Macroinvertebrate Monitoring at Selected Sites in Whychus Creek, Sisters, OR, 2019

Simulium black fly larvae, Whychus Creek 2019; C.A. Searles Mazzacano

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Summary

The benthic macroinvertebrate community in Whychus Creek was sampled on 23-24 August, 2019 in five regions: Road 6360 (WC0600; index site), Rimrock Ranch (WC1025; baseline data), Whychus Canyon (WC1100 restoration WC1150 untreated control site), Camp Polk (WC1925, WC1950; restoration sites), and Whychus Floodplain (WC2600; index site). A single habitat riffle-targeted sample (RT) and a proportional multihabitat sample (PM) was taken at each index site, and a single PM sample was taken at the baseline and untreated control sites. At restored sites, RT and PM samples were taken in primary and side channel reaches, with RT sampling concentrated in the primary channel. The ORDEQ PREDATOR predictive model and Index of Biotic Integrity (IBI) was applied to all RT samples. Taxonomic and biological traits were assessed for all samples, including: community optima for temperature and fine sediment; tolerances to sediment and organic pollution; functional feeding group; habit (locomotion); annual generations (voltinism); rheophily (flow preference); water temperature association; and maximum body length.

Samples contained 155 unique taxa in 54 families. Order-level diversity was highest among true flies (Diptera; 63 unique taxa in 10 families), especially non-biting midges (Chironomidae). Other families with high diversity included mayflies (Ephemeroptera; 17 unique taxa in six families); caddisflies (Trichoptera; 17 unique taxa in nine families); beetles (Coleoptera; 14 unique taxa in four families); and stoneflies (Plecoptera; eight unique taxa in five families). Eleven taxa not found in any prior sampling year were collected, mainly in PM samples and from sites spanning RM19 to RM26 (three beetle, two mayfly, two caddisfly, one dragonfly, one damselfly, one true fly, and one coelenterate group), including two new families (Aeshnidae; darner dragonfly; Leptoceridae; longhorned caddisfly). In addition, at least one taxon not seen in prior sampling years was collected at all but one of the sites that had been sampled in multiple years.

Taxa richness among all samples ranged from 36-67 (mean = 32 taxa $\pm$ 27), and was significantly greater in PM (55 $\pm$ 9) vs. RT samples; 45 $\pm$ 5), but the mean number of EPT (Ephemeroptera, Plecoptera, Trichoptera) taxa was identical in both sample types (18 EPT). PM samples had a significantly higher community sediment optima and greater numbers of high sediment and warm temperature indicator taxa, reflecting taxa adapted to the slower flows and smaller sediment sizes captured in the pools and glides included in PM sample collection.

Overall, ongoing restoration along Whychus has resulted in communities that are both more diverse and more balanced in recent years. For the most part, macroinvertebrate communities in the same general river mile of the creek are most similar; primary and side channels in the same general location have similar macroinvertebrate communities, and their differences reflect the variations in diversity of habitat and flow. Communities at sites where recent restoration projects were done recover substantially within two years. While there are no significant differences in the pre- and post-project means for community temperature or sediment optima or numbers of DEQ indicator taxa for low/high sediment or cool/warm temperatures, post-restoration communities are usually more diverse and include more taxa with cool/cold temperature, erosional flow, and/or low sediment associations. Some longterm downstream sites are indicating higher temperature and sediment signals, while the sampling site farthest upstream on the creek has one of the highest numbers of low sediment indicator taxa and lowest community temperature optima.

Background

Whychus Creek watershed is a designated priority watershed for conservation and restoration in the upper Deschutes Basin. Projects implemented since 1999 have restored perennial flow to the creek and increased in-stream flow volume and channel; complexity. The aquatic macroinvertebrate community has been monitored regularly to assess changes following restoration and relate them to changes in habitat conditions. More recent creation of side channel habitat for salmonids led to additional focus on macroinvertebrate communities in these more heterogenous habitats. The goals of macroinvertebrate monitoring in Whychus Creek are twofold: 1. to assess ongoing changes at the watershed level through continued monitoring at selected long-term index sites; and 2. to analyze communities at the project level before and after restoration to increase fine-scale resolution at targeted sites.

Methods

Sampling sites

Benthic macroinvertebrate sampling was done on 23-24 August 2019 in multiple regions of Whychus Creek (Table 1): Road 6360 (WC0600), Rimrock Ranch (WC21025), Whychus Canyon (WC1100, WC1150), Camp Polk (WC1925, WC1950), and Whychus Floodplain (WC2600). A riffle-targeted sample (RT) and a proportional multihabitat sample (PM) was taken at each index site, and a single PM sample was taken at the baseline and untreated control sites. At restored sites, RT and PM samples were taken in primary channel and side channel reaches, with RT sampling concentrated in the primary channel. A duplicate RT sample was taken at WC1950 for quality control.

Macroinvertebrate sampling techniques

Sampling was done by CASM Environmental and UDWC staff in conjunction with volunteers from natural resource agencies (23 August) and the community (24 August). On each day, CASM Environmental staff demonstrated sampling techniques and explained data sheet entries. Teams received sampling kits and directions and dispersed into the field. All teams worked in the same general area each day, so CASM Environmental and UDWC staff were available to answer questions. Teams returned their samples, data sheets, and equipment to CASM Environmental, who inspected each sample to ensure it was properly labeled and preserved.

Single habitat riffle-targeted protocol (RT)

Benthic macroinvertebrates were collected from mainstem riffle habitats according to Oregon Department of Environmental Quality (ORDEQ) protocols for Oregon's wadeable streams (OWEB, 2003). Reach lengths were calculated as 40 times the average wetted stream width at the desired sampling point (min. 500 ft./max 1000 ft.) and the upstream and downstream limit was flagged by UDWC staff. A site sample consisted of eight individual net sets taken in riffle habitat in the designated reach, each collected from a 1 ft^2 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 was taken in each of eight randomly selected riffles; in reaches with fewer riffles, two net sets were taken in each of four randomly selected riffles.

Table 1. Whychus Creek sampling sites in 2019

Site ID	Description	Coordinates	Year(s) sampled
WC0600	RM 6, u/s Rd 6360	44.40412, -121.40259	2005, 2009, 2011-2019
WC1025[a]	Rimrock Ranch u/s	44.371534, -121.415865	2011-2012, 2014-2017, 2019
WC1100[b]	Whychus Canyon Reach 4	44.36493, -121.422232	2014, 2015, 2017-2019
WC1150[c]	Whychus Canyon Reach 3	44.35862, -121.43023	2014-2019
WC1925	Camp Polk		2019
WC1950	Camp Polk upstream	44.318741, -121.514961	2009, 2011-2017, 2019
WC2600	Whychus floodplain; RM 26, 4606 Rd. footbridge	44.27322, -121.5552	2005, 2009, 2011-2018

[a] *designated as WC1050 in 2016 & 2017, and as WC0950 in 2011-2015;* [b] *designated WC1025 in 2014;*
[c] *designated WC1075 in 2014*

Large rocks and debris in the sampling area were rubbed and rinsed into the net to collect clinging organisms and set aside, then the substrate was disturbed thoroughly to a depth of 6-10 cm (2-4 in.) for 1-2 minutes. All eight net sets were pooled in a bucket, large debris was rinsed and removed, and sample material was poured through a sieve lined with a 500 µm Nitex membrane. This concentrated sample was transferred to a 1-liter Nalgene sample jar half-filled with 80% ethanol as a preservative. Jars were filled no more than 2/3 full of volume; sample material was divided among multiple jars if needed. CASM Environmental staff replaced the 80% ethanol in all jars with fresh within 48 hours to ensure preservation.

Proportional multihabitat sampling (PM)

A multihabitat approach samples a representative portion of all habitat types in a reach, including mineral and organic substrates, which improves sample representativeness and assessment of ecological condition and is also preferred in streams or reaches where riffle habitat is poorly represented (Barbour et al., 2006). Reach lengths for proportional multihabitat (PM) sampling were calculated and flagged as described above. At the index sites (WC0600, WC2600) and one restoration site (WC1950), PM and RT samples were taken in the same reach and at the same time. In sample reaches that included side channel habitats, UDWC staff flagged turning points and paths along the channel. Prior to sampling, teams walked the reach and used a worksheet to determine types of in-stream habitat present and their relative proportions. Habitat types were designated as follows:

- bedrock/boulder (continuous rock/large mineral substrate > basketball size)
- cobble (tennis ball- to basketball-size)
- gravel (marble- to tennis ball-size)
- sand/silt (fine sediment)
- filamentous algae (long, flowing strands)
- aquatic vegetation (herbaceous plants rooted or floating in the channel; excludes trees, shrubs, mosses, algae)
- wood (tangles/piles of small wood < 30 cm diameter and large woody debris ≥ 30 cm diameter in wetted channel)
- rootwads/undercut banks (root tangles extruding into flowing channel due to undercut banks)

Each sample was a composite of 10 net sets; the number of net sets taken in each type of habitat was determined by its proportional representation in the reach (Table 2). Flow type in the habitat where each net set was taken was recorded (rapid, riffle, run, glide, pool), but no particular flow types were targeted.

Table 2. Whychus Creek sample and channel types in 2019.
RT = riffle-targeted, PM = proportional multihabitat; PC = primary channel, SC = side channel; PC/SC = reaches that contained both PC and SC. Average wetted widths were calculated from wetted widths recorded by volunteers at each point where a net set was taken at sampling time.

Sample	Site type	sample type	Loc.	# net sets in each habitat type	flow type in net sets	avg wetted width (ft)
WC0600-1	index	RT	PC	8 riffle	8 riffles	25.7 ± 1.8
WC0600-1	index	PM	PC	1 boulder, 3 cobble, 2 gravel, 2 silt, 2 wood	4 riffle, 6 run	25.1 ± 2.5
WC1025-1	baseline	PM	PC	1 boulder, 6 cobble, 1 gravel, 1 sand/silt, 1 wood	3 riffle, 4 glide, 3 pool	26.1 ± 6.6
WC1100-1	restoration	PM	PC	5 cobble, 3 gravel, 2 silt/sand	1 rapid, 6 riffle, 3 pool	22.6 ± 8.5
WC1100-2	restoration	RT	PC	8; mostly cobble/gravel, some sand and wood	8 riffles	17.3 ± 4.2
WC1100-2	restoration	PM	PC	4 cobble, 2 gravel, 3 silt/sand, 1 fil. algae	6 riffle, 2 glide, 2 pool	15.4 ± 3.6
WC1100-3	restoration	PM	SC	3 cobble, 1 gravel, 5 silt/sand, 1 wood	4 riffle, 6 pool	14.7 ± 5.0
WC1100-4	restoration	PM	PC/SC	2 cobble, 3 gravel, 4 sand/silt, 1 wood	5 riffle, 1 run, 4 glide	17.3 ± 6.3
WC1100-5	restoration	PM	PC/SC	8 cobble, 1 gravel, 1 silt/sand	2 riffle, 7 run, 1 glide	21.4 ± 8.0
WC1150-1	untreated control	PM	PC	2 boulder, 5 cobble, 2 gravel, 1 wood	2 riffle, 6 run, 2 glide	24.7 ± 3.7
WC1925-1	restoration	PM	SC	1 cobble, 3 gravel, 4 silt/sand, 1 wood, 1 aq. veg. (*Elodea*)	4 riffle, 3 glide, 3 pool	14.3 + 6.9
WC1925-2	restoration	PM	SC	3 gravel, 1 sand/silt, 6 aq veg	9 glide, 1 pool	5.9 ± 4.3
WC1925-3	restoration	PM	PC	5 gravel, 4 algae, 1 wood	4 riffle, 3 glide, 3 pool	16.1 ± 6.6
WC1925-4	restoration	PM	SC	1 boulder, 1 cobble, 4 sand/silt, 2 aq. veg, 2 wood	2 riffle, 8 glide	16.4 ± 5.6
WC1950-1	restoration	RT	PC	8; mostly gravel & sand, some cobble & silt	5 riffle	25.7 ± 11.4
WC1950-1 DUP	restoration	RT	PC	8; mostly gravel & sand, some cobble & silt	5 riffle	25.7 ± 11.4
WC1950-1	restoration	PM	PC	5 cobble, 1 gravel, 1 silt/sand, 1 algae, 1 wood, 1 aq. veg	4 riffle, 2 run, 4 glide	22.9 ± 6.4
WC2600-1	index	PM	PC/SC	3 cobble, 3 gravel, 2 silt/sand, 2 wood	2 riffle, 5 run, 2 glide, 1 pool	23.0 ± 5.6
WC2600-1	index	RT	PC/SC	8; mainly cobble/gravel, some silt/sand	8 riffle	22.5 ± 10.2

Where there was sufficient current to carry suspended material into the net, cobble and gravel substrates were sampled as described above for RT sampling. To sample bedrock and boulders, the D-net was held perpendicular to the substrate with the mouth facing upstream and the rock surface was rubbed clean in a 1 ft² area in front of the net. In slow/still waters and in sediment, the substrate was disturbed manually in a 1 ft² area as the net was swept upwards to capture suspended/disturbed material. Clumps of filamentous algae and plants were shaken into the net mouth to collect any clinging organisms, and the net was jabbed firmly into clumps of plants. Woody materials were rubbed or picked into the net, then kicked vigorously while the net was held below. Rootwads were sampled by jabbing the net into the tangle or kicking into the rootwad while holding the net below. All net sets were composited and processed as described for RT samples.

Sample identification

Samples were identified by Cole Ecological, Inc. (www.coleecological.com) after being first sub-sampled to a target count of 500 individuals by splitting the entire sample into equal aliquots which were then selected randomly and all individuals picked out. An aliquot in which the target number was reached was picked to completion, which explains differences in organismal abundance between samples (see Table 3 in Results).

Organisms were identified to the lowest practical taxonomic level using the standard taxonomic effort recommended by the Pacific Northwest Aquatic Monitoring Partnership (PNAMP, 2015). The 2019 dataset reflects taxonomic changes resulting from recently published updates to taxonomic keys in the seminal reference *Aquatic Insects of North America* (Merritt et al., 2019). For ease of comparison to prior years, any changes are noted with the historic name first and the new current name in parentheses. Most of the changes occurred in the former family Tipulidae (crane flies); this group has now been elevated to a superfamily (Tipuloidea) containing four families, and multiple genera have undergone name changes.

Biological/ecological traits of taxa

Assessing functional traits (i.e., biological properties and ecological preferences) of macroinvertebrate taxa helps infer habitat conditions that shape the community, diagnose stressors or environmental filters, and predict restoration-related changes (Poff et al., 2006; Tullos et al., 2009; Culp et al., 2011; Van den Brink et al., 2011; White et al., 2017). Trait states relating to the ecology and life history of the macroinvertebrate community were assigned to species, genera, or families where data were available. Trait data were drawn from sources specific to Oregon and/or the west (ORDEQ, 2003; Vieira et al., 2006; Meyer & McCafferty, 2007; Huff et al., 2008; Richards & Rogers, 2011; Relyea et al., 2012; IDDEQ, 2015; SAFIT, 2016), as well as general and family-specific references (Pinder, 1986; Wiggins, 1996; Larson et al., 2000; Thorp & Covich, 2001; Stewart & Stark, 2002; Anderson et al., 2013; Merritt et al., 2019). Where multiple modalities existed for a given trait, the primary one for the genus or family was used. Community measures calculated from traits included:

- community optima values for temperature and % fine suspended sediment (weighted averages): Some taxa are more strongly associated with cool/cold or warm flow conditions, either as stenotherms (narrow range) or

eurytherms (wide range). Fine suspended sediment (FSS) is an environmental filter on macroinvertebrates with certain traits. Increasing sediment loads can decrease overall richness as well as the abundance of taxa that feed as scrapers or filterers, have a large maximum body size, soft exposed body, external exposed gills, associations with larger mineral substrata, and a crawling or sprawling habit. Conversely, taxa with operculate gills, smaller and more sclerotized bodies or cases/tubes, and a swimming or climbing/clinging habit may increase in abundance with increasing fine sediment stress (Beche & Statzner, 2009; Sutherland et al., 2012; Buendia et al., 2013; Bona et al., 2015; Murphy et al., 2017; Doretto et al., 2018; Akamagwuna et al., 2019).

- trophic guild (functional feeding group), i.e., relative abundances of predator (PR), scraper (SC), shredder (SH), and collector (C; includes filterers and gatherers) organisms: Filterers can be negatively impacted by sedimentation as their feeding structures become clogged (Rabení et al., 2005; Wilkes et al., 2017); predator abundance may increase as increasing habitat diversity and/or stability creates more abundant and diverse prey (Arce et al., 2014); scrapers can be more abundant on algae- and biofilm-coated mineral substrates; and shredders indicate more plant material and leaf litter input.

- habit (locomotion) i.e., relative abundances of swimmer, clinger, burrower, climber, and sprawler organisms: Swimmers may be able to more rapidly escape disturbances such as sedimentation; burrowers may be selected for in sedimented habitat; sprawlers, clingers, and crawlers can be smothered and/or lose habitat as interstitial spaces are filled (Mathers et al., 2017; Murphy et al., 2017).

- voltinism (# generations per year) i.e., relative abundances of multivoltine (>1 generation/year), univoltine (one generation/year), and semivoltine <1 generation/yr) organisms. Multivoltinism is associated with more tolerant organisms and/or greater resilience in disturbed habitats, while semivoltine taxa require more stable conditions.

- rheophily (flow preference), i.e, relative abundances of organisms associated with erosional, depositional, and mixed flow (members of taxon found in lotic and lentic habitats);

- temperature associations, i.e., relative abundances of organisms with cool/cold or warm water temperature preferences (taxa with mixed or no particular preference were omitted from this analysis); and

- maximum length, i.e., relative abundances of organisms with small (< 9 mm), medium (9-16 mm), and large (>16 mm) body length: Small body size is often associated with greater tolerance and rapid recolonization, which can be an advantage in disturbed sites, while larger-bodied insects may be slower to develop and more abundant in sites with greater habitat stability (Townsend & Hildrew, 1994; Castro et al., 2018).

Data analysis

Analyses were done using PAST 4.0 statistical software (Hammer et al., 2001). CLUSTER ordinations and SIMPER tests were run on a Bray-Curtis similarity matrix of square-root transformed taxa abundances. Principal Component

Analysis (PCA) was done using a variance-covariance matrix. When doing t tests to compare means, a cutoff value of $p \leq 0.05$ was used for statistical significance.

Biological condition of RT sample reaches was assessed using the ORDEQ multimetric invertebrate-based index of biotic integrity (IBI), and the probability-based PREDATOR model (Hubler, 2008). For the IBI, 10 trait values are scored individually (1, 3, 5) then summed to give a number that corresponds to a level of impairment (Table 3). PREDATOR calculates the ratio of taxa observed at a sampling site to taxa expected if the site is not impaired (O/E), based on comparison to established reference communities. The model uses site elevation, slope, and longitude to select appropriate reference streams. O/E scores associated with a probability of capture (P_c) > 0.5 are used to avoid rare taxa bias and are assigned to biological condition categories of: poor (most disturbed; ≤ 0.78); fair (moderately disturbed; 0.79-0.92); good (least disturbed; 0.93-1.23); and enriched (>1.23). Whychus Creek is an outlier for the PREDATOR model because it has lower annual precipitation than any of the reference streams the model selects as most appropriate (Shannon Hubler, pers. comm. 2017).

Table 3. ORDEQ genus-level macroinvertebrate-based IBI metrics and scoring.

I-IBI			
Scoring Criteria			
Metric	5	3	1
Taxa richness	>35	19-35	<19
Mayfly richness	>8	4-8	<4
Stonefly richness	>5	3-5	<3
Caddisfly richness	>8	4-8	<4
# sensitive taxa	>4	2-4	<2
# sediment-sensitive taxa	>2	1	0
% dominance[a]	<20	20-40	>40
% tolerant taxa	<15	15-45	>45
% sediment-tolerant taxa	<10	10-25	>25
MHBI[b]	<4	4-5	>5
Summed score & condition			
Severely impaired		<20	
Moderately impaired		20-29	
Slightly impaired		30-39	
Minimally/not impaired		>39	

[a] *relative abundance of the most abundant taxon;* [b] *modified Hilsenhoff Biotic Index (Hilsenhoff, 1987), which reflects tolerant to organic pollution and ranges from 1 (lot tolerance) to 10 (high tolerance)*

Results

Overall macroinvertebrate community in 2019 samples

A total of 155 unique taxa in 54 families (37 insect,17 non-insect) was collected across all sites and samples, only nine of which were found at every sampling site. Order-level diversity was highest among Diptera (true flies), with 63 unique taxa in 10 families, including 40 unique genera of non-biting midge (Chironomidae). Other well-represented families included mayflies (Ephemeroptera), with 17 unique taxa in six families; caddisflies (Trichoptera), with 17 unique taxa in nine families; beetles (Coleoptera), with 14 unique taxa in four families; and stoneflies (Plecoptera), with eight unique taxa in five families. Taxa taken in 2019 but not in any prior sampling year occurred in low numbers and at a small number of sampling sites, though the majority were found in samples from RM 19-26, and include:

- *Haliplus*, a tolerant genus of crawling water beetle (Haliplidae) associated with macrophytes in slow water; one individual in WC1925 PM sample
- *Laccobius*, a water scavenger beetle (Hydrophilidae) that prefers warmer waters; low numbers in PM samples from WC1100-3 and WC1925
- *Tropisternus*, a water scavenger beetle that prefers warmer waters; one individual in WC1925 PM sample
- *Trichoclinocera*, a dance fly (Empididae) found on rocks in riffles with open canopy; low to moderate numbers in PM and RT samples from WC1925, WC1950, and WC2600
- *Neoleptophlebia*, a prong-gilled mayfly (Leptophlebiidae) that prefers colder flowing waters; one individual in the duplicate RT sample at WC1950
- *Siphlonurus*, a primitive minnow mayfly (Siphlonuridae) that prefers slower-moving water; low numbers in PM samples at WC1050 and WC1925-2
- Aeshnidae, darner dragonflies, whose larvae climb on aquatic plants and adults of which have been seen flying during sampling in past years (C.A. Searles Mazzacano, pers. obs.); one in the WC1925-1 PM sample
- *Calopteryx*, a jewelwing damselfly often seen at stream margins, in a family (Calopterygidae) also not found in prior years; one individual in the WC1050 PM sample
- Leptoceridae, longhorned caddisflies, which inhabit a variety of lentic and lotic habitats; one individual in the WC1100-1 PM sample
- *Glyphopsyche irrorata*, a Northern caddisfly (Limnephilidae) that sprawls in detritus in slow-moving water; one individual in the WC1925-2 PM sample
- Hydra, a tolerant coelenterate that clings to rocks in shallow waters; eight individuals in the WC1925-4 PM sample

Invertebrate abundance was high, with the target sub-sampling number of 500 individuals attained for all but one sample (WC1100-2) with 5.8-100% of the total sample picked (Table 4). There was no significant difference between the proportion of RT vs. PM samples required for subsampling. Numerical abundance across the dataset was dominated by *Tanytarsus*, a non-biting midge that prefers warmer waters but is found in all types of freshwater habitats, present in all but three samples in abundances ranging from 2 to 202; and *Simulium*, a black fly that clings to rocks and trailing vegetation in flowing water, present in every sample except the WC1925-2 PM side channel sample (the only PM sample that did not include any riffle habitat), in numbers ranging from two to 294.

The number of unique taxa in each sample ranged from 36 to 67 (mean = 32 taxa ± 27), and was significantly greater in PM (55 taxa ± 9) vs. RT samples; 45 taxa ± 5). For reference, in the ORDEQ IBI, taxa richness receives the highest scaled score for >35 unique taxa in a sample. Simpson's Diversity Index (1-D), which considers both richness and evenness, did not differ significantly between RT and PM samples (Table 4), indicating that while PM samples were more diverse, they were not overly dominated by a subset of taxa at any site. This is also seen in the relative abundances of the top (numerically dominant) taxon at each site, which ranged from 11.3% to 53.3% (mean 24.9% ± 11.1) and was not significantly different between PM and RT samples. The dominance of the top taxon was ≤ 37% in every sample except WC1950 RT; for reference, a top taxon relative abundance of <20% is considered to reflect a balanced community and receives the highest scaled score in the IBI.

Table 4. Richness, abundance, and diversity among sampling sites in 2019. *DUP = duplicate sample; RT = riffle-targeted, PM = proportional multihabitat; PC = primary channel, SC = side channel; PC/SC = both channel types in sampling reach*

Sample	Type	Reach	% of sample picked	Abundance[a] (# individuals)	Richness (# unique taxa)	#EPT taxa	Simpson's Diversity Index (1-D)
WC0600-1	RT	PC	21.7	538	43	15	0.93
WC0600-1	PM	PC	23.3	532	45	13	0.86
WC1025-1	PM	PC	20.8	548	60	18	0.92
WC1100-1	PM	PC	63.3	549	51	20	0.87
WC1100-2	RT	PC	21.7	520	51	21	0.93
WC1100-2	PM	PC	100	122	36	16	0.93
WC1100-3	PM	SC	28.3	550	58	17	0.76
WC1100-4	PM	PC/SC	25	537	60	20	0.81
WC1100-5	PM	PC/SC	43.3	553	55	22	0.93
WC1150-1	PM	PC	20	524	47	19	0.90
WC1925-1	PM	SC	30	553	65	20	0.89
WC1925-2	PM	SC	15	530	56	9	0.84
WC1925-3	PM	PC	10.8	546	67	23	0.91
WC1925-4	PM	SC	100	541	64	19	0.94
WC1950-1	RT	PC	5.8	552	46	20	0.70
WC1950-1 DUP	RT	PC	11.7	531	46	19	0.84
WC1950-1	PM	PC	23.3	508	56	18	0.90
WC2600-1	PM	PC/SC	30	516	49	22	0.82
WC2600-1	RT	PC/SC	21.7	524	37	18	0.76

[a] *total number of individuals subsampled in proportion of sample picked; target subsampling number is 500.*

Although RT samples might be expected to have more sensitive and/or EPT taxa due to the greater representation of riffle habitat, the mean number of EPT (range = 9-23) and of sensitive taxa (range = 3-7) was not significantly different between PM and RT samples. The number of sediment-sensitive taxa (range = 1-3) was higher in RT samples, while the relative abundance of both tolerant (range = 2.1-40.7%) and sediment-tolerant organisms (range = 0.4-11%) was greater in PM samples, but none of the differences were significant. The means for community temperature optima (range = 16.7-18.0°F) and number of DEQ cool temperature indicator taxa (range = 0-7) were the same in RT and PM samples (17.3°F; 3 cool indicator taxa), but the mean number of DEQ warm temperature indicators (range = 0-9 taxa) was significantly greater in PM samples. The mean community sediment optima (range = 6.9-10.3% FSS) was significantly lower in RT samples (7.1% FSS ± 0.2 vs. 8.5% FSS ± 1.0), as was the mean number of DEQ high sediment indicator taxa (range = 1-11), while the mean number of DEQ low sediment indicator taxa (range = 0-10) was significantly greater in RT samples.

As in past years, macroinvertebrate community composition was strongly influenced by location (Figure 1), with greater similarity among samples taken in upstream reaches (i.e., RM 19.25 to 26), regardless of the type of sample reach (primary/side channel), with the exception of the WC1925-2 side channel sample, which was an outlier. The paired samples at WC1950 for quality control were most similar to each other (Bray-Curtis Index = 0.77), confirming consistency of sampling technique between different operators. In a PCA ordination of taxa abundances (Figure 2), axis 1 explained 27% of the variation among samples, and taxa with the highest loading values were the black fly *Simulium* (very abundant in WC2600 and WC1950 samples); and the non-biting midge tribes Tanytarsini (more abundant in many WC1100 and WC1150 samples) and Chironomini (low abundances in samples from RM 19.25 through RM 26), which are tolerant of warmer and more sedimented habitats. Axis 2 explained an additional 22% of variation among samples, and taxa with the highest loading values were the flatheaded mayfly *Rhithrogena* (few to none in WC1925 and WC1950 samples), which is generally found on rocks in colder running waters; Tanytarsini; and the riffle beetles *Optioservus* and *Zaitzevia* (less abundant in sample reaches from RM19 to RM 26), which inhabit gravels and sediments in faster waters.

