

Attachment A

Aquatic Benthic Macroinvertebrate Communities of Mammoth and Hot Creeks, California

Section	Page
1.0 INTRODUCTION	1
2.0 METHODS	2
2.1 1992 through 1994 Methods - Mammoth Creek	2
2.2 1993 Methods - Hot Creek.....	2
2.3 2000 through 2004 Methods	3
2.3.1 Cluster Analysis.....	4
2.3.2 Multi-Metric Analysis.....	4
2.4 California Stream Bioassessment Procedure Methods	4
2.4.1 Determining Monitoring Reach Length	5
2.4.2 Physical/Habitat and Ambient Chemical Characteristics.....	5
2.4.3 Biological Sampling.....	5
2.4.4 Laboratory Methodology	6
2.5 2005 and 2006 Methods	6
3.0 RESULTS.....	7
3.1 1992 through 1994 Results - Mammoth Creek	7
3.2 1993 Results - Hot Creek	7
3.3 2000 through 2004 Results	8
3.3.1 Review of 2000-2004 Hot Creek Hatchery Bioassessment Reports	8
3.3.2 Physical Habitat Characteristics.....	10
3.3.3 Summary of Benthic Macroinvertebrate Metrics from 2000 through 2004.....	10
3.3.4 Analysis of taxon-specific differences among sites	12
3.3.5 Cluster Analysis of 2004 Bioassessment Data	13
3.3.6 Multi-Metric Analysis on 2004 Bioassessment Data.....	14
3.4 2007 Summary of Results.....	15
4.0 DISCUSSION AND CONCLUSIONS.....	16
5.0 REFERENCES	34

LIST OF FIGURES

Figure		Page
Figure A-1.	BMI sample collection locations in Mammoth Creek during 1992 through 1994.....	18
Figure A-2.	BMI sample collection locations in Mammoth and Hot Creeks during 2000 through 2004 (from Jellison et al. 2005a).....	18
Figure A-3.	Relative abundance of <i>Coleoptera</i> (beetles), <i>Diptera</i> (flies, gnats, midges, and mosquitoes), <i>Ephemeroptera</i> (mayflies), <i>Plecoptera</i> (stoneflies), and <i>Trichoptera</i> (caddisflies) in Reaches B through E of Mammoth Creek. Data are compiled from Vinson (1995) and represent the actual number of organisms collected (from MCWD and USFS 2000).	19
Figure A-4.	Cumulative taxonomic richness in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	19
Figure A-5.	Cumulative EPT taxonomic richness in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	20
Figure A-6.	EPT Index (percentage of EPT taxa) in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	20
Figure A-7.	Sensitive EPT index (percentage of sensitive EPT taxa) in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).	21
Figure A-8.	Shannon diversity index values in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	21
Figure A-9.	Percent of organisms in the family Tubificidae in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	22
Figure A-10.	Mean BMI tolerance values in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).	22
Figure A-11.	Percentage of intolerant BMI taxa in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	23
Figure A-12.	Percentage of tolerant BMI taxa in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	23
Figure A-13.	Percentage of dominant BMI taxa in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	24
Figure A-14.	Percentage of collector-gatherers in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	24
Figure A-15.	Relative abundance (%) of riffle beetles (<i>Optioservus sp.</i>) in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).	25

Figure A-16.	Relative abundance (%) of riffle beetles (<i>Zaitzevia sp.</i>) in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	25
Figure A-17.	Relative abundance (%) of black flies (<i>Simulium sp.</i>) in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	26
Figure A-18.	Relative abundance (%) of the mayfly <i>Fallceon quilleri</i> in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	26
Figure A-19.	Relative abundance (%) of caddisflies in the genus <i>Brachycentrus</i> in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	27
Figure A-20.	Relative abundance (%) of micro-caddisflies in the genus <i>Ochrotrichia</i> in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	27
Figure A-21.	Relative abundance (%) of micro-caddisflies in the genus <i>Oxyethria</i> in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	28
Figure A-22.	Relative abundance (%) of ostracods in the genus <i>Cyprididae</i> in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	28
Figure A-23.	Relative abundance (%) of tubificid worms in the family Tubificidae Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	29
Figure A-24.	Relative abundance (%) of tubificid worms in the family Naididae in Mammoth Creek and Hot Creek During 2000 Through 2004 (from Jellison et al. 2005a).....	29
Figure A-25.	Relative abundance (%) of planarid flatworms in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	30
Figure A-26.	Cluster analysis of 2004 BMI relative abundance data obtained from all transects (from Jellison et al. 2005a).....	30
Figure A-27.	Cluster analysis of 2004 BMI relative abundance data with replicate transects averaged (from Jellison et al. 2005a).	31
Figure A-28.	Hot Creek multi-metric index (from Jellison et al. 2005a).....	31

LIST OF TABLES

Table	Page
Table A-1. Sampling site codes, GPS coordinates, and site descriptions for the ten monitoring stations where biological and physical/habitat assessments were conducted during 2000 through 2004 (from CDFG 2004).....	32
Table A-2. BMI sampling sites in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).....	32
Table A-3. Bioassessment metrics used to describe characteristics of the benthic macroinvertebrate community for the ten monitoring stations where biological and physical/habitat assessments were conducted.....	33

Attachment A

Aquatic Benthic Macroinvertebrate Communities of Mammoth and Hot Creeks, California

1.0 INTRODUCTION

Water Right Permit 17332, under which the District may divert water for beneficial uses, requires the District to remain in compliance with Fish and Game Code Sections 5937 and 5946. Specifically, Section 5937 requires “the owner of any dam to allow sufficient water at all times to pass through a fishway, or over, or around the dam to keep in good condition any fish that may be planted or exist below the dam.” Additionally, definition of “fish” as specified in Fish and Game Code sections 5937 and 5946 includes aquatic invertebrates, as well as vertebrate fishes. The same standard of “good condition” applies to invertebrates and includes the same standard of ecological health that applies to fish species.

It was suggested by the Mammoth Creek Technical Team during August 2005 that reduced flows in Mammoth Creek resulting from existing bypass flow requirements have reduced water quality and increased substrate consolidation (cementing of gravels and cobbles) and embeddedness (accumulation of fine sediments between gravels and cobbles), thereby reducing habitat availability for benthic macroinvertebrates (BMI) in Mammoth and Hot creeks. Additionally, it was suggested by the Mammoth Creek Technical Team during August 2006 that streambed cleansing (via scouring flows) may result in additional substrate interstitial space availability for colonization of BMIs. Reduced habitat availability could result in BMI communities not remaining in “good condition.”

Available information on BMI communities in Mammoth and Hot Creeks was examined to identify potential trends in BMI community metrics in Mammoth Creek and potential differences BMI communities between Mammoth and Hot creeks. BMI information was obtained from the Draft Mammoth Creek EIR (MCWD and USFS 2000), the Hot Creek Hatchery Stressor Identification reports (Jellison et al. 2005a, 2005b, 2007), and the 2004 Hot Creek Biomonitoring Report published by the California Department of Fish and Game (Harrington 2005). Information from the Draft Mammoth Creek EIR included BMI sampling data obtained during 1992 through 1994 that was analyzed and reported in *Aquatic Benthic Macroinvertebrate Monitoring Report* (Vinson 1995). However, original data and analyses provided in Vinson (1995) were not available for use in this evaluation. Information obtained from the Hot Creek Hatchery Stressor Identification reports included a description of a 1993 bioassessment report conducted for the Hot Creek Hatchery and data obtained during 2000 through 2004 BMI monitoring. The CDFG report (Harrington 2005) included additional information regarding the 2004 data described in the Hot Creek Hatchery Stressor Identification reports. The Hot Creek Hatchery Stressor Identification Final Report (Jellison et al. 2007) included a re-analysis of BMI data across all years employing comparable data sets collected from 2000-2006.

2.0 METHODS

2.1 1992 THROUGH 1994 METHODS – MAMMOTH CREEK

According to MCWD and USFS (2000) BMIs were collected from each fish population sample site in Mammoth Creek coincident with the fish population sampling conducted during 1992 through 1994. **Figure A-1** shows the location of fish population and BMI sampling sites during 1992 through 1994. BMI samples were subsequently analyzed using the U.S. Environmental Protection Agency (EPA) Rapid Bioassessment Protocols (Vinson 1995 *in* MCWD and USFS 2000).

Several measures of community health were calculated for these three years of data, including measures of richness and diversity. Richness is described by the abundance (numbers) of invertebrates as well as the number of taxa (e.g., species or families). Diversity is a measure of community structure defined by the relationship between the number of distinct taxa and their relative abundance. The indices used to describe and compare the BMI communities during 1992 through 1994 include three measures of richness including: (1) taxa richness; (2) ephemeroptera, plecoptera, and trichoptera (EPT) taxa richness; and (3) family richness (MCWD and USFS 2000).

Taxa richness refers to the number of individual taxa, and normally decreases with decreased water quality. Generally, rapid bioassessment protocols utilize genus as the lowest taxonomic level to which individual organisms are identified. However, the taxonomic level utilized by Vinson (1995) was not confirmed for this report. EPT taxa richness refers to the taxa richness within the insect orders ephemeroptera (mayflies), plecoptera (stoneflies), and trichoptera (caddisflies). These orders are considered to be sensitive to water quality, and EPT richness generally decreases with decreasing water quality. Family richness refers to the number of families, which typically decreases with decreasing water quality. In general, low richness (total taxa, EPT taxa, and family) is indicative of degraded water quality affecting the invertebrate community (MCWD and USFS 2000).

Other standard measures of diversity calculated for the Mammoth Creek samples include Shannon's H, Simpson's D, and evenness. Shannon's H is widely used in community ecology and is a measure of the average degree of uncertainty in predicting a taxon to which an individual chosen at random will belong. This uncertainty increases as the number of taxa increases and the distribution of taxa becomes more even (the community diversity increases). Simpson's D is defined as the probability of picking two individuals that are of the same group, usually reported as (1-D), such that the index increases with diversity. Evenness is a measure of the distribution of individuals among taxa. Values range from 0-1 and approach zero as a single taxon becomes dominant.

2.2 1993 METHODS – HOT CREEK

The 1993 bioassessment survey (Harrington 1993) was conducted as part of a larger study, which included an assessment of the effectiveness of the Hot Creek Hatchery settling ponds, the impact of untreated discharges from the brood ponds at the Hot Creek Hatchery (Hatchery II), and toxicity tests. A full description of the survey and analysis of the data were not included in either of the available Hot Creek Hatchery Stressor Identification reports (Jellison et al. 2005a, 2005b). Specifically, Jellison et al. (2005a) stated... *"The 1993 bioassessment should be considered*

preliminary due to the limited design and small number of individuals counted.” However, Jellison et al. (2005a) indicated that the 1993 report provided some notable conclusions, and therefore is discussed briefly in this report.

2.3 2000 THROUGH 2004 METHODS

During 2000 through 2004 BMI monitoring in Hot Creek was conducted as required by the Lahontan Regional Water Quality Control Board (LRWQCB) as a condition of CDFG’s Hot Creek Hatchery National Pollution Discharge Elimination System (NPDES) permit. Based on the monitoring reports produced after the 2000 through 2004 monitoring efforts, LRWQCB determined that the receiving waters from the Hot Creek Hatchery were impaired and ordered CDFG to determine the cause of impairment. CDFG subsequently entered into an interagency agreement with the University of California to determine the causes of impairment by assembling a team including CDFG biologists, UC scientists, and consultants with combined expertise in limnology, aquatic bioassessment, geomorphology and aquatic toxicology to conduct the stressor identification (SI) employing EPA guidelines (US EPA 2000). The first and second of four stressor identification reports (Jellison et al. 2005a, 2005b), which reviewed bioassessment monitoring data, other relevant reports, and available scientific literature, were reviewed to identify potential temporal and spatial trends in BMI communities, and potential differences among sites in Mammoth and Hot creeks.

During 2000, the bioassessment survey methods were modified from the 1993 survey by adding an additional Hot Creek monitoring site immediately upstream of the Hatchery II discharge and increasing the number of organisms identified to the lowest practical taxonomic level (typically genus) from each sample to 300 individual organisms. During 1993, identification of 100 organisms was considered representative of each sample. The macroinvertebrate sampling also was conducted later in the year (26 August 2000) compared to the 1993 sampling (Jellison et al. 2005a).

During 2001, two bioassessment monitoring sites were added on the springbrooks immediately below the two major hatchery source springs, AB and CD springs. Additionally, Big Springs was sampled to determine whether it could be used as a reference site. Sampling was conducted during late August (August 28-29, 2001) (Jellison et al. 2005a).

During 2002 (Harrington 2003), the same six monitoring sites sampled during 2001 were sampled on 10 September 2002. Additionally, physical/habitat dimensions, substrate composition and water column measurements (temperature, D.O., conductivity, and pH) were determined at each monitoring site (Jellison et al. 2005a).

For the 2003 annual report (Harrington 2004), CDFG was directed to summarize the bioassessment data from 2000-2003. A detailed description of variation across stations and years for each of the eleven metrics employed is included in the report (Jellison et al. 2005a).

Ten sites (**Table A-1**) were sampled on September 7 through 9, 2004 by CDFG staff from the Water Pollution Control Laboratory in Rancho Cordova (CDFG 2004).

Ongoing bioassessment surveys were conducted at the ten sites in Mammoth and Hot creeks, from 2000 through 2004. Two sites (HC-AB and HC-CD) are located in Hot Creek immediately above the hatchery on springbrooks fed by hatchery source springs, and two sites (HC-H3 and HC-H2) are located immediately below the hatchery. HC-H3 samples the benthic community

immediately below settling pond 1, while HC-H2 samples Hot Creek below the combined discharges of all three settling ponds (i.e. ponds 1 and 2, and McBurney pond). Three sites (MC-H1, MC-H2, and MC-H4) are located on Mammoth Creek upstream of the confluence with Hot Creek and three sites (HC-UH7, HC-H7, and HC-H8) are located on Hot Creek below the confluence with Mammoth Creek (Jellison et al. 2005a). The Mammoth Creek BMI sampling sites were used as reference samples for comparisons to the Hot Creek sampling sites below the confluence of the two creeks to control for the hydrological influence of the seasonal Mammoth Creek flows and associated sediment loading. Additionally, comparison of Mammoth Creek BMI data to data obtained from the sites below the hatchery and below the confluence with Mammoth Creek allow inferences to be drawn about the influence of the hatchery on Hot Creek BMI communities, relative to the influence of Mammoth Creek inflow on Hot Creek communities. **Figure A-2** shows the locations of the 10 BMI sampling sites utilized during 2000 through 2004. **Table A-2** shows the locations and years during which each location was sampled from 2000 through 2004.

2.3.1 CLUSTER ANALYSIS

Cluster analysis permits an evaluation of community similarity in the taxonomic composition and relative abundance between sites. A Bray-Curtis cluster analysis of BMI data collected during 2004 was presented by Jellison et al. (2005a) as a quantitative measure of the differences among sites based on the full data set.

Jellison et al. (2005a) performed two cluster analyses using the Bray-Curtis dissimilarity distance measure and Ward clustering algorithm. The first analysis examined the entire suite of 30 BMI samples (10 stations each with three replicates). The natural clustering of the replicate transects at each monitoring site provides a good measure of within versus across site variation. The second analysis was based on a composite (simple sum) sample of the three replicates at each site (Jellison et al. 2005a).

2.3.2 MULTI-METRIC ANALYSIS

In addition to the statistical examination of the individual metrics, Jellison et al. (2005a) also examined a simple multi-metric index, which considers the relative differences in each of the individual metrics for bioassessment data collected during 2004. The multi-metric index was calculated by equally weighting each of the 11 individual metrics employed in the bioassessment monitoring reports. Individual metric scores were scaled from the 0 to 10 based on the observed range in each metric (or 10-0 for the 5 metrics which decrease with increasing biotic integrity). The scaled scores of the individual metrics were then summed and multiplied by 10/11 to provide a range from 0 to 100 (Jellison et al. 2005a).

2.4 CALIFORNIA STREAM BIOASSESSMENT PROCEDURE METHODS

The California Stream Bioassessment Procedure (CSBP) developed by DFG (Harrington 1996) was used for BMI monitoring during 2000 through 2004. The CSBP is a regional adaptation of the U.S. EPA Rapid Bioassessment Protocols (utilized by Vinson 1995 for conducting the Mammoth Creek monitoring during 1992 through 1994) that has undergone multiple revisions since it was first introduced. However, Jellison et al. (2005a) indicated that an early version of the CSBP was used for all sampling events with differences in sampling protocols among years indicated in Sections 2.1 through 2.3, above. The Hot Creek Hatchery bioassessments

considered 11 metrics including richness (cumulative taxa richness, cumulative number of EPT taxa), composition (EPT index, sensitive EPT index, Shannon Diversity, percent Tubificida), tolerance (tolerance value, percentage of organisms in intolerant taxa, percentage of organisms in tolerant taxa, percent composition of the single most dominant taxon), and functional feeding group measures (percent of collector, gatherer, and filterer) (Jellison et al. 2005a).

