	6	6	2	11.5	4	22.4	3	26.7	3	121.7	7	42.3	
		Potthastia gaedi group	6	2			2	1.5	1	8.3			1	0.2	
		Potthastia longimana group	6	2	1	2.1					1	12.5			
		Procladius(Holotanypus) spp	6	9							3	40.0			
		Prodiamesia spp	6	3			1	1.3							
		Pseudodiamesa spp	6	6	1	0.4									
		Pseudorthocladius spp	6	0											
		Psilometriocnemus	6	5	1	7.1									
		Rheocricotopus(Rheocricotopus) eminellobus	6	6	2	4.9	3	131.7			2	27.5			
		Rheocricotopus(Rheocricotopus) pauriseta	6	6					1	8.3					
		Rheosmittia spp	6	6			1	1.7					1	0.1	
		Rheotanytarsus spp	6	6			2	25.4			4	316.7	2	1.2	
		Saetheria tylus	6	4											
		Stempellina bausei group	6	2									1	0.5	
		Stempellina spp	6	2	1	9.4					1	212.5			
		Stempellinella spp	6	4	1	4.7	4	9.7			5	124.2	2	0.5	
		Stictochironomus spp	6	9			1	2.8					1	0.2	
		Stilocladius spp	6	6			2	12.0							
		Sublettea coffmani	6	4			1	0.8	1	4.2	2	75.0			
		Symposiocladius lignicola	6	5											
		Syndiamesa spp	6	6											
		Synorthocladius semivirens	6	2			1	0.9			1	12.5			
		Tanytarsus spp	6	6	3	9.6	6	141.3	5	50.8	6	1493.8	4	5.4	
		Thienemanniella spp	6	6	1	3.1	1	0.9	1	3.3					
		Thienemannimyia group	6	6			2	18.0					2	1.4	
		Tribelos spp	6	5							1	25.0			
		Tvetenia bavarica group	6	5	4	62.9	8	509.8	2	20.8	5	101.3	3	0.5	
		Tvetenia discoloripes group	6	5			2	3.7							
		Unknown Chironominae ⁺	6				1	3.7							
		Unknown Diamesinae ⁺	6				1	0.8							
		Unknown Orthocladinae ⁺	6		1	2.1	7	45.9	1	2.8	5	60.8			
		Unknown Tanypodiinae ⁺	6				1	12.8							
		Zavrelimyia spp	6	8	1	28.1	3	167.0			5	215.0	1	0.1	
	Deuterophlebiidae	Deuterophlebia coloradensis	0	0	1	2.1									
	Dixidae	Dixa spp	2	2							1	12.5			
	Empididae	Chelifera spp	6	6			7	27.2	1	8.3	2	31.3	4	3.6	
		Clinocera spp	6	6	3	6.3	1	0.8			2	62.5	4	1.9	
		Oreogeton spp	6	6	2	12.5	2	3.5			2	29.2	1	0.1	
	Muscidae	Unknown Muscidae ⁺	6		1	0.5							1	0.1	
	Pelicerhynchidae	Glutops spp	3	3					1	3.3					
	Psychodidae	Maruina spp	10	2											
		Pericoma/Thelmatoscopus spp	10	4	1	3.1	3	84.8	3	10.8	3	141.7			
	Simuliidae	Prosimulium spp	6	3	1	1.8	3	24.7			3	87.5	2	0.2	
		Simulium spp	6	6	2	10.9					1	25.0			
	Stratiomyidae	Caloparyphus spp	8	8											
	Tabanidae	Unknown Tabanidae ⁺	6												
	Tanyderidae	Protanyderus margarita	5	5			1	4.2	1	4.2			2	1.7	
	Thaumaleidae	Thaumalea spp	5	5											
	Tipulidae	Antocha monticola	3	3	1	1.8			2	33.3	1	12.5			
		Dicranota spp	3	3	3	14.3	3	4.8			4	54.2	2	0.2	
		Gonomyodes spp	3	5	2	2.3									
		Hexatoma spp	3	2	1	6.3	1	1.7	4	24.2	5	52.1	3	0.7	
		Pseudolimnophila spp	3	5			3	2.6					3	1.0	
		Rhabdomastix spp	3	3	1	2.1							1	0.1	
		Tipula spp	3	4											
Ephemeroptera	Ameletidae	Ameletus spp	0	0	1	1.8	4	10.8	1	3.3	1	12.5	8	11.6	
	Ametropodidae	Ametropus ammophilus	11	11									1	0.6	
	Baetidae	Acentrella insignificans	4	4	1	2.4	1	11.1	3	43.3					
		Acentrella macdunnoughi	4	4											
		Baetis bicaudatus	4	5			3	99.9			6	1140.0	1	7.2	
		Baetis spp	4	5					4	248.3			3	1.5	
		Baetis tricaudatus	4	5	6	171.4	8	723.0	1	19.4	5	554.6	1	5.1	
		Centropetium spp	4	2											

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No. sites					Chilko		Clearwater		Coldwater		Euchiniko		Fraser	
			F-Tot.	S-Tot.	Sites	Mean	Sites	Mean	Sites	Mean	Sites	Mean	Sites	Mean
Order	Family	Species			present		present		present		present		present	
		Diphetor hageni	4	5	2	5.2	4	503.1	1	1.7	3	925.0		
		Fallceon quilleri	4	5									2	20.9
		Unknown Baetidae*	4				2	23.9					1	0.6
	Ephemereillidae	Caudatella heterocaudata heterocaudata	1	1			1	11.3						
		Caudatella hystrix	1	1										
		Caudatella spp	1	1	2	9.5	2	7.8					1	0.8
		Drunella doddsi	1	0	4	10.5	7	57.1	1	8.3			7	3.0
		Drunella grandis ingens	1	0										
		Drunella spinifera	1	0	1	15.6	1	0.3	1	2.8	2	40.0		
		Ephemerella inermis	1	1	2	22.3							1	2.3
		Ephemerella infrequens	1	1	1	18.8					1	337.5	4	27.7
		Ephemerella mollita	1	1							2	1437.5		
		Ephemerella spp	1	1	1	18.5	8	199.3	3	544.4	2	41.7	4	4.7
		Serratella spp	1	2			2	74.2	2	1733.3				
		Serratella tibialis	1	2					1	525.0				
		Unknown Ephemerellidae*	1											
	Ephemeridae	Ephemera spp	4	4										
	Heptageniidae	Cinygma spp	4	2										
		Cinygmula spp	4	4	2	124.1	1	1.7	1	40.0	2	154.2		
		Epeorus deceptivus	4	0	5	39.7							1	0.2
		Epeorus grandis	4	0					1	8.3			1	0.5
		Epeorus longimanus	4	0	2	9.8							1	0.1
		Epeorus spp	4	0	1	2.1	1	8.3						
		Heptagenia spp	4	3	1	43.8	3	22.6			1	262.5		
		Leucrocota spp	4	1	3	25.3	6	190.5						
		Rhithrogena spp	4	0	7	220.8	8	92.8	6	201.1	1	4.2	9	35.4
		Stenonema spp	4	5										
		Unknown Heptageniidae*	4				4	236.0	5	389.4	6	667.9	4	12.4
	Leptohyphidae	Tricorythodes minutes	4	4										
	Leptophlebiidae	Paraleptophlebia spp	2	4	3	25.3	8	144.0	6	357.5	5	868.3		
Gastropoda	Lymnaeidae	Unknown Lymnaeidae*	8											
	Physidae	Physella spp	8	8										
	Planorbidae	Gyraulus circumstriatus	5	5										
		Menetus opercularis	5	5							1	50.0		
	Valvatidae	Valvata humeralis	5	5							1	12.5		
		Valvata sincera	5	5										
Hirudinea	Piscicolidae	Piscicola milneri		6										
Megaloptera	Sialidae	Sialis spp	4	4										
Nematoda	Nematoda family*	Unknown Nematoda*			3	28.3	4	44.7			1	4.2	1	0.2
Oligochaeta	Enchytraeidae	Unknown Enchytraeidae*			3	20.2	8	91.1	1	8.3	4	166.7	8	8.7
	Lumbriculidae	Eclipidrilus spp	7	7	1	0.5					1	12.5	4	3.5
		Kincaidiana hexatheca	7	7										
		Lumbriculus spp	7	7									1	0.1
		Lumbriculus variegatus	7	7										
		Rhynchelmis spp	7	7										
		Unknown Lumbriculidae*	7											
	Naididae	Chaetogaster diaphanus	8	8			1	0.8						
		Dero digitata	8	8	1	8.9								
		Nais alpina	8	8	2	122.9	1	3.3					1	0.1
		Nais behningi	8	8			1	1.4						
		Nais simplex	8	8										
		Nais variabilis	8	8			1	0.8						
		Pristina aequisetata	8	8					1	3.3			1	0.1
		Pristinella jenkiniae	8	8										
		Specaria fraseri	8	8	2	55.1	1	25.6	5	268.9			5	10.2
		Specaria hellei	8	8										
		Specaria josinae	8	8	1	18.8								
		Uncinails uncinata	8	8			1	0.9						
	Tubificidae	Immatures with hair chaetae		10			1	3.5					1	0.1
		Immatures without hair chaetae		10			1	0.5					1	7.0
		Limnodrilus profundicola		9									1	0.2
		Limnodrilus udekemianus		9										
Ostracoda	Ostracoda family*	Unknown Ostracoda*			3	5.5	2	390.2			8	1594.2	2	0.2