In a PCA ordination of traits measured as relative abundances, axis 1 explained 57% of the variation between samples (Figure 3). Factors with the highest loading values included relative abundance of organisms associated with erosional habitats (greater overall in RT samples), and relative abundances of climbers and warm water-associated organisms, which were greater in samples taken around RM 11 and RM 19.

Figure 1. CLUSTER ordination of the macroinvertebrate community among all sampling sites in 2019.
RT = riffle-targeted, PM = proportional multihabitat; PC = primary channel, SC = side channel; PC/SC = both channel types in sampling reach; DUP = duplicate sample taken for quality control
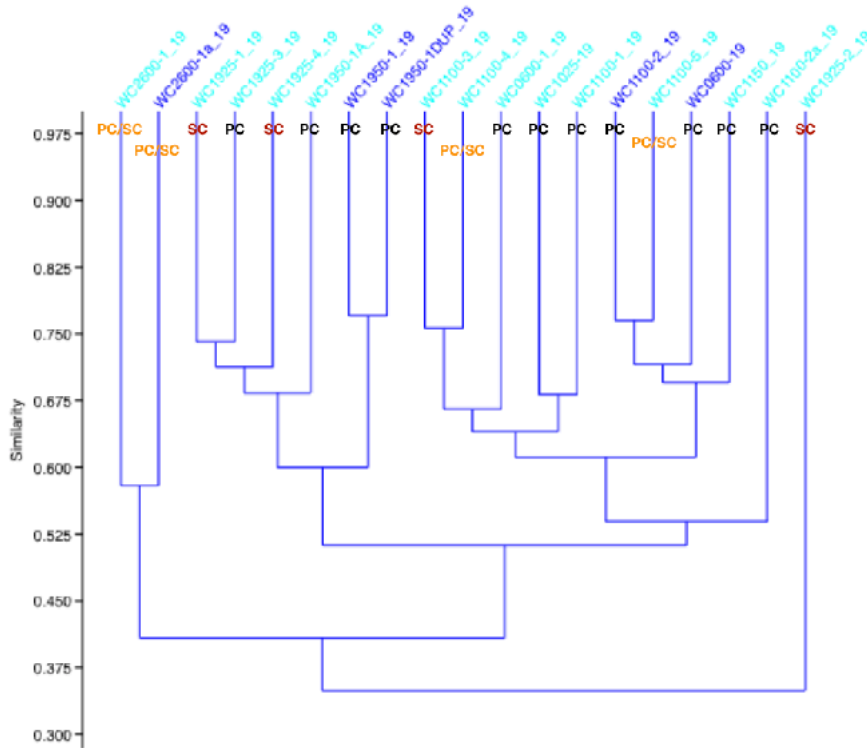
Figure 2. Ordination plot from a Principal Components Analysis (PCA) of taxa abundances among all 2019 samples.
Eigenvectors show dominant taxa contributions, where the length of the vector is related to the strength of its contribution. Dark blue = RT sample, aqua = PM sample.
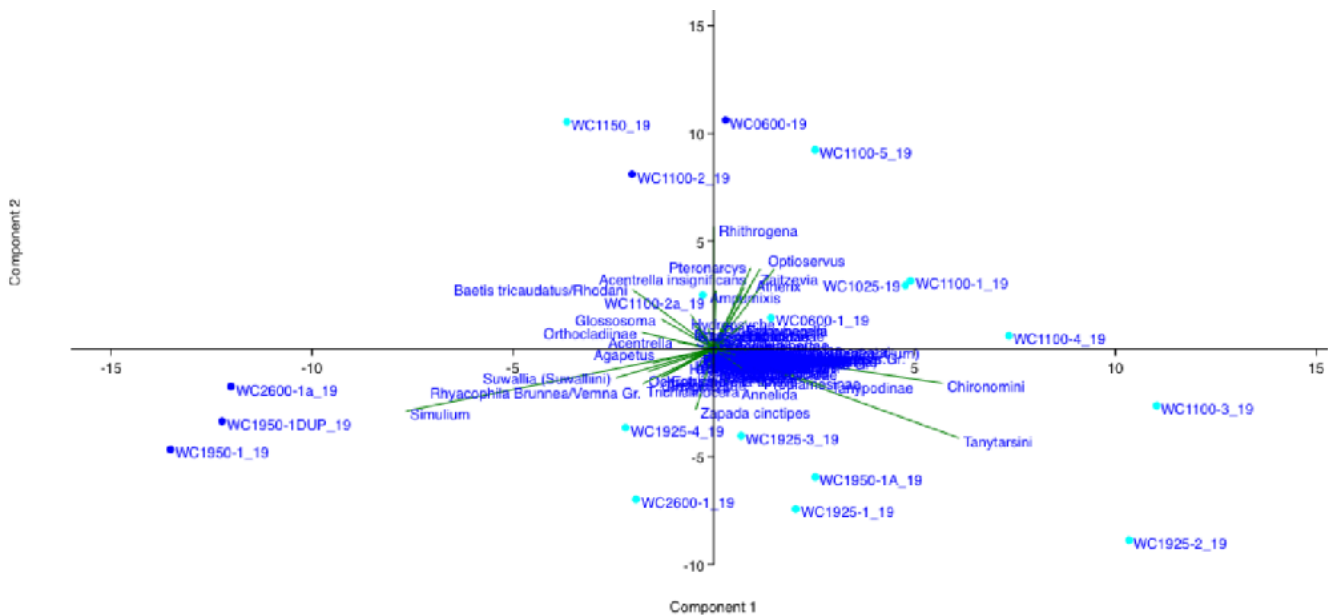
Figure 3. Ordination plot from PCA of traits calculated as relative abundances among all 2019 samples. *Eigenvectors show dominant contributions, where length of the vector is related to the strength of its contribution. Dark blue = RT sample, aqua = PM sample.*
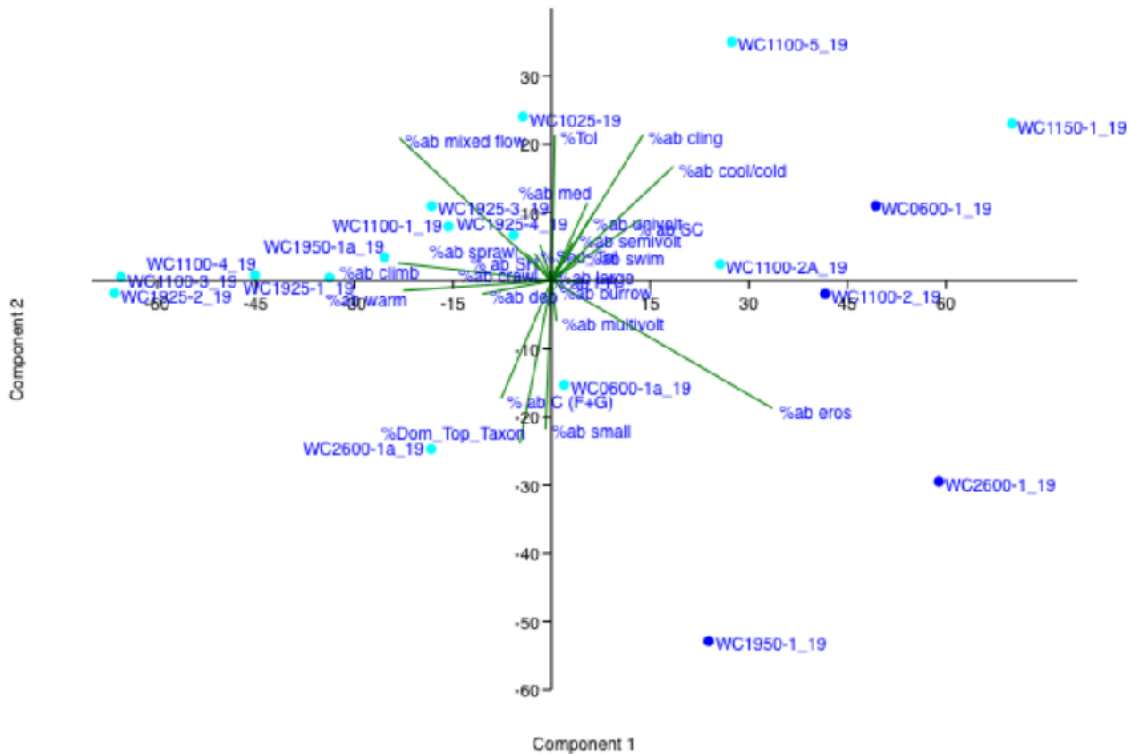
Individual site characteristics

<u>WC0600</u>

Riffle-targeted (RT) samples were taken in the primary channel of Whychus Creek around RM 6.0 in every sampling year since 2005; in 2018 and 2019, a PM sample was also taken in the same reach. PM and RT samples in 2019 were similar (Bray-Curtis similarity index = 0.64) and had similar numbers of total taxa (43 and 45 taxa, respectively) and of EPT taxa (15 vs. 13 taxa). As expected, the RT sample had more cool/cold- and erosional-associated organisms, but both samples had very few sediment-tolerant organisms (<1% of total organismal abundance in each sample). Community temperature optima were almost identical (18.0°F in RT, 17.9°F in PM), and were at the upper end of the range seen in 2019 (16.7-18.0°F among all 2019 samples). The PM sample had a higher community sediment optima (8.7% FSS vs. 6.9% FSS) and more DEQ high sediment (7 vs. 3) and high temperature (9 vs. 5) indicator taxa than the RT sample. The community in both sample types was dominated by small-bodied, rapidly-developing (multivoltine) collectors and clingers, and while there were more warm-and depositional habitat-associated organisms in the PM sample compared to the RT, the majority in both were associated with erosional habitats. The only taxon in the 2019 sample not taken in previous years at this site was *Ochrotrichia* (one individual in RT sample), a tolerant purse-case caddisfly that inhabits both erosional and depositional habitats.

The target sub-sample of 500 organisms was attained in eight of 11 sampling years, including every year since 2015 (Figure 4). Sample richness increased overall; from 2017-2019, taxa numbers received the highest scaled score in the IBI (>35 taxa), and richness in the last two years is almost twice that of earlier years (Figure 5). The number of EPT taxa fluctuated, and the overall average dissimilarity among the EPT community in all years is 55%. More changes occurred among the mayflies and include increasing abundances of lotic-associated taxa such as *Rhithrogena*, a flatheaded mayfly found in cold flowing waters that is a DEQ low sediment indicator; *Hydropsyche*, a net-spinning caddisfly found in a variety of flowing waters that is a DEQ warm temperature indicator; *Acentrella*, a small minnow mayfly associated with lotic-erosional habitat; *Diphetor hageni*, a flatheaded mayfly that inhabits gravel and cobble in a variety of flows and is a DEQ warm temperature indicator; *Attenella*, a spiny crawler mayfly found in waters with

Figure 4. Proportion of sample needed for sub-sampling and resulting organismal abundance at WC0600 in all sampling years. RT samples were taken every year; a PM sample was taken in the same reach as the RT in 2018-2019.
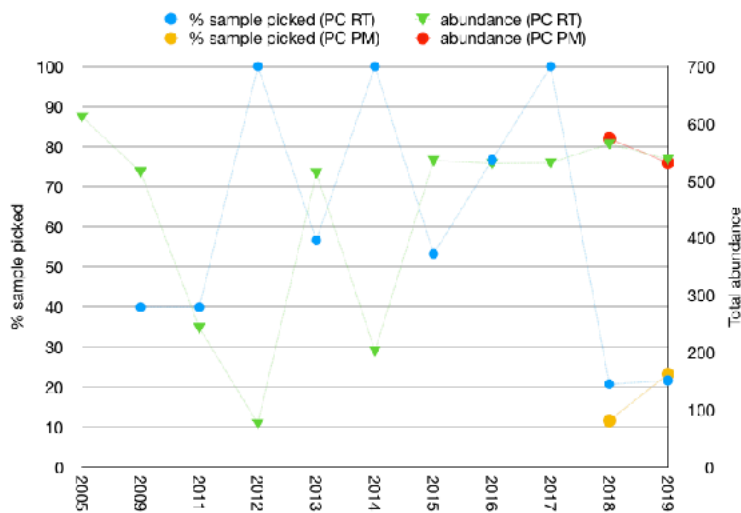
Figure 5. Sample richness and number of EPT taxa at WC0600 in all sampling years. RT samples were taken every year; a PM sample was taken in the same reach as the RT in 2018-2019. For this metric in the ORDEQ IBI, >35 total taxa receives the highest scaled score.
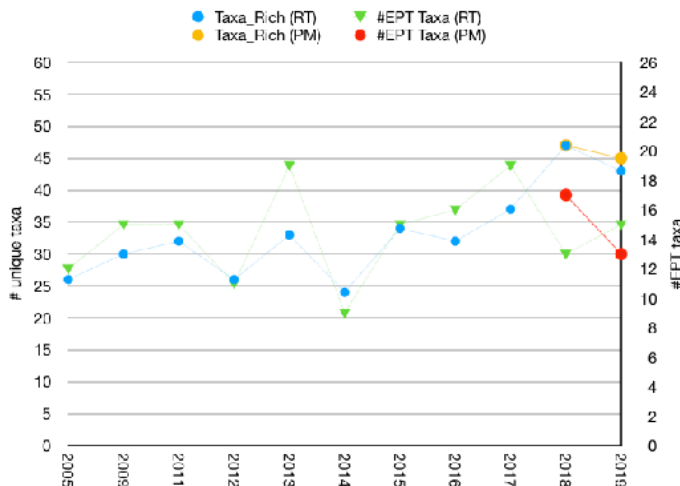
moderate flow along the margins among silt and moss-covered rocks and gravel; and *Wormaldia*, a finger-net caddisfly found on rocks in flowing waters.

IBI and PREDATOR scores have fluctuated (Figure 6) but both increased after 2014 to values reflecting slight/minimal impairment (IBI) or fair condition (O/E). The number of sensitive taxa and sediment-sensitive taxa increased overall since 2016 in both RT and PM samples (Figure 7) and while this site has never had enough sensitive taxa to receive the highest scaled IBI score, 2019 was the first year in which both the RT and PM sample had sufficient sediment-sensitive taxa (3) to be in the range for the highest scaled IBI score. Relative abundances of tolerant and sediment-tolerant taxa fluctuated through 2016 but decreased overall since (Figure 8), and relative abundance of sediment-tolerant taxa (range = 0.4-4.4%) has always been low enough to receive the highest scaled IBI score (<10%).

The macroinvertebrate community has also become much more balanced at this site over time (Figure 9), and from 2015-2019 the relative abundance of the top taxon in RT samples was low enough to receive the highest scaled score in the IBI (<20%). With the exception of some earlier sampling years when the top taxon included non-biting midge groups, the community at WC0600 has been dominated by taxa associated with faster-flowing water, though with a mixture of temperature preferences and sediment tolerances.

*Figure 6. PREDATOR O/E and ORDEQ IBI scores at WC0600 in all sampling years.*
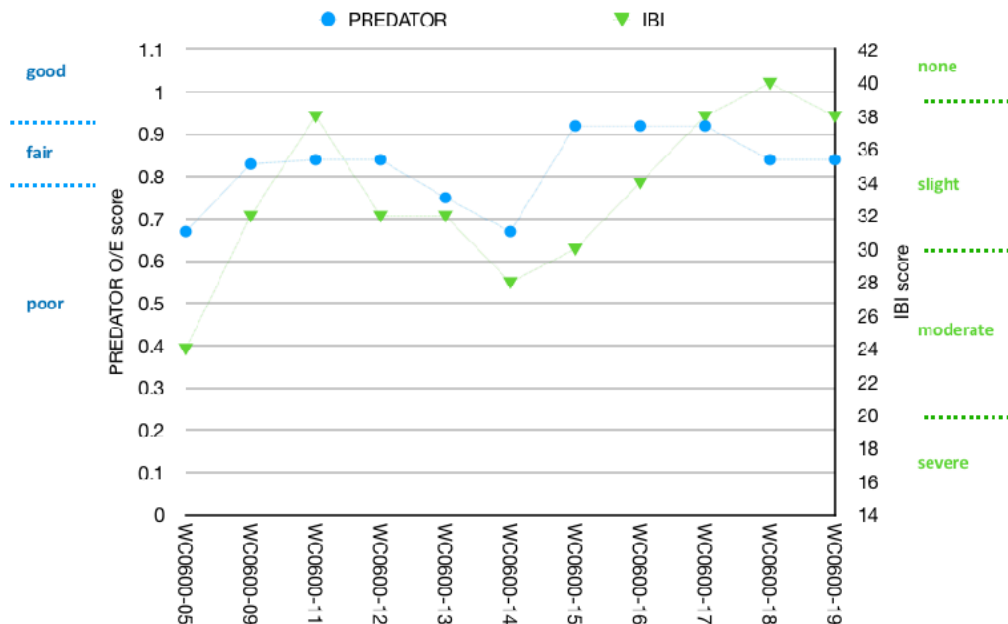
Figure 7. Numbers of sensitive and sediment-sensitive taxa at WC0600 in all sampling years. *RT samples were taken every year; a PM sample was also taken in the same reach as the RT in 2018-2019. For these metrics in the ORDEQ IBI, the highest scaled score correlates with >4 sensitive and >2 sediment-sensitive taxa.*
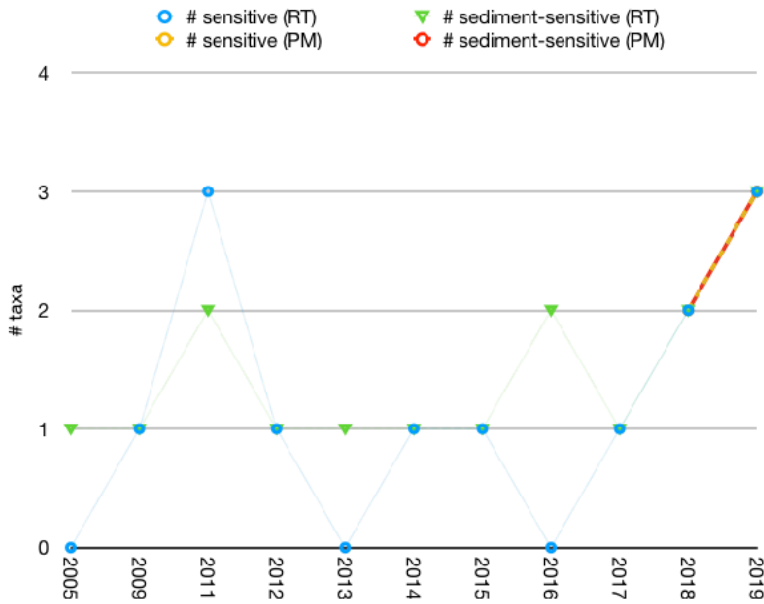
Figure 8. Relative abundance of tolerant and sediment-tolerant organisms at WC0600 in all sampling years. *RT samples were taken every year; a PM sample was also taken in the same reach as the RT in 2018-2019. For these metrics in the ORDEQ IBI, the highest scaled score correlates with <15% tolerant and <10% sediment-tolerant.*
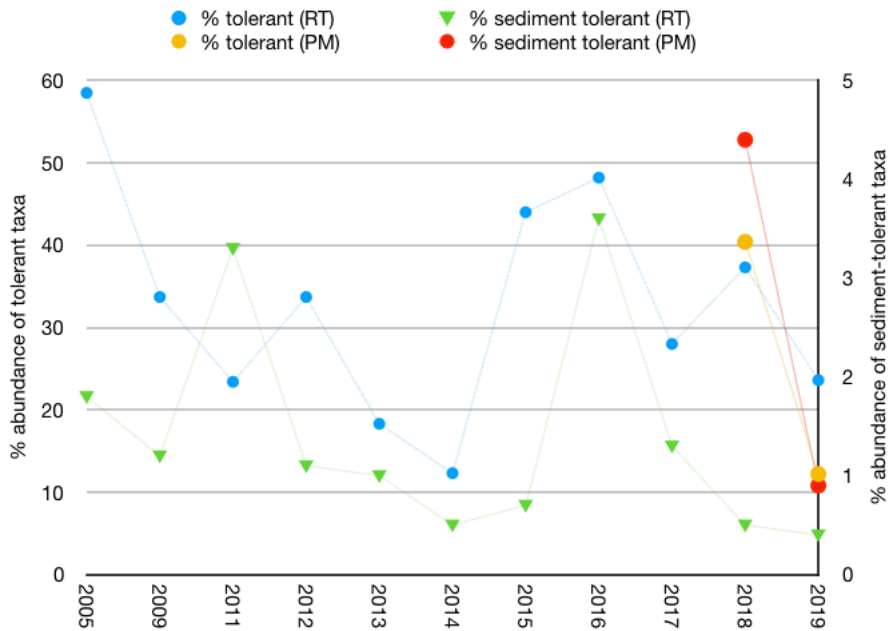
Figure 9. Relative abundance of the numerically dominant taxon at WC0600 in all sampling years. *RT samples were taken every year; a PM sample was also taken in the same reach as the RT in 2018-2019. For this metric in the ORDEQ IBI, the highest scaled score correlates with <20% abundance of the top taxon.*
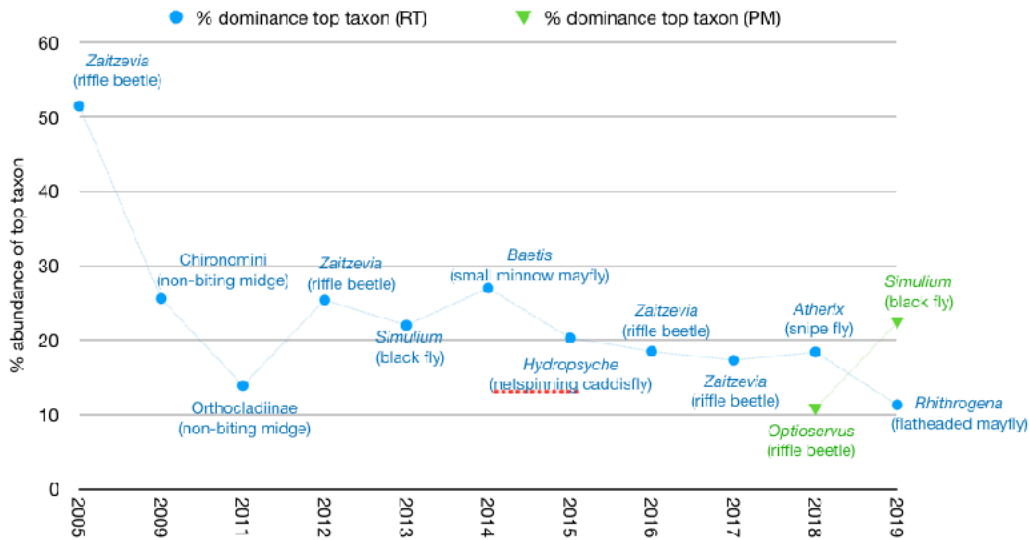
Community temperature optima in RT samples decreased from 2005-2013 but increased since then (Figure 10), and the number of DEQ warm temperature indicator taxa exceeded the number of cool indicator taxa in all but a single sampling year (Figure 11). However, the difference in the mean temperature optima from 2005-2013 and 2014-2019 is not significant, and the temperature optima in PM samples was lower in 2019 compared to 2018, though the difference was not significant. Community sediment optima in RT samples decreased overall (Figure 10); higher and increasing optima in PM samples in 2018-2019 is likely due in part to sampling different flow and sediment types. The number of DEQ high sediment indicator taxa exceeded the number of low sediment indicators in most sampling years, but decreased more than two-fold in RT samples from 2018 to 2019 (Figure 12).

Figure 10. Temperature and fine sediment optima of the community (weighted means) at WC0600 in all sampling years. *RT samples were taken every year; a PM sample was also taken in the same reach as the RT in 2018-2019.*
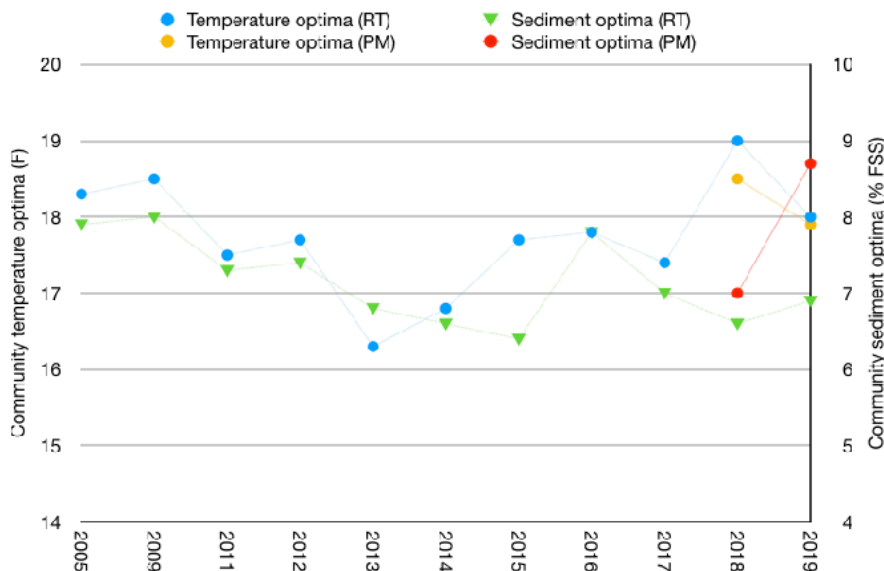
Figure 11. Number of ORDEQ cool and warm temperature indicator taxa at WC0600 in all sampling years. RT samples were taken every year; a PM sample was also taken in the same reach as the RT in 2018-2019. Note that the ORDEQ taxa do not account for the temperature associations of all taxa in a sample.
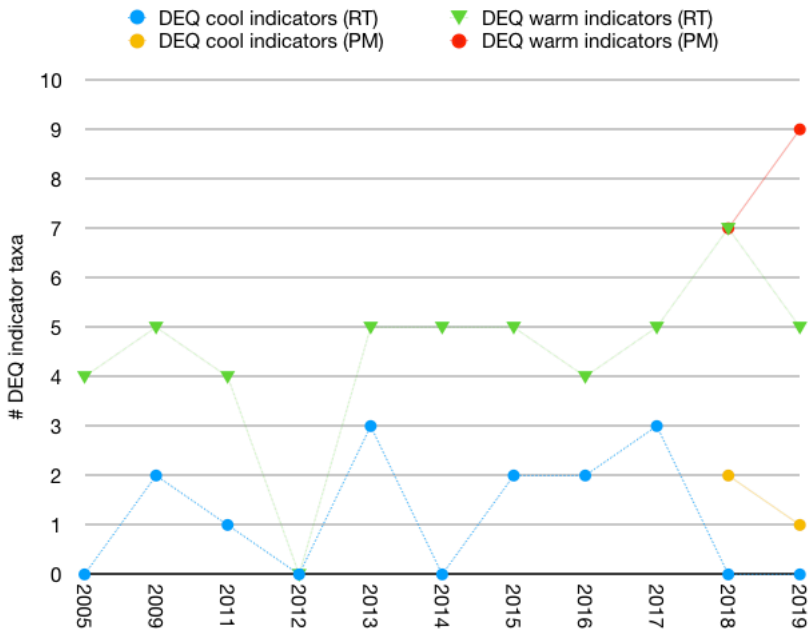
Figure 12. Number of ORDEQ low and high sediment indicator taxa at WC0600 in all sampling years. RT samples were taken every year; a PM sample was also taken in the same reach as the RT in 2018-2019. Note that the ORDEQ taxa do not account for the sediment tolerances of all taxa in a sample.
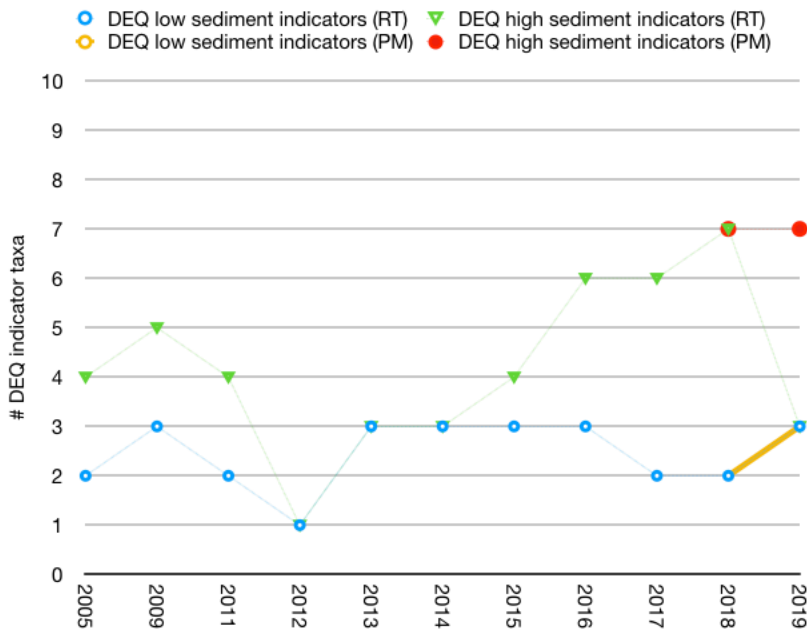
A CLUSTER dendrogram shows greater community similarity among samples in earlier vs. later years (Figure 13), with an overall average dissimilarity among all years of 45%. Taxa that accounted most for differences were those that dominated the community in different years, i.e., *Zaitzevia*, *Rhithrogena*, and *Simulium*. In a PCA ordination of taxa (Figure 14), axis 1 explained only 25% of the variation; factors with the highest loading were *Rhithrogena*, *Acentrella*, and *Optioservus,* all of which were more abundant in recent sampling years. Axis 2 explained an additional 20% of variation, and factors with the highest loading were *Zaitzevia,* a tolerant riffle beetle in erosional habitats on cobble and gravel that is a DEQ warm temperature and high sediment indicator (more abundant in earlier sampling years); the tolerant non-biting midge tribe Chironomini (high abundance in 2019 PM sample); and *Baetis tricaudatus*, a small minnow mayfly associated with fast flows that is often an early recolonizer after disturbance and is a DEQ low sediment indicator taxon (more abundant in later sampling years).

