Spatial and temporal patterns of benthic cyanobacteria proliferations and anatoxin in the Klamath River Watershed, summer 2021

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Risk from benthic cyanobacteria

Toxin-producing cyanobacteria are an emerging public health threat in lakes and rivers (Testai et al., 2016). Although cyanobacteria are a natural component of algal biofilms, proliferations of cyanobacteria-dominated mats appear to be increasing or are more widespread than previously expected (McAllister et al., 2016; Bouma-Gregson et al., 2018; Fetscher et al., 2015). Cyanobacteria can produce toxins that when ingested, can cause illness and death to humans, pets, and wildlife (Chorus and Welker, 2021; Wood, 2016). Increasingly, dog deaths following visits to rivers have been associated with anatoxin, a potent neurotoxin produced by cyanobacteria (Puschner et al., 2008; Backer et al., 2013; Catherine et al., 2013). Our understanding of the drivers and impacts of toxin-producing cyanobacterial blooms has relied largely on research of planktonic blooms dominated by taxa with different toxin-production dynamics and habitat requirements than benthic cyanobacteria proliferations (Wood et al., 2020; Scott and Marcarelli, 2012). Understanding of benthic cyanobacteria occurrence, toxin-production dynamics, and ecology lags public health concerns that these toxins pose, in part due to challenges associated with observing and documenting benthic algae.

The heterogeneous, patchy nature of benthic algae at the reach scale poses challenges to documenting their distribution and toxin dynamics in rivers and streams where they proliferate (Ledger et al., 2008). Even in small patches that appear homogeneous at a macroscopic scale, benthic algal mats can be dominated by different taxa and strains, resulting in differential toxin-production within very small patches (Wood et al., 2010, 2012). Sampling recommendations include collecting composite samples from algae mats across observed patches to capture some of the variation (Wood et al., 2020), but the extreme heterogeneity of benthic algae and inability of surveyors to collect samples from inaccessible river habitats may result in misrepresented toxin levels.

While sampling benthic material poses challenges to adequately capturing algal mat variation in a reach, water column grab samples are known to under-represent the biomass of benthic algae by orders of magnitude (Tekwani et al., 2013). Further, anatoxin degrades rapidly when exposed to sunlight, especially in warm temperatures and alkaline waters (Colas et al., 2021), reducing the likelihood of detecting anatoxin in the water column. Such under-representation translates to underestimates or even a total lack of detection of possible toxin exposure when benthic algae are the source of toxins. Still, water column grab sample methods developed for plankton are currently the sampling norm in many rivers dominated by benthic algae, and public health thresholds are based on water column concentrations of cyanotoxins (USEPA, 2019). Sloughed algal material

may provide a useful indicator of reach-scale toxin production and export from benthic cyanobacteria (Bouma-Gregson et al., 2017; Perry and Perry, 1991). Thus, due to the highly patchy nature of benthic algae and surveyor limitations in rivers, nets capturing transported coarse algal material may provide a sampling strategy to monitor water quality and public health risk associated with benthic cyanobacteria mats.

Benthic cyanobacteria in the Klamath River and tributaries

Limited sampling of anatoxin from ambient water column grab samples in the Klamath River and tributaries has generally resulted in non-detectable levels of the toxin, with detection only found in 15 of 236 samples (6%)(Genzoli and Kann, 2020). Although the sample size is much lower, recent targeted samples of cyanobacterial mats in 2019 confirmed benthic cyanobacteria proliferations along the length of the Klamath River, as well as in tributaries. All eight samples of these benthic algal mats analyzed for anatoxin resulted in detectable levels of anatoxin, indicating the potential for benthic algal mats to be a source of anatoxin in the Klamath River and its tributaries (Genzoli and Kann, 2020).

Similar sampling in the Russian River has also shown higher concentration of anatoxin in cyanobacterial mats, compared to both Solid Phase Adsorption Toxin Tracking (SPATT) and grab samples, which both reflect concentrations of toxins in the water column (Fadness, R. unpublished data). Although the 2019 data suggests that benthic cyanobacteria mats are a source of anatoxin in the Klamath River, we know little about the extent of mats and toxins, how to efficiently monitor anatoxin for public health, or how prevalent cyanobacteria are within the algal community.

Study objectives

The objectives of the summer 2021 benthic cyanobacteria study were to sample the distribution and extent of benthic cyanobacteria and associated anatoxins to gain baseline information about the public health risk that benthic cyanobacteria may pose in the Klamath River and tributaries. This sampling effort represents the first extensive sampling of benthic cyanobacteria and associated anatoxin over a large geographical area in the Klamath Basin. The specific goals of the sampling were to address the following questions:

1. What is the spatial and temporal distribution of benthic cyanobacteria and anatoxin in the Middle and Lower Klamath River Watershed?
2. What sampling and analysis methods are appropriate for regular public health monitoring?

Table 1. Klamath River and tributary sites, with site code, location, and indication ("o") of which samples were collected in each of three sampling efforts (July, August, and September).