Since the first sampling event conducted as part of the Hot Creek Hatchery BMI monitoring efforts during 1993, all sampling sites were chosen to have similar physical/habitat characteristics to the extent possible. The majority of the sampling sites would be characterized as “runs” with swift velocity, relatively deep, but wadeable channels and bottom substrates consisting of cobble, gravel, and fine sediment. Most of the monitoring locations had low level vegetation growing on the stream banks and no substantial canopy cover. Most monitoring reaches, especially in Hot Creek had vegetation growing on the benthos.

2.4.1 DETERMINING MONITORING REACH LENGTH

The length of each sampling reach was determined in the field based on the extent of similar channel characteristics present at each predetermined monitoring reach. Usually, similar depth and water velocity were the overriding factors determining reach length. After the reach length was determined it was quantified by extending a measuring tape along the edge of the bank. The measuring tape was left in place throughout the sampling event and used to determine the positions of three randomly located transects, along which biological and physical habitat sampling was conducted (CDFG 2004).

2.4.2 PHYSICAL/HABITAT AND AMBIENT CHEMICAL CHARACTERISTICS

Sampling reach width, depth, and water velocity were determined by averaging three measurements from each of the three randomly chosen transects. The geometric mean substrate particle size was determined by measuring 10 pieces of substrate along five randomly chosen transects. Transects were chosen randomly from all possible one meter intervals on the measuring tape used to determine reach length. Substrate composition was determined through visual observation of the entire monitoring reach. Ambient chemical characteristics were determined using a Yellow Springs Instruments (YSI) Model 85 and pH probe (CDFG 2004).

2.4.3 BIOLOGICAL SAMPLING

At all monitoring reaches, samples were collected along the three transects for which width, depth, and water velocity data were obtained. Along each transect three locations representing the left margin, right margin, and center of the transect were sampled within a 2 ft² area upstream of the sample location. Benthic organisms were collected at each sample location using a one-foot wide D-frame net with 0.5 mm mesh. The three collections obtained from each transect were combined into a single composited sample representing a 6 ft² area. Sampling of the benthos was performed manually by rubbing cobble and boulder substrates in front of the net followed by “kicking” the upper layers of substrate to dislodge any invertebrates remaining in the substrates. The duration of sampling ranged from 60 to 120 seconds, depending on the amount of boulder and cobble-sized substrates that required rubbing by hand. The composite sample was transferred into a 500 ml wide-mouth plastic jar containing approximately 200 ml of

95% ethanol. Samples were submitted to the Aquatic Bioassessment Laboratory (ABL) in Rancho Cordova along with a Chain of Custody form and stored in the ABL Sample Repository until processing (CDFG 2004).

2.4.4 LABORATORY METHODOLOGY

Samples were processed at the ABL in Rancho Cordova, California and at the ABL - Chico State University, Chico, California. Sample contents were rinsed through a 0.5 mm mesh sieve to remove excess ethanol during sorting. The sample contents were then evenly distributed on the bottom of a tray divided into 25 cm² grids. BMIs were separated from benthic material with the aid of a stereomicroscope from one randomly selected grid at a time and transferred to vials containing 70% ethanol and 5% glycerol. The process continued until 300 organisms were counted or until all organisms were removed from the tray if it contained fewer than 300 organisms. For subsequent quality control analysis, the material left from the processed grids was transferred into a jar with 70% ethanol and labeled as “remnant” (CDFG 2004).

All organisms were identified to the lowest practical taxonomic level using: Baumann et al. (1977); Brown (1972); Edmunds et al. (1976); Merritt and Cummins (1995); Pennak (1991); Stewart and Stark (1993); Surdick (1985); Thorp and Covich (1991); Usinger (1963); Weaver (1988); Wiederholm (1983, 1986); Wiggins (1996); and Wold (1974). Organisms in each taxon were saved in individual vials containing 70% ethanol and 5% glycerol and retained as a voucher collection (CDFG 2004).

Taxonomic lists, functional feeding group composition, and the bioassessment metrics (**Table A-3**) were generated for each of the samples using an application developed in Microsoft Excel™ (CDFG 2004).

2.5 2005 AND 2006 METHODS

BMI data are highly spatially and temporally variable. Rather than reviewing and compiling the findings of each of the years individually, Jellison et al. (2007) conducted a re-analysis of BMI data across all years employing comparable data sets collected from 2000-2006. They considered eleven commonly used metrics of biotic integrity including measures of richness, community composition, tolerance, and functional feeding groups.

Jellison et al. (2007) included additional benthic monitoring sites in both 2005 and 2006, the characterization of sediment size composition and organic content across all sampling sites, a quantitative assessment of macrophyte biomass, the collection of two longitudinal time-series of water quality data during cleaning operations, and broodstock tissue analysis. They calculated the 12-metric IBI values for the 2005 and 2006 bioassessment data based on methods and reference sites provided in Herbst and Silldorff (2004). The index can only be calculated for 2005 and 2006 data because it employs higher taxonomic resolution of midge taxa than employed in earlier bioassessments. They calculated the metric for each individual transect so that a measure of site variability (e.g. standard error) also could be calculated, which differed from the methodology employed in Herbst and Silldorff (2004). Consequently, the Hot Creek Hatchery calculations are not directly comparable to Herbst and Silldorff (2004).

BMI metrics were compared across three site-specific reference-test sets of site: (1) reference springbrooks immediately above the hatchery (AB & CD) against stream reaches immediately

below hatchery discharges (H2 & H3); (2) reference sites on Mammoth Creek above the confluence of Hot Creek (MC1, MC2, MC4) against Hot Creek sites below the confluence (UH7 and H7); and (3) a reference site above (H7) against a test site below (H8) inflows from the Hatchery II spring complex (Jellison et al. 2007).

3.0 RESULTS

3.1 1992 THROUGH 1994 RESULTS – MAMMOTH CREEK

Data obtained from sampling conducted during 1992 through 1994 were first presented in MCWD and USFS (2000) and are presented in **Figure A-3**. Total abundance of BMIs was generally higher in the downstream reaches (i.e., reaches D and E). Mayflies (ephemeroptera) and caddisflies (trichoptera) were relatively abundant in all stream reaches. The relative proportion of midges (dipterans) and caddisflies was higher in the downstream reaches. The relative abundance of stoneflies (plecoptera) was lower than that of other species and tended to decrease towards the downstream reaches (MCWD and USFS 2000).

The results from Mammoth Creek reported in MCWD and USFS (2000) show the same pattern for the richness indices (taxa richness, EPT richness, and family richness), with the 1992 and 1994 indices nearly identical and 1993 slightly lower. For example, the values for EPT richness are 13, 11, and 12 for 1992, 1993, and 1994, respectively, indicating that the number of taxa within these sensitive groups remained constant during those three years. The values of all three measures of richness were reported as typical of mountain streams in the Sierra Nevada and are considered indicative of moderate to good conditions (MCWD and USFS 2000).

Results for all diversity indices calculated using data obtained during 1992 through 1994 including Shannon's H, Simpson's D, and evenness reportedly showed a slight increase in BMI diversity in Mammoth Creek from 1992 to 1994 (MCWD and USFS 2000).

3.2 1993 RESULTS – HOT CREEK

The report describing the 1993 bioassessment survey conducted for the Hot Creek Hatchery monitoring program concluded, "*The biotic condition of Hot Creek below the effluent discharge from Hot Creek Hatchery is severely impaired and the degree of organic pollution improves downstream from the source of the hatchery effluent*" (Jellison et al. 2005a).

Jellison et al. (2005a) indicated that the 1993 bioassessment survey conducted for the Hot Creek Hatchery monitoring program should be considered preliminary due to the limited study design and small number of individuals counted. However, Jellison et al. (2005a) also noted that the following observations warranted mention:

- ❑ The samples were collected during early summer (14 June 1993) during a relatively wet (114 % of 1933-1996 average) year, a period in which significant flushing flows would have occurred immediately prior to sampling at three of the four survey sites.
- ❑ The degraded condition of Hot Creek, relative to Mammoth Creek, extended far downstream of the hatchery to lower Hot Creek Ranch where the monitoring site

was chosen to represent “best” conditions. This was true for all 6 metrics analyzed.

- ❑ There was little change in any of the metrics between the monitoring sites immediately below Hatchery II and downstream on Hot Creek Ranch.
- ❑ The IAI index (ratio of the numbers of EPT to chironomids and annelids) showed the most marked changes across the four monitoring sites (Jellison et al. 2005a).

3.3 2000 THROUGH 2004 RESULTS

During the Hot Creek Hatchery stressor identification process, several analyses were conducted on data collected during 2000 through 2004. Results of the review of annual BMI monitoring reports, enumeration and calculation of selected biometrics, and the results of analysis of taxon-specific differences among years are presented below.

3.3.1 REVIEW OF 2000-2004 HOT CREEK HATCHERY BIOASSESSMENT REPORTS

3.3.1.1 2000 MONITORING REPORT

During 2000, 18 different metrics were evaluated instead of the six metrics evaluated during 1993. Jellison et al. (2005a) reported that few differences among stations were statistically significant ($\alpha = 0.05$). However, most metrics suggested the Hot Creek monitoring stations were degraded compared to the Mammoth Creek station (during 2000 only one Mammoth Creek site was sampled). The EPT metrics (EPT taxa, EPT Index, Sensitive EPT Index) were the exceptions with higher values often observed below the hatchery (Jellison et al. 2005a). Jellison et al. (2005a) also noted that the 2000 annual monitoring report (Harrington 2001) concluded that:

- ❑ There is organic enrichment downstream of the Hot Creek Hatchery and the problem is evident throughout the sampled reach.
- ❑ Some metrics including percent collector-filterers and percent tubificidae were stronger indicators than others of organic richness in the sites below the hatchery. Toxic contamination was an unlikely cause of the increased richness because richness and composition metrics yielded mixed results and there were more sensitive organisms in Hot Creek, relative to Mammoth Creek.
- ❑ Mammoth Creek is not a suitable control site to judge Hot Creek conditions (Jellison et al. 2005a).

3.3.1.2 2001 MONITORING REPORT

Jellison et al. (2005a) noted that the 2001 report (Harrington 2002) concluded that:

- ❑ The percent tubificidae and percent collector-filterer metrics at springbrook monitoring sites (HC-AB and HC-CD) were high, and using them as controls indicates the hatchery has a smaller impact on Hot Creek than previously indicated.

- ❑ The benthic community at Big Springs differed significantly from that at Mammoth Creek or the Hot Creek springbrooks and thus cannot provide an appropriate control.
- ❑ Most of the biological metric values showed minor increases or decreases between the 2000 and 2001 sampling events. However, there are still obvious signals showing an influence of organic enrichment downstream of the Hatchery.
- ❑ The relatively high sensitive EPT index values observed for Hot Creek samples below the hatchery during 2000 may have been anomalous and were lower for 2001 samples.
- ❑ Statistical comparisons of metrics across sites were not performed because the assumptions of the experimental design could not be adequately met in an uncontrolled natural setting such as Hot Creek (Jellison et al. 2005a).

3.3.1.3 2002 MONITORING REPORT

Jellison et al. (2005a) indicated that, generally, the variation in the suite of metrics analyzed during 2002 was similar to the variation observed during previous years with the exception of the metric percent tubificida. Additionally, Jellison et al. (2005a) noted:

- ❑ Percent tubificida declined markedly at Hot Creek monitoring sites below the hatchery, relative to 2001.
- ❑ Percent collector-filterers also declined at these sites, although less markedly.
- ❑ The report concludes that the decreases in percent tubificida and percent collector-filterers indicated a decrease in the influence of organic enrichment downstream of the hatchery (Jellison et al. 2005a).

3.3.1.4 2003 MONITORING REPORT

For the 2003 annual report (Harrington 2004), DFG summarized the bioassessment data from 2000 through 2003. A detailed description of variation across stations and years for each of the eleven metrics employed was included in the report. Jellison et al. (2005a) noted:

- ❑ Generally, the biological metrics indicated Mammoth Creek was in better condition than Hot Creek sites.
- ❑ The Mammoth Creek site contained pool/riffle sequences typical of a higher gradient channel and had coarse substrate compared to Hot Creek sites which contained run habitat and fine substrates.
- ❑ Using AB and CD springbrook sites as reference sites led to 7 of 11 biological metrics indicating more degraded conditions immediately below the hatchery and only 5 of 11 metrics indicating more degraded conditions at the furthest downstream sites (H7 and H8) with the remaining 6 indicating improvement (Jellison et al. 2005a).

3.3.1.5 2004 MONITORING REPORT

Jellison et al. (2005a) indicated that the 2004 data (Harrington 2005) generally were similar to those collected during 2000 through 2003 and CDFG concluded:

- For the 11 biological metrics used to indicate responses to impairment, only 2 met the expectation for the above and below hatchery comparison using the AB and CD spring supply channels for a control and only 4 met this expectation for the Mammoth Creek and Hot Creek comparison. However, as in years past, the number of tubificid worms increased downstream of the hatchery discharge.

3.3.2 PHYSICAL HABITAT CHARACTERISTICS

Physical habitat characteristics were recorded during all sampling events during all years. However, no analysis was conducted on physical habitat data within or among years, in part because physical habitat was reported as similar among years (Jellison et al. 2005) and physical habitat data obtained prior to the 2004 sampling event are not readily available. Therefore, physical habitat data are not presented in this report. However, the 2004 physical habitat data are available in Jellison et al. (2005a) and Harrington (2005).

3.3.3 SUMMARY OF BENTHIC MACROINVERTEBRATE METRICS FROM 2000 THROUGH 2004

BMI sampling sites were not consistent among all years because sites were added as deemed necessary and appropriate during the monitoring program. Table A-2 shows the locations and years during which each location was sampled from 2000 through 2004.

Cumulative taxonomic richness values varied from 16 to 45 across all sites and years and was lower at the springbrook sites upstream of the Hot Creek Hatchery (HC-AB and HC-CD) and immediately below the hatchery (HC-H2 and HC-H3), compared to Mammoth Creek and Hot Creek sites below the confluence with Mammoth Creek (**Figure A-4**). The year-to-year variation in this metric was highest at the Mammoth Creek sites and ranged from 27 to 44 at MC-H4. The 4-year mean value, 20, at the shallower springbrook site (HC-CD) was significantly less (t-test, $p < 0.02$) than the 4-year mean value at the deeper springbrook site (HC-AB) but neither was significantly different from the Mammoth Creek site (MC-H4) due to the high inter-year variation observed at that Mammoth Creek site. The taxonomic richness of HC-H3 was significantly less than HC-AB but not HC-CD. The 5-year mean taxonomic richness decreased from 36 at MC-H4 to 32.2 at HC-H7 and 30.8 at HC-H8 but this decrease was not statistically significant ($p > 0.05$) (Jellison et al. 2005a).

The cumulative EPT taxonomic richness metric shows similar patterns among stations except that Hot Creek monitoring sites below the confluence with Mammoth Creek are intermediate between those of Mammoth Creek and the springbrook monitoring stations (**Figure A-5**). The comparisons between Mammoth Creek sampling sites and Hot Creek sampling sites below the confluence with Mammoth Creek were statistically significant (Jellison et al. 2005a). The Mammoth Creek sites generally were richer than the springbrook or other Hot Creek sites.

The EPT Index is the percentage of organisms in ephemeroptera, plecoptera, or trichoptera taxa (**Figure A-6**). As with most measures of relative abundance, this index varied more among years than the richness metrics and is thus less well-suited to detect differences among stations.

The EPT Index is expected to decrease due to impairment. Indices at the Hot Creek stations below the confluence with Mammoth Creek were generally higher (overall mean, 17.6 %) than the indices at the Mammoth Creek stations (mean 9.9 %) (Jellison et al. 2005a).

The sensitive EPT index is the percentage of organisms that are in the ephemeroptera, plecoptera, or trichoptera orders that are considered sensitive to impairment (i.e., tolerance values less than 3). The sensitive EPT index is expected to decrease in response to impairment. As with the EPT Index, the sensitive EPT Index was highly variable (within stations among years, and among stations) (**Figure A-7**). This metric was significantly lower at the Mammoth Creek monitoring stations than all the other stations. However, there was no significant difference among the other stations (Jellison et al. 2005a).

The Shannon Diversity index, a general measure of sample diversity, is expected to decrease in response to impairment. Shannon Diversity ranged from 1.1 to 2.6 among all stations and all years (**Figure A-8**). Values were low at the HC-CD monitoring site for three of the four years, but a high value at this site during 2001 made differences between this site and others statistically insignificant ($p > 0.05$). The Shannon Diversity at the settling pond outflow site (HC-H3) was significantly less than the Shannon Diversity at the AB springbrook (HC-AB), Mammoth Creek (MC-H4) and lower Hot Creek (HC-H7, HC-H8) sites (Jellison et al. 2005a).

