

**A Review of the Issues Related to Taxonomic Resolution in Biological Monitoring of
Aquatic Ecosystems with an Emphasis on Macroinvertebrates**

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Introduction

Arguably the most debated issue related to bioassessment methods is the establishment of appropriate taxonomic resolution levels. There are numerous reasons why the taxonomic resolution debate remains unresolved, but all of the potential issues can be summed up into three categories: information loss or redundancy, level of discrimination necessary in the decision process, and monitoring costs. Theoretically the use of lower taxonomic units such as species or genera provides us access to most appropriate and accurate autecological information that can be used in assessing ecological condition. On the other hand, it maybe true that larger hierarchal taxonomic groupings (e.g. families, orders) may possess quit similar ecological traits and provide redundant ecological functions. Thus these higher taxonomic units contain redundant and similar information which suggest that new information would not be made avail by a further taxonomic break down. All biological metrics commonly used in aquatic bioassessments are based on counts of the kinds and numbers of organisms found in a sample or derived from ecological and toxological information inferred from each taxon that makes up the sample. Determining statistical and observational differences between samples, sites and treatments is dependant upon many things but invariably the more similar any two populations are to each other the more (e.g. more samples) or finer resolution (e.g. more group or class distinctions) data is need to identify and quantify potential differences. Often the level of discrimination necessary to meet study or program objectives is ill defined and thus the necessary level of information about the biota (e.g. taxonomic resolution or sufficiency) remains undefined. Concurrent with defining study needs and objectives is estimation of resources needs and limitation to

meet program and study objectives (e.g. cost/benefit considerations). Of all the aspects of bioassessment, the identification of organisms generally requires the most resources and specialized knowledge. It is the desire of most bioassessment researches to obtain the information required to make accurate assessments of ecological health while expending as little resources as possible, thus the first area scrutinized to save resources is often the identification of organisms.

The simplest way to make identification of aquatic macroinvertebrates less resource demanding would be the use of coarser taxonomic resolutions (e.g. family instead of genus or genus instead of species). In the literature there are numerous recommendations, contradictions, and caveats regarding the use of different taxonomic resolutions. Many authors call for species-level identifications to ensure accurate assessments of ecosystem health (see Resh & Unzicker 1975, Resh 1979, Lenat & Penrose 1980, Simpson & Bode 1980, Rosenberg *et al.* 1986, Moog & Chovanec 2000, Lenat & Resh 2001, Schmidt-Kloiber & Nijboer 2004). Some authors (especially those working in marine and estuarine habitats) argue that the family, order, class, or even phylum level can be used to accurately assess the ecological health of a system (e.g. Heip *et al.* 1988, Herman & Heip 1988, Warwick 1988a, Warwick 1988b, Warwick 1988c, Ferraro & Cole 1990, Gray *et al.* 1990, Warwick *et al.* 1990, Ferraro & Cole 1992, Ferraro & Cole 1995, Somerfield & Clark 1995, Vanderklift *et al.* 1996, Olsgard *et al.* 1997, Olsgard *et al.* 1998, Olsgard & Somerfield 2000, Dalby *et al.* 2003, Defeo & Lercari 2004). Still others recommend a mix of taxonomic levels (see De Pauw & Vanhooren 1983, Bailey *et al.* 2001, Waite *et al.* 2004) or taxonomic sufficiency (see Ellis 1985, Kingston & Riddle 1989, Ammann *et al.* 1997)

This paper discusses the difficulties associated with aquatic macroinvertebrate identification as they relate to the problems of information loss, information redundancy, analytic discrimination and resource expenditure through a review of the literature from the past thirty years and an analysis of current data on aquatic macroinvertebrates. The paper discusses the potential effects redundancy and information loss have on the types of analysis typically done in bioassessment studies. Finally, a set of recommendations is given that may assist workers to better determine what level of taxonomic resolution is most appropriate based on the desired outcome of a study or objectives of a monitoring program that uses macroinvertebrates as an indicator group. Many of the principal concerns and issues surround the debate as to what level of taxonomic resolution is necessary or desirable in addressing bioassessment needs using macroinvertebrates are the same as those for fish and algae. However, because the number of freshwater fish species is relative small and the adult and juvenile taxonomic keys well developed, most aquatic scientists are able to work at the species level. Nearly all bioassessment programs and researchers who use algae as an indicator group in disturbance studies with aquatic ecosystems rely on data from generic-level taxonomy (e.g. Barber *et al.* 1999, Charles *et al.* 2002). The taxonomy of most algae groups is well study and keys are generally available for identification to the genus and sometimes species level. However, sample preservation is critical in preserving intact and undamaged specimen material that is necessary for identification at lower taxonomic levels.

Difficulties with Identifying Aquatic Organisms

Ideally all bioassessment programs would take all specimens to the species level to obtain the most complete analysis of ecosystem health, but this is not a practical goal for most programs and laboratories. Species-level identifications are often avoided for biological reasons, such as ontogenetic changes between instars and/or life stages, the small size of aquatic invertebrates, limitations of the taxonomic literature, availability of expertise, need for intensive preparation or rearing, and the allocation of limited time and resources (Resh & McElravy 1993, Ammann *et al.* 1997, Cummins 1994, Feminella 2000, Chessman & Royal 2004).

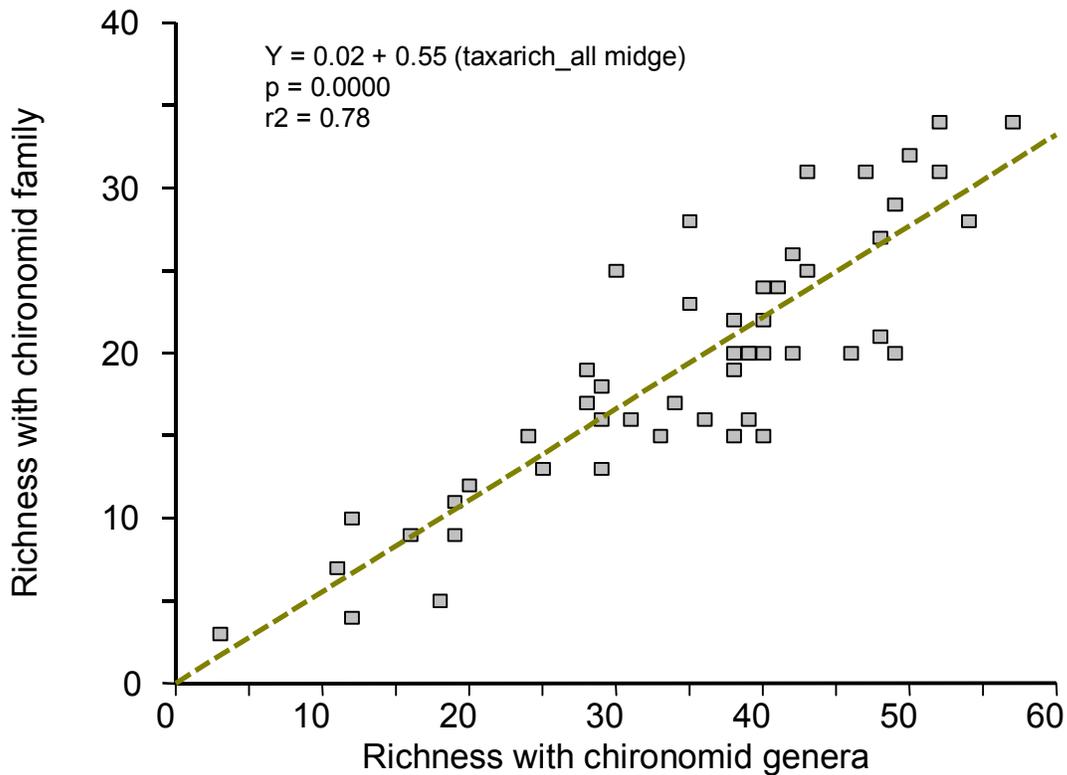
Finer taxonomic resolutions can decrease the accuracy of identifications because some level of expertise is required (Stribling *et al.* 2004). The difficulty of finer-resolution identification imparts a degree of error as the more difficult the identification, the more likely it will be incorrect and differ among laboratories and taxonomists. Undescribed or difficult species are often placed in morphospecies units such as Cranston's *recognizable taxonomic units* (Cranston 1990) and Resh's *operational taxonomic units* (Resh 1979). However, since morphospecies units are user defined and can vary in what they actually represent their use greatly reduces precision among taxonomists and impairs comparisons between samples, studies, and laboratories. There are also questions regarding the degree of improvement morphospecies provide since no environmental requirements can be associated with these units except for their higher-level taxa, in which case, there is little reason to identify morphospecies.

