



Sediment bacteria in an urban stream: Spatiotemporal patterns in community composition



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ARTICLE INFO

Article history:

Received 31 October 2017

Received in revised form

4 January 2018

Accepted 20 January 2018

Keywords:

Bacterial community composition

Urban drainage

WWTPs

Spatiotemporal effects

Streams

ABSTRACT

Sediment bacterial communities play a critical role in biogeochemical cycling in lotic ecosystems. Despite their ecological significance, the effects of urban discharge on spatiotemporal distribution of bacterial communities are understudied. In this study, we examined the effect of urban discharge on the spatiotemporal distribution of stream sediment bacteria in a northeast Ohio stream. Water and sediment samples were collected after large storm events (discharge > 100 m) from sites along a highly impacted stream (Tinkers Creek, Cuyahoga River watershed, Ohio, USA) and two reference streams. Although alpha (α) diversity was relatively constant spatially, multivariate analysis of bacterial community 16S rDNA profiles revealed significant spatial and temporal effects on beta (β) diversity and community composition and identified a number of significant correlative abiotic parameters. Clustering of upstream and reference sites from downstream sites of Tinkers Creek combined with the dominant families observed in specific locales suggests that environmentally-induced species sorting had a strong impact on the composition of sediment bacterial communities. Distinct groupings of bacterial families that are often associated with nutrient pollution (i.e., *Comamonadaceae*, *Rhodobacteraceae*, and *Pirellulaceae*) and other contaminants (i.e., *Sphingomonadaceae* and *Phyllobacteriaceae*) were more prominent at sites experiencing higher degrees of discharge associated with urbanization. Additionally, there were marked seasonal changes in community composition, with individual taxa exhibiting different seasonal abundance patterns. However, spatiotemporal variation in stream conditions did not affect bacterial community functional profiles. Together, these results suggest that local environmental drivers and niche filtering from discharge events associated with urbanization shape the bacterial community structure. However, dispersal limitations and interactions among other species likely play a role as well.

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1. Introduction

Urban discharge, consisting of stormwater run-off (SWR) and wastewater treatment plant (WWTP) effluent, is among the greatest source of diffuse pollution of surface waters (Paul and Meyer, 2001), including nutrients (PO₄-P and ammonia [NH₄-N]), carbon (Carey and Migliaccio, 2009), bacteria, organic pollutants, road salt, suspended solids, and metals (Gilliom et al., 2006; Lewis et al., 2007; Paul and Meyer, 2001; Poff et al., 2006; Wenger et al., 2009). Chemical degradation of these water bodies can have a negative effect on lotic ecosystem function, resulting in reduced nutrient retention efficiency, decreased biological diversity, and

increased dominance of pollution-tolerant species (reviewed by House et al., 1993; Roy et al., 2014). Additionally, the altered hydrological regime and geomorphic adjustment from WWTPs and SWR can scour streambeds and increase erosion (Walsh et al., 2005), reducing habitat quality and altering ecosystem dynamics (Konrad et al., 2005; Roy et al., 2008). Although the severity of hydrogeomorphic (Fitzpatrick and Peppler, 2010), chemical (Beaulieu et al., 2014), and biological (Bryant and Carlisle, 2012) alterations from urban discharge depends on spatial and temporal differences within catchments, the overall effects on aquatic ecosystems are well documented (Coles et al., 2004; Cuffney et al., 2005; Paul and Meyer, 2001; Walker and Pan, 2006; Wenger et al., 2009). Thus, urban discharge can constitute as an environmental filter that potentially impacts benthic bacterial communities.

Benthic bacterial communities perform important functions in lotic ecosystems, such as biodegradation and biogeochemical

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cycling (Zeglin, 2015), and thus are ideal candidates for monitoring ecological effects of urban discharge on functional characteristics of aquatic environments (Lear et al., 2009). Additionally, stream benthic bacteria are highly responsive to changes in the environment; they are the first to interact with dissolved substances and can be severely impacted by perturbations (Ancion et al., 2010; Beaulieu et al., 2014; Paerl et al., 2014). As a result of their fast growth rates and responses to small physical and chemical changes (Schwermer et al., 2008; Paerl et al., 2014), benthic bacterial community composition may differ temporally and spatially (i.e. longitudinally within a stream or among different streams) in response to environmental stimuli from urban discharge.