Figure 13. CLUSTER dendrogram of the WC0600 macroinvertebrate community in all sampling years. Blue = RT, aqua = PM. The numeral in each label indicates the sampling year.
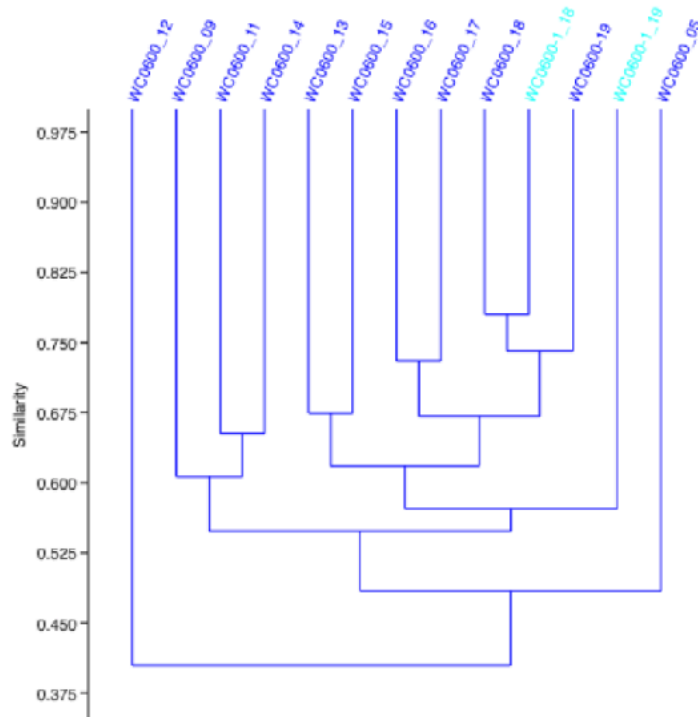
In a PCA ordination of traits measured as relative abundances in all years (Figure 15), axis 1 explained 65% of the variation; factors with the highest loading were relative abundance of scrapers (SC; most abundant in 2005 and 2016) and collectors (C (F+G); less abundant in earlier sampling years). Axis 2 explained an additional 15% of the variation, with relative abundance of tolerant organisms and of collectors having the highest loading. In a PCA ordination of all traits measured since 2018, when additional traits such as flow and temperature preference, maximum body length, voltinism, and habit were assessed, axis 1 explained 60% of the total variation (Figure 16); factors with the highest loading were relative abundance of small and medium organisms, which differed most in the

2019 PM sample. Axis 2 explained an additional 35% of the variation; factors with the highest loading were cool/cold- and erosional-associated taxa, which differed more between RT and PM samples.

Figure 14. PCA ordination of the WC0600 macroinvertebrate taxa in all sampling years. Blue = RT, aqua = PM. The numeral in each label indicates the sampling year. Eigenvectors show dominant contributions, where vector length is related to the strength of its contribution.
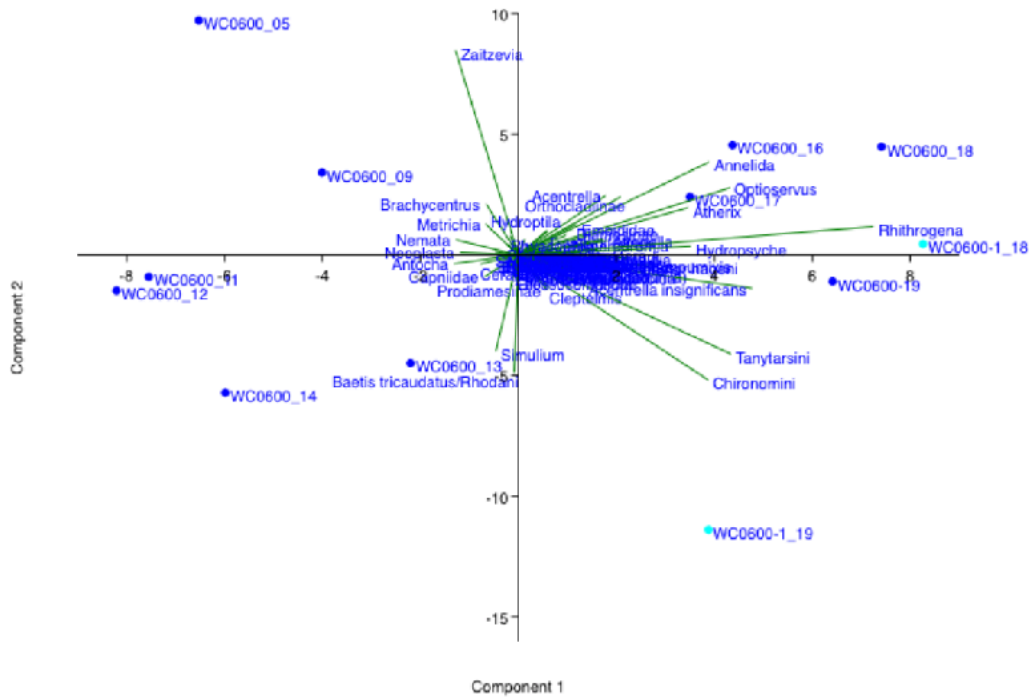

Figure 15. PCA ordination of WC0600 macroinvertebrate community traits measured as relative abundances in all sampling years. Blue = RT, aqua = PM. The numeral in each label indicates the sampling year. Eigenvectors show dominant contributions, where vector length is related to the strength of its contribution.
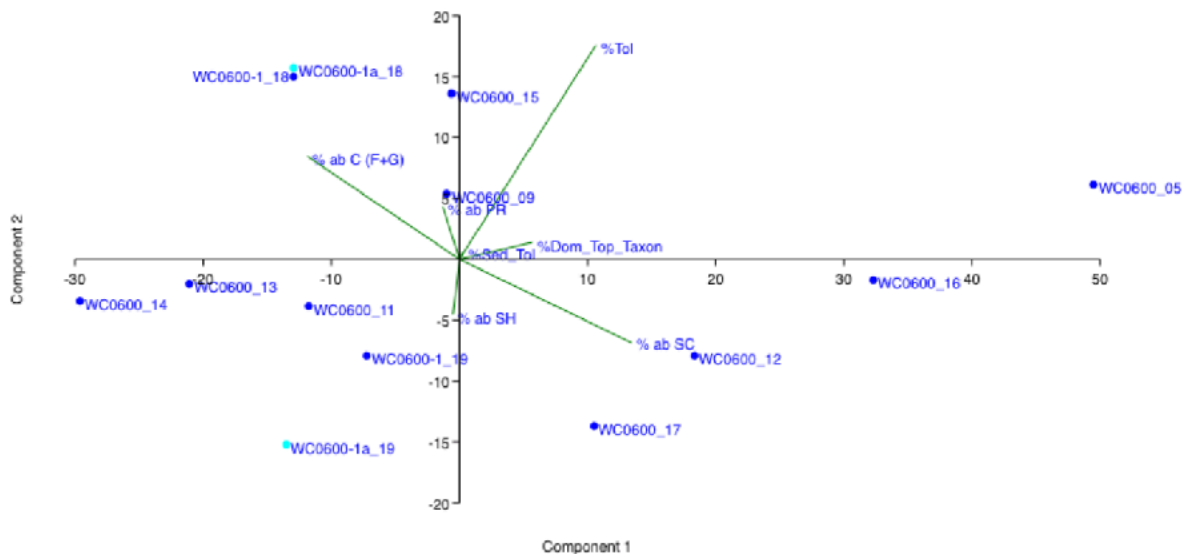
Figure 16. PCA ordination of the WC0600 macroinvertebrate community traits measured as relative abundances in 2018-2019. Blue = RT, aqua = PM. The numeral in each label indicates the sampling year. Eigenvectors show dominant contributions, where vector length is related to the strength of its contribution.
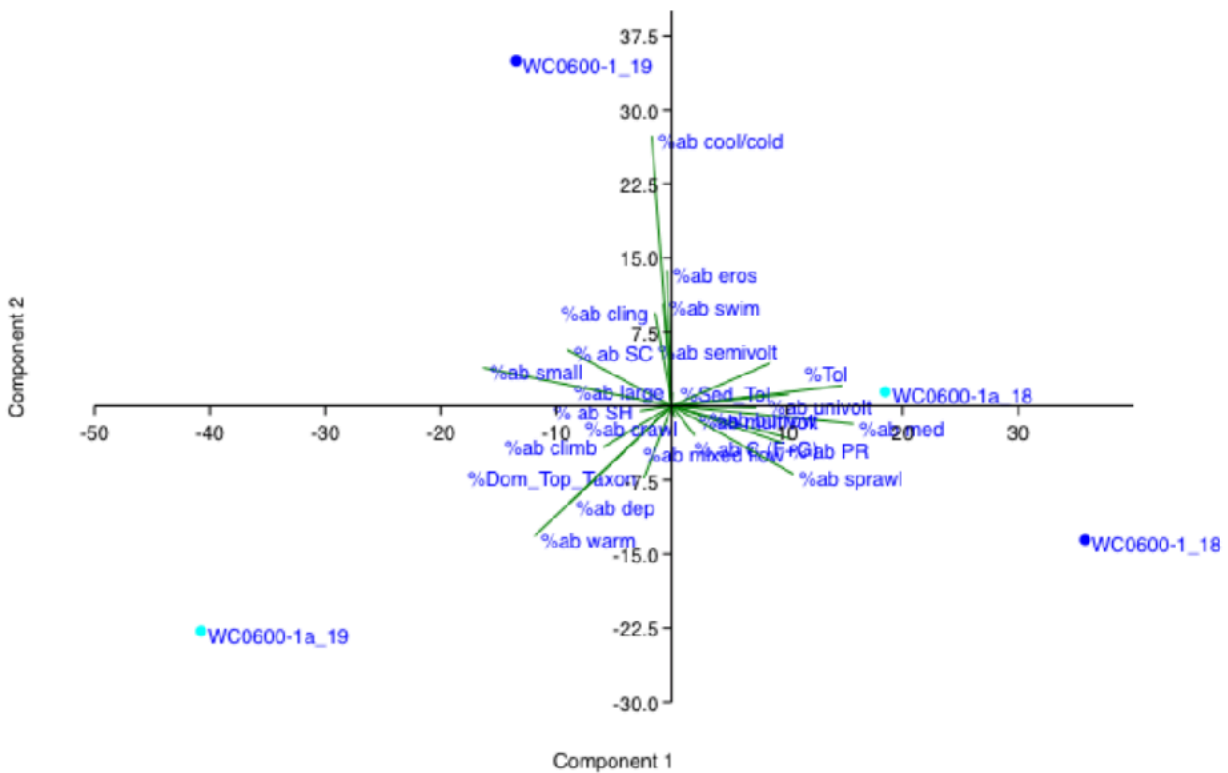
WC1025

Riffle-targeted (RT) samples were taken in the primary channel of Whychus Creek around RM 10.25 from 2011-2017. The site was not sampled in 2018, and a proportional multihabitat sample was taken in 2019. The community in 2019 was dominated by a tolerant and sediment-tolerant taxon (sludge worms), but at only 18% of total organismal abundance. This sample also had the highest relative abundances of tolerant and sediment-tolerant taxa in the 2019 sample set (40.7% and 23%, respectively) and of Tanypodinae (15.6% of total), a predaceous non-biting midge subfamily that is a DEQ high sediment indicator taxon. Sample richness was high (60 taxa), however, and at the upper end of this year's sample set (range = 36-67 total taxa). The majority of organisms were small-bodied, fast-developing (multivoltine and univoltine) collectors with mixed temperature and flow associations.

IBI and PREDATOR sores for RT samples changed little over time (Figure 17) and indicated moderate to slight disturbance (IBI) and fair to good (PREDATOR) biological condition. Because both models were developed using riffle-targeted sampling, they were not appropriate for the 2019 PM sample. The target subsampling number of 500 organisms was attained in every RT sample except in 2017 (Figure 18), when the entire sample had only 315 organisms. However, picking just 21% of the 2019 PM sample yielded 548 organisms.

Figure 17. PREDATOR O/E and ORDEQ IBI scores at WC1025 from 2011-2017. The site was not sampled in 2018, and these models are not applicable to the PM sample in 2019.
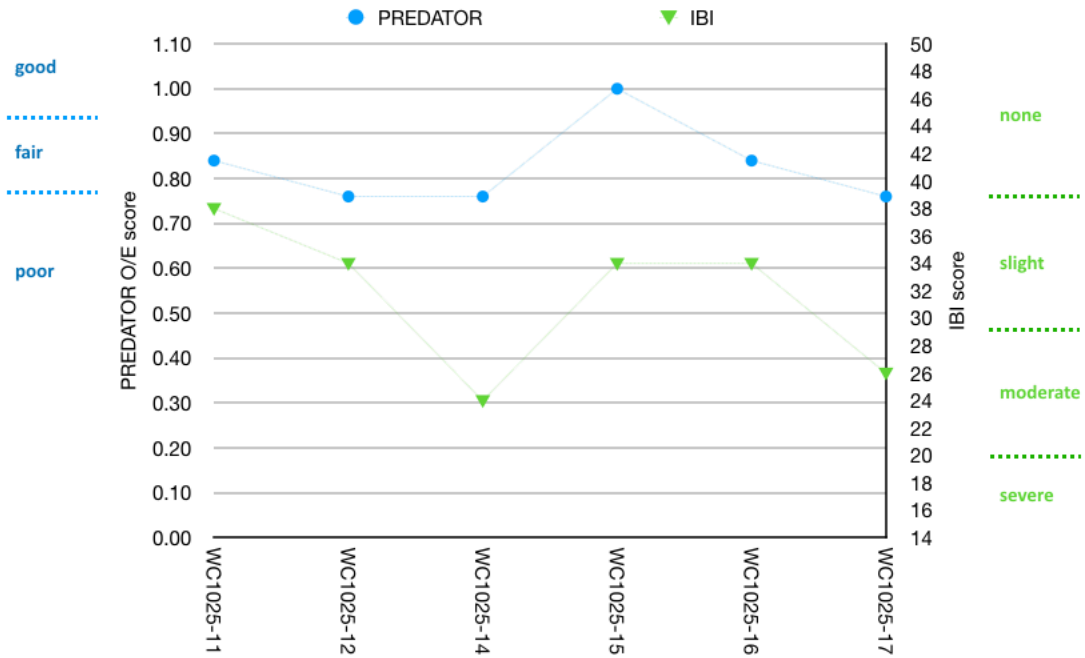
Figure 18. Proportion of sample needed for sub-sampling and resulting organismal abundance at WC1025 in all sampling years. RT samples were taken every sampling year except 2019, when a PM sample was taken.
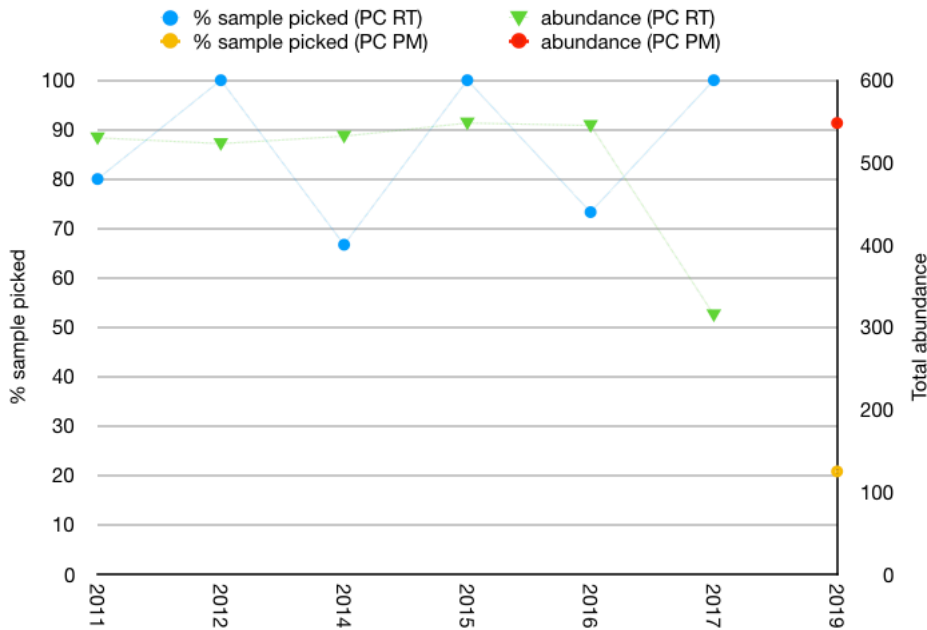
Sample richness and EPT diversity were fairly consistent from 2011-2017 (Figure 19), but both increased in 2019. Before 2019, samples contained 29-37 taxa, and were diverse enough to receive the highest scaled IBI score in only a single year. Richness was almost two-fold greater in 2019 (60 unique taxa), likely due in part to the fact that richness in PM samples has been significantly higher overall in years in which PM and RT samples are taken. Seven taxa in the 2019 sample had not been taken at this site in any prior sampling year, including a sensitive non-biting midge subfamily (Prodiamesinae), two mayflies (*Acentrella insignificans, Paraleptophlebia*), a broad-winged damselfly (Calopterygidae), a stonefly (*Sweltsa*), and two types of snail (*Ferrissia*, Planorbidae).

EPT diversity was higher in 2019 (18) than in any year except 2011, and this was the first year in which three EPT taxa were taken at this site: *Paraleptophlebia*, a prong-gilled mayfly in sediments and detritus in erosional parts of streams, and a DEQ high sediment indicator taxon; *Sweltsa*, a green stonefly found in a variety of flowing water habitats; and *Acentrella insignificans*, small minnow mayfly found in erosional habitat in rivers and streams. Overall average dissimilarity among the EPT community in all years was 47%; both taxa that contributed most to the differences decreased in abundance over time: the saddlecase-maker caddisfly *Brachycentrus*, typically found in larger cool streams on logs, branches, and vascular hydrophytes in erosional habitat; and *Baetis tricaudatus*, a small minnow mayfly found in swift streams that is a DEQ low sediment indicator taxon.

Figure 19. Sample richness and EPT diversity at WC1025 in all sampling years. RT samples were taken sampling year except 2019, when a PM sample was taken. For this metric in the ORDEQ IBI, >35 total taxa receives the highest scaled score.
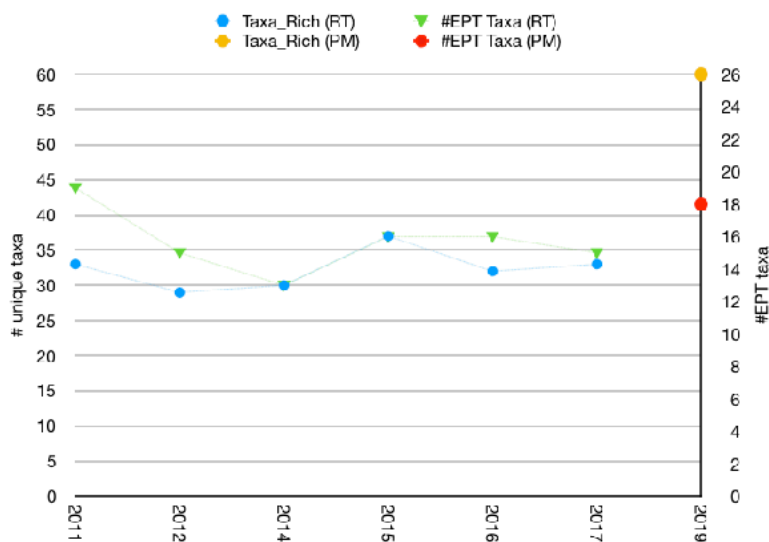

Sensitive and sediment-sensitive taxa have been scarce at this site (Figure 20), but the 2019 PM sample had more sensitive taxa (4) than any prior sampling year and the most sediment-sensitive taxa (2) since 2011. However, relative abundances of tolerant and sediment-tolerant taxa have also been increasing (Figure 21), and dominant taxa in the last two years are tolerant and sediment-tolerant burrowing worms (Oligochaeta and Naididae), although relative abundance of Naididae in 2019 was low enough to receive the highest scaled IBI score (Figure 22). Community

temperature optima fluctuated in a narrow range (Figure 23) and 2019 was the highest of any sampling year (18.0°F); that may be partly because PM samples include slower and warmer portions of the stream, but it is also the same as the 2019 temperature optima for the WC0600 samples. Furthermore, the number of DEQ cool indicator taxa has decreased while the number of warm indicator taxa is increasing overall (Figure 24). Community sediment optima also increased over time (Figure 23), and while the number of DEQ low sediment indicator taxa has been almost unchanged since 2011, the number of high sediment indicator taxa has increased substantially (Figure 25).