To circumvent identification problems with fine resolution, it has been suggested by some that certain prominent taxonomic groups would be sufficient to evaluate

biodiversity or anthropogenic impact assessments and thereby reduce both the number/kinds of taxa identified and associated time and resource costs ((e.g. Juutinen and Mönkkönen 2005, Lawler, *et al.* 2001). Addressing biodiversity and species conservation issues, through the assessment of surrogate or restricted taxonomic groups seems to be of limited value. (see Jaarsveld *et al.* 1998). In the biological assessment of aquatic ecosystems, it is often argued that Chironomidae would be an ideal indicator group because they are ubiquitous and often a substantial component of a system's aquatic fauna (Cranston 1995, Armitage 1995, King & Richardson 2002). Chironomidae exhibit a wide range of intra-generic and inter-species variability in habitat preference and tolerance measures (Clements *et al.* 1988). However, it was determined that the exclusion of Chironomidae from RIVPACS models had no effect on the ability of the model to distinguish between impacted and reference sites (Hawkins & Norris 2000). The authors also determined that using Chironomidae at the species level alone in RIVPACS models was not as effective at assessing differences between aquatic systems as using the entire faunal assemblage. Based on the results of this single study it would appear that Chironomidae would have some limitation as a "stand alone" indicator group. However, many authors suggest that groups such as the Ephemeroptera, Plecoptera and Trichoptera (EPT) (Lenat & Resh 2001, Bauernfeind & Moog 2000), Oligochaeta (Brinkhurst *et al.* 1969, Howmiller & Scott 1977), Polychaeta (Pocklington & Wells 1992), and Chironomidae (King & Richardson 2002, Carew *et al.* 2003, Wymer & Cook 2003) could be good indicator species when other factors related to the specific aquatic system are considered. Donley (1999) found that metrics based only on Chironomidae community measures performed equally well in discerning reference from non-reference

streams located in the Western Corn Belt Plains ecoregion when compared to metrics based on whole macroinvertebrate community measures. In a suite of wadeable streams in Iowa for which we had standardized taxonomic resolution, we found that number of chironomid genera in a sample was highly correlated to whole sample richness (Figure 1)

Figure 1. Linear regression between macroinvertebrate sample richness using only Chironomidae level information and sample richness with midge larvae taken to genus.



The most common identification level in aquatic bioassessment is a heterogeneous classification due to difficulties in achieving a uniform species-, genus-, or even family-level identifications for aquatic macroinvertebrates (Cranston 1990). This is often done with no account for how the identification levels were selected (i.e. on a purely pragmatic basis) (Ellis 1985). This creates a mosaic of identifications at ranks from species to class. Heterogeneous identifications are common because they permit inclusion of the entire community while extracting the maximum amount of information

given limited taxonomic resources. However, heterogeneous identifications make comparisons among studies difficult because each agency produces varying suites of heterogeneous identifications depending on the study purpose and the experience of workers and not on any ecological principle. Comparison problems can be corrected by implementing a standard taxonomic level or suite of identifications that are feasible for most laboratories. However, the logistics of setting a standard mixed resolution for all agencies, even those within the same region, is extremely difficult.

All pragmatic issues in the taxonomic resolution debate are obviously in favor of higher-level identifications, because the more coarse the resolution, the easier and cheaper the identification. Ferraro and Cole (1995) estimated that the savings of phylum-, class-, order-, and genus-level identification compared to species level were 95, 80, 55, and 23%, respectively. Clearly there is a considerable opportunity to reduce the resources needed for identification by utilizing coarser taxonomic resolutions, but what, if any, are the losses in discriminating the level of health or impact of a system? Is there significant redundancy between different taxonomic resolution levels or does the use of a coarser taxonomic level result in a meaningful loss of ecological information?

Loss of information

Species-level identifications are generally considered to be important in studies utilizing indicator organisms, invertebrate bioassays, productivity studies, and conservation studies (Resh 1979, Simpson & Bode 1980, Bailey et al. 2001, Lenat & Resh 2001, Waite *et al.* 2004). (See Williams & Gaston (1994), Gaston *et al.* (1995), Balmford *et al.* (1996b), Balmford *et al.* (1996a), Williams *et al.* (1997) for a different opinion on taxonomic resolution in conservation studies.) Over the past 25 years various

researchers have made the case that species-level identifications may be the only reliable method for obtaining accurate biological assessments of the ecological health of aquatic ecosystems, especially lotic systems (e.g. Resh & Unzicker 1975, Resh 1979, Lenat & Penrose 1980, Simpson & Bode 1980, Rosenberg *et al.* 1986, Moog & Chovanec 2000, Lenat & Resh 2001, Schmidt-Kloiber & Nijboer 2004). The most common and maybe the best argument for species-level resolution is that species occurrence relates the most exact information regarding ecological condition. Environmental requirements, life history traits, and sensitivity to anthropogenic contaminants are often unique to individual species, but may vary considerably within genera (Resh & Unzicker 1975, Wiggins & MacKay 1978, Cranston 1990, Resh & McElravy 1993, Barbour *et al.* 1999, Lenat & Resh 2001). The differences among species within a taxon may be the result of ecological specialization of sister taxa, resulting in a loss of information with coarser identifications (Cranston 1990).