Overall, urban discharge impacts sediment bacterial communities in lotic ecosystems, and these impacts are spatiotemporally variable (Fisher et al., 2015; Drury et al., 2013; Newton et al., 2013; Parent-Raoult et al., 2008; Parent-Raoult and Boisson, 2007; Perryman et al., 2011). Yet, the majority of studies that have focused on microbial communities in urban aquatic ecosystems have studied the effects of urbanization on microbial-mediated nutrient cycling (Claessens et al., 2010; Groffman et al., 2004; Harbott and Grace, 2005; Imberger et al., 2008; Merbt et al., 2015; Perryman et al., 2008, 2011; Rosa et al., 2013) or sewage-derived bacteria (Baudart et al., 2000; Cha et al., 2010; Chigbu et al., 2004; Chu et al., 2014). Effects of urban discharge on native bacterial communities have largely been ignored (Gosset et al., 2016). In this study, urban discharge impacts on spatiotemporal variation in benthic bacterial community composition and environmental drivers were examined in Tinkers Creek—a tributary of the Cuyahoga River in Northeast Ohio (USA). Effluent from WWTPs constitutes up to ~80% of streamflow in Tinkers Creek (Tertuliani et al., 2008) and input from nonpoint sources causes increased turbidity and sedimentation after heavy rain events (Ohio EPA, 2003). As a result, the stream is exposed to a wide range of physicochemical variation and various sources of inorganic and organic contamination.

Along the length of Tinkers Creek, the extent of urban land use and the number of WWTPs increases with distance from the headwaters; physicochemical conditions were expected to reflect this pattern through higher nutrient loads and greater conductivity downstream (Tertuliani et al., 2008). We hypothesized there would be a longitudinal decrease in bacterial richness (α -diversity) concurrently with the urban gradient and that there would be high compositional dissimilarity (β -diversity) between Tinkers Creek and two reference streams. Further, we hypothesized that the urbanization gradient reflected in Tinkers Creek physicochemistry would result in increased compositional dissimilarity between upstream and downstream sites and that these changes would be reflected by fluctuations in specific functional traits. Additionally, we anticipated that seasonal variability in stream physicochemical parameters would result in a successional change in community composition over the course of the sampling season. Specifically, prior studies have shown seasonal fluctuations in temperature (Boyer et al., 2011; Sliva and Williams, 2005; Zhang et al., 2012), nutrient concentrations (Dodds et al., 2002; Gessner and Chauvet, 1994; Findlay and Sinsabaugh, 2003), and streamflow (Chiaromonte et al., 2013; Fazi et al., 2013; Sliva and Williams, 2005; Valett et al., 1997; Zoppini et al., 2010) to be selective forces for the temporal shifts observed in microbial communities.

2. Methods

2.1. Study site

Tinkers Creek, a 7th-order stream, drains a 250 km² watershed with a rural/agriculture to an urban land cover gradient that spans the length of the stream (Tertuliani et al., 2008). A small percentage

(0.3%) of the watershed is classified as agricultural land use, while >70% is classified as commercial/industrial/transportation and residential, and 25.5% as wetlands, grasslands/pasture or forest (Tertuliani et al., 2008). The stream's flow is highly influenced by discharge from 8 WWTPs (Fig. S1) and stormwater run-off. The five sites selected for sampling were chosen to represent a wide range of physicochemical parameters and various sources of inorganic and organic contamination (Tertuliani et al., 2008), with only the most upstream site not receiving WWTP effluent. Qualitatively, substrate composition differed along Tinkers Creek, with silt/sand occurring at the most upstream locations, which shifted to pebbles/cobbles at downstream sampling locations. Additionally, single sampling sites were established in Furnace Run and Yellow Creek, 4th and 3rd-order tributaries of the Cuyahoga River, respectively, to serve as reference sites. Both streams are tributaries of the Cuyahoga River, and their watersheds are less developed compared to that of Tinkers Creek, and they lack WWTPs (Tertuliani et al., 2008; Table S1). Both streams meet biocriteria for attainment as specified by the Ohio Water Quality Standards (WQS; Ohio Administrative Code Chapter 3745-1) and Ohio EPA biological criteria (OAC Rule 3745-1-07; Ohio Environmental Protection Agency, 2003). In contrast, Tinkers Creek is impaired based on these metrics, with significant departures from biocriteria for fish and invertebrate communities.