Figure 20. Numbers of sensitive and sediment-sensitive taxa at WC1025 in all sampling years. RT samples were taken sampling year except 2019, when a PM sample was taken. For this metric in the ORDEQ IBI, the highest scaled score correlates with >4 sensitive and >2 sediment-sensitive taxa.
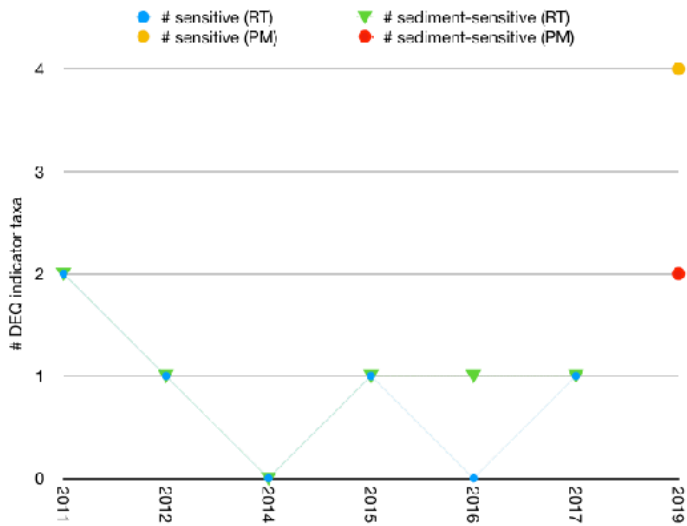
Figure 21. Relative abundance of tolerant and sediment-tolerant organisms at WC1025 in all sampling years. For this metric in the ORDEQ IBI, the highest scaled score correlates with <15% tolerant and <10% sediment-tolerant taxa.
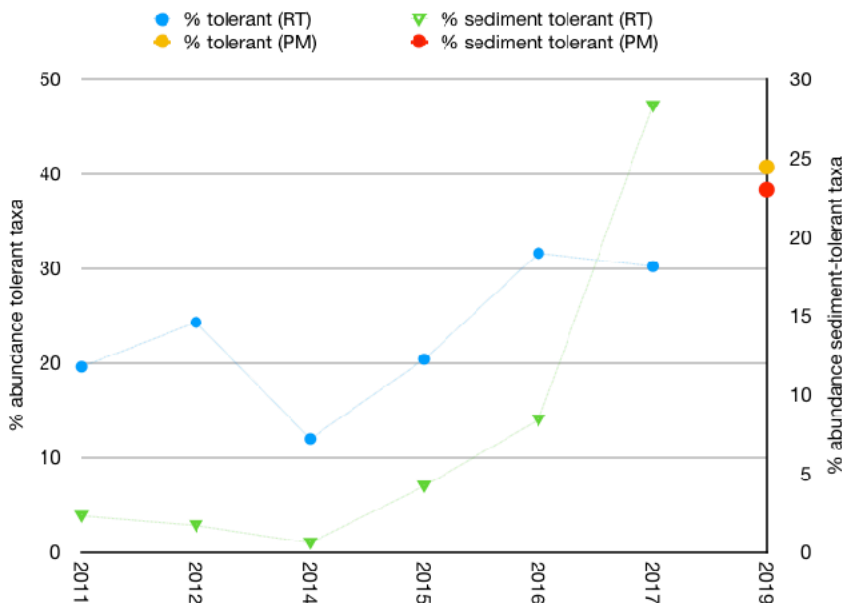
Figure 22. Relative abundance of the numerically dominant taxon at WC1025 in all sampling years. RT samples were taken sampling year except 2019, when a PM sample was taken. For this metric in the ORDEQ IBI, the highest scaled score correlates with <20% abundance of the top taxon.
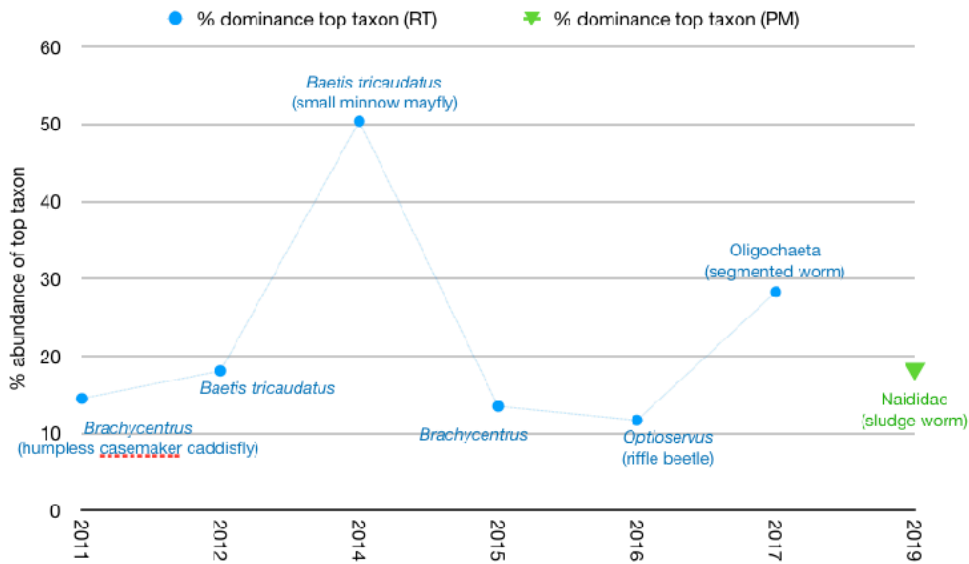
Figure 23. Temperature and fine sediment optima of the community at WC1025 in all sampling years. RT samples were taken sampling year except 2019, when a PM sample was taken.
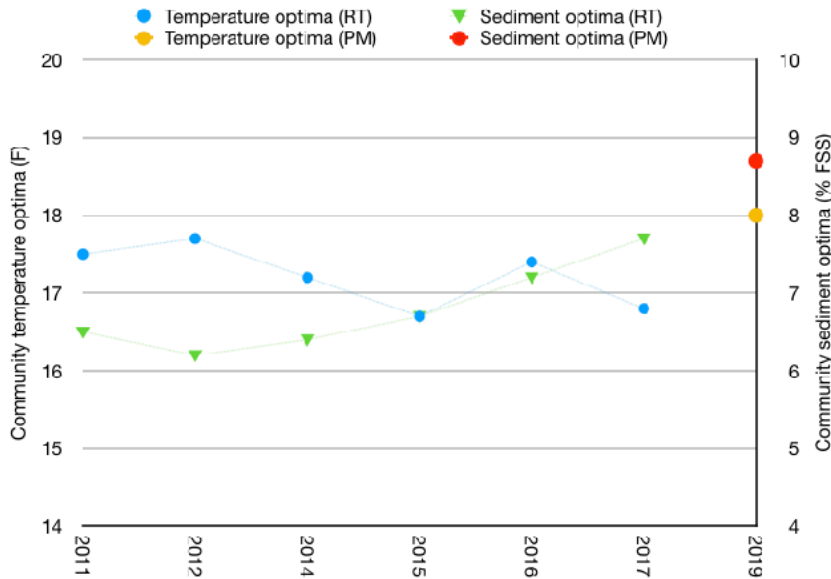
Figure 24. Number of ORDEQ cool and warm temperature indicator taxa at WC1025 in all sampling years. *RT samples were taken sampling year except 2019, when a PM sample was taken. Note that these taxa do not account for the temperature associations of all taxa in a sample.*
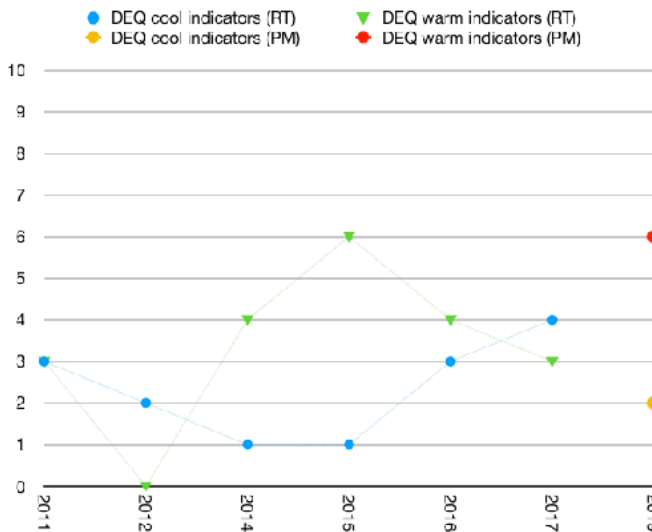
Figure 25. Number of ORDEQ low and high sediment indicator taxa at WC1025 in all sampling years. *RT samples were taken sampling year except 2019, when a PM sample was taken. Note that these taxa do not account for the sediment associations of all taxa in a sample.*
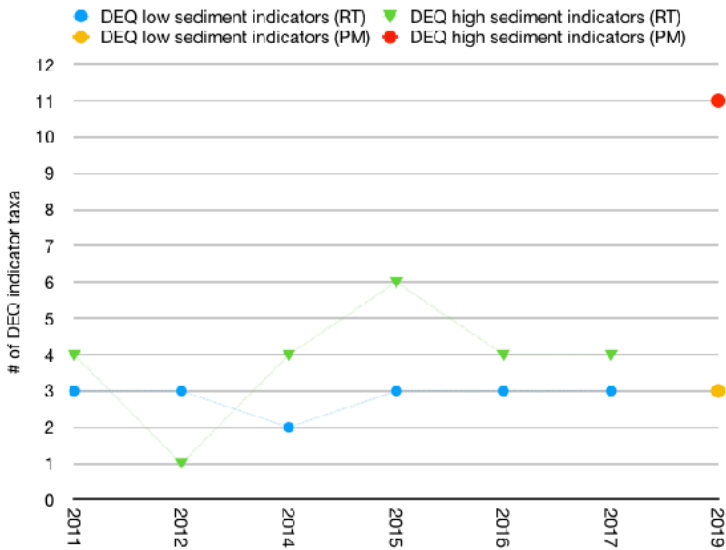
CLUSTER analysis separates early from later sampling years, with the 2017 and 2019 communities as outliers (Figure 26). Overall average dissimilarity among all years was 42%; taxa that contributed most were *Brachycentrus* and *Baetis tricaudatus*, which dominated the communities in 2011-2015 and then decreased in abundance. In a PCA ordination of taxa (Figure 27), axis 1 explained 38% of the variation, and taxa with the highest loading again reflected changes in the dominant taxon (segmented worms, *Baetis tricaudatus*). Axis 2 explained an additional 21% of the variation; taxa with the highest loading were *Brachycentrus,* which was abundant only in 2011, 2012, and 2015, and *Baetis*. PCA ordination of traits measured as relative abundances reflected the dominant taxa influences (Figure 28). Axis 1 explained 57% of the variation, and the traits with the highest loading were relative abundance of collectors and of the top taxon, both of which had the highest abundances in 2014 and 2017 at this site; axis 2 explained an additional 23% of the variation, with relative abundance of tolerant and sediment-tolerant taxa, both of which were greatest in the 2019 PM sample, having the highest loading.

Figure 26. CLUSTER dendrogram of the WC1025 macroinvertebrate community in all sampling years. Blue = RT, aqua = PM. The numeral in each label indicates the sampling year.
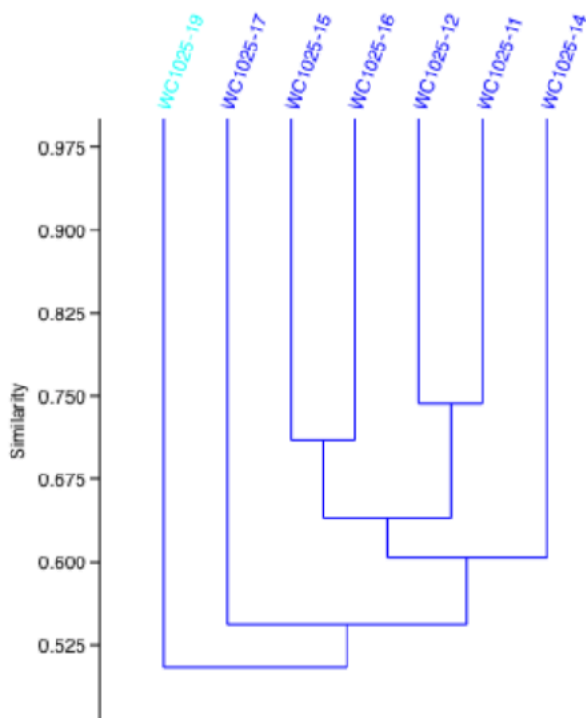
Figure 27. PCA ordination of the macroinvertebrate community at WC1025 in all sampling years. *Blue = RT, aqua = PM. The numeral in each label indicates the sampling year. Eigenvectors show dominant contributions, where vector length is related to the strength of its contribution.*
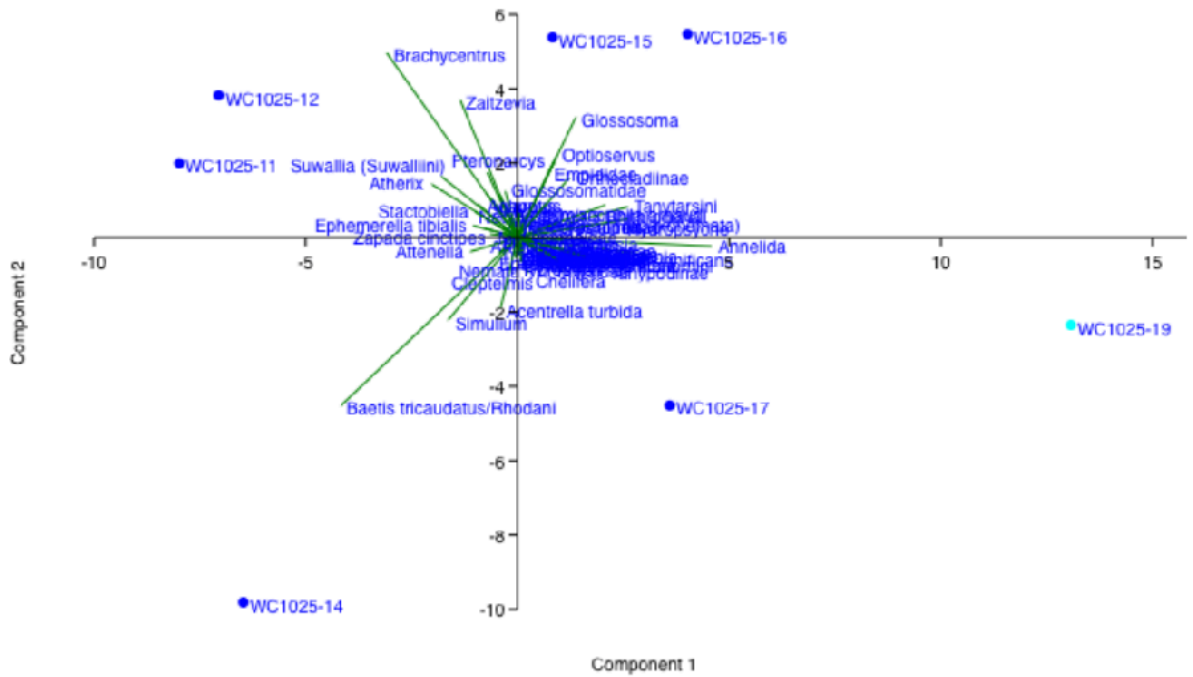
Figure 28. PCA ordination of WC1025 macroinvertebrate community traits measured as relative abundances. *Blue = RT, aqua = PM. The numeral in each label indicates the sampling year. Eigenvectors show dominant contributions, where vector length is related to the strength of its contribution.*
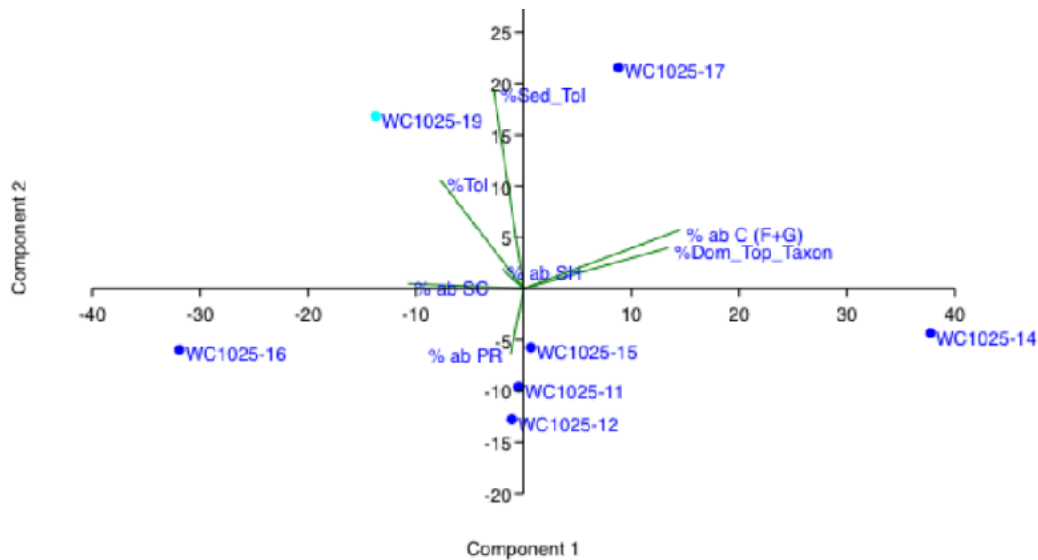
<u>WC1100</u>

The Whychus Canyon restoration project implemented in 2016 created new side channel habitat at WC1100. Pre-project data were collected in 2014-2015; no sampling was done in 2016, as work was just completed, and in 2017, the primary channel and new side channels were sampled. In 2019, a PM and RT sample were taken in the same reach of the primary channel (WC1100-2, WC1100-2a), and another PM sample was taken in a different primary channel reach (WC1100-1). Three additional PM samples included a side channel (WC1100-3) and reaches with both primary and side channels (WC1100-4, WC1100-5).

Overall average dissimilarity among all 2019 samples was only 35%, and taxa that contributed the most were the tolerant non-biting midge tribes Tanytarsini and Chironomini (more abundant in WC1100-3 and WC1100-4 samples). The RT and PM sample taken in the same primary channel reach were not the most similar (Bray-Curtis similarity index = 0.58); the community in the primary channel RT sample was most similar to WC1100-5 primary/side channel PM sample (Bray-Curtis index = 0.77), and the WC1100-1 primary channel PM sample also grouped with these samples (Figure 29). The WC1100-2 RT and WC1100-5 PM samples had similar numbers of EPT, sensitive taxa, sediment-sensitive taxa, DEQ indicator taxa for temperature and sediment conditions, as well as low relative abundances of sediment-tolerant organisms (<4%) and similar sediment and temperature optima. Most organisms were small-bodied collectors and clingers associated with erosional habitats. The WC1100-3 and WC1100-4 PM samples were closely similar (Bray-Curtis index = 0.76); these side channel communities were dominated by the tolerant non-biting midge *Tanytarsus* and had lower EPT richness and total richness, greater relative abundance of non-biting midges, higher temperature optima, more shredders and climbers, fewer organisms with cool/cold water or erosional habitat associations and more that prefer warmer waters and mixed flow conditions. The community in the WC1100-2a PM sample, taken in the same primary channel reach as the RT sample, was an outlier, (Bray-Curtis index = 0.55-0.58 with all other samples). The dominant taxon was the same as in the RT sample (*Baetis tricaudatus*) and there was a similarly high relative abundance of organisms with erosional flow preference, but this sample had the fewest organisms, lowest total and EPT diversity, and the lowest community temperature optima (17.1°F) of all the WC1100 samples (range = 17.1-17.5°F).

There was no significant difference between the pre- and post-project means for sediment or temperature optima or the number of any DEQ sediment or temperature indicator taxa. However, most metrics assessed in samples taken in the primary channel show an immediate strong negative impact from restoration activities followed by a rapid recovery. The only year in which the target number of subsampled organisms was not attained was 2017 (45 organisms total; Figure 30). Total diversity and EPT richness increased post-restoration in RT and PM primary channel samples, and the numbers of both in RT samples were significantly greater post-restoration (Figure 31). Similarly, IBI and PREDATOR scores, which plummeted in 2017, recovered post-restoration to indicate undisturbed (IBI) or good to near-fair (PREDATOR) conditions (Figure 32).

Figure 29. CLUSTER dendrogram of the WC1100 macroinvertebrate community in 2019 sample reaches. Blue = RT, aqua = PM. SC = side channel, PC = primary channel, PC/SC = sample reach included both channel types. WC1100-2 and WC1100-2a were taken in the same reach.
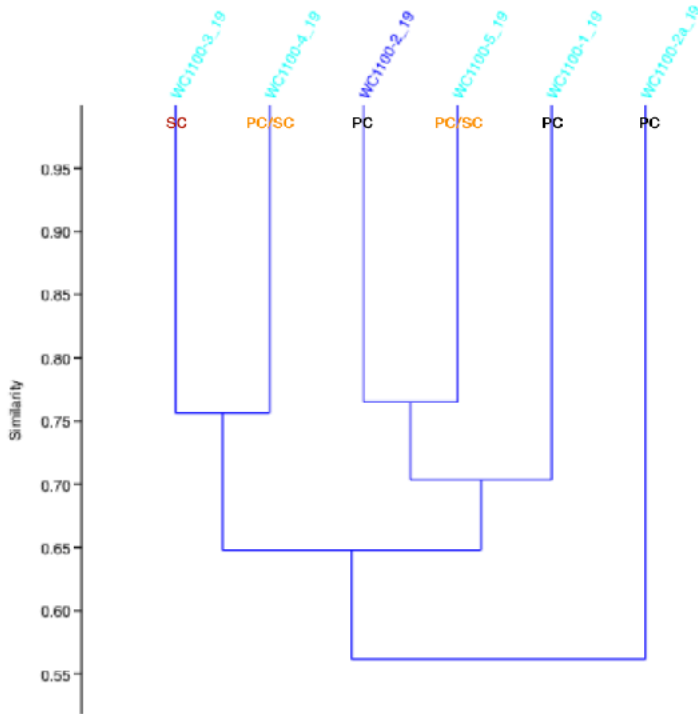

Figure 30. Proportion of sample needed for sub-sampling and resulting organismal abundance at WC1100 in all sampling years. Only samples taken in the primary channel are shown. The PM1 and RT samples were taken in the same reach at the same time in 2018-2019.
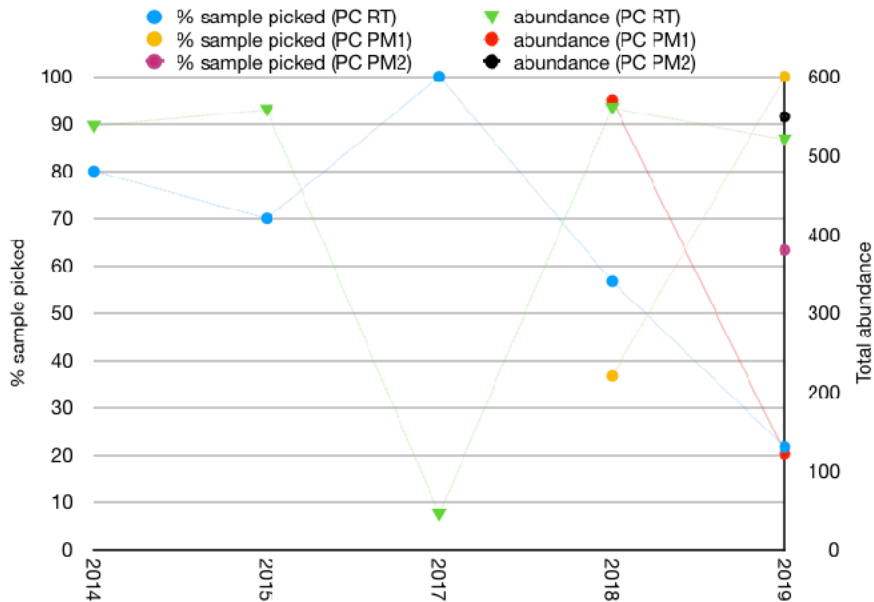
Figure 31. Sample richness and EPT diversity at WC1100 in all sampling years. *Only samples taken in the primary channel are shown. The PM1 and RT samples were taken in the same reach at the same time in 2018-2019. For this metric in the ORDEQ IBI, >35 total taxa receives the highest scaled score.*
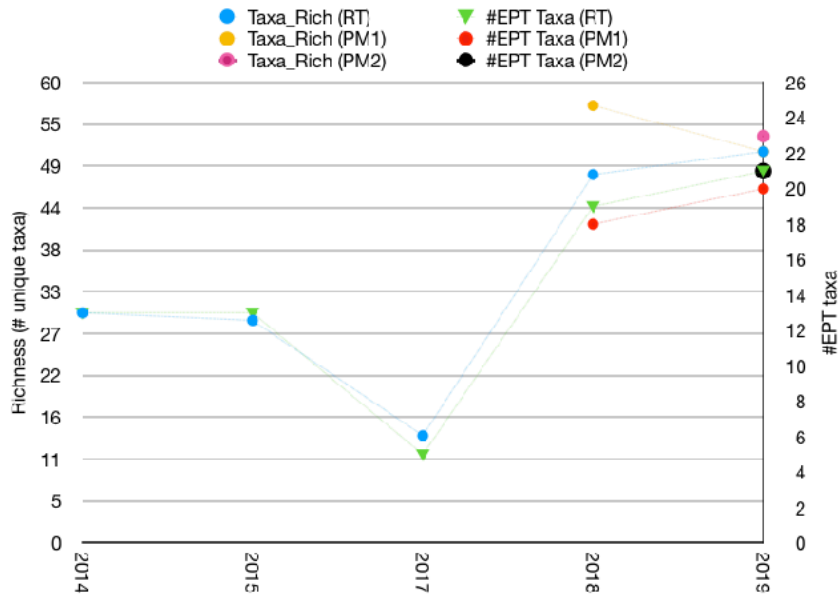
Figure 32. PREDATOR O/E and ORDEQ IBI scores at WC1100 from 2011-2017. *Only RT samples taken in the primary channel are shown.*
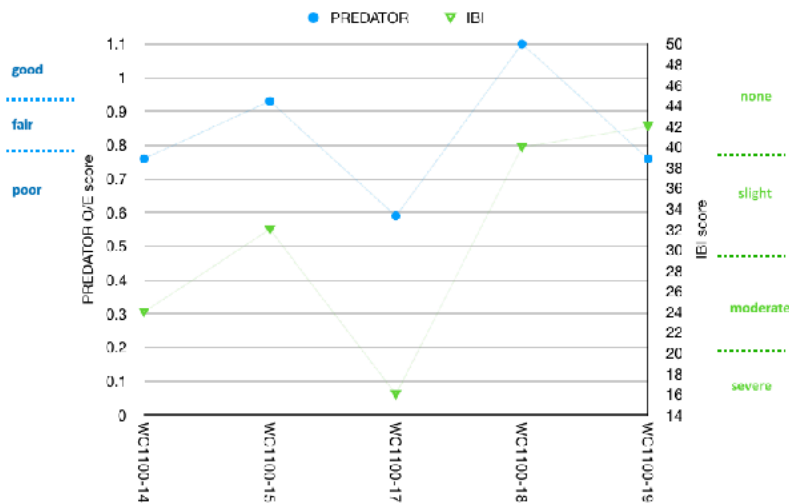
Sensitive taxa were not seen in any samples prior to 2018 but were found in numbers ranging from 3-5 in recent RT and PM samples (Figure 33), and the number of sediment-sensitive taxa, while low, also increased after 2017. The relative abundances of tolerant and sediment-tolerant taxa decreased after peaking in 2017 (Figure 34). In 2019, the relative abundance of tolerant organisms was at or above the cutoff to receive the highest scaled IBI score (<15%) in RT and PM samples, but the proportion of sediment-tolerant taxa was very low (<1%) in the RT and PM sample from the same reach.

Figure 33. Numbers of sensitive and sediment-sensitive taxa at WC1100 in all sampling years. *Only samples taken in the primary channel are shown. The PM1 and RT samples were taken in the same reach at the same time in 2018-2019. In the ORDEQ IBI, the highest scaled score correlates with >4 sensitive and >2 sediment-sensitive taxa.*
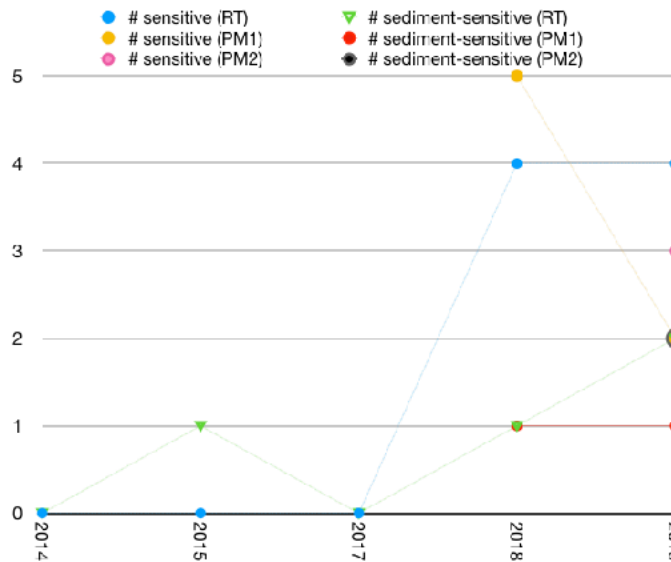
Figure 34. Numbers of tolerant and sediment-tolerant taxa at WC1100 in all sampling years. *Only samples taken in the primary channel are shown. The PM1 and RT samples were taken in the same reach at the same time in 2018-2019. In the ORDEQ IBI, the highest scaled score correlates with <15% tolerant and <10% sediment-tolerant taxa.*
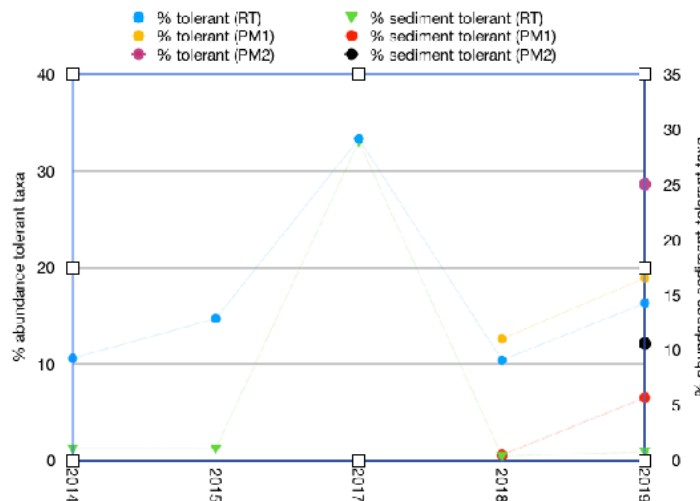
Since restoration, the community in RT samples is also more balanced, with dominant taxa that prefer faster flows and are present at lower overall abundances (Figure 35). Prior to 2018, top taxon abundance was always too great to receive the highest scaled score in the IBI for this metric and in 2017, almost a third of the RT sample consisted of tolerant and sediment-tolerant burrowing worms (Oligochaeta). Recently, the dominant taxon in RT samples is the small minnow mayfly *Baetis tricaudatus*, which prefers clear flowing waters and is a DEQ low sediment indicator taxon, though PM samples have been dominated by a ubiquitous non-biting midge adapted to a wide range of habitats and ecological conditions (*Tanytarsus*).

Figure 35. Relative abundance of the numerically dominant taxon at WC1100 in all sampling years. Only samples taken in the primary channel are shown. The PM1 and RT samples were taken in th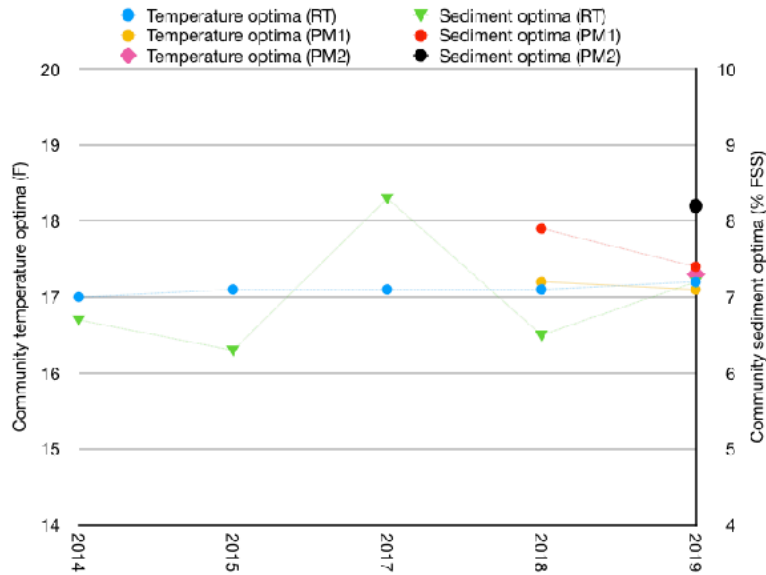e same reach at the same time in 2018-2019. In the ORDEQ IBI, the highest scaled score correlates with <20% abundance of the top taxon.
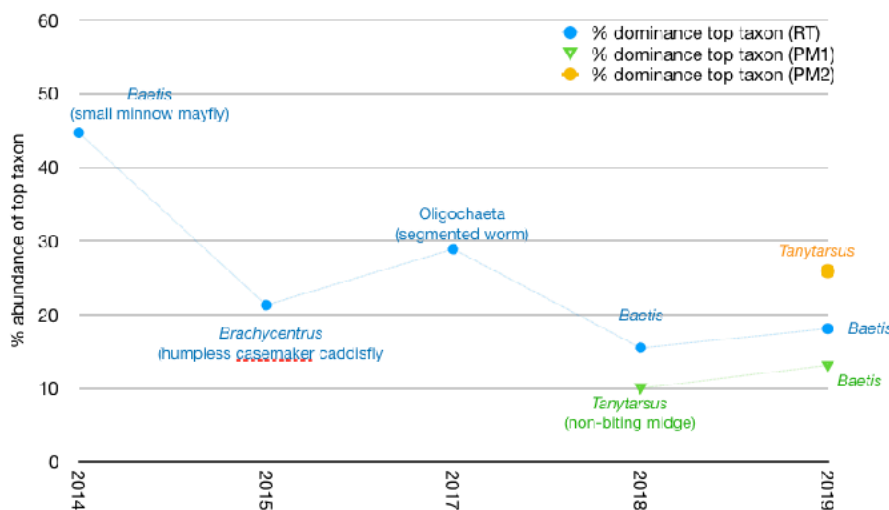
Community temperature optima were almost identical in every sampling year (17.0-17.1oF) and are similar though slightly higher in PM samples, but community sediment optima reflect the pattern described above for sediment-tolerant organisms (Figure 36). The number of DEQ warm temperature indicators has always exceeded cool indicators at this site (Figure 37), but cool indicator taxa recovered after restoration and there were more in the 2019 RT sample than in any other year. Sediment indicator taxa show a similar pattern, with high sediment indicators outnumbering low in every sampling year, but the number of low sediment indicators in RT samples increased after 2017 (Figure 38). There was no significant difference between the pre- and post-project means of any of these traits.