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No. sites					Chilko		Clearwater		Coldwater		Euchiniko		Fraser	
			F.Tol.	S.Tol.	8 Sites present	Mean	12 Sites present	Mean	6 Sites present	Mean	8 Sites present	Mean	12 Sites present	Mean
Order	Family	Species												
Platyhelminthes - Turbellaria	Platyhelminthes - Turbellaria family*	Unknown Platyhelminthes - Turbellaria*			3	9.2	2	1.8	2	10.0			1	0.2
Plecoptera	Capniidae	Capnia spp	1	3	7	229.2	6	64.5			8	1443.3	12	76.0
		Unknown Capniidae*	1											
	Chloroperlidae	Haploperla brevis	1	0	3	28.8	1	2.8	1	8.3			3	6.6
		Plumiperla diversa	1	0	2	9.9							2	0.9
		Suwallia spp	1	0			1	1.4						
		Sweltsa spp	1	1	3	34.0	8	50.6	2	16.7	4	250.0	4	1.5
		Unknown Chloroperlidae*	1											
	Leuctridae	Paraleuctra spp	0	3	3	11.5	5	52.0	3	13.6			1	0.8
		Unknown Leuctridae*	0											
	Nemouridae	Podmosta spp	2	2	1	11.8	2	120.3						
		Unknown Nemouridae*	2		3	15.6			1	5.6	3	293.8		
		Visoka cataractae	2	0	1	3.1	2	9.5						
		Zapada cinctipes	2	2	3	42.3	4	516.2	3	22.8	6	240.0		
		Zapada columbiana	2	2	5	76.9	4	13.2					2	2.3
		Zapada oregonensis	2	2										
		Zapada spp	2	2			7	187.6			3	75.0	5	1.4
	Peltoperlidae	Yoraperla mariana	0	1			1	14.5						
	Perlidae	Calineuria californica	1	2										
		Claasenia sabulosa	1	3										
		Hesperoperla pacifica	1	2			2	1.6			1	12.5	1	0.5
	Perlodidae	Cultus spp	2	2										
		Isogenoides spp	2	2									2	1.1
		Isoperla spp	2	2	4	53.0	1	6.7	1	12.5	5	135.0	5	15.8
		Megarcys spp	2	2	1	1.4	1	1.6						
		Perlinodes aureus	2	2										
		Rickera sorta	2	2										
		Setvena bradleyi	2	2			1	1.3						
		Setvena spp	2	2	1	0.1								
		Skwala spp	2	2	3	2.9					1	25.0	2	2.2
		Unknown Perlodidae*	2				6	11.7	2	4.4	1	12.5	2	0.9
	Pteronarcyidae	Pteronarcella regularis	0	0										
		Pteronarcys californica	0	0										
		Pteronarcys spp	0	0										
	Taeniopterygidae	Taenionema spp	2	2	5	32.9	5	149.6			1	7.5	7	20.8
Porifera	Spongiillidae	Unknown Spongiillidae*									1	25.0	2	0.4
Trichoptera	Apataniidae	Allomyia spp	4	3										
		Apatania spp	4	1			1	2.8						
		Apatania zonella	4	1									1	0.2
		Pedomoeus sierra	4	0										
	Brachycentridae	Amiocentrus aspilus	1	3							1	12.5		
		Brachycentrus americanus	1	1	3	11.7	4	20.1	5	62.5	2	175.0	3	1.6
		Brachycentrus occidentalis	1	1							2	125.0	1	0.3
		Micrasema bactro	1	1			2	88.0			2	35.0		
		Micrasema spp	1	1							2	54.2		
	Glossomatidae	Anagapetus spp	0	0										
		Glossosoma spp	0	1	3	4.9			3	8.6				
		Protophila spp	0	1										
	Hydropsychidae	Arctopsyche grandis	4	1	1	4.7	2	3.6	1	3.3	1	25.0	3	2.9
		Cheumatopsyche spp	4	5										
		Diplectrona spp	4	4										
		Hydropsyche alhedra	4	4										
		Hydropsyche ambilis	4	4										
		Hydropsyche morosa	4	4										
		Hydropsyche slossanae	4	4										
		Hydropsyche spp	4	4			3	15.9	5	299.4	3	204.2		
		Hydropsyche tana	4	4	1	7.1			1	30.0	1	12.5		
		Parapsyche almota	4	2										
		Parapsyche elsis	4	2	2	5.0	1	2.2					1	0.5
		Parapsyche spp	4	2									1	0.7
	Hydroptilidae	Hydroptila spp	4	6			2	32.5					1	1.5
		Leucotrichia pictipes	4	6							1	12.5		
		Oxyethira spp	4	3							1	12.5		

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No. sites					Chilko		Clearwater		Coldwater		Euchiniko		Fraser	
			F-Tol.	S-Tol.	8	Mean	12	Mean	6	Mean	8	Mean	12	Mean
Order	Family	Species			Sites present		Sites present		Sites present		Sites present		Sites present	
		Stactobiella spp	4	4			5	100.5						
		Unknown Hydroptilidae ⁺	4								1	12.5		
	Lepidostomatidae	Lepidostoma astaneum group	1	1							1	212.5		
		Lepidostoma cinereum	1	1							1	4.2		
		Lepidostoma pluviale group	1	1			2	7.9	2	762.5				
		Lepidostoma spp	1	1			3	7.8	4	878.9	4	300.0	1	0.1
		Lepidostoma unicolor	1	1							1	25.0		
	Leptoceridae	Ceraclea spp	4	3										
		Oecetis avara	4	8			1	11.3						
		Oecetis disjuncta	4	8										
	Limnephilidae	Chyranda centralis	4	1										
		Clostoea disjuncta	4	4										
		Ecclosocmoecus scylla	4	0										
		Ecclosomyia spp	4	2	1	1.8								
		Grammotaulius spp	4	4										
		Hesperophylax spp	4	3							1	6.3		
		Limnephilus spp	4	3										
		Psychoglypha spp	4	0	2	32.8	1	0.8			1	12.5	2	0.4
		Unknown Limnephilidae ⁺	4		1	0.1	1	5.6			1	50.0	3	0.3
	Philopotamidae	Wormaldia spp	3	3										
	Polycentropodidae	Polycentropus spp	6	6										
	Rhyacophilidae	Rhyacophila acropedes group	0	0	2	5.2	1	0.8			1	2.5	1	0.1
		Rhyacophila alberta group	0	0	2	2.3							1	0.1
		Rhyacophila angelita group	0	0	3	6.3	2	3.4					4	1.1
		Rhyacophila arnaudi	0	0										
		Rhyacophila betteni group	0	0										
		Rhyacophila blarina	0	0										
		Rhyacophila grandis	0	0			2	3.2						
		Rhyacophila narvae	0	0							1	12.5		
		Rhyacophila rotunda group	0	0										
		Rhyacophila spp	0	0			1	5.6	1	3.3			1	0.1
		Rhyacophila vagrita	0	0	1	1.8					1	15.0		
		Rhyacophila valuma	0	0										
		Rhyacophila velora	0	0					2	25.0				
		Rhyacophila verrula	0	0										
		Rhyacophila vocala	0	0	3	19.9	2	1.9						
	Uenoidae	Neothremma spp	4	0							1	2.5		
		Oligophlebodes spp	4	0	1	0.3								