The percent of organisms in the family tubificidae is expected to increase in response to impairment, and specifically organic enrichment, and varied from 1 percent to 57 percent among sites and years (**Figure A-9**). This metric was lowest at Mammoth Creek monitoring sites, intermediate at the hatchery springbrook sites, and high at all Hot Creek sites below the hatchery, including below the confluence with Mammoth Creek. This metric at the Mammoth Creek monitoring site (MC-H4) was significantly lower ($p < 0.05$) than the percent tubificidae at all Hot Creek sites except the CD springbrook site (HC-CD) (Jellison et al. 2005a).

The mean tolerance value is a calculated value between 0 and 10, weighted for the abundance of individuals designated as pollution tolerant (higher values) or intolerant (lower values). The mean tolerance value among sites and years ranged from 5.2 to 8 among Hot Creek stations with a mean of 6.5, which indicates a benthic community dominated by organisms with a relatively high tolerance (**Figure A-10**). While there were no significant differences in values among Hot Creek stations, the values at the Mammoth Creek monitoring stations were lower than the values at all the other stations, with a 5-year mean of 5.1 at station MC-H4 (Jellison et al. 2005a).

The multi-year mean percent intolerant organisms ranged from 1.25 percent at the CD springbrook site to 4.25 percent at the AB springbrook site, with values on Mammoth Creek and Hot Creek below the confluence with Mammoth Creek intermediate to these values (**Figure A-11**). Intolerant taxa were completely absent at Hot Creek sites immediately below the settling ponds (HC-H3) and hatchery discharge (HC-H2) (Jellison et al. 2005a).

The multi-year mean percentage of organisms in tolerant taxa (Tolerance Value [TV] 8 to 10) was highly variable (**Figure A-12**). The percentage of tolerant taxa at Mammoth Creek (MC-H4) was lower than the percentage of tolerant taxa all other Hot Creek sites (Jellison et al. 2005a).

The multi-year mean value for the metric of the percentage of dominant taxa (i.e., percent composition of the single most dominant taxon) ranged from 19 percent to 27 percent for Hot Creek sites above the confluence with Mammoth Creek to 31 percent to 44 percent below the confluence (**Figure A-13**). The Mammoth Creek site (MC-H4) had a mean value of 36 percent.

Thus, while this metric increased from the springbrooks to the most downstream sites, the Mammoth Creek monitoring site had values similar to those below the confluence with Hot Creek (Jellison et al. 2005a).

Functional feeding group metrics differ in their responses to impairment. The percentage of organisms in the collector-gatherer group is expected to increase in response to impairment. The percentage (multi-year mean = 46.6 percent) of collector-gatherers at the Mammoth Creek monitoring site was lower than the percentage at all other Hot Creek monitoring sites (multi-year means ranged from 59 percent to 74 percent) except for the settling pond outflow (HC-H3), which had a similar percentage (mean = 51) (**Figure A-14**) (Jellison et al. 2005a).

3.3.4 ANALYSIS OF TAXON-SPECIFIC DIFFERENCES AMONG SITES

Bioassessment metrics are utilized to condense and summarize species changes occurring in complex benthic communities. In some cases a taxon-by-taxon analysis of observed changes may provide more useful or additional information. Jellison et al. (2005a) analyzed changes in abundance of individual taxa for all taxa that showed a “marked difference” between Mammoth Creek and Hot Creek sample sites, and which constituted a “significant proportion (>5%) of sampled individuals.” The results of the analysis conducted by Jellison et al. (2005a) are presented below.

3.3.4.1 COLEOPTERA

Riffle beetles feed on periphyton and reportedly are somewhat tolerant of fine sediment (Relyea et al. 2000). Both larvae and adults are found in streams and typically inhabit shallow, rocky, turbulent areas (riffles). Riffle beetles in the genus *Optioservus* (TV = 4), were abundant at all three Mammoth Creek sites, constituting 25 to 60 percent of the total abundance (**Figure A-15**, from Figure 17 in Jellison et al. (2005a)). They also were present, but were substantially less abundant at both springbrook sites (HC-AB and HC-CD). *Optioservus* was completely absent at Hot Creek sites immediately below the hatchery and only in low abundances at Hot Creek sites below the confluence with Mammoth Creek (Jellison et al. 2005a).

Riffle beetles in the genus *Zaitzevia* (TV = 4) were present in lower abundances than *Optioservus* at the Mammoth Creek sites but were completely absent from all Hot Creek sites including monitoring sites on the springbrooks (**Figure A-16**, from Figure 18 in Jellison et al. (2005a)).

3.3.4.2 DIPTERA

Black flies, *Simulium sp.* (TV = 6), were present in low (0 to 3%) relative abundance at all stations except Hot Creek below the confluence with Mammoth Creek (**Figure A-17**, from Figure 21 in Jellison et al. (2005a)). At HC-H7 their relative abundances ranged from 3 to 28 percent over the five years sampled (Jellison et al. 2005a).

3.3.4.3 EPHEMEROPTERA

The moderately sensitive mayfly, *Fallceon quilleri* (TV = 4), was present in low (1.5-4.5%) relative abundance at Mammoth Creek sites and Hot Creek sites below the confluence with Mammoth Creek but mostly absent from other Hot Creek sites (**Figure A-18**, from Figure 22 in Jellison et al. (2005a)).

3.3.4.4 TRICHOPTERA

Sensitive caddisflies in the genus *Brachycentrus* (TV = 1) were present in low relative abundance in Mammoth Creek and increased slightly in lower Hot Creek (**Figure A-19**, from Figure 23 in Jellison et al. (2005a)). They were not observed at any Hot Creek sites immediately above or below the hatchery. Individuals in the Hot Creek samples likely were *B. echo* (D. Herbst, pers. comm. in Jellison et al. 2005a), which display a greater tolerance to sediment and warm temperatures than its congeners *B. americanus* and *B. occidentalis* (Jellison et al. 2005a).

Micro-caddisflies in the genera *Ochrotrichia* (TV = 4) and *Oxyethira* (TV = 3) were mostly absent from Mammoth Creek (**Figures A-20** and **A-21**, from Figures 24 and 25 in Jellison et al. (2005a)). Relative abundance of *Ochrotrichia sp.* increased slightly below McBurney Pond and further at the lower Hot Creek sites. Relative abundance of *Oxyethira sp.* increased across the hatchery and remained relatively high at the downstream Hot Creek sites compared to Mammoth Creek (Jellison et al. 2005a).

3.3.4.5 PODOCOPIDA

Ostrocods in the family Cyprididae (TV = 8) were moderately abundant at the springbrook monitoring stations and immediately below the hatchery (**Figure A-22**, from Figure 28 in Jellison et al. (2005a)). Their relative abundance was substantially lower in Mammoth Creek and in Hot Creek below the confluence (Jellison et al. 2005a).

3.3.4.6 TUBIFICIDA

Worms in the Tubificidae family (TV = 10) were present in moderate (1 to 18 percent) but variable relative abundances at the springbrook monitoring sites, increased across the hatchery, and increased in Hot Creek downstream of the confluence with Mammoth Creek where they constituted between 18 and 57 percent of the total number of organisms (**Figure A-23**, from Figure 29 in Jellison et al. (2005a)). Tubificid worms were least abundant at the Mammoth Creek sites. These oligochaetes are classic indicators of organic enrichment and sediments in streams. Naididae (TV = 10) were less abundant (0 to 10 percent) and variable across the stations (**Figure A-25**, from Figure 30 in Jellison et al. (2005a)).

3.3.4.7 PLANARIDS

Planarid flatworms (Turbellaria: Planariidae, TV = 4) showed a similar increase immediately below the hatchery and moderately high relative abundance at the lower Hot Creek stations (**Figure A-25**, from Figure 31 in Jellison et al. (2005a)).

3.3.5 CLUSTER ANALYSIS OF 2004 BIOASSESSMENT DATA

Generalized metrics greatly simplify the information contained in BMI samples, but in so doing lose information. The taxon-specific analysis suggests there are significant differences among the monitoring sites that require additional analysis that are not fully captured in the analysis of metrics (Jellison et al. 2005a).

Cluster analysis permits an evaluation of community similarity in the taxonomic composition and relative abundance between sites. A Bray-Curtis cluster analysis of BMI data collected during 2004 was presented by Jellison et al. (2005a) as a quantitative measure of the differences among sites based on the full data set.

Jellison et al. (2005a) performed two cluster analyses using the Bray-Curtis dissimilarity distance measure and Ward clustering algorithm. The first analysis examined the entire suite of 30 BMI samples (10 stations each with three replicates). The natural clustering of the replicate transects at each monitoring site provides a good measure of within versus across site variation. The second analysis was based on a composite (simple sum) sample of the three replicates at each site (Jellison et al. 2005a).

The cluster analysis indicates that differences among sites are large, relative to within site variation because most replicate transects cluster closely together (**Figures A-26 and A-27**). The most notable exception is the 3rd transect from Hot Creek below McBurney Pond (HC-H2 Transect 3) which was much more similar to the Mammoth Creek samples than other Hot Creek samples. Samples from the most upstream Mammoth Creek monitoring site (MC-H1) cluster closely together and are most similar to the two other Mammoth Creek sites (MC-H2 and MC-H4). Samples from the two springbrook monitoring sites (HC-AB and HC-CD) are tightly clustered in two different groups. HC-CD springbrook clusters with the Mammoth Creek sites, while HC-AB springbrook is more similar to the other Hot Creek sites (Jellison et al. 2005a).

Cluster analysis on the composite samples reveals similar affinities. The most similar sites are the three Mammoth Creek monitoring sites (MC-H1, MC-H2, and MC-H4). The HC-CD springbrook site is more closely related to the Mammoth Creek samples than to the HC-AB springbrook site or other Hot Creek samples. The HC-AB springbrook site is most similar to the site immediately below the hatchery (HC-H3) although not as similar as the Mammoth Creek sites are to each other. Additionally, the HC-AB springbrook sites are not as similar to the HC-H3 sites as the downstream Hot Creek sites are to each other (HC-UH7, HC-H7, and HC-H8). The downstream Hot Creek sites (HC-H7 and HC-H8) are very similar and next most similar to the Hot Creek site immediately upstream (HC-UH7), followed by those below the Hatchery (HC-H2 and HC-H3) (Jellison et al. 2005a).

The only difference in clustering that arises from using the composite samples as opposed to the individual transects is that the two lowest Hot Creek samples (HC-H7 and HC-H8) are most closely clustered with the site immediately upstream (HC-UH7) rather than the Hot Creek site below the hatchery but immediately above the confluence with Mammoth Creek (HC-H2) (Jellison et al. 2005a).

3.3.6 MULTI-METRIC ANALYSIS ON 2004 BIOASSESSMENT DATA

In addition to differences in BMI communities identified by cluster analyses, there are also differences in individual metrics between Mammoth Creek sites and those on Hot Creek below the confluence with Mammoth Creek. An equal weighting of the 11 metrics would suggest that while biotic integrity is low in the springbrooks (HC-AB and HC-CD) and immediately downstream of the hatchery (HC-H2 and HC-H3), it does not change across either of the two comparisons (i.e. springbrooks versus immediately below the hatchery, and Mammoth Creek versus Hot Creek below the confluence).

Figure A-28, obtained from Jellison et al. (2005a) presents the multi-metric analysis to allow a summary comparison of all the various metrics across stations, but Jellison et al. (2005a) cautions the reader against attaching unwarranted significance to the overall score.

3.4 2007 SUMMARY OF RESULTS

Jellison et al. (2007) conducted a re-analysis of BMI data across all years employing comparable data sets collected from 2000-2006. They considered eleven commonly used metrics of biotic integrity including measures of richness, community composition, tolerance, and functional feeding groups. While they found that there were significant differences, especially in EPT metrics, between the data collected from 2000-2004 and two additional years of data collected in 2005 and 2006 following above average runoff years, the previous findings are largely confirmed.

Tubificid worms are often abundant in aquatic environments with heavy loads of organic detritus because they can tolerate low levels of dissolved oxygen and reproduce throughout the year (Jellison et al. 2007). Tubificidae constituted a relatively minor portion of the Mammoth Creek sites and increased markedly in downstream Hot Creek samples.

Riffle beetles (*Optioservus sp.* and *Zaitzevia sp.*), stoneflies (Perlodidae), and the sensitive caddisfly (*Lepidostoma sp.*) were observed in Mammoth Creek but not in Hot Creek.

The size composition and organic content of sediments also affects benthic community composition. Although the Mammoth-Hot Creek control/test sites were both dominated by gravel, there was a higher percentage of cobble at the Mammoth Creek sites and generally more fines at the Hot Creek sites. Thus, the D-50 of lower Hot Creek sites (7.5-14 mm) was smaller than that of the Mammoth Creek sites (15.5-27 mm).

Cumulative taxonomic richness was generally lower at the springbrook sites (AB and CD) and below the Hot Creek Hatchery compared to Mammoth Creek and the Hot Creek sites above the hatchery but below the confluence with Mammoth Creek. Biotic integrity, as implied by richness, below the confluence of Mammoth and Hot Creek was intermediate between Mammoth Creek and Hot Creek downstream of the hatchery but above the confluence of Mammoth and Hot creeks. Biotic integrity (i.e., richness) was higher in Mammoth Creek compared to the springbrooks above the hatchery, and biotic integrity was higher in the springbrooks than immediately below the hatchery.

The EPT Index is the percentage of organisms in Ephemeroptera, Plecoptera, or Trichoptera taxa. As with most measures of relative abundance, it varied more among years than the richness metrics and is less suited for detecting differences among sites. Only three of the seven trends were statistically significant. EPT Index was higher at Mammoth Creek compared to CD springbrook ($p < 0.05$) and probably AB springbrook ($p < 0.1$) (Jellison et al. 2007).

The Shannon Diversity index ranged from 1.1 to 2.8. Values were generally above 2 at springbrook AB, Mammoth Creek, and all Hot Creek sites below the confluence with Mammoth Creek.

The mean tolerance value, often termed biotic index, ranged from 5.2 to 8 among Hot Creek stations with a mean of 6.0 indicating a benthic community dominated by organisms with a relatively high tolerance (2.12). The biotic index at Mammoth Creek sites was lower ($p < 0.02$) than all sites on Hot Creek. The percent of the community that was tolerant organisms at Mammoth Creek sites was much lower with intermediate values below the confluence of the two creeks (Jellison et al. 2007).

The percent intolerant organisms ranged from near zero immediately below the hatchery to over 20 percent on Mammoth and Hot Creeks.

Jellison et al. (2007) state that the spatial variation in the BMI metrics and relative abundance of individual taxa clearly indicate that benthic communities supported by hatchery springbrook waters *above and below* the hatchery are very different from those of Mammoth Creek fed by snowmelt runoff. Despite high year-to-year variability in BMI metrics, six of eleven commonly used metrics indicate statistically significant lower biotic integrity at springbrooks *above* the hatchery compared to Mammoth Creek and none indicated higher biotic integrity. Furthermore, most measures of biotic integrity below the confluence of Mammoth and Hot Creek are intermediate to the two sets of reference conditions (Jellison et al. 2007).

Further increases in biotic integrity due to flows from Mammoth Creek are supported by 6 of 11 metrics. In summary, the overall pattern of higher biotic integrity in Mammoth Creek compared to the springbrooks, with intermediate values after the waters mix, is strongly supported (Jellison et al. 2007).

The higher index of biotic integrity at Mammoth Creek sites compared to the springbrook and hatchery sites is primarily due to higher scores for Intolerant Taxon Richness, Biotic Index, %EPT taxa, Ephemeroptera Taxa, EPT Taxa, and overall Taxa Richness. The differences between scores at Mammoth Creek and downstream Hot Creek sites are due to contributions from many of the metrics and these vary between the two years. However, Taxonomic Richness, EPT Taxa, Intolerant Taxa Richness, and Ephemeroptera Taxa are consistently higher at Mammoth Creek (Jellison et al. 2007).

Jellison et al. (2007) note that all of the sites in the study area, both site-specific reference conditions and treatment (or test) sites, have low IBI scores relative to reference streams in the Lahontan region with only the Mammoth Creek sites reaching 50 on a 0-100 scale. In Herbst and Silldorff (2004) the 12-metric IBI for 24 reference streams ranged from 57 to 100. However, Jellison et al. (2007) further note that this 12-metric IBI was developed to discriminate between impaired and reference streams in the Lahontan Region where impairment was due to land development and/or grazing, and that the strict applicability of this multi-metric IBI to the hatchery bioassessment data in which nutrient-rich source springs are a major stressor is unknown. Jellison et al. (2007) simply consider this 12-metric IBI as another way to summarize and visualize the Hot Creek bioassessment data.

4.0 DISCUSSION AND CONCLUSIONS

The previously described CDFG interpretation of maintaining “good condition” addresses the macroinvertebrate community, and the term “fish” as defined in California Fish and Game Code Section 45 includes both vertebrate and invertebrate aquatic life.