From the literature, Lenat and Resh (2001) used Lewis' (1974) revision of the mayfly genus *Stenonema*, to illustrate a wide range of infrageneric differences in decomposable organic waste tolerances within a single genus. In this revision, 14 species and subspecies were listed as intolerant, 8 moderately tolerant, and 10 as tolerant. There even existed differences in tolerances between some of the subspecies. It is worthwhile to note that this revision only dealt with one form of pollution, so the examination of other pollutants would likely create a mosaic of tolerances for this one genus and further complicate analyses. Assuming accurate and precise identifications can be made, species-level information would provide more accurate results and improve the ability of metrics to detect differences between sites and subtle changes in environmental quality

(Simpson & Bode 1980, Wright *et al.* 1995, Moog & Chovanec 2000, Schmidt-Kloiber & Nijboer 2004).

The variability in tolerance value within selected families and genera can be seen in Table 1 and Table 2, respectively. These taxa were selected because they were the only taxa in our large data set (see www.cpcb.ku.edu/ for details on the regional macroinvertebrate database used in this study) that had five lower taxa (e.g. 5 genera within a family or 5 species within a genus) that had a recorded tolerance value. The mean tolerance value was calculated from a set of five regional tolerance values. The small number of taxa presented in these tables illustrates the general lack of knowledge regarding generic- and species-level autoecology. In general, there is a fairly high degree of variation in tolerance values within the listed mayfly (Ephemeroptera) families, Perlidae, most Trichoptera families, Chironomidae, Tipulidae and the dragonfly (Odonata) families (Table 1). Most of the stonefly (Plecoptera) families are comprised of genera that all appear to be very sensitive. This same pattern is reflected in the tolerance values displayed in genera within families (Table 2) which maybe the result of so few species having listed values.

Table 1. Variation within selected aquatic insect families and the snail family Hydrobiidae (minimum 5 genera with tolerance values)

	n	mean	median	minimum	maximum	std. dev.
Ephemeroptera						
Baetidae	11	5.08	4.70	3	8.7	1.90
Ephemerellidae	8	2.19	1.74	0	7	2.69
Heptageniidae	12	2.37	3.14	0	4	1.69
Plecoptera						
Chloroperlidae	6	0.70	0.75	0	1.2	0.45
Leuctridae	5	0.07	0.00	0	0.35	0.16
Nemouridae	6	2.36	2.00	2	3.37	0.59
Perlidae	8	1.93	1.90	0	3.17	1.11
Perlodidae	15	2.00	2.00	2	2	0.00
Trichoptera						
Hydropsychidae	6	2.35	2.10	0	4.9	1.96

Hydroptilidae	9	5.19	5.60	2	6.85	1.49
Leptoceridae	6	4.05	3.77	1.45	6.54	1.93
Limnephilidae	15	2.16	1.00	0	6	1.97
Coleoptera						
Dytiscidae	13	5.79	5.00	5	9	1.25
Elmidae	18	3.90	4.00	1	5.42	1.00
Hydrophilidae	11	6.15	5.00	4.95	8.27	1.41
Diptera						
Ceratopogonidae	8	6.33	6.00	5.77	8.83	1.02
Chironomidae	101	5.79	6.00	0	10	1.86
Empididae	7	5.86	6.00	5	6	0.38
Tipulidae	18	4.30	4.00	1	8	1.86
Heteroptera						
Corixidae	5	7.00	8.00	5	9	1.87
Odonata						
Coenagrionidae	6	7.31	7.39	5	9.1	1.83
Gomphidae	6	3.62	3.37	1	6.3	1.88
Neotaenioglossa						
Hydrobiidae	5	6.88	6.50	4.9	10	2.16

Violin plots (Hintze and Nelson 1998) were used to show the loss of information that can occur when coarser taxonomic resolutions are utilized. Most of the selected families of Ephemeroptera, Plecoptera, and Trichoptera (EPT) have mean tolerance values < 5.0, indicating the family-level resolution could be used to distinguish between reference and highly perturbed sites (Figure 2). The Baetidae, Hydroptilidae, and Leptoceridae exhibit a range of tolerance values that extend above 5.0 and near 9.0 for

Table 2. Variation within selected aquatic insect genera and the fingernail clam genus *Pisidium* (minimum 5 species with tolerance value

	n	mean	median	minimum	maximum	std. dev.
Ephemeroptera						
Baetis	6	3.54	4.26	1	5.1	1.71
Drunella	5	0.52	0.20	0	1.3	0.59
Epeorus	7	0.63	0.00	0	2	0.84
Ephemerella	5	1.44	1.30	0	2.8	0.96
Heptagenia	5	2.24	2.30	0.5	4	1.26
Paraleptophlebia	5	3.60	4.00	2	4	0.89
Serratella	5	1.31	1.50	0	2.2	0.86
Stenonema	13	2.61	2.30	0.3	5.2	1.22
Plecoptera						
Acroneuria	6	1.90	2.08	1.1	2.8	0.66
Isoperla	12	2.19	2.00	0	5.6	1.78
Paragnetina	5	1.86	2.00	0	3.5	1.25

Trichoptera						
Brachycentrus	8	0.93	1.00	0	2.2	0.72
Ceratopsyche	7	1.86	2.00	0	3.85	1.23
Hydropsyche	18	3.23	2.80	0	6.03	1.51
Micrasema	7	0.56	0.00	0	2.6	0.97
Nectopsyche	8	3.22	3.08	3	3.8	0.31
Neophylax	7	2.06	2.60	0	3	1.16
Rhyacophila	21	0.68	1.00	0	3.4	0.84
Coleoptera						
Optioservus	5	3.86	4.00	3.3	4	0.31
Diptera						
Cricotopus	5	7.51	7.23	4.5	10	1.63
Dicrotendipes	5	7.52	6.70	5.8	10	1.76
Eukiefferiella	6	6.10	5.60	4.85	8	1.24
Eurylophella	5	2.61	2.60	0.3	4.8	1.61
Nanocladius	5	4.07	3.65	2.6	6.1	1.32
Orthocladius	7	5.26	5.80	0.9	8.8	2.84
Parachironomus	6	6.10	6.60	3.7	8	2.09
Polypedilum	9	5.80	6.00	2.6	8.7	2.14
Simulium	8	6.13	6.00	6	6.925	0.32
Veneroidea						
Pisidium	7	8.00	8.00	8	8	0.00

some Baetidae (Figure 2). For these groups assuming that family-level resolution is adequate could underestimate the amount of perturbation. In habitats dominated by any of these families, at minimum, the generic level is likely required for accurate assessment of ecosystem health. Looking at the non-EPT families it is clear that a great deal of information could be lost when Chironomidae are not identified to a finer resolution than family (Figure 3). Unfortunately, this group is often identified only to the family level because of the difficulty in identifying the group to genera and species. Similar losses of information could also occur if Tipulidae (Diptera) and Gomphidae (Odonata) are analyzed at the family level. Information loss does not appear to be an issue for the selected genera of EPT (Figures 4 and 5). For two common and diverse Diptera genera, Orthocladius and Polypedilum, it appears that loss of information at the generic level should be a concern, because tolerance values range from 1.0 to 9.0 and < 3.0 to 9.0, respectively among species (Figure 6). Based on this information, species-level analysis

may be required in many aquatic habitats that contain these taxa to obtain accurate measures of the ecological condition of the community. There is a great amount of variation within Chironomidae genera, which reinforces the point that there could be significant loss of information within the Chironomidae if not identified beyond family. Based on our analysis, it is clear that generalizing tolerance values at coarser taxonomic levels could potentially lead to a significant loss of information for some taxa.

