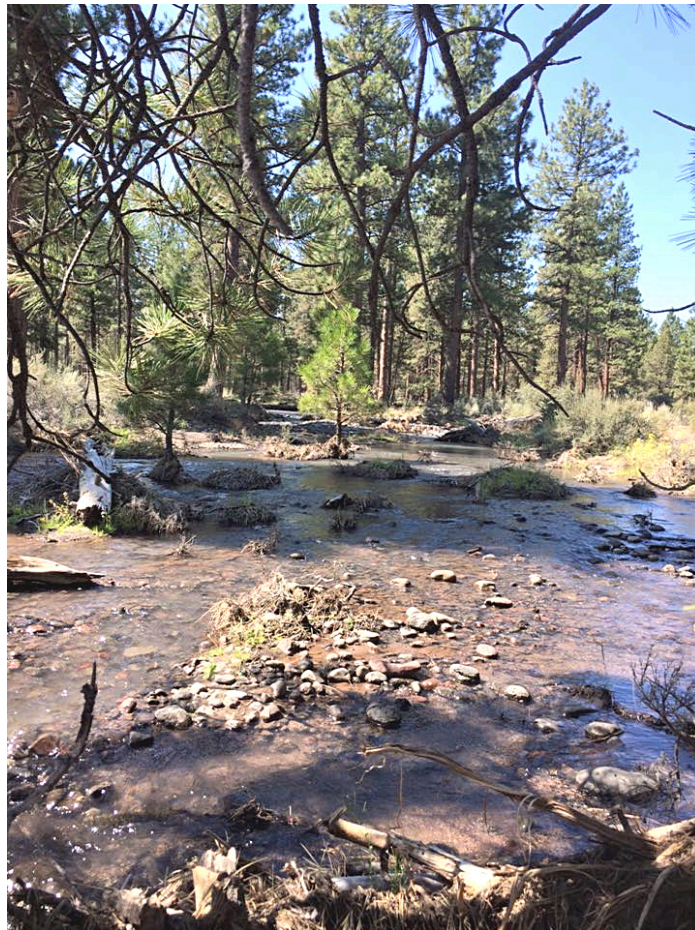


Macroinvertebrate-based Biomonitoring in Whychus Creek



Whychus Creek restored channel; C.A. Searles Mazzacano

Prepared for: Lauren Mork, Monitoring Coordinator, Upper Deschutes Watershed Council
Prepared by: Celeste A. Searles Mazzacano, Principal Scientist, CASM Environmental, LLC
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Executive Summary

This is the 8th season in which aquatic macroinvertebrate monitoring has been done in Whychus Creek to assess changes in the community and related them to ongoing restoration activities. Benthic macroinvertebrate sampling is done in each year according to Oregon Department of Environmental Quality (ORDEQ) standardized protocols for wadeable streams. Kick sampling was done using D-frame nets at 12 sampling sites spanning RM26 to RM1.5 on 20 August 2016; duplicate samples were collected at two sites for quality control. Samples were collected in riffle habitats by teams of volunteers trained by CASM Environmental. Each site sample was subsequently sub-sampled to a target count of 500 organisms and identified to the lowest practical level of taxonomic resolution.

Taxa data were analyzed via the ORDEQ PREDATOR predictive model and invertebrate-based index of biotic integrity (I-IBI). Multivariate analysis was done to assess changes in community composition and identify taxa contributing most to observed community dissimilarities, and multiple taxonomic and ecological traits were assessed. As in previous years, there was good agreement between the original and duplicate samples, providing assurance that observed macroinvertebrate community changes are not strongly influenced by differences between operators. The macroinvertebrate community in Whychus Creek continues to change, much of it in ways that indicate improved biotic conditions and a healthier macroinvertebrate community. Nine new taxa were collected in 2016, five of which have habitat preferences that include cooler and/or faster-flowing waters. The most dramatic changes in the Whychus community occurred between 2005 and 2009; since then, the community in the downstream, mid-stream, and upstream sampling reaches generally shows stronger within-year similarity than within-site similarity. The taxa that account most for the differences between years at the same site tend to be tolerant and/or more lentic taxa that are more abundant in earlier sampling years, and sensitive and/or more lotic taxa that are more abundant in later years (especially Ephemeroptera, Plecoptera, and Trichoptera). The communities have also become more balanced over time, and are less dominated by a single highly abundant taxon.

PREDATOR and I-IBI scores were higher in 2016 than in several previous years and indicated improved biotic conditions at many sites. PREDATOR scores in 2016 scored more sites as good or fair and fewer as poor than in several earlier years. I-IBI scores were also higher overall in 2016; this is the first year since 2013 that any sites received a score indicating minimal impairment, and the only site that scored as moderately disturbed is currently undergoing channel restoration. Scores fluctuate over the years, but no sites have ever scored as severely impaired, and overall the proportion of sites scoring as moderately impaired has decreased since sampling began in 2005, while the proportion scoring as slightly impaired has increased.

Many community indicators such as the number of sensitive taxa, taxa richness, and diversity of sensitive EPT (Ephemeroptera, Plecoptera, Trichoptera) have improved over time, and sediment conditions have also been a strong driver. In earlier sampling years, the community also appeared to be responding positively to lower stream temperatures, and the mean community temperature optima among downstream and mid-stream sites initially

decreased significantly through 2013. However, these means began to rise again in 2014 and have continued to do so among all sampling reaches through 2016. The number of ORDEQ warm indicator taxa in the community has also been increasing in recent years among downstream and mid-stream sites. Given that the last three years have been the hottest in recorded history (NOAA, 2016), this sustained trend may be a signal that the stream community is being impacted by larger climate stressors.

Background

The Whychus Creek watershed is a designated priority watershed for conservation and restoration in the upper Deschutes Basin. Since 1999, restoration projects have restored perennial flows to the creek and increased instream flow volumes. The aquatic invertebrate community has been systematically monitored in Whychus Creek since 2005, with sampling done annually in eight of the years during 2005-2016 (2005, 2009, 2011-2016) at 10-13 reaches between RM 30.25 to RM 0.5, with the most consistently sampled sites between RM 26 and 1.5. Multiple approaches are used to examine the benthic macroinvertebrate community and investigate the ecological implications of changes in community composition. Standard biotic assessment techniques are applied to assign levels of biological impairment to sampling sites: general Invertebrate Index of Biotic Integrity (I-IBI), Grande Ronde IBI (GR-IBI), and PREDATOR predictive model (Hubler, 2008), all developed by the Oregon Department of Environmental Quality (ORDEQ). Changes in individual IBI metrics as well as community tolerances for percent fine sediment and temperature and diversity of ORDEQ temperature and sediment indicator taxa are assessed. Multivariate analysis is done to determine between-year macroinvertebrate community similarities and to identify taxa contributing the most to observed community differences.

Methods

Sampling sites

In 2016, benthic macroinvertebrate sampling was done at 12 reaches along Whychus Creek, with duplicate samples taken at two sites for quality control (Table 1). Sites are distributed into downstream (RM 1.6 - 11.5; DS), mid-stream (RM 18-19.5; MS), and upstream (RM 24.25-26; US) regions. Some sites have been added, moved, or removed since sampling began in 2005 based on access, changes in land use, or re-assessment of their importance, and some site names changed following more precise GIS mapping done in 2014. Not shown in Table 1 are two additional downstream sites were sampled only in 2005 (RM 0.50 and 3.0), and three additional upstream sites not sampled after 2011 (i.e., RM 26.5, 27.0, and 30.25).

Table 1. *Whychus Creek sampling sites, 2016*

Site ID	Description	Coordinates	Year(s) sampled
WC0150	RM 1.5, d/s Alder Springs	44.44491, -121.34543	2009, 2011-2016
WC0600	RM 6, u/s Rd 6360	44.40412, -121.40259	2005, 2009, 2011-2016
WC0850	RM 8.75, Rimrock Ranch d/s	44.391278, -121.406182	2011-2015
WC0900	RM 9, Rimrock Ranch	44.384198, -121.407892	2005, 2009, 2011-2015
WC1050^a	RM 10.25, Rimrock Ranch u/s	44.371534, -121.415865	2011-2012, 2014-2016
WC1150	RM 10.75	44.361288, -121.427525	2014-2016
WC1825	RM 18.25, d/s end DBLT property	44.32781, -121.495406	2009, 2011-2016
WC1850	RM 18.5, DBLT property	44.326601, -121.500229	2009, 2011-2016
WC1900	RM 19, DBLT property	44.321523, -121.507461	2005, 2009, 2011-2016
WC1950^b	RM 19.5, d/s Camp Polk Bridge, DBLT property	44.318741, -121.514961	2009, 2011-2016
WC2425^b	RM 24.25, City Park, d/s gauge	44.287806, -121.544229	2005, 2009, 2011-2015
WC2600	RM 26, 4606 Rd. footbridge	44.2730592, -121.555297	2005, 2009, 2011-2015

^a prior to 2016, sampling site was at RM 10.25

^b duplicate samples taken for QA/QC

Sampling method

The same index period has been used across all sampling years (17-20 August) to minimize seasonal variations in macroinvertebrate populations between years; in 2016, sampling was done on 20 August. Benthic macroinvertebrates were collected from riffle habitats according to standardized protocols developed by ORDEQ for Oregon's wadeable streams (OWEB, 2003). Sample reach lengths are calculated as 40 times the average wetted width of the stream at the desired sampling point, with a minimum reach length of 500 feet and a maximum of 1000 feet. A few days prior to sampling, UDWC staff perform these calculations and flag the upstream and downstream extent of each reach to make it easier for volunteers to find their designated sites. On the morning of 20 August, volunteers gathered at City Park in Sisters, OR to be trained in macroinvertebrate sampling methods by CASM Environmental, who demonstrated the sampling technique and explained each item on the data sheet. Teams received sampling kits and detailed instructions for finding their sites and dispersed into the field. Each team returned samples, data sheets, and equipment to the park when they had finished their site(s), and CASM Environmental staff inspected each sample to be sure it was properly labeled and preserved.

A site sample comprises eight individual net sets taken from riffle habitat within a designated reach. Each net set is collected from a 1 ft² area using a D-frame kick net with 500 µm mesh and a 1-ft opening. In reaches with eight or

more riffles, a single net set is taken in each of eight randomly selected riffles; in reaches with fewer than eight riffles, two kick net samples are taken in each of four riffles. Large rocks and debris in the sampling area are first rubbed and rinsed into the net to dislodge and collect any clinging organisms, and set aside. The substrate is then disturbed thoroughly using a boot heel to a depth of 6-10 cm for 1-2 minutes. The eight net sets at each site are pooled into a bucket; large debris is rinsed and removed, and any vertebrates such as fish are noted on the data sheet and carefully replaced in the stream. Sample material is concentrated by being poured through a 500 μm sieve lined with a flexible square of 500 μm Nitex membrane; the membrane is lifted out and the concentrated sample carefully scooped and rinsed into a 1-liter Nalgene sample jar half-filled with 80% ethanol as a preservative.

Samples that contained excessive amounts of sand or gravel were elutriated, a process that allows lighter, soft-bodied invertebrates to be separated from heavier mineral material and placed in different sample jars to avoid crushing or grinding the specimens. Elutriation is done by adding water to the composited sample in the bucket, swirling it thoroughly, then pouring the suspended organic material through the sieve. After two to three rinses, the organic material is placed in one sample jar and the mineral material in another; all sample material from each site is retained for subsequent examination in the lab so that heavier-bodied organisms (i.e., snails, stonecase-making caddisflies) are not lost. Jars are filled no more than halfway with sample to ensure preservation, and the ethanol is replaced with within 48 hours by CASM Environmental to maintain an 80% concentration, since water leaches from the sample and dilutes the preservative. Each jar receives an interior and exterior label, written in pencil on waterproof paper. A simple physical habitat assessment is also done at each site to provide data on human use and landscape alterations, substrate composition, water temperature and appearance, and wetted width and depth at each riffle sampled (see Appendix A for data sheet).

Macroinvertebrate identification

Samples were identified by Cole Ecological, Inc. (<http://www.coleecological.com>). Each composite sample was randomly sub-sampled to a target count of 500 organisms. If a sample contains fewer than 500 organisms it is picked and identified in its entirety, but the target count was attained for all 2016 samples. Organisms were identified to the level of taxonomic resolution currently recommended by ORDEQ and the Southwestern Association of Freshwater Invertebrate Taxonomists (SAFIT; Richards & Rogers, 2011), which is generally genus or species, although some groups should be left to family or order. If a specimen is too immature for critical taxonomic characters to be fully developed or visible, identification is done only to family level.

Data analysis

Biological condition of each sampling site was assessed using both multimetric and probability-based models. Two multimetric indices developed by ORDEQ were used: a general macroinvertebrate-based Index of Biotic Integrity (I-IBI) and a more regional northeastern (Grande Ronde) GR-IBI (Table 2). A higher scaled score (5) is given

to metric ranges considered typical of a healthy stream, while a lower scaled score (3 or 1) reflects values associated with more degraded conditions. Scaled scores for all metrics are summed to generate single value that reflects the level of site impairment.

Table 2. ORDEQ general macroinvertebrate-based IBI and Grande Ronde IBI metrics and scoring. Both use taxa identified to genus level.

I-IBI				GR-IBI		
Scoring Criteria						
Metric	5	3	1	5	3	1
Taxa richness	>35	19-35	<19	>31	24-31	<24
Mayfly richness	>8	4-8	<4	>7	6-7	<6
Stonefly richness	>5	3-5	<3	>6	5-6	<5
Caddisfly richness	>8	4-8	<4	>4	2-4	<2
# sensitive taxa	>4	2-4	<2	>4	3-4	<3
# sediment-sensitive taxa	>2	1	0	>1	1	0
% dominance ^a	<20	20-40	>40	<39	39-42	>42
% tolerant taxa	<15	15-45	>45	<24	24-36	>36
% sediment-tolerant taxa	<10	10-25	>25	<10	10-15	>15
MHBI ^b	<4	4-5	>5	<3.9	3.9-4.3	>4.3
Summed score & condition						
Severely impaired	<20			<15		
Moderately impaired	20-29			15-25		
Slightly impaired	30-39			N/A		
Minimally/not impaired	>39			>26		

^a for I-IBI, dominance (% abundance) of most abundant taxon is assessed; for GR-IBI, dominance of the three most abundant taxa is assessed.

^b Modified Hilsenhoff Biotic Index (Hilsenhoff, 1987), reflecting tolerance to organic pollution/enrichment; values range from 1 (low tolerance) to 10 (high tolerance)

The macroinvertebrate community in Whychus Creek was also analyzed using the probability-based PREDATOR model (Predictive Assessment Tool for Oregon; Hubler, 2008) developed for the Western Cordillera and Columbia Plateau (Klamath Mountain, Cascades, East Cascades, Blue Mountains, and Columbia Plateau ecoregions; WCCP). PREDATOR calculates the ratio of taxa observed at a sampling site to taxa expected at that site if no impairment exists (O/E), based on community data collected previously at a large number of reference streams. The model incorporates environmental gradients such as elevation, slope, and longitude to select the most

appropriate reference streams. An O/E value <1 indicates loss of taxa, while values >1.2 indicate taxa enrichment, potentially in response to pollution or nutrient loading. PREDATOR scores are generated from a habitat file and a macroinvertebrate data file for each site, which are uploaded to the model software at the Western Center for Monitoring & Assessment of Freshwater Ecosystems (www.qcnr.usu.edu/wmc). Model outputs include a site test result, which indicates whether the habitat data falls within the model parameters; an O/E score for each sample, which provides a measure of biological condition; a site probability matrix that identifies missing taxa (taxa expected to occur at each site but absent) and replacement taxa (taxa present at a site but not predicted by the model to occur there); and a sensitivity index that reveals “increaser” and “decreaser” taxa in the overall community (i.e., taxa collected at more or fewer sites than predicted by the model). Invertebrate community data were uploaded to the PREDATOR WCCP model (Hubler, 2008) by Cole Ecological. O/E scores associated with a probability of capture (P_c) > 0.5 were used in the subsequent analyses to avoid rare taxa bias (i.e. the model considers only invertebrates with over 50% likelihood of being collected at reference sites). Site biological condition is assigned based on the following O/E scores: ≤ 0.78 = poor (most disturbed); $0.79 - 0.92$ = fair (moderately disturbed); $0.93 - 1.23$ = good (least disturbed); and > 1.23 = enriched.

The macroinvertebrate community in Whychus Creek in 2016 was analyzed independently, and was also examined as part of a larger assessment of community changes and trends across the entire dataset in all sampling years. Additional characteristics were assessed, including temperature and percent fine sediment optima and presence of high/low temperature and sediment indicators (established by the ORDEQ; see Hubler, 2008). Richness (number of taxa), relative abundance, and relative diversity of different macroinvertebrate groups was assessed. All univariate and multivariate analyses of community composition and characteristics were done using the PAST statistical software package (Hammer et al., 2001). CLUSTER, one-way ANOSIM, and SIMPER analyses were done on Bray-Curtis similarity matrices of square root-transformed abundance data to investigate macroinvertebrate community similarity between sites and across years. CLUSTER analyses were also done on presence/absence datasets to examine the communities of increaser/decreaser and missing/replacement taxa. SIMPER tests were used to find taxa that contributed the most to community differences between years and sampling reaches (DS, MS, and US). Scatter plots and box plots were also done in PAST. Note: in previous years, trophic guilds (functional feeding groups) of the macroinvertebrate communities were analyzed and compared; however, they have proved uninformative and thus were omitted from the 2016 analysis. In addition, box-and-whisker plots are used in 2016 to show ranges and median values for various metrics, instead of the bar graphs of mean values shown in past years, as these present a more useful visual representation of the data and differences between groups. Mean values for metrics were compared using unpaired two-sample t tests, and a cutoff value of $p < 0.05$ was used to determine significant differences between means.

Results & Discussion

Macroinvertebrate community 2016

The target count of 500 organisms was achieved for all site samples, with anywhere from 15-77% of the total sample being picked. A total of 79 unique taxa was collected across all sites, which is in the same range as previous years (76-83 unique taxa per year in 2005-2015). Nine taxa were collected for the first time since sampling began in 2005; these new taxa were present at low abundances (≤ 10) and at a small number of sites (1-2). New taxa included two genera of predaceous diving beetle (*Agabus* at WC0600; *Stictotarsus* at WC1900); although dytiscid beetles are seen in Whychus samples in every year except 2009 and 2012, they have not been identifiable any further than subfamily (Hydroporinae) in the past. The remaining new taxa are *Heterlimnius*, a riffle beetle (WC1950); *Limonia*, a crane fly (WC1825); Prodiamesinae, a subfamily of non-biting midge (WC0600); *Helodon*, a black fly (WC2425 and WC2600); *Amiocentrus*, a brachycentrid caddisfly (WC0150); *Apatania*, an apataniid caddisfly (WC0900); and Lymnaeidae, a family of bassomatophorid snail (WC1050).

Restoration of perennial and higher flows in Whychus is expected to support an increased diversity of sensitive taxa, and new taxa found across the years support this. The new taxa in 2016 are a mixture of sensitive and tolerant groups, but the majority require faster and/or cooler running waters. *Apatania* is a sensitive genus in a caddisfly family known from northern montane habitats, generally in small, cool mountain streams and occasionally high-elevation cold lakes. *Amiocentrus* is a sensitive genus of humpless case-making caddisfly, a family found in a variety of habitats from fast, cold springs to larger, slower rivers. *Heterlimnius* is a somewhat tolerant genus of riffle beetle that inhabits faster-flowing waters. Prodiamesinae are a subfamily of nonbiting midges associated with springs, streams, ponds, and the littoral zone of lakes. Black flies such as *Helodon* are restricted to running waters, and this genus can be more characteristic of higher-elevation sites. New taxa associated with slower waters include the tolerant predaceous diving beetles *Agabus* and *Stictotarsus*, as well as *Limonia*, a tolerant crane fly generally inhabiting exposed objects on the margins of aquatic habitats, and Lymnaeidae, a tolerant snail family generally found in shallower waters.