CLUSTER analysis separates early from recent sampling years, with the highly disrupted post-restoration community in 2017 as an outlier (Figure 39), and shows greater similarity among side channel vs. primary channel samples in recent years. The overall average dissimilarity between pre-project (primary channel) and post-project (2018-2019, primary and primary/side channel only) samples was 47.5%; taxa that contributed the most were Chironominae, a tolerant tribe of non-biting midge (greater abundance pre-project); *Baetis tricaudatus* (lower abundance post-project, but the dominant taxon in RT samples in 2018-2019); and Tanytarsini (greater abundance post-project).

Figure 36. Temperature and fine sediment optima of the community at WC1100 in all sampling years. *Only samples taken in the primary channel are shown. The PM1 and RT samples were taken in the same reach at the same time in 2018-2019.*
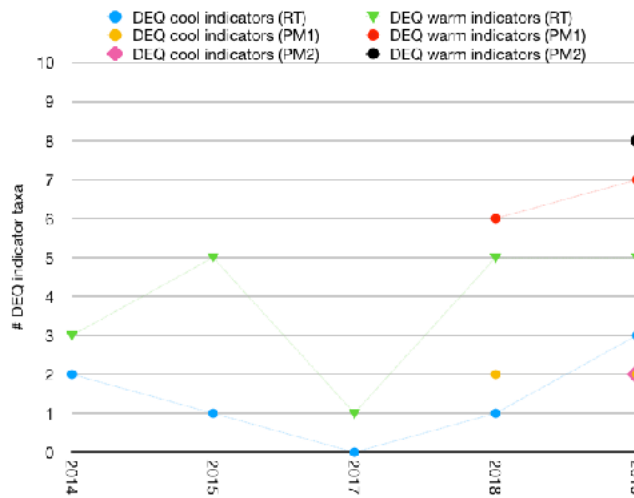

Figure 37. Number of ORDEQ cool and warm temperature indicator taxa at WC1100 in all sampling years. *Only samples taken in the primary channel are shown. The PM1 and RT samples were taken in the same reach at the same time in 2018-2019. Note that these taxa do not account for the temperature associations of all taxa in a sample.*

Figure 38. Number of ORDEQ low and high sediment indicator taxa at WC11100 in all sampling years. Only samples taken in the primary channel are shown. The PM1 and RT samples were taken in the same reach at the same time in 2018-2019. Note that these taxa do not account for the sediment associations of all taxa in a sample.
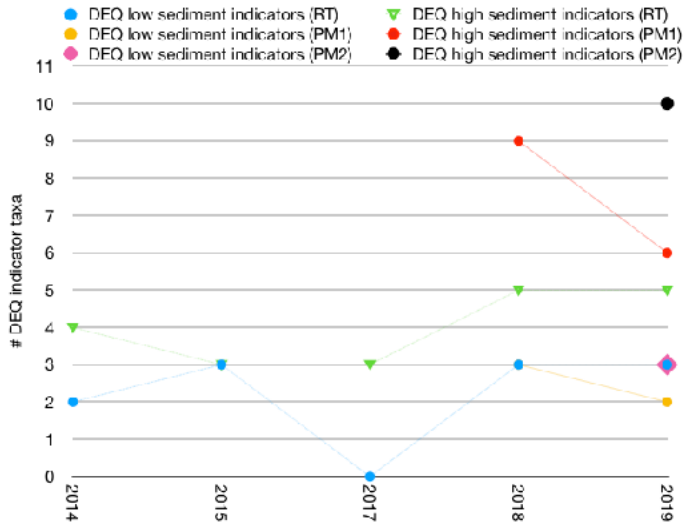
Figure 39. CLUSTER dendrogram of the WC1100 macroinvertebrate community in all sampling years. Blue = RT, aqua = PM. The numeral in each label indicates the sampling year.
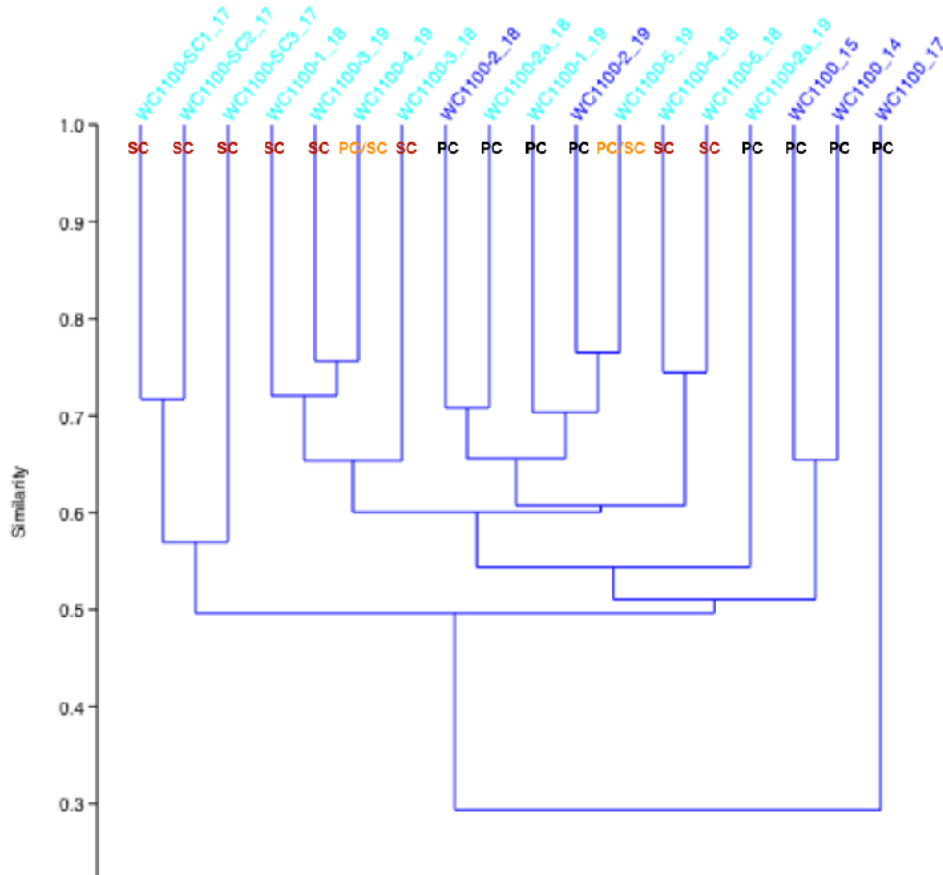
Similarly, in a PCA ordination of taxa from all years and channel types (Figure 40), taxa with the highest loading on axis 1, which explained 26% of the total variation, were Chironomini and Tanytarsini; taxa with the highest loading on axis 2, which explained an additional 17% of variation, were *Simulium* black flies, collector-filterers in fast waters and often a post-restoration pioneer species; and *Zapada cinctipes*, a spring stonefly that feeds by shredding and is associated with cold waters in a variety of flows (abundant in 2017 side channel samples).

In a PCA ordination of traits measured as relative abundances for all years and channel types (Figure 41), axis 1 explained 57% of the variation; factors with the highest loading were relative abundances of collectors (overall more abundant in RT samples prior to 2018) and of predators (more abundant in 2017 side channels). Axis 2 explained an additional 17% of variation, with relative abundance of the dominant taxon (lower after 2017) and of scrapers (overall more abundant in 2019) having the highest loading. In traits from just the 2018-2019 communities (Figure 42), axis 1 of the PCA explained 50% of the variation, with relative abundance of erosional- and mixed flow-associated taxa, which tend to distinguish RT from PM samples, having the highest loading; and on axis 2, which explained an additional 27% of the variation, relative abundance of multivoltine (higher in 2018 samples) and cool/cold-associated individuals (higher in 2019 samples) had the highest loading.

Figure 40. PCA ordination of the WC1100 macroinvertebrate community in all years. *Blue = RT, aqua = PM. The numeral in each label indicates the sampling year. Eigenvectors show dominant contributions, where vector length is related to the strength of its contribution.*
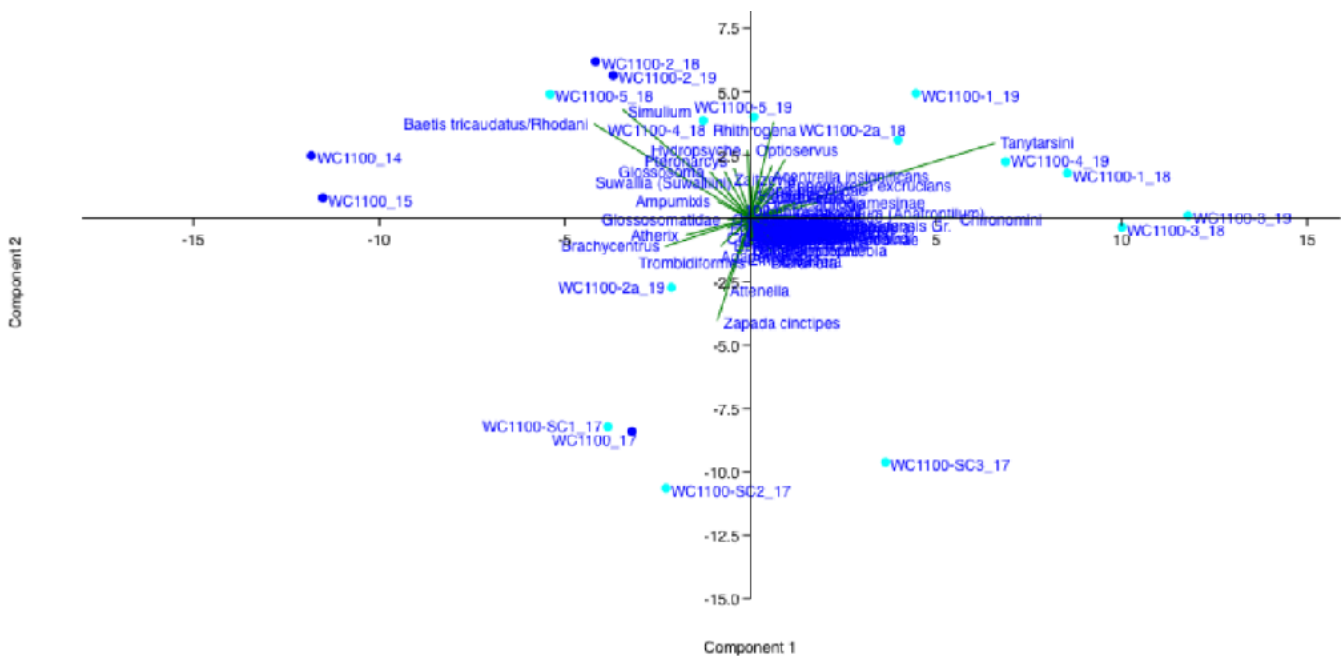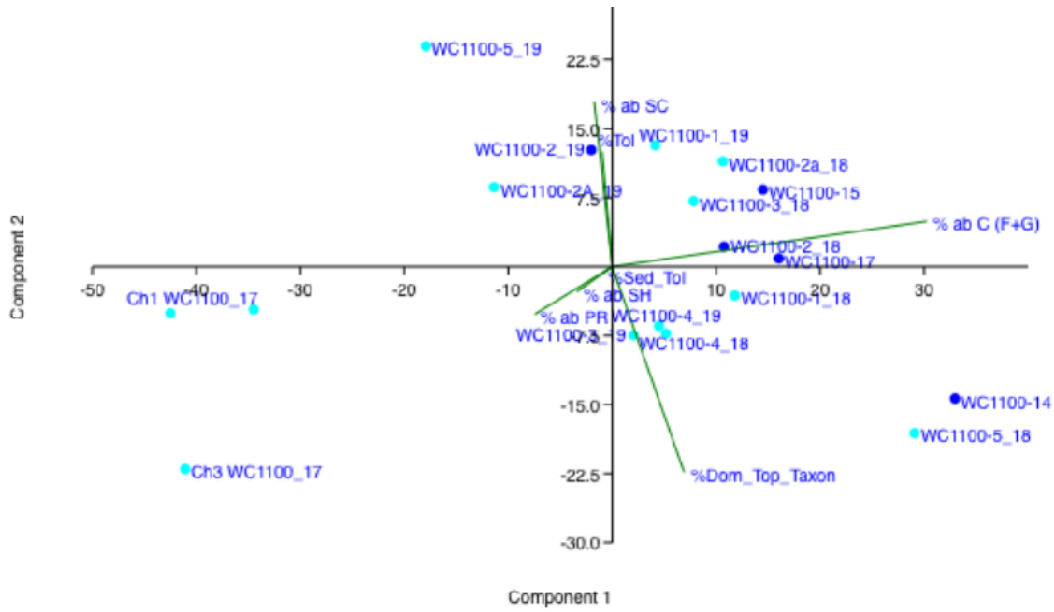
Figure 41. PCA ordination of WC1100 macroinvertebrate community traits measured as relative abundances in all sampling years. *Blue = RT, aqua = PM. The numeral in each label indicates the sampling year. Eigenvectors show dominant contributions, where vector length is related to the strength of its contribution.*

Figure 42. PCA ordination of WC1100 macroinvertebrate community traits measured as relative abundances in 2018-2019. *Blue = RT, aqua = PM. The numeral in each label indicates the sampling year. Eigenvectors show dominant contributions, where vector length is related to the strength of its contribution.*
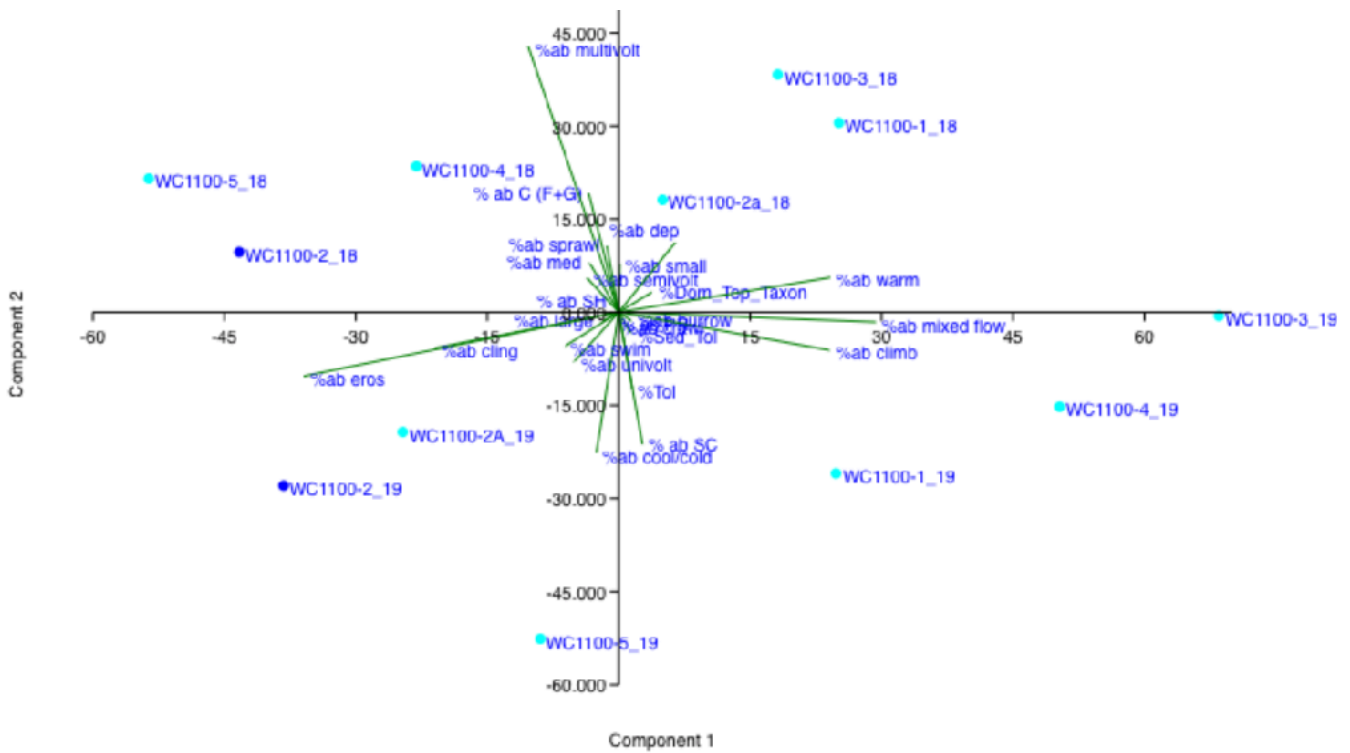
Sampling began at WC1150 in 2014 to provide an upstream reference for the WC1100 project site. An RT sample was taken in the primary channel in each year from 2014-2018; in 2018, a PM sample was taken in the same reach as the RT sample, and in 2019 only a PM sample was taken. The community in 2019 was most similar to that in the WC0600 RT sample (Figure 1) and was dominated by *Cricotopus* (*Nostococladius)* (19.8% of total abundance), a sensitive and sediment-intolerant non-biting midge found in cold, clear, flowing waters. *Nostococladius* has a specialized life history; larvae burrow into *Nostoc*, a blue-green colonial algae found in many types of fresh water that is abundant on cobbles in many parts of Whychus Creek. Sample richness (47 taxa) was intermediate for the 2019 sample set (range = 37-67), and all taxa in the 2019 samples had been taken at this site in at least one other sampling year. Most organisms were small-bodied scrapers and clingers with a preference for cool/cold and fast-flowing water. Compared to all other 2019 samples, this site had the lowest relative abundance of sediment-tolerant organisms (0.2%; 2019 sample range = 0.2-23%), one of the lowest community sediment optima (7.0% FSS; 2019 sample range = 6.9-10.3 % FSS), and few DEQ high sediment indicator taxa (2; range in 2019 samples = 1-13). This site also had the most scrapers (50.8% of total; 2019 range = 4.3-50.8%) and fewest collectors (33% of total; range = 33-77.2), the greatest relative abundances of semivoltine (14.7%; 2019 sample range = 1.0-14.7% of total) and of cold water-associated organisms (72.9%; 2019 sample range = 14.0-72.9%), and one of the lowest relative abundances of warm water-associated organisms (2.3% of total; 2019 sample range = 2.2-49.8% of total).

PREDATOR scores increased overall since sampling began (Figure 43), rising from poor biological condition in 2014 to fair or good. IBI scores indicated slight disturbance in early sampling years, and after a dramatic drop in 2017 the site scored as undisturbed for the first time in 2018. The target subsampling number of 500 organisms was attained for almost all samples (Figure 44), with the PM samples requiring much less of the total sample to be picked.

Figure 43. PREDATOR O/E and ORDEQ IBI scores at WC1150 from 2011-2018. *Only RT samples taken in the primary channel are shown.*
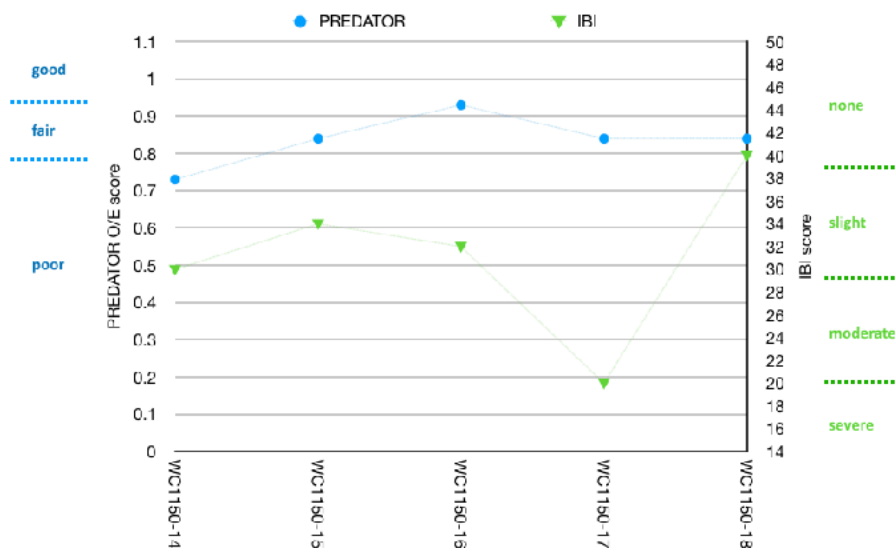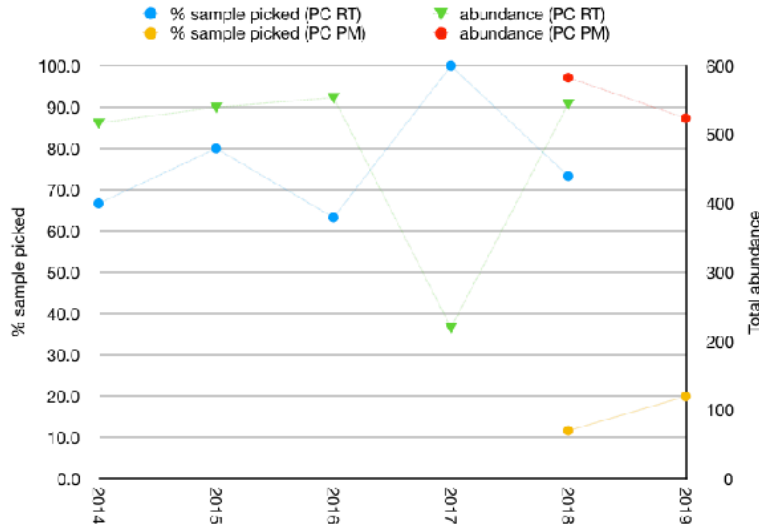
Figure 44. Proportion of sample needed for sub-sampling and resulting organismal abundance at WC1150 in all sampling years. Only samples taken in the primary channel are shown. The PM1 and RT samples were taken in the same reach at the same time in 2018-2019.

Total taxa and EPT richness increased after 2017 (Figure 45). Taxa richness was in the range for the highest scaled IBI score in two RT samples during 2014-2018 and in all PM samples; this is likely due in part to the greater richness in PM vs. RT samples in general. The number of EPT is also much higher in recent PM samples, even though they include fewer riffles, and 2019 was the first time a sample included *Micrasema*, a humpless casemaker caddisfly that inhabits wood, vascular plants, and moss clumps in cool/cold fast-flowing waters, and is a DEQ cool temperature indicator taxon. Overall average dissimilarity among the EPT community in all years was 47%; taxa that accounted most for the differences were *Baetis tricaudatus*, a small minnow mayfly with mixed flow and temperature preferences that is a DEQ low sediment indicator taxon (more abundant in 2014 and 2015); and *Glossosoma*, a sediment-

Figure 45. Sample richness and EPT diversity at WC1150 in all sampling years. In the ORDEQ IBI, >35 total taxa receives the highest scaled score.
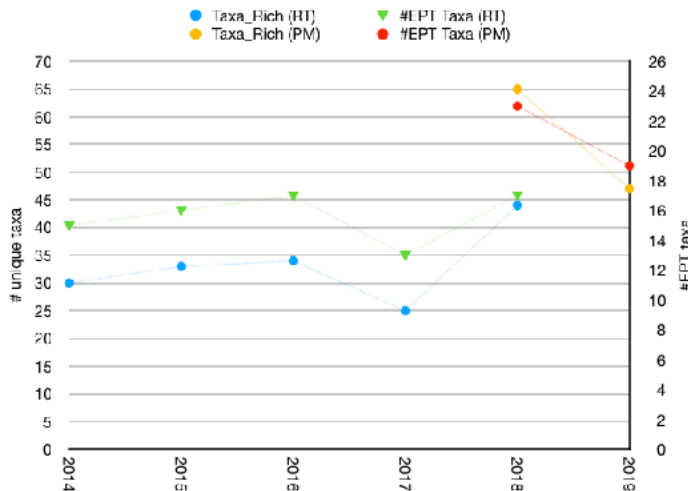
intolerant saddlecase-maker caddisfly that prefers clear, cool, flowing waters and is a DEQ low sediment indicator taxon (much lower abundance [2-3 individuals] in 2014 and 2017).

The number of sensitive taxa increased 4-5 fold since 2017 in both PM and RT samples, and in 2018 corresponded to the highest scaled score in the IBI (>4); sediment-sensitive taxa numbers increased to a lesser extent (Figure 46), while relative abundances of tolerant and sediment-tolerant organisms increased through 2017 but have since dropped, and are <1% in recent PM samples (Figure 47). The community has been generally dominated by taxa associated with colder, fast-flowing waters (Figure 48), and in most years at abundances low enough to score in the top range of the IBI. A notable exception is the 2017 sample community, which was dominated by a high proportion of tolerant segmented worms (42.7%). The PM samples taken in recent years, despite including non-riffle habitats, are well-balanced and dominated by taxa associated with cold water and erosional habitat.