2.2. Sample collection

Water (125 mL) and sediment (100 g) samples (N = 3) were collected from each of the seven study sites after large rain events (discharge > 100 m³/s; USGS discharge gauge at site 5 in Tinkers Creek) in October and November of 2012, and in April, May, June, July, August and September of 2013. Sampling after large rain events was performed so as to achieve maximum levels of urban discharge from WWTPs and stormwater. Samples were stored on ice for transport to the lab. Water samples were collected in polypropylene acid washed bottles. Sediments (top 10 cm) were collected with a scoop, homogenized, and divided into subsamples for nutrient analysis and DNA extraction. All samples were collected following standard USGS field collection procedures (Wagner et al., 2006).

2.3. Physicochemical variables

Dissolved oxygen (DO), conductivity, redox potential, pH, and turbidity were measured using a Hqd/IntelliCAL Rugged Field kit (Hach Company, Loveland, CO) and Hach turbidimeter model 2100P, respectively, during sample collection. Additionally, flow velocity (portable water flow meter model 201; Marsh-McBirney, Inc), and water depth and width were used to calculate discharge.

Surface water was sub-sampled, filtered and acidified as appropriate before analysis. Dissolved organic carbon (DOC) and dissolved total nitrogen (TN) were measured from 50 mL subsamples using a Shimadzu TOC/TN analyzer (Eaton et al., 2005). Soluble reactive phosphorus (SRP) was determined from 50 mL subsamples following Eaton et al. (2005), while dissolved ammonium (NH₄⁺-N), nitrate (NO₃⁻-N), and nitrite (NO₂⁻-N) were measured from 15 mL subsamples colorimetrically via a modified microplate analysis (Hood-Nowotny et al., 2010; Weatherburn, 1967).

For determination of nutrient content in sediments, subsamples (20 g) were treated with a 0.5M K₂SO₄ solution (1:5 ratio [soil: 0.5M K₂SO₄]) (Ettema et al., 1999), filtered, and nitrogen and P concentrations were measured colorimetrically as above (Eaton et al., 2005; Hood-Nowotny et al., 2010; Weatherburn, 1967). Benthic organic matter (BOM) was measured via combustion on 5 g sub-

samples of fresh sediments; percent organic matter was calculated based on the ratio of ash-free dry mass and dry mass.

2.4. Bacterial community composition

DNA from stream sediment samples was extracted using PowerSoil DNA Isolation Kits following the manufacturer's instructions (MoBio Laboratories, Carlsbad, CA). Bacterial community composition was assessed using Terminal Restriction Length Polymorphism (T-RFLP) of the 16S rRNA gene as described in Blackwood et al. (2003). PCR used primers Eub338F-0-II and Eub338F-I-III (forward), which were labeled at the 5' termini with 6-carboxyfluorescein (6-FAM, Integrated Technologies) and 1392R (reverse) (Blackwood et al., 2003). Each reaction contained 0.5 μ M of each primer, 400 ng BSA (New England Biolabs, Ipswich, MA), and approximately 10 ng of total DNA in 30 μ l reaction volumes. Thermal cycling conditions were as follows: 1 cycle at 95 °C for 3 min followed by 40 cycles at 94 °C for 30s, 57 °C for 30s, and 72 °C for 1 min 30s, and 1 cycle at 72 °C for 7 min. PCR products were pooled from three reactions per sample and digested with endonuclease HhaI (New England Biolabs). Digested products were cleaned using E.Z.N.A DNA probe cleanup kit (Omega bio-tek, Norcross, Georgia) and were separated by automated capillary electrophoresis (3730 DNA analyzer; Applied Biosystems, Foster City, CA) at The Ohio State Plant-Microbe Genomics Facility to produce a community profile. Analysis of T-RFLP reads generated was performed with T-REX software (Culman et al., 2009), T-RFLPs were processed to remove peak noise and to align fragments before further analysis in R (see below).