The rate of addition of new taxa to the Whychus community had slowed in recent years. The greatest number of new taxa (35) was seen in 2009, which was only the second year in which the creek had been sampled, following a four-year gap in which substantial work that restored summer flows and increased instream flows was done, so habitat conditions changed dramatically. Subsequent years saw anywhere from 3-10 new taxa, but the number of new taxa in 2016 is the highest since 2011. In all prior years except 2014, the majority of new taxa (71-100%) were mayflies (Ephemeroptera), stoneflies (Plecoptera), and caddisflies (Trichoptera); in 2016 and 2014, only 20% of new taxa were EPT. This suggests that the regional pool of EPT colonists is now better represented in Whychus Creek, especially as EPT are in general considered poor overland dispersers due to weaker flight capabilities. A combination of slow dispersal, changing habitat conditions in Whychus, and the need to compete against more tolerant taxa that are established in the stream explains the continuing expansion of the taxa set. Because new

taxa are generally found in low abundance at a small number of sites, their presence reflects both chance (likelihood of sampling a taxon present at low abundance) and responses to changing stream conditions.

Indices of Biotic Integrity

Of the 12 sites sampled in 2016, two (17%) received a score indicating minimal impairment and nine (75%) received a score indicating slight impairment. Only one site, WC2600, scored as moderately impaired; that site has been undergoing extensive restoration recently, and changes to the channel in this reach account for the decreased IBI, as it has scored as slightly impaired for the past three years. This year is the first time that any sites received a score indicating minimal impairment since 2013 (Figure 1; Table 3). Scores have fluctuated over the years, although no sites have ever scored as severely impaired, but overall the proportion of sites scoring as moderately impaired has decreased since sampling began in 2005, while the proportion scoring as slightly impaired has increased, demonstrating a shift to better biological conditions.

Figure 1. Comparison of site biological condition categories indicated by IBI scores across time.

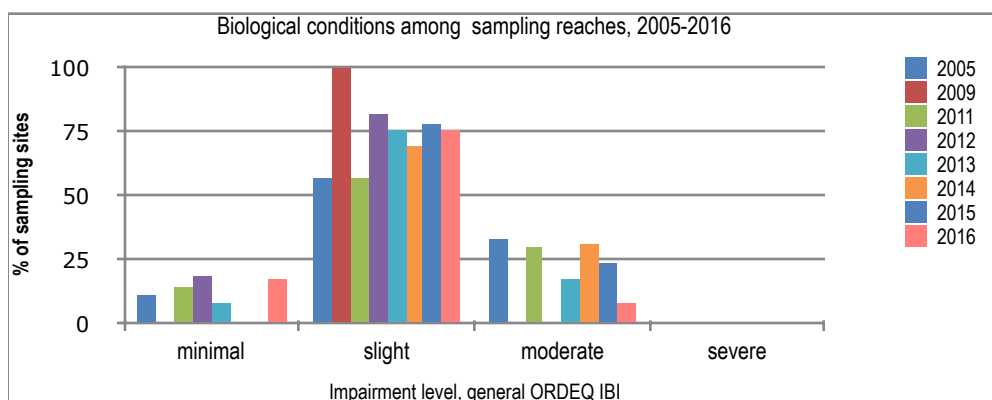


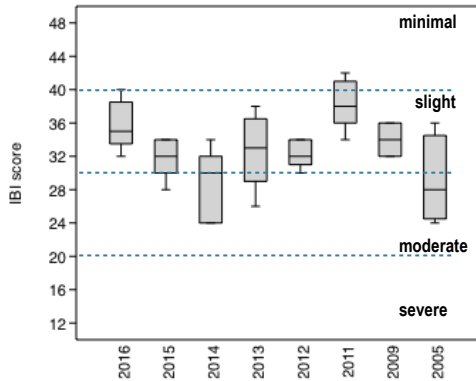
Table 3. I-IBI scores across time. Colors indicate biological conditions corresponding to I-IBI score (minimal impairment = green, slight impairment = blue, moderate impairment = red)

Site	2005	2009	2011	2012	2013	2014	2015	2016
WC0050	30	---	---	---	---	---	---	---
WC0150	---	38	44	34	36	34	28	38
WC0300	26	—	—	—	—	—	—	—
WC0600	24	32	38	32	32	28	30	34
WC0650	—	—	—	—	34	—	—	—
WC0875	—	—	40	30	26	30	30	36
WC0900	36	36	34	32	38	32	32	40
WC0950*	—	—	38	34	30	24	34	—
WC1025 (WC1100)	—	—	—	—	—	24	32	34
WC1075 (WC1150)	—	—	—	—	—	30	34	32
WC1800	32	—	—	—	—	—	—	—
WC1825	—	36	34	34	32	32	20	34
WC1850	—	34	22	36	26	28	32	36
WC1900	40	34	28	34	36	34	32	32
WC1950	—	34	34	36	36	36	34	42
WC2325	28	—	—	—	—	—	—	—
WC2425	28	34	26	42	40	38	24	38
WC2600	30	38	28	46	32	36	30	28
WC2650	—	—	32	—	—	—	—	—
WC2700	—	—	36	—	—	—	—	—
WC3025	38	38	36	—	—	—	—	—

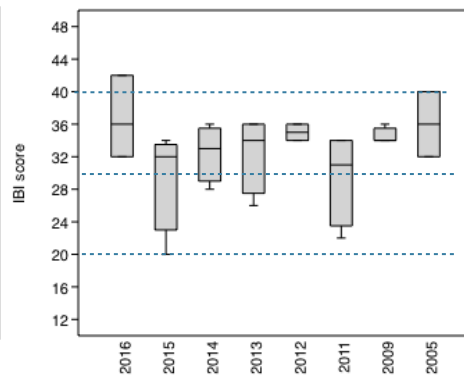
Examination of I-IBI scores among different sampling reaches shows annual variation among all reaches (Figure 2). Median scores in most years fall into the range indicating slight impairment, but scores have gone further into the moderately impaired range among downstream and mid-stream sites. Mean I-IBI scores for downstream sites sampled in 2016 are significantly higher than those in 2015, 2014, and 2005, and were higher but not quite significant compared to 2012 ($p=0.0561$). Among both mid-stream and upstream sites, mean IBI scores in 2016 were not significantly different from those in other sampling years.

Figure 2. I-IBI scores across time. Horizontal line in each box indicates the median value; filled box shows the interquartile range; whiskers depict data range. Dotted lines show cutoff points for impairment levels in I-IBI scoring.

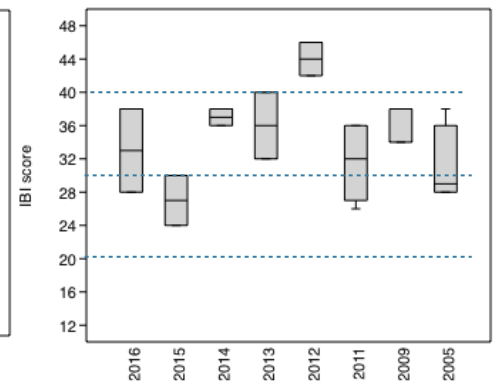
A. Downstream sampling sites



B. Mid-stream sites

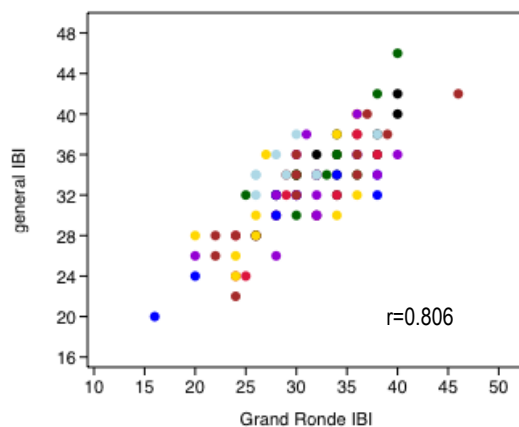


C. Upstream sites



Grande Ronde IBI (GRIBI) scores continue to show better overall biological condition scores than indicated by the standard I-IBI, with all sites in 2016 scoring as minimally impaired. Part of this difference is due to the fact that the GRIBI has only three biological condition categories while the I-IBI has four, and the site score that corresponds to minimal impairment is much lower for the GRIBI (≥ 26) than for the I-IBI (> 39). However, the GRIBI was developed specifically for streams in northeastern Oregon, with scoring ranges designed to reflect the biotic community conditions expected in those settings, and the general and Grande Ronde IBI site scores show a strong correlation (Figure 3; Pearson's $r = 0.806$)

Figure 3. Correlation between site scores for the general I-IBI and the GR-IBI developed for northeastern Oregon. Yellow=2005, light blue=2009, brown=2011, green=2012, purple=2013, red=2014, dark blue=2015, black=2016.

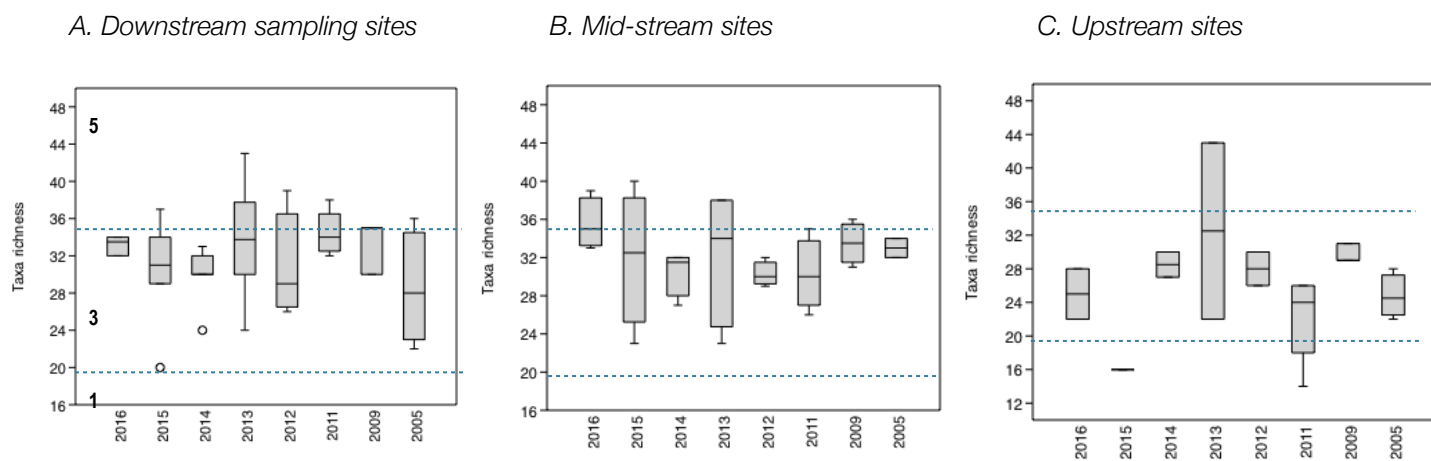


Changes in individual metrics

Changes in the individual metrics used to generate the I-IBI score were examined to determine if any have undergone greater changes and are exhibiting a stronger driving force on the overall IBI scores.

Taxa richness: The median number of unique taxa present among downstream and mid-stream sites has increased overall (Figure 4), while this metric has varied more among upstream sampling sites. The range of taxa richness across all reaches is generally in the intermediate scoring range for the IBI. Among downstream sites, mean taxa richness in 2016 was significantly greater than in 2014, and greater but not quite significant compared to 2005 ($p=0.0892$). Among mid-stream sites, mean taxa richness in 2016 was significantly greater than in 2014 and 2012, and greater but not quite significant compared to 2011 ($p=0.0599$). Among upstream sites, mean taxa richness in 2016 was not significantly different from other years, although the difference was not quite significant compared to 2015 (higher in 2016; $p=0.0955$).

Figure 4. Taxa richness across time. Horizontal line in each box indicated the median value; filled box shows the interquartile range; whiskers depict data range; points show outlier values. Dotted lines show cutoff points for IBI scoring; bold numbers show scaled scores for IBI.



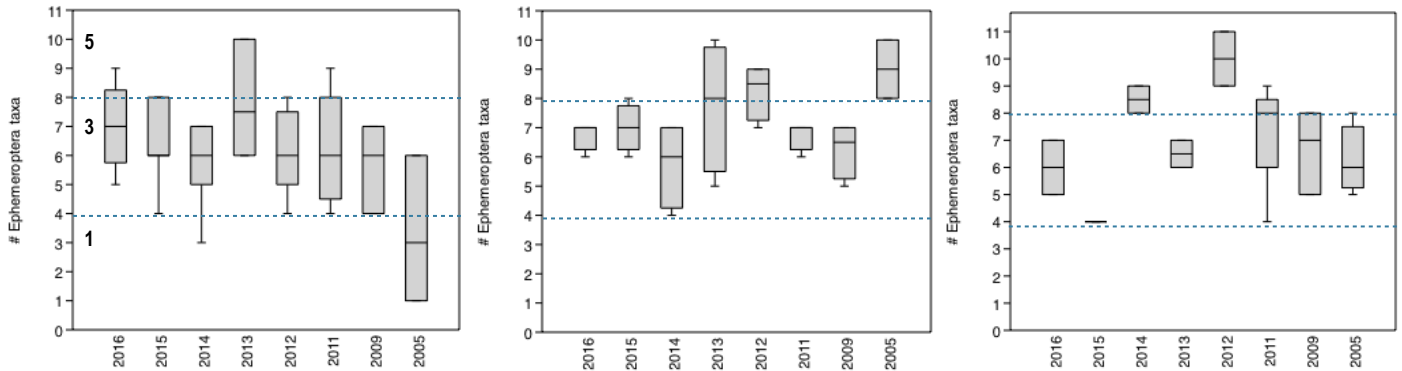
Ephemeroptera richness: The number of mayfly taxa has increased fairly steadily among downstream sites, but shows much between-year variation among mid-stream and upstream sites, with no sustained pattern (Figure 5). The range of mayfly taxa across all reaches is generally in the intermediate scoring range for the IBI. Among downstream sites, the mean number of mayfly taxa in 2016 was significantly greater than in 2005. Among mid-stream sites, the mean number of mayfly taxa in 2016 was significantly lower than in 2012 and 2005, and among upstream sites, the mean in 2016 did not differ significantly from any other year.

Figure 5. Ephemeroptera richness across time. Horizontal line in each box indicates the median value; filled box shows the interquartile range; whiskers depict data range. Dotted lines show cutoff points for IBI scoring; bold numbers show scaled scores for I-BI.

A. Downstream sampling sites

B. Mid-stream sites

C. Upstream sites



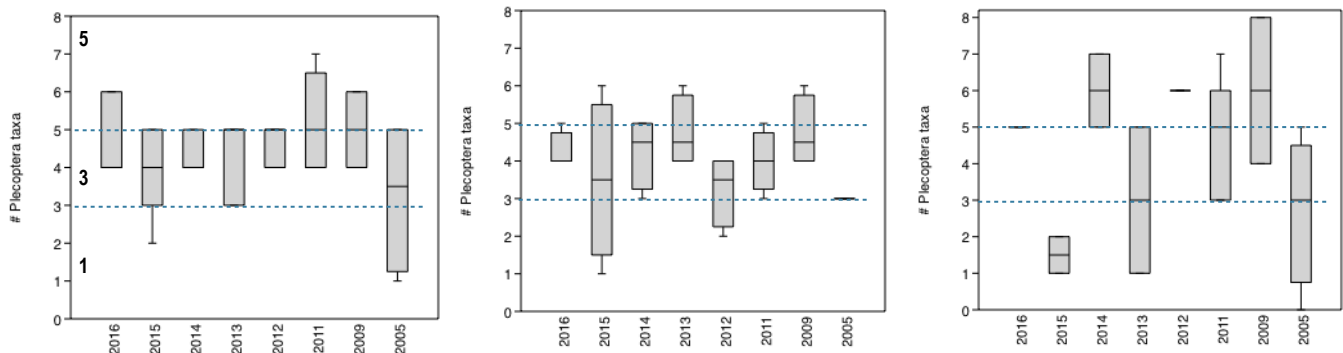
Plecoptera richness: The number of stonefly taxa in each year shows the greatest variation among upstream and mid-stream sites, with downstream sites more stable (Figure 6). The range of stonefly richness across downstream and mid-stream sites is generally in the intermediate scoring range for the IBI, while the taxa number at upstream sites ranges more frequently into the highest scoring zone. Among downstream sites, the mean number of stonefly taxa in 2016 did not differ significantly from that seen in any other year, but the mean among mid-stream sites was significantly greater than in 2005, and among upstream sites the mean was significantly greater than in 2009.

Figure 6. Plecoptera richness across time. Horizontal line in each box indicated the median value; filled box shows the interquartile range; whiskers depict data range. Dotted lines on graphs show cutoff points for IBI scoring; bold numbers show scaled scores for IBI.

A. Downstream sampling sites

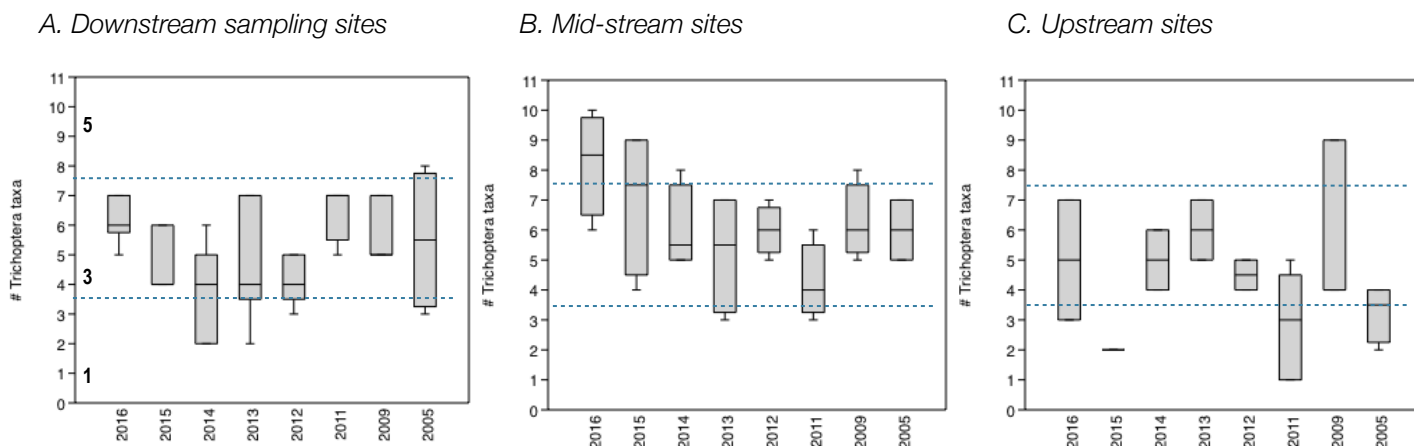
B. Mid-stream sites

C. Upstream sites



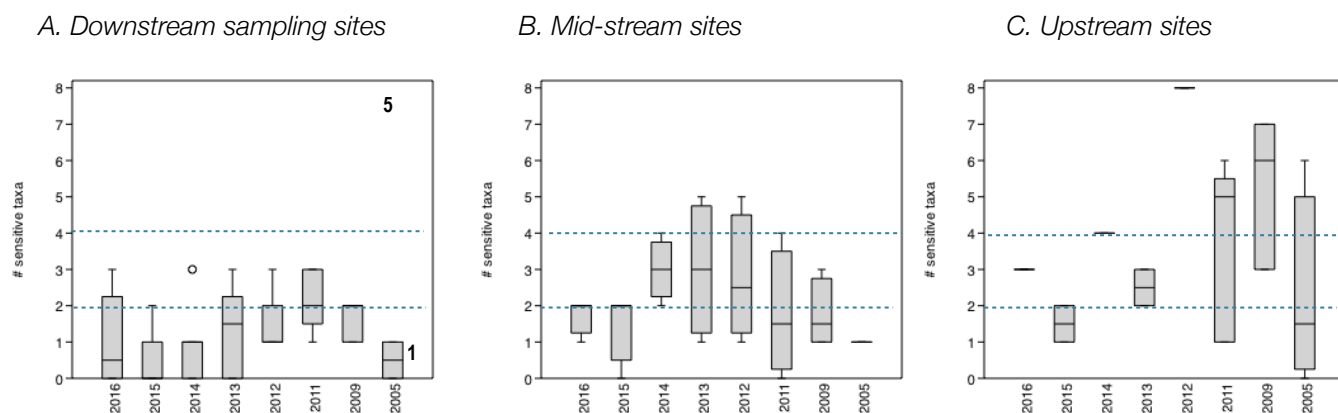
Trichoptera richness: The range of caddisfly taxa richness shows a sustained increase among mid-stream sites. Downstream and upstream sites vary more, with some indication of recovery in recent years following an early decrease in caddisfly richness (Figure 7). The number of caddisfly taxa in most years has been in the intermediate scoring range among all reaches, although the range in recent years at mid-stream sites has climbed into the highest IBI scoring zone. Among downstream sites, the mean number of caddisfly taxa in 2016 was significantly greater than in 2015, 2014, and 2012. Among mid-stream sites, the mean number of taxa in 2016 was significantly greater than in 2011, and greater but not quite significant compared to 2014 ($p=0.0887$), 2013 ($p=0.0662$), and 2012 ($p=0.0550$). Among upstream sites, mean number of caddisfly taxa in 2016 was not significantly different than in any other year.