Figure 46. Numbers of sensitive and sediment-sensitive taxa at WC1150 in all sampling years. *For this metric in the ORDEQ IBI, the highest scaled score correlates with >4 sensitive and >2 sediment-sensitive taxa.*
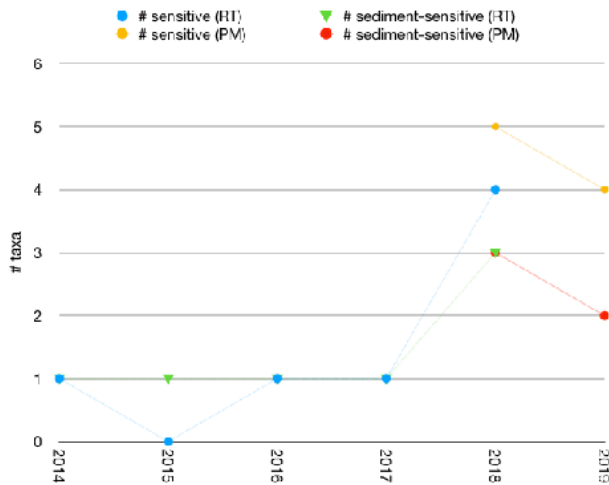

Figure 47. Numbers of tolerant and sediment-tolerant taxa at WC1150 in all sampling years. *For this metric in the ORDEQ IBI, the highest scaled score correlates with <15% tolerant and <10% sediment-tolerant taxa.*
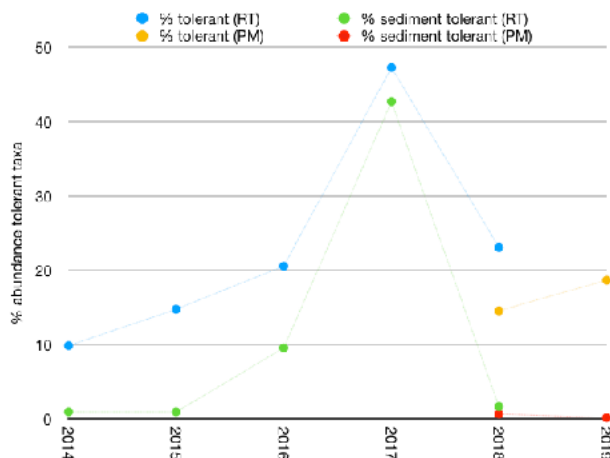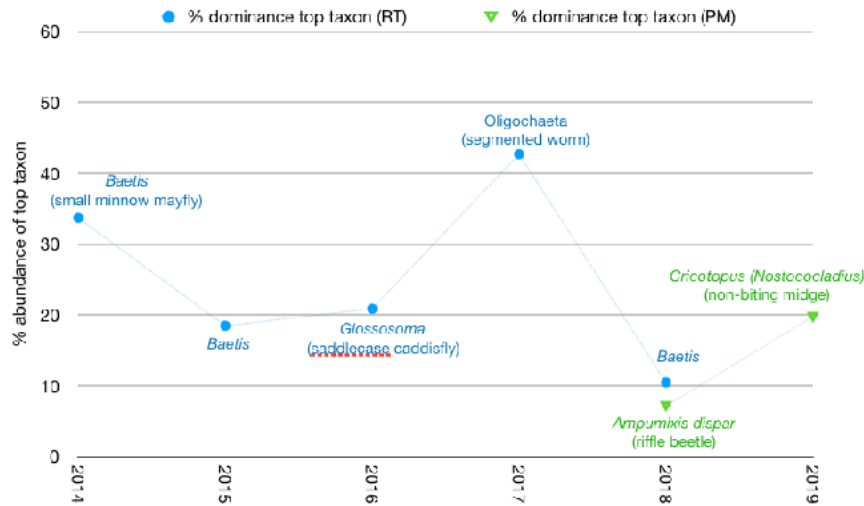
Figure 48. Relative abundance of the numerically dominant taxon at WC1150 in all sampling years. For this metric in the ORDEQ IBI, the highest scaled score correlates with <20% abundance of the top taxon.

Community temperature optima fluctuated over time and have increased overall (Figure 49); however, the number of DEQ cool temperature indicator taxa has increased over time while the number of warm indicators has dropped (Figure 50). Community sediment optima fluctuated annually without an overall trend, and the number of DEQ low and high sediment indicator taxa has also been consistent (Figure 51), except for a spike in the number of high sediment indicators in the 2018 PM sample; however, the 2019 PM sample contained the fewest high sediment indicator taxa of any sampling year.

Figure 49. Temperature and fine sediment optima of the community at WC1150 in all sampling years. RT = riffle-targeted, PM = proportional multihabitat.
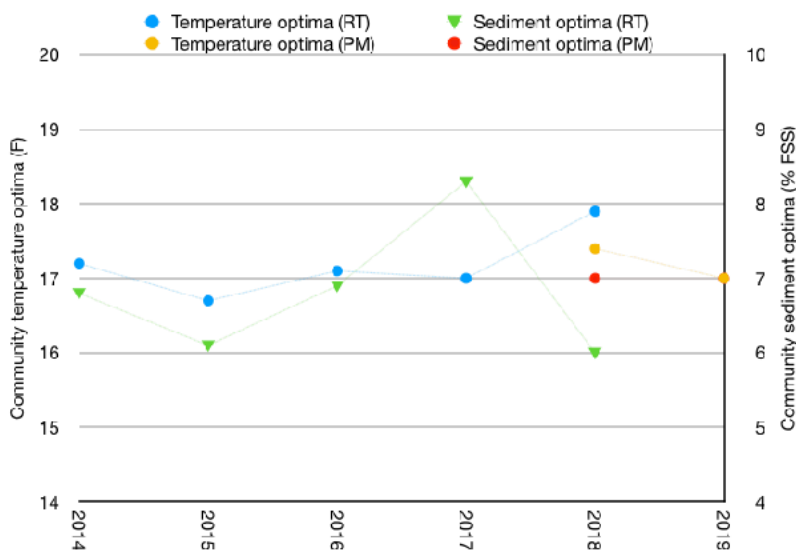
Figure 50. Number of ORDEQ cool and warm temperature indicator taxa at WC1150 in all sampling years. Note that these taxa do not account for the temperature associations of all taxa in a sample.
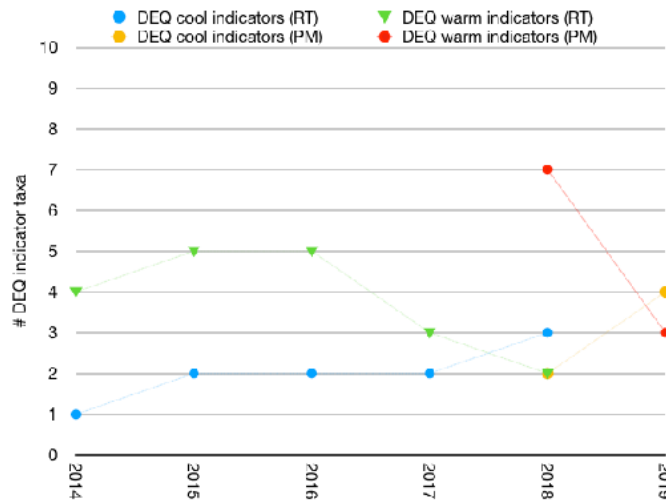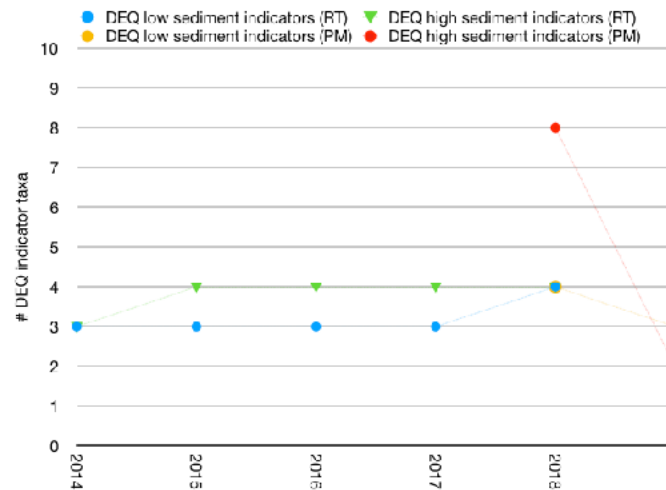

Figure 51. Number of ORDEQ low and high sediment indicator taxa at WC1150 in all sampling years. Note that these taxa do not account for the sediment associations of all taxa in a sample.

Communities in the 2018 PM and RT samples were most similar, but the 2019 PM sample community was more similar to earlier years (Figure 52). Overall average dissimilarity among all years was 42%; taxa that contributed the most were Annelida (tolerant segmented worms; dominant in 2017); and *Glossosoma* (high abundance in 2016). In a PCA ordination of taxa (Figure 53), axis 1 explained only 25% of variation; taxa with the highest loading were *Ampumixis* (riffle beetle associated with fast cold flows; higher abundances in 2018-2019) and *Rhithrogena* (flatheaded mayfly associated with cold fast flows and a DEQ low sediment indicator; increasing abundance over time). Axis 2 explained an additional 23% of the variation, with the mayfly *Baetis* (mixed temperature preferences in flowing waters and a DEQ low sediment indicator; greater abundances in 2014-2015) and Annelida having the

highest loading values. In a PCA ordination of traits measured as relative abundances (Figure 54), axis 1 explained 60% of the variation, with relative abundances of scrapers (particularly abundant in 2016 and 2019 and the feeding guild of the dominant taxa in those years [*Glossosoma* and *Nostococladius*]) and collectors (lower relative abundances in 2016 and 2019) having the highest loading values; on axis 2, which explained an additional 31% of

Figure 52. CLUSTER dendrogram of the WC1150 macroinvertebrate community in all sampling years. Blue = RT, aqua = PM. The numeral in each label indicates the sampling year.
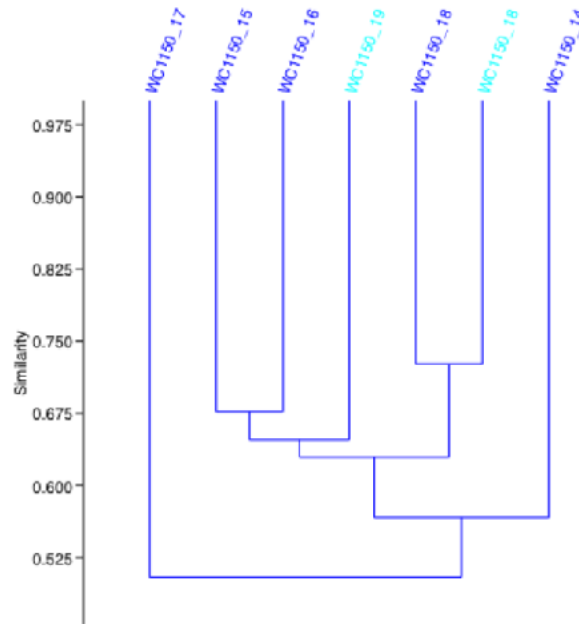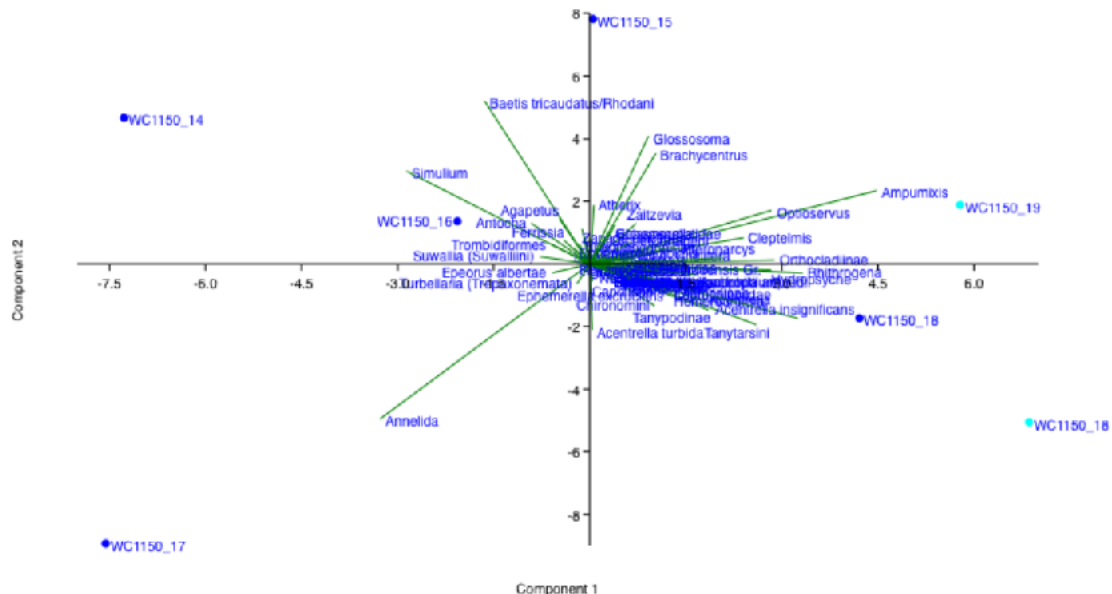

Figure 53. PCA ordination of the WC1100 macroinvertebrate community in all years. Blue = RT, aqua = PM. The numeral in each label indicates the sampling year. Eigenvectors show dominant contributions, where vector length is related to the strength of its contribution.

variation, relative abundances of sediment-tolerant (high abundance in 2017, including the numerically dominant Annelida) and scraper organisms had the highest loadings.

Figure 54. PCA ordination of the WC1150 macroinvertebrate community traits measured as relative abundances in all years. *Blue = RT, aqua = PM. The numeral in each label indicates the sampling year. Eigenvectors show dominant contributions, where vector length is related to the strength of its contribution.*
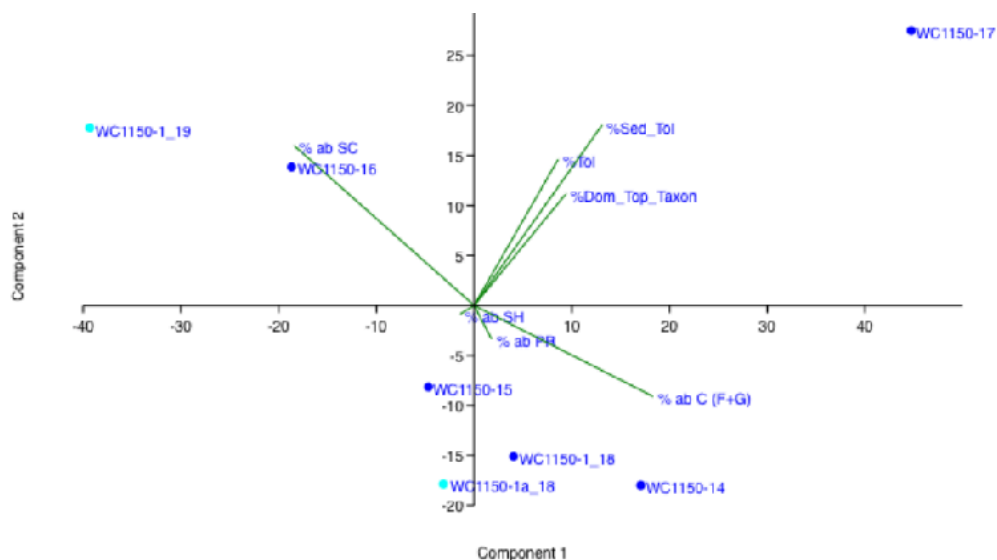
WC1925

WC1925 was sampled for the first time in 2019, with a single PM sample taken in a reach of the primary channel (WC1925-3) and three PM samples taken in reaches of connected braided side channels. Three of the four WC1925 samples were most similar to the RT and PM samples from WC1950 (Figure 1). The WC1925-2 (side channel) community had the lowest similarity to any other sample in 2019, which likely reflects greater habitat differences, as this was the only PM sample in 2019 that did not include any net sets in riffle habitat (nine glide and one pool net set). The subsampling target of 500 organisms was attained for all four samples, and all were dominated at fairly low relative abundances (range = 10-30.8%) by *Tanytarsus*, a non-biting midge associated with warmer temperatures in all types of fresh water. Taxa richness was high in all samples and at the upper end of the range for the 2019 dataset (WC1925 samples = 56-67 unique taxa; remaining 2019 samples = 36-60 unique taxa), although the outlier WC1925-2 had fewer taxa (56) than other WC1925 samples. Community temperature optima were similar among all WC1925 samples and lowest in the sample from the primary channel (range = 17.1-17.6°F). The number of warm temperature and high sediment indicator taxa outnumbered that of cool and low sediment indicators respectively in all samples except WC1925-2, which had no cool temperature or low sediment indicator taxa (Figure 55).

The WC1925-3 primary channel sample had more EPT taxa than any other sample in 2019 (23) and the greatest caddisfly diversity (11 taxa; 2019 samples range = 4-11), while WC1925-2 had the fewest EPT taxa (9) in the 2019

sample set. With the exception of WC1925-3, the numbers of sensitive (4 taxa) and sediment-sensitive (1-3 taxa) were comparable to those seen in other site samples, and the relative abundance of sediment-tolerant organisms in all WC1925 samples (3.0-8.7% of total) was at the lower end of the range for the 2019 sample set (0.2-23% of total in remaining 2019 samples).

The following trait means differed significantly between the WC1925 samples and all other 2019 site samples:

- taxa richness: WC1925 samples = 63 ± 4.8 taxa; remaining 2019 samples = 49 ± 7.6 taxa
- community sediment optima: WC1925 samples = 9.2% FSS ± 1.2; remaining 2019 samples = 7.8% FSS ± 1.8
- relative abundance of predators: WC1925 samples = 12.3% ± 3.4; remaining 2019 samples = 7.4 ± 2.2
- relative abundance of organisms with erosional habitat preferences: WC1925 samples = 30.4% ± 13.0; remaining 2019 samples = 56.1% ± 22.9
- relative abundance of organisms with mixed flow associations: WC1925 samples = 54.6% + 5.7; remaining 2019 samples = 32.5% + 17.3
- relative abundances of crawlers: WC1925 samples = 3.7% ± 1.9; remaining 2019 samples = 1.1% ± 1.1
- relative abundance of sprawlers: WC1925 samples = 16.7% + 3.6; remaining 2019 samples = 10.3% + 4.8

Figure 55. DEQ indicator taxa for temperature and sediment conditions in WC1925 samples taken in 2019. SC = side channel, PC = primary channel.
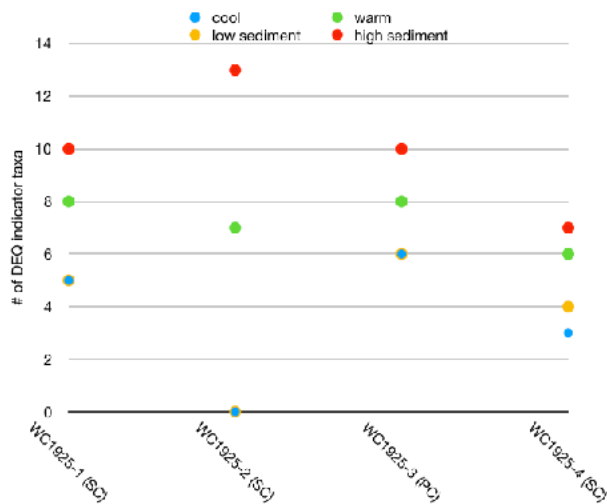

WC1950

An RT sample was taken in a primary channel reach at WC1950 in each sampling year from 2009-2019 except in 2018, when restoration was ongoing. A PM sample was taken in the same reach as the RT sample at this site for the first time in 2019, and a duplicate RT sample was also taken for quality control. The two RT sample communities had a 78% similarity, and the PM sample was overall 60% similar to the RT samples. *Simulium* black flies dominated RT

sample communities in 2019 (53.3% and 36.9% of total abundance), and the primary RT sample was the least balanced (lowest Simpson Diversity Index) of all the 2019 samples. *Tanytarsus* midges dominated the PM sample community, but at just 17.7% of total abundance. In addition to differences in the top taxon, the PM sample had more beetles, while the RT samples had no Chironomini, a tribe of tolerant non-biting midge whose larvae burrow in sediment and are DEQ indicators for warm temperatures and high sediment conditions. Both RT and PM communities were dominated by small-bodied collectors and clingers, and the PM sample had one of the highest relative abundances of multivoltine organisms (50%; range in 2019 samples = 19-58.9%). Most organisms in RT samples were associated with erosional habitat, while the majority in the PM sample had mixed flow associations. However, the number of EPT taxa in both sample types was similar (19/20 in RT samples, 18 in PM) and at the upper end of the range for all 2019 samples (range = 9-23 EPT taxa).

PREDATOR scores have been consistent since 2015, indicating fair biological condition, although the duplicate RT sample in 2019 scored as "good condition" (Figure 56). IBI scores rose slightly overall, indicating slight disturbance in all sampling years except 2016, which scored as undisturbed. The target subsampling number of 500 organisms was attained in every year except 2011 (Figure 57), when the entire sample had only 385 organisms. However, whereas from 2009-2014 it required 67-100% of the total sample to attain the 500 organism target, every sampling year since then has yielded the target with only 6-23% of the sample being picked.

Figure 56. PREDATOR O/E and ORDEQ IBI scores at WC1950 from 2009-2019. *Only RT samples taken in the primary channel are shown. Asterisks indicate scores for duplicate RT sample taken in 2019 for quality control.*
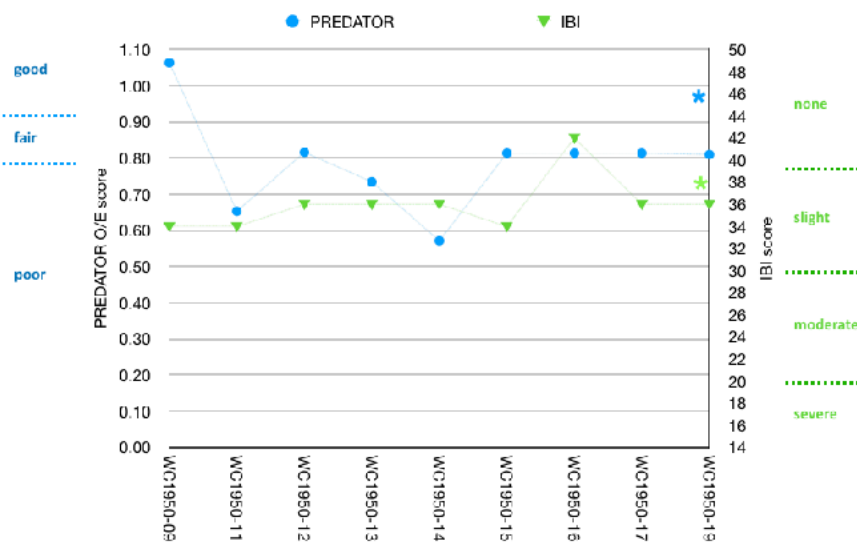
Total richness and EPT richness have increased overall (Figure 58). For the last two sampling years, total richness has been in the range of the highest scaled score in the IBI, and the 2019 PM sample had the most taxa of any sampling year at this site. All taxa seen for the first time at this site in 2019 samples prefer cooler and faster-flowing habitats, and include: Prodiamesinae (PM), a subfamily of non-biting midge that prefers cool lotic and lentic habitats, feeds by

collecting, and is associated with fine sediments; *Trichoclinocera* (PM, RT), a predatory dance fly found among rocks in riffles in lotic habitats; *Neoleptophlebia* (RT), a genus of prong-gill mayfly that inhabits sediment and detritus in lotic erosional habitats; and *Pteronarcys* (RT), a giant stonefly genus that is a shredder in swift areas of streams where detritus accumulates.

Figure 57. Proportion of sample needed for sub-sampling and resulting organismal abundance at WC1950 in all sampling years. The PM1 and RT samples were taken in the same reach at the same time in 2019.
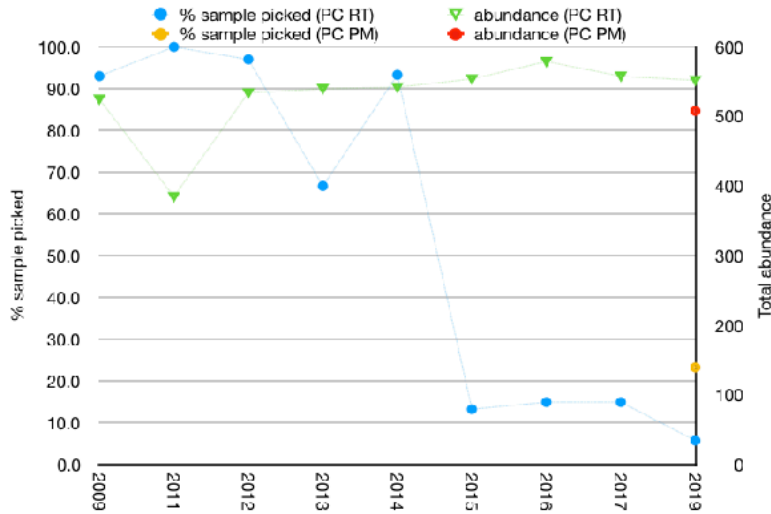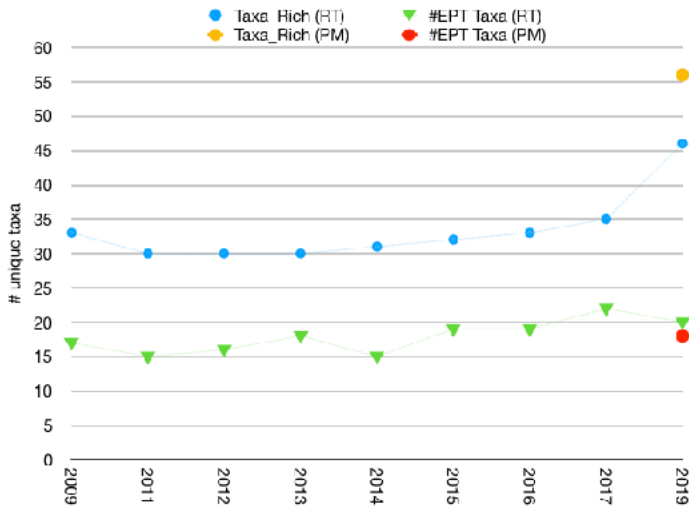

Figure 58. Sample richness and EPT diversity at WC1950 in all sampling years. For this metric in the ORDEQ IBI, >35 total taxa receives the highest scaled score.

Numbers of sensitive and sediment-sensitive taxa fluctuate annually but are higher post-project than in the years immediately preceding (Figure 59), and the number of sediment-sensitive taxa in the 2019 RT sample was the highest of any sampling year. Relative abundances of tolerant and sediment-tolerant taxa decreased sharply in earlier sampling years, but fluctuated since; a pre-project increase appears to have reversed in the 2019 RT sample, though the proportions in the PM sample are still higher (Figure 60). The dominant taxa shifted from more tolerant types in earlier sampling years (i.e., segmented worms, non-biting midges) to more sensitive lotic types in 2016-2017 (*Suwallia* green stonefly, *Agapetus* saddlecase caddisfly; Figure 61). In 2019, over half of the RT sample consisted of *Simulium*; this is not uncommon at newly-restored sites, where black flies are often pioneer species that create new

Figure 59. Numbers of sensitive and sediment-sensitive taxa at WC1950 in all sampling years. In the ORDEQ IBI, the highest scaled score correlates with >4 sensitive and >2 sediment-sensitive taxa.
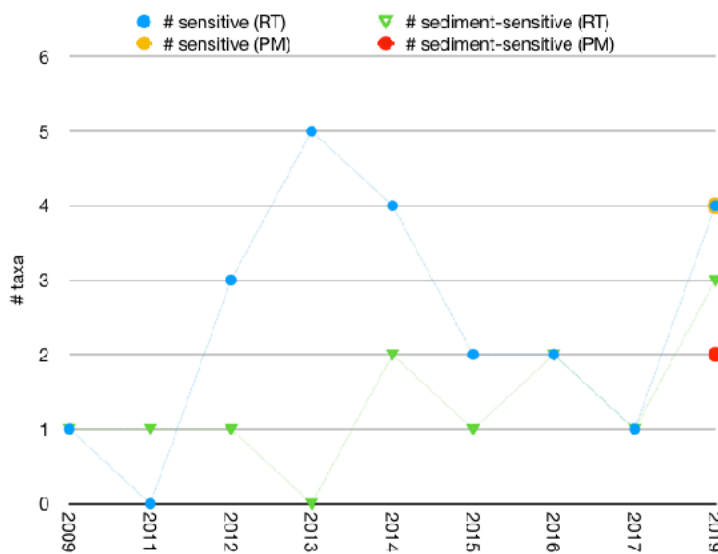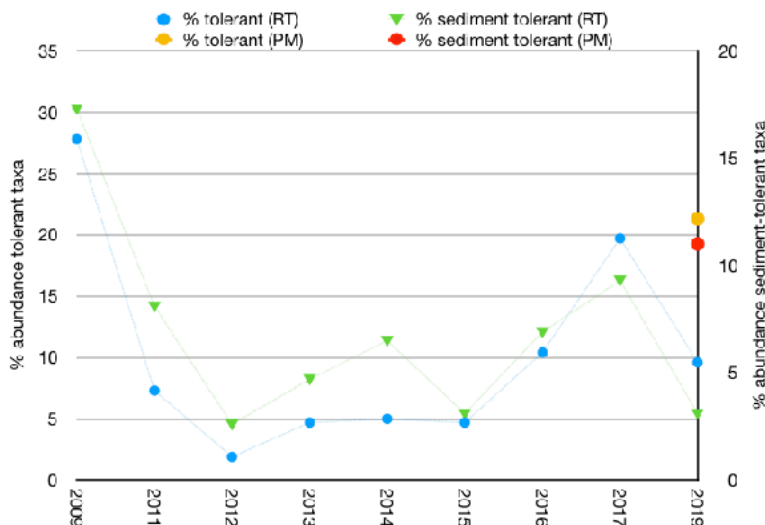

Figure 60. Numbers of tolerant and sediment-tolerant taxa at WC1950 in all sampling years. For this metric in the ORDEQ IBI, the highest scaled score correlates with <15% tolerant and <10% sediment-tolerant taxa.

habitat and additional food resources for later colonists (Hammock & Bogan, 2014). The top taxon in the 2019 PM sample was *Tanytarsus*, a non-biting midge genus that prefers warmer temperatures and feeds as a collector in all types of freshwater habitats, but it dominated the community to a lesser extent than the top taxon in the RT sample (17.7% of total abundance).