Given that redundancy analysis of T-RFLPs revealed spatial and temporal differences (but no interaction effect) in bacterial communities, samples were pooled and subjected to 16S rRNA gene sequencing. DNA concentrations were standardized (10 ng μ L⁻¹) and pooled by sampling location (samples were pooled across sampling dates for each site) and sampling date (samples were pooled across sites for each date). The V4-V5 hypervariable region of 16S rRNA genes was sequenced at The Ohio State Molecular and Cellular imaging center, via Illumina Miseq sequencing technology. iTags generated were processed in the QIIME pipeline v1.9.1 (Caporaso et al., 2010). Paired forward and reverse reads with ambiguities, homopolymers, as well as low-quality scores were removed using QCing in QIIME. Reads were then assembled into single contigs or iTags via PANDASeq (Masella et al., 2012). iTag primer sequences and barcodes were subsequently eliminated, contigs were edited to a uniform length of 250 bp, and then chimeric reads detected and removed with USEARCH v 6.1 (Edgar, 2010). Quality-filtered contigs were then processed using the de novo and reference-based OTU clustering platforms in QIIME, and based on a >97% similarity to 16SrRNA sequences in the Greengenes reference database (Version 13.8) were assigned to operational taxonomic units (OTUs). Singletons were removed, and results were summarized at the phylum and family levels. Reads occurring in more than two samples with relative abundances greater than 1% were retained for α - and β -diversity analyses. Reads were then rarefied to 14,648 sequences per sample and used in further analysis.

PICRUSt (Langille et al., 2013) was used to predict functional characteristics of stream bacterial populations. PICRUSt utilized associations between 16S rRNA gene markers found in the Greengenes database and functional genes found in the Kyoto Encyclopedia of Genes and Genomes (KEGG) database to reconstruct potential functional gene families present in the sampled communities. De novo OTUs were removed and the remaining OTUs were normalized to create a closed reference OTU table consisting of samples with Greengenes IDs which were then used to predict

metagenomics functional profiles. To compare differences in the functional profiles of communities among sampling sites and dates, the relative abundance of predicted KEGG Orthologs (KOs) were examined across three tiers of increasing functional resolution (tiers 1–3). KOs associated with tier 1 functions “organismal systems” and “human disease” were considered irrelevant to environmental samples and were discarded prior to further analysis. Accession numbers: Tinkers Creek Site 1: SAMN08245559; Tinkers Creek Site 2: SAMN08245560; Tinkers Creek Site 3: SAMN08245561; Tinkers Creek Site 4: SAMN08245562; Tinkers Creek Site 5: SAMN08245563; Reference Site Yellow Creek: SAMN08245564; Reference Site Furnace Run: SAMN08245565; April_pooled: SAMN08245566; May_pooled: SAMN08245567; June_pooled: SAMN08245568; July_pooled: SAMN08245569; August_pooled: SAMN08245570; September_pooled: SAMN08245571; October_pooled: SAMN08245572; November_pooled: SAMN08245573 can be found at NCBI BioSample database.

2.5. Statistical analysis

All statistical analyses were performed using R statistical software version 3.2.0 (R Development Core Team, 2014). Grubb's tests (package: outliers [Lukasz, 2015]), were used to identify outliers in stream physicochemical data, which were removed before further analysis. Physicochemical data failed to meet assumptions of normality and homoscedasticity, and attempts at data transformation were not successful. Consequently, Spearman's rank correlations were used to explore general spatial trends in environmental conditions within Tinkers Creek and to identify seasonal patterns. In addition, permutational one-way analysis of variance (PERMANOVA) (coin package; Hothorn et al., 2008) followed by permutational multiple comparison tests (nparcomp package [Maintainer and Konietzschke, 2015]) were used to identify site-specific differences in environmental conditions between Tinkers Creek and reference streams. All univariate P values were corrected following the Benjamini-Hochberg (B-H) procedure for reducing false discovery rates (Hochberg and Benjamini, 1995).

To evaluate differences in community composition among sampling sites and dates relative abundance data from T-RFLP profiles were Hellinger transformed and measures associated with α - (richness, evenness, Shannon's entropy, and inverse Simpson's index) and β -diversity (as Bray-Curtis distances) were calculated using the vegan package (Oksanen et al., 2007). Measures of α -diversity were log-transformed to reduce homoscedasticity and both α - and β -diversity data were tested using a permutational multivariate analysis of variance. PERMANOVA (coin package; Hothorn et al., 2008) followed by permutational multiple comparison tests (nparcomp package [Maintainer and Konietzschke, 2015]) were used to identify site-specific or month-specific differences. All univariate P values were corrected following the Benjamini-Hochberg procedure for reducing false discovery rates (Hochberg and Benjamini, 1995). Nonmetric multidimensional scaling was used to compare and visualize β -diversity data (ggplot2 package; Wickham et al., 2016). Partial redundancy analysis (vegan package; Oksanen et al., 2007) was then performed on Hellinger transformed community T-RFLP relative abundance data to assess effects of sampling site and month on community composition. Additionally, α -diversity indices (Chao 1 richness and Shannon diversity index) were calculated to determine within sample diversity from rarefied sequences. A Bray-Curtis distance matrix was generated and used to generate multidimensional scaling axes to visualize trends in communities over time and among sampling sites. Finally, partial redundancy analyses were used to compare community KO profiles between sampling locations and between sampling months.