Figure 7. Trichoptera richness across time. Horizontal line in each box indicates the median value; filled box shows the interquartile range; whiskers depict data range. Dotted lines show cutoff points for IBI scoring; bold numbers show scaled scores for IBI.



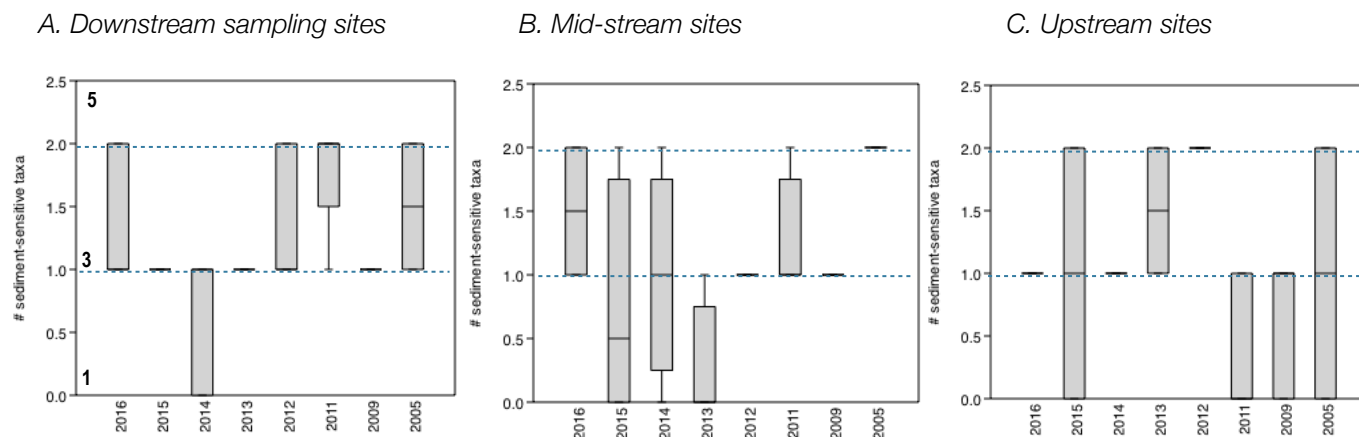
Number of sensitive taxa: The range of values for the number of sensitive taxa varies greatly within all sampling reaches, but shows some indication of an early increase followed by a decrease (Figure 8), especially among mid-stream and upstream sites. Downstream sites consistently exhibit the lowest numbers of sensitive taxa, and the range in most years falls into the lowest or intermediate I-BI scoring zone. Upstream sites consistently have the greatest number of sensitive taxa, and more values that correspond to the highest scaled I-BI scoring zone. The mean number of sensitive taxa in 2016 among all downstream sites did not differ significantly from that in any other year. Among mid-stream sites, the mean in 2016 was significantly lower than in 2014, and among upstream sites, the mean number in 2016 was significantly lower than in 2012.

Figure 8. Number of sensitive taxa across time. Horizontal line in each box indicates the median value; filled box shows the interquartile range; whiskers depict data range; points show outlier values. Dotted lines show cutoff points for IBI scoring; bold numbers show scaled scores for IBI.



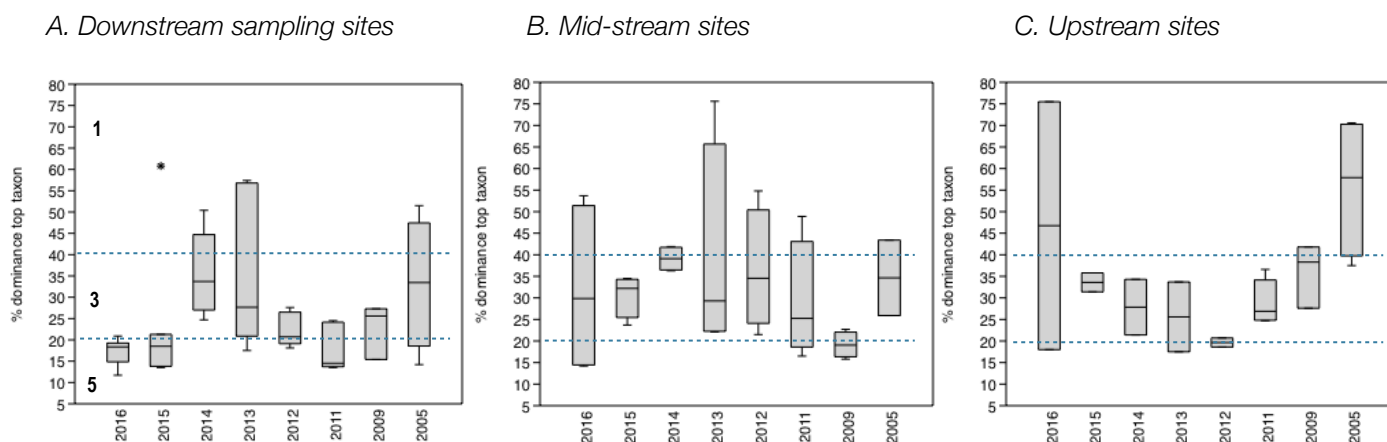
Number of sediment sensitive taxa: The I-BI model considers the presence of any sediment-sensitive taxa to warrant a scaled score in the intermediate range, and the presence two of these taxa receives the highest scaled score. With this in mind, although the number of sediment-sensitive taxa has never exceeded two at any site, and while some sites have lacked sediment-sensitive taxa in particular sampling years, there are no years in which at least one sediment-sensitive taxon was not found within the broader sampling reaches (Figure 9). The very low number of these taxa limits the information content of this metric, but the mean number of sediment-sensitive taxa in 2016 was significantly greater than in 2014 among all downstream sites, significantly greater than in 2013 among mid-stream sites, and significantly lower than in 2012 among upstream sites.

Figure 9. Number of sediment-sensitive taxa across time. Horizontal line in each box indicates the median value; filled box shows the interquartile range; whiskers depict data range. Dotted lines on graphs show cutoff points for IBI scoring; bold numbers show scaled scores for IBI.



Dominance of the top taxon: A balanced biological community is considered to be one that is not heavily dominated by a particular group; for this reason, a lower relative abundance of the most abundant taxon at a site receives a higher scaled score in the I-IBI. Raw values for this metric have shown the broadest range of any I-IBI metric across time, with individual site scores in many years indicating a “top heavy”, unbalanced community. However, in recent years, the range of values for % dominance have decreased, and more sites, especially in the downstream reach, are scoring in the highest range of the I-IBI (Figure 10). The upstream sampling sites in 2016 are a glaring exception; this is due to the fact that the sample from WC2600, where new channel restoration is still ongoing, was comprised mostly (75%) of *Simulium* black flies. The other upstream site sampled in 2016, WC2425, had a more balanced community dominated by the sensitive chloroperlid stonefly *Suwallia*, which comprised 18% of the total sample abundance. *Simulium* were previously seen in sudden large abundance soon after channel restoration was done on Whychus at Camp Polk, so they may be early colonizers of newly-restored running waters where rocky substrates are available. Among downstream sites, the mean % dominance of the top taxon in 2016 was significantly lower than in 2014, 2013, 2012, and 2005, but the mean value among mid-stream and upstream sites in 2016 did not differ significantly from any other sampling years.

Figure 10. Dominance (relative abundance) of the top taxon across time. Horizontal line in each box indicates the median value; filled box shows the interquartile range; whiskers depict data range; points show outlier values. Dotted lines show cutoff points for IBI scoring; bold numbers show scaled scores for IBI.

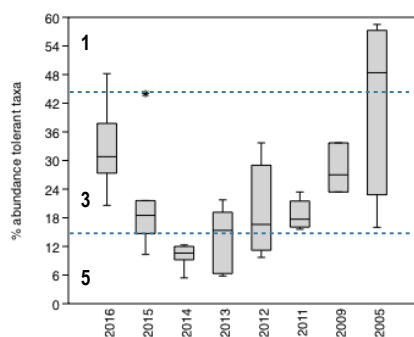


% Tolerant taxa: The relative abundance of tolerant taxa is another negative metric in the I-IBI, where a lower raw value receives a higher scaled score. The upstream reach of Whychus Creek consistently has the lowest proportions of tolerant taxa, and all reaches have seen an overall decrease in % tolerant taxa since the earliest sampling years (Figure 11). These numbers have continued to decrease in recent years among upstream sites, but the proportion of tolerant taxa at sites in the mid-stream and downstream have been increasing in the last two

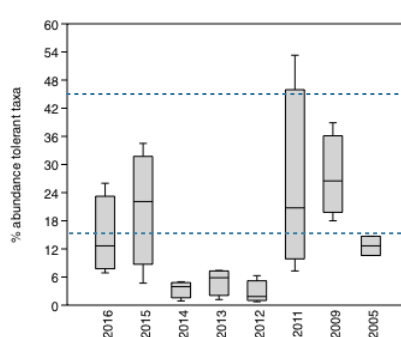
years. The mean relative abundance of tolerant taxa among downstream sites in 2016 was significantly higher than in 2011-2014, and was higher but not quite significant compared to 2015 ($p=0.0614$). Among mid-stream sites, mean relative abundance of tolerant taxa in 2016 was significantly higher than in 2014 and 2012, and higher but not quite significant compared to 2013 and 2009 ($p=0.0742$ and 0.0748 , respectively). Among upstream sites, mean abundance of tolerant taxa in 2016 was significantly higher than in 2012, and was lower but not quite significant compared to 2011 ($p=0.0882$).

Figure 11. Relative abundance of tolerant taxa across time. Horizontal line in each box indicates the median value; filled box shows the interquartile range; whiskers depict data range; points show outlier values. Dotted lines show cutoff points for IBI scoring; bold numbers show scaled scores for IBI.

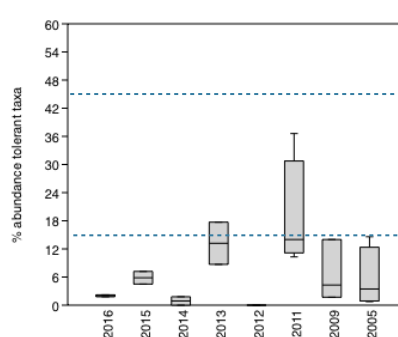
A. Downstream sampling sites



B. Mid-stream sites



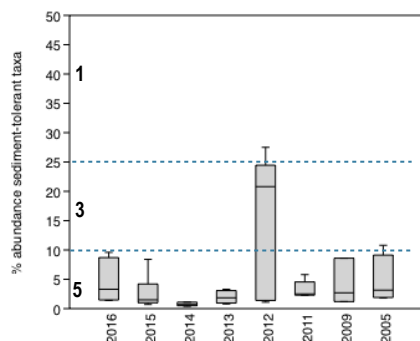
C. Upstream sites



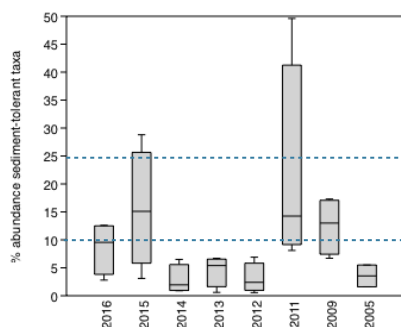
% Abundance of sediment-tolerant taxa: The relative abundance of sediment-tolerant taxa is a negative metric, where a lower raw value receives a higher scaled score. Sediment has always appeared to be a strong driver of the macroinvertebrate community in Whychus Creek, and the raw value for this metric among most sampling sites falls into the highest scoring range of the I-IBI, especially within the downstream reach (Figure 12). Sediment-tolerant taxa abundance varies more among mid-stream and upstream reaches, but proportions are lower overall in recent years after having increased in earlier sampling years. The % abundance of sediment-tolerant taxa among downstream sites in 2016 was significantly higher than in 2014 and lower but not quite significant compared to 2012 ($p=0.0886$), but the range for this metric remains low. Among mid-stream sites, the mean % sediment-tolerant taxa in 2016 did not differ significantly from that in any other years, although the difference was close to significant in 2014 and 2012 (higher in 2016; $p = 0.0730$ and 0.0851 , respectively). The mean % sediment-tolerant taxa among upstream sites was significantly lower in 2016 than in 2015, and lower but not quite significant compared to 2011 ($p = 0.0785$).

Figure 12. Relative abundance of sediment-tolerant taxa across time. Horizontal line in each box indicates the median value; filled box shows the interquartile range; whiskers depict data range. Dotted lines show cutoff points for IBI scoring; bold numbers show scaled scores for IBI.

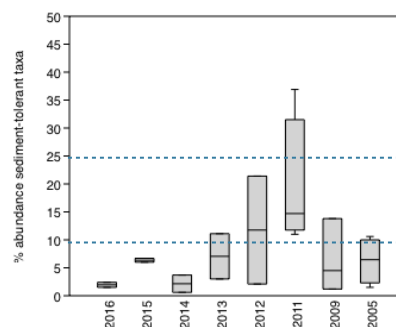
A. Downstream sampling sites



B. Mid-stream sites



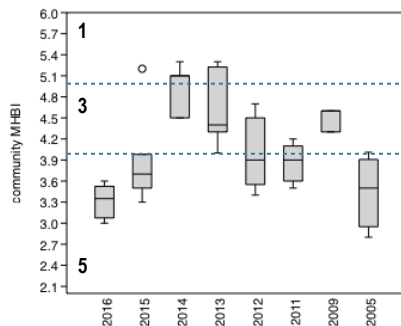
C. Upstream sites



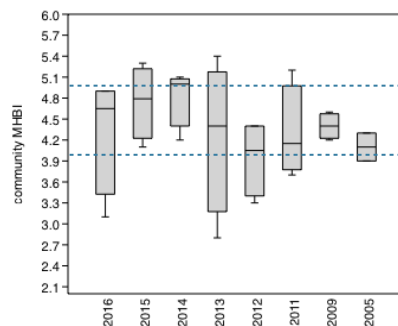
Modified Hilsenhoff Biotic Index (MHBI): MHBI is a measure of tolerance to organic pollution, with a lower value indicating a more sensitive taxon or community; values range from 0 to 10. Community MHBI is calculated for each sample site in each year as the weighted mean of individual taxon MHBI values. Mean community MHBI scores have varied little among mid-stream sites over time, with most score ranges in each year falling within the intermediate I-BI scoring zone (Figure 13). The range of community MHBI scores among downstream sites increased fairly steadily since 2005, but has decreased in recent years, dropping into the zone that receives the highest I-BI scaled score. In contrast, MHBI scores among upstream sampling sites decreased through 2012, but have been rising again in recent years. The mean community MHBI among downstream sites was significantly lower in 2016 than in all other sampling years except 2015 and 2005, and was lower but not quite significant compared to 2015 ($p = 0.0695$). Mean community MHBI values among mid-stream and upstream sites in 2016 were not significantly different from those in other sampling years.

Figure 13. Mean community MHBI across time. Horizontal line in each box indicates the median value; filled box shows the interquartile range; whiskers depict data range; points show outlier values. Dotted lines show cutoff points for IBI scoring; bold numbers show scaled scores for IBI.

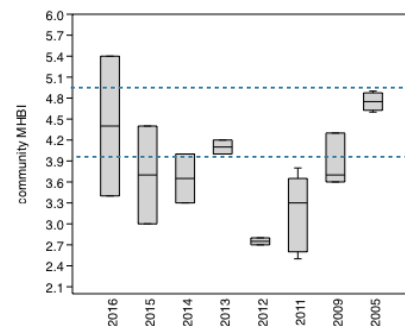
A. Downstream sampling sites



B. Mid-stream sites



C. Upstream sites

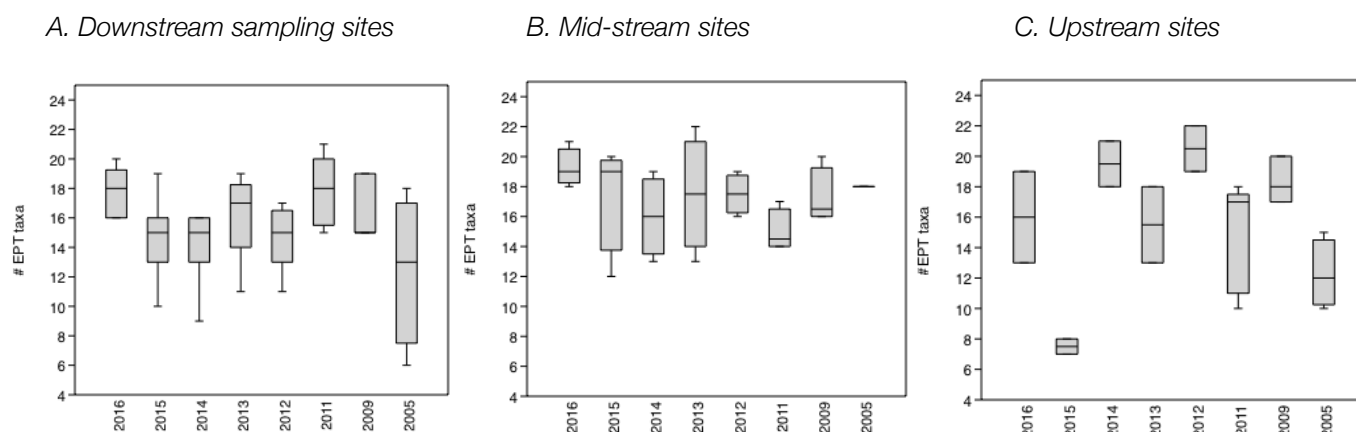


Additional Community Metrics

EPT richness:

Many indices of biotic integrity examine EPT richness as a combined group that comprises the most sensitive stream taxa. While the number of EPT taxa has varied annually (especially among upstream sites), overall the median number of EPT taxa has increased at downstream and mid-stream sites compared to earlier sampling years (Figure 14). The mean number of EPT taxa among downstream sites was significantly greater in 2016 than in 2015, 2014, 2012, and 2005. Among mid-stream sites, the mean number of EPT taxa in 2016 was significantly greater than in 2011 and greater but not quite significant compared to 2014 ($p = 0.0643$). Among upstream sites, the mean number of EPT taxa in 2016 was not significantly different than that in any other year, although the median and range were much higher than in 2015.