MCWD and USFS (2000) reported that the aquatic invertebrate sampling conducted from 1992 to 1994 suggests that the aquatic invertebrate community in Mammoth Creek is relatively healthy, being composed of a relatively large number of taxa (around 20), representing a number of different families (around 15), and with good representation of the more sensitive taxa within the EPT orders.

Subsequent BMI sampling conducted as a requirement of the Hot Creek Hatchery NPDES permit from 2000 through 2004 indicated that six of twelve metrics strongly support the

hypothesis that the Hot Creek Hatchery springbrook inflows have lower biotic integrity than Mammoth Creek (Jellison et al. 2005a).

Jellison et al. (2007) conducted a re-analysis of BMI data across all years employing comparable data sets collected from 2000-2006. Biotic integrity (i.e., richness) was higher in Mammoth Creek compared to the springbrooks above the hatchery. EPT Index was higher at Mammoth Creek compared to CD springbrook ($p < 0.05$) and probably AB springbrook ($p < 0.1$). The percent of the benthic macroinvertebrate community comprised of tolerant organisms was much lower in Mammoth Creek than in Hot Creek, including the headsprings. Six of eleven commonly used metrics indicate statistically significant lower biotic integrity at springbrooks *above* the hatchery compared to Mammoth Creek and none indicated higher biotic integrity.

For Mammoth Creek, available benthic macroinvertebrate data and information is focused on the lowermost sections of the creek. The lowermost section of Mammoth Creek exhibits higher benthic macroinvertebrate biotic integrity than in Hot Creek below the Hot Creek Hatchery, above the Hot Creek Hatchery and even in the headsprings area which serves as inflow to the hatchery.

Jellison *et al.* (2007) note that only the sites located in the lowermost section of Mammoth Creek exhibited IBI scores approaching those in reference streams in the Lahontan Region. However, Jellison *et al.* (2007) further note that this 12-metric IBI was developed to discriminate between impaired and reference streams where impairment was due to land development and/or grazing, and that the 12-metric IBI is simply another way to summarize and visualize the Hot Creek bioassessment data.

The lowermost section of Mammoth Creek would be most subject to the cumulative influences of contaminant inputs, nutrient loading, livestock grazing effects and associated sediment deposition, due to the low-gradient nature of this section of the creek. The lowermost section of Mammoth Creek would be expected to exhibit the lowest benthic macroinvertebrate biotic integrity of the entire creek. Therefore, it is reasonable to assume that the sections of Mammoth Creek located upstream of the lowermost section would exhibit higher indices of benthic macroinvertebrate biotic integrity, and that Mammoth Creek benthic macroinvertebrates are in good condition.

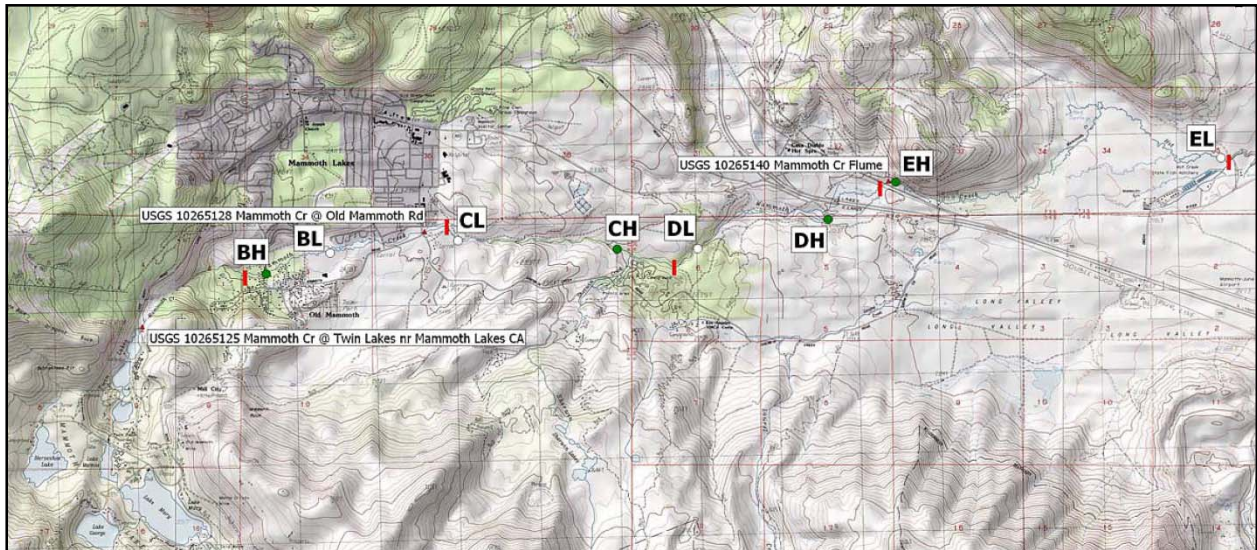


Figure A-1. BMI sample collection locations in Mammoth Creek during 1992 through 1994.

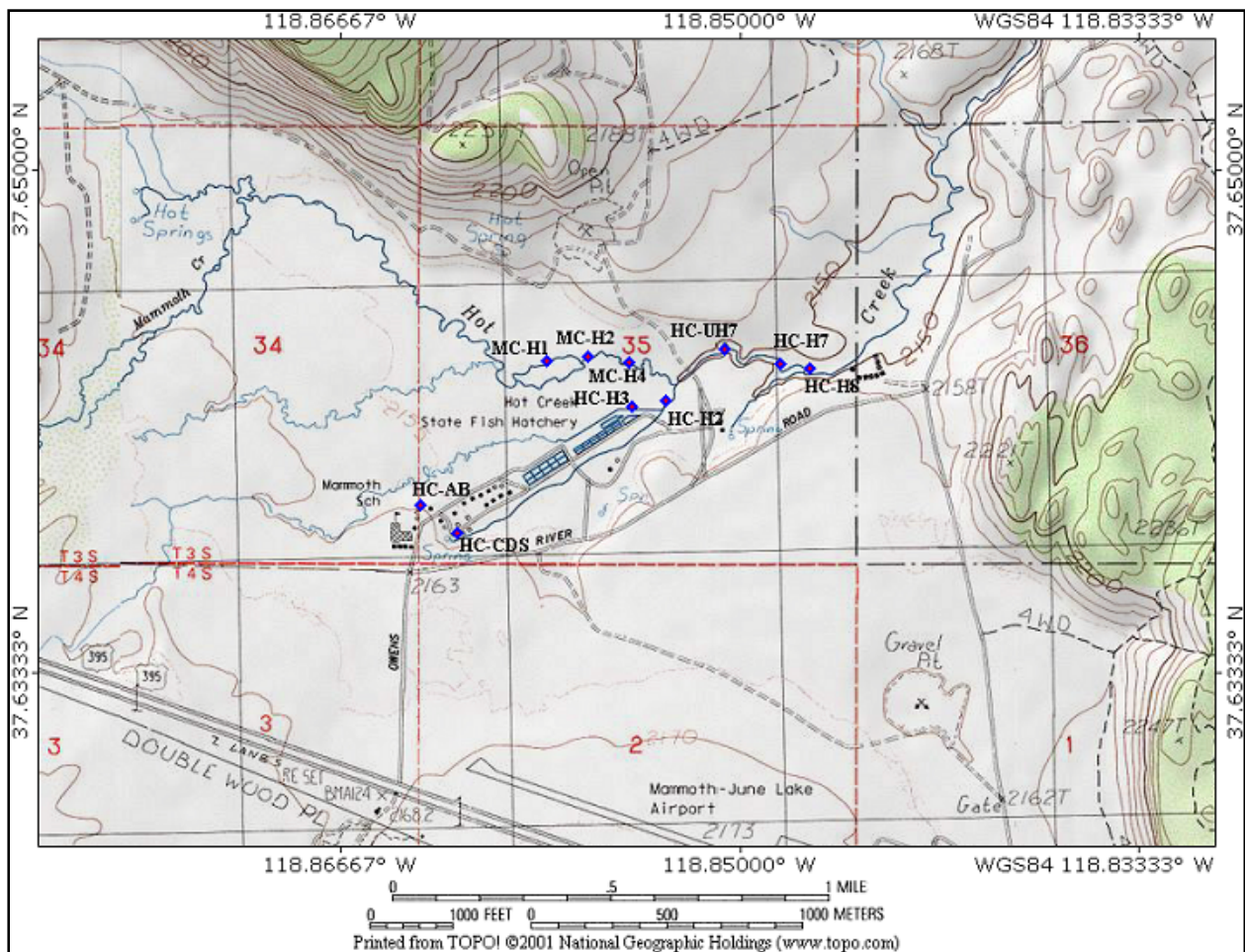


Figure A-2. BMI sample collection locations in Mammoth and Hot Creeks during 2000 through 2004 (from Jellison et al. 2005a).

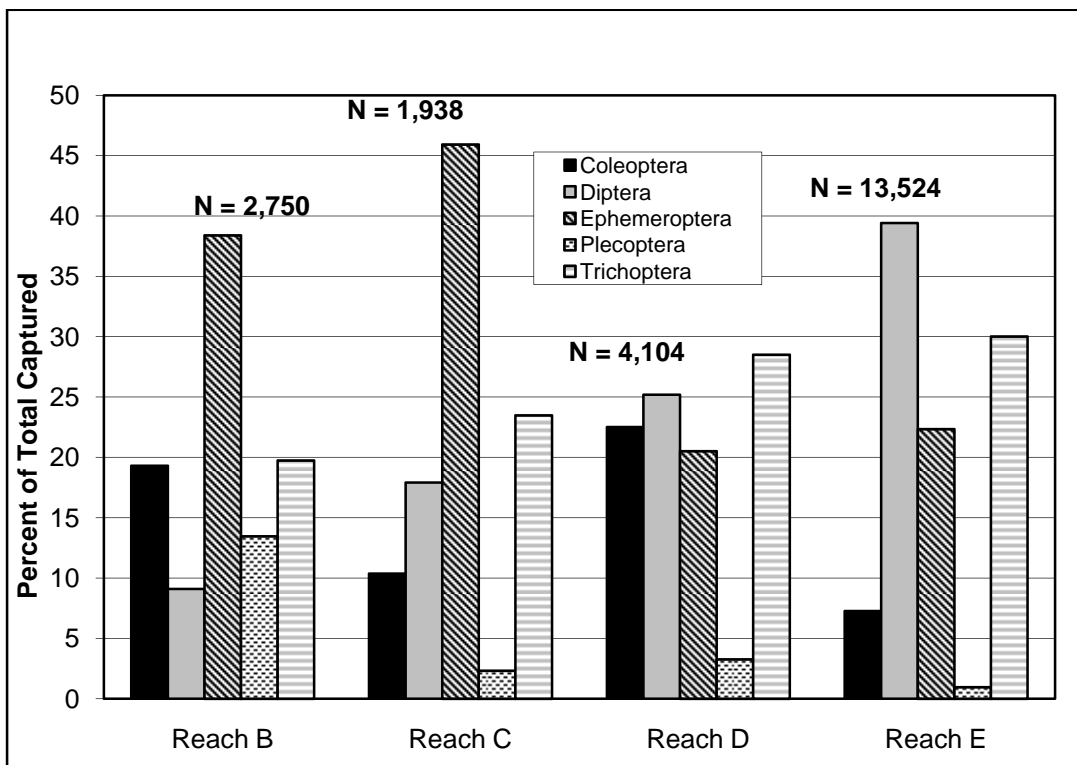


Figure A-3. Relative abundance of *Coleoptera* (beetles), *Diptera* (flies, gnats, midges, and mosquitoes), *Ephemeroptera* (mayflies), *Plecoptera* (stoneflies), and *Trichoptera* (caddisflies) in Reaches B through E of Mammoth Creek. Data are compiled from Vinson (1995) and represent the actual number of organisms collected (from MCWD and USFS 2000).

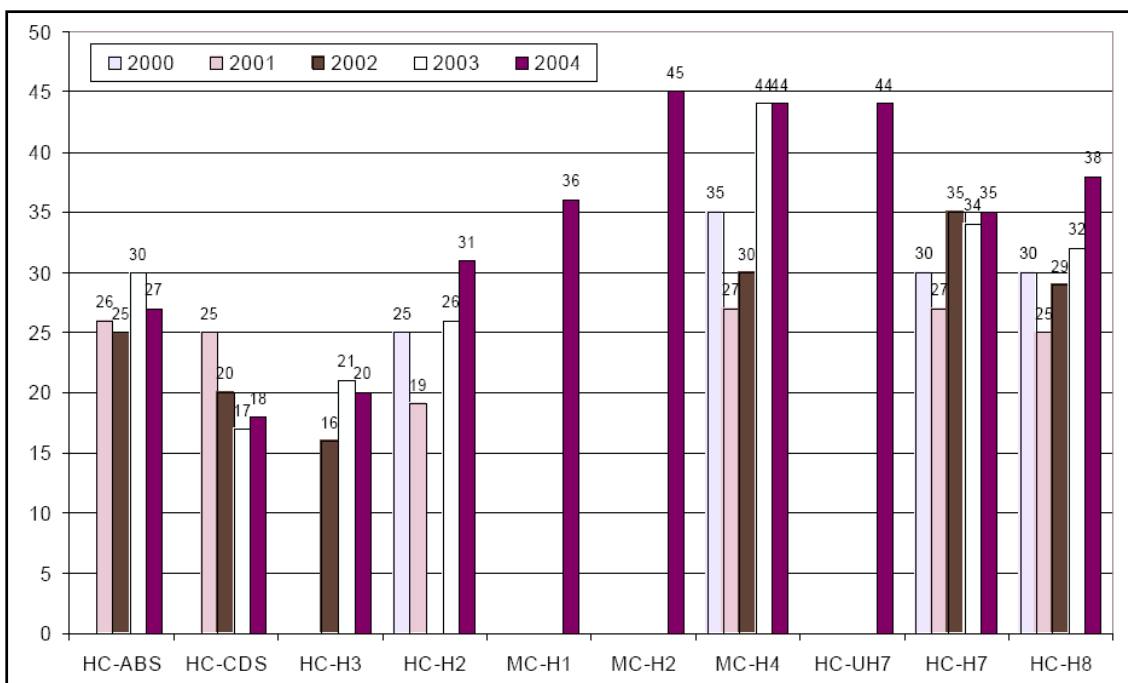


Figure A-4. Cumulative taxonomic richness in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

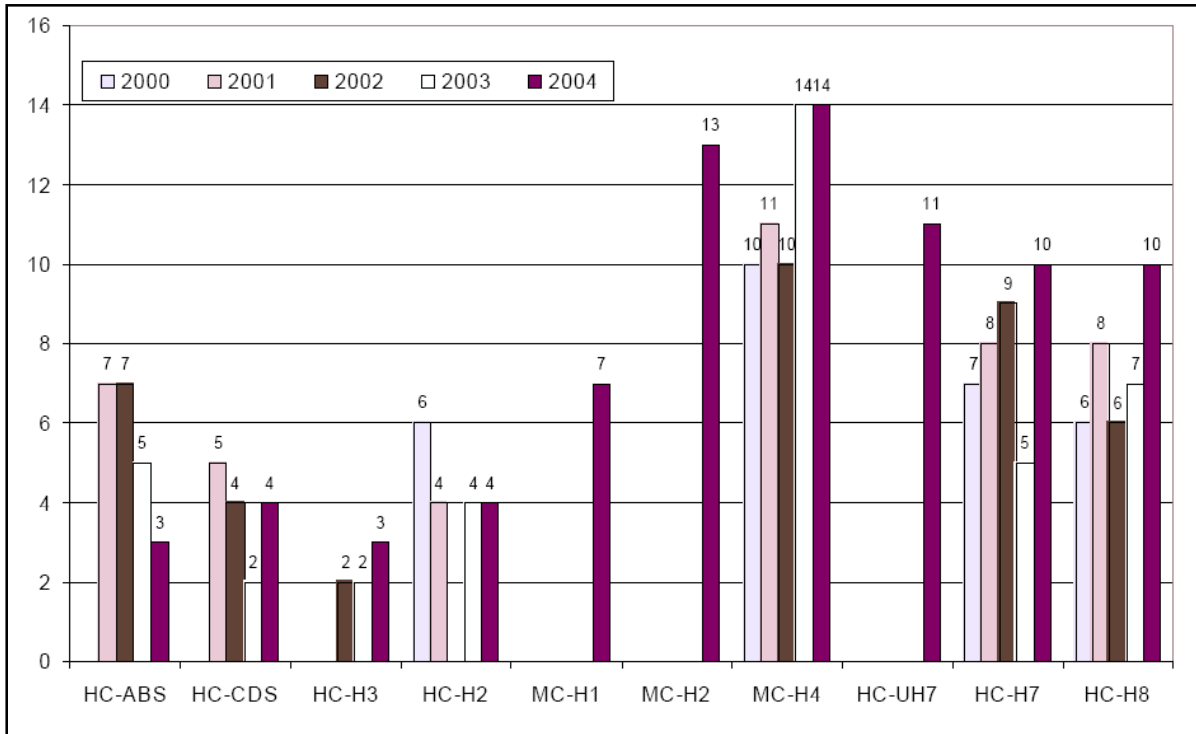


Figure A-5. Cumulative EPT taxonomic richness in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