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No. sites					Herrick 12 Sites present	Mean	Lillooet 12 Sites present	Mean	Nicola 10 Sites present	Mean	Pitt 16 Sites present	Mean	Stein 12 Sites present	Mean	Stuart 10 Sites present	Mean
Order	Family	Species	F-Tol.	S-Tol.												
Acariformes	Acariformes family*	Unknown Acariformes*							1	5.0	2	0.4	1	4.2		
	Anisitsiellidae	Unknown Anisitsiellinae*	4						1	5.0						
	Aturidae	Unknown Axonopsinae*	4		1	1.7										
	Hydryphantidae	Protzia spp	4	5	1	5.0					1	0.1	1	1.4		
		Wandesia spp	4	5												
	Lebertidae	Lebertia spp	4	2	3	3.2	1	0.2	3	40.0	2	2.5	1	10.4	2	0.9
	Limnesiidae	Limnesia spp	4	5	1	2.1			1	5.0					2	2.2
		Unknown Tyrellinae*	4													
	Sperchontidae	Sperchon spp	4	4	1	1.7	3	3.8	2	70.0	7	6.7	3	30.6	2	2.5
	Stygothrombidiidae	Stygothrombium spp		5	2	0.5					1	0.6				
	Torrencicolidae	Testudacarus spp	4	5					2	7.0			2	8.3	2	3.0
		Torrencicola spp	4	5			1	1.7	3	17.5	1	4.7			1	5.0
Amphipoda	Crangonyctidae	Crangonyx richmodensis-occidentalis	5	5												
	Gammaridae	Gammarus lacustris	4	6												
	Talitridae	Hyaella azteca	8	8												
Bivalvia	Margaritiferidae	Margaritifera falcata		5												
	Sphaeriidae	Pisidium casertanum	8	7												
		Pisidium nitidum	8	7					1	4.0						
		Pisidium spp	8	7												
		Sphaerium spp	8	7	1	8.3					1	0.1	1	4.2		
		Sphaerium striatum	8	7												
		Unknown Sphaeriidae*	8												1	2.5
Cladocera	Cladocera family*	Unknown Cladocera*														
	Daphniidae	Unknown Daphniidae*														
Coelentrata	Hydriidae	Hydra polyps	5	5												
Coleoptera	Elmidae	Cleptelmis ornata	4	4												
		Heterlimnius corpulentus	4	4					2	55.0						
		Heterlimnius spp	4	4					2	37.7	1	0.3			1	22.5
		Lara spp	4	4							2	2.6				
		Narpus concolor	4	4												
		Optioservus quadrimaculatus	4	4					5	297.5						
		Optioservus spp	4	4												
		Zaitzevia parvula	4	4					1	140.0						
		Zaitzevia spp	4	4					6	105.8	2	46.0				
Collembola	Hypogastruridae	Unknown Hypogastruridae*	5													
		Xenylla spp	5	5												
	Isotomidae	Semicerura spp	5	5												
Copepoda	Copepoda family*	Unknown Copepoda*							1	20.1			1	4.2		
Diptera	Athericidae	Atherix pachypus	2	4					2	20.0						
	Blephariceridae	Blephariceridae	0	0			1	0.2			1	1.3				
	Ceratopogonidae	Atrichopogon spp	6	6												
		Bezzia/Palpomyia spp	6	6	1	1.7			1	5.0					2	3.1
		Culicoides spp	6	6												
		Forcipomyia spp	6	6												
		Monohelea spp	6	6					1	5.0	1	0.3				
		Probezzia spp	6	6												
		Stilobezzia spp	6	6												
		Unknown Ceratopogonidae*	6								1	0.1				
	Chironomidae	Ablabesmyia spp	6	8												
		Brillia flavifrons	6	5							1	0.1				
		Brillia retifinis	6	5							1	0.1				
		Brillia spp	6	5	4	12.8	3	4.0	2	15.0	7	5.8	9	138.9	3	41.4
		Cardiocladius spp	6	5												
		Chaetocladius spp	6	6												
		Chaetocladius vittatus group	6	6												
		Chironomus spp	6	10												
		Cladotanytarsus spp	6	7					4	152.5	1	0.6	1	8.3	1	0.4
		Corynoneura spp	6	7					1	10.1			2	11.1		
		Cricotopus spp	6	7												
		Cricotopus(Cricotopus) bicintus group	6	7	4	19.6	1	3.3	2	20.0			3	83.3	1	45.0
		Cricotopus(Cricotopus) cylindraceus group	6	7												
		Cricotopus(Cricotopus) festivellus group	6	7					1	6.0						

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No. sites					Herrick		Lillooet		Nicola		Pitt		Stein		Stuart	
			F-Tol.	S-Tol.	12 Sites	Mean	12 Sites	Mean	10 Sites	Mean	16 Sites	Mean	12 Sites	Mean	10 Sites	Mean
Order	Family	Species			present		present		present		present		present		present	
		Cricotopus(Cricotopus) fuscus group	6	7												
		Cricotopus(Cricotopus) spp	6	7					1	25.0	1	1.1	1	4.2		
		Cricotopus(Cricotopus) tremulus group	6	7	1	0.4			1	30.2	1	0.7				
		Cricotopus(Cricotopus) trifasciatus group	6	7					3	17.5						
		Cricotopus(Isocladus) laricomalis group	6	7												
		Cricotopus(Isocladus) obnixus group	6	7												
		Cricotopus(Isocladus) spp	6	7	1	0.2	2	1.2	1	20.1			4	19.8		
		Cricotopus(Nostocoladus) spp	6	7												
		Cryptochironomus spp	6	8												
		Diamesa spp	6	5	2	29.3	6	25.3			6	4.3			4	23.0
		Diplociadus spp	6	6			1	0.2								
		Endochironomus spp	6	10									1	2.8	3	24.6
		Eukiefferiella brehmi group	6	8	5	55.4	2	2.3	5	116.3	4	13.8	7	51.8	5	19.1
		Eukiefferiella brevicar group	6	8							2	6.5				
		Eukiefferiella claripennis group	6	8			2	1.0								
		Eukiefferiella devonica group	6	8	2	3.7			1	2.5	2	0.8	1	20.8		
		Eukiefferiella gracei group	6	8	2	0.7	1	0.3			3	1.1			1	3.4
		Eukiefferiella rectangularis group	6	8												
		Eukiefferiella similis group	6	8			1	0.2					2	6.3		
		Eukiefferiella spp	6	8							1	2.7				
		Euryhopsis spp	6	5											1	1.4
		Heleniella spp	6	5											1	1.7
		Heterotanytarsus spp	6	5											1	3.3
		Heterotrissocladus changi	6	0	2	8.7	1	0.1	1	10.0			3	23.6	3	26.2
		Heterotrissocladus spp	6	0												
		Hydrobaenus spp	6	8			1	3.3								
		Krenomittia spp	6	5											1	1.7
		Larsia spp	6	6											2	0.9
		Lopesocladus(Cordiella) hyporheicus	6	6					1	10.0						
		Metriocnemus spp	6	6												
		Micropsectra spp	6	7	8	293.1			9	542.0	6	45.6	11	360.7	10	918.2
		Microtendipes spp	6	6					3	135.0	1	14.1				
		Monodiamesia spp	6	7												
		Nanocladus (Nanocladus) distinctus	6	3												
		Nanocladus (Plecopteracalathus) branchicolus	6	3												
		Nanocladus(Nanocladus) balticus	6	3												
		Nanocladus(Nanocladus) parvulus group	6	3												
		Nanocladus(Plecopteracalathus)	6	3					2	40.0			1	12.5		
		Nilotanytus frimbriatus	6	6												
		Odontomesa spp	6	4												
		Orthocladus spp	6	6												
		Orthocladus(Eudactylocladius) spp	6	6					4	340.2			1	4.2		
		Orthocladus(Euorthocladus) spp	6	6	1	8.3	1	3.3			1	0.1	3	117.0	3	25.0
		Orthocladus(Orthocladus) doreus	6	6	5	18.8	3	8.4	3	110.7			1	2.8		
		Orthocladus(Orthocladus) nigratus	6	6	1	4.2										
		Orthocladus(Orthocladus) obumbratus	6	6	3	5.9	4	3.3	4	286.3			5	96.7		
		Orthocladus(Orthocladus) spp	6	6							4	5.3			5	17.8
		Pagastia spp	6	1	2	11.7	2	11.8	3	30.1	1	0.1	4	16.0		
		Parachironomus arcuatus group	6	10												
		Parachironomus frequens group	6	10											1	2.7
		Paracladopelma camptolabis group	6	7												
		Paracladopelma spp	6	7												
		Paracladopelma winnelli	6	7												
		Paracricotopus spp	6	6												
		Parakiefferiella spp	6	4	1	16.7	1	0.8	1	40.3			3	13.9	4	17.1
		Paramerina spp	6	6								0.3				
		Parametriocnemus spp	6	5							1	4.7	2	4.9		
		Paraphaenocladus spp	6	4	5	26.4	4	1.7	2	15.1	1	0.1	5	22.9	3	12.6
		Parapsectra spp	6	5												
		Paratanytarsus spp	6	6												
		Paratendipes spp	6	8												
		Paratrachocladus spp	6	6	2	16.7			2	25.1	5	1.0	1	4.2	1	1.7
		Parorthocladus spp	6	6			1	0.1			3	1.3				
		Phaenopsectra spp	6	7			1	0.3								