Figure 14. Number of EPT taxa (Ephemeroptera, Plecoptera, Trichoptera) across time. Horizontal line in each box indicates the median value; filled box shows the interquartile range (25-75th quartiles); whiskers depict data range.

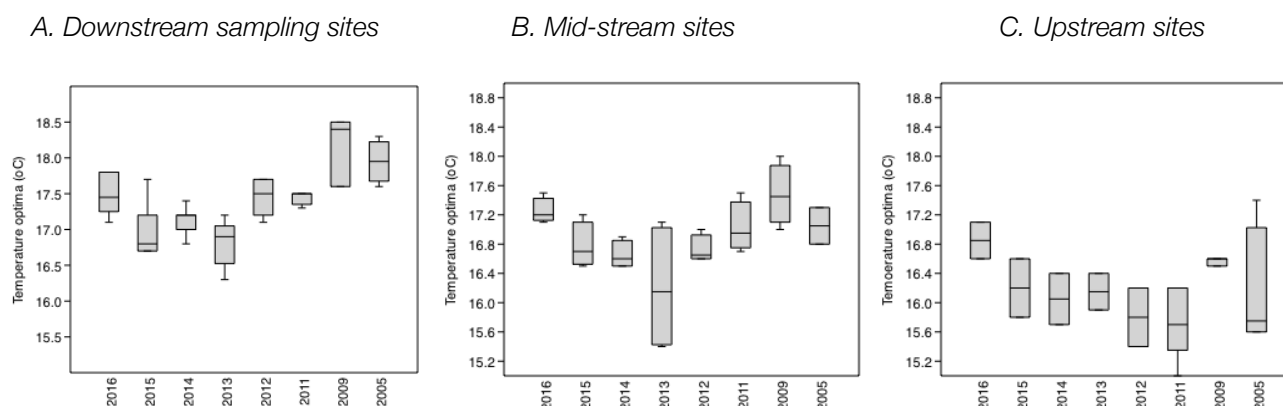


Community temperature optima:

ORDEQ developed a dataset of individual taxa optima values for seasonal maximum temperature (i.e. the temperature under which a taxon can maximize its abundance). Community temperature optima are calculated for each sampling site as the weighted mean of optima for individual taxa in the sample. Temperature optima among upstream sampling sites are overall lower than those in mid-stream and downstream sites, but they have increased since sampling began (Figure 15). In addition, a period of steadily decreasing temperature optima among mid-stream and downstream sites from 2005-2013 has been reversing itself in recent years.

The mean temperature optima for communities at downstream sites was significantly higher in 2016 than in 2015, 2014, and 2013, although still significantly lower than in 2009 and 2005. Among mid-stream sites, mean community temperature optima was significantly higher in 2016 than in 2015, 2014, and 2012, and higher but not quite significant compared to 2013 ($p = 0.0568$). Among upstream sites, the mean community temperature optima was significantly higher in 2016 than in 2011, and this is the first time since 2011 that an annual temperature optima has differed significantly from that of an earlier year. Given that the last three years have been the hottest in recorded history (NOAA, 2016), this may be a signal that the stream community is responding to larger climate stressors.

Figure 15. Mean community temperature optima across time. Horizontal line in each box indicates the median value; filled box shows the interquartile range; whiskers depict data range.



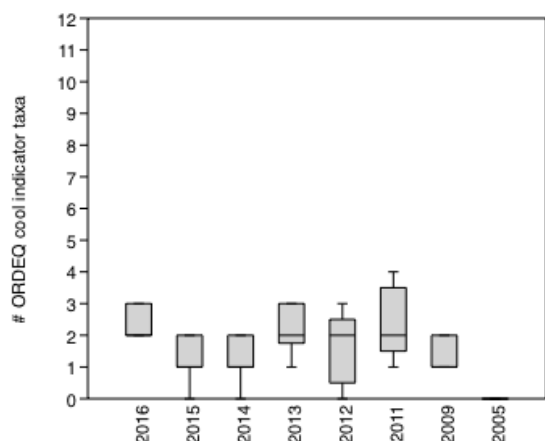
ORDEQ indicator taxa for temperature:

ORDEQ has also developed a dataset of taxa that are considered indicators of cool or warm temperate conditions (see Appendix B). For the first few years in which sampling was done, the number of warm temperature indicator taxa declined among all sampling reaches, while the number of cool indicator taxa increased (Figure 16). However, since 2013, the number of cool indicator taxa among mid-stream and upstream reaches sampling reaches has decreased, and the number of warm indicator taxa has risen among downstream and mid-stream sites.

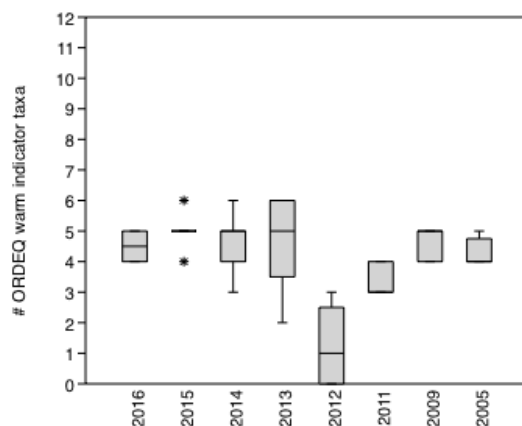
The mean number of cool indicator taxa among downstream sites in 2016 was significantly higher than in 2015, 2014, 2009, and 2005 (which lacked cool indicator taxa), but the mean number of warm indicator taxa among downstream sites in 2016 was significantly greater than in 2012 and 2013. Among mid-stream sites, the mean number of cool indicator taxa in 2016 was significantly lower than in 2012, and lower but not quite significant compared to 2013 and 2009 ($p=0.0550$ and 0.0941 , respectively). The mean number of warm indicator taxa in 2016 at mid-stream sites was significantly greater than in 2014, 2012, and 2011, and greater but not quite significant compared to 2013 ($p = 0.0941$). Among upstream sites, the mean number of cool indicator taxa in 2016 was significantly lower than in 2012, and overall, there have been very few warm indicator taxa among upstream sampling communities since 2009, with no more than one in any year.

Figure 16. Number of DEQ indicator taxa for cool and warm temperatures. Horizontal line in each box indicates the median value; filled box shows the interquartile ranges; whiskers depict data range; points show outlier values.

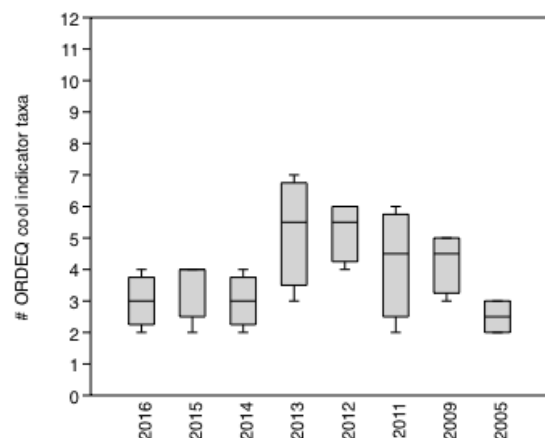
A. Downstream, cool indicators



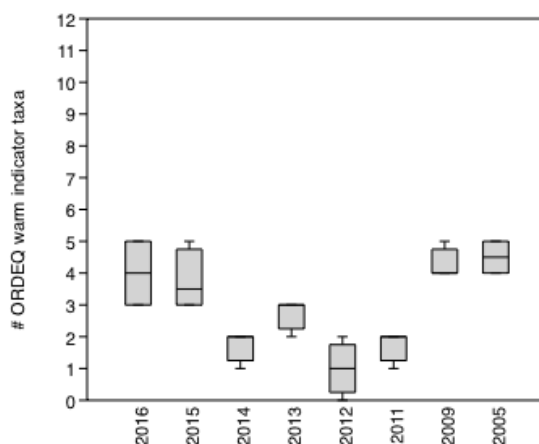
B. Downstream, warm indicators



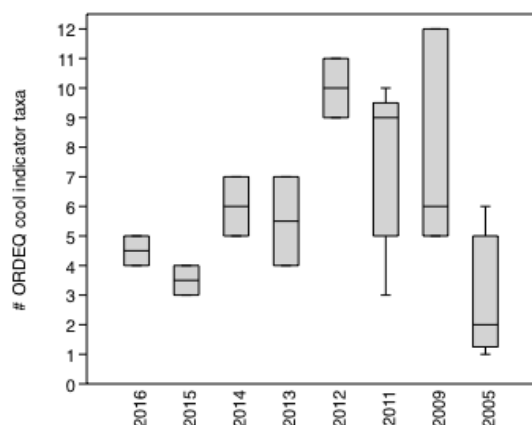
C. Mid-stream, cool indicators



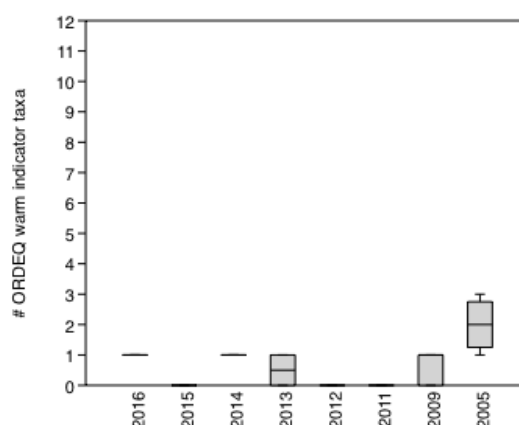
D. Mid-stream, warm indicators



E. Upstream, cool indicators



F. Upstream, warm indicators

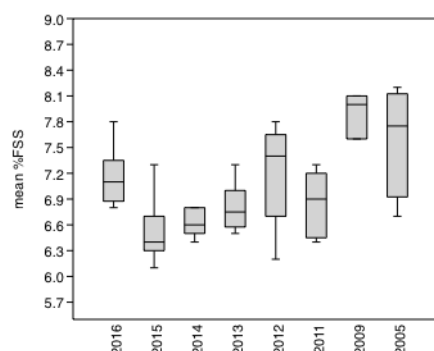


Community sediment optima:

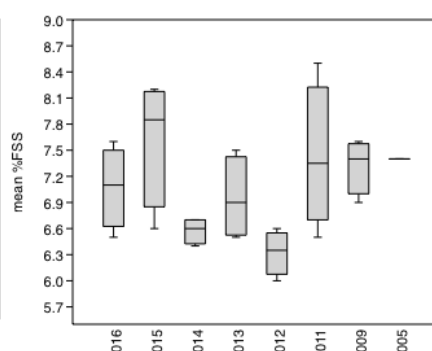
ORDEQ developed a dataset of individual taxa optima values for percent fine sediments (%FSS under which a taxon can maximize its abundance). Community sediment optima are calculated for each sampling site as the weighted mean of optima for individual taxa in the sample. Community sediment optima vary greatly between years, although they have decreased more steadily over time among downstream sites (Figure 17). Mean %FSS optima among downstream sites in 2016 was significantly greater than in 2015 and 2014, though it was significantly lower than in 2009. Among mid-stream sites, mean %FSS optima in 2016 was significantly higher than in 2012, and higher but not quite significant compared to 2014 ($p = 0.0830$). The mean FSS optima in 2016 among upstream sites was not significantly different compared to that in any other year.

Figure 17. Mean % fine suspended sediment optima (FSS) across time. Horizontal line in each box indicates the median value; filled box shows the interquartile ranges; whiskers depict data range.

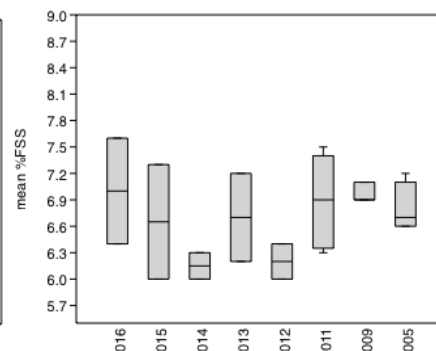
A. Downstream sampling sites



B. Mid-stream sites



C. Upstream sites

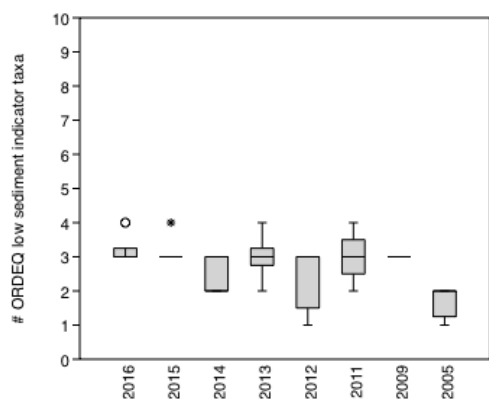


ORDEQ indicator taxa for sediment:

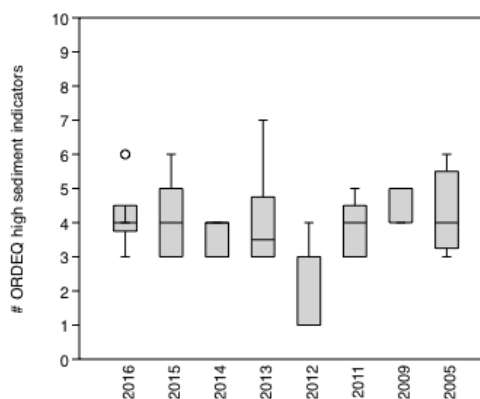
ORDEQ has developed a dataset of taxa that are considered indicators of low or high sediment conditions (see Appendix B). The number of ORDEQ taxa considered indicative of low sediment conditions varies between years, has increased overall since the earliest sampling years, while the number of high sediment indicator taxa dropped and then stabilized among all reaches (Figure 18). The mean number of low sediment indicator taxa among downstream sites in 2016 was significantly greater than in 2014 and 2005, and greater but not quite significant compared to 2012 ($p = 0.0911$). Among mid-stream sites, the mean number of low sediment indicator taxa in 2016 was not significantly different compared to those in other years, though the difference was close to significant compared to 2015 and 2005 (greater in 2016; $p = 0.0633$ and 0.0709 , respectively), and the mean number of high sediment indicator taxa in 2016 was significantly higher than in 2014. Among upstream sites, the mean number of low sediment indicator taxa in 2016 was significantly greater than in 2005, and lower but not quite significant compared to 2012 ($p = 0.0887$). The mean number of high sediment indicator taxa at upstream sites in 2016 did not differ significantly from any other year.

Figure 18. Number of ORDEQ indicator taxa for low and high % fine suspended sediment (FSS). Horizontal line in each box indicates the median value; filled box shows the interquartile ranges; whiskers depict data range; point show outlier values.

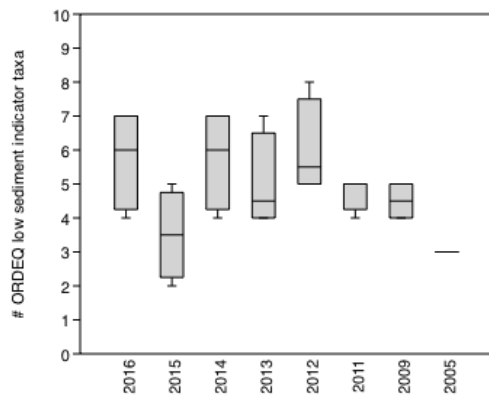
A. Downstream, low sediment indicators



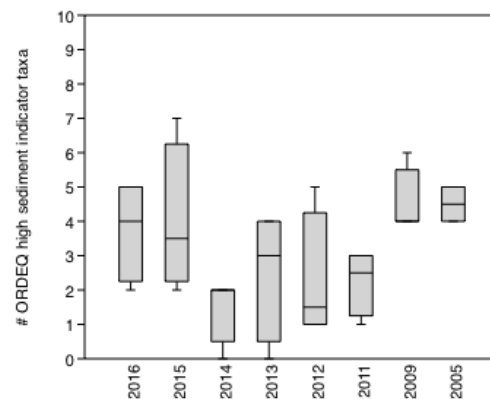
B. downstream, high sediment indicators



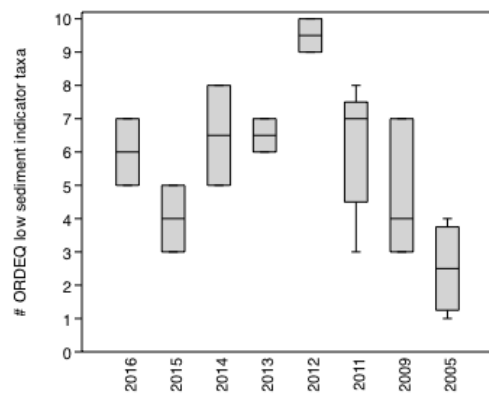
C. Mid-stream, low sediment indicators



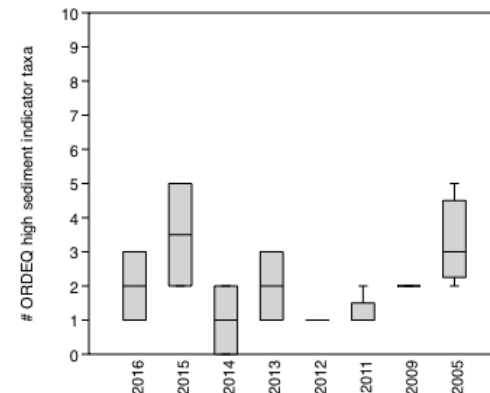
D. Mid-stream, high sediment indicators



E. Upstream, low sediment indicators



F. Upstream, high sediment indicators



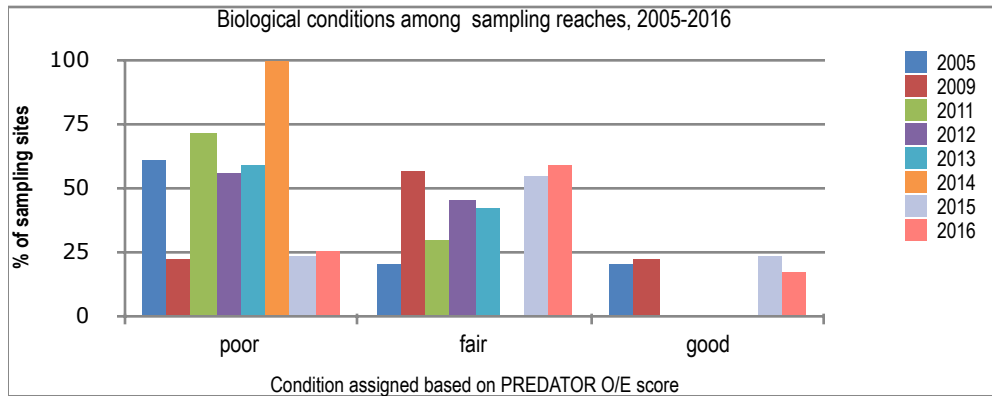
PREDATOR model

Of the 12 sites sampled in 2016, two (17%) had site O/E scores indicating good biological conditions, seven (58%) had scores indicating fair biological conditions, and three (25%) scored as having poor biological conditions. Overall, these scores represent an improvement over those seen in recent years (Table 4). In comparison to previous years, PREDATOR scores for 2015 and 2016 show an increase in the number of sites scoring as good and fair biological condition, and a decrease in those scoring as poor (Figure 19).