Redundancy

In some cases, genus- or family-level information may contain a high degree of redundancy. Congenerics and confamilials may be ecological equivalents and add little to the interpretation of the structural and functional health of a community while increasing the expenditure of resources (Olsgard & Somerfield 2000).

In samples dominated by one species the numerically dominant members of a taxon determines the most important ecological information, thus the taxon assumes the traits and characteristics of the numerically dominant species (Wu 1982). For example, there may be several species from a single genus present in a sample, but if 95% of the individuals belong to a single species, the few individuals from the remaining species contribute only a small portion to the community and are thus much less important in analysis. It has been argued that genus-, family-, or order-level identification may be adequate for specific taxonomic groups, regions, or habitats when taxa are well studied and known to have similar ecological requirements and responses to impact (Resh & McElravy 1993). Baumann (1979) indicated that most members of the order Plecoptera have similar responses to environmental change, and thus lower taxonomic resolution would be redundant and contribute little to assessment.

The redundancy in tolerance value within selected families and genera can be seen in Table 1 and Table 2, respectively. Violin plots based on the data from these tables were used to show that redundancy does exist within some genera. Within the selected families of EPT only the Hydroptilidae showed a mean tolerance value > 5.0 (Figure 2). This indicates that for the selected families there may be little information gained by analyzing tolerance values at the generic level, family-level analysis maybe sufficient to assess ecological health. For the selected Coleoptera families it appears that some redundancy does exist when identifications are left at the family level (Figure 3). The amount of redundancy at the generic level is quite high in the selected EPT (Figures 4 and 5). For all EPT genera the mean tolerance value is < 5.0 and in most genera < 2.5 . This indicates that analysis of EPT tolerance values at the species level for the selected genera is likely redundant supports the hypothesis that family-level identification could be sufficient to perform bioassessment. Within the selected Diptera genera, there is little meaningful variation within the genera *Dicrotendipes*, *Eukiefferiella*, *Eurylophelia*, *Nanocladius*, and *Simulium* (Figure 6). This indicates that species-level analysis for tolerance value is likely not required for an accurate assessment of ecosystem health in habitats dominated by these genera.

Our data support the hypothesis that within some groups, there is a large amount of ecological redundancy that does not aid in assessments (Tables 1 and 2). A serious problem with the redundancy argument is that most biological and ecological knowledge is the result of incomplete information at the species level, resulting in the extrapolation of ecological characteristics for poorly known species from congenetics or confamilials, thereby creating artificial redundancy (Lenat & Resh 2001). The small number of taxa

presented in Tables 1 and 2, with at least five recorded tolerance values in our data set, illustrated this point as well.

Effects of taxonomic resolution on analysis

Few studies have examined the effects that different taxonomic resolutions have on the suite of simple metrics (e.g. richness, dominance, composition, trophic structure, etc.) commonly used in biological assessment studies. Lenat and Resh (2001) state that to compare richness measures, ratios of taxonomic levels need to be compared (e.g. genus:family). Ratios with large values indicate a substantial discrepancy between the taxonomic levels and suggest a coarser resolution should be avoided or used with care, while ratios at or near unity indicate little effect of taxonomic resolution. For example, in North America there are a larger number of species within the family of Chironomidae (approximately 2000) than are found within families of Ephemeroptera (mean = 28 species per family) so the identification of the Chironomidae to lower levels may be more informative (Lenat & Resh 2001; data from Merritt & Cummins 1996). However, the 28 species average per family in Ephemeroptera may be large enough to make generalizations questionable. The ratio of taxonomic levels and its significance are dependent upon the regional, habitat, and historical factors of the aquatic system (Lenat & Resh 2001). Thus a fair amount of autoecological information is required before assessment of the effects on richness indices can be made.

Schmidt-Kloiber and Nijboer (2004) examined how the use of coarser taxonomic resolution affected multimetric analysis tools such as the AQEM (Integrated Assessment System for the Ecological Quality of Streams and Rivers through Europe Using Benthic Macroinvertebrates) Assessment Software (AAS). The AAS was constructed using

species information and therefore should offer the most accurate assessments when utilized at that level. The authors found this to be true, but they hypothesized that similar models constructed with data from higher resolutions would likely work well with coarser taxonomic level data (Usseglio-Polatera et al. 2000, Schmidt-Kloiber & Nijboer 2004). The ability of predictive models to measure biological integrity of stream systems has been tested. The River Invertebrate Prediction and Classification System models (RIVPACS) ability to detect biological impairment in montane streams of California was tested. The RIVPACS models have been applied and work well at both species and family taxonomic levels in Europe and Australia, but had been relatively untested in North America. It was determined that RIVPACS models used at the species level could distinguish between logging-perturbed areas and unperturbed areas. The models could not do so at the family-level however (Hawkins *et al.* 2000). The authors believe that predictive models can be useful in all geographic regions, but they emphasize that how and to what taxonomic level the models are applied will vary among regions.

Diversity indices for the most part were developed from data at the species level and many authors argue that they are not reliable at higher taxonomic levels due to the errors that are introduced (Lenat & Penrose 1980, Resh & McElravy 1993, Lenat & Resh 2001). Wu (1982) argues that using coarser taxonomic resolution with diversity indices decreased the magnitude of detectable diversity within samples.

Multivariate analysis is a popular method of analyzing bioassessment data because many variables can be included in a model. However, in most cases the methods of multivariate analysis require that rare taxa be eliminated. This creates an analysis similar to one in which a coarser taxonomic resolution was used because a portion of the

community is ignored (Cao *et al.* 1998, Cao & Williams 1999, Cao *et al.* 2001, Lenat & Resh 2001). In most cases, these rare taxa are species represented by only a one or a few specimens, seldom are entire families or genera rare within a given sample. Cao and co-workers (Cao *et al.* 1998 & 2001 and Cao & Williams 1999) illustrated that the elimination of rare taxa affects the least impacted sites because these sites are typically more diverse and single species specimens are more likely to occur. This could lead to an underestimation of the difference between impacted and unimpacted sites, which could result in misallocation of funding away from sites that are in need of rehabilitation. It should be noted that while the above authors make valid points regarding multivariate analysis, many authors argue that coarser resolution has no effect or even improves multivariate analysis by eliminating environmental noise (Furse *et al.* 1984, Armitage *et al.* 1987, Marchant *et al.* 1995, Olsgard *et al.* 1997, Bowman & Bailey 1997, Marchant 1999, Hewlett 2000, Bailey *et al.* 2001, Marchant 2002).