No. sites					Herrick 12 Sites present		Lillooet 12 Sites present		Nicola 10 Sites present		Pitt 16 Sites present		Stein 12 Sites present		Stuart 10 Sites present	
Order	Family	Species	F-Tol.	S-Tol.	Mean	Mean	Mean	Mean	Mean	Mean	Mean	Mean	Mean	Mean	Mean	Mean
		Polypedium spp	6	6	2	4.3	1	0.1	5	1547.7	4	31.3	5	31.3	6	49.3
		Potthastia gaedi group	6	2												
		Potthastia longimana group	6	2												
		Procladius(Holotanypus) spp	6	9												
		Prodiamesia spp	6	3												
		Pseudodiamesa spp	6	6	1	0.2	1	0.3					1	25.0		
		Pseudorthocladius spp	6	0												
		Psilometriocnemus	6	5					1	5.0						
		Rheocricotopus(Rheocricotopus) eminellus	6	6	3	14.6			5	185.8	2	0.8	5	52.8	7	28.4
		Rheocricotopus(Rheocricotopus) paucisetatus	6	6												
		Rheosmittia spp	6	6	3	14.1	2	5.2								
		Rheotanytarsus spp	6	6	2	8.4			2	17.5	1	0.3	1	0.7	5	14.0
		Saetheria tylus	6	4											1	3.3
		Stempellina bausei group	6	2	1	83.3			3	40.1						
		Stempellina spp	6	2												
		Stempellinella spp	6	4	2	10.0			2	90.0	2	18.3	5	29.2	5	62.9
		Stictochironomus spp	6	9												
		Stilocladius spp	6	6	1	2.8							1	4.2	2	5.0
		Sublettea coffmani	6	4												
		Symposiocladius lignicola	6	5			1	0.1	1	5.0	1	4.7				
		Syndiamesa spp	6	6			1	0.1			2	0.8				
		Synorthocladius semivirens	6	2												
		Tanytarsus spp	6	6	3	75.7			3	105.0	2	17.3	1	4.2	8	295.8
		Thienemanniella spp	6	6	2	10.0	1	1.7			1	0.3	4	18.8	3	5.5
		Thienemannimyia group	6	6					1	5.0	1	0.1	1	2.8	5	31.8
		Tribelos spp	6	5												
		Tvetenia bavarica group	6	5	7	127.4	1	1.7	6	75.2	4	6.6	10	155.3	6	42.7
		Tvetenia discoloripes group	6	5					1	5.0	1	0.3				
		Unknown Chironominae*	6				2	0.3			1	0.6				
		Unknown Diamesinae*	6													
		Unknown Orthocladiinae*	6		1	0.4					4	1.6	1	4.2		
		Unknown Tanyptodinae*	6										1	2.1		
		Zavrelimyia spp	6	8	1	16.7					1	0.4	2	22.2		
	Deuterophlebiidae	Deuterophlebia coloradensis	0	0												
	Dixidae	Dixa spp	2	2												
	Empididae	Chelifera spp	6	6	4	13.3	2	0.6	5	34.1	3	3.4	3	20.1	5	9.3
		Clinocera spp	6	6	1	6.7	1	0.1	3	40.0	1	0.1	3	14.2		
		Oreogeton spp	6	6			2	7.5	1	2.5	1	0.1	2	4.9	2	6.8
	Muscidae	Unknown Muscidae*	6													
	Pellicorhynchidae	Glutops spp	3	3												
	Psychodidae	Maruina spp	10	2												
		Pericoma/Thelmatoscopus spp	10	4					3	57.5						
	Simuliidae	Prosimulium spp	6	3	1	4.2			1	15.0	2	1.0	3	10.8	2	7.1
		Simulium spp	6	6	2	60.4			1	5.0	2	1.7	1	0.7	2	11.4
	Stratiomyidae	Caloparyphus spp	8	8												
	Tabanidae	Unknown Tabanidae*	6													
	Tanyderidae	Protanyderus margarita	5	5												
	Thaumaleidae	Thaumalea spp	5	5												
	Tipulidae	Antocha monticola	3	3			1	3.3	5	59.0	1	0.1	1	0.4	1	0.4
		Dicranota spp	3	3	3	2.4	4	2.5	2	20.1	6	4.2	5	16.1	2	16.0
		Gonomyodes spp	3	5	1	0.2	1	0.8								
		Hexatoma spp	3	2	2	4.5			1	10.0	3	4.0	2	5.6	5	18.2
		Pseudolimmophila spp	3	5			1	0.9			3	1.3	3	14.6		
		Rhabdomastix spp	3	3	3	3.3										
		Tipula spp	3	4					1	10.0						
Ephemeroptera	Ameletidae	Ameletus spp	0	0	5	27.8	5	6.0	4	50.0	7	3.1	2	9.7	5	35.6
	Ametropodidae	Ametropus ammophilus	11	11												
	Baetidae	Acentrella insignificans	4	4	2	14.1			1	5.0						
		Acentrella macdunnoughi	4	4												
		Baetis bicaudatus	4	5	10	1500.5	6	75.6	5	289.5	8	52.5	3	200.0	2	20.1
		Baetis spp	4	5					1	10.0	6	47.3	5	316.0		
		Baetis tricaudatus	4	5			1	1.3	6	675.5	2	7.6	2	213.6	2	154.8
		Centroptilum spp	4	2												

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* - not identified to Family level.

No. sites					Herrick		Lillooet		Nicola		Pitt		Stein		Stuart	
			F-Tol.	S-Tol.	12 Sites	Mean	12 Sites	Mean	10 Sites	Mean	16 Sites	Mean	12 Sites	Mean	10 Sites	Mean
Order	Family	Species	present	present	present	present	present	present	present	present	present	present	present	present	present	present
		Dipheter hageni	4	5	1	56.3			4	34.5	1	2.7	2	22.9	7	216.6
		Fallceon quilleri	4	5	1	2.1										
		Unknown Baetidae*	4													
	Ephemerellidae	Caudatella heterocaudata heterocaudata	1	1					2	4.5	1	0.7			1	4.1
		Caudatella hystrix	1	1			1	0.3								
		Caudatella spp	1	1									1	0.9		
		Drunella doddsi	1	0	10	89.0	9	160.8	4	25.1	12	35.7	8	176.6	5	64.7
		Drunella grandis ingens	1	0					1	2.5					1	7.5
		Drunella spinifera	1	0			2	0.2	2	35.2	3	1.0	1	0.3		
		Ephemerella inermis	1	1							1	3.3				
		Ephemerella infrequens	1	1	3	27.0	2	1.0			1	1.1			1	2.4
		Ephemerella mollita	1	1												
		Ephemerella spp	1	1	7	886.9					4	35.5			7	36.2
		Serratella spp	1	2					5	70.1	3	6.3	6	166.8	1	27.5
		Serratella tibialis	1	2	2	4.0			4	181.5			5	67.4		
		Unknown Ephemerellidae*	1													
	Ephemeridae	Ephemerella spp	4	4												
	Heptageniidae	Cinygma spp	4	2			1	6.4							1	8.6
		Cinygmula spp	4	4							1	0.1				
		Epeorus deceptivus	4	0	1	2.8	1	2.9			5	19.1	2	22.2		
		Epeorus grandis	4	0			4	45.4	1	2.5	3	12.1	2	13.5	1	0.5
		Epeorus longimanus	4	0							1	0.1				
		Epeorus spp	4	0			2	27.6	4	105.0			3	177.1	4	28.6
		Heptagenia spp	4	3	2	8.8	3	9.8	3	200.0	3	24.0	6	369.0		
		Leucrocota spp	4	1			2	70.1	3	500.5			1	181.3	7	173.1
		Rhithrogena spp	4	0	10	765.9	10	81.5	2	75.0	16	158.3	9	236.8	6	163.6
		Stenonema spp	4	5												
		Unknown Heptageniidae*	4		5	1036.1			4	2166.1	3	64.4	4	806.9	1	63.7
	Leptohyphidae	Tricorythodes minutes	4	4												
	Leptophlebiidae	Paraleptophlebia spp	2	4					6	232.3	2	46.7	5	86.1	3	48.8
Gastropoda	Lymnaeidae	Unknown Lymnaeidae*	8													
	Physidae	Physella spp	8	8												
	Planorbidae	Gyraulus circumstriatus	5	5												
		Menetus opercularis	5	5												
	Valvatidae	Valvata humeralis	5	5												
		Valvata sincera	5	5							1	0.3				
Hirudinea	Piscicolidae	Piscicola milneri		6												
Megaloptera	Sialidae	Sialis spp	4	4												
Nematoda	Nematoda family*	Unknown Nematoda*							1	5.0	1	0.7	1	5.6		
Oligochaeta	Enchytraeidae	Unknown Enchytraeidae*			3	50.7	1	0.1	1	5.0	3	10.2	1	4.2		
	Lumbriculidae	Eclipidrilus spp	7	7							1	0.1				
		Kincaidiana hexatheca	7	7							2	2.6				
		Lumbriculus spp	7	7							1	0.2				
		Lumbriculus variegatus	7	7							1	7.0				
		Rhynchelmis spp	7	7												
		Unknown Lumbriculidae*	7						1	5.0						
	Naididae	Chaetogaster diaphanus	8	8												
		Dero digitata	8	8												
		Nais alpina	8	8							1	0.1				
		Nais behningi	8	8					1	10.0	1	0.5			1	6.7
		Nais simplex	8	8												
		Nais variabilis	8	8												
		Pristina aequisetata	8	8												
		Pristinella jenkiniae	8	8												
		Specaria fraseri	8	8					5	205.1	4	11.7	2	177.1	1	15.0
		Specaria hellei	8	8			1	0.1								
		Specaria josinae	8	8												
		Uncinails uncinata	8	8												
	Tubificidae	Immatures with hair chaetae		10	1	16.7					1	0.3	1	2.8		
		Immatures without hair chaetae		10	1	16.7										
		Limnodrilus profundicola		9												
		Limnodrilus udekemianus		9	1	8.3										
Ostracoda	Ostracoda family*	Unknown Ostracoda*			1	40.0			4	117.6	2	3.2	9	445.5	4	21.5