Table 4. Site PREDATOR O/E scores. Colors indicate biological conditions corresponding to O/E score (good = green, fair = blue, poor = red)

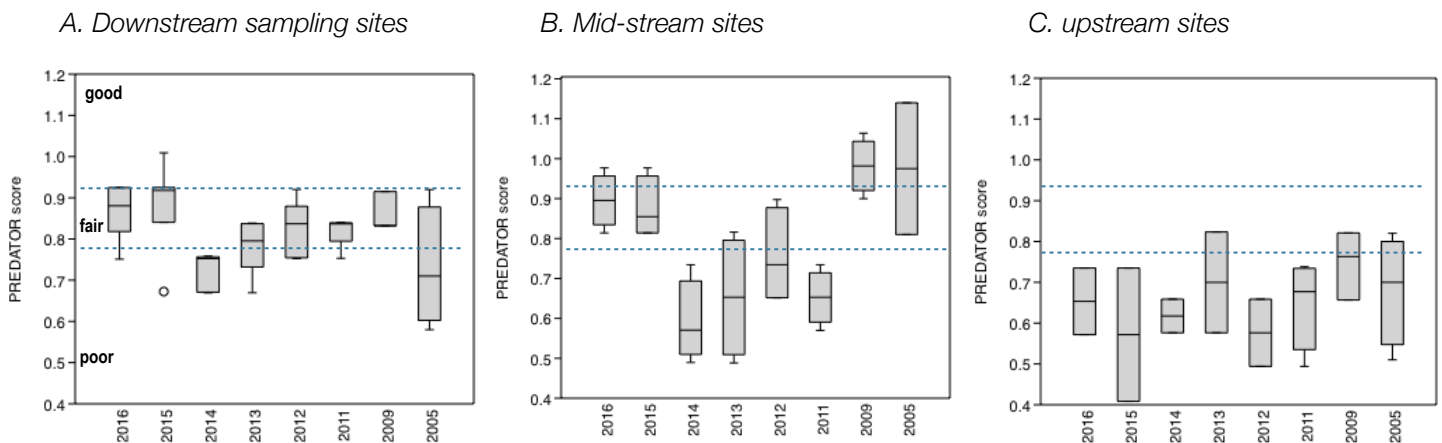
Site	2005	2009	2011	2012	2013	2014	2015	2016
WC0050	0.92	---	---	---	---	---	---	---
WC0150	---	0.83	0.84	0.75	0.84	0.75	0.92	0.75
WC0300	0.58	—	—	—	—	—	—	—
WC0600	0.67	0.83	0.84	0.84	0.75	0.67	0.92	0.92
WC0650	—	—	—	—	0.84	—	—	—
WC0875	—	—	0.75	0.84	0.67	0.75	0.67	0.92
WC0900	0.75	0.92	0.84	0.92	0.84	0.67	0.84	0.84
WC0950*	—	—	0.84	0.76	0.75	0.76	1.01	—
WC1025 (WC1100)	—	—	—	—	—	0.76	0.93	0.84
WC1075 (WC1150)	—	—	—	—	—	0.73	0.84	0.93
WC1800	0.81	—	—	—	—	—	—	—
WC1825	—	0.98	0.65	0.65	0.57	0.49	0.90	0.98
WC1850	—	0.90	0.57	0.65	0.49	0.57	0.81	0.90
WC1900	1.14	0.98	0.73	0.90	0.82	0.73	0.98	0.90
WC1950	—	1.06	0.65	0.82	0.73	0.57	0.81	0.81
WC2325	0.82	—	—	—	—	—	—	—
WC2425	0.74	0.82	0.49	0.49	0.82	0.66	0.74	0.74
WC2600	0.66	0.66	0.58	0.66	0.58	0.58	0.41	0.57
WC2650	—	—	0.73	—	—	—	—	—
WC2700	—	—	0.74	—	—	—	—	—
WC3025	0.51	0.76	0.68	—	—	—	—	—

Figure 19. Comparison of site biological condition categories indicated by PREDATOR O/E scores across time.



The range of scores in each year in downstream and mid-stream sampling sites shows an interesting trend, decreasing through 2014 and then rising again in 2015 and 2016 (Figure 20). Mean PREDATOR scores among downstream sites were significantly higher in 2016 than in 2014, and higher but not quite significant compared to 2013 and 2005 ($p = 0.0572$ and 0.0761 , respectively). Mean PREDATOR scores were also significantly higher among mid-stream sites in 2016 compared to 2014, 2013, and 2011, and higher but not quite significant compared to 2012 ($p = 0.0901$). Mean PREDATOR scores among upstream sites in 2016 did not differ significantly from those in any other year, and the range of site scores for this reach have generally been in the zone that scores as poor biological condition.

Figure 20. PREDATOR O/E scores across time. Horizontal line in each box indicates the median value; filled box shows the interquartile range; whiskers depict data range; points show outlier values. Dotted lines show cutoffs for impairment categories.



Biological conditions generated via the PREDATOR model generally indicate a more impaired state than those generated by the I-IBI. This is particularly true for the upstream reach; while I-IBI scores among upstream sites vary more between years and score more frequently as slightly impaired, these same sites have less variation in O/E scores from year to year, and scores usually indicate poor biological conditions. The upstream sampling set includes a site with the heaviest human usage (WC2425); this sampling reach runs through Sisters City Park in the middle of a heavily used campground, there is a high level of both human and dog activity in the stream itself, and a highway delimits the downstream end of the reach. Because there are few upstream sampling sites in each year, this more anthropogenically-impacted site could contribute disproportionately to lower biotic condition scores. However, I-IBI scores have increased overall at this reach since 2011, and several individual community metrics have improved among upstream sites since the earliest sampling years, especially those related to sediment conditions.

Overall, there is poor correlation between PREDATOR and I-IBI scores for all sites in all years (Pearson's $r = 0.185$, $p = 0.072$). When examined by reach, there is better (though still low) correlation between I-IBI and PREDATOR scores for downstream ($r = 0.3505$, $p = 0.0211$) and mid-stream ($r = 0.3364$, $p = 0.0691$) sites, but no correlation among the upstream sampling sites ($r = 0.0676$, $p = 0.7651$). This lack of agreement between the two models has been something of a conundrum for Whychus Creek. Although in every year the PREDATOR site test score indicates that the model is suitable for the sites and that appropriate reference streams within the model were identified for comparison, Whychus Creek has lower annual precipitation than any of the reference streams the model selects as most appropriate (Shannon Hubler, pers. comm.), making it somewhat of an outlier for the PREDATOR model itself. Predictive models are often considered to be more sensitive and accurate than IBIs, but it should be noted that the PREDATOR model has not been re-calibrated since it was created using stream survey data from 1998-2004, and the WCCP model applicable to the Cascades has lower precision than the MWCF model developed for the Willamette Valley (Hubler, 2008; Hubler, pers. comm.). Periodic sampling of reference streams used to build the models and model re-calibration is needed to detect any shifts arising from altered environmental conditions such as climate change, so it is possible that the sensitivity of this model has changed over time. The impacts of climate change on the PREDATOR model are worth considering in light of the increasing community temperature optima that have been seen in recent years among all sampling reaches.

Missing/replacement taxa

For each sampling site, the PREDATOR model also identifies taxa that are expected to occur but were not collected (missing taxa), and taxa that were not expected but were collected in samples (replacement taxa), based on comparison to appropriate reference sites. The missing/replacement communities are investigated in each year to provide further details about community changes.

Community composition:

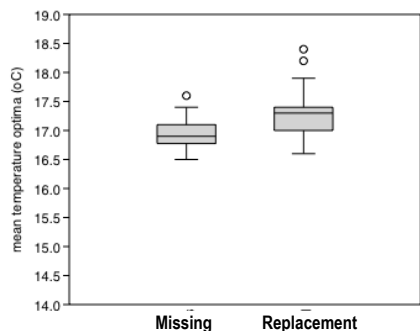
A SIMPER test on presence/absence data for missing and replacement taxa showed much greater similarity between the missing community in 2016 compared to all years than for the 2016 replacement community vs. that in other years. The average dissimilarity between the 2016 missing taxa community and the missing community in 2009-2015 ranged from 24.1-30.3% (mean = 27.5% + 2.1); however, the difference between the 2005 and 2016 missing taxa community was almost two times greater (50.2% overall average dissimilarity). The replacement taxa community in 2016 differed more overall from those in other sampling years than the missing community did, ranging from 52.4-57.6% in 2005-2015 (mean = 55.2 + 1.7). This could indicate a greater degree of community dynamism and colonization by different taxa that may not persist in the long-term due to existing or changing stream conditions.

Temperature optima:

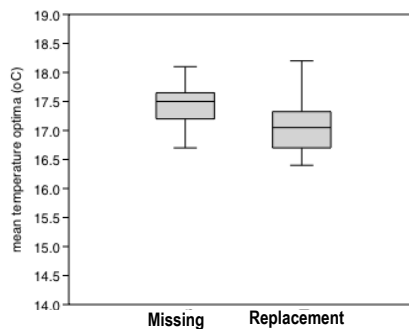
Community temperature optima were determined for missing and replacement communities at sites that were sampled in each year from 2005-2016. Among upstream and mid-stream sites, the median values for temperature optima were lower in the replacement taxa community (Figure 21); the means for replacement community temperature optima were also significantly lower than those of the missing taxa community at the same reaches. In contrast, the median value for temperature optima at downstream sites is higher among the replacement community, and the difference between the means is also significant. In 2016, the mean temperature optima of the replacement community among downstream sites was significantly higher than for missing taxa, virtually the same between the two communities among mid-stream sites, and lower but not quite significantly different in the replacement community at upstream sites ($p = 0.0794$).

Figure 21. Mean temperature optima among missing and replacement communities for sites sampled in all eight sampling years between 2005-2016. Horizontal line in each box indicates the median value; filled box shows interquartile ranges; whiskers depict data range; points show outliers.

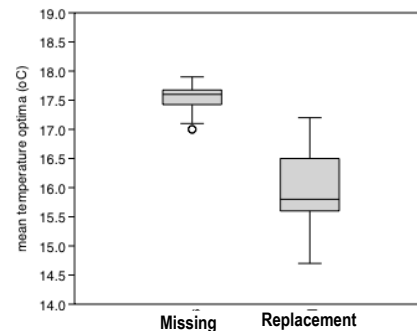
A. Downstream sampling sites, all years



B. Mid-stream sites



C. Upstream sites

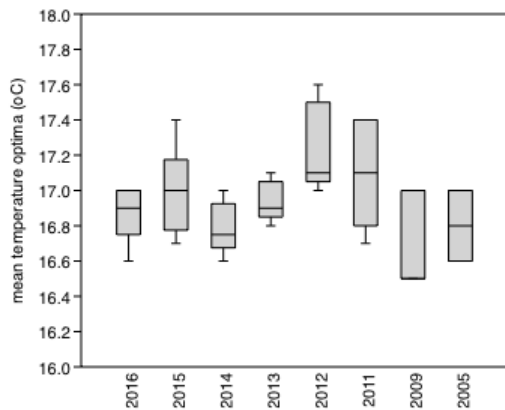


Examination of community temperature optima between all years shows a more dynamic picture (Figure 22). Between 2005 and 2012, the median value for replacement community temperature optima decreased steadily among downstream, mid-stream, and upstream sites, then rose again slightly in 2013 and remained more or less stable through 2016. This is similar to what was seen in the overall sampling community. Changes in the mean temperature optima of the missing community mirrored this, increasing through 2012. This suggests changing stream conditions following restoration improved temperatures and supported taxa that required lower water temperature ranges to survive. However, the recent increase in temperature optima among the replacement taxa community and decreases in the temperature optima among the missing community may indicate temperature as an increasing stressor.

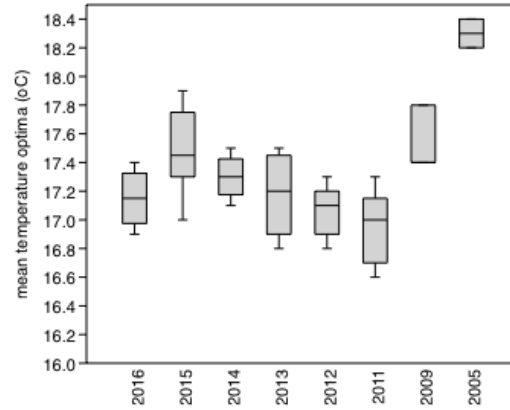
The mean temperature optima for the replacement community among downstream sites in 2016 was significantly lower than in 2015 and 2005, while the mean for the missing community in 2016 differed significantly only from that in 2012, which had the highest range of mean temperature optima values in all sampling years. Among mid-stream sites, the mean optima for the 2016 replacement community was significantly higher compared to 2012 and 2011, and mean for the missing community in 2016 was significantly lower compared to 2014, 2013, and 2012, and significantly higher than in 2005. Among upstream sites, the mean temperature optima for the missing and replacement community in 2016 did not differ from those in any other year.

Figure 22. Mean temperature optima among missing and replacement taxa between years. Horizontal line in each box indicates the median value; filled box shows the interquartile ranges; whiskers depict data range.

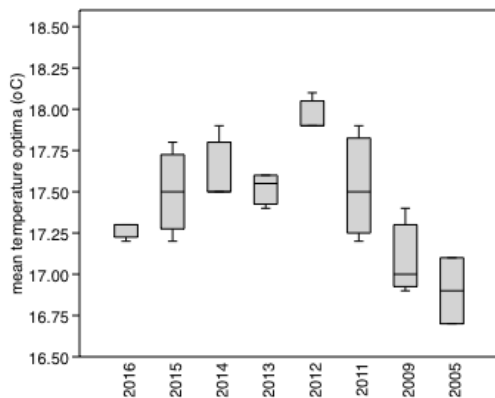
A. downstream sites, missing taxa



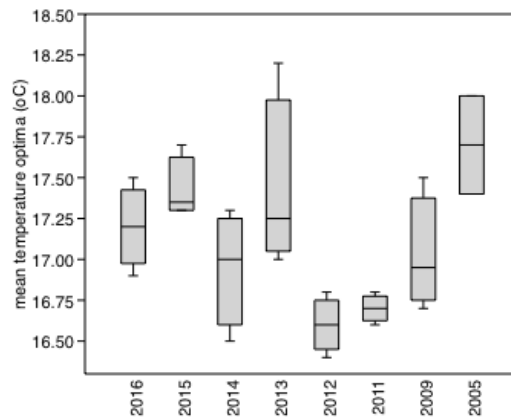
B. downstream sites, replacement taxa



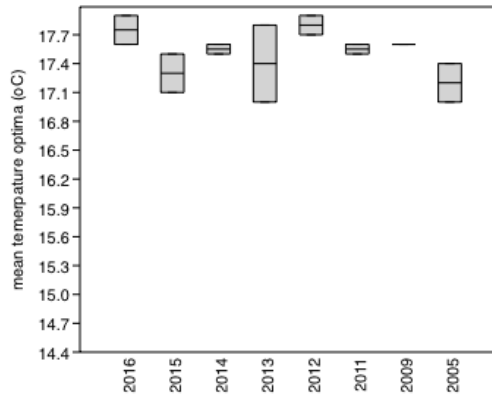
C. Mid-stream sites, missing taxa



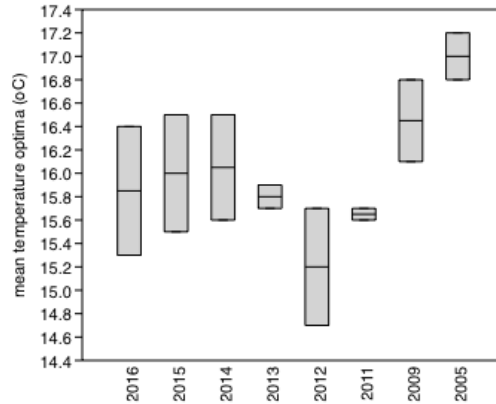
D. Mid-stream sites, replacement taxa



E. Upstream sites, missing taxa



F. Upstream sites, replacement taxa

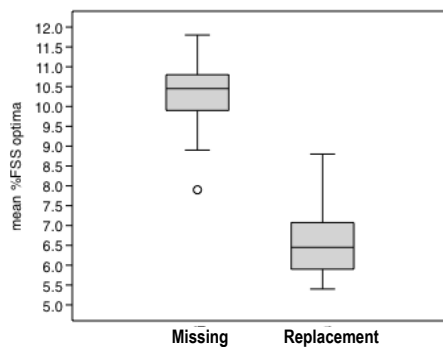


Fine suspended sediment (%FSS) optima:

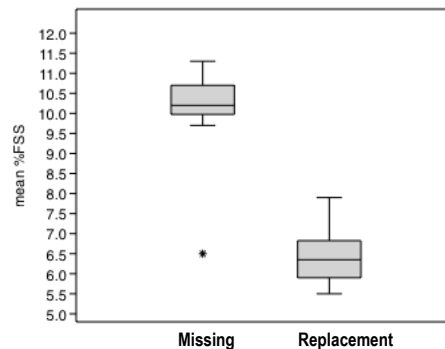
When considering sites that were sampled each year from 2005-2016, median values for sediment optima of the missing taxa community are almost twice as high as those of the replacement taxa community among downstream, mid-stream, and upstream reaches (Figure 23), and the mean %FSS optima for the missing community was also significantly greater than the replacement community among all sampling reaches. This indicates that sediment continues to be a strong community driver among all sampling reaches.

Figure 23. Mean % fine suspended sediment optima (FSS) among missing and replacement taxa across time. Horizontal line in each box indicates the median value; filled box shows the interquartile ranges; whiskers depict data range; points show outlier values.

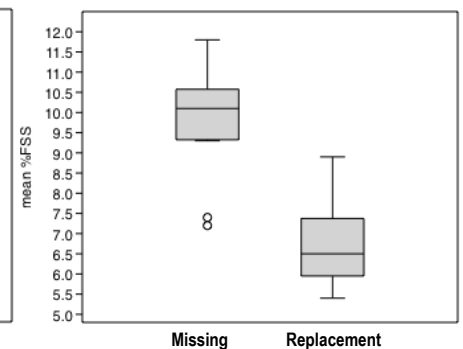
A. Downstream sampling sites



B. Mid-stream sites



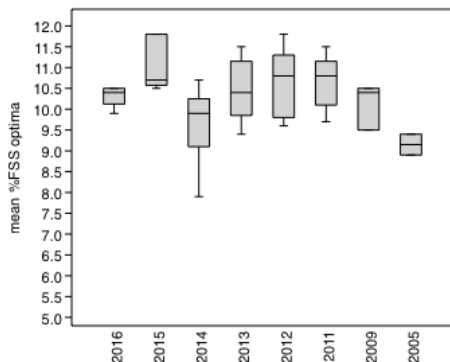
C. Upstream sites



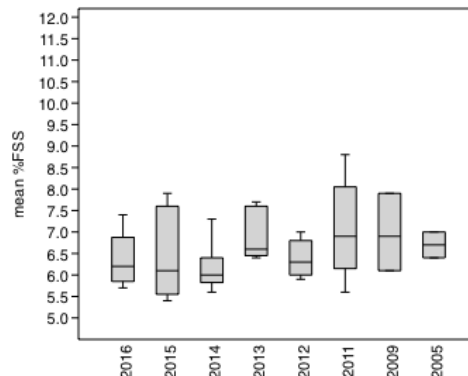
When %FSS optima is examined by year, a similar pattern is seen for the missing community among all sampling sites, with an increase in mean %FSS optima from 2005 to 2009 that stabilizes throughout later sampling years; this is especially evident at mid-stream and upstream sites (Figure 24). The past few years have not seen large changes in the ranges or median values, however. Median values for %FSS among the replacement taxa community have varied from year to year, and do not show as marked a change from 2005, but are overall lower in recent sampling years. This is again more evident among mid-stream and upstream sampling sites; furthermore, a period of what appeared to be sustained increase in the mean %FSS optima among the replacement community at upstream sampling sites in 2014 and 2015 appears to have ended in 2016. However, mean sediment optima for the 2016 replacement community among downstream, mid-stream, and upstream sites was not significantly different that that in any other year at corresponding reaches, although among mid-stream sites, the 2016 mean replacement community sediment optima was not quite significantly lower than in 2013 ($p = 0.0609$), and among upstream sites, the 2016 mean was not quite significantly lower compared to 2005 ($p = 0.0877$).