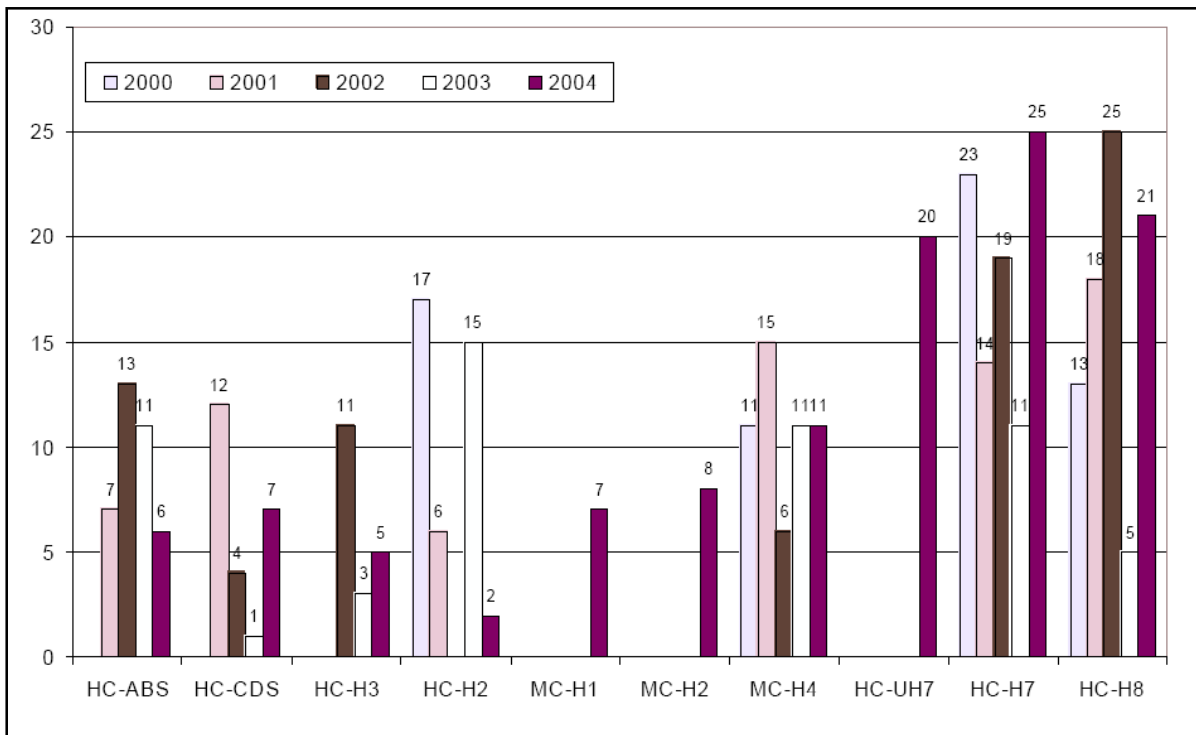


Figure A-6. EPT Index (percentage of EPT taxa) in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

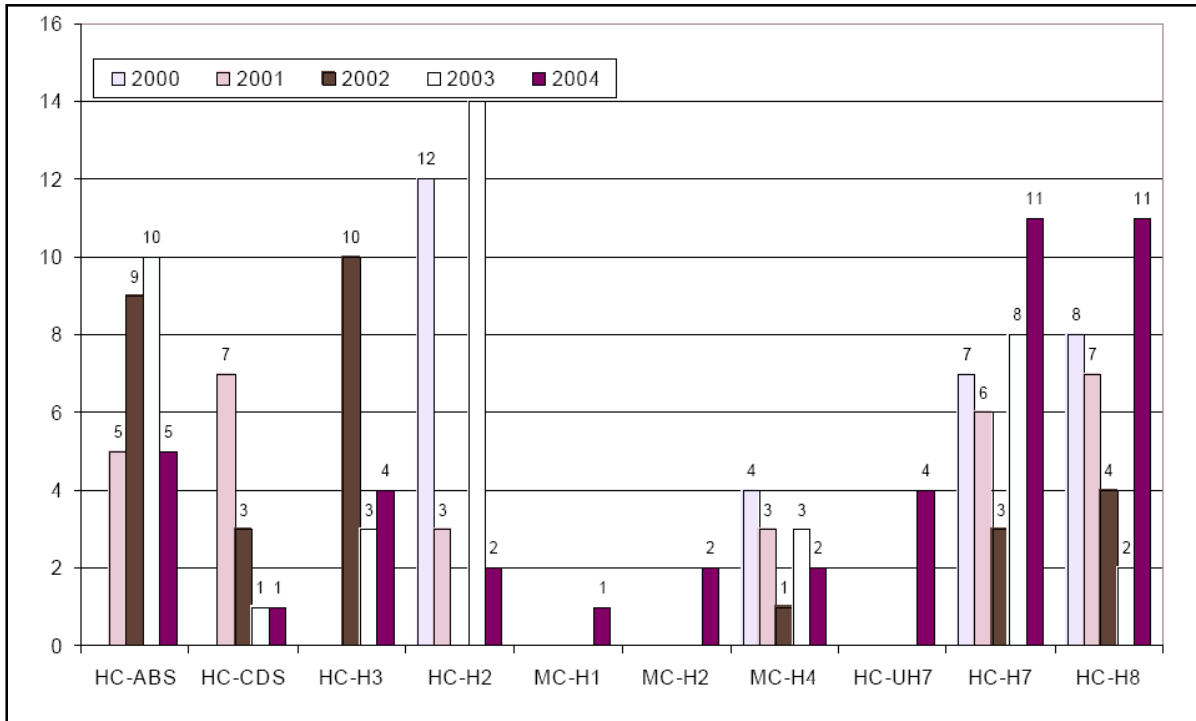


Figure A-7. Sensitive EPT index (percentage of sensitive EPT taxa) in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

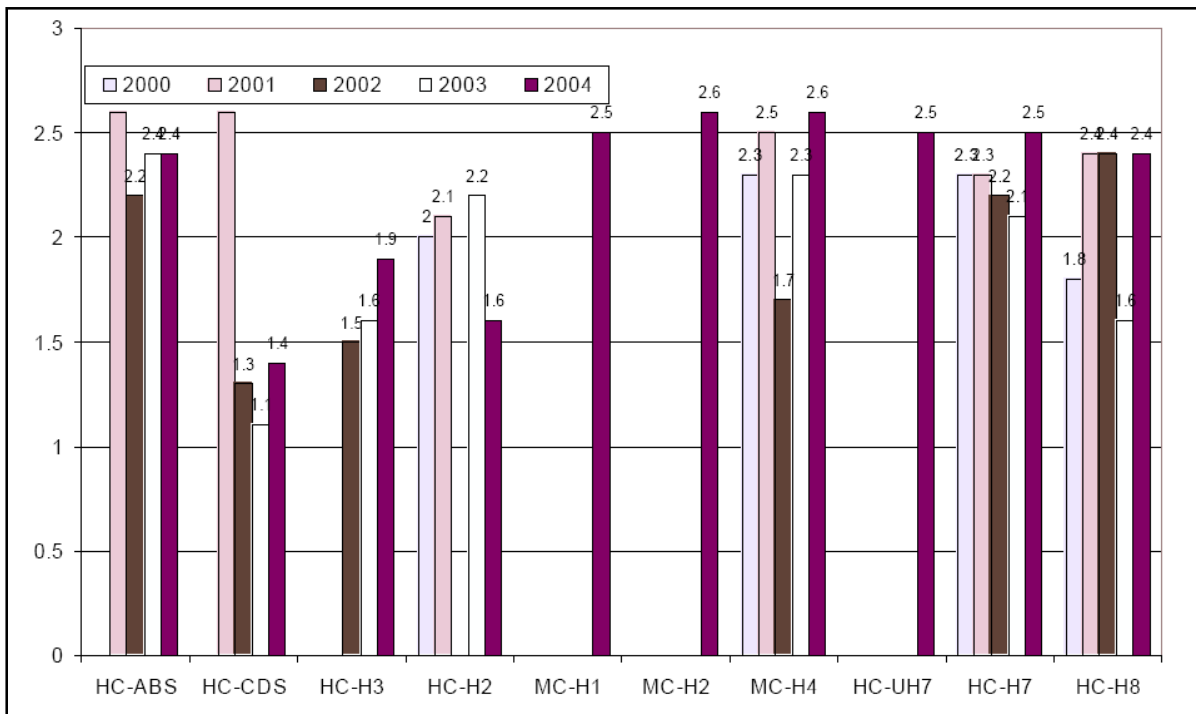


Figure A-8. Shannon diversity index values in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

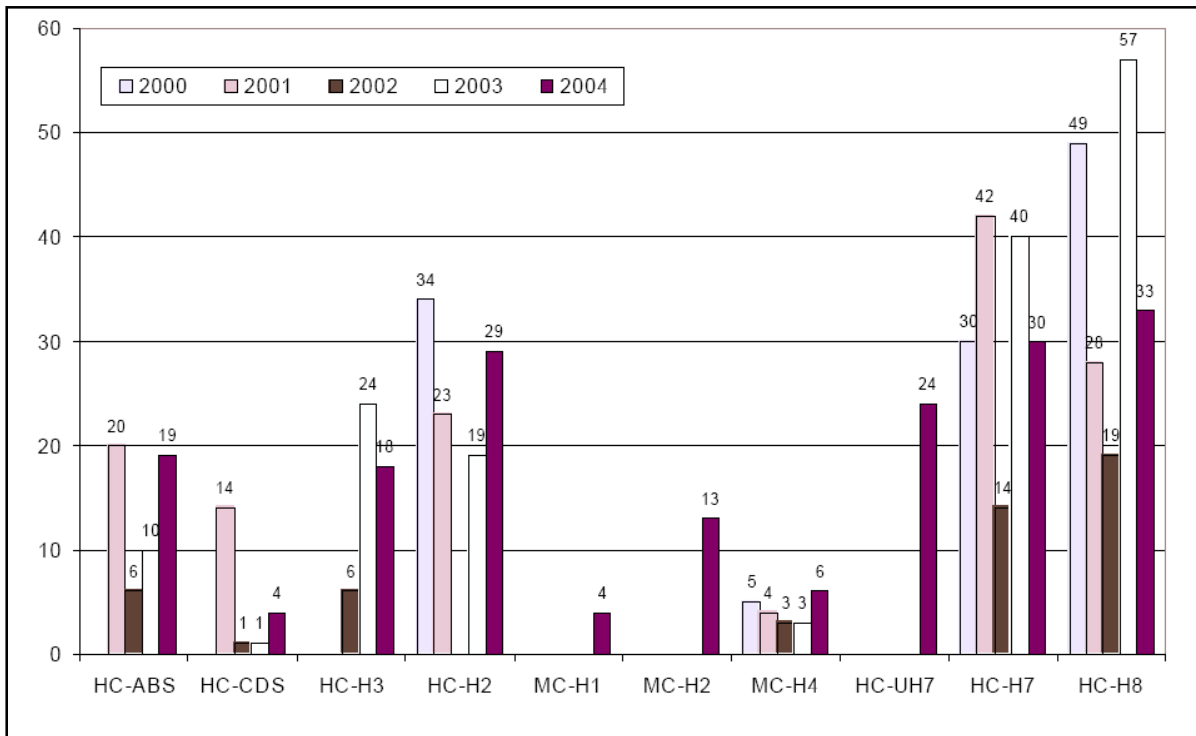


Figure A-9. Percent of organisms in the family Tubificidae in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

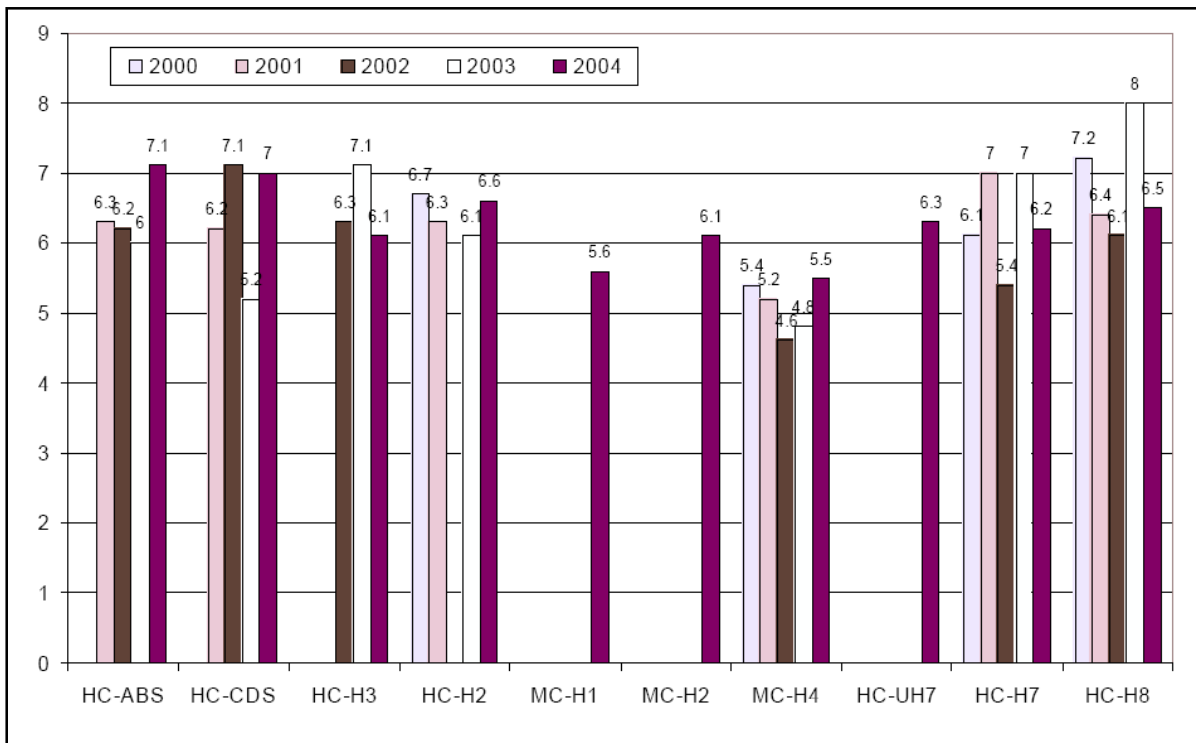


Figure A-10. Mean BMI tolerance values in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

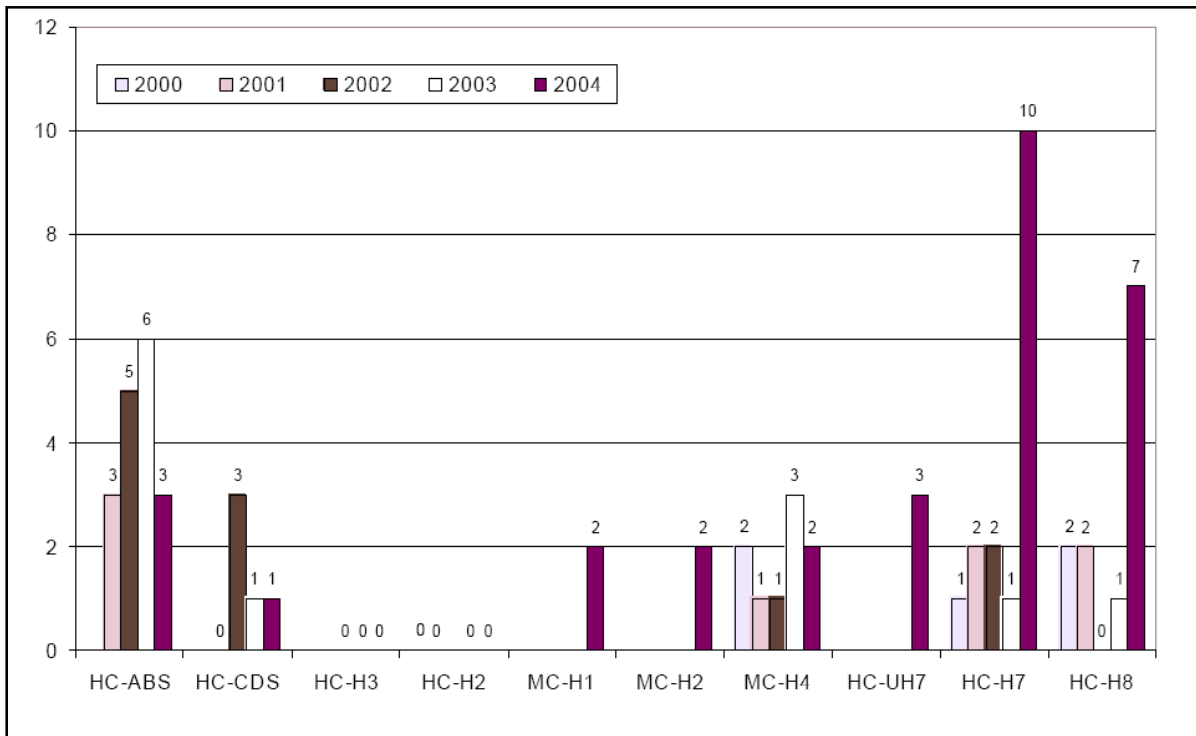


Figure A-11. Percentage of intolerant BMI taxa in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

