

Quality Assurance Report

Biological Data Prepared by Boris Kondratieff from Samples Collected in Vail, Colorado

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Introduction

The Watershed Management Institute (WMI) entered into a contract with the Town of Vail, Colorado to study the effectiveness of nonstructural stormwater controls in protecting stream biota. The Town of Vail contracted with the U.S. Geological Survey (USGS) in Denver to manage the collection and processing of macroinvertebrate and physical habitat data at sites throughout the towns of Vail, Beaver Creek, and Copper Mountain, Colorado. Samples were collected at 50 sites by the USGS during the period September 23-28, 1998.

The USGS contracted with Dr. Boris Kondratieff (BK) of the University of Colorado for sorting, taxonomic identifications, and the preparation of a reference collection. The sorted samples, reference collection, and data files were delivered to the WMI for quality assurance on October 1, 1998. The data and samples were also sent to Mike Winnell of Freshwater Benthic Service (FBS) on November 15, 1998 for further taxonomic evaluations. Work by FBS was completed on February 1, 1999 under contract with WMI.

After review by WMI and FBS, it was concluded that portions of the data did not meet QA objectives as specified in the Scope of Work. Agreement was reached between WMI, USGS, and BK on the procedures to be followed to correct the data. This included the generation of 100-organism subsamples from the sorted samples and applying QA checks to the new data. A Scope of Work to subsample and re-identify the samples was prepared (Attachment B), and the work was completed by BK June 20, 1999. The data and samples were sent to FBS for further QA analysis. FBS completed additional QA analysis of 10 samples on November 9, 1999. This report documents the problems encountered in the original data and the QA results of the new data generated by BK.

QA Problems with the Original Data

The reference collection passed QA with regard to taxonomic quality assurance (Attachment A). However, several problems were documented in the review of the sample data. These problems are summarized below.

- Sorted detritus was not saved to allow for quality assurance checks on sorting accuracy. This provision was specified in the Scope of Work for sample processing. Independent QA review of sorting efficiency and accuracy was not possible without the sorted detritus samples.

- Several of the sample vials were poorly labeled. 39 samples (about 50%) did not specify the replicate number. Thus, there was no way to match samples with data. In addition, the caps on 3 vials did not match correctly with the vial label, and some labels were hard to read and contained extraneous information.
- One-third of the reference material came from other projects. The Scope of Work specified that reference material come from samples collected for the project.
- Reference collection documentation did not specify what samples the reference specimens came from, as specified in the Scope of Work. The samples could not be “rebuilt” and matched to the data without sample numbers assigned to reference specimens.
- The Scope of Work specified that the samples be subsampled. BK requested that the samples be whole picked. The WMI (John Maxted) objected to this change because whole picking, data recording, and QA would be difficult for very large (> 300 individuals) samples. WMI allowed the change provided the data met the QA objectives of the original Scope of Work (i.e., subsampling). 17 samples were whole picked and the remainder had 25% of the sample sorted (i.e., subsampled). WMI did not approve this combined “whole pick/subsample” approach. The total number of individuals processed using the combined whole pick/subsampling approach was 61,514 individuals. The total number of individuals in all of the samples was estimated to be 217,381. This number of individuals justifies the use of subsampling in sample processing.
- Midges and pupa were not permanently mounted.

Given the problems encountered in review of the data and samples, the WMI contracted with FBS to have 5 randomly selected samples re-identified and checked against the data reported by BK. The purpose of this QA analysis was to provide objective review of quality of the sample data. This review was completed by FBS on November 11, 1998. The report prepared by FBS identified unacceptable differences between the BK data and data generated by FBS (attachment A). FBS found 1300 more specimens in the 5 samples than reported by BK for an increase of 64%; well above the QA threshold of 5%. There were unacceptable differences in 4 of the 5 samples checked. In one sample (BMP-5), FBS found 955 *Neothremma alicia* (Trichoptera) as compared to 77 reported by BK.

No explanation was provided to explain the differences. It was concluded that the remaining samples had to be re-identified. This decision was agree upon by all parties involved.

QA Results for the New (subsampled) Data

The samples were subsampled (100-organisms) and re-identified by BK following procedures agreed to by all parties (Attachment B). BK began work on May 6, 1999 and completed work in September 1999. The samples and data were sent to FBS for QA. QA by FBS involved re-identification of 10 randomly selected samples. The taxonomy and recording of data by BK would pass QA if less than 5% of the individuals were recorded differently between the two sets of data.

FBS completed the review and delivered a final QA report on November 10, 1999. The report concluded that the samples met the QA threshold of 5% (Attachment C). A summary of the report is presented below.

- Analysis A – The total counts between the two sets of 10 samples were compared. The two sets of data were different by 30 individuals (out of 1157) for an error rate of 2.59% and within the QA threshold of 5%.
- Analysis B – The counts between individual samples were compared. The differences between the two data sets ranged from a low of 2 individuals to a high of 18 individuals. There were a total of 77 individuals (out of 1157) recorded differently between the two data sets for an error rate of 6.6%. This difference was considered to be equivalent to the QA threshold of 5% given the accuracy of the analysis.
- Analysis C – The total number of taxa (richness) between the two sets of data were compared. There were 11 taxonomic differences (out of a total of 161 taxa) between the two sets of data for an error rate of 6.83%. This difference was considered to be equivalent to the QA threshold of 5% given the accuracy of the analysis.

Conclusions and Recommendations for Data Analysis

The new subsampled data generated by BK has met all QA requirements and is acceptable for data analysis. Given the problems encountered in sample processing and QA, the following actions are recommended. First, only the new subsampled data should be used in data analysis. Second, no attempt should be made to estimate total abundance (organisms per meter² of substrate sampled) for each site. The variability introduced into the data associated with sample collection, processing, and QA makes such estimates of little value in the ecological assessment. The 100 organisms removed from each sample are the best estimate of the community at each site, regardless of the hypothetical number in the field or in the samples originally sorted. Third, the samples should have individuals randomly removed from each data set down to 100 organisms using a random numbers table. Thus, all of the samples should have 100 organisms before calculating metrics. Fourth, the following metrics should be calculated from the adjusted data:

- Total richness
- EPT richness
- % EPT
- Hilsenhoff biotic index (HBI)

Other metrics may also be calculated if documented to be important metrics for streams of the region.