	Site Name	Code	Latitude	Longitude	July				August				September			
					Composite-mat	Disturbance	Thalweg	Net-capture	Composite-mat	Disturbance	Thalweg	Net-capture	Composite-mat	Disturbance	Thalweg	Net-capture
Klamath River Sites	I5 at Screw Trap	**I5**	41.863138	-122.56472	o	o	o	o	o	o	o	o	o	o	o	o
	Tree of Heaven	**TH**	41.863040	-122.56465	o	o	o	o	o				o			
	Brown Bear	**BB**	41.823420	-122.96181		o	o	o	o	o	o	o	o	o	o	o
	Seiad Valley at Sluice Box	**SV**	41.842464	-123.22012	o	o	o	o	o	o			o	o	o	o
	Happy Camp	**HC**	41.793273	-123.36821	o	o	o	o	o	o	o	o	o	o	o	o
	Orleans	**OR**	41.302890	-123.53452	o	o	o	o	o	o	o	o	o	o	o	o
	Weitchpec	**WE**	41.186310	-123.69920	o	o	o	o	o	o	o	o		o	o	o
	Klamath at Terwer	**KAT**	41.510010	-123.97944	o	o	o	o								
Tributary Sites	Scott River Jones Beach	**SRJB**	41.639660	-123.05978		o	o		o	o	o	o	o	o	o	o
	Scott River Indian Scotty	**SRIS**	41.635610	-123.07732	o				o	o			o	o		
	Scott River nr Klamath	**SRMO**	41.775195	-123.03501		o	o									
	Dillon Creek	**DILL**	41.576099	-123.53879	o				o				o			
	Salmon River Hippo Rock	**SALM**	41.378490	-123.47554	o	o	o	o	o	o	o	o	o	o	o	o
	Trinity River Tish Tang	**TRTT**	41.021284	-123.63491					o	o	o			o	o	
	Trinity River Near Mouth	**TRMO**	41.184620	-123.70662		o	o	o	o	o	o	o	o	o	o	o

Study Sites

We sampled cyanobacteria at 15 sites in the Klamath River Watershed, including eight sites along the mainstem of the Klamath River between Iron Gate Dam and the Klamath River Estuary, and seven sites on tributaries, including the Scott, Salmon, and Trinity Rivers and Dillon Creek (Table 1). To the extent possible, we chose mainstem sites that were evenly spaced. In addition, we prioritized sites utilized by the public and that are established water quality monitoring sites by the Karuk, Yurok, Hoopa and Quartz Valley Tribes, including sites with long-term water quality sondes when possible.

Methods

In order to document patterns of cyanobacteria and anatoxin production throughout the summer, and at sites across the Middle and Lower Klamath Watershed, we assessed benthic cyanobacteria and anatoxin using multiple sample collection methods targeting benthic mats, river water, and transported algal material during the summer of 2021. Samples were analyzed for a suite of parameters to compare methods with respect to

feasibility and identification of methods most protective of public health.

Field Methods

Targeted benthic mat sampling

We conducted semi-quantitative surveys of wadeable river margins and collected composite samples from conspicuous algal mats at 10 - 14 sites monthly in July, August and September of 2021. From each river access point we surveyed an area of shoreline that was accessible by wading, and where benthic algae were visible given current water clarity conditions. Surveys consisted of walking either along the shoreline or in shallow river margins for 10 minutes. We documented the width and length of each survey area and composited up to 20 pinches of cyanobacterial mat material into a 60 mL amber glass jar to 40% full. Upon completion of the survey and mat sample collection effort we filled the jar with water to 80% full and placed the samples on ice. In addition, we qualitatively estimated conspicuous cyanobacteria mat cover using a scale of 0-3, where "0" indicated no conspicuous cyanobacteria mats, "1" indicated few isolated patches totaling less than 0.4 m^2, "2" indicated moderate cover between 0.4–2 m^2, and "3" indicated >2 m^2 of conspicuous cyanobacteria mat cover. We also recorded a qualitative description of the cyanobacteria conditions present at the site, including suspected taxa, associations with non-cyanobacteria taxa, river habitat occupied.

Disturbance sampling

Disturbance samples were taken to mimic increased water column levels of suspended algal material created when people wade into the river and dislodge benthic algal mats. We first agitated the algal material with our feet in an area of dense algae, and then collected a grab sample of dislodged, suspended materials in a 125 mL amber glass jar. At most sites we identified conspicuous cyanobacteria mats, and thus collected disturbance samples where these mats were present. At the few sites where we did not identify conspicuous mats, we collected disturbance samples from other types of dense algae to see if cyanobacteria cells and anatoxins were present in the absence of conspicuous cyanobacterial mats.

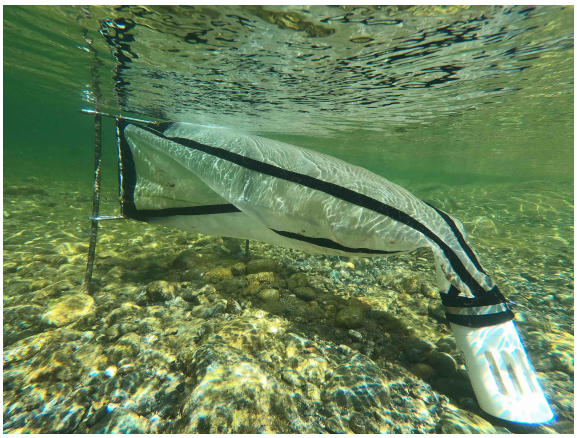


Figure 1. Algal drift net capturing coarse algal particles suspended in the water column