Figure 61. Relative abundance of the numerically dominant taxon at WC1950 in all sampling years. In the ORDEQ IBI, the highest scaled score correlates with <20% abundance of the top taxon.
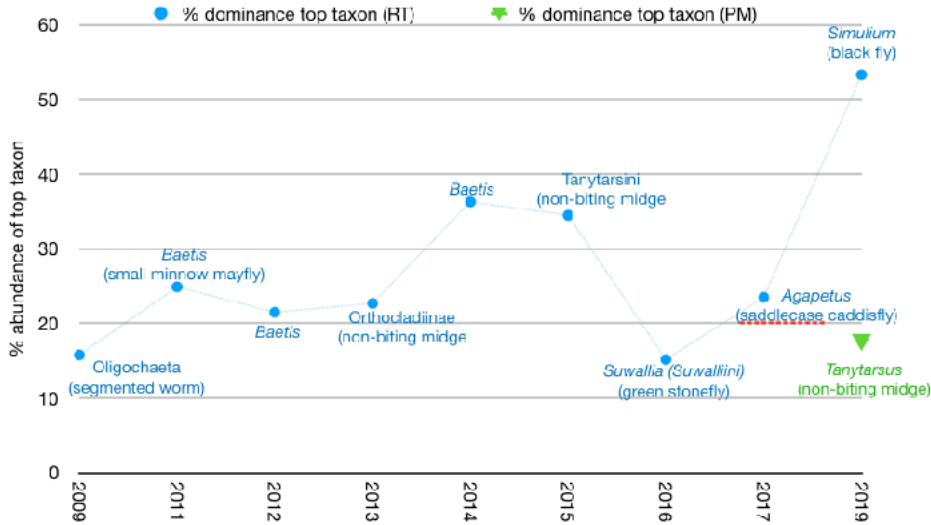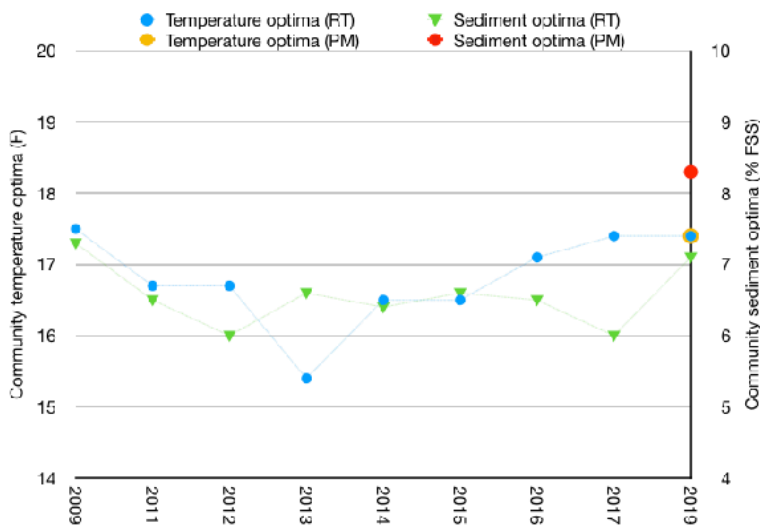

Figure 62. Temperature and fine sediment optima of the community at WC1950 in all sampling years.

Community temperature and sediment optima over time exhibit a somewhat U-shaped curve (Figure 62). The number of DEQ cool and warm temperature indicator taxa fluctuated in a similar manner (Figure 63), although there were more cool than warm indicators in six of the nine sampling years The number of DEQ low sediment indicator taxa increased overall in RT samples and exceeded the number of high sediment indicators in seven of the sampling years, while the number of high sediment indicator taxa decreased (Figure 64).

Figure 63. Number of ORDEQ cool and warm temperature indicator taxa at WC1950 in all sampling years. Note that these taxa do not account for the temperature associations of all taxa in a sample.
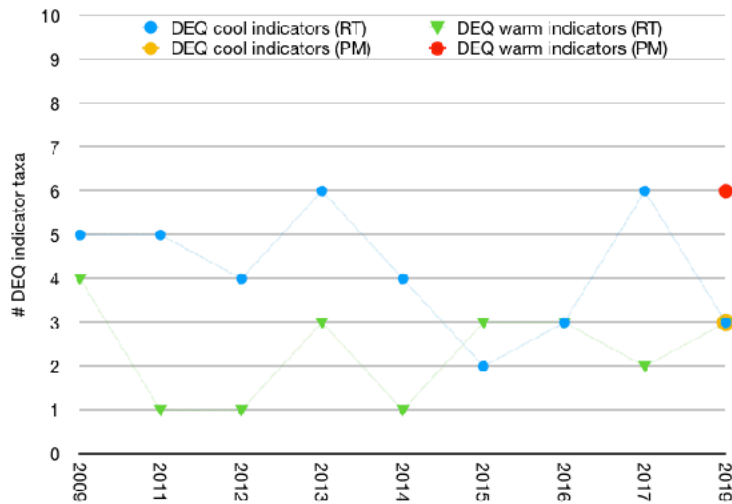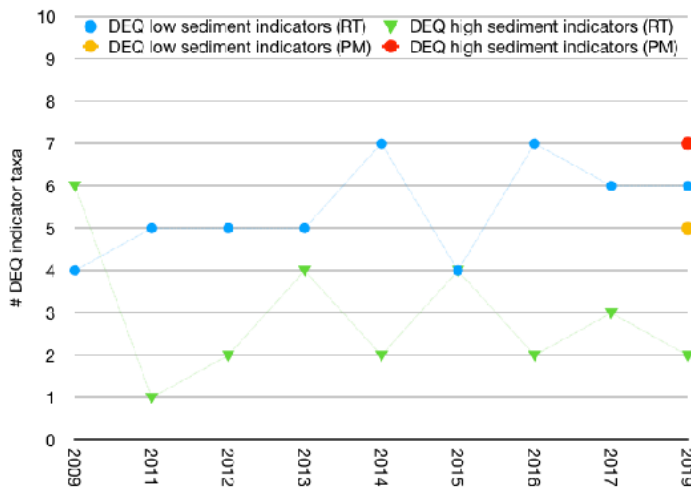

Figure 64. Number of ORDEQ low and high sediment indicator taxa at WC1950 in all sampling years. Note that these taxa do not account for the sediment associations of all taxa in a sample.

Macroinvertebrate community composition was more similar among samples from later years (2015-2019) with the exception of 2017 (Figure 65). Overall average dissimilarity among all years was 43%; taxa that contributed the most were Tanytarsini, a tribe of non-biting midge whose members generally feed as collectors in warmer lentic and lotic waters; and *Simulium* black flies, both of which were more abundant in 2016 and 2019. In a PCA ordination of taxa (Figure 66), axis 1 explained 32% of the total variation; taxa with the highest loading were Tanytarsini and *Baetis*, a small minnow mayfly that is a DEQ low sediment indicator (more abundant in 2009-2014). Axis 2 explained an additional 18% of variation, and taxa with the highest loading were *Simulium* and *Agapetus*, a saddlecase-maker caddisfly found in cool fast flows (none in 2009; increased abundances after 2013).

In a PCA ordination of traits measured as relative abundances (Figure 67), axis 1 explained 60% of the variation, and traits with the highest loading were relative abundance of collectors (greatest in 2013 and 2019 RT samples and two-fold lower in 2017) and dominance of the top taxon (1.5-3 times greater in the 2019 RT sample than in other years). Axis 2 explained an additional 20% of the variation; factors with the highest loading were relative abundance of tolerant organisms (highest in 2009 RT and 2019 PM sample) and relative abundance of the collector feeding guild (highest in 2013 RT and 2019 PM samples).

Figure 65. CLUSTER dendrogram of the WC1950 macroinvertebrate community in all sampling years. *Blue = RT, aqua = PM. The numeral in each label indicates the sampling year.*
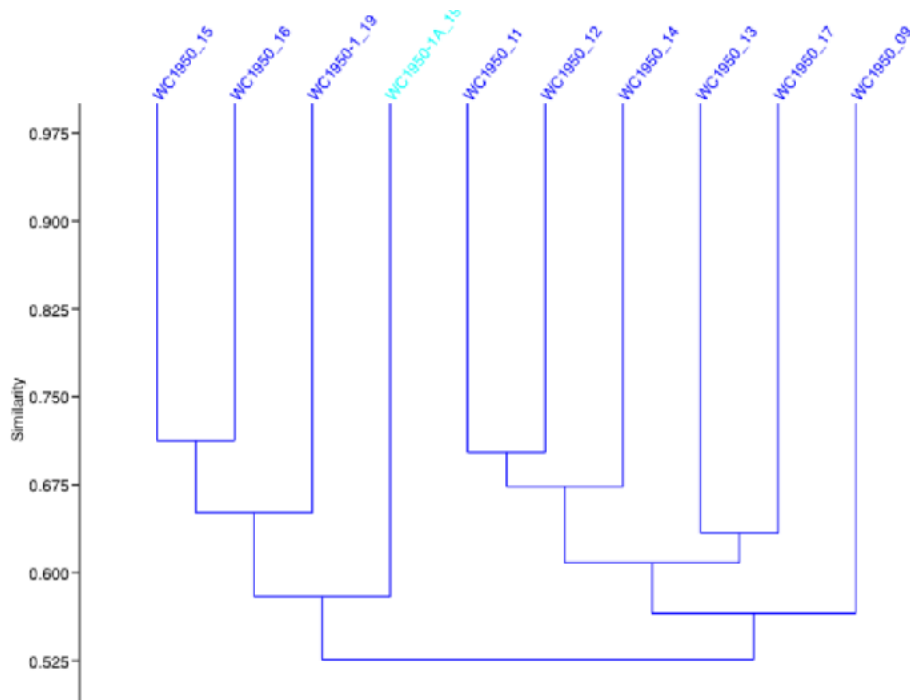
Figure 66. PCA ordination of the WC1950 macroinvertebrate community in all years. *Blue = RT, aqua = PM. The numeral in each label indicates the sampling year. Eigenvectors show dominant contributions, where vector length is related to the strength of its contribution.*

Figure 67. PCA ordination of WC1950 macroinvertebrate community traits measured as relative abundances in all years. *Blue = RT, aqua = PM. The numeral in each label indicates the sampling year. Eigenvectors show dominant contributions,*

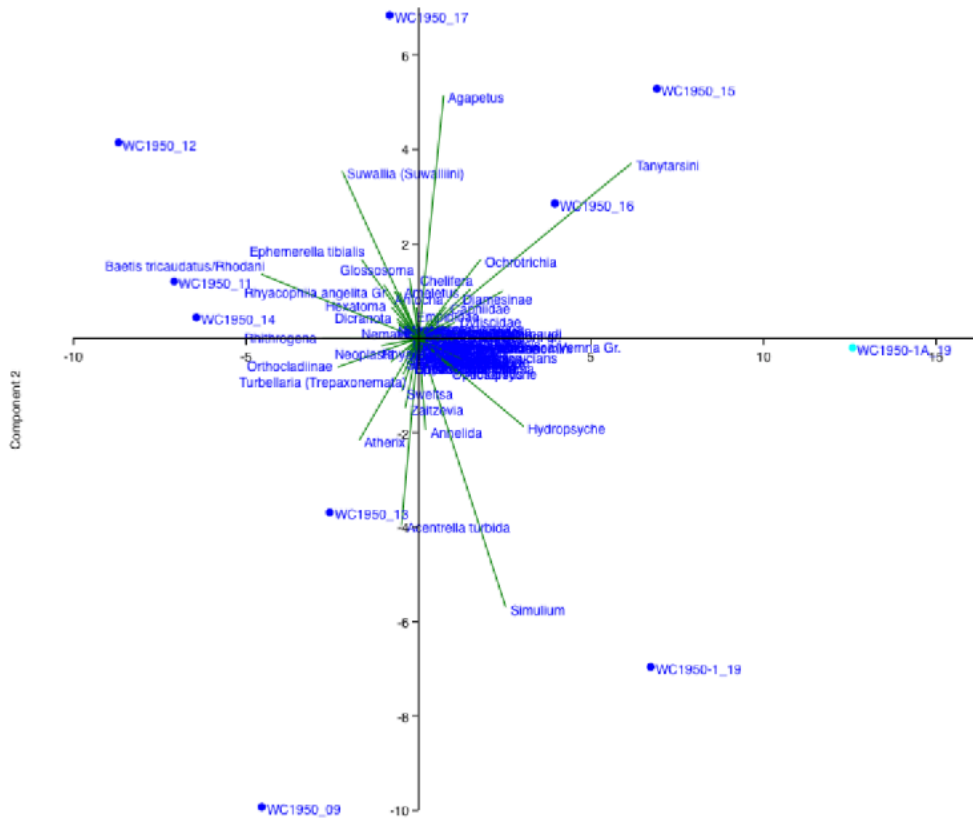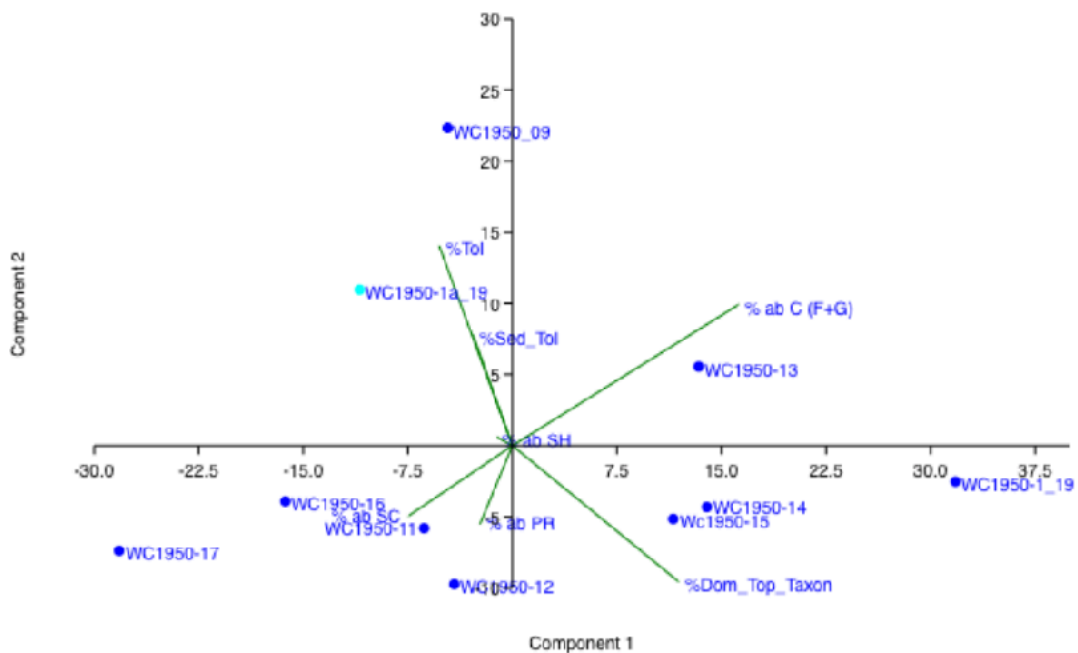Riffle-targeted sampling was done at WC2600 since 2005 including 2014, when the creek was directed into a new meandering channel at this site. Addition PM samples were taken in four side channels in 2018; the sample reach in 2019 contained primary and side channel habitat and both RT and PM samples were taken. The 2019 RT and PM communities had a relatively low similarity (Bray-Curtis Similarity Index = 0.58). Both were dominated by non-biting midge taxa at similar and moderate relative abundances (32.6% and 30.2%, respectively), but in different genera. The top taxon in the RT sample was *Cricotopus (Nostococladius)*, a sensitive, sediment-intolerant taxon found in cold, clear, flowing waters; the PM sample was dominated by *Micropsectra*, a member of the Tanytarsini tribe that prefers warmer, slower habitats and is characteristic of muddy deposits in slow regions of flowing waters. The target sub-sampling number of organisms was attained after picking similar proportions of the sample (21.7% and 30%), but the PM sample was more diverse (49 vs. 37 unique taxa in RT sample) and had more EPT taxa (22 vs. 18). The PM sample also had more stonefly and sensitive taxa (7 of each) than any other site sample in 2019 (range = 2-5 in remaining 2019 samples for both groups). The RT sample had very few shredders (1.7% of total; range in 2019 samples = 1.7-17.5%) and more scrapers than the PM sample, while PM sample contained almost a six-fold higher proportion of shredders (10.5%) and half as many scrapers. Both communities were dominated by small-bodied, multivoltine organisms; the majority in the RT sample were associated with cold/cold erosional habitat, but the PM sample contained similar proportions of cold/cold- and warm-associated taxa in a wider range flow conditions.

In comparison to the samples taken in 2019 at other sites, the macroinvertebrate communities in WC2600 samples had the lowest community temperature optima (16.7°F in both RT and PM; range in remaining 2019 samples = 17.0-18.0°F), and the PM sample had more DEQ low temperature indicator taxa (WC2600 PM = 7 taxa; range in remaining 2019 samples = 0-6). The proportion of tolerant organisms in both WC2600 samples was also significantly lower (mean = 2.5% $\pm$ 0.6) than at any other site in 2019 (mean = 19.0% $\pm$ 8.2).

PREDATOR scores at this site increased overall (Figure 68). Scores consistently indicated poor biological condition from 2005-2014, with a further drop in 2015 due to the immediate impacts of restoration, but increased afterwards and are higher in 2018 and 2019 than in any previous year at the site, indicating fair biological conditions. IBI scores fluctuated more, indicating moderate to slight disturbance in most years from 2005-2016 and showing a similar decrease immediately post-restoration, but increasing into the "no disturbance" range since then. Organismal abundance in samples has varied more here than at other sites (Figure 69), and the target subsampling number was not attained in four of the 10 RT samples taken at this site in different years, including 2018 (although the PM sample from the same reach that year had 540 organisms).

Figure 68. PREDATOR O/E and ORDEQ IBI scores at WC2600 from 2011-2018. Only RT samples are shown.
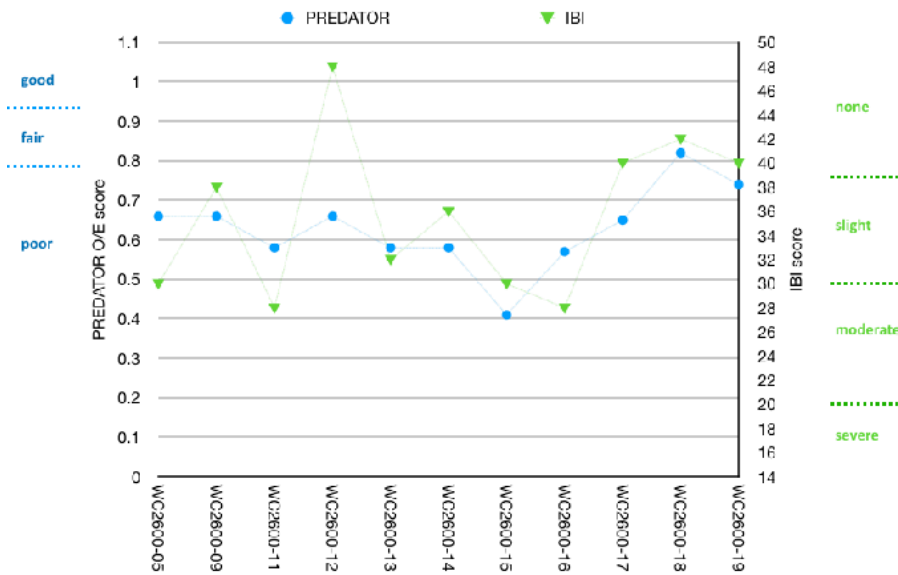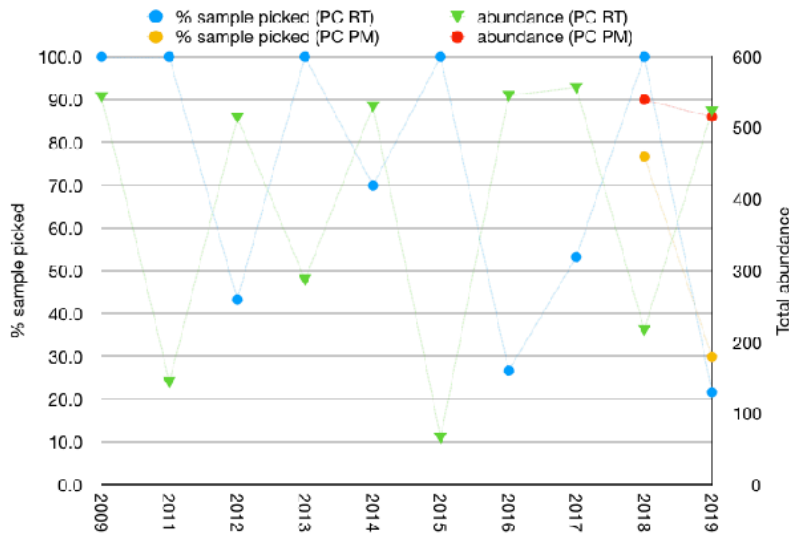
Figure 69. Proportion of sample needed for sub-sampling and resulting organismal abundance at WC2600 in all sampling years. Only samples taken in the primary channel are shown. The PM and RT samples was taken in the same reach at the same time in 2018-2019.

Total richness and EPT richness show a similar pattern of a post-restoration drop followed by sustained increase (Figure 70). In recent years, RT sample richness was in the range of the highest scaled IBI score, and PM samples have even more taxa. All taxa taken for the first time at this site in 2019 occurred in low numbers and are associated with cooler and/or fast-flowing habitats: Prodiamesinae (RT), a subfamily of non-biting midge that feeds as a collector in cool lotic and lentic habitats and is associated with fine sediment; *Trichoclinocera* (RT, PM), a predatory dance fly found among rocks on riffles in lotic habitats; *Ephemerella aurivillii* (RT), a DEQ cool temperature indicator taxon associated with cool/cold erosional flows; and *Cinygma* (RT), a sensitive flatheaded mayfly that prefers woody substrates in cold, lotic-erosional habitats.

Figure 70. Sample richness and EPT diversity at WC2600 in all sampling years. *For this metric in the ORDEQ IBI, >35 total taxa receives the highest scaled score.*
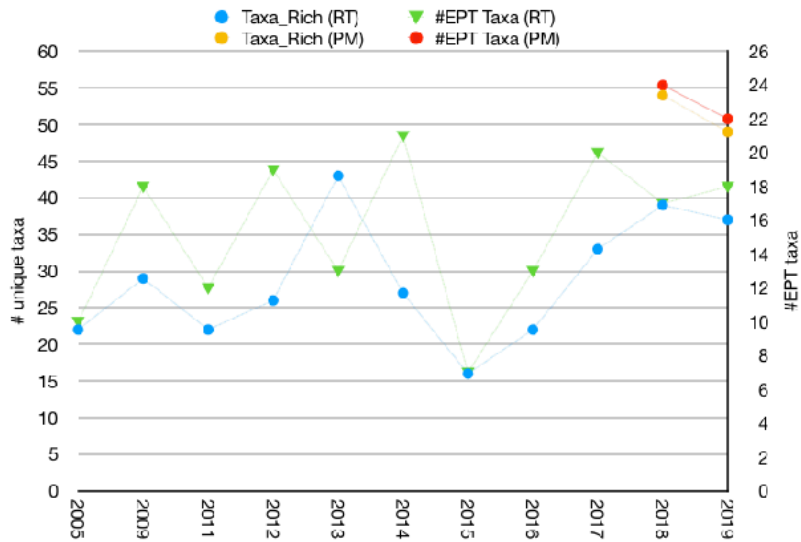
The number of sensitive taxa fluctuated greatly in early sampling years (Figure 71) but increased steadily post-restoration, with a slight drop in 2019. The number of sediment-sensitive taxa in each year varies less, but also increased after 2016 and was in the range for the highest scaled score in the IBI in 2018 and 2019. Somewhat unexpectedly, the number of both in PM samples was the same or higher than in the RT sample from the same year. Relative abundances of tolerant and sediment-tolerant taxa (Figure 72) fluctuate as well but are low overall, even in the PM samples, which often have higher proportions of tolerant organisms as sampling includes lentic and/or sedimented habitats. Relative abundance of tolerant taxa was low enough to receive the highest scaled IBI score (<15%) in all years and samples except in 2013 (17.7%), and relative abundance of sediment-tolerant taxa was low enough to receive the highest scaled IBI score in every year except 2009 and 2013.

Figure 71. Numbers of sensitive and sediment-sensitive taxa at WC2600 in all sampling years. *In the ORDEQ IBI, the highest scaled score correlates with >4 sensitive and >2 sediment-sensitive taxa.*
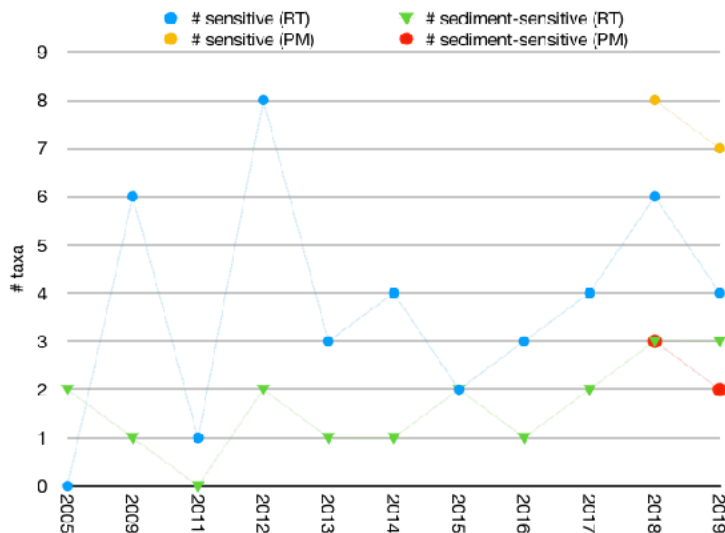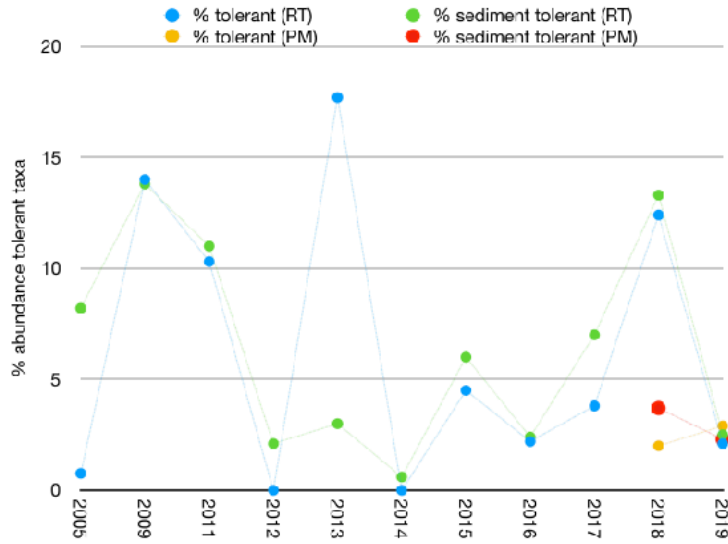
Figure 72. Relative abundance of tolerant and sediment-tolerant taxa at WC2600 in all sampling years. In the ORDEQ IBI, the highest scaled score correlates with >4 sensitive and >2 sediment-sensitive taxa.