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No. sites					Herrick		Lillooet		Nicola		Pitt		Stein		Stuart	
			F-Tol.	S-Tol.	12 Sites present	Mean	12 Sites present	Mean	10 Sites present	Mean	16 Sites present	Mean	12 Sites present	Mean	10 Sites present	Mean
Order	Family	Species														
Platyhelminthes - Turbellaria	Platyhelminthes - Turbellaria family*	Unknown Platyhelminthes - Turbellaria*			5	104.3	4	38.5	1	40.3	6	32.9	7	59.8	5	26.5
Plecoptera	Capniidae	Capnia spp	1	3	9	308.8	6	3.7	8	572.0	5	3.9	10	169.8	10	289.8
		Unknown Capniidae*	1													
	Chloroperlidae	Haploperla brevis	1	0	8	73.1	6	47.7	1	30.0	1	0.4	4	19.4		
		Plumiperla diversa	1	0	1	16.7	5	26.7			4	84.6	2	25.6		
		Suwallia spp	1	0							8	15.9				
		Sweltsa spp	1	1	4	17.4			6	182.8	2	2.1	6	66.0	10	119.2
		Unknown Chloroperlidae*	1													
	Leuctridae	Paraleuctra spp	0	3	4	56.9			4	27.5	5	3.5	3	37.5	7	43.5
		Unknown Leuctridae*	0		1	11.7										
	Nemouridae	Podmosta spp	2	2					1	5.0						
		Unknown Nemouridae*	2													
		Visoka cataractae	2	0	2	8.8			1	20.1	1	0.1	3	15.4		
		Zapada cinctipes	2	2	2	100.0			7	304.0	4	12.5	4	36.8	5	20.9
		Zapada columbiana	2	2	5	16.0	4	2.7	3	351.0	4	1.3	6	145.7	2	11.2
		Zapada oregonensis	2	2	4	9.2	2	8.4	2	7.0	1	9.4	2	5.3		
		Zapada spp	2	2	6	426.6	2	5.6			5	4.2	8	121.2	2	28.4
	Peltoperlidae	Yoraperla mariana	0	1	1	71.7										
	Perlidae	Calineuria californica	1	2					3	55.1	3	28.5				
		Claasenia sabulosa	1	3												
		Hesperoperla pacifica	1	2					1	20.0			3	16.0		
	Perlodidae	Cultus spp	2	2												
		Isogenoides spp	2	2	2	0.6							1	4.2		
		Isoperla spp	2	2	9	69.2	6	21.3	9	124.1	4	9.4	7	31.6		
		Megarcys spp	2	2	2	11.1	7	22.9			6	5.7				
		Perlinodes aureus	2	2	3	3.0										
		Rickera sorpta	2	2												
		Setvena bradleyi	2	2												
		Setvena spp	2	2	2	4.5			2	15.0	1	0.4	3	5.6		
		Skwala spp	2	2					1	2.0	1	0.2				
		Unknown Perlodidae*	2		1	16.7					4	4.4			4	7.5
	Pteronarcyidae	Pteronarcella regularis	0	0												
		Pteronarcys californica	0	0					2	35.0						
		Pteronarcys spp	0	0							1	0.1				
	Taeniopterygidae	Taenionema spp	2	2	10	959.8	12	742.8	4	60.1	13	258.0	8	152.5	7	43.8
Porifera	Spongillidae	Unknown Spongillidae*														
Trichoptera	Apataniidae	Allomyia spp	4	3	1	0.2										
		Apatania spp	4	1											2	13.8
		Apatania zonella	4	1												
		Pedomoeus sierra	4	0									1	0.7		
	Brachycentridae	Amiocentrus aspilus	1	3					1	10.0					1	0.4
		Brachycentrus americanus	1	1	2	8.4			2	167.5					4	7.6
		Brachycentrus occidentalis	1	1												
		Micrasema bactro	1	1					4	31.1	2	5.0	2	3.1	2	10.5
		Micrasema spp	1	1												
	Glossosomatidae	Anagapetus spp	0	0					1	5.0						
		Glossosoma spp	0	1	4	12.8	1	0.5	2	12.6	1	28.1	4	32.6	1	2.7
		Proptilia spp	0	1												
	Hydropsychidae	Arctopsyche grandis	4	1	2	4.5							4	7.3	3	2.3
		Cheumatopsyche spp	4	5												
		Diplectrona spp	4	4							1	3.5				
		Hydropsyche alhedra	4	4					1	10.0					1	0.5
		Hydropsyche ambilis	4	4							1	14.1				
		Hydropsyche morosa	4	4					1	10.0						
		Hydropsyche slossanae	4	4					1	10.0						
		Hydropsyche spp	4	4					5	212.5	2	0.8	1	1.4	2	10.2
		Hydropsyche tana	4	4					2	29.5						
		Parapsyche aimota	4	2							1	0.3				
		Parapsyche elsis	4	2	2	10.6	2	0.4			1	2.1	1	0.4	1	0.5
		Parapsyche spp	4	2			1	0.8	1	10.1	1	1.1				
	Hydroptilidae	Hydroptila spp	4	6			1	0.3							5	89.0
		Leucotrichia pictipes	4	6												
		Oxyethira spp	4	3												

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No. sites					Herrick		Lillooet		Nicola		Pitt		Stein		Stuart	
			F-Tol.	S-Tol.	12 Sites present	Mean	12 Sites present	Mean	10 Sites present	Mean	16 Sites present	Mean	12 Sites present	Mean	10 Sites present	Mean
Order	Family	Species														
		Stactobiella spp	4	4											1	0.5
		Unknown Hydroptilidae ⁺	4													
	Lepidostomatidae	Lepidostoma astaneum group	1	1					2	12.5					1	10.4
		Lepidostoma cinereum	1	1					2	7.5					1	2.5
		Lepidostoma pluviale group	1	1							1	42.2			1	1.2
		Lepidostoma spp	1	1					4	282.5	2	1.0	3	31.3	5	108.9
		Lepidostoma unicolor	1	1												
	Leptoceridae	Ceraclea spp	4	3												
		Oecetis avara	4	8					1	5.0						
		Oecetis disjuncta	4	8												
	Limnephilidae	Chyranda centralis	4	1					1	5.0						
		Clostoea disjuncta	4	4	1	3.3							1	0.4		
		Ecclisocosmoecus scylla	4	0							2	0.4				
		Ecclisomyia spp	4	2			4	8.1	1	10.0	6	1.1			1	0.4
		Grammotaulius spp	4	4												
		Hesperophylax spp	4	3												
		Limnephilus spp	4	3												
		Psychoglypha spp	4	0					1	2.5					1	0.5
		Unknown Limnephilidae ⁺	4		1	8.3	3	1.2	2	15.0			7	24.4	1	0.4
	Philopotamidae	Wormaldia spp	3	3							2	21.4				
	Polycentropodidae	Polycentropus spp	6	6							1	0.3				
	Rhyacophilidae	Rhyacophila acropedes group	0	0	2	4.4	1	0.1	1	10.1			4	7.9		
		Rhyacophila alberta group	0	0	2	11.7	1	0.1					1	0.4		
		Rhyacophila angelita group	0	0	2	13.9					1	2.3	3	5.9	4	7.0
		Rhyacophila arnaldi	0	0											1	1.7
		Rhyacophila betteni group	0	0	3	11.2			2	40.2	3	3.0				
		Rhyacophila blarina	0	0							1	4.7				
		Rhyacophila grandis	0	0												
		Rhyacophila narvae	0	0					2	35.2			2	8.3	2	1.4
		Rhyacophila rotunda group	0	0			1	0.3								
		Rhyacophila spp	0	0	1	0.4	1	3.3	2	20.0	2	12.1	2	4.3		
		Rhyacophila vagrita	0	0	1	0.1							1	2.8	4	22.0
		Rhyacophila valuma	0	0											1	0.4
		Rhyacophila velora	0	0												
		Rhyacophila verrula	0	0												
		Rhyacophila vocala	0	0			3	4.2			3	1.0	1	0.9		
	Uenoidae	Neothremma spp	4	0									2	11.1	1	6.7
		Oligophlebodes spp	4	0			7	41.0			3	7.3	3	45.2	1	1.7