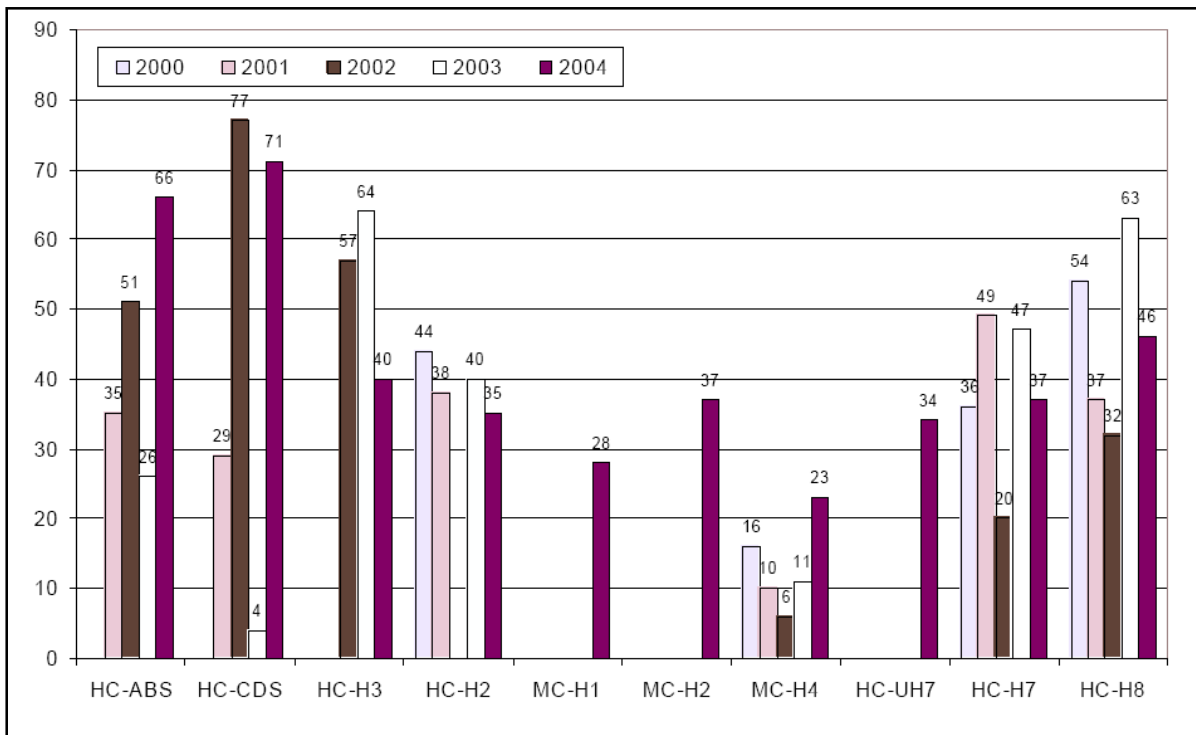


Figure A-12. Percentage of tolerant BMI taxa in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

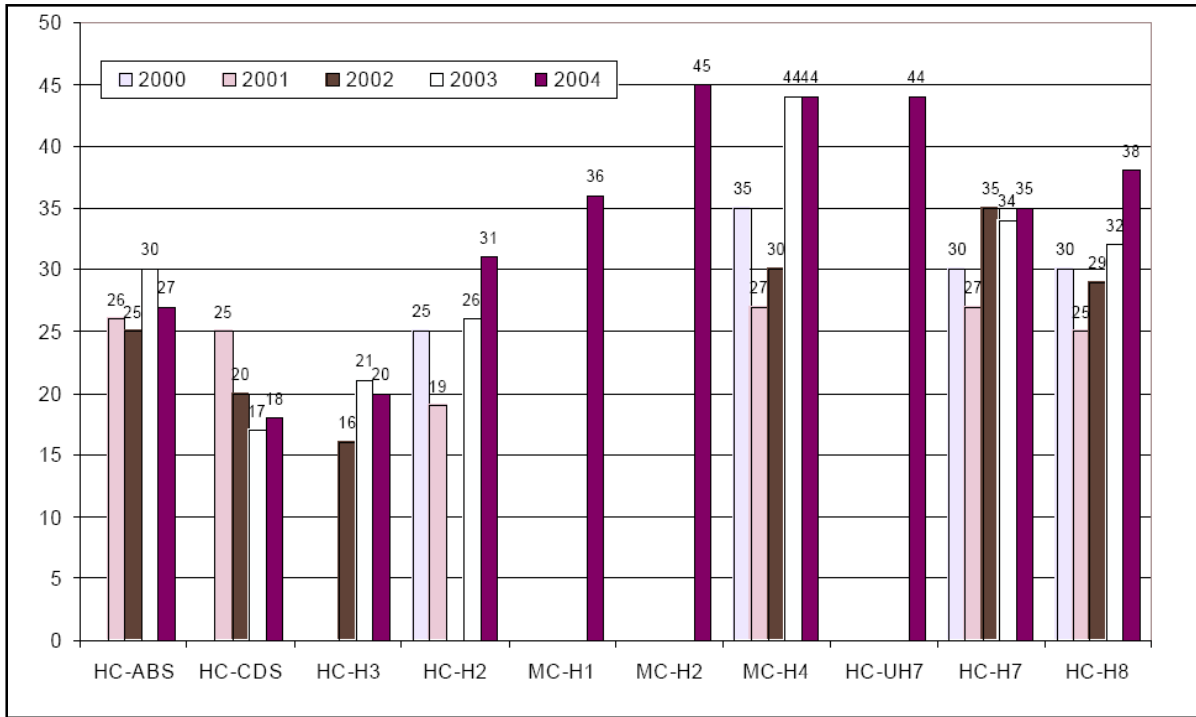


Figure A-13. Percentage of dominant BMI taxa in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

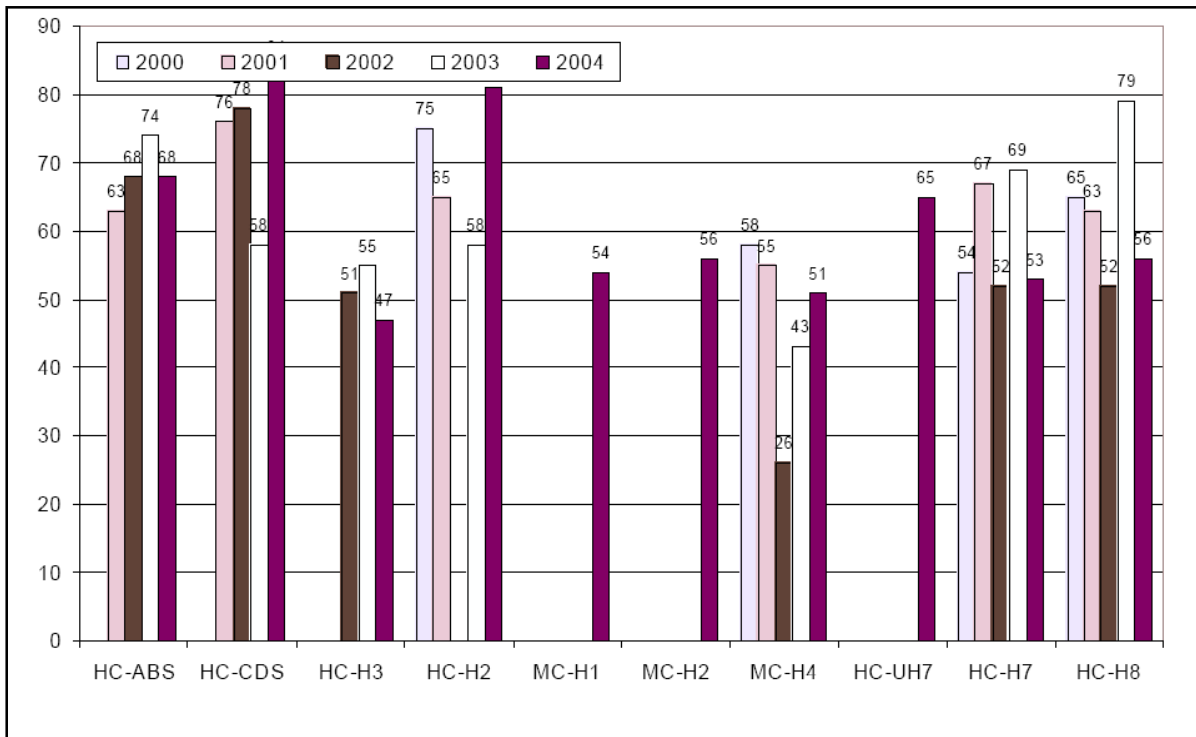


Figure A-14. Percentage of collector-gatherers in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

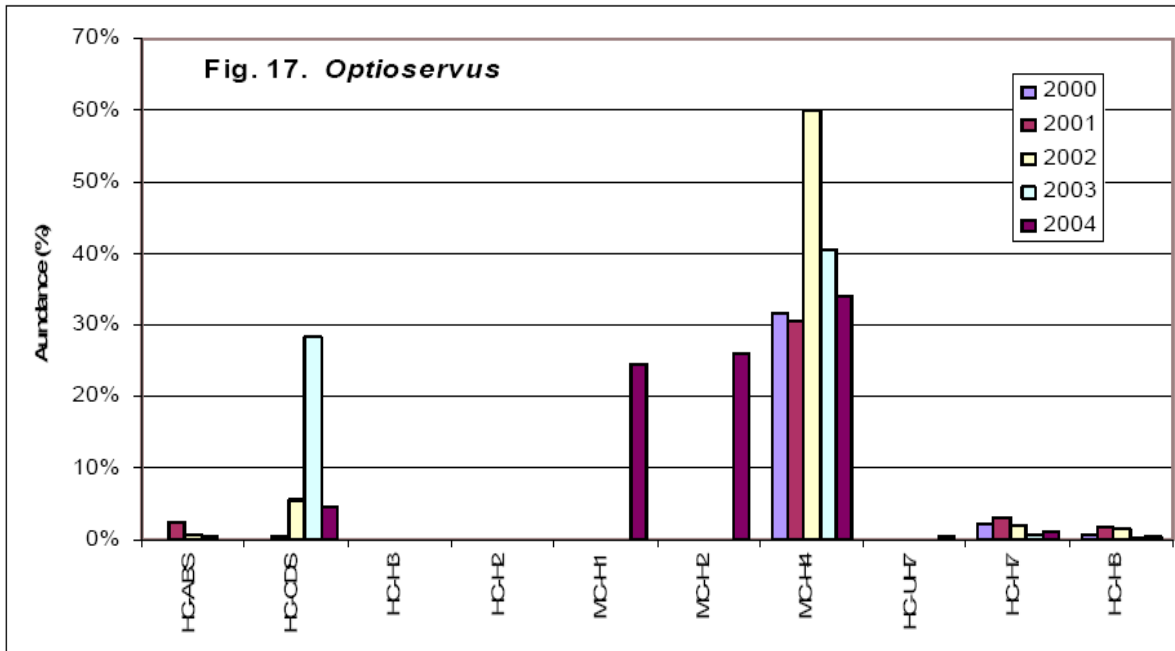


Figure A-15. Relative abundance (%) of riffle beetles (*Optioservus sp.*) in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

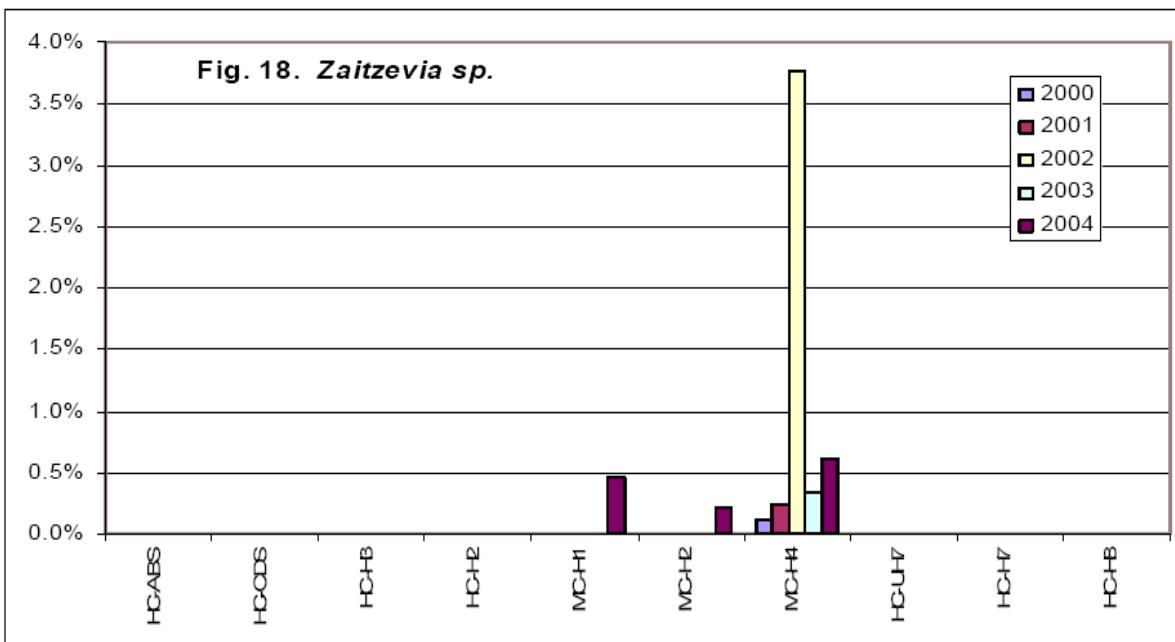


Figure A-16. Relative abundance (%) of riffle beetles (*Zaitzevia sp.*) in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

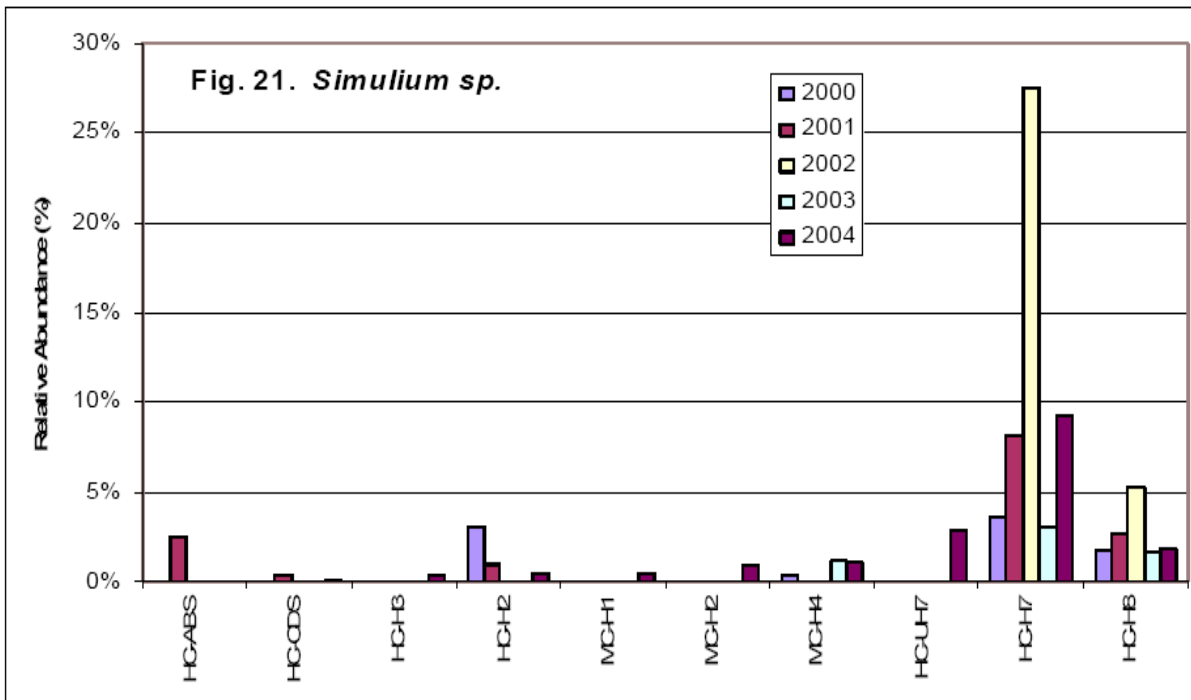


Figure A-17. Relative abundance (%) of black flies (*Simulium* sp.) in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