3. Results

Several significant (Spearman rank test; $P < 0.05$) correlations between environmental variables associated with urban discharge and the upstream-downstream Tinkers Creek sampling gradient were observed (Table S2). Dissolved nutrients (TN, NO_3^- , NO_2^- , and PO_4^-), as well as other abiotic variables (conductivity, pH, DO, and rates of discharge), increased from upstream to downstream within Tinkers Creek. In contrast, sediment nutrients (BOM, NH_4^+ , NO_2^- , and PO_4^-) and turbidity decreased. Additionally, Tinkers Creek had significantly greater concentrations of dissolved and sediment (extractable) nutrients compared to reference streams (PERMANOVA [$P < 0.001$; Table S3]). Specifically, nearly all sites in Tinkers Creek had greater concentrations of DOC, TN, sediment NH_4^+ , and higher readings of conductivity, pH, redox, DO, and turbidity. Dissolved nitrogen species (NH_4^+ , NO_3^- , and NO_2^-) and PO_4^- , and rates of discharge were significantly higher in downstream Tinkers sites (2–5) compared to reference sites.

Seasonal changes in stream physicochemical characteristics demonstrated significant variation ($P < 0.05$) (Table S4). Dissolved (NH_4^+ , NO_3^- , PO_4^-), BOM, and sediment-extractable (NO_2^- , NO_3^- , PO_4^-) nutrients and DO exhibited significant increases over time; nutrients and higher DO measurements were observed during summer months as compared to autumn sampling periods. This trend was opposite for both nutrient (DOC, dissolved NO_2^- , and sediment NH_4^+) and other physicochemical variables (conductivity, temperature, redox potential, turbidity, and discharge), which generally decreased as sampling dates approached September.

Bacterial community α -diversity calculated from T-RFLP profiles did not differ significantly among sites, and no longitudinal pattern was observed in Tinkers Creek (Table 1). However, strong seasonal differences were observed (PERMANOVA [$p < 0.001$; Table 1]); richness ($\rho = -0.22$), evenness ($\rho = -0.62$), Shannon entropy ($\rho = -0.35$), and inverse Simpson ($\rho = -0.32$) indices were all significantly, and negatively correlated with the month of sampling. There were significant increases in diversity between November and April, and then relatively stable values until a sharp, significant increase in August. Although there was a 5-month lag between the November and April sampling dates, the increase in diversity coincided with increased nutrient concentrations (data not shown).

Sampling location and date significantly ($p = 0.025$ and $p < 0.001$, respectively) affected community β -diversity based on T-RFLP profiles. However, due to considerable variance at each site, it was difficult to discern clear spatial patterns in β -diversity (Fig. 1a). Seasonal effects on β -diversity were much more apparent, with a clear separation of October and November from other months, which exhibited far more overlap in community profiles (Fig. 1b).

Redundancy analysis of T-RFLP data revealed significant differences in community composition among sites ($p = 0.02$; Fig. 2a) and dates ($p = 0.001$; Fig. 2b); site and date interactions were not significant (data not shown). Therefore, site and date were considered separately. Sampling site explained 8% of the variance among communities when partitioning out the effects of sampling date. Ordination of the significant RDA axes showed most of the sites clustered relatively close to one another, except for the most

upstream site in Tinkers Creek (TC1) and reference site 2 (Furnace Run) (Fig. 2a). Despite this clustering, there was little overlap in ordination space, as demonstrated by standard errors of community profile means, indicating significant compositional dissimilarity among sites. Of the environmental variables examined, BOM, dissolved and sediment nutrients, conductivity, pH, redox, DO, and discharge rates were all strong predictors of bacterial community composition (Table 2; $p \leq 0.05$). Analysis of the community KO profiles revealed that there was no significant difference in functional groups regardless of functional resolution (e.g., levels 1 [Fig. 3], 2 or 3 [data not shown]) between sampling locations. However, the majority (~51%) of functional genes were related to metabolic function.