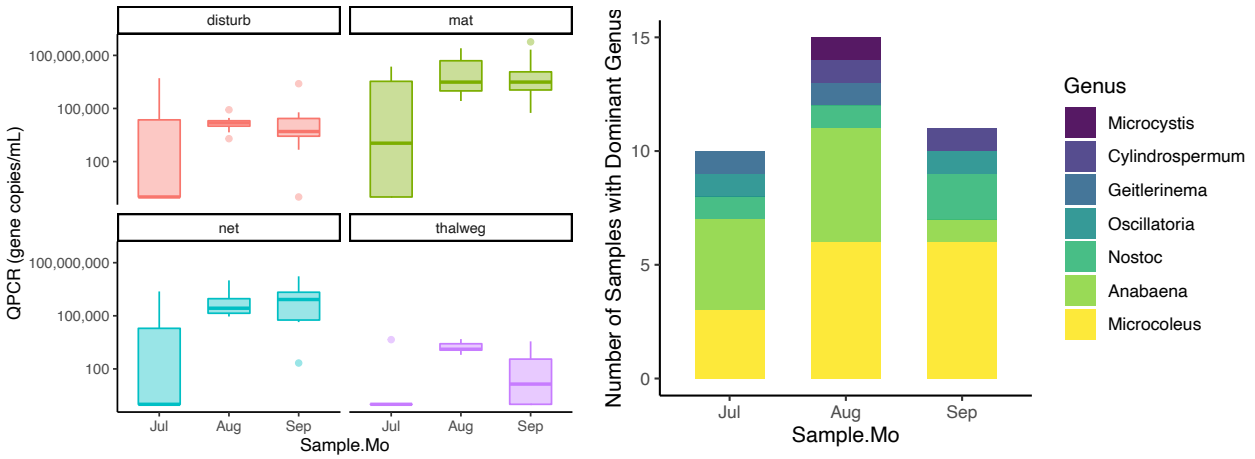
Water column and algal drift sampling

To estimate transported algal material, anatoxin, and the proportion of toxin-producing cyanobacteria, we sampled ambient water column conditions both instantaneously and over time via grab sampling and by employing drift nets at each site. We collected water column grab samples for indicators of cyanotoxin production from a well-mixed area of the water column in a 250 mL amber glass jars, and immediately transferred samples to a dark cooler.

To assess algal drift as a source of toxin export, we placed an invertebrate drift net in the current and secured the net with rebar stakes (Fig. 1). The net was deployed until enough drifting algal material was collected for analysis of both anatoxin and dry mass, which ranged from a few minutes to >30 minutes depending on quantity of algae suspended in the water column. We repeated the net deployment three times at a new location in the river during each deployment and composited the coarse algal material from the three deployments into a single jar, which was placed in a dark cooler until processing. Measurements of dry mass, paired with net deployment time and incoming velocity, which was recorded at three points in front of the net, will be used in subsequent analyses to calculate coarse particulate algal loads and anatoxins associated with those loads.

Lab Methods

We sent all sample types (net capture, composite mat, water column, and disturbance) to Bend Genetics for analysis of toxins, toxin production genes, and qualitative microscopy. Prior to sending the net samples for analysis of anatoxin and dry mass, we partitioned the samples after homogenizing the captured coarse particulates by cutting coarse material (primarily macrophytes and filamentous algae) into small pieces (1 cm) and then utilizing an immersion blender to further homogenize the sample. For each sample, we measured the total volume, partitioned 40 mL into an amber glass jar for toxin analysis, and reserved the remainder for analysis of dry mass. All samples were analyzed via QPCR for the anatoxin-production gene (AnaC gene), and were examined under a microscope for qualitative identification of dominant and subdominant taxa. Net samples, mat samples, and any other samples with QPCR results >10,000 AnaC gene copies/mL were also analysed for anatoxin concentration by ELISA.



(a). Box plots show median and ranges of AnaC gene copies by month for the four sample types collected

(b). Count of composite mat samples for each sampling event with colors showing the dominant taxa in each sample by month

Figure 2. AnaC gene copies in four sample types and dominant species in benthic cyanobacteria mat samples by month in the Klamath Watershed

Results

Spatial and Temporal Patterns

Of the 141 benthic cyanobacteria samples from 15 sites and three sampling efforts in the summer of 2021, cyanobacteria and associated anatoxins were present at all sites and months, with increasing coverage and toxin indicators later in the summer (Data Appendix, Fig. 2). Although we encountered conspicuous cyanobacteria mats during the majority of surveys, the extent of mat coverage and toxin indicators were higher in August and September than in July. Toxin-production genes were highest in August in all sample types, except the net samples, which were slightly higher in September (Fig. 2a). All mat samples collected in the field contained cyanobacteria, confirming that we were successful in field-identifying cyanobacteria. *Microcoleus* and *Anabaena* were the most common taxa in benthic mats, but five other taxa were at times found to be dominant in mat samples (Fig. 2b). *Microcystis* was the dominant cyanobacteria in one mat sample in August, but this was due to large numbers of planktonic cells settling out of the water column onto cyanobacteria mats where benthic species were sub-dominant in the sample.

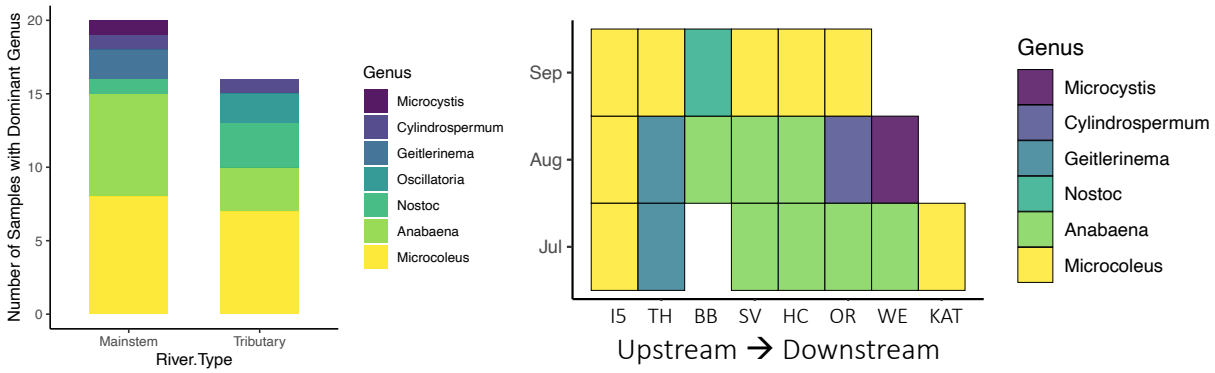
Spatial patterns of dominant cyanobacteria taxa and toxin production were generally weak. *Microcoleus* and *Anabaena* were commonly dominant in both the mainstem and tributary sites, although *Anabaena* was more commonly dominant at mainstem sites. *Ocillatoria* was only dominant at tributary sites, whereas *Microcystis* was only dominant at

Table 2. Anatoxin by ELISA (µg/L) from composite cyanobacteria mat samples at Klamath River and tributary sites. Mat samples in July were only analyzed by QPCR. Sites with two samples (TRMO and TRTT) were of different taxa observed at the same site. "ns" indicates that no mats were observed and sampled.