Figure 24. Mean sediment optima among missing and replacement taxa between years. Horizontal line in each box indicates the median value; filled box shows the interquartile ranges; whiskers depict data range.

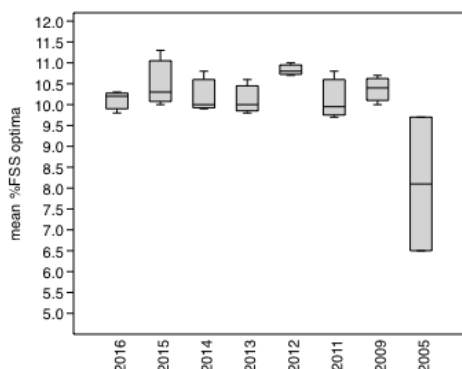
A. downstream sites, missing taxa



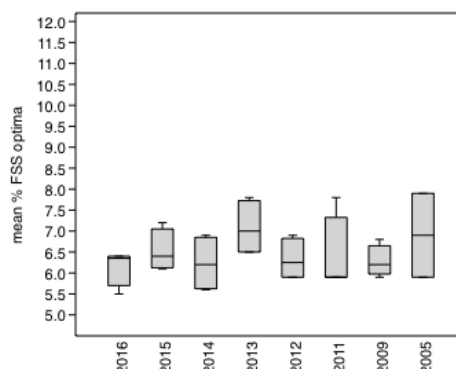
B. downstream sites, replacement taxa



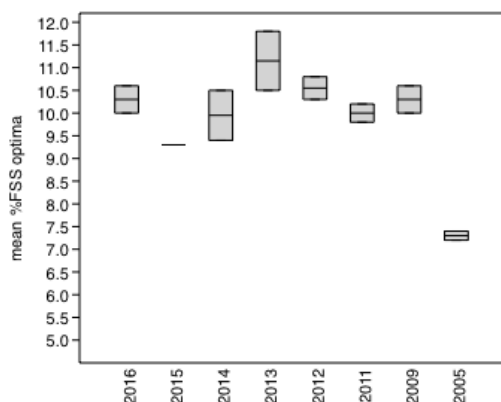
C. mid-stream sites, missing taxa



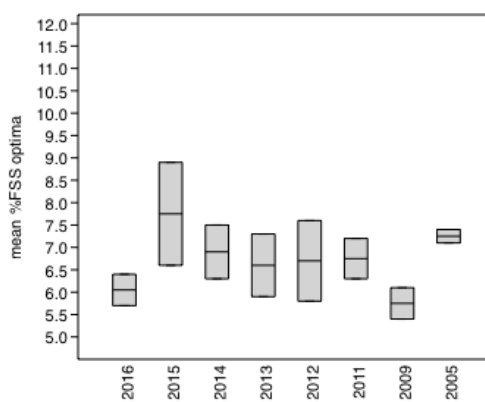
D. mid-stream sites, replacement taxa



E. Upstream sites, missing taxa



F. Upstream sites, replacement taxa



Increaser/decreaser taxa

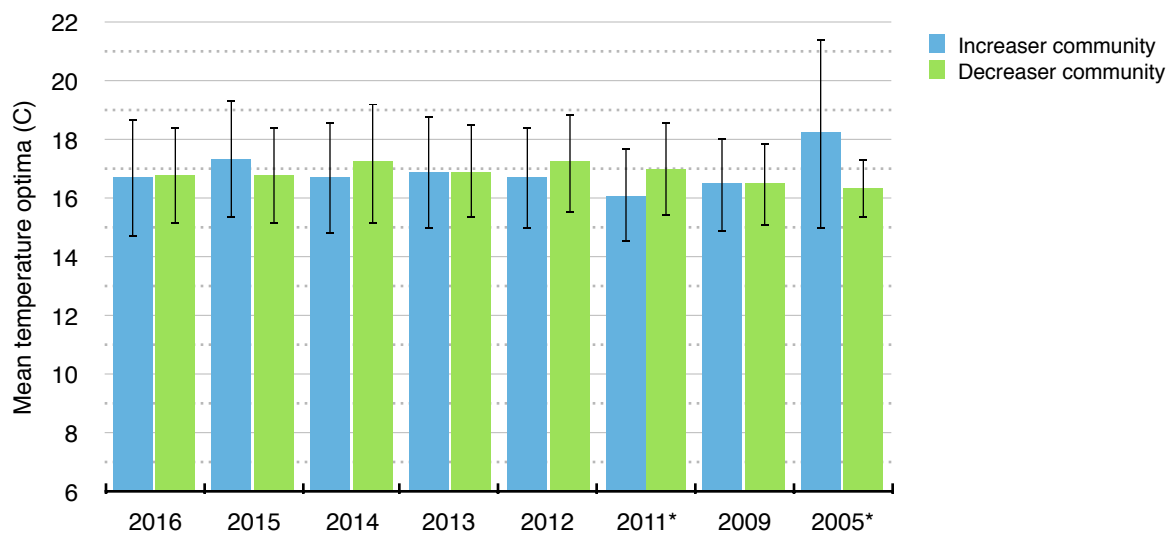
The PREDATOR model generates a sensitivity index, calculated as the total number of sites at which a taxon was collected divided by the number of sites at which it was expected to be collected (So/Se), such that a single sensitivity index score is generated for each taxon across the entire sampling set. Taxa with $So/Se > 1$ are considered to be “increasers” (collected more frequently than expected); taxa with $So/Se < 1$ are “decreasers” (collected less frequently than expected). Increaser and decreaser taxa for each sampling site in Whychus Creek were analyzed across all sampling years. To avoid a bias for rare taxa, increasers were identified using $So/Se > 1.3$, while taxa with $So/Se < 0.8$ were identified as decreasers.

As expected, there is overlap among the missing/replacement taxa at individual sites and the increaser/decreaser community identified across all sites in each year, and thus some community characteristics are similar. As was observed with the missing and replacement taxa, the mean sediment optima among increaser vs. decreaser communities shows greater separation than that between the mean temperature optima in each year (Figure 25). The mean sediment optima has been lower in the increaser community than in the decreaser in every sampling year, and difference between the increaser/decreaser means was significant in 2016 as well as in 2014 and 2012.

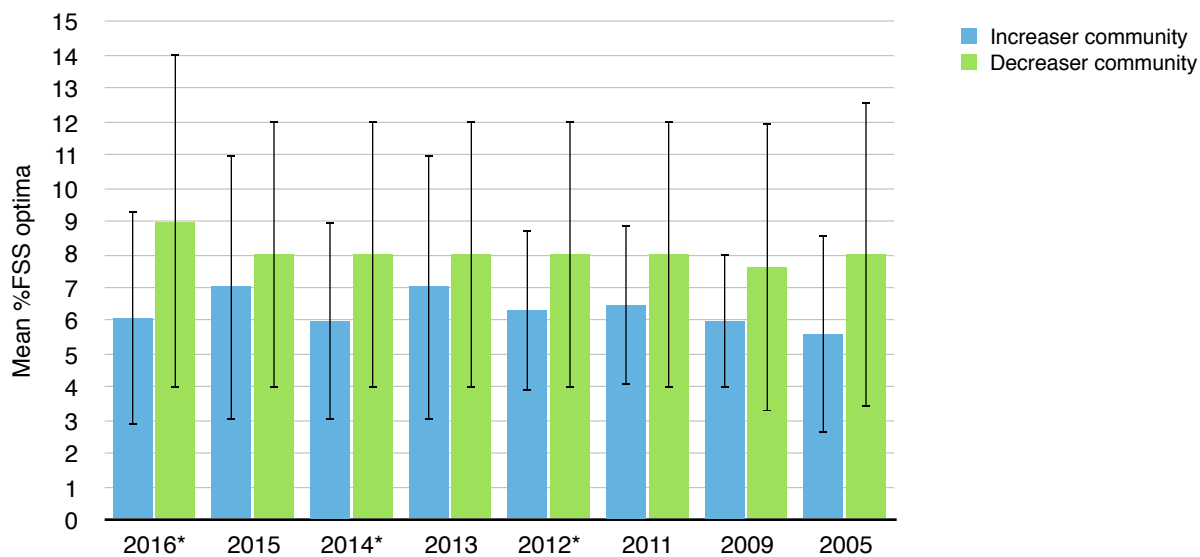
The mean temperature optima of the increaser and decreaser communities in 2016 are very similar, though slightly lower in the increaser community (Figure 25). This has been the case in almost every sampling year, although the only year in which the increaser community temperature optima was significantly lower than the decreaser community was 2011. There are only two years in which the mean temperature optima was higher in the increaser community: 2005 (significant difference between means) and 2015 (no significant difference between means).

Figure 25. Temperature and sediment optima of communities identified in each year as increaser and decreaser taxa by the PREDATOR model. Asterisk by a year indicates significant difference ($p < 0.05$) between increaser and decreaser community means in that year.

A. Community temperature optima of increaser and decreaser taxa

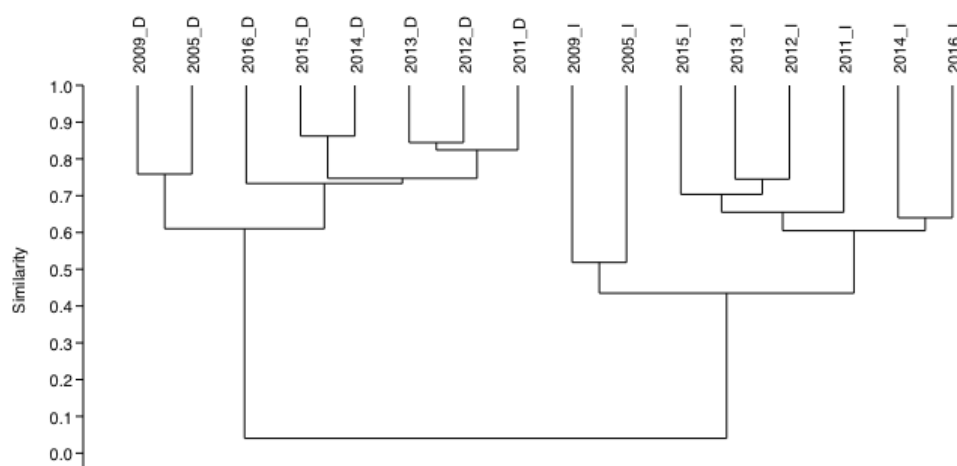


B. Community sediment optima of increaser and decreaser taxa



A CLUSTER analysis of presence/absence data for increaser and decreaser taxa showed virtually no overlap between the two communities (Figure 26). The pattern for the increaser and decreaser communities was similar to that seen for the complete macroinvertebrate community collected across time, with the 2005/2009 communities forming a separate cluster from later years. Overall, the decreaser community showed greater between-cluster similarities, with the 2005/2009 cluster 61% similar to the communities in all subsequent years. More recently, decreaser communities in contiguous years were generally more similar to each other. The 2005/2009 increaser communities were also more closely related to each other (52% similarity) than to the communities in later years (43% overall similarity).

Figure 26. CLUSTER analysis on a Bray-Curtis similarity matrix of presence/absence taxa data for increaser (I) and decreaser (D) communities.



The 2016 increaser community contained six taxa not seen as increasers in any earlier years (*Apatania*, Blephariceridae, Ephydriidae, Lymnaeidae, *Limonia*, *Wiedemannia*), two of which are sensitive taxa. *Apatania* is a genus of apataniid caddisfly, a family of northern montane habitats usually known from small, cool mountain streams and occasionally high-elevation cold lakes; it was collected for the first time in Whychus Creek in 2016 (site WC0900). Blephariceridae (net-winged midge) is a very sensitive true fly family associated with cool, fast-flowing montane waters, where larvae use abdominal suckers to cling to rocks in the current; individuals were found at WC0150. Ephydriidae (shore flies) are another true fly family, a moderately tolerant group found near shoreline habitat in a wide variety of waters; they were collected in Whychus from site WC1825. Lymnaeidae is a family of tolerant snails with high diversity in northern North America, generally found in shallow waters; a single individual was found for the first time in Whychus Creek at site WC1050. *Limonia* is a tolerant crane fly (Tipulidae) genus, generally inhabiting exposed objects on the margins of aquatic habitats; it was also found for the first time in Whychus in 2016 (site WC1825). *Wiedemannia*, which has not been seen in samples since 2005, is a

moderately tolerant dance fly (Empididae) generally found on submerged and emergent rocks in cool, fast-flowing streams; larvae are considered important consumers of black fly larvae (Simuliidae), and it is worth noting that 75% of the sample at the site where this genus was collected in 2016 (WC2600) consisted of *Simulium*.

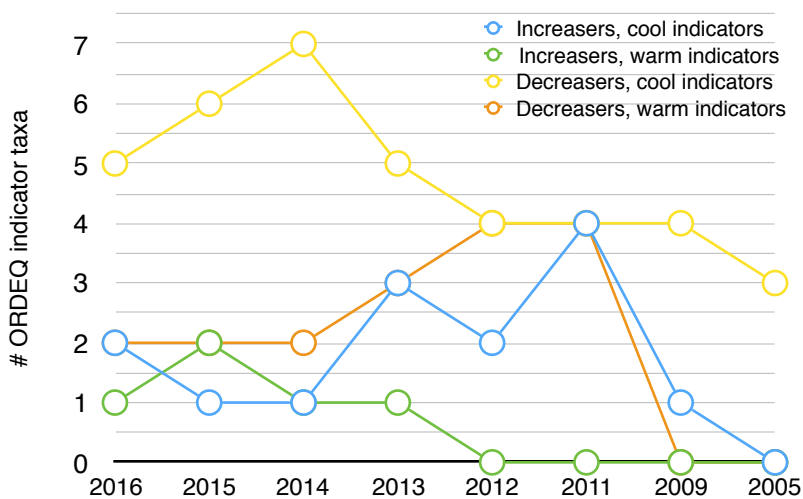
The decreaser community contained five taxa not seen as decreasers in previous years (*Cleptelmis*, *Dicranota*, Dytiscidae, *Hexatoma*, *Isoperla*), all but one of which are fairly tolerant. *Cleptelmis*, which was expected to occur at three sites but was present at none, is a moderately tolerant riffle beetle that has been collected in every other sampling year, generally at low abundances but from multiple sites each year. *Dicranota* and *Hexatoma* are sediment-tolerant crane fly (Tipulidae) genera that have been collected in almost every sampling year. Dytiscidae (predaceous diving beetles) are a tolerant group associated with slower waters and have been found almost every year, generally left at subfamily but with two genera new to the Whychus community added in 2016 (*Agabus*, *Stictotarsus*). The only sensitive member of the 2016 decreaser community is *Isoperla*, a sensitive stripetail (Perlodidae) stonefly that prefers cool, fast waters with rocky or sandy substrates; this genus was found in several previous years, generally at low abundances and a small number of sites.

The increaser and decreaser communities also contain ORDEQ indicator taxa for sediment and temperature (Figure 27), and the way they have changed throughout time offers insights into community responses to environmental factors. In 2005, the increaser community had no cool indicator taxa, but from 2009-2013, the number of cool indicators ranged from 1-4, and has since leveled off and stabilized. In contrast, there were no warm temperature indicator taxa in the increaser community from 2005-2012, and subsequent years have seen no more than 1-2 warm indicators per year in the increaser community. In contrast, the decreaser community had no warm indicator taxa in 2005 or 2009, but their numbers increased through 2012 and then dropped slightly and leveled off. The overall greatest number of temperature indicator taxa has always been the number of cool indicators in the decreaser community; this number stayed relatively stable from 2005-2012, increased through 2014, and has decreased again in recent years. These results suggest a community response to improved temperature conditions during the first few years of sampling, with more cool indicator taxa able to colonize and survive.

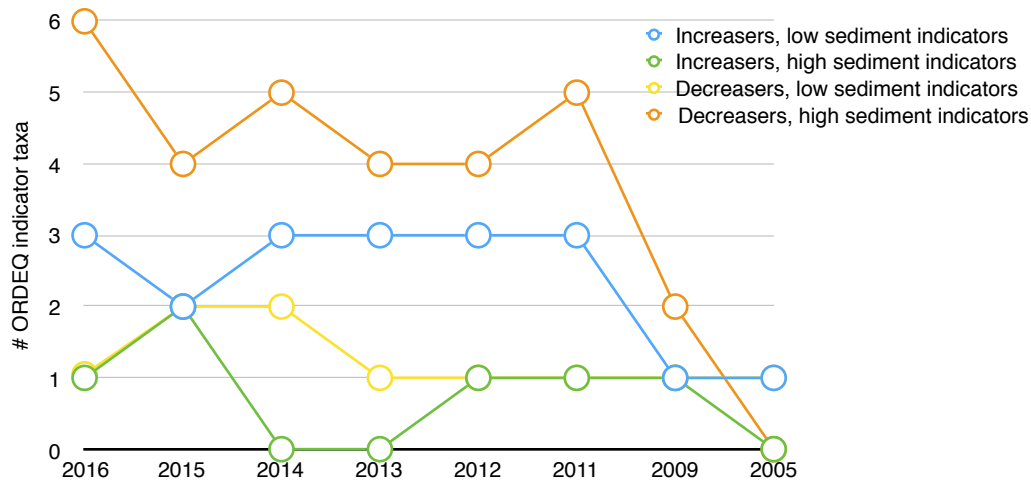
Indicator taxa for sediment suggest a response to low sediment conditions. The number of high sediment indicator taxa in the decreaser community, which was zero in 2005, has increased steadily over time and reached its highest point (6 taxa) in 2016; in contrast, the number of high sediment indicator taxa in the increaser community has remained low, ranging from 0-2 throughout the sampling period. The number of low sediment indicators in the decreaser community is consistently low (0-2 across all sampling years); in contrast, while there were no low sediment indicators in the 2005 increaser community, that number rose through 2011 (3 taxa) and has remained stable since then.

Figure 27. ORDEQ indicator taxa for temperature and fine suspended sediment (%FSS) present in increaser and decreaser communities.