Several authors have proposed that higher-level identifications would be less sensitive to natural influences on communities, thereby making the effects of perturbations more evident (Warwick 1988a, Warwick 1988c, Bailey *et al.* 2001). This hypothesis is based on the idea that species' presence is determined by a narrow range of natural variables, which is not reflected in higher classification levels, and that perturbations affect taxa at higher levels (Bowman & Bailey 1997). There is little evidence for the general applicability of this mechanism, although some research has documented "noise" resulting from lower resolutions (Smith & Simpson 1993, Bowman & Bailey 1997, Feminella 2000). Wright *et al.* (1995) and Olsgard *et al.* (1998) argue that this mechanism may not exist if both higher and lower levels are affected similarly

by impacts and environmental factors. The reverse may also be true in that subtle disturbances may only affect a limited set of ecological and/or taxonomic specialists that are most often represented at species-level. These hypotheses require further analysis.

The usefulness of the species concept has sometimes come into question in the biomonitoring debate (Wiley 1978, Cummins 1994). For many involved in biomonitoring, the concept of species is generally accepted as fact (Resh & McElravy 1993) although the use of species as a naturally distinct unit may be academic, misleading, or simplified and thus a possible source of interpretive error. An author determines the designation of species, but a lack of evolutionary information could result in a determination that is meaningless to an ecologist. Such effects may be more pronounced with coarser resolution, where the taxonomy of a group is not based solely on phylogenetic principles, but also the prerogative of the author of the phylogeny (i.e. splitter or lumpers). Subspecies and even populations may have different characteristics and responses to impact, so why not use these levels to assess impact? These differences may not be relevant if the taxonomic units correctly describe the ecological characteristics, but discrepancies in taxonomy among regions and groups could potentially interfere with analyses. In determining an optimal level of taxonomic resolution, the mechanisms of speciation must be considered. The evolution of a species can be the result of two important factors: (1) allopatry or (2) ecological differentiation among sister taxa (Cranston 1990). If allopatry is the overriding mode for speciation, then ecological differences between species may be minimal, and the use of higher-level classifications would be adequate and justified. If speciation is driven by ecological differences between sister taxa, species-level identification is important to prevent the

loss of ecological information and interpretation (Cranston 1990). These comments are not meant to suggest that the species concept is not useful, but these ideas deserve some consideration.

Taxonomic Sufficiency

Resh & McElravy (1993) state that in the determination of proper taxonomic resolution for a study, “It depends.” This simple idea is central to taxonomic sufficiency, is the concept of determining a meaningful compromise between species-level and higher-level resolution (see Ellis 1985). Numerous factors (e.g. spatial scales, sieve mesh size, sample unit size, stream size, seasonality, region, perturbation type, etc.) need to be explored before a taxonomic classification system can be applied to a study. Doledec et al. (2000) tested the effect of spatial scales on taxonomic resolution and found that at large spatial scales (catchments), species-level identifications were best to describe communities, whereas genus- or family-level identifications were sufficient on the local habitat scale. Biotic (i.e., saprobic) indices (e.g. Hilsenhoff 1982, Lenat 1993) are still used in many biological-monitoring programs, so there is still a need for information on the characteristics of taxa. Although current trends place more emphasis on determining scientifically and statistically robust metrics to characterize sites in a way that allows discrimination between sites of varying impacts. Using modern approaches, identifications to the species level may not be necessary, but study designs still require a method to determine the taxonomic resolution necessary to distinguish impact levels between sites.

The idea of taxonomic sufficiency is useful and may be the best current method to solve the problem of taxonomic resolution. As stated by Ellis (1985), “Taxonomic

sufficiency is the concept that in any project organisms must be identified to a level (species, genera, family, etc.) which balances the need to indicate the biology (including for example such matters as diversity) of organisms present with accuracy in making the identifications.” Omitting pragmatic constraints (e.g. resource or knowledge limitations), four aspects of a study can influence the taxonomic sufficiency: (1) the purpose of the study, (2) sensitivity required, (3) type of analysis, and (4) the group of organisms of interest (Resh & McElravy 1993).

There is little doubt that species-level identifications have the potential to provide more community information, but is this level of detail needed to determine whether an ecosystem deviates from the reference condition? The purpose of bioassessment programs is not to describe the macroinvertebrate community, but rather to identify potential impacts or differences from the reference condition (Bailey *et al.* 2001).

It has been hypothesized that there is a hierarchical response in macroinvertebrate communities to increasing impact (Pearson & Rosenberg 1978, Boesch & Rosenberg 1981, Ferraro & Cole 1990 and 1992, Bowman & Bailey 1997). Species resolution will be able to detect subtle impacts because species exhibit a wide range of ecological characteristics and tolerances to a variety of disturbances (Nijboer & Schmidt-Kloiber 2004). When genus resolution is employed, these more subtle and specific impacts may be missed because the loss of species can be masked by the replacement of more tolerant congeners. The replacement of taxonomic groups occurs in steps as stress increases. First the individual is affected, and then the species, genus, family, etc. are removed from a community as levels of stress increase (Ferraro & Cole 1992). As resolution becomes coarser, the ability to detect impact decreases to the point where only gross pollution can

be identified. The hierarchical response to stress provides a framework to analyze the taxonomic resolution needed to identify various levels of impact.

It is generally agreed that family- or even order-level classifications can be utilized for the assessment and monitoring of gross impacts or dramatic changes, while species- or genus-level classification, may be more applicable to the assessment of more subtle changes in stream quality (Simpson & Bode 1980, Kingston & Riddle 1989, Resh & McElravy 1993, Young 1999; Lenat & Resh 2001, Waite *et al.* 2004). It has also been suggested that family level could be used to distinguish between unimpaired, moderately impaired, and severely impaired systems (Plafkin *et al.* 1989, Hewlett 2000, Lenat & Resh 2001, Chessman & Royal 2004, Waite *et al.* 2004). Coarser taxonomic resolution may also be applied as an “early warning system” to identify potential changes in stream quality (Resh & McElravy 1993). However, in most situations when finer scales of impact or specific impacts must be identified or when management decisions are based on such research, genus- or species-level identifications are likely required (Lenat & Resh 2001, King & Richardson 2002, Schmidt-Kloiber & Nijboer 2004).

The following example illustrates the need to base taxonomic sufficiency on specific study needs. Results from a study designed to compare predictive modeling with a multimetric ICI approach in assessing biological conditions for a number of wadeable streams in the Western Corn Belt Plains (WCBP) ecoregion suggested that genus-level taxonomy may be necessary to better differentiate reference and non-reference streams (Bouchard 2002). Impacted and reference streams were determined independently using land use/land cover, water quality, and habitat information that was combined into a numeric watershed model (see Donley 1999 and Bouchard 2002).

Classification accuracy and precision were assessed for both modeling approaches using both genus and family-level taxonomy to evaluate their performance in discriminating impacted and reference streams within this heavily disturbed ecoregion. Both taxonomic resolutions were able to separate reference from non-reference streams using either model but genera-level resolution resulted in better accuracy and precision especially within the predictive model. Multimetric and predictive model scores using genus-level identifications displayed smaller variances when examining both reference and test sites.