	Site Code	Anatoxin by ELISA (µg/L)	
		August	September
Klamath River Sites	I5	278.8	45.6
	TH	14.2	17.5
	BB	0.3	0.9
	SV	21.0	25.5
	HC	0.7	2227.5
	OR	4.1	710.4
	WE	0.8	ns
Tributary Sites	DILL	0.4	1.1
	SRIS	1584.5	6.3
	SRJB	16.1	17.9
	SALM	891.5	11.7
	TRMO (1)	204.2	0.4
	TRMO (2)	1.6	ns
	TRTT (1)	9302.0	ns
	TRTT (2)	1.4	ns

one mainstem site, associated with upstream transport and cell settling (Fig. 3a). In the mainstem of the Klamath River, *Microcoleus* was always the dominant taxa at the most upstream site, and was dominant at most sites during September. *Anabaena* was more common at sites lower on the river, but only in the July and August samples (Fig. 3b). Little is known about conditions favoring specific cyanobacteria taxa or toxin production, but the patterns observed in the Klamath provide opportunities for further study aimed at identifying the conditions that favor specific taxa and associated toxin-production dynamics.

As with dominant taxa, patterns in toxin indicators across the watershed were generally weak or overshadowed by temporal variability. AnaC gene copies were overall slightly higher in tributary than mainstem mat samples (Fig. 4a), but there was substantial overlap in gene copies between site types. Of the six samples with the highest anatoxin and AnaC gene copies, two were in the mainstem and four were in tributaries, including the Salmon, Trinity and Scott rivers. High toxins in tributary streams show that cyanotoxins are a risk not only in the mainstem of the Klamath River where most river users are aware of concerns associated with reservoir-sourced cyanotoxins (Table 2).

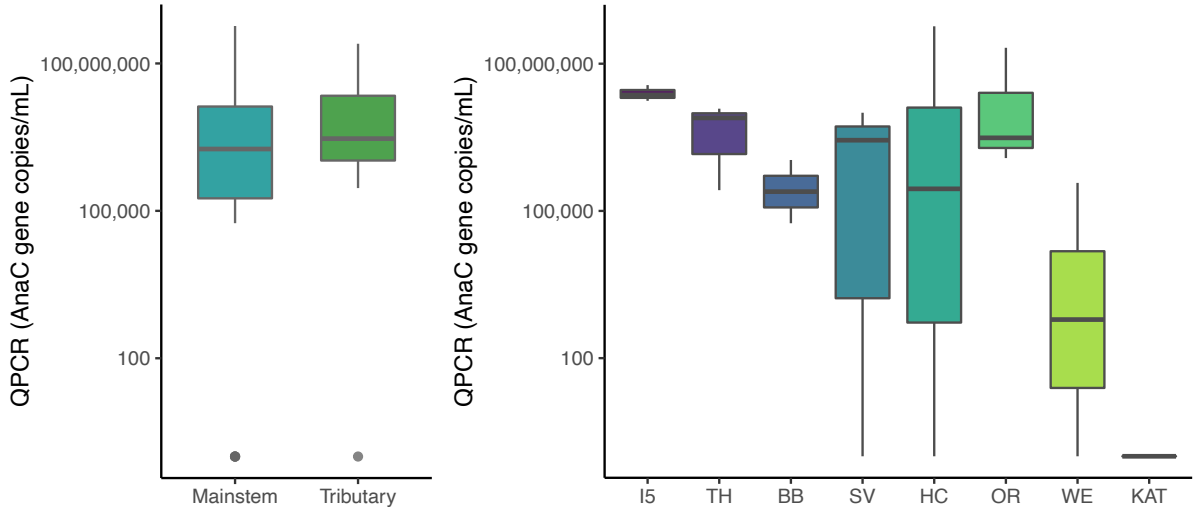


(a). Count of composite mat samples with colors indicating dominant taxa from the mainstem of the Klamath River and from tributaries.

(b). Dominant taxa by month and site in the Klamath River. KAT was only sampled in July, and white rectangles at BB and WE indicate no mats found during surveys.

Figure 3. Dominant taxa from composite mat samples for each sampling event

Similar to toxin production between mainstem and tributary sites, the Klamath River showed weak longitudinal patterns in toxin-production genes. Mat samples showed a decrease in AnaC gene copies in the most upriver three sites, but mid-river sites had a large range in gene copies and no trend in median gene copy concentrations (Fig. 4b). Gene copies from net, disturbance and thalweg samples did not show longitudinal trends, indicating that cyanobacteria growth and toxin-production dynamics may be tied to local conditions. Research investigating the drivers that promote cyanobacteria, specific taxa, and toxin production is needed to better predict where cyanobacteria and associated toxins will present water quality and public health concerns.



(a). AnaC gene copies from mainstem and tributary sites.

(b). AnaC gene copies from mainstem sites, shown from upriver to downriver

Figure 4. Box plots show median and ranges of AnaC gene copies

Informing Monitoring Methods

We compared field sampling techniques and lab analytical methods to consider what types of samples are logistically feasible and protective of public health. QPCR methods, which quantify the number of toxin-production genes in a sample and thus should represent the number cyanobacteria cells with toxin production capacity, were representative of toxin concretions measured by ELISA (Fig. 5). The adjusted r^2 of the slope of the log-log relationship was 0.70 considering all sample types, and 0.82 when only assessing the relation among the composite mat samples. Assessing this relationship on a log scale requires acknowledging a large range in absolute toxin and gene copy concentrations at high concentrations. However, due to the high level of heterogeneity of riverbed algae, toxin production, and environmental conditions that promote, dilute, and degrade toxins, both ELISA and QPCR results from benthic cyanobacteria should be viewed as indicators of risk, rather than absolute quantities. The relatively strong relationship between QPCR and toxin by ELISA indicates that the more affordable QPCR lab method can be used to inform toxicity of benthic mats. The increased affordability allows for greater spatial and temporal coverage of sampling, as well as the use of plastic bottles instead of the amber glass that is required in toxin samples.