No. sites					Taseko 8		Thompson 1		Torpy 8		Tyaughton 8		Upper Fraser 12		West Road 18	
Order	Family	Species	F-Tol.	S-Tol.	Sites present	Mean	Sites present	Mean	Sites present	Mean	Sites present	Mean	Sites present	Mean	Sites present	Mean
Acariformes	Acariformes family*	Unknown Acariformes*			1	0.1			2	5.1						
	Anisitsiellidae	Unknown Anisitsiellinae*	4		1	0.1									2	8.3
	Aturidae	Unknown Axonopsinae*	4													
	Hydryphantidae	Protzia spp	4	5									1	0.1	1	0.7
		Wandesia spp	4	5	1	0.6									3	4.6
	Lebertidae	Lebertia spp	4	2	5	29.6			4	15.4	2	0.7	6	56.9	6	21.5
	Limnesiidae	Limnesia spp	4	5	3	16.9			1	1.4	1	0.1	2	8.4	3	18.5
		Unknown Tyrellinae*	4													
	Sperchontidae	Sperchon spp	4	4	5	6.3	1	21.7	3	6.2	4	5.1	6	10.2	5	19.9
	Stygothrombidiidae	Stygothrombium spp		5					1	1.3					2	7.4
	Torrenicolidae	Testudacarus spp	4	5							1	1.8			8	30.1
		Torrenicola spp	4	5					1	1.0					6	16.0
Amphipoda	Crangonyctidae	Crangonyx richmodensis-occidentalis	5	5											2	8.3
	Gammaridae	Gammarus lacustris	4	6												
	Talitridae	Hyalella azteca	8	8												
Bivalvia	Margaritiferidae	Margaritifera falcata		5												
	Sphaeriidae	Pisidium casertanum	8	7												
		Pisidium nitidum	8	7												
		Pisidium spp	8	7			1	4.3								
		Sphaerium spp	8	7	1	62.5									1	5.6
		Sphaerium striatum	8	7											5	217.6
		Unknown Sphaeriidae*	8												1	2.8
Cladocera	Cladocera family*	Unknown Cladocera*														
	Daphniidae	Unknown Daphniidae*														
Coelentrata	Hydridae	Hydra polyps	5	5												
Coleoptera	Elmidae	Cleptelmis ornata	4	4												
		Heterolimnius corpulentus	4	4	1	0.3			2	317.5					1	4.9
		Heterolimnius spp	4	4					2	15.8					5	146.8
		Lara spp	4	4												
		Narpus concolor	4	4												
		Optioservus quadrimaculatus	4	4											3	29.2
		Optioservus spp	4	4											10	310.6
		Zaitzevia parvula	4	4	1	0.6									5	46.3
		Zaitzevia spp	4	4											4	11.1
Collembola	Hypogastruridae	Unknown Hypogastruridae*	5		1	0.1					1	0.1				
		Xenylla spp	5	5												
	Isotomidae	Semicerura spp	5	5												
Copepoda	Copepoda family*	Unknown Copepoda*													2	18.1
Diptera	Athericidae	Atherix pachypus	2	4											2	3.2
	Blephariceridae	Blephariceridae grandis	0	0											1	0.7
	Ceratopogonidae	Atrichopogon spp	6	6												
		Bezzia/Palpomyia spp	6	6							1	6.3			2	2.5
		Culicoides spp	6	6												
		Forcipomyia spp	6	6												
		Monohelea spp	6	6												
		Probezzia spp	6	6					2	5.8					1	2.8
		Stilobezzia spp	6	6							2	0.3				
		Unknown Ceratopogonidae*	6													
	Chironomidae	Ablabesmyia spp	6	8												
		Brillia flavifrons	6	5												
		Brillia retifinis	6	5	3	8.8			5	11.9	5	45.8			6	25.9
		Brillia spp	6	5												
		Cardiocladius spp	6	5			1	139.1								
		Chaetocladius spp	6	6												
		Chaetocladius vittatus group	6	6												
		Chironomus spp	6	10												
		Cladotanytarsus spp	6	7												
		Corynoneura spp	6	7							1	50.0			10	689.1
		Cricotopus spp	6	7											5	20.8
		Cricotopus(Cricotopus) bicintus group	6	7									1	170.8	4	37.5
		Cricotopus(Cricotopus) cylindraceus group	6	7											2	16.7
		Cricotopus(Cricotopus) festivellus group	6	7												

+ - not identified to Genus/Species level.
 * - not identified to Family level.

No. sites					Taseko		Thompson		Torpy		Tyaughton		Upper Fraser		West Road	
			F-Tol.	S-Tol.	8 Sites present	Mean	1 Sites present	Mean	8 Sites present	Mean	8 Sites present	Mean	12 Sites present	Mean	18 Sites present	Mean
Order	Family	Species														
		Cricotopus(Cricotopus) fuscus group	6	7	1	0.7					1	3.6			4	54.9
		Cricotopus(Cricotopus) spp	6	7	2	25.6			3	8.3					1	11.1
		Cricotopus(Cricotopus) tremulus group	6	7			1	252.2								
		Cricotopus(Cricotopus) trifasciatus group	6	7			1	4.3								
		Cricotopus(Isocladus) laricomalis group	6	7											7	33.1
		Cricotopus(Isocladus) obnixus group	6	7											2	27.8
		Cricotopus(Isocladus) spp	6	7	1	0.7					1	6.3	2	10.3		
		Cricotopus(Nostocoladus) spp	6	7												
		Cryptochironomus spp	6	8											2	6.9
		Diamesa spp	6	5	3	17.1	1	4.3	1	0.7			3	0.9	1	1.1
		Diplociadus spp	6	6												
		Endochironomus spp	6	10			1	8.7							2	3.5
		Eukiefferiella brehmi group	6	8	5	35.6	1	4.3	4	41.0	7	47.3	6	6.6	10	164.8
		Eukiefferiella brevicar group	6	8												
		Eukiefferiella claripennis group	6	8												
		Eukiefferiella devonica group	6	8	1	2.1	1	8.7			1	2.1	2	0.7	3	47.0
		Eukiefferiella gracei group	6	8					2	7.9	1	0.7			2	9.7
		Eukiefferiella rectangularis group	6	8												
		Eukiefferiella similis group	6	8			1	21.7	1	1.0			2	1.4		
		Eukiefferiella spp	6	8												
		Euryhopsis spp	6	5											1	2.8
		Heleniella spp	6	5												
		Heterotanytarsus spp	6	5												
		Heterotrissocladus changi	6	0									4	94.3		
		Heterotrissocladus spp	6	0												
		Hydrobaenus spp	6	8							2	1.9				
		Krenosmittia spp	6	5												
		Larsia spp	6	6												
		Lopesocladus(Cordiella) hyporheicus	6	6	1	0.6									6	32.6
		Metriocnemus spp	6	6	1	4.2			1	2.1	5	14.9			1	8.3
		Micropsectra spp	6	7	7	748.3			6	83.5	4	379.1	4	302.2	13	356.8
		Microtendipes spp	6	6											8	77.5
		Monodiamesia spp	6	7												
		Nanocladus (Nanocladus) distinctus	6	3											1	5.6
		Nanocladus (Plecopteracalathus) branchicolus	6	3												
		Nanocladus(Nanocladus) balticus	6	3												
		Nanocladus(Nanocladus) parvulus group	6	3												
		Nanocladus(Plecopteracalathus)	6	3												
		Nilotanytus frimbriatus	6	6											2	3.2
		Odontomesa spp	6	4												
		Orthocladus spp	6	6												
		Orthocladus(Eudactylociadus) spp	6	6					1	1.0	3	13.6			6	95.4
		Orthocladus(Euorthocladus) spp	6	6	2	0.8									2	24.1
		Orthocladus(Orthocladus) doreus	6	6	1	1.8	1	21.7					1	0.1	5	46.3
		Orthocladus(Orthocladus) nigratus	6	6												
		Orthocladus(Orthocladus) obumbratus	6	6	1	0.8	1	4.3			1	3.6	4	54.8	8	65.7
		Orthocladus(Orthocladus) spp	6	6												
		Pagastia spp	6	1	3	26.8			1	28.1	4	9.3	3	22.9	3	9.7
		Parachironomus arcuatus group	6	10												
		Parachironomus frequens group	6	10											6	103.2
		Paracladopelma camptolabis group	6	7												
		Paracladopelma spp	6	7												
		Paracladopelma winnelli	6	7									1	5.6		
		Paracricotopus spp	6	6												
		Parakiefferiella spp	6	4			1	4.3			2	16.1			1	0.7
		Paramerina spp	6	6												
		Parametriocnemus spp	6	5												
		Paraphaenocladus spp	6	4	2	1.5			3	11.1	6	56.6	6	8.4	7	21.8
		Parapsectra spp	6	5											1	2.8
		Paratanytarsus spp	6	6												
		Paratendipes spp	6	8												
		Paratrachocladus spp	6	6	5	115.1	1	65.2	2	1.7	6	34.6	2	0.6	5	41.4
		Parorthocladus spp	6	6					1	59.4						
		Phaenopsectra spp	6	7												