Finally the determination of taxonomic sufficiency can be difficult because of the natural variability present in most aquatic systems and the inability of sampling and analysis techniques to avoid classification errors resulting from this variability. Few studies have examined the effects of water body type and environmental or regional characteristics on the natural diversity and composition of aquatic fauna even though these factors potentially have substantial effects on taxonomic sufficiency (Hawkins & Norris 2000, Bailey et al. 2001, Lenat & Resh 2001).

Conclusion

There are two apparent things that could be done to help resolve the issues of taxonomic resolution relative to individual or collective biological assessment studies. First, there needs to be continued improvements in our taxonomic keys and tools as well as more research into the pollution ecology of nearly all macroinvertebrate taxa. These improvements can only come through continuing investigations into the life history of individual species and integrating this knowledge with applied aspects of bioassessment (Hart 1994). This area of research has decreased in funding and thus effort over recent

decades. If there is going to be future emphasis on indicator groups to decrease resources required for bioassessment, then this type of research must continue. The identification of good indicator groups is dependent upon a thorough understanding of species' biology and ecology. There also needs to be continued development of more complete keys and the examination of new techniques such as molecular identification (Carew *et al.* 2003, Sharley *et al.* 2004). The most crucial element to a better understanding of taxonomy is communication between researchers, agencies, academics, and the public (Penrose & Call 1995, Cullen *et al.* 1999). This involves not only open lines of communication, but also data sharing, accurate record keeping, an emphasis on metadata, and a willingness to share reference specimens.

The second key to settling the taxonomic resolution debate involves finding an understanding of the taxonomic sufficiency required for specific study methods and objectives. This can be accomplished through the continued investigation of the effects of taxonomic resolution on different types of analysis in different ecosystems. There must also be continued research on individual taxa looking for the presence of redundancy and loss of information. This type of information can only be obtained through species level life history studies. An understanding of what taxonomic level is needed for a specific type of study could eventually lead to a method standardized, objective set of taxonomic resolution criteria.

Lenat and Resh (2001) offer a set of recommendations for appropriate taxonomic levels. The authors state that family-level identifications are appropriate in situations where resources (money, time, or expertise) are very limited. Essentially they are stating that family-level analysis is better than no biological monitoring. They contend that very

large between-site differences are detectable at the family level. Finally, the authors suggest that when sampling is done in areas known to exhibit low taxa richness, family-level identification could be sufficient. However, Bouchard's (Bouchard 2002) work in wadeable streams in the Western Corn Belt Plains ecoregion indicates that even in systems with limited taxon richness, genus-level resolution is more informative in discerning impacts to these stream systems. Lenat and Resh (2001) argue that many cases require more precise identifications such as genus or species. When conclusions are to be made with a high degree of confidence and when small between-site differences are investigated a level lower than family should be utilized. If the study is interested in deducing both the magnitude and type of perturbation the authors argue that only genus- or species-level identifications should be analyzed. The authors argue for the use of species-level identifications in conservation studies because rare species are likely missed when higher taxonomic levels are used. Finally, the authors state that ideally any multipurpose federal/state survey should be done at the lowest possible taxonomic level. This would increase comparability between studies over time and it would make subtle changes in systems over long periods of time (decades) much more detectable because more organisms would be catalogued.

In this paper we have attempted to address some of the issues related to taxonomic resolution and biological assessment needs and objectives – not all have clear scientific answers. Final determination of appropriate taxonomic resolution often comes down to a balance between information (gain or loss) and available resources. If the long-term goal were to make bioassessment as inexpensive and quick as possible it would seem that studies using both coarser and finer taxonomic resolutions are still required.

The question that must be answered is this: does the cost of finer taxonomic resolution outweigh the potential loss of information? In many cases, yes, the cost of increased resolution is greater than the potential loss of information. Studies interested in the detection of gross between-site differences, studies in areas of known low diversity, and studies utilizing multimetric and multivariate techniques can likely utilize coarser taxonomic resolutions. However, studies dealing with conservation, life histories, indicator groups, and those looking at specific type of perturbation are likely to require genus-level or preferably species-level identifications. At this point the key to finding quick and inexpensive methods for bioassessment is the continued investigation into genus- and species-level traits of aquatic macroinvertebrates.

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Figure 2. Violin plots of Ephemeroptera, Plecoptera and Trichoptera families based on literature assigned tolerance values (mean values used in violin plots if multiple literature values were identified). Violin plots show median value (circle) and 95 and 25 quartiles (bars) for each taxon and the general distribution on values within each plot.