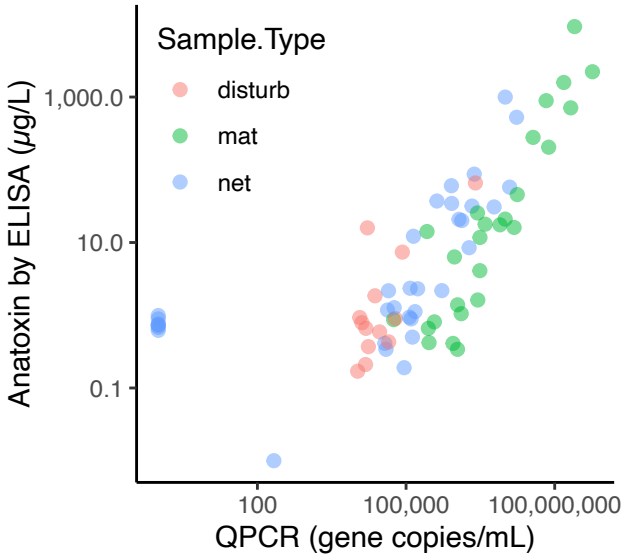


Figure 5. The log of anatoxin concentrations by the log of AnaC gene copies from a sample; colors indicate sample type (disturbance, composite mat, and net-capture).

In comparing four types of field samples, composite samples of conspicuous cyanobacteria mat material were the most protective of public health (i.e., they typically showed the highest concentrations) and were logistically feasible to collect. Although public health thresholds exist for toxin concentrations in water column samples, we found that water from the well-mixed water column was always low in anatoxin production genes (AnaC gene copies mean = 923, max = 4833), confirming that the well-mixed water generally presents a low risk of anatoxin exposure to river users, unless cyanobacterial material is suspended in the water column.

The drift net samples captured floating algal material in the water column, but by design were set to capture substantially more material than a river user or pet would be exposed to. However, these samples can be scaled and used to predict the likelihood that a swimmer would encounter toxins from suspended cyanobacteria. Additionally, drift net samples capture a mixed sample of what is floating in the water both near the site and from upstream, thus capturing material from a much larger area than what can be surveyed from shore. Of multiple sites sampled where no benthic mats were visible, we found toxins to be present in the drift nets, indicating upstream presence of mats. Drift nets may be especially useful early in the season to indicate the onset of benthic proliferations. Because drift nets need to be set in an area of flowing water and to sit for up to 30 minutes, they may be more challenging to deploy as part of currently scheduled site visits.

Mat samples consistently had the highest toxin concentrations and were reflective of paired disturbance samples taken at the same sampling location (Fig. 6). Mat samples represent a realistic "worst-case" exposure because they are present along shorelines, including in calm pools where parents may be comfortable allowing children to play and where dogs wade and drink, allowing both of these vulnerable groups access to play with and possibly ingest these anatoxin-containing mats. Understanding the worst-case

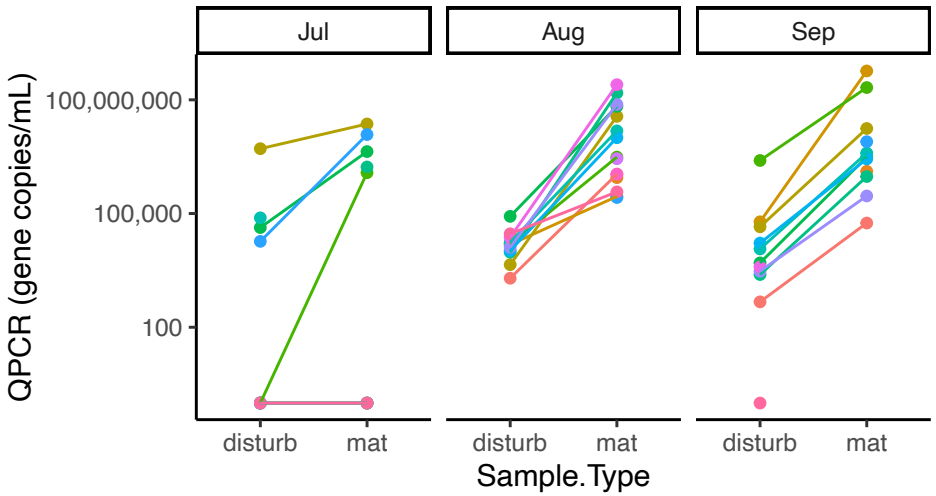


Figure 6. Disturbance samples with paired mat samples from from the same site and sampling day.

scenario and communicating this risk to the public will help mitigate the health risk associated with anatoxin exposure.

Conclusions

Benthic cyanobacteria and associated anatoxins were widespread in the Klamath River Watershed in summer 2021. We collected 141 samples from 15 sites during three sampling efforts on the Klamath River and tributaries. Benthic cyanobacteria and indicators of anatoxin were found at all sites and sampling efforts. Cyanobacteria extent and toxin indicators were higher in August and September than in July, but the extent of mat coverage, toxin-production genes, toxin concentrations, and patterns in dominant taxa were variable among sites, making predicting occurrence of toxins difficult. The Salmon and Trinity Rivers, generally considered to have good water quality compared to the Klamath River, had high anatoxins, indicating that future sampling and public health messaging should include tributary streams of high water quality.