A. Temperature indicator taxa



B. Sediment indicator taxa



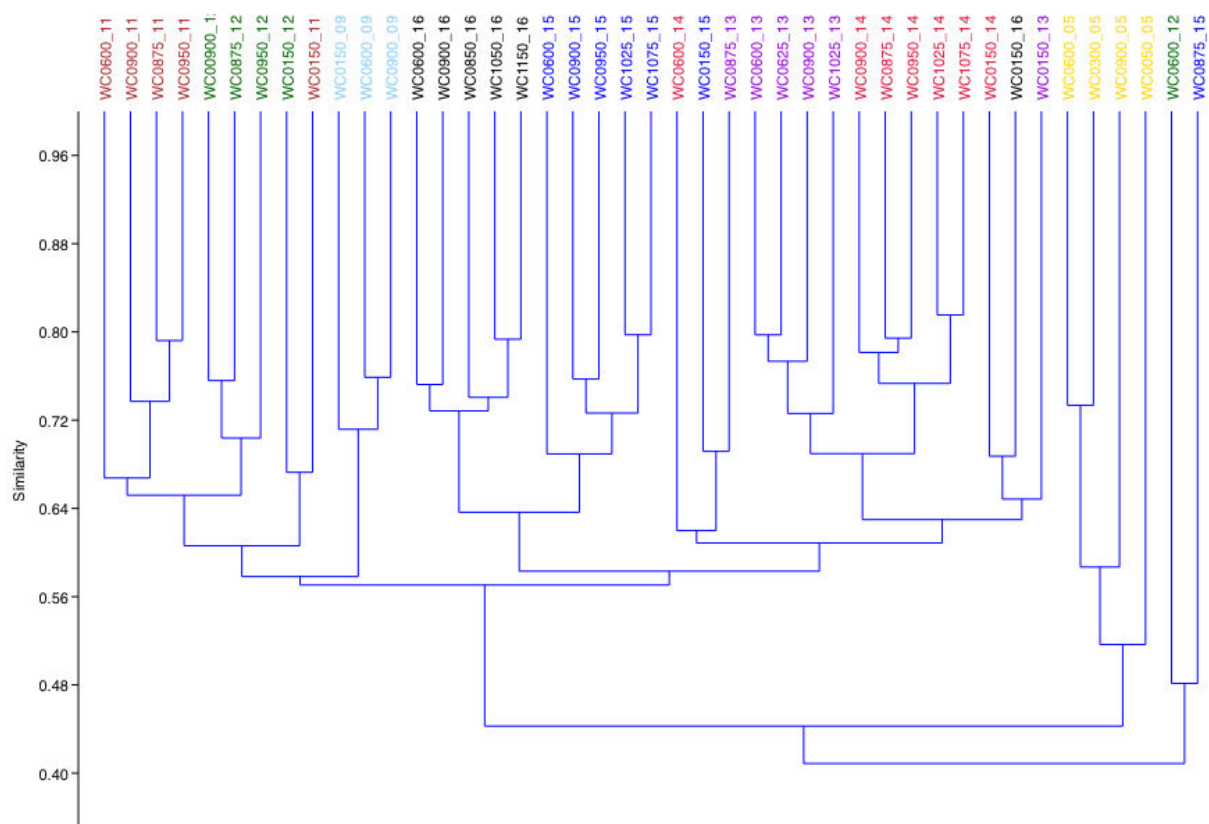
Community composition

The macroinvertebrate community in Whychus Creek continues to change, although the most dramatic changes occurred during the first years of monitoring. A two-way ANOSIM showed separation of sites by both year ($R=0.7122$, $P=0.0001$) and location (i.e. DS, MS, US; $R=0.8538$, $p=0.0001$). The duplicate samples taken in 2016 for quality control were from a mid-stream (WC1950) and upstream (WC2425) site; the two samples taken at WC1950 were most similar to each other, based on a cluster analysis, while the WC2425 duplicate showed greater similarity to the WC2600 sample.

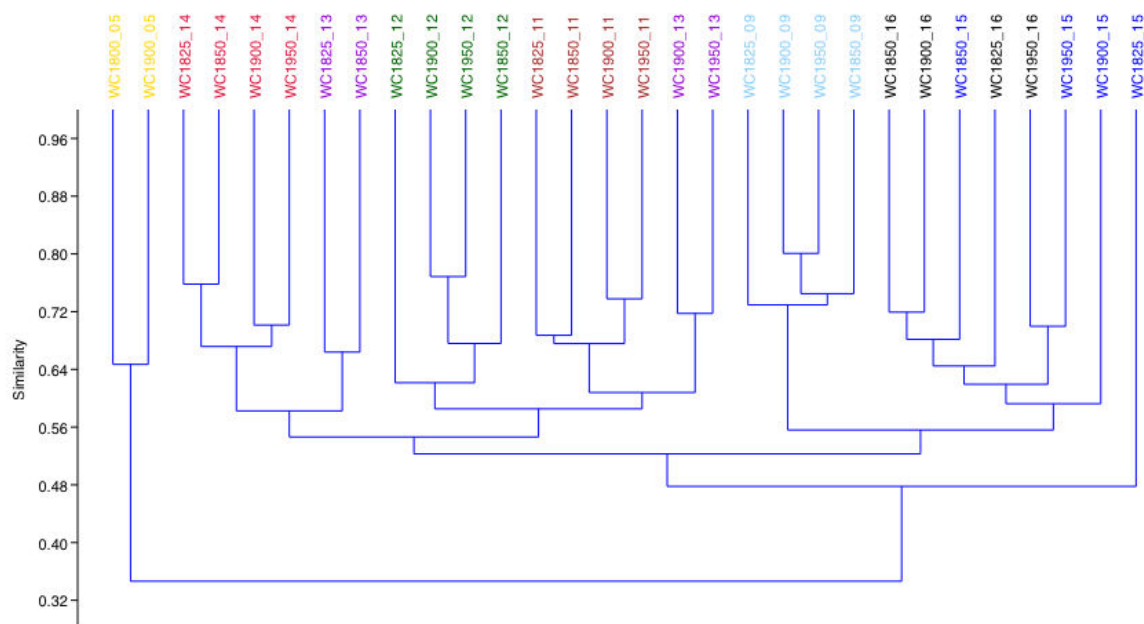
For the complete dataset, sampling sites clustered based on reach location, and between years, sampling sites from the same reaches showed the greatest similarities. The exception is the 2005 sampling set, which forms a separate cluster with only 35% similarity to all other sampling year clusters. When examined by reach (Figure 28), CLUSTER analyses shows the greatest community difference between 2005 and all other years for downstream, mid-stream, and upstream sites. Among downstream sites, earlier sampling year communities (2009-2012) form a separate cluster from later sampling years (2013-2016), with contiguous years more similar to each other (2009-2012; 2013/2014; and 2015/2016), and sites sampled within the same year overall more similar to each other than to the same sites sampled in different years. Similarly, among the mid-stream sampling sites, the communities in 2016, 2015, and 2009 form a separate cluster from the 2011-2014 communities (52% similarity), with the 2005 community clustering alone, and within-year similarity is greater than within-site similarity. The relationship between the upstream sampling sites is more variable. All upstream sites sampled in 2005 formed a separate cluster from sites sampled in any other year, as was seen for the other reaches. However, while upstream sites sampled in 2009, 2011, and 2012 showed greater within-year than within-site similarity, in other years there was greater within-site similarity; for example, the communities at site WC2425 clustered together for the 2013, 2014, and 2016 samples.

Figure 28. Cluster analyses of Whychus Creek macroinvertebrate community by reach (DS, MS, and US) across all sampling years. Analyses were done on a Bray-Curtis similarity matrix of square root-transformed abundance data.

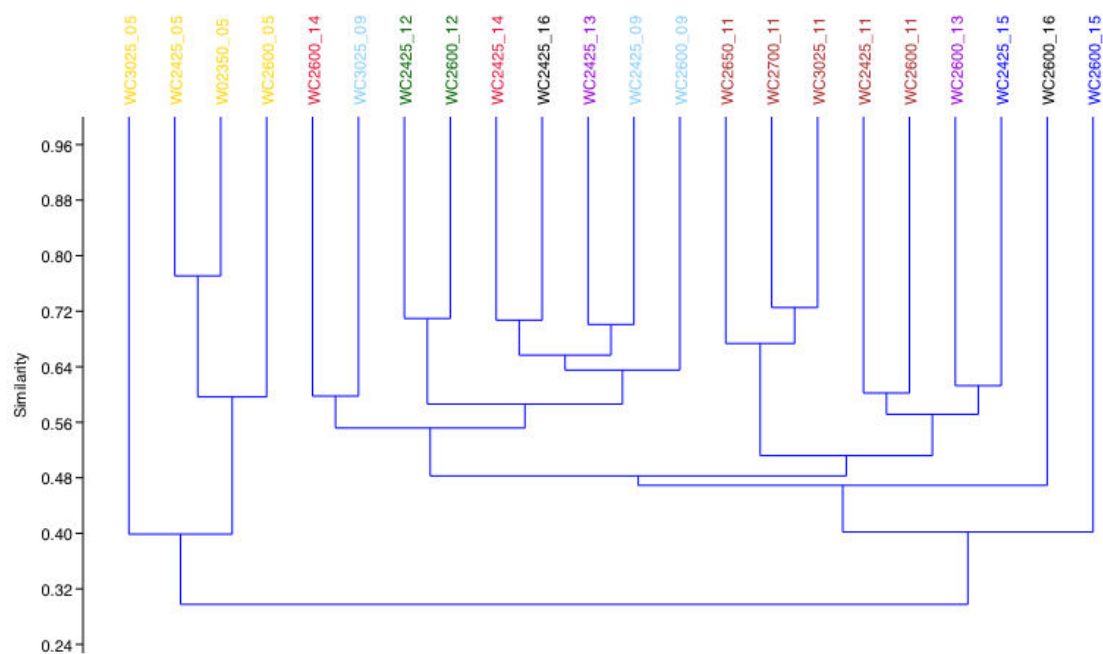
A. Downstream sampling sites, 2005-2016. Yellow=2005, light blue=2009, brown=2011, green=2012, purple=2013, red=2014, dark blue=2015, black=2016



B. Mid-stream sampling sites 2005-2016. Yellow=2005, light blue=2009, brown=2011, green=2012, purple=2013, red=2014, dark blue=2015, black=2016



C. Upstream sampling sites 2005-2016. Yellow=2005, light blue=2009, brown=2011, green=2012, purple=2013, red=2014, dark blue=2015, black=2016



Invertebrate communities often show substantial annual variation, and changes in macroinvertebrate community composition over time due to stressors or changing habitat conditions will always have an underlying background of normal between-year fluctuations. Examination of missing/replacement and increaser/decreaser taxa have revealed some of the drivers behind macroinvertebrate community changes across time. To investigate this further on a site-specific basis, a SIMPER test was done on data from seven sites at which macroinvertebrates have been collected in every sampling year to assess changes in the community across time, and the three taxa that contributed the most to observed between-year community dissimilarity at each site were identified (Appendix C). The data tables in Appendix C show the three taxa that contribute the most to observed difference between the macroinvertebrate community in different sampling years.

Some cosmopolitan, generalist taxa are seen in both early and later sampling years as driving between-year sample differences, such as Orthocladiinae (a widespread subfamily of chironomid midge common in rock and gravel substrates) and Oligochaeta (aquatic earthworms). However, in all sampling reaches (DS, MS, and US), there is a pattern wherein taxa that account for a large proportion of the between-year difference at an individual site and are more abundant in samples from earlier years (2005-2011) are more tolerant and/or more frequently associated with slower waters, such as Chironominae (a diverse subfamily of non-biting midge with many tolerant genera, common in sand and silt sediment) and *Zaitzevia* (tolerant riffle beetle; ORDEQ indicator for warm temperatures and high sediment). However, it should be noted that more sensitive taxa can occasionally drive between-year differences with greater abundance in an earlier year, notably *Rhithrogena* (a flatheaded mayfly with low tolerance for organic pollution; low sediment indicator) and *Zapada* (small brown stonefly sensitive to organic pollution). In contrast, many of the taxa that account for a large proportion of the between-year difference at an individual site and are more abundant in samples from later years (2012-2016) are those associated with faster-flowing and/or cooler waters and include more of the sensitive EPT, i.e., *Optioservus* (tolerant riffle beetle; associated with lotic waters but ORDEQ indicator for warm temperatures and high sediment), *Glossosoma* (sensitive saddle case-maker caddisfly; ORDEQ low sediment indicator), *Hydropsyche* (free-living caddisfly; ORDEQ warm temperature indicator), *Baetis* (small minnow mayfly; DEQ low sediment indicator), *Ephemerella* (spiny crawler mayfly; ORDEQ cool temperature indicator), and *Suwallia* (sensitive genus of green stonefly).

Taxa that drove between-year differences in SIMPER tests that were more abundant in the 2016 community included *Glossosoma*, *Hydropsyche*, *Optioservus*, *Zaitzevia*, *Ampumixis* (riffle beetle), *Brachycentrus* (humpless case-maker caddisfly sensitive to organic pollution), *Simulium*, *Rhyacophila* (diverse genus of caddisfly with low tolerances for organic pollution, cool-water associated; several species are ORDEQ cool temperature/low sediment indicators), *Baetis tricaudatus* (small minnow mayfly; ORDEQ low sediment indicator), *Suwallia*, and *Cinygmula* (flatheaded mayfly; ORDEQ cool temperature and low sediment indicator).

Thus, it can be seen that overall, there is a shift in the taxa that are driving the macroinvertebrate community differences between years at individual sites, with more common/tolerant being more abundant in earlier years, and higher abundances of more sensitive or lotic taxa in later years

Conclusions

The macroinvertebrate community collected in Whychus Creek in 2016 continues to show signs of change, much of it in a direction that indicates improved biotic conditions and a healthier macroinvertebrate community. Nine new taxa were collected in 2016 for the first time since sampling began, the highest number of new taxa found in a year since 2011; five of these have habitat preferences that include cooler or faster-flowing waters. The macroinvertebrate community continues to change in each year, due to a combination of normal annual variations commonly seen in invertebrate populations as well as responses to changes habitat and potentially to changing climate conditions. The most dramatic changes in the Whychus community occurred between 2005 and 2009; since then, the community at downstream, mid-stream, and upstream sites shows overall stronger the within-year similarity than within-site similarity, especially at downstream and mid-stream sites. The community at individual sites continues to change over time, and the taxa that account most for the differences between years at the same site tend to be tolerant and/or more lentic taxa that are more abundant in earlier sampling years and sensitive and/or more lotic taxa that are more abundant in later years, especially the sensitive Ephemeroptera, Plecoptera, and Trichoptera. The macroinvertebrate communities have also become more balanced over time, and with a few exceptions (often related to new restoration work) are less dominated by a single highly abundant taxon.

The I-IBI and PREDATOR bioassessment models used to assess the macroinvertebrate communities indicate a shift to improved biotic conditions over time, though this has fluctuated throughout the sampling period. PREDATOR site O/E scores in 2016 and 2015 have been higher than in the past several years, with more sites scoring as having good or fair biological conditions and fewer as poor. Upstream sites continue to have the lowest PREDATOR scores; however, that region includes a site at Sisters City Park, which experiences heavy human use, and a site affected by substantial disturbance in recent years due to an ongoing channel restoration project. I-IBI scores were also higher overall in 2016, and this is the first year that any sites received a score indicating minimal impairment since 2013. Only one site in 2016 scored as being moderately disturbed based in the I-IBI, the upstream site at which channel restoration is occurring; the macroinvertebrate community there in 2016 consisted mainly of *Simulium* black flies. Scores fluctuate over the years, but no sites have ever scored as severely impaired, and overall the proportion of sites scoring as moderately impaired has decreased since sampling began in 2005, while the proportion scoring as slightly impaired has increased.

Sediment and temperature have been examined in every year as potential drivers of observed macroinvertebrate community changes, within both the total collected community as well as the communities identified by the PREDATOR model as missing or replacement taxa at each site and as increasing or decreasing taxa across the

dataset. The increaser/decreaser community contained six taxa that had not been identified as increasers in previous years, two of which are sensitive taxa; and five taxa that had not been seen as decreasers in previous years, four of which are tolerant species. The pattern of changes in ORDEQ temperature indicator taxa among increasers/decreasers suggests a community response to improved temperature conditions during the first few years of sampling, with more cool indicator taxa able to colonize and survive. The response to sediment conditions is stronger; the number of high sediment indicator taxa in the decreaser community has risen steadily from 2005 through 2016, and there are very few high sediment indicator taxa in the increaser community, but the number of low sediment indicators in the increaser community rose through 2011 and appears to have stabilized. In addition, the sediment optima of the increaser community is much lower than that of the decreaser community. The missing/replacement community also shows a stronger influence of sediment conditions; although there has been an overall decrease since sampling began in the temperature optima of the replacement communities, there is a much larger and significant separation between the sediment optima of the missing and replacement communities, with consistently lower optima among the replacement taxa.

One trend emerging from examination of the 2016 data may point to an emerging issue with temperature. The mean community temperature optima decreased significantly over time among downstream and mid-stream sites, with higher values in 2005/2009 that decreased steadily in 2011-2013. However, these means began to increase again in 2014, and have continued to do so among all sampling reaches through 2016, with the most significant increases seen among downstream and mid-stream sites. The mean temperature optima for the downstream and mid-stream communities were significantly higher in 2016 than in the previous three years, although still lower than the means in 2009 and 2005. Among upstream sites, the mean community temperature optima was significantly higher in 2016 than in 2011; the mean temperature optima of the upstream community has been increasing since 2011, but this is the first year in which the difference has been significant. The number of ORDEQ warm indicator taxa in the community has also been increasing in recent years among downstream and mid-stream sites. Given that the last three years have been the hottest in recorded history (NOAA, 2016), this sustained trend may be a signal that the stream community is being impacted by larger climate stressors.

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Appendix A. Macroinvertebrate Monitoring Data Sheet

Site ID _____ Date: 20 August 2016

Sampled by: _____

Start time: _____ End time: _____ Air temp.: _____ °C Water temp.: _____ °C

Sample Information:

of riffles sampled: _____ # of kicks composited: 8 x 1 ft² # sample jars _____

Duplicate collected? ☐ yes ☐ no If yes, total # duplicate jars _____

Human use & influence (right & left bank relative to observer facing downstream)

A = absent	B = on bank		C = ≤ 30 ft from bank		D = > 30 ft from bank	
Disturbance	Left bank	Right bank		Disturbance	Left bank	Right bank
Riprap/wall/armored bank				Landfill/dump		
Buildings				Park/lawn		
Industrial				Row crops		
Rural residential				Pasture/range/hayfield		
Urban residential				Livestock access		
Pavement/cleared lot				Logging in last 5 years		
Road/railroad				Sand or gravel mining		
Pipes (inlet/outlet)				Forest/woodland		
Other:						

Qualitative observations (circle 1 choice for each):

Water odors: none / organic / rotten eggs / fishy / chlorine / petroleum / other (describe):

Water appearance: clear / turbid / milky / dark brown / foamy / oily sheen / other (describe):

Dominant land use: Forest / agriculture (crops / pasture) / urban (industrial / residential) / other:

Extent of algae covering submerged materials: none / 1-25% / 25-50% / 50-75% / 75-100%

Type of algae: none / close-growing / filamentous (i.e. strands >2") / floating clumps

Physical characteristics: (if fewer than 8 riffles, record only for the riffles sampled)

Substrate (estimate % each type present; each column should add to 100%)

% composition of riffle	Riffle1	Riffle2	Riffle3	Riffle4	Riffle5	Riffle6	Riffle7	Riffle8
Bedrock (continuous rock)								
Boulder (> 12 in.; larger than basketball)								
Cobble (2.5-12 in.; tennis ball to basketball)								
Gravel (0.6-2.5 in.; marble to tennis ball)								
Sand (< 0.6 in.; smaller than marble)								
Silt/clay/muck (fine particles)								
Woody debris								
Other (describe)								

Water depth (in feet and inches)

Parameter	Riffle1	Riffle2	Riffle3	Riffle4	Riffle5	Riffle6	Riffle7	Riffle8
Wetted width								
Depth @ ¼ wetted width								
Depth @ ½ wetted width								
Depth @ ¾ wetted width								

Additional notes or observations (including other wildlife noted):

Appendix B. ORDEQ indicator taxa for temperature and percent fine sediment.

Values in parentheses indicate temperature (°C) or sediment (% fine sediment) optima for each taxon.