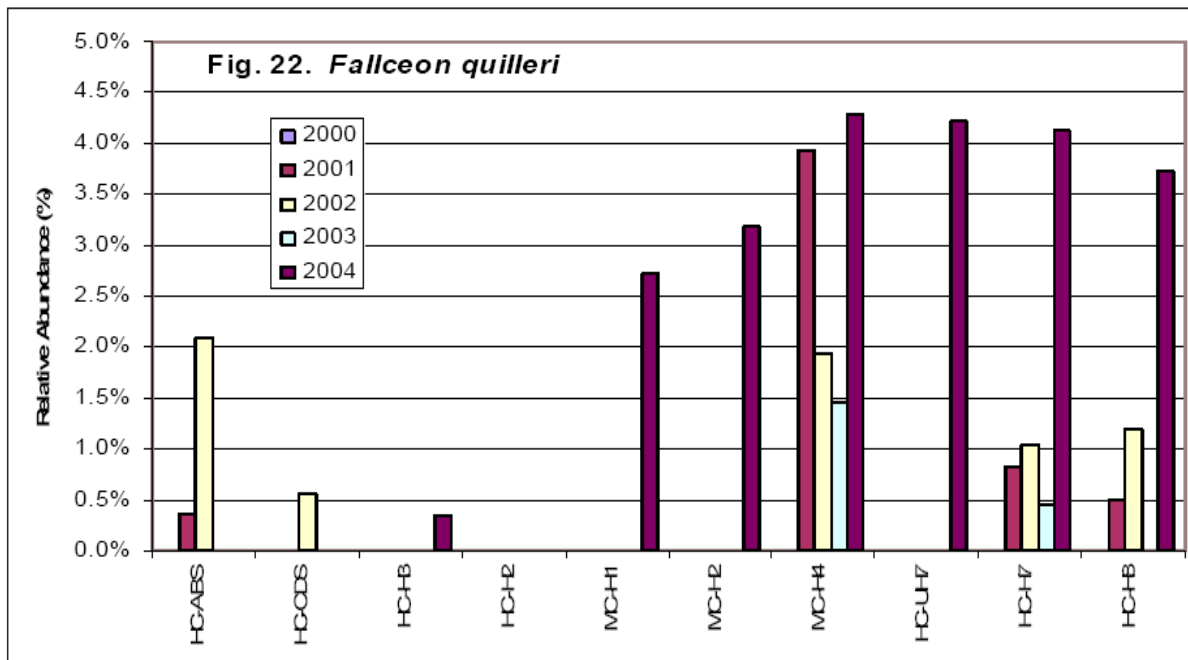


Figure A-18. Relative abundance (%) of the mayfly *Fallceon quilleri* in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

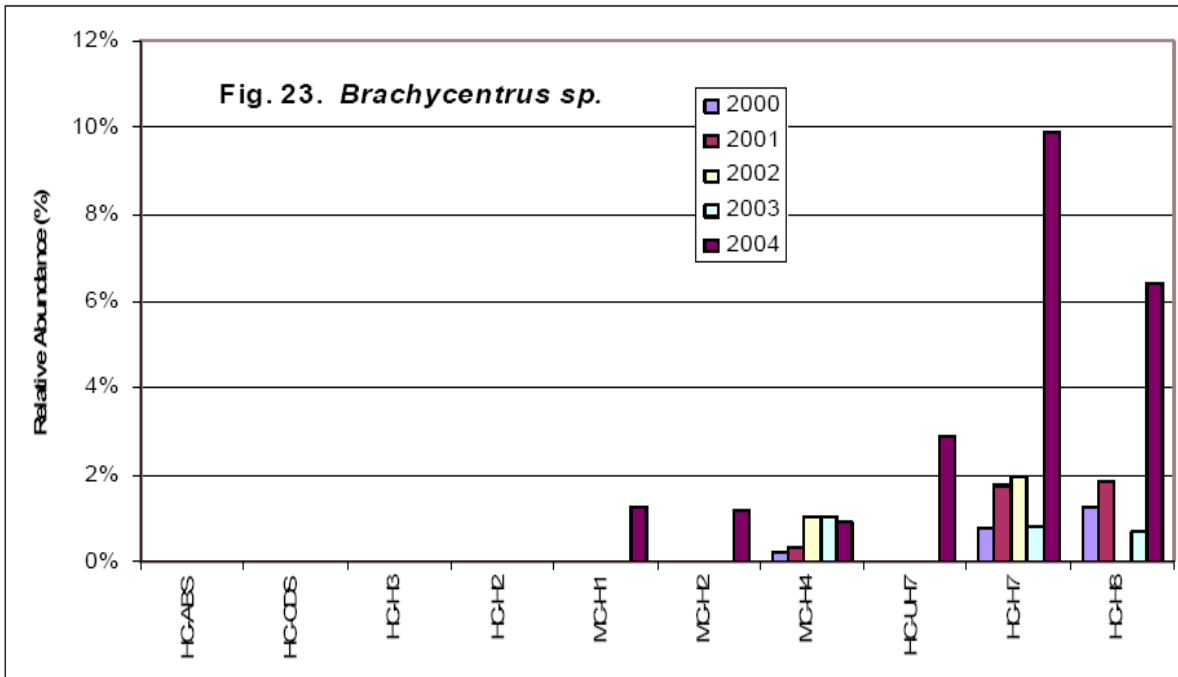


Figure A-19. Relative abundance (%) of caddisflies in the genus *Brachycentrus* in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

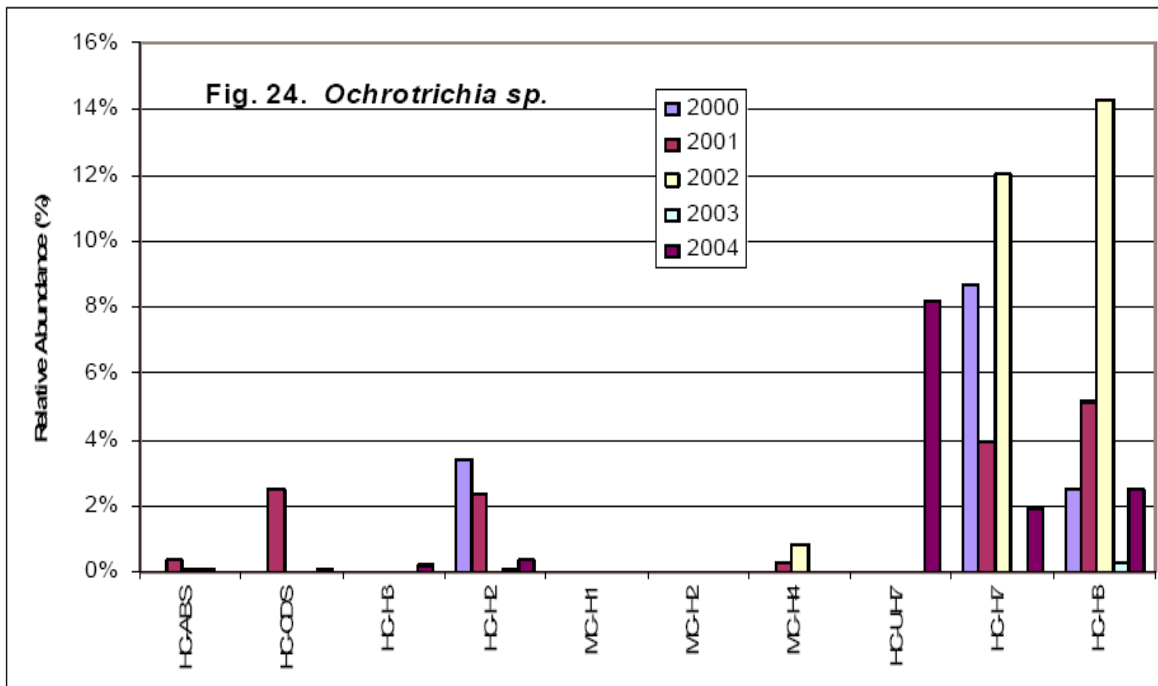


Figure A-20. Relative abundance (%) of micro-caddisflies in the genus *Ochrotrichia* in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

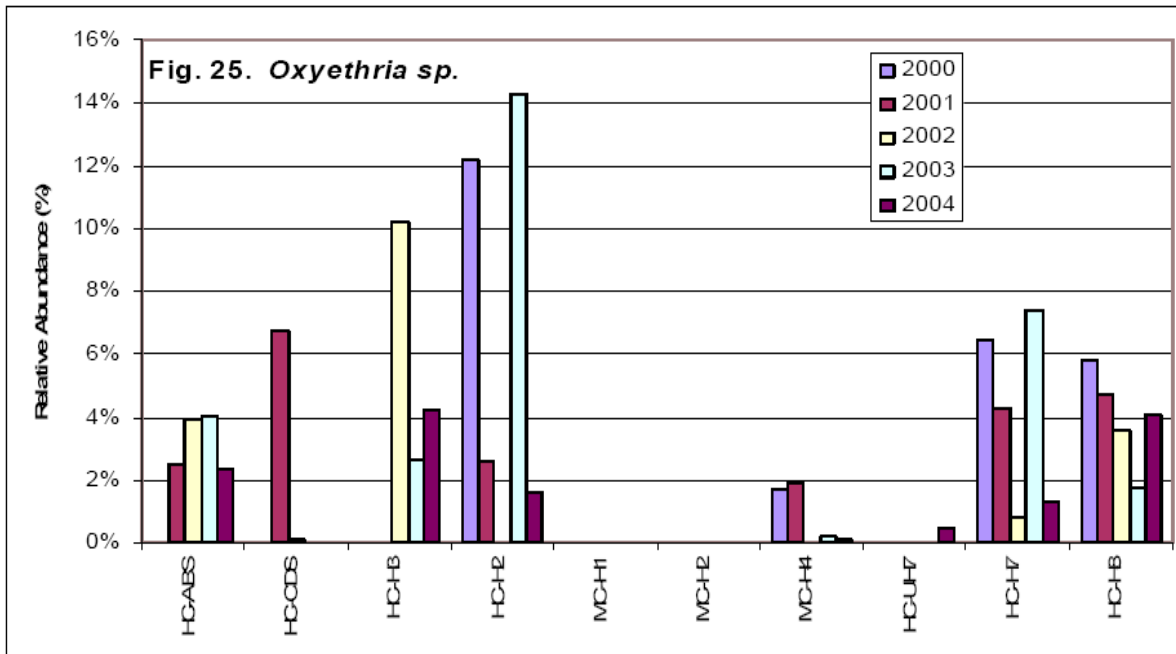


Figure A-21. Relative abundance (%) of micro-caddisflies in the genus *Oxyethria* in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

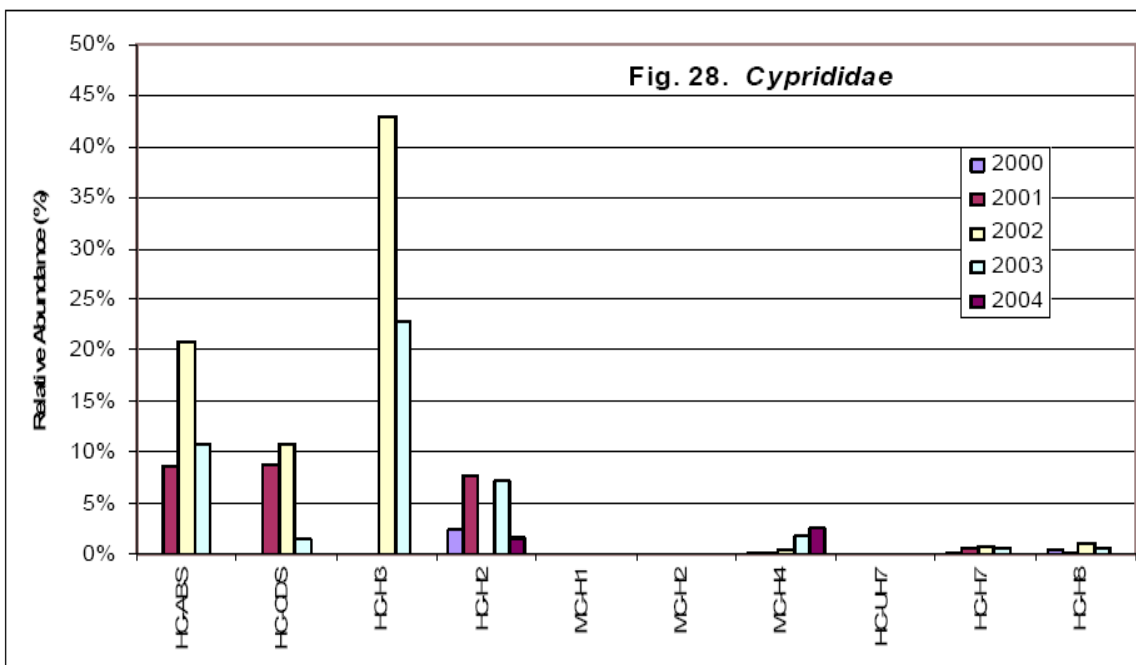


Figure A-22. Relative abundance (%) of ostracods in the genus *Cyprididae* in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

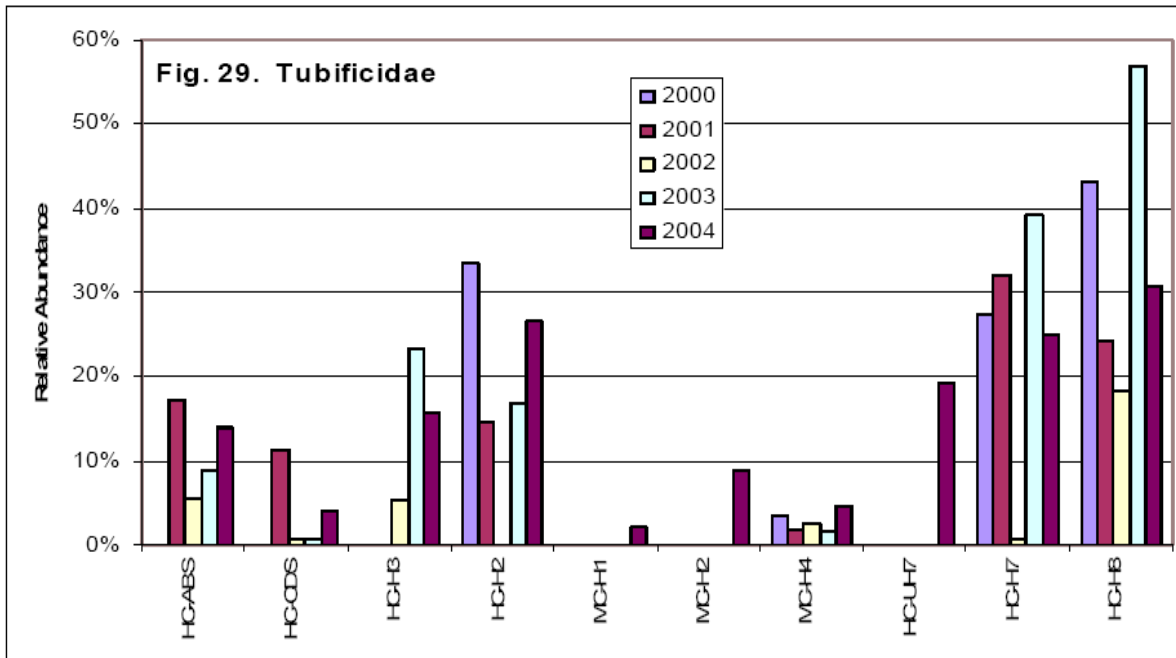


Figure A-23. Relative abundance (%) of tubificid worms in the family Tubificidae Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

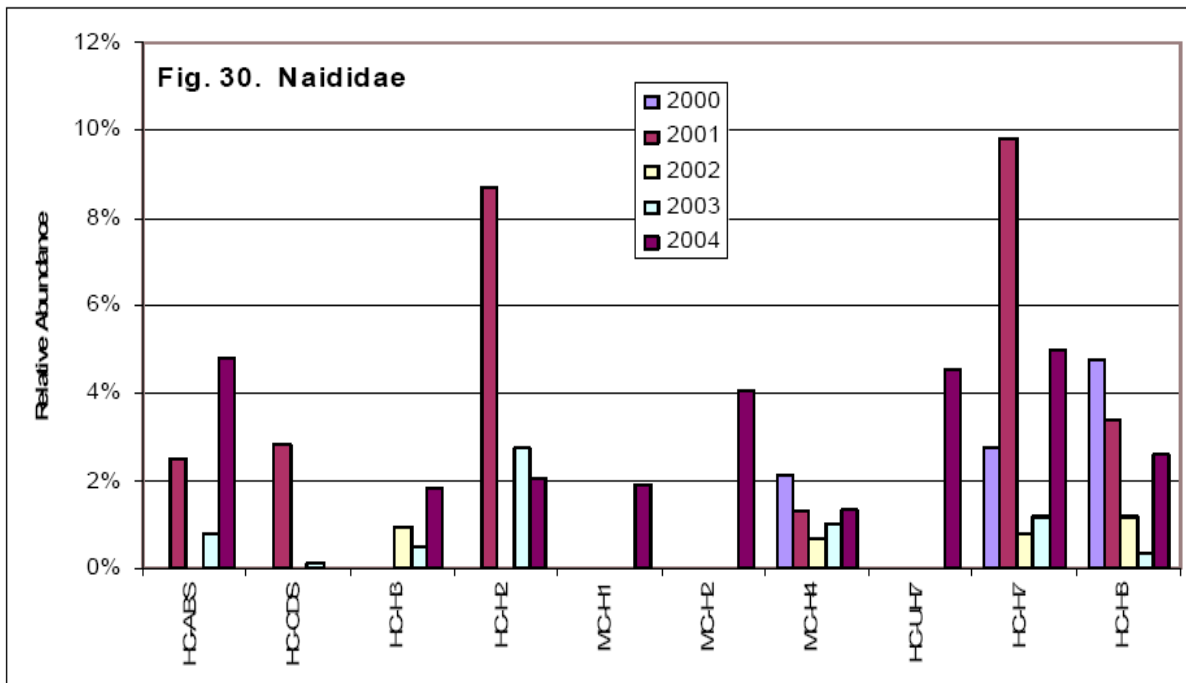


Figure A-24. Relative abundance (%) of tubificid worms in the family Naididae in Mammoth Creek and Hot Creek During 2000 Through 2004 (from Jellison et al. 2005a).