Continued surveying and sampling for benthic cyanobacteria will add to current understanding of their extent and the risk they pose to public health. Selecting sampling methods most likely to result in positive detections will help efficiently use sampling resources. Despite a history of sampling the water column for anatoxin, anatoxin in the water column was always low compared to other sample types and thus not the most protective indicator of public health risk. Drift nets, set to capture coarse particles of sloughed algae transported in the water column, required more survey effort but reflected

toxins from sloughed algae from an area upstream which could not easily be surveyed otherwise. These drift net samples could be used early in the season to trigger more thorough search efforts once anatoxin detections rise in these samples. Although disturbance samples reflected benthic cyanobacteria mats samples at a site, they were always lower due to not being concentrated. Thus, composite samples of conspicuous cyanobacteria mats, which can easily be eaten by a dog or accessed by children, provided the most protective measure of public health risk at a site. Quantitative PCR methods, which assess the number of toxin-production genes in a sample, were reflective of toxin concentrations and are less costly to process, suggesting that QPCR lab analysis is a good option when sampling resources need to be extended to more sites.

Although benthic cyanobacteria is a naturally occurring part of the algal community, they can become a problem for water quality and public health when proliferations become extensive and produce anatoxin. Due to the widespread documentation of benthic cyanobacteria and anatoxin in the Klamath River in the summer of 2021, more sampling should be conducted to inform public health messaging, to better understand the extent of toxin-producing proliferations, and to understand the conditions driving cyanobacteria and toxin production in the Klamath River and tributaries.

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Sample.ID	Date	Site	Sample.Type	ELISA	QPCR	Dominant	Sub.Dominant	Also.Present
(site.day.mo.samp)	(yyyy-mm-dd)			(µg/L)	(copies/mL)	(genus)	(genus)	(genus)
BB0507DIST	2021-07-05	BB	disturb	NA	nd	nd	nd	nd
BB0507NET	2021-07-05	BB	net	0.75	nd	nd	nd	nd
BB0507THAL	2021-07-05	BB	thalweg	NA	nd	nd	nd	nd
DIL0407MAT	2021-07-04	DILL	mat	NA	nd	Nostoc	nd	nd
HC0407DIST	2021-07-04	HC	disturb	NA	nd	Microcoleus	Oscillatoria	nd
HC0407MAT	2021-07-04	HC	mat	NA	nd	Anabaena	Microcystis	nd
HC0407NET	2021-07-04	HC	net	0.89	nd	nd	nd	nd
HC0407THAL	2021-07-04	HC	thalweg	NA	nd	nd	nd	nd
I50507DIST	2021-07-05	I5	disturb	NA	5136658	Microcoleus	Microcystis	Oscillatoria
I50507MAT	2021-07-05	I5	mat	NA	23097094	Microcoleus	Oscillatoria	Microcystis
I50507MATWAT	2021-07-05	I5	mat-water	nd	nd	nd	nd	nd
I50507NET	2021-07-05	I5	net	0.99	nd	nd	nd	nd
I50507THAL	2021-07-05	I5	thalweg	NA	nd	nd	nd	nd
KAT0307DIST	2021-07-03	KAT	disturb	NA	nd	nd	nd	nd
KAT0307MAT	2021-07-03	KAT	mat	NA	nd	Microcoleus	nd	nd
KAT0307MATWAT	2021-07-03	KAT	mat-water	nd	nd	nd	nd	nd
KAT0307NET	2021-07-03	KAT	net	0.72	nd	Microcoleus	nd	nd
KAT0307THAL	2021-07-03	KAT	thalweg	NA	nd	nd	nd	nd
OR0407DIST	2021-07-04	OR	disturb	NA	nd	Anabaena	nd	nd
OR0407MAT	2021-07-04	OR	mat	NA	1194301	Anabaena	nd	nd
OR0407MATWAT	2021-07-04	OR	mat-water	nd	nd	nd	nd	nd
OR0407NET	2021-07-04	OR	net	2.18	528505	nd	nd	nd
OR0407THAL	2021-07-04	OR	thalweg	NA	4498	nd	nd	nd
SAL0407DIST	2021-07-04	SALM	disturb	NA	42635	nd	nd	nd
SAL0407MAT	2021-07-04	SALM	mat	NA	4316411	Microcoleus	Oscillatoria	nd
SAL0407NET	2021-07-04	SALM	net	87.08	2379221	Microcoleus	nd	nd
SAL0407THAL	2021-07-04	SALM	thalweg	NA	nd	nd	nd	nd
SCM0507DIST	2021-07-05	SRMO	disturb	NA	nd	Geitlerinema	Oscillatoria	nd
SCM0507THAL	2021-07-05	SRMO	thalweg	NA	nd	nd	nd	nd
SJB0507DIST	2021-07-05	SRJB	disturb	NA	76948	nd	nd	nd
SJB0507THAL	2021-07-05	SRJB	thalweg	NA	nd	nd	nd	nd