Sampling date accounted for a greater percentage of described variance (14.5%) in community composition than did study site. This was apparent in the lack of overlap in community profiles by month and clear clustering that reflected seasonal environmental differences (Fig. 2b). For example, spring and summer months clustered near one another while mid to late fall communities (October and November) clustered together. These patterns were significantly correlated with seasonal changes in environmental conditions (i.e., dissolved NH_4^+ , NO_2^- , sediment NO_3^- , conductivity, temperature, DO, turbidity, flow, and discharge [Table 2; $p \leq 0.05$]). September exhibited the greatest divergence from other community profiles, which correlated with elevated sediment NO_3^- .

Because there was no site by date interaction from the T-RFLP data, samples for 16S rRNA gene sequencing were pooled by date and by site. Nonmetric multidimensional scaling (NMDS) of sequencing data revealed marked differences in bacterial community composition among sites and dates at phylum (Figs. S2a and S2b), order (Figs. S3a and S3b), and family (Fig. 4a and b) levels. Nutrients (water and sediment), and other stream abiotic properties (e.g., conductivity, redox, DO, turbidity, pH, and discharge) were related to differences in composition among sampling site (Fig. 4a; Tables S5a and S5b). When comparing the relative abundances of specific families of bacteria across all sampling locations, the most abundant sequences were classified as members of the *Betaproteobacteria* (*Burkholderiales Comamonadaceae*), which made up ~16.4% of the sequencing reads, followed by and *Bacteroidia* (*[Saprospirales] Chitinophagaceae*) (10.9% of the reads), *Planctomycetia* (*Pirellulales Pirellulaceae*) and *Verrucomicrobiae* (*Verrucomicrobia Verrucomicrobiae*) (7.1% and 6.9% of the reads, respectively), and *Alphaproteobacteria* (*Rhodobacterales Rhodobacteraceae* and *Rhizobiales Phyllobacteriaceae*) (6.8% and 4.7% of the reads, respectively).

Communities in Tinkers Creek were more similar among sites with greater spatial proximity to each other (e.g., site 1 was more similar to site 2 than to sites 3–5; Fig. 5a and b, Fig. S3a). Upstream sites (TC 1–2) had a higher prevalence of families in the class *Acidobacteria*-6 (iii 1–15 unassigned), *Bacteroidia* (unassigned *Bacteroidales*), *BSV26*, *Ignavibacteria*, *Anaerolineaea*, *Gemm-1*, *Nitrospira*, *Verrucomicrobiae*, *Betaproteobacteria* (SC-1-84 unassigned), *Deltaproteobacteria*, *Gammaproteobacteria* ($p \leq 0.05$; Fig. 5a and b). In contrast, downstream sites (TC 3–5) were dominated by families from the class [*Chloracidobacteria*], *Acidobacteria*-6 (iii1–15 mb2424), *Solibacteres*, [*Saprospirales*], *Flavobacteriia*, *Planctomycetia*

Table 1
Sampling date^a and location^b effect on α -diversity of Hellinger transformed 16S T-RFLP OTU profiles. Mean \pm SE.

Date ^a	October	November	April	May	June	July	August	September
Richness	10.67 (1.00)	9.57 (0.71)	17.14 (0.960)	16.95 (2.38)	23.33 (4.59)	12.67 (1.37)	18.74 (1.84)	21 (1.02)
Evenness	0.95 (0.006)	0.93 (0.007)	0.98 (0.002)	0.98 (0.003)	0.97 (0.003)	0.97 (0.005)	0.96 (0.003)	0.95 (0.003)
Location ^b	1	2	3	4	5	Ref.1	Ref.2	
Richness	15.67 (2.03)	16.46 (2.07)	17.58 (1.58)	15.29 (1.29)	15.54 (1.42)	15.33 (1.51)	17.92 (4.02)	
Evenness	0.96 (0.006)	0.96 (0.007)	0.96 (0.004)	0.96 (0.006)	0.96 (0.006)	0.96 (0.004)	0.96 (0.004)	

