A Case Study for Comparison of NAWQA and EMAP Protocols for Benthic Macroinvertebrates and Habitat

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Introduction

Benthic macroinvertebrate communities and habitat measurements are compared for data collected following protocols established by the U.S. Geological Survey for the National Water-Quality Assessment (NAWQA) program (Cuffney and others, 1993, Fitzpatrick and others, 1987) and by the U.S. Environmental Protection Agency for the Western Pilot Environmental Monitoring and Assessment Program (EMAP) (Peck and others, 2000). Samples and measurements at 12 sites were collected by the same personnel for both protocols, in a side-by-side fashion at streams in Wyoming, Montana, and Colorado (fig. 1) during 2000-2001.

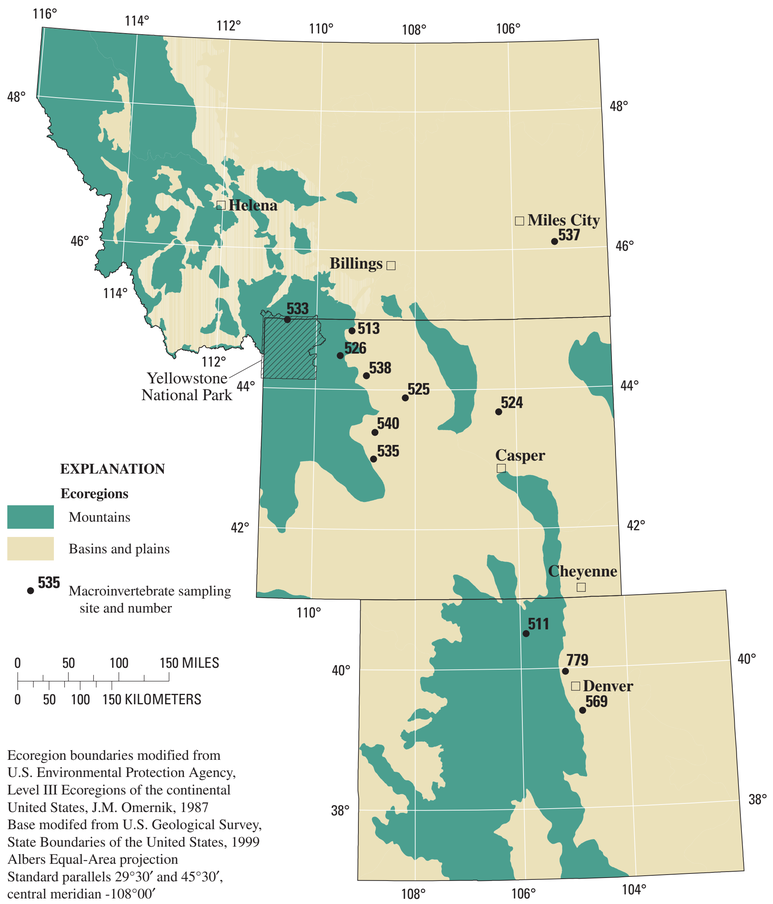

Figure 1. Locations of the sampling sites, NAWQA-EMAP comparative study, Wyoming, Colorado, and Montana, 2000–01.

Clarks Fork Yellowstone River, Wyoming (site 513). Photograph by Ron Zelt, USGS.

Caddisfly *Neophylax* (Trichoptera: Uenoidae). Photo courtesy of James L. Carter, National Research Program, USGS.

1. Initial Macroinvertebrate Data Set

Ambiguous taxa in the NAWQA and EMAP macroinvertebrate data sets were resolved using the IDAS software (Cuffney, 2003). After treatment of ambiguous taxa, pair-wise differences in total taxa richness and Ephemeroptera taxa richness (fig. 2 and table 1) were statistically significant between the data sets. Other metrics tested, such as Chironomid taxa richness, relative abundance of EPT and non-insects, and macroinvertebrate density, were not significantly different between the data sets, in spite of differences in net mesh-opening size and area sampled between the NAWQA (425 micron mesh, 1.25 m^2 per sample) and EMAP protocols (500 micron mesh, 0.72 m^2 per sample). Sample scores calculated using a multi-metric index, the Wyoming Stream Integrity Index (WSII) were not significantly different between the data sets.