Sample.ID	Date	Site	Sample.Type	ELISA	QPCR	Dominant	Sub.Dominant	Also.Present
SRIS0507CHUNK	2021-07-05	SRIS	chunk	NA	3609761	Oscillatoria	Geitlerinema	nd
SRIS0507MAT	2021-07-05	SRIS	mat	NA	1693346	Oscillatoria	Microcoleus	nd
SRIS0507MATWAT	2021-07-05	SRIS	mat-water	nd	nd	Oscillatoria	nd	nd
SV0507DIST	2021-07-05	SV	disturb	NA	nd	nd	nd	nd
SV0507MAT	2021-07-05	SV	mat	NA	nd	Anabaena	nd	nd
SV0507NET	2021-07-05	SV	net	0.75	nd	nd	nd	nd
SV0507THAL	2021-07-05	SV	thalweg	NA	nd	nd	nd	nd
TH0507DIST	2021-07-05	TH	disturb	NA	18446	Geitlerinema	nd	nd
TH0507MAT	2021-07-05	TH	mat	NA	12119550	Geitlerinema	Microcoleus	nd
TH0507NET	2021-07-05	TH	net	0.68	nd	nd	nd	nd
TH0507THAL	2021-07-05	TH	thalweg	NA	nd	Geitlerinema	nd	nd
TR0407DIST	2021-07-04	TRMO	disturb	NA	nd	Anabaena	Microcystis	nd
TR0407NET	2021-07-04	TRMO	net	8.48	1875283	Nostoc	Microcoleus	nd
TR0407THAL	2021-07-04	TRMO	thalweg	NA	nd	Microcoleus	nd	nd
WE0407DIST	2021-07-04	WE	disturb	NA	nd	Anabaena	nd	nd
WE0407MAT	2021-07-04	WE	mat	NA	nd	Anabaena	Microcoleus	nd
WE0407MATWAT	2021-07-04	WE	mat-water	NA	nd	Anabaena	Microcystis	nd
WE0407NET	2021-07-04	WE	net	0.62	nd	nd	nd	nd
WE0407THAL	2021-07-04	WE	thalweg	NA	nd	Anabaena	nd	nd
BB0208BLEND	2021-08-02	BB	blend	0.34	39446	Microcystis	Microcoleus	nd
BB0208DIST	2021-08-02	BB	disturb	NA	1965	Microcystis	nd	nd
BB0208MAT	2021-08-02	BB	mat	0.34	1091667	Anabaena	Microcystis	nd
BB0208NET	2021-08-02	BB	net	0.19	91501	Microcystis	nd	nd
BB0208THAL	2021-08-02	BB	thalweg	NA	1149	Microcystis	nd	nd
DIL0408MAT	2021-08-04	DILL	mat	0.41	885772	Anabaena	Microcoleus	nd
HC0208BLEND	2021-08-02	HC	blend	2.35	120956	Microcystis	Microcoleus	nd
HC0208DIST	2021-08-02	HC	disturb	0.21	15207	Microcystis	nd	nd
HC0208MAT	2021-08-02	HC	mat	0.66	281783	Anabaena	Microcystis	Microcoleus
HC0208NET	2021-08-02	HC	net	2.31	171530	Anabaena	Fisherella	Microcoleus
HC0208THAL	2021-08-02	HC	thalweg	NA	623	Microcystis	nd	nd
I50108BLEND	2021-08-01	I5	blend	1.18	42248	Microcystis	nd	nd
I50108DIST	2021-08-01	I5	disturb	NA	4478	Microcystis	nd	nd

Sample.ID	Date	Site	Sample.Type	ELISA	QPCR	Dominant	Sub.Dominant	Also.Present
I50108MAT	2021-08-01	I5	mat	278.8	36631823	Microcoleus	Oscillatoria	Kamptonema
I50108NET	2021-08-01	I5	net	0.5	134473	Microcystis	nd	nd
I50108THAL	2021-08-01	I5	thalweg	NA	1158	Microcystis	nd	nd
OR0308DIST	2021-08-03	OR	disturb	0.66	15496	Microcystis	Cylindrospermum	Microcoleus
OR0308MAT	2021-08-03	OR	mat	4.1	3085672	Cylindrospermum	Microcystis	Microcoleus
OR0308NET	2021-08-03	OR	net	37.17	419689	Microcystis	Microcoleus	Oscillatoria
OR0308THAL	2021-08-03	OR	thalweg	NA	2639	Microcystis	nd	nd
SAL0308DIST	2021-08-03	SALM	disturb	7.37	84160	Microcoleus	Oscillatoria	Anabaena
SAL0308MAT	2021-08-03	SALM	mat	891.5	67278662	Microcoleus	Anabaena	nd
SAL0308NET	2021-08-03	SALM	net	999.2	10046817	Microcoleus	nd	nd
SAL0308THAL	2021-08-03	SALM	thalweg	NA	4618	nd	nd	nd
SJB0208DIST	2021-08-02	SRJB	disturb	0.37	17380	Microcoleus	nd	nd
SJB0208MAT	2021-08-02	SRJB	mat	16.11	15160230	Microcoleus	Oscillatoria	Kamptonema
SJB0208NET	2021-08-02	SRJB	net	20.04	1333286	Microcoleus	Oscillatoria	nd
SJB0208THAL	2021-08-02	SRJB	thalweg	NA	1409	nd	nd	nd
SRIS0208DIST	2021-08-02	SRIS	disturb	NA	9530	Microcoleus	Oscillatoria	nd
SRIS0208MAT	2021-08-02	SRIS	mat	1584.5	152381994	Microcoleus	Cylindrospermum	Oscillatoria
SV0208DIST	2021-08-02	SV	disturb	0.17	10541	Microcystis	nd	nd
SV0208MAT	2021-08-02	SV	mat	20.97	10021033	Anabaena	Microcoleus	Oscillatoria
TH0108MAT	2021-08-01	TH	mat	14.15	264854	Geitlerinema	Microcystis	Microcoleus
TR0408DIST	2021-08-04	TRMO	disturb	0.79	12856	Anabaena	Microcoleus	Oscillatoria
TR0408MAT-ANAB	2021-08-04	TRMO	mat	1.62	2803646	Nostoc	Microcoleus	Oscillatoria
TR0408MAT-PHOR	2021-08-04	TRMO	mat	204.2	75547836	Microcoleus	Anabaena	nd
TR0408NET	2021-08-04	TRMO	net	60.36	822513	Microcoleus	Anabaena	Microcystis
TR0408THAL	2021-08-04	TRMO	thalweg	NA	4833	nd	nd	nd
TTTR0308DIST	2021-08-03	TRTT	disturb	1.85	23609	Microcoleus	Anabaena	Kamptonema
TTTR0308MAT-ANAB	2021-08-03	TRTT	mat	1.39	1097229	Anabaena	Cylindrospermum	Microcystis
TTTR0308MAT-PHOR	2021-08-03	TRTT	mat	9302	251730853	Microcoleus	nd	nd
TTTR0308THAL	2021-08-03	TRTT	thalweg	NA	794	nd	nd	nd
WE0408DIST	2021-08-04	WE	disturb	0.59	29242	Microcystis	Microcoleus	Anabaena
WE0408MAT	2021-08-04	WE	mat	0.81	372832	Microcystis	Nostoc	nd
WE0408NET	2021-08-04	WE	net	12.19	140865	Nostoc	Microcoleus	nd