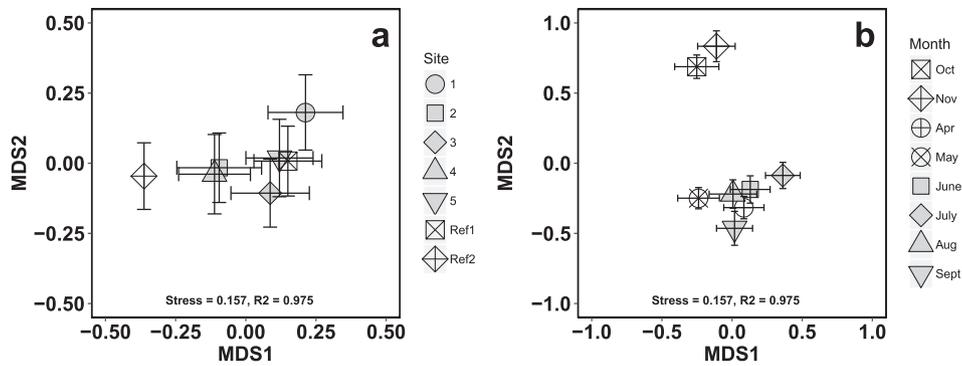


Fig. 1. Sampling location (a) and date (b) effect on β -diversity of Hellinger transformed 16S T-RFLP OTU profiles. The greater the dissimilarity between communities, the further apart data points are from one another. Each data point is the mean, with error bars representing the standard error.

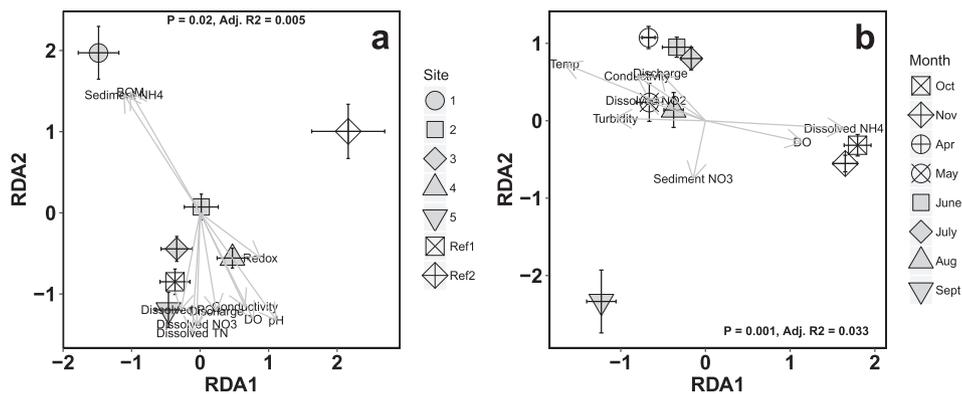


Fig. 2. RDA plot of sampling location (N = 21; a) and date (N = 24; b) effect on TRFLP 16S OTU profiles of Tinkers Creek (sites 1–5), Yellow Creek (R1) and Furnace Run (R2). Each data point is the mean, with error bars representing the standard error. Significant differences are based on redundancy analysis with post hoc testing. Physicochemical parameters influencing differences in 16S OTU profiles were determined via environmental fit ($\alpha \leq 0.05$). Arrows indicate the direction of the environmental gradient, and their lengths are proportional to their correlations with the ordination.

Table 2

Results of putative physicochemical factors affecting bacterial community composition by sampling date and location via *envifit*.

	Dis. ^a NH ₄ mg L ⁻¹	Dis. NO ₂ μg L ⁻¹	S.E. ^b NO ₃ mg kg ⁻¹	Conductivity EC μS/cm	Temperature °C	DO mg L ⁻¹	Turbidity NTU	Discharge m ³ s ⁻¹			
Sampling Date	R ² = 0.67 P = 0.001	R ² = 0.14 P = 0.021	R ² = 0.15 P = 0.015	R ² = 0.25 P = 0.001	R ² = 0.83 P = 0.001	R ² = 0.35 P = 0.001	R ² = 0.28 P = 0.001	R ² = 0.1 P = 0.007			
	BOM g ⁻¹ C	Dis. TN mg L ⁻¹	Dis. NO ₃ mg L ⁻¹	SRP μg μg L ⁻¹	S.E. NH ₄ mg L ⁻¹	Conductivity EC μS/cm	pH	Redox mV	DO mg L ⁻¹	Discharge m ³ s ⁻¹	
Sampling Location	R ² = 0.36 P = 0.001	R ² = 0.25 P = 0.001	R ² = 0.21 P = 0.003	R ² = 0.17 P = 0.010	R ² = 0.37 P = 0.001	R ² = 0.20 P = 0.006	R ² = 0.33 P = 0.001	R ² = 0.12 P = 0.038	R ² = 0.26 P = 0.00	R ² = 0.17 P = 0.010	

^aDis. means dissolved; ^bS.E. means sediment extracted.