Taxon	Temperature indicator	Fine sediment indicator
<i>Prosimulium</i>	Cool (12.2)	---
<i>Baetis bicaudatus</i>	Cool (12.3)	---
<i>Zapada columbiana</i>	Cool (12.9)	---
<i>Neothremma</i>	Cool (12.9)	---
<i>Parapsyche elsis</i>	Cool (13.5)	Low (4)
<i>Caudatella</i>	Cool (13.6)	Low (4)
<i>Megarcys</i>	Cool (13.6)	Low (4)
<i>Visoka</i>	Cool (13.7)	---
<i>Epeorus grandis</i>	Cool (14.2)	Low (2)
<i>Yoraperla</i>	Cool (14.2)	---
<i>Ephemerella</i>	Cool (14.4)	---
<i>Drunella coloradensis/flavilinea</i>	Cool (14.5)	---
<i>Doroneuria</i>	Cool (14.5)	---
<i>Despaxia</i>	Cool (14.5)	---
<i>Turbellaria</i>	Cool (14.6)	---
<i>Ironodes</i>	Cool (14.9)	---
<i>Drunella doddsi</i>	Cool (15.2)	Low (3)
<i>Ameletus</i>	Cool (15.2)	---
<i>Rhyacophila Brunnea Gr.</i>	Cool (15.5)	Low (4)
<i>Cinygmula</i>	Cool (15.5)	Low (6)
<i>Micrasema</i>	Cool (15.6)	---
<i>Dipheter hageni</i>	Warm (17.9)	---
<i>Antocha</i>	Warm (18.3)	---
<i>Hydropsyche</i>	Warm (18.5)	---
<i>Juga</i>	Warm (18.6)	High (15)
Chironomini	Warm (18.8)	High (10)

Taxon	Temperature indicator	Fine sediment indicator
<i>Zaitzevia</i>	Warm (19.0)	High (9)
<i>Optioservus</i>	Warm (19.6)	High (12)
<i>Dicosmoecus gilvipes</i>	Warm (20.6)	---
<i>Physa</i>	Warm (21.1)	High (21)
<i>Arctopsyche</i>	---	Low (2)
<i>Rhyacophila Hyalinata Gr.</i>	---	Low (3)
<i>Rhyacophila Angelita Gr.</i>	---	Low (3)
<i>Drunella grandis</i>	---	Low (3)
<i>Epeorus longimanus</i>	---	Low (4)
<i>Rhithrogena</i>	---	Low (5)
<i>Rhyacophila Betteni Gr.</i>	---	Low (5)
<i>Glossosoma</i>	---	Low (5)
<i>Baetis tricaudatus</i>	---	Low (6)
<i>Oligochaeta</i>	---	High (10)
<i>Paraleptophlebia</i>	---	High (11)
Tanypodinae	---	High (12)
Ostracoda	---	High (17)
<i>Hydroptila</i>	---	High (17)
Lymnaeidae	---	High (18)
<i>Cheumatopsyche</i>	---	High (20)
Sphaeriidae	---	High (21)
Coenagrionidae	---	High (25)

Appendix C. SIMPER analyses of sites sampled across multiple years.

The three taxa that contribute most to the overall between-year dissimilarity in macroinvertebrate communities are shown; number in parentheses indicates the year in which the mean abundance of the indicated taxon was greater.

WC0150

	WC0150_16	WC0150_15	WC0150_14	WC0150_13	WC0150_12	WC0150_11
WC0150_16	—	—	—	—	—	—
WC0150_15	Simulium (15), Glossosoma (16), Optioservus (16)	—	—	—	—	—
WC0150_14	Glossosoma (16), Optioservus (16), Baetis tricaudatus (14)	Acentrella turbida (14), Simulium (15), Baetis tricaudatus (14)	—	—	—	—
WC0150_13	Glossosoma (16), Ampumixis (16), Optioservus (16)	Simulium (15), Rhithrogena (13), Acentrella turbida (13)	Rhithrogena (13), Baetis tricaudatus (14), Oligochaeta (13)	—	—	—
WC0150_12	Glossosoma (16), Oligochaeta (12), Hydropsyche (16)	Simulium (15), Oligochaeta (12), Orthocladinae (12)	Oligochaeta (12), Acentrella turbida (14), Simulium (14)	Oligochaeta (12), Acentrella turbida (13), Simulium (13)	—	—
WC0150_11	Glossosoma (16), Dasyhelea (11), Simulium (16)	Simulium (15), Dasyhelea (11), Acentrella (11)	Simulium (14), Acentrella turbida (14), Dasyhelea (11)	Dasyhelea (12), Simulium (13), Acentrella turbida (13)	Oligochaeta 912), Dasyhelea (11), Tanytarsini (12)	—
WC0150_09	Glossosoma (16), Optioservus (16), Hydropsyche (16)	Simulium (15), Chironominae (09), Orthocladinae (09)	Chironominae (09), Oligochaeta (09), Simulium (14)	Chironominae (09), Glossosoma (13), Simulium (13)	Chironominae (09), Acentrella turbida (09), Tanytarsini (12)	Dasyhelea (11), Acentrella turbida (09), Chironominae (09)

WC0600

	WC0600_16	WC0600_15	WC0600_14	WC0600_13	WC0600_12	WC0600_11	WC0600_09
WC0600_16	—	—	—	—	—	—	—
WC0600_15	Hydropsyche (15), Rhithrogena (16), Optioservus (16)	—	—	—	—	—	—
WC0600_14	Optioservus (16), Rhithrogena (16), Zaitzevia (16)	Hydropsyche (15), Ampumixis (15), Brachycentrus (15)	—	—	—	—	—
WC0600_13	Simulium (13), Baetis tricaudatus (13), Acentrella turbida (13)	Hydropsyche (15), Brachycentrus (15), Simulium (13)	Simulium (13), Ampumixis (13), Zaitzevia (13)	—	—	—	—

WC0600_12	Rhithrogena (16), Optioservus (16), Glossosoma (16)	Hydropsyche (15), Ampumixis (15), Simulium (15)	Simulium (14), Baetis tricaudatus (14), Orthocladiinae (14)	Simulium (13), Baetis tricaudatus (13), Acentrella turbida (13)	—	—	—
WC0600_11	Rhithrogena (16), Optioservus (16), Zaitzevia (16)	Hydropsyche (15), Ampumixis (15), Rhithrogena (15)	Brachycentrus (11), Suwallia (14), Zaitzevia (01)	Simulium (13), Brachycentrus (11), Rhithrogena (13)	Brachycentrus (11), Orthocladiinae (11), Simulium (11)	—	—
WC0600_09	Chironominae (09), Rhithrogena (16), Optioservus (16)	Chironominae (09), Hydropsyche (15), Ampumixis (15)	Chironominae (09), Zaitzevia (09), Baetis tricaudatus (14)	Chironominae (09), Baetis tricaudatus (13), Simulium (13)	Chironominae (09), Orthocladiinae (09), Zaitzevia (12)	Chironominae (09), Zaitzevia (11), Brachycentrus (11)	—
WC0600_05	Zaitzevia (05), Rhithrogena (16), Ampumixis (16)	Zaitzevia (05), Hydropsyche (15), Ampumixis (15)	Zaitzevia (05), Baetis tricaudatus (14), Brachycentrus (05)	Zaitzevia (05), Baetis tricaudatus (13), Brachycentrus (05)	Zaitzevia (09), Simulium (05), Brachycentrus (05)	Zaitzevia (05), Baetis tricaudatus (11), Chironominae (05)	Zaitzevia (05), Chironominae (09), Brachycentrus (05)

WC0900

	WC0900_16	WC0900_15	WC0900_14	WC0900_13	WC0900_12	WC0900_11	WC0900_09
WC0900_16	—	—	—	—	—	—	—
WC0900_15	Brachycentrus (15), Optioservus (15), Baetis tricaudatus (15)	—	—	—	—	—	—
WC0900_14	Baetis tricaudatus (14), Glossosoma (16), Optioservus (16)	Glossosoma (15), Brachycentrus (15), Oligochaeta (15)	—	—	—	—	—
WC0900_13	Baetis tricaudatus (13), Glossosoma (16), Optioservus (16)	Brachycentrus (15), Oligochaeta (15), Acentrella turbida (13)	Chironominae (13), Ephemerella tibialis (13), Suwallia (14)	—	—	—	—
WC0900_12	Optioservus (16), Glossosoma (16), Rhithrogena (16)	Simulium (15), Glossosoma (15), Orthocladiinae (15)	Oligochaeta (12), Baetis tricaudatus (14), Acentrella turbida (14)	Oligochaeta (12), Baetis tricaudatus (13), Acentrella turbida (13)	—	—	—
WC0900_11	Simulium (11), Optioservus (16), Brachycentrus (11)	Oligochaeta (15), Simulium (11), Narpus (11)	Tanytarsini (14), Attenella (14), Zaitzevia (11)	Brachycentrus (11), Simulium (11), Baetis tricaudatus (13)	Simulium (11), Oligochaeta (12), Acentrella turbida (12)	—	—
WC0900_09	Chironominae (09), Glossosoma (16), Optioservus (16)	Chironominae (09), Glossosoma (15), Acentrella turbida (09)	Chironominae (09), Baetis tricaudatus (14), Tanytarsini (14)	Chironominae (09), Baetis tricaudatus (13), Ephemerella tibialis (13)	Chironominae (09), Acentrella turbida (09), Orthocladiinae (09)	Chironominae (09), Simulium (11), Nemata (11)	—

WC0900_05	Zaitzevia (05), Ampumixis (16), Glossosoma (16)	Zaitzevia (05), Baetis tricaudatus (15), Simulium (15)	Baetis tricaudatus (14), Zaitzevia (05), Tanytarsini (14)	Baetis tricaudatus (13), Zaitzevia (05), Acentrella turbida (13)	Zaitzevia (05), Optioservus (05), Rhithrogena (05)	Simulium (11), Baetis tricaudatus (11), Optioservus (05)	Chironominae (09), Rhithrogena (05), Zaitzevia (05)
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WC1825

	WC1825_16	WC1825_15	WC1825_14	WC1825_13	WC1825_12	WC1825_11	WC1825_09
WC1825_16	—	—	—	—	—	—	—
WC1825_15	Baetis tricaudatus (16), Brachycentrus (16), Optioservus (16)	—	—	—	—	—	—
WC1825_14	Oligochaeta (16), Brachycentrus (16), Baetis tricaudatus (14)	Baetis tricaudatus (14), Oligochaeta (15), Suwallia (14)	—	—	—	—	—
WC1825_13	Simulium (13), Hydropsyche (16), Brachycentrus (16)	Simulium (13), Oligochaeta (15), Baetis tricaudatus (13)	Baetis tricaudatus (14), Simulium (13), Oligochaeta (13)	—	—	—	—
WC1825_12	Hydropsyche (16), Glossosoma (12), Brachycentrus (16)	Baetis tricaudatus (12), Glossosoma (12), Simulium (12)	Simulium (14), Glossosoma (12), Oligochaeta (12)	Simulium (13), Baetis tricaudatus (12), Glossosoma (12)	—	—	—
WC1825_11	Hydropsyche (16), Zapada cinctipes (11), Chironomidae (11)	Simulium (15), Zapada cinctipes (11), Atherix (11)	Simulium (14), Oligochaeta (11), Baetis tricaudatus (14)	Simulium (13), Zapada cinctipes (11), Brachycentrus (11)	Glossosoma (12), Acentrella turbida (11), Baetis tricaudatus (12)	—	—
WC1825_09	Brachycentrus (16), Hydropsyche (09), Tanytarsini (09)	Hydropsyche (09), Atherix (09), Oligochaeta (15)	Hydropsyche (09), Baeti tricaudatus (14), Oligochaeta (09)	Hydropsyche (09), Simulium (13), Atherix (09)	Hydropsyche (09), Baetis tricaudatus (12), Acentrella turbida (09)	Hydropsyche (09), Simulium (09), Brachycentrus (11)	—
WC1825_05	Zapada (05), Simulium (05), Baetis tricaudatus (05)	Zapada (05), Simulium (05), Optioservus (05)	Zapada (05), Baetis tricaudatus (14), Optioservus (05)	Zapada (05), Optioservus (05), Baetis tricaudatus (13)	Zapada (05), Simulium (05), Baetis tricaudatus (12)	Simulium (05), Zapada (05), Baetis tricaudatus (11)	Zapada (05), Simulium (05), Optioservus (05)

WC1900

	WC1900_16	WC11900_15	WC1900_14	WC1900_13	WC1900_12	WC1900_11	WC1900_09
WC1900_16	—	—	—	—	—	—	—
WC1900_15	Simulium (16), Tanytarsini (15), Hydroptila (15)	—	—	—	—	—	—
WC1900_14	Simulium (16), Baetis tricaudatus (14), Orthoclaadiinae (14)	Baetis tricaudatus (14), Tanytarsini (15), Oligochaeta (15)	—	—	—	—	—
WC1900_13	Simulium (16), Ephemerella tibialis (13), Hydropsyche (16)	Tanytarsini (15), Simulium (13), Acentrella turbida (13)	Baetis tricaudatus (14), Simulium (13), Orthoclaadiinae (14)	—	—	—	—
WC1900_12	Simulium (16), Ephemerella tibialis (12), Baetis tricaudatus (12)	Tanytarsini (15), Baetis tricaudatus (12), Oligochaeta (15)	Ephemerella tibialis (12), Acentrella turbida (14), Ameletus (12)	Simulium (11), Acentrella turbida (13), Diamesinae (13)	—	—	—
WC1900_11	Simulium (16), Chironomidae (11), Orthoclaadiinae (11)	Tanytarsini (15), Hydroptila (15), Diamesinae (15)	Baetis tricaudatus (14), Oligochaeta (11), Chironomidae (11)	Simulium (13), Diamesinae (13), Glossosoma (11)	Ephemerella tibialis (12), Oligochaeta (11), Chironomidae (11)	—	—
WC11900_09	Simulium (16), Sweltsa (09), Acentrella turbida (09)	Tanytarsini (15), Simulium (09), Hydroptila	Orthoclaadiinae (14), Oligochaeta (09), Baetis tricaudatus (14)	Diamesinae (13), Sweltsa (09), Hydroptilidae (13)	Acentrella turbida (09), Suwallia (12), Oligochaeta (09)	Orthoclaadiinae (11), Simulium (09), Sweltsa (09)	—
WC1900_05	Zapada (05), Simulium (16), Chironominae (05)	Zapada (05), Tanytarsini (15), Chironominae (05)	Zapada (05), Baetis tricaudatus (14), Chironominae (05)	Zapada (05), Chironominae (05), Acentrella (05)	Zapada (05), Chironominae (05), Baetis tricaudatus (12)	Zapada (05), Chironominae (05), Acentrella (05)	Zapada (05), Acentrella (05), Chironominae (05)

WC2425

	WC2425_16	WC2425_15	WC2425_14	WC2425_13	WC2425_12	WC2425_11	WC2425_09
WC2425_16	—	—	—	—	—	—	—
WC2425_15	Suwallia (16), Baetis tricaudatus (16), Glossosoma (16)	—	—	—	—	—	—
WC2425_14	Simulium (16), Rhyacophila Brunnea/Vemna (16), Glossosoma (16)	Suwallia (14), Baetis tricaudatus (14), Rhithrogena (14)	—	—	—	—	—

WC2425_13	Baetis tricaudatus (16), Simulium (16), Glossosoma (16)	Suwallia (13), Rhithrogena (13), Ephemerella tibialis (13)	Baetis tricaudatus (14), Ephemerella tibialis (13), Acentrella turbida (13)	—	—	--	—
WC2425_12	Simulium (16), Oligochaeta (12), Zapada columbiana (12)	Suwallia (12), Simulium (15), Oligochaeta (12)	Oligochaeta (12), Zapada columbiana (12), Orthoclaadiinae (14)	Oligochaeta (12), Simulium (13), Zapada columbiana (12)	—	—	—
WC2425_11	Simulium (16), Baetis tricaudatus (16), Suwallia (16)	Simulium (15), Suwallia (11), Ameletus (11)	Baetis tricaudatus (14), Orthoclaadiinae (14), Suwallia (14)	Simulium (13), Orthoclaadiinae (13), Rhithrogena (13)	Oligochaeta (12), Zapada columbiana (12), Suwallia (12)	—	—
WC2425_09	Orthoclaadiinae (09), Baetis tricaudatus (16), Chironominae (09)	Orthoclaadiinae (09), Chironominae (09), Suwallia (09)	Baetis tricaudatus (14), Chironominae (09), Orthoclaadiinae (09)	Orthoclaadiinae (09), Chironominae (09), Narpus (13)	Oligochaeta (12), Orthoclaadiinae (09), Simulium (09)	Orthoclaadiinae (09), Simulium (09), Chironominae (09)	—
WC2425_05	Suwallia (16), Chironominae (05), Rhithrogena (16)	Orthoclaadiinae (05), Chironominae (05), Diamesinae (05)	Suwallia (14), Chironominae (05), Rhithrogena (14)	Chironominae (05), Rhithrogena (13), Suwallia (13)	Orthoclaadiinae (05), Suwallia (12), Chironominae (05)	Orthoclaadiinae (05), Chironominae (05), Diamesinae (05)	Rhithrogena (09), Suwallia (09), Chironominae (05)

WC2600

	WC2600_16	WC2600_15	WC2600_14	WC2600_13	WC2600_12	WC2600_11	WC2600_09
WC2600_16	—	—	—	—	—	—	—
WC2600_15	Simulium (16), Cinygmula (16), Suwallia (16)	—	—	—	—	—	—
WC2600_14	Simulium (16), Baetis tricaudatus (14), Rhithrogena (14)	Baetis tricaudatus (14), Orthoclaadiinae (14), Simulium (14)	—	—	—	—	—
WC2600_13	Simulium (16), Orthoclaadiinae (13), Cinygmula (16)	Orthoclaadiinae (13), Simulium (13), Suwallia (13)	Baetis tricaudatus (14), Oligochaeta (13), Rhithrogena (14)	—	—	--	—
WC2600_12	Simulium (16), Prosimulium (12), Orthoclaadiinae (12)	Orthoclaadiinae (12), Suwallia (12), Prosimulium (12)	Simulium (14), Prosimulium (12), Suwallia (12)	Prosimulium (12), Suwallia (12), Zapada columbiana (12)	—	—	—
WC2600_11	Simulium (16), Orthoclaadiinae (11), Prosimulium (11)	Orthoclaadiinae (11), Prosimulium (11), Suwallia (11)	Baetis tricaudatus (14), Simulium (14), Rhithrogena (14)	Simulium (13), Prosimulium (11), Orthoclaadiinae (13)	Rhithrogena (12), Suwallia (12), Zapada columbiana (12)	—	—

WC2600_09	Simulium (16), Orthoclaadiinae (09), Rhithrogena (09)	Orthoclaadiinae (09), Oligochaeta (09), Suwallia (09)	Oligochaeta (09), Simulium (14), Baetis tricaudatus (14)	Rhithrogena (09), Simulium (13), Ephemerella tibialis (09)	Prosimulium (12), Oligochaeta (09), Epeorus deceptivus (12)	Rhithrogena (09), Orthoclaadiinae (09), Oligochaeta (09)	—
WC2600_05	Simulium (16), Orthoclaadiinae (05), Antocha (05)	Orthoclaadiinae (05), Antocha (05), Chironominae (05)	Baetis tricaudatus (14), Orthoclaadiinae (14), Simulium (14)	Orthoclaadiinae (05), Antocha (05), Chironominae (05)	Orthoclaadiinae (05), Suwallia (12), Prosimulium (12)	Orthoclaadiinae (05), Antocha (05), Chironominae (05)	Oligochaeta (09), Orthoclaadiinae (05), Baetis tricaudatus (09)