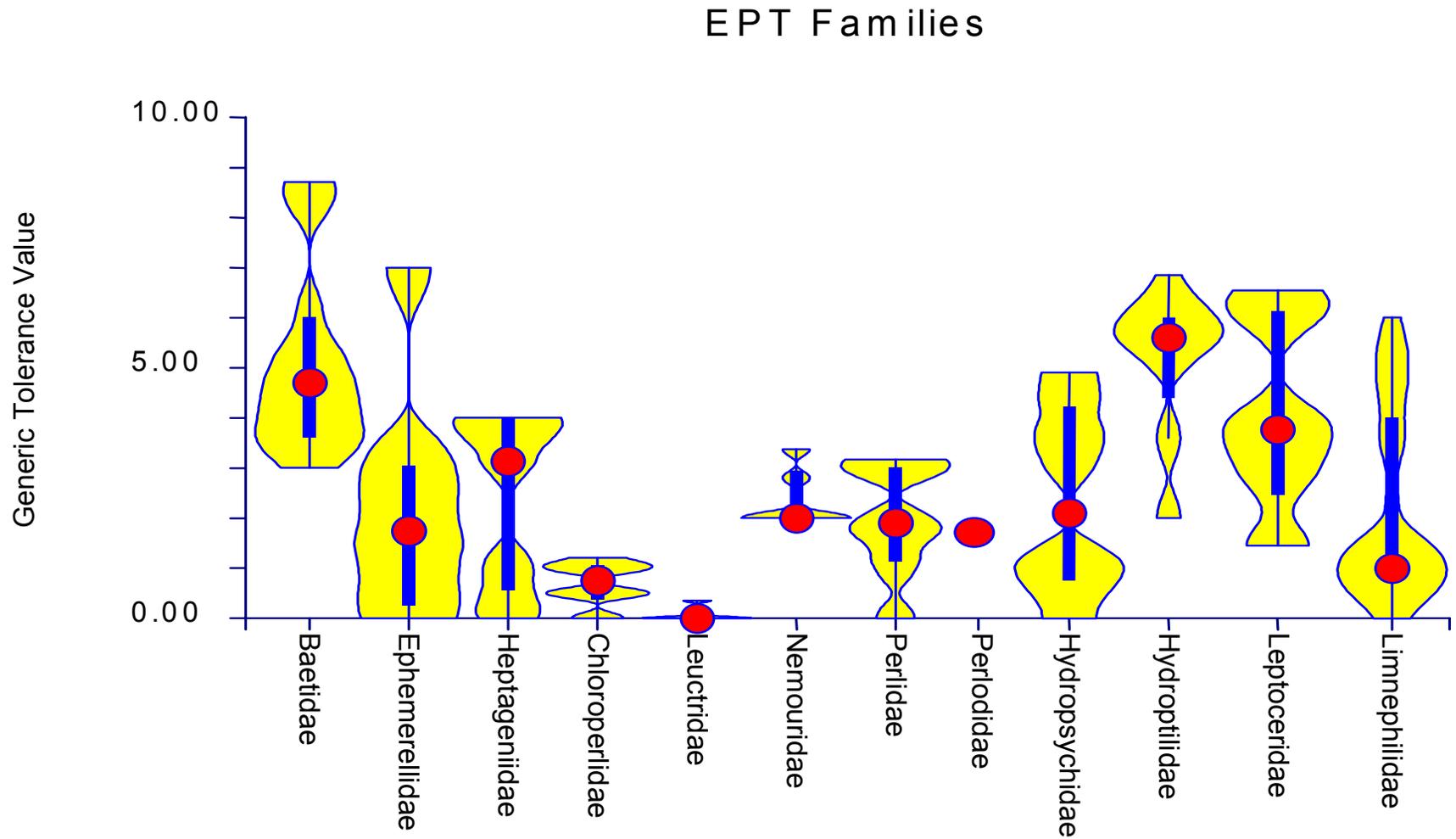


Figure 3. Violin plots of Coleoptera, Heteroptera, Diptera and Odonata families based on literature assigned tolerance values (mean values used in violin plots if multiple literature values were identified). Violin plots show median value (circle) and 95 and 25 quartiles (bars) for each taxon and the general distribution on values within each plot.

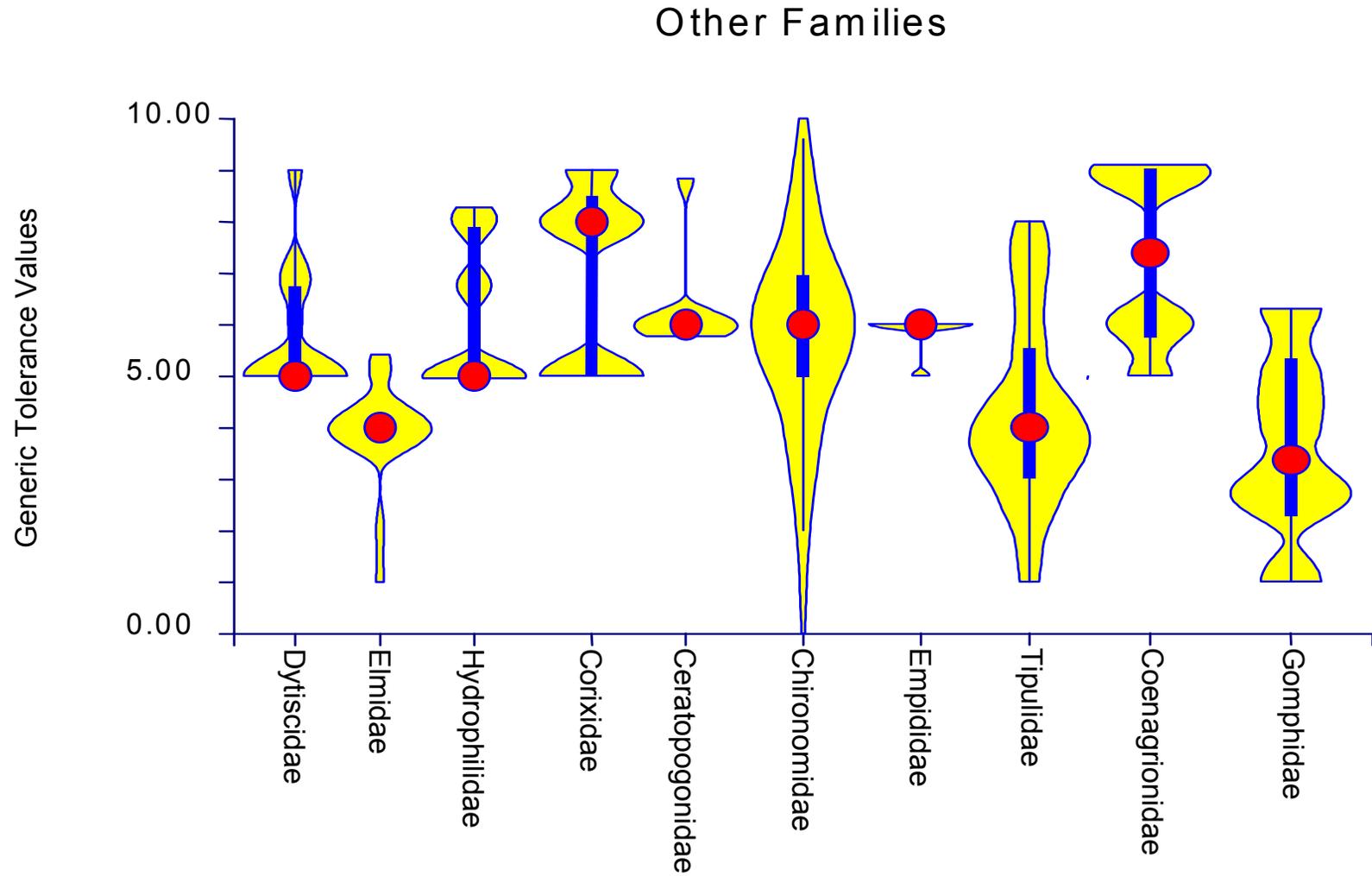


Figure 4. Violin plots of Ephemeroptera genera based on literature assigned tolerance values (mean values used in violin plots if multiple literature values were identified). Violin plots show median value (circle) and 95 and 25 quartiles (bars) for each taxon and the general distribution on values within each plot.