No. sites					Taseko 8		Thompson 1		Torpy 8		Iyaughton 8		Upper Fraser 12		West Road 18	
			F-Tol.	S-Tol.	Sites present	Mean	Sites present	Mean	Sites present	Mean	Sites present	Mean	Sites present	Mean	Sites present	Mean
Order	Family	Species														
		Polypedium spp	6	6	2	15.5							1	2.8	16	785.9
		Potthastia gaedi group	6	2												
		Potthastia longimana group	6	2											1	8.3
		Procladius(Holotanypus) spp	6	9												
		Prodiamesia spp	6	3												
		Pseudodiamesa spp	6	6									3	36.2	2	3.5
		Pseudorthocladius spp	6	0	1	1.0										
		Psilometriocnemus	6	5												
		Rheocricotopus(Rheocricotopus) eminellobus	6	6	2	7.1			1	1.0	3	53.9	1	2.8	4	22.4
		Rheocricotopus(Rheocricotopus) pauriseta	6	6					1	0.7						
		Rheosmittia spp	6	6												
		Rheotanytarsus spp	6	6											7	48.1
		Saetheria tylus	6	4												
		Stempellina bausei group	6	2												
		Stempellina spp	6	2											4	26.4
		Stempellinella spp	6	4							1	0.3			4	24.3
		Stictochironomus spp	6	9												
		Stilocladus spp	6	6	2	2.3					1	31.3				
		Sublettea coffmani	6	4											3	14.6
		Symposiocladius lignicola	6	5	1	0.4										
		Syndiamesa spp	6	6	1	12.5										
		Synorthocladius semivirens	6	2	1	0.1	1	17.4							1	2.8
		Tanytarsus spp	6	6	2	87.9					2	14.6			11	202.1
		Thienemanniella spp	6	6					1	6.3			1	0.6	2	2.5
		Thienemannimyia group	6	6	5	14.8	1	13.0					1	0.3	1	1.9
		Tribelos spp	6	5											1	2.8
		Tvetenia bavarica group	6	5	5	65.7	1	13.0	5	23.0	7	248.6	4	8.9	3	15.7
		Tvetenia discoloripes group	6	5							1	1.8			2	2.5
		Unknown Chironominae ⁺	6				1	13.0								
		Unknown Diamesinae ⁺	6													
		Unknown Orthocladiinae ⁺	6		5	18.1	1	13.0	1	0.7	1	1.8			4	8.1
		Unknown Tanyptodinae ⁺	6													
		Zavrelimyia spp	6	8	2	62.6			1	0.8					9	43.8
	Deuterophlebiidae	Deuterophlebia coloradensis	0	0							1	0.1				
	Dixidae	Dixa spp	2	2							1	6.3				
	Empididae	Chelifera spp	6	6	1	0.6			1	3.1			4	6.1	5	22.0
		Clinocera spp	6	6					2	12.2	4	7.6			5	18.8
		Oreogeton spp	6	6	1	2.0			4	20.4	4	16.3	4	1.1	3	13.0
	Muscidae	Unknown Muscidae ⁺	6								2	2.2				
	Pellicorhynchidae	Glutops spp	3	3												
	Psychodidae	Maruina spp	10	2												
		Pericoma/Thelmatoscopus spp	10	4					1	4.2	1	14.3			2	97.9
	Simuliidae	Prosimulium spp	6	3	1	25.0			1	2.5	2	15.1	1	0.3	4	26.4
		Simulium spp	6	6							1	0.4			3	111.8
	Stratiomyidae	Caloparyphus spp	8	8					1	1.3						
	Tabanidae	Unknown Tabanidae ⁺	6								3	2.3				
	Tanyderidae	Protanyderus margarita	5	5												
	Thaumaleidae	Thaumalea spp	5	5							2	2.4				
	Tipulidae	Antocha monticola	3	3	4	14.5			1	0.8	1	0.1			5	61.1
		Dicranota spp	3	3	3	39.8			2	2.6	1	2.1			2	11.1
		Gonomyodes spp	3	5					1	2.1			1	0.2		
		Hexatoma spp	3	2	1	0.1			2	7.1	2	2.4	1	0.1	6	21.3
		Pseudolimnophila spp	3	5	1	0.5					1	0.4				
		Rhabdomastix spp	3	3									1	0.2		
		Tipula spp	3	4												
Ephemeroptera	Ameletidae	Ameletus spp	0	0	4	11.8			6	86.6	5	67.0	10	20.3	1	5.6
	Ametropodidae	Ametropus ammophilus	11	11												
	Baetidae	Acentrella insignificans	4	4					1	1.9					2	11.1
		Acentrella macdunnoughi	4	4											1	9.3
		Baetis bicaudatus	4	5	2	10.4			7	1980.6	7	112.3	8	289.2	9	1162.2
		Baetis spp	4	5									1	0.8		
		Baetis tricaudatus	4	5	5	234.4					1	0.6			10	1062.5
		Centroptilium spp	4	2												

+ - not identified to Genus/Species level.

* - not identified to Family level.

No. sites					Taseko		Thompson		Torpy		Tyaughton		Upper Fraser		West Road	
			F-Tol.	S-Tol.	8	Mean	1	Mean	8	Mean	8	Mean	12	Mean	18	Mean
Order	Family	Species			present		present		present		present		present		present	
		Dipheter hageni	4	5	1	75.0	1	52.2			1	2.1	2	22.6	8	128.5
		Fallceon quilleri	4	5											1	0.7
		Unknown Baetidae*	4													
	Ephemerellidae	Caudatella heterocaudata heterocaudata	1	1							3	9.4			1	0.7
		Caudatella hystrix	1	1												
		Caudatella spp	1	1												
		Drunella doddsi	1	0	6	15.6			6	108.9	7	36.9	4	6.1	2	13.2
		Drunella grandis ingens	1	0	2	25.3									1	1.9
		Drunella spinifera	1	0	1	0.1			1	6.3	2	5.5			1	2.8
		Ephemerella inermis	1	1							1	1.5				
		Ephemerella infrequens	1	1	3	53.8									6	416.7
		Ephemerella mollita	1	1											3	195.4
		Ephemerella spp	1	1	2	54.3	1	52.2	2	115.0	7	353.4	1	0.1	7	165.6
		Serratella spp	1	2									7	85.2		
		Serratella tibialis	1	2												
		Unknown Ephemerellidae*	1												1	8.3
	Ephemeridae	Ephemerella spp	4	4					4	606.9						
	Heptageniidae	Cinygma spp	4	2									1	3.2		
		Cinygmula spp	4	4	6	772.1			4	406.3	3	34.2			1	166.7
		Epeorus deceptivus	4	0	1	3.3					3	11.7	1	0.1		
		Epeorus grandis	4	0							1	5.4	3	4.8		
		Epeorus longimanus	4	0					2	10.8	2	11.3				
		Epeorus spp	4	0												
		Heptagenia spp	4	3	1	25.0			1	3.3			7	600.2	4	162.5
		Leucrocota spp	4	1												
		Rhithrogena spp	4	0	7	86.5	1	30.4	7	711.3	7	116.0	6	46.9	10	283.1
		Stenonema spp	4	5	4	75.3			1	3.1					9	151.6
		Unknown Heptageniidae*	4		4	593.9			6	212.1	4	99.7	3	18.4	10	382.2
	Leptohyphidae	Tricorythodes minutes	4	4												
	Leptophlebiidae	Paraleptophlebia spp	2	4	1	75.0			2	7.1	1	125.0			12	247.0
Gastropoda	Lymnaeidae	Unknown Lymnaeidae*	8												1	5.6
	Physidae	Physella spp	8	8											1	1.4
	Planorbidae	Gyraulus circumstriatus	5	5	1	0.7										
		Menetus opercularis	5	5												
	Valvatidae	Valvata humeralis	5	5												
		Valvata sincera	5	5												
Hirudinea	Piscicolidae	Piscicola milneri		6												
Megaloptera	Sialidae	Sialis spp	4	4												
Nematoda	Nematoda family*	Unknown Nematoda*			1	1.0			3	31.7	1	0.3			4	37.5
Oligochaeta	Enchytraeidae	Unknown Enchytraeidae*			2	1.1			5	22.4	2	5.4	2	1.4	3	22.2
	Lumbriculidae	Eclipidrilus spp	7	7											1	2.1
		Kincaidiana hexatheca	7	7												
		Lumbriculus spp	7	7												
		Lumbriculus variegatus	7	7												
		Rhynchelmis spp	7	7												
		Unknown Lumbriculidae*	7													
	Naididae	Chaetogaster diaphanus	8	8												
		Dero digitata	8	8												
		Nais alpina	8	8	4	5.6	1	8.7							6	22.2
		Nais behningi	8	8												
		Nais simplex	8	8											1	2.8
		Nais variabilis	8	8											2	4.6
		Pristina aequisetata	8	8	1	1.0										
		Pristinella jenkiniae	8	8												
		Specaria fraseri	8	8	4	98.7							1	0.2	4	30.3
		Specaria hellei	8	8												
		Specaria josinae	8	8												
		Uncinails uncinata	8	8											1	0.7
	Tubificidae	Immatures with hair chaetae		10	1	12.5			1	6.3					4	19.4
		Immatures without hair chaetae		10											2	9.7
		Limnodrilus profundicola		9												
		Limnodrilus udekemianus		9												
Ostracoda	Ostracoda family*	Unknown Ostracoda*			2	12.8			6	100.2	7	461.9			12	72.1

+ - not identified to Genus/Species level.