(Fig. 5a), *Alphaproteobacteria*, and *Betaproteobacteria* (*Comamonadaceae*) (Fig. 5b). Reference streams had similar community makeup as upstream sites in Tinkers Creek; however several families were either only present in reference streams or had greater relative abundance compared to upstream sites, including *Bacteroidia* (*Bacteroidales* SB-1), *Flavobacteriia* (*Flavobacteriales* *Flavobacteriaceae*) (Fig. 5a), and *Betaproteobacteria* (*Rhodocyclales* *Rhodocyclaceae*) (Fig. 5b).

Seasonal differences were also apparent at all taxonomic levels (Figs. S2b and S3b; Fig. 4b). Although dissolved NH₄⁺ was the only abiotic parameter to correlate with July community composition (Fig. 4b), significant correlations were apparent with specific family groups (Tables S6a and S6b). Specifically, dissolved and sediment-extracted nutrients positively and negatively, respectively, correlated with abundance within the phylum *Acidobacteria*, whereas taxa within the classes [*Saprospirae*], *Alphaproteobacteria* and

Gammaproteobacteria negatively correlated with dissolved nutrients and/or sediment nutrients (Table S6a). Additionally, all non-nutrient stream measurements (Table S6b) positively correlated with different taxa over time, except for DO concentration which was negatively correlated to *Nitrospiraceae* abundance.

Seasonal differences in the prevalence of dominant families (abundances > 3% of sequence reads) were apparent for the *Chitinophagaceae*, *Pirellulaceae*, *Verrucomicrobiaceae* (Fig. 6a), *Rhodobacteraceae*, and *Comamonadaceae* (Fig. 6b). The *Comamonadaceae* was the most dominant sediment community member over the course of this study (except during October); with abundances peaking in June at 10.3% of sequencing reads. In October, *Verrucomicrobiaceae* and *Rhodobacteraceae* were the most prevalent groups, making up 10% of the reads. Both families peaked again in abundance (7.4% and 4.6% of reads, respectively) during spring (April). Similarly, *Chitinophagaceae* made up a large proportion (7.3%

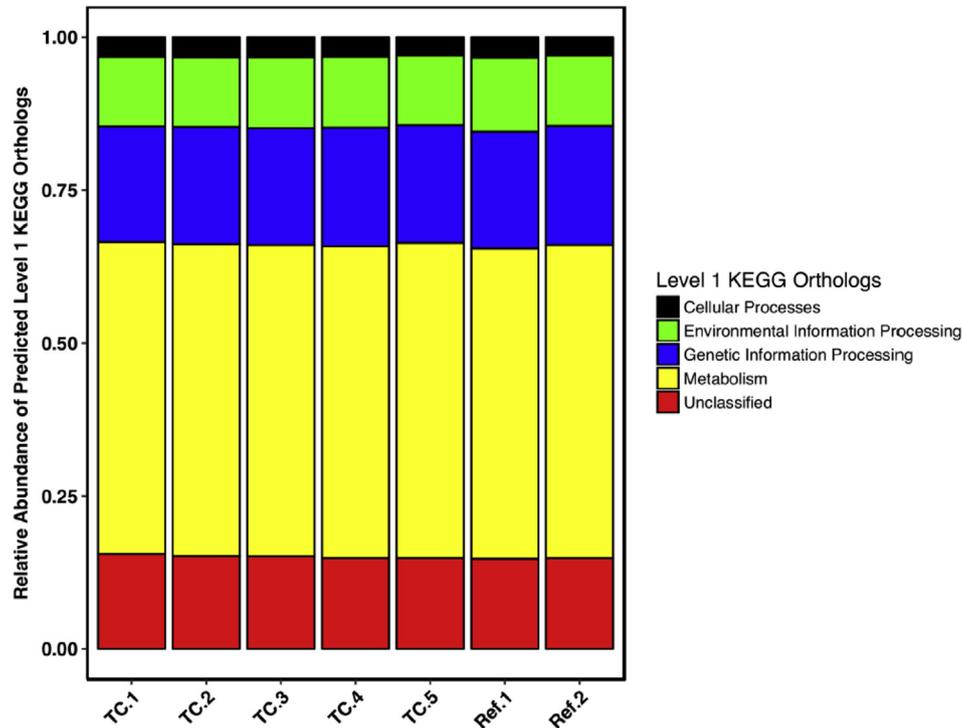


Fig. 3. Sampling location effects on predicted functional groups of OTUs in stream sediment bacteria based on KEGG database. Functional groups with less than 1% relative abundance are not included.