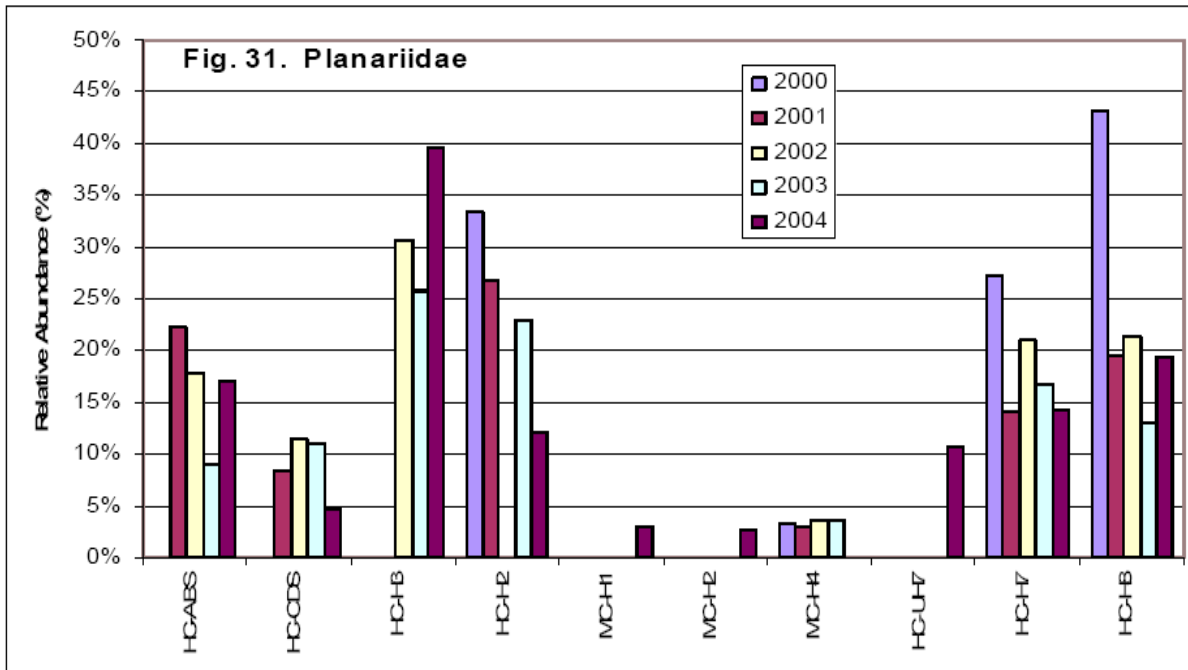
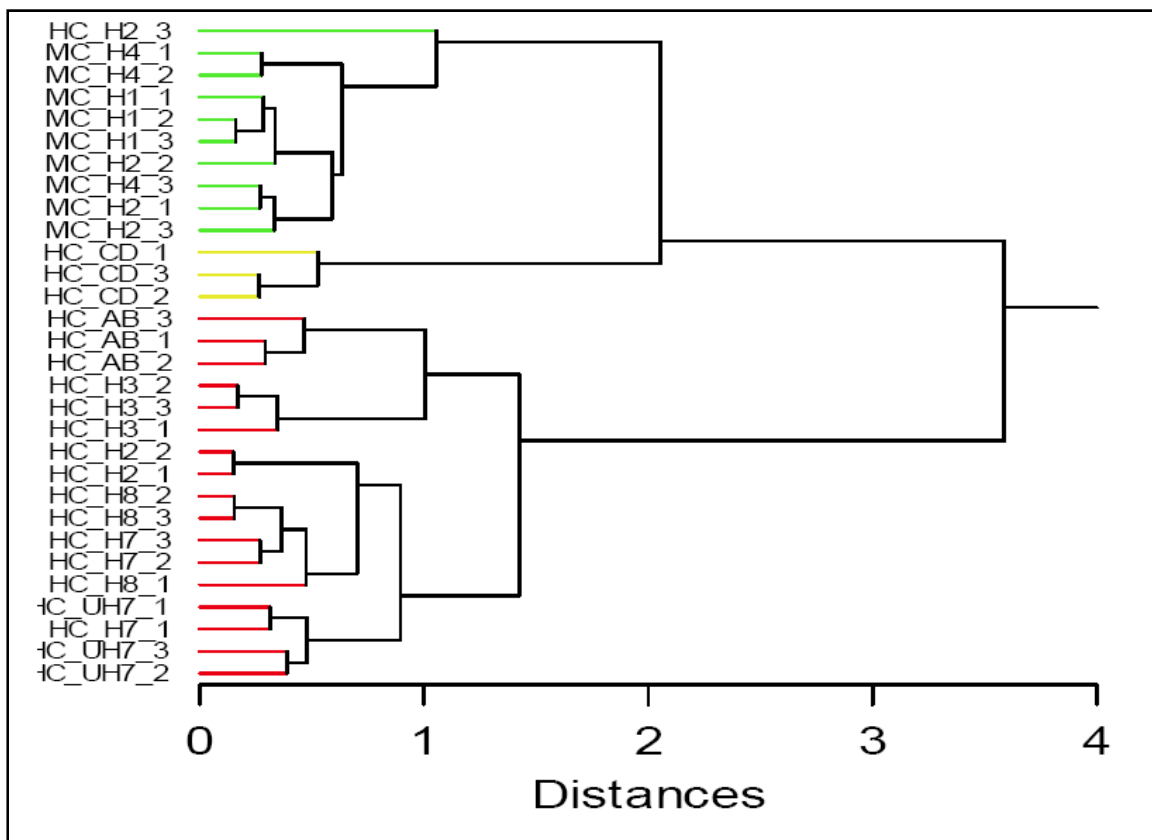


Figure A-25. Relative abundance (%) of planariid flatworms in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).



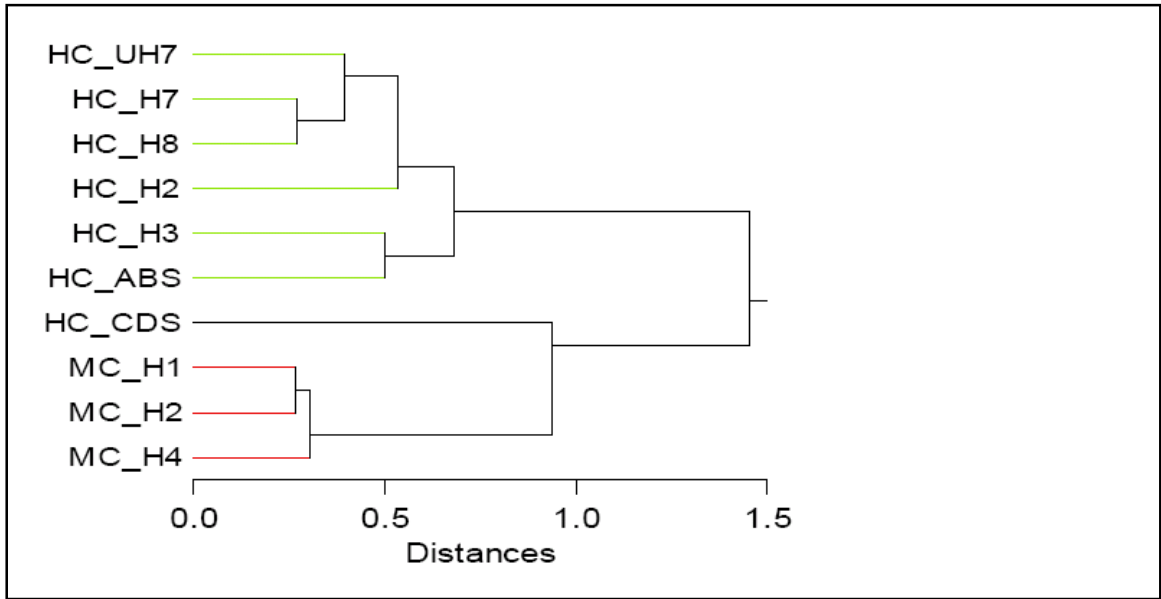


Figure A-27. Cluster analysis of 2004 BMI relative abundance data with replicate transects averaged (from Jellison et al. 2005a).

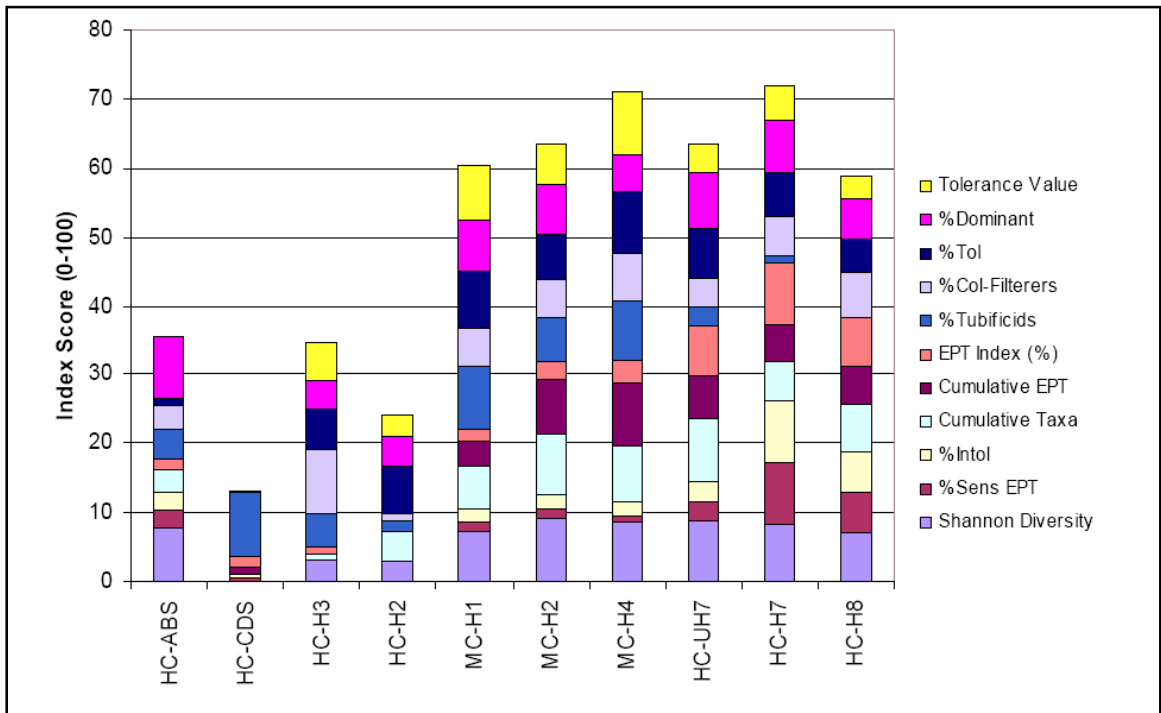


Figure A-28. Hot Creek multi-metric index (from Jellison et al. 2005a).

Table A-1. Sampling site codes, GPS coordinates, and site descriptions for the ten monitoring stations where biological and physical/habitat assessments were conducted during 2000 through 2004 (from CDFG 2004).

Sampling Site Codes	GPS Coordinates	Site Description
Sites Used in Above Hatchery and Below Hatchery Comparison		
HC-ABS	N 37° 38' 20.2" W 118° 51' 44.8"	AB Spring upstream of the Hatchery
HC-CDS	N 37° 38' 16.9" W 118° 51' 39.3"	CD Spring upstream of the Hatchery
HC-H3	N 37° 38' 32.1" W 118° 51' 13.0"	Hot Creek below Settling Pond Outflow
HC-H2	N 37° 38' 32.8" W 118° 51' 08.0"	Hot Creek below Hatchery
Sites Used in Mammoth Creek and Below Hatchery Comparison		
MC-H1	N 37° 38' 37.5" W 118° 51' 25.7"	Mammoth Creek above MC-H2
MC-H2	N 37° 38' 38.0" W 118° 51' 19.7"	Mammoth Creek above MC-H4
MC-H4	N 37° 38' 37.4" W 118° 51' 13.4"	Mammoth Creek near confluence with Hot Creek
HC-UH7	N 37° 38' 38.9" W 118° 50' 59.0"	Hot Creek above HC-H7
HC-H7	N 37° 38' 37.1" W 118° 50' 50.8"	Hot Creek above Brood Pond Discharge
HC-H8	N 37° 38' 36.6" W 118° 50' 46.2"	Hot Creek below Brood Pond Discharge

Table A-2. BMI sampling sites in Mammoth Creek and Hot Creek during 2000 through 2004 (from Jellison et al. 2005a).

Site Code	Site Description	Years Sampled				
		2000	2001	2002	2003	2004
HC-ABS	AB springbrook upstream of the Hatchery		X	X	X	X
HC-CDS	CD springbrook upstream of the Hatchery		X	X	X	X
HC-H3	Hot Creek below Settling Pond#1 Outflow			X	X	X
HC-H2	Hot Creek below hatchery and settling ponds	X	X		X	X
MC-H1	Mammoth Creek above MC-H2					X
MC-H2	Mammoth Creek above MC-H4					X
MC-H4	Mammoth Creek near confluence with Hot Creek	X	X	X	X	X
HC-UH7	Hot Creek immediately below confluence with Mammoth Creek					X
HC-H7	Hot Creek above Hatchery II Discharge	X	X	X	X	X
HC-H8	Hot Creek below Hatchery II Discharge	X	X	X	X	X

Table A-3. Bioassessment metrics used to describe characteristics of the benthic macroinvertebrate community for the ten monitoring stations where biological and physical/habitat assessments were conducted.

BMI Metric	Description	Response to Impairment
Richness Measures		
Taxa Richness	Total number of individual taxa	Decrease
EPT Taxa	Number of taxa in the Ephemeroptera (mayfly), Plecoptera (stonefly) and Trichoptera (caddisfly) insect orders	Decrease
Composition Measures		
EPT Index (%)	Percent composition of mayfly, stonefly and caddisfly larvae	Decrease
Sensitive EPT Index (%)	Percent composition of mayfly, stonefly and caddisfly larvae with tolerance values between 0 and 3	Decrease
Shannon Diversity Index	General measure of sample diversity that incorporates richness and evenness (Shannon and Weaver 1963)	Decrease
Percent Tubificida	Percent composition of the tolerant oligochaete order Tubificida	Increase
Tolerance/Intolerance Measures		
Tolerance Value	Value between 0 and 10 weighted for abundance of individuals designated as pollution tolerant (higher values) or intolerant (lower values)	Increase
Percent Intolerant Organisms	Percent of organisms in sample that are highly intolerant to impairment as indicated by a tolerance value of 0, 1 or 2	Decrease
Percent Tolerant Organisms	Percent of organisms in sample that are highly tolerant to impairment as indicated by a tolerance value of 8, 9 or 10	Increase
Percent Dominant Taxa	Percent composition of the single most abundant taxon	Increase
Functional Feeding Groups (FFG)		
Percent Collectors	Percent of macrobenthos that collect or gather fine particulate matter	Increase
Percent Filterers	Percent of macrobenthos that filter fine particulate matter	Increase
Percent Grazers	Percent of macrobenthos that graze upon periphyton	Variable
Percent Predators	Percent of macrobenthos that feed on other organisms	Variable
Percent Shredders	Percent of macrobenthos that shreds coarse particulate matter	Decrease

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