Sample.ID	Date	Site	Sample.Type	ELISA	QPCR	Dominant	Sub.Dominant	Also.Present
WE0408THAL	2021-08-04	WE	thalweg	NA	1290	Microcystis	nd	nd
BB1009BLEND	2021-09-10	BB	blend	0.41	37351	Microcoleus	nd	nd
BB1009DIST	2021-09-10	BB	disturb	NA	467	Microcystis	nd	nd
BB1009MAT	2021-09-10	BB	mat	0.87	56126	Nostoc	Microcystis	Microcoleus
BB1009NET	2021-09-10	BB	net	nd	215	Microcystis	Microcoleus	nd
BB1009THAL	2021-09-10	BB	thalweg	NA	nd	Microcystis	nd	nd
DIL1209MAT	2021-09-12	DILL	mat	1.05	1298129	Anabaena	Cylindrospermum	Microcystis
HC1109DIST	2021-09-11	HC	disturb	0.9	60547	Microcoleus	Geitlerinema	nd
HC1209BLEND	2021-09-12	HC	blend	57.73	12307528	Microcoleus	nd	nd
HC1209MAT	2021-09-12	HC	mat	2227.5	578067098	Microcoleus	Microcystis	Oscillatoria
HC1209NET	2021-09-12	HC	net	30.85	5992328	Microcoleus	nd	nd
HC1209THAL	2021-09-12	HC	thalweg	NA	1127	Microcystis	Microcoleus	nd
I51009BLEND	2021-09-10	I5	blend	0.89	126312	nd	nd	nd
I51009DIST	2021-09-10	I5	disturb	0.43	44623	Microcoleus	Microcystis	nd
I51009MAT	2021-09-10	I5	mat	45.58	17536960	Microcoleus	Microcystis	nd
I51009NET	2021-09-10	I5	net	1.12	151726	Microcystis	Microcoleus	nd
I51009THAL	2021-09-10	I5	thalweg	NA	375	Microcystis	Microcoleus	nd
OR1109DIST	2021-09-11	OR	disturb	65.87	2510040	Nostoc	Cylindrospermum	Microcoleus
OR1109MAT	2021-09-11	OR	mat	710.4	210927093	Microcoleus	Cylindrospermum	Microcystis
OR1109NET	2021-09-11	OR	net	526.7	17014522	Microcoleus	nd	nd
OR1109THAL	2021-09-11	OR	thalweg	NA	3598	Microcystis	Kamptonema	nd
SAL1109DIST	2021-09-11	SALM	disturb	NA	4982	Microcoleus	nd	nd
SAL1109MAT	2021-09-11	SALM	mat	11.73	3099565	Cylindrospermum	Microcoleus	Microcystis
SAL1109NET	2021-09-11	SALM	net	20.83	1168623	Microcoleus	Oscillatoria	nd
SAL1109THAL	2021-09-11	SALM	thalweg	NA	310	nd	nd	nd
SJB1209DIST	2021-09-12	SRJB	disturb	0.93	11644	Microcoleus	nd	nd
SJB1209MAT	2021-09-12	SRJB	mat	17.86	3944430	Nostoc	Microcoleus	Cylindrospermum
SJB1209NET	2021-09-12	SRJB	net	31.68	2143913	Microcoleus	nd	nd
SJB1209THAL	2021-09-12	SRJB	thalweg	NA	nd	nd	nd	nd
SRIS1209DIST	2021-09-12	SRIS	disturb	NA	2457	Oscillatoria	Microcoleus	nd
SRIS1209MAT	2021-09-12	SRIS	mat	6.33	947154	Oscillatoria	Microcoleus	Anabaena
SV1109MAT	2021-09-11	SV	mat	25.48	2760999	Microcoleus	Microcystis	nd

Sample.ID	Date	Site	Sample.Type	ELISA	QPCR	Dominant	Sub.Dominant	Also.Present
SV1209BLEND	2021-09-12	SV	blend	0.94	116600	Microcoleus	nd	nd
SV1209DIST	2021-09-12	SV	disturb	15.9	16612	Microcoleus	Microcystis	Geitlerinema
SV1209NET	2021-09-12	SV	net	1.27	57646	Microcoleus	nd	nd
SV1209THAL	2021-09-12	SV	thalweg	NA	nd	Microcystis	Microcoleus	nd
TH1009MAT	2021-09-10	TH	mat	17.5	7856874	Microcoleus	Microcystis	Anabaena
TR1109DIST	2021-09-11	TRMO	disturb	NA	3003	Tolypothrix	Microcoleus	Microcystis
TR1109MAT	2021-09-11	TRMO	mat	0.42	290680	Microcoleus	nd	nd
TR1109NET	2021-09-11	TRMO	net	2.17	44225	Tolypothrix	Microcoleus	nd
TR1109THAL	2021-09-11	TRMO	thalweg	NA	nd	nd	nd	nd
TTTR1109DIST	2021-09-11	TRTT	disturb	NA	3899	Tolypothrix	Microcoleus	Microcystis
TTTR1109THAL	2021-09-11	TRTT	thalweg	NA	nd	nd	nd	nd
WE1109DIST	2021-09-11	WE	disturb	NA	nd	Microcystis	nd	nd
WE1109NET	2021-09-11	WE	net	34.47	832799	Microcystis	nd	nd
WE1109THAL	2021-09-11	WE	thalweg	NA	193	Microcystis	nd	nd