Prior to restoration, this site was dominated by the same taxon each year: Orthocladiinae, a cosmopolitan subfamily of non-biting midge whose members are warm water-associated burrowers and tube builders in a wide variety of habitats (Figure 73). Dominant taxa since then are associated more with colder and/or faster-flowing waters, including the flatheaded mayflies *Baetis* and *Rhithrogena*, non-biting midges *Cricotopus* (*Nostococladius*) and *Micropsectra*, and *Simulium*, a pioneer species that composed 3/4 of the numerical abundance of the post-restoration 2016 sample. Despite this, pre- and post-project community temperature and sediment optima have changed little overall (Figure 74), and the number of DEQ cool temperature taxa, while still higher than at many other sites on Whychus, has decreased since 2017 (Figure 75). However, the number of high sediment indicator taxa has been consistently low (0-3 taxa; Figure 76), while the number of low sediment indicators increased overall and is among the highest in Whychus samples (4-10). Pre- and post-project means are not significantly different for any of these traits.

Figure 73. Relative abundance of the numerically dominant taxon at WC2600 in all sampling years. For this metric in the ORDEQ IBI, the highest scaled score correlates with <20% abundance.
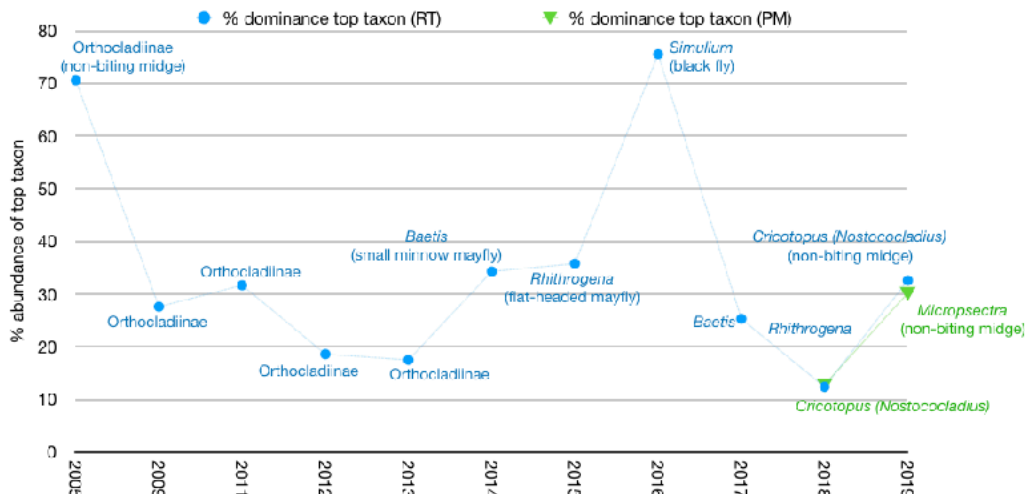
Figure 74. Temperature and fine sediment optima of the community at WC2600 in all sampling years.
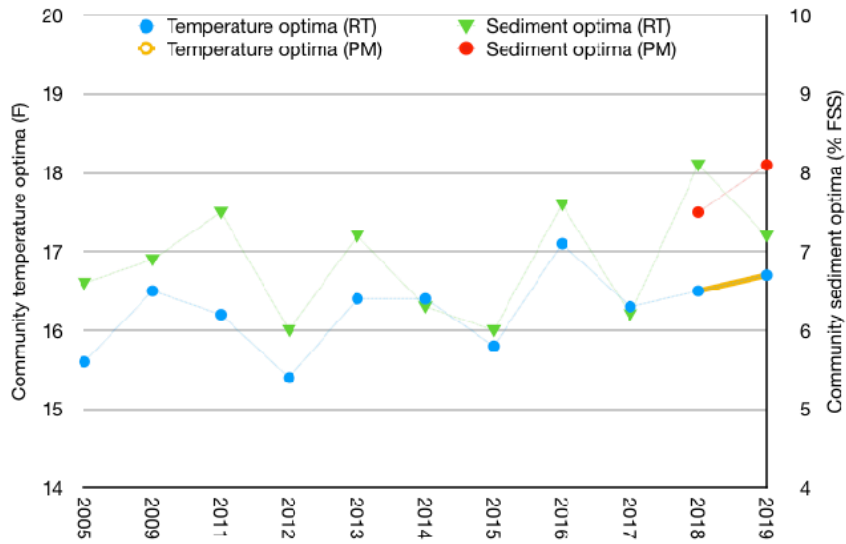

Figure 75. Number of ORDEQ cool and warm temperature indicator taxa at WC2600 in all sampling years. Note that these taxa do not account for the temperature associations of all taxa in a sample.
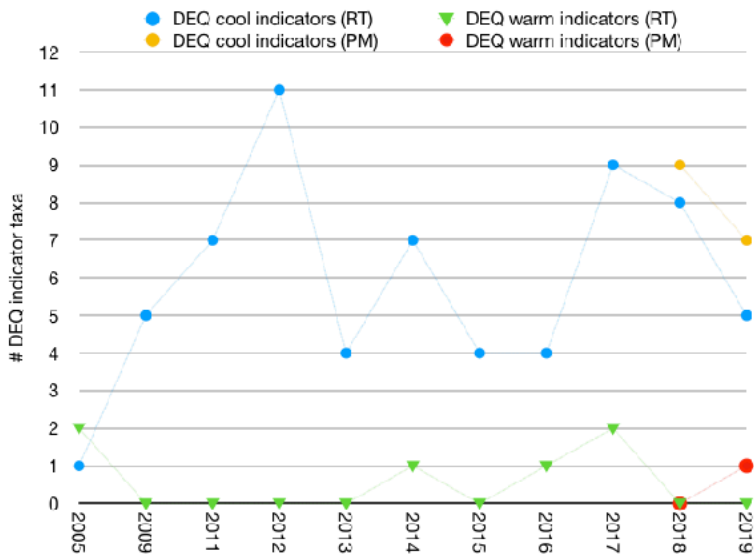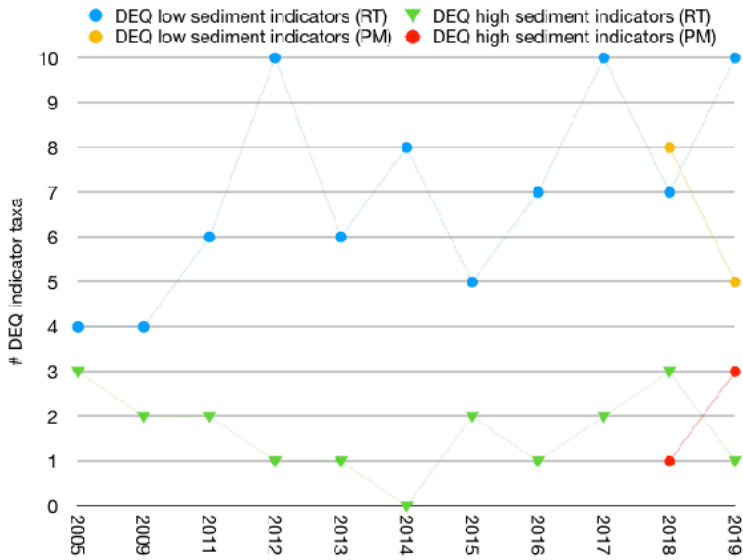
Figure 76. Number of ORDEQ low and high sediment indicator taxa at WC2600 in all sampling years. *Note that these taxa do not account for the sediment associations of all taxa in a sample.*

The macroinvertebrate communities in 2005 (prior to instream flow restoration in Whychus) and 2015 (immediate after site restoration) differed most from those in all other years at this site (Figure 77). Samples from recent years were most similar regardless of method (RT or PM) or channel type (primary or side channel) except for the 2019 RT sample, which was more similar to earlier years. In a PCA ordination of taxa (Figure 78), axis 1 explained 35% of the total variation and primarily separated RT from PM samples; taxa with the highest loading included Tanytarsini, a non-biting midge tribe that was absent or present in low abundance (1-2 individuals) until 2018-2019, when abundances ranged from 9-177; and *Zapada cinctipes,* a stonefly associated with cold water that feeds as a shredder in a variety of lotic and some lentic habitats that was also absent or present in low abundance (1-5 individuals) until 2018-1019, when abundance ranged from 22-62 in all but the 2019 RT sample (1 individual). Axis 2 explained an additional 17% of variation; taxa with the highest loading included *Simulium,* which was more abundant in RT samples from 2014, 2016, and 2019; and Orthocladiinae, the non-biting midge subfamily that was the dominant group from 2005-2013.

In a PCA ordination of traits measured as relative abundances in all years (Figure 79), axis 1 explained 64% of the variation; factors with the highest loading were relative abundance of the top taxon (unusually high in 2005 and 2016) and of collectors (related to the feeding guild of the dominant taxa). Axis 2 explained an additional 22% of variation, with relative abundance of scrapers (higher in the 2018 and 2019 RT samples) and of the top taxon having the highest loading. In a PCA ordination of total traits measured in 2018-2019, which included additional factors such as flow and temperature associations, maximum body length, voltinism, and habit, axis 1 explained 55% of the total variation (Figure 80); factors with the highest loading were relative abundance of erosional-associated organisms and of scrapers, both of which were greatest in the 2019 RT sample. Axis 2 explained an additional 35% of variation; factors with the highest loading were cool/cold-associated taxa, which was greatest in the 2019 RT sample, and of erosional-associated taxa.

Figure 77. CLUSTER dendrogram of the WC2600 macroinvertebrate community in all sampling years. Blue = RT, aqua = PM. The numeral in each label indicates the sampling year.
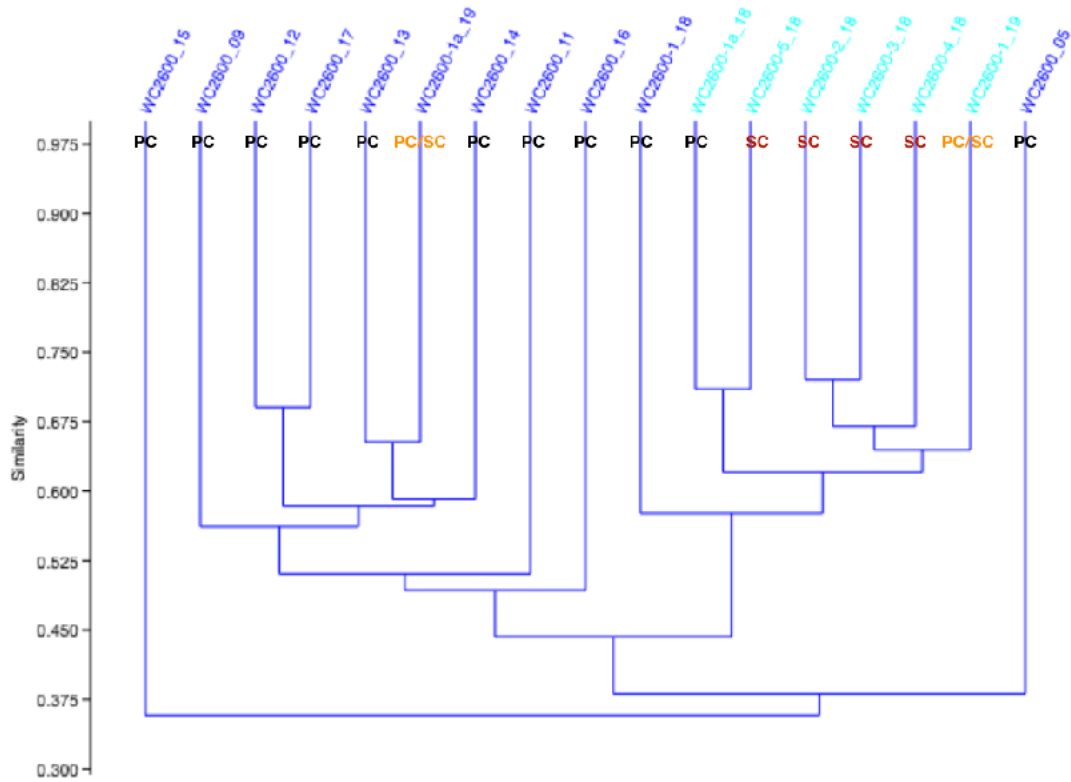
Figure 78. PCA ordination of the WC2600 macroinvertebrate community in all years. Blue = RT, aqua = PM. The numeral in each label indicates the sampling year. Eigenvectors show dominant contributions, where vector length is related to the strength of its contribution.
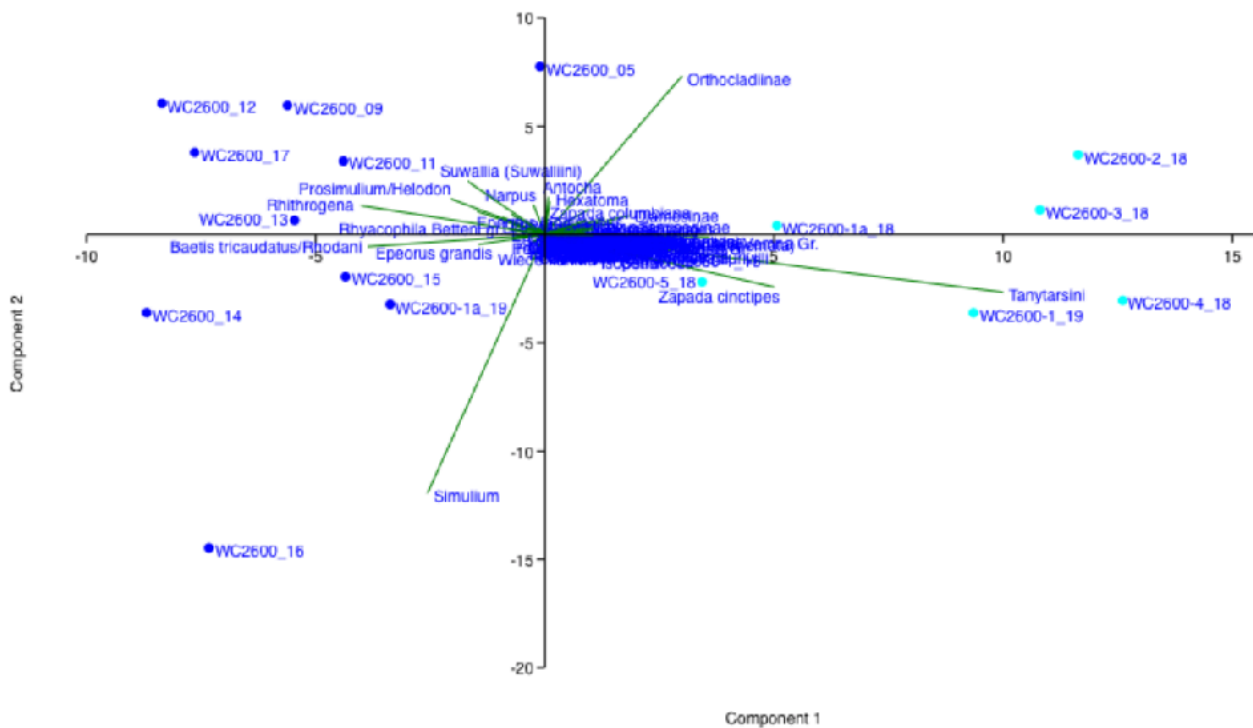
Figure 79. PCA ordination of WC2600 macroinvertebrate community traits measured as relative abundances in all years. *Blue = RT, aqua = PM. The numeral in each label indicates the sampling year. Eigenvectors show dominant contributions, where vector length is related to the strength of its contribution.*

Figure 80. PCA ordination of WC260 macroinvertebrate community traits measured as relative abundances in 2018-2019. *Blue = RT, aqua = PM. The numeral in each label indicates the sampling year. Eigenvectors show dominant contributions, where vector length is related to the strength of its contribution.*
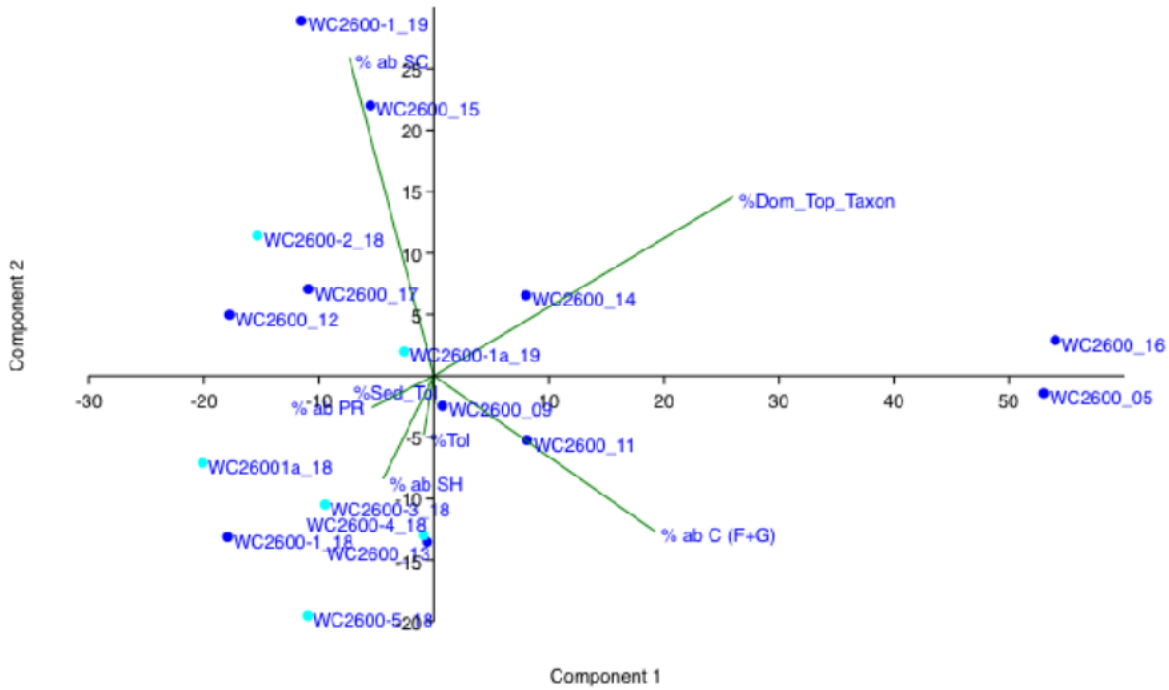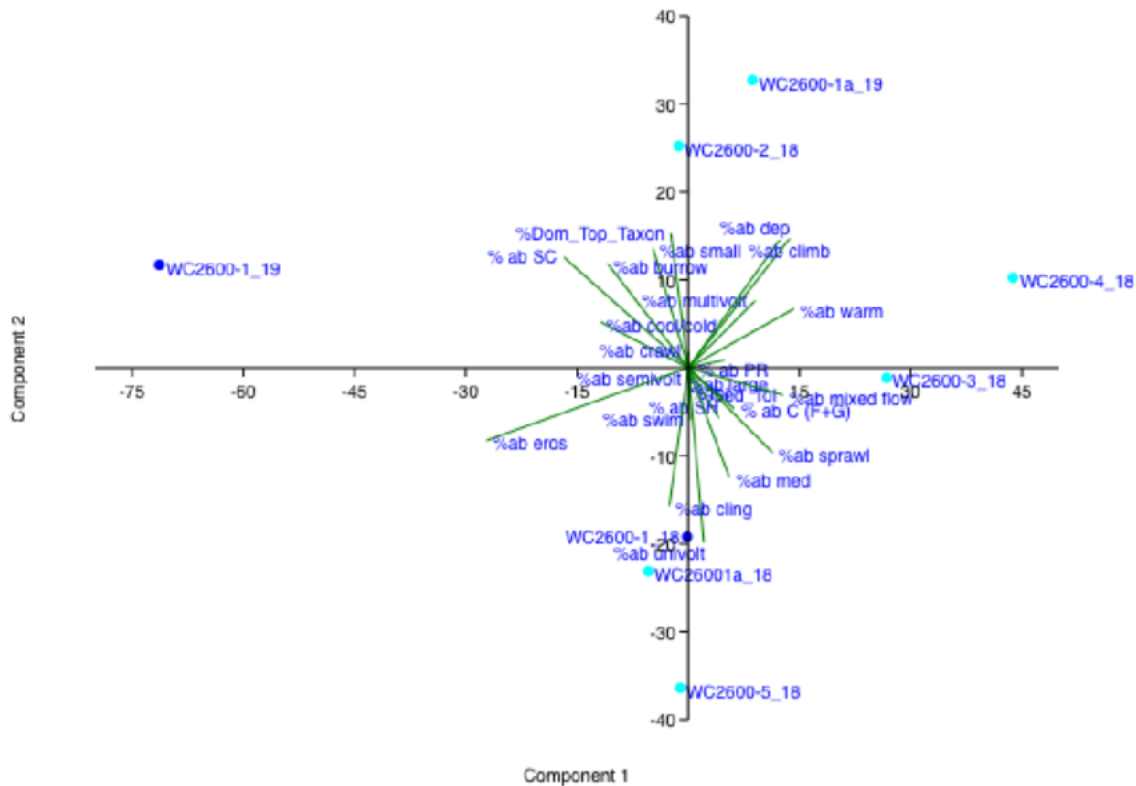
Discussion

Sampling has been done in Whychus Creek in 11 of the past 14 years, but the species accumulation curve has not yet plateaued. Eleven taxa in six different orders that had not been taken in any previous year or site were seen in the 2019 sample set, the majority of which were taken in the more upstream sampling reaches and in samples obtained using the primary multihabitat (PM) technique, and at least one new taxon was seen at any site that had been sampled in multiple years except WC1150. PM sampling is more representative and ensures that rare habitats in aren't oversampled and abundant habitats aren't under-sampled (Barbour et al., 2006), and thus provides a more accurate picture of the total biota a stream supports. Riffle-targeted sampling is used to increase the likelihood of capturing more sensitive taxa that require the faster, colder, better-oxygenated flows in this habitat. However, data from this second year of PM and RT sampling in Whychus indicate that PM sampling provides an accurate assessment of site biodiversity without sacrificing capture of sensitive riffle-associated taxa. PM samples have significantly higher richness and similar if not greater numbers of EPT taxa. Because the random selection of available habitat types in PM sampling also includes a range of flow types, including riffles, and all PM samples taken in the same reach as RT samples in 2019 included net sets from at least two riffles, differences between the two sampling methods in the same reach appear to be minimized.

The macroinvertebrate community in different reaches of Whychus Creek is influenced by both site-level (i.e., restoration in different reaches) and basin-level (i.e., restoration of perennial flow, surrounding landscape use) factors, as well as the more global impacts of climate, which can complicate identifying changes due solely to an individual site restoration project. Overall, restoration along Whychus has resulted in communities that are both more diverse and more balanced in recent years, which implies habitat that is more stable and/or subject to less harsh environmental filters. It should be noted that some of the observed increases in diversity is related to the shift from RT to PM sampling at some sites. However, for the most part, macroinvertebrate communities in the same general river mile of the stream are most similar (i.e., RM 19.25-26; RM 10.25-11.50), regardless of sampling method or channel type, though there are a few exceptions from year to year. Direct comparisons of the community in side channel vs. primary channel habitat in restored reaches was more difficult this year, as increased channel braiding at restored sites made separation of channels more difficult and several samples included both primary and side channel habitat in the reach, but primary and side channels in the same general location had similar macroinvertebrate communities.

Restoration projects to improve water quality and flow and habitat conditions are predicted to support a greater diversity and/or abundance of sensitive taxa, and there have been some concerns as the means for community temperature and sediment optima have not been significantly different pre- and post-project at any restoration site; in addition, DEQ warm temperature and high sediment indicator taxa generally outnumber cool temperature and low sediment indicators at most sites. However, the communities at sites where recent restoration projects have been done appear to recover substantially from disruption within two years, and include more taxa with cool/cold temperature, erosional flow, and/or low sediment associations. The geographic setting of Whychus Creek should also be considered when evaluating sediment optima. In developing a Biological Sediment Tolerance Index for Oregon, Hubler et al. (2016) assessed fine sediment conditions across the state via direct measurement of substrate

composition and macroinvertebrate taxa tolerances; their data indicate that most watersheds in the Cascades are in the 0-10% fine sediment class. Community sediment optima of Whychus samples are in this range (i.e., 6.9-10.3% FSS in 2019 samples), so significant decreases following restoration may not be likely to occur.

Communities in the primary and mainstem channels at restoration sites are similar, but their differences reflect variation in the quantity and type of habitat and flow present. For example, samples taken in side channels at WC1100 had a higher proportion of shredders and climbers, suggesting a greater abundance of macrophytes in these habitats, as well as a greater diversity and abundance of organisms associated with mixed flow, reflecting more heterogenous conditions and thus more ecological niches in the side channels. Despite the lack of a significant difference in pre- and post project means at WC1100 for traits relating to temperature and sediment, sensitive taxa were only seen at this site after restoration, and the dominant taxon, which is a member of the EPT in RT samples, occurs at lower relative abundances. In contrast, the PM sample taken at WC1150, the upstream reference for the WC1100 project site, had an abundance of scraper and clinger organisms and the lowest relative abundance of warm water-associated taxa in the 2019 dataset, suggesting a habitat with fast flows over rocky substrates, as well as more semivoltine organisms, which is indicative of greater habitat stability. Interestingly, in 2017, the year in which restoration was implemented at WC1100, values of many traits in the WC1150 sample decreased, including IBI score, total richness, and number of EPT taxa, and the community was dominated by a high abundance of segmented worms. These values all increased again in subsequent sampling years, suggesting some impact of the restoration activities on this upstream site.

WC1950 seems to have recovered even more quickly from restoration activities. The community in 2019 was dominated by *Simulium*, a pioneer species whose abundance often increases immediately following restoration (Hammock & Bogan, 2014), but the number of EPT taxa was at the higher end of the range for the 2019 dataset and total richness was higher in 2019 than in any other sampling year at this site. Interesting, there were no Chironomini in the RT sample; absence of this tolerant cosmopolitan tribe of non-biting midge may indicate substrate conditions too dynamic to sustain this sediment burrower. Most of the four taxa taken for the first time at this site in 2019 were associated with cooler faster flows, as well as with sediment and/or detritus. However, WC1950 is the only site among those sampled in 2019 where cool temperature indicator have outnumbered warm indicators in most years (although the number of each was the same in the 2019 RT sample), and there were more sediment-sensitive taxa in 2019 samples than in any prior sampling year at the site.

The WC1925 reach was a new sampling reach for 2019. The primary channel and three side channels all had the same dominant taxon, a non-biting midge (*Tanytarsus*) associated with warmer slower flows. The greatest total richness (64-67 taxa) was seen in three of the four samples at this site, and one side channel (WC1925-3) had more EPT than any other 2019 site sample. Overall this site had significantly higher richness, more sprawlers and predators, more organisms associated with varied flows, as well as a higher community sediment optima, reflecting reaches with slower flow and more sedimented substrate but sustaining a very diverse community.

Some longterm downstream sites are indicating higher temperature and sediment signals. WC0600 has consistently had a low enough relative abundance of sediment-tolerant organisms to receive the highest scaled score in the ORDEQ IBI for this metric and the community sediment optima was the lowest of all 2019 samples, but both of the WC0600 samples and the WC1025 sample had the highest community temperature optima in the 2019 dataset (17.9-18.0°F), while the lowest community temperature optima was seen in the WC2600 samples (16.7°F in PM and RT). In addition, the macroinvertebrate community at WC1025 has been dominated by tolerant burrowing segmented worms for the past two years, and this sample had more tolerant and sediment-tolerant taxa than any other 2019 sample. However, WC1025 also had a high taxon diversity, and the three taxa taken for the first time at this site in 2019 were all members of the EPT. In contrast, WC2600, the most upstream sampling site on Whychus Creek, has had more low sediment indicator taxa (7-10) in the last four sampling years than any of the other 2019 sites that were sampled in multiple years. In 2019, the WC2600 community had the lowest temperature optima and relative abundance of tolerant organisms compared of all other 2019 samples, and the four taxa taken here for the first time were all associated with colder and/or faster-flowing habitats.

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