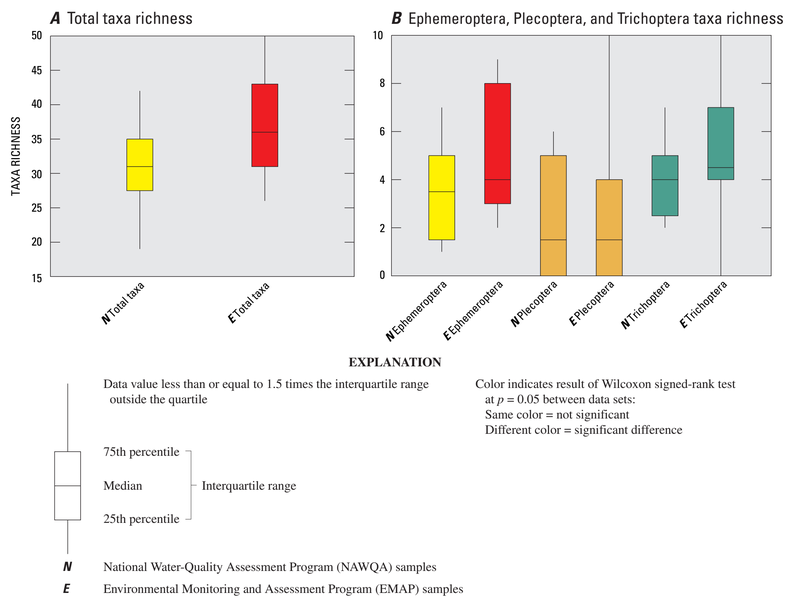

Figure 2. Selected macroinvertebrate metrics for 12 paired NAWQA and EMAP samples.

Table 1. Comparison of metric values between initial NAWQA and EMAP data sets, using the Wilcoxon signed-ranks test.

Difference significant ($p < 0.05$)	Difference not significant ($p > 0.05$)
Total taxa richness	Trichoptera taxa richness
Ephemeroptera taxa richness	Plecoptera taxa richness
	Chironomid taxa richness
	Relative abundance of EPT, non-insects, and Oligochaeta
	Tolerance values
	Semivoltine taxa
	Functional feeding groups (scraper, filterer-collector, and collector-gatherer)
	Abundance of 5 dominant taxa
	Shannon diversity
	Macroinvertebrate density

Mayfly *Ironodes* (Ephemeroptera: Heptageniidae) Photograph courtesy of James L. Carter, National Research Program, USGS.

2. Macroinvertebrate Taxa Reconciliation

A total of 29 taxa were identified to species in the NAWQA samples, and 35 taxa were identified to species in the EMAP samples. The NAWQA laboratory identified mites to Acari (class Arachnida), Oligochaeta to family, and discarded Ostracoda, whereas the EMAP laboratory identified mites to genus, Oligochaeta to class, and counted Ostracoda. As a test of the effect of the laboratory procedures on the results, both data sets were reconciled to set genus as the minimum level of identification, all Oligochaeta and mites were lumped to one respective taxon each, and Ostracoda were deleted. The total number of taxa in each reconciled data set (fig. 3) was reduced from those of the initial data set, but the difference in total taxa richness and Ephemeroptera taxa richness between the reconciled data sets was still significant ($p < 0.05$).

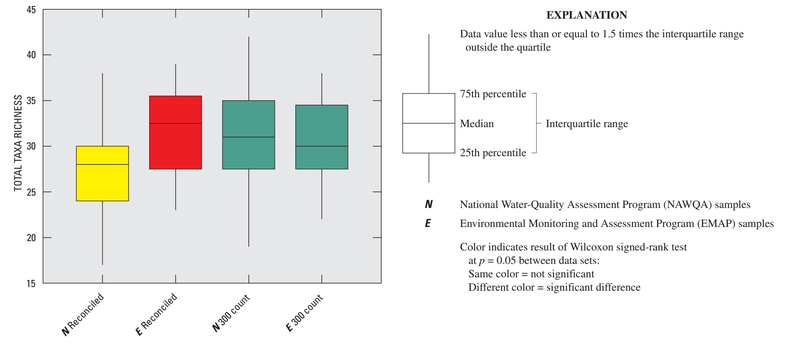

Figure 3. Total taxa richness in NAWQA and EMAP data sets after taxa reconciliation and subsampling.

3. Adjustment of Macroinvertebrate Samples for Subsampling

The NAWQA laboratory used a fixed-count target of 300 organisms whereas the EMAP laboratory used a fixed-count target of 500 organisms. In order to test the effects of the different-sized fixed counts used by the laboratories, a software routine (Daren Carlisle, U.S. Geological Survey, written commun., 2005) was used to estimate taxa present if the EMAP samples were identified to 300 organisms instead of 500. Using a 300-organism, species-level count for EMAP and NAWQA data sets, the total number of taxa and the Ephemeroptera taxa richness were not significantly different between the data sets ($p > 0.05$) (fig. 3).

The effects of taxa reconciliation and subsampling on community structure also were tested using non-metric multi-dimensional scaling (NMDS) ordinations of Bray-Curtis similarity coefficients between the samples (Clarke and Warwick, 2005). NMDS ordinations of log-transformed abundance data were tested for combinations of species-level data, before and after subsampling, and taxa reconciled data, before and after subsampling. All of the NMDS ordinations of log-transformed abundance data, as well as presence/absence data at the species level, showed a mirror image similar to that shown in figure 4A, indicating greater affinity by program than by site. The NMDS ordinations using presence/absence data after reconciliation of taxa showed a stronger affinity by site than by program, but the additional step of subsampling did not improve the ordination (Peterson and Zumberge, in press). Of the various ordinations performed, taxa reconciliation of presence/absence data (fig. 4B) provided the best indicator of similar macroinvertebrate community structure between the NAWQA and EMAP data sets.