* - not identified to Family level.

No. sites					Taseko		Thompson	Torpy		Tyaughton		Upper Fraser		West Road		
			F-Tol.	S-Tol.	8 Sites	Mean	1 Sites	Mean	8 Sites	Mean	8 Sites	Mean	12 Sites	Mean	18 Sites	Mean
Order	Family	Species			present		present		present		present		present		present	
Platyhelminthes - Turbellaria	Platyhelminthes - Turbellaria family*	Unknown Platyhelminthes - Turbellaria*							1	6.3	6	81.9	4	26.5	1	2.8
Plecoptera	Capniidae	Capnia spp	1	3	7	448.4			3	14.7	8	63.0	6	73.5	13	359.5
		Unknown Capniidae*	1						1	1.4					1	20.4
	Chloroperlidae	Haploperla brevis	1	0	5	19.8			5	45.6	4	16.4	1	0.1	1	6.7
		Plumiperla diversa	1	0					2	36.8	1	8.3	5	25.1		
		Suwallia spp	1	0	1	4.2			2	13.2					1	6.7
		Sweltsa spp	1	1	4	14.4			6	47.5	1	31.3			15	128.2
		Unknown Chloroperlidae*	1													
	Leuctridae	Paraleuctra spp	0	3	3	2.8			4	50.9	5	36.2	5	4.2	5	11.3
		Unknown Leuctridae*	0													
	Nemouridae	Podmosta spp	2	2												
		Unknown Nemouridae*	2		2	66.7			3	4.7	5	66.1			6	107.8
		Visoka cataractae	2	0					1	2.1	2	11.6	2	2.7	1	2.8
		Zapada cinctipes	2	2	2	2.2			3	9.7	2	3.8	1	0.2	8	138.8
		Zapada columbiana	2	2	2	42.9			5	62.2	8	157.3	5	31.9	2	22.5
		Zapada oregonensis	2	2								4	25.6			
		Zapada spp	2	2	3	13.5					2	27.7	6	64.1	2	29.2
	Peltoperlidae	Yoraperla mariana	0	1					1	3.5			2	0.2		
	Perlidae	Calineuria californica	1	2												
		Claasenia sabulosa	1	3												
		Hesperoperla pacifica	1	2	1	0.7							1	0.2	1	11.1
	Perlodidae	Cultus spp	2	2												
		Isogenoides spp	2	2												
		Isoperla spp	2	2	2	1.0	1	13.0	1	4.2	3	11.5	5	10.9	5	23.8
		Megarcys spp	2	2	3	3.1			1	2.1	4	4.6				
		Perlinoes aureus	2	2												
		Rickera sorpta	2	2												
		Setvena bradleyi	2	2												
		Setvena spp	2	2									5	23.8		
		Skwala spp	2	2	1	0.1					2	26.3	1	0.1	5	22.9
		Unknown Perlodidae*	2		5	105.6			5	12.4	3	20.0			4	20.1
	Pteronarcyidae	Pteronarcella regularis	0	0	1	0.6			1	0.8					1	2.8
		Pteronarcys californica	0	0											2	13.9
		Pteronarcys spp	0	0									1	0.1	1	0.7
	Taeniopterygidae	Taenionema spp	2	2	6	36.0			5	223.0	7	148.9	5	27.1	6	91.2
Porifera	Spongillidae	Unknown Spongillidae*			2	1.1									1	2.8
Trichoptera	Apataniidae	Allomyia spp	4	3												
		Apatania spp	4	1							1	1.8				
		Apatania zonella	4	1							1	31.3				
		Pedomoecus sierra	4	0	1	1.0					2	0.5			1	3.7
	Brachycentridae	Amiocentrus aspilus	1	3											6	29.9
		Brachycentrus americanus	1	1	2	0.7			3	14.8			1	0.1	4	44.4
		Brachycentrus occidentalis	1	1			1	8.7								
		Micrasema bactro	1	1											5	50.0
		Micrasema spp	1	1											2	3.2
	Glossosomatidae	Anagapetus spp	0	0							1	6.3				
		Glossosoma spp	0	1	4	65.4			3	8.2	2	20.5	2	23.3	5	26.4
		Protoptila spp	0	1											4	11.8
	Hydropsychidae	Arctopsyche grandis	4	1	1	0.6			1	1.3			3	0.4		
		Cheumatopsyche spp	4	5											1	9.3
		Diplectrona spp	4	4												
		Hydropsyche alhedra	4	4												
		Hydropsyche ambilis	4	4												
		Hydropsyche morosa	4	4												
		Hydropsyche slossanae	4	4												
		Hydropsyche spp	4	4	3	3.4	1	17.4					1	0.4	8	199.5
		Hydropsyche tana	4	4			1	21.7							3	84.3
		Parapsyche almota	4	2												
		Parapsyche elsis	4	2	2	6.5			1	2.1	4	18.8	2	1.4		
		Parapsyche spp	4	2							3	8.0	1	5.6		
	Hydroptilidae	Hydroptila spp	4	6	2	13.8	1	4.3							6	19.9
		Leucotrichia pictipes	4	6											1	2.8
		Oxyethira spp	4	3												

+ - not identified to Genus/Species level.

* - not identified to Family level.

No. sites					Taseko		Thompson		Torpy		Tyaughton		Upper Fraser		West Road	
					8		1		8		8		12		18	
			F-Tol.	S-Tol.	Sites present	Mean	Sites present	Mean	Sites present	Mean	Sites present	Mean	Sites present	Mean	Sites present	Mean
Order	Family	Species														
		Stactobiella spp	4	4												
		Unknown Hydroptilidae ⁺	4													
	Lepidostomatidae	Lepidostoma astaneum group	1	1			1	4.3							6	45.6
		Lepidostoma cinereum	1	1												
		Lepidostoma pluviale group	1	1												
		Lepidostoma spp	1	1					1	1.0			1	0.7	6	118.1
		Lepidostoma unicolor	1	1												
	Leptoceridae	Ceraclea spp	4	3												
		Oecetis avara	4	8											5	15.3
		Oecetis disjuncta	4	8												
	Limnephilidae	Chyranda centralis	4	1							1	6.3			1	1.9
		Clostoea disjuncta	4	4												
		Ecclisocosmoecus scylla	4	0												
		Ecclisomyia spp	4	2	1	0.1					2	0.8	3	23.6		
		Grammotaulius spp	4	4												
		Hesperophylax spp	4	3											1	5.6
		Limnephilus spp	4	3												
		Psychoglypha spp	4	0											1	0.7
		Unknown Limnephilidae ⁺	4								1	5.4	1	0.1		
	Philopotamidae	Wormaldia spp	3	3												
	Polycentropodidae	Polycentropus spp	6	6												
	Rhyacophilidae	Rhyacophila acropedes group	0	0	1	0.1			2	7.5	2	7.3	2	0.3	5	37.3
		Rhyacophila alberta group	0	0	2	10.1			1	0.7	2	24.8	1	2.8		
		Rhyacophila angelita group	0	0					1	3.1	3	2.7	2	0.5		
		Rhyacophila arnaldi	0	0												
		Rhyacophila betteni group	0	0					2	3.8	3	16.7	3	16.9	2	5.1
		Rhyacophila blarina	0	0							1	6.6				
		Rhyacophila grandis	0	0												
		Rhyacophila narvae	0	0	1	0.6			2	5.1					4	11.6
		Rhyacophila rotunda group	0	0												
		Rhyacophila spp	0	0					3	19.7	3	2.3	1	0.1	1	5.6
		Rhyacophila vagrita	0	0					1	2.1						
		Rhyacophila valuma	0	0												
		Rhyacophila velora	0	0									3	10.3		
		Rhyacophila verrula	0	0					2	8.3						
		Rhyacophila vocala	0	0	4	4.3			1	4.2	5	30.2	2	0.8	1	2.8
	Uenoidae	Neothremma spp	4	0							3	17.2	2	9.8		
		Oligophlebodes spp	4	0	1	16.7			1	0.7	5	59.2	1	12.8	1	2.8