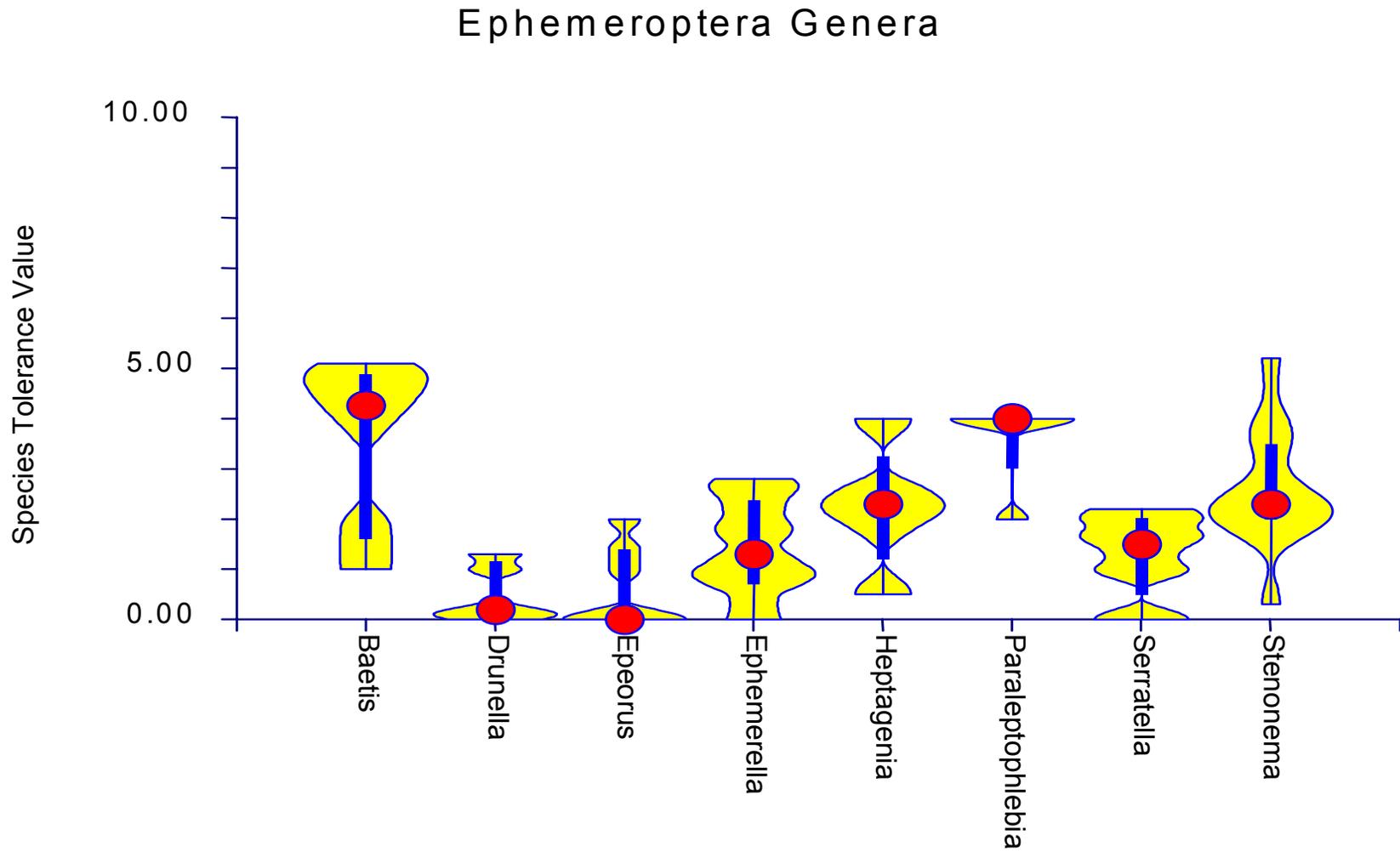


Figure 5. Violin plots of Plecoptera and Trichoptera genera based on literature assigned tolerance values (mean values used in violin plots if multiple literature values were identified). Violin plots show median value (circle) and 95 and 25 quartiles (bars) for each taxon and the general distribution on values within each plot.

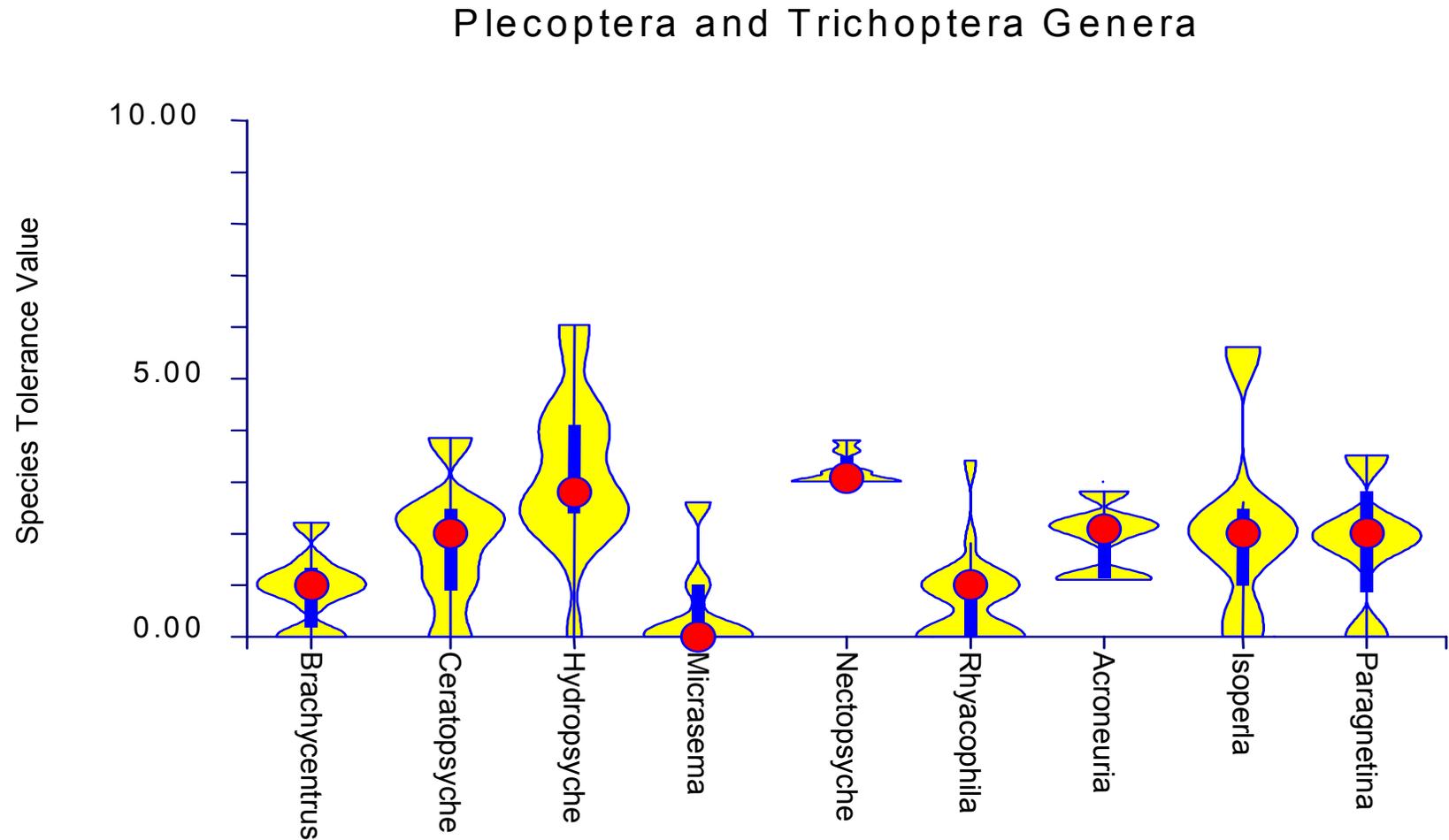


Figure 6. Violin plots of Chironomidae and Simuliidae (Diptera) genera based on literature assigned tolerance values (mean values used in violin plots if multiple literature values were identified). Violin plots show median value (circle) and 95 and 25 quartiles (bars) for each taxon and the general distribution on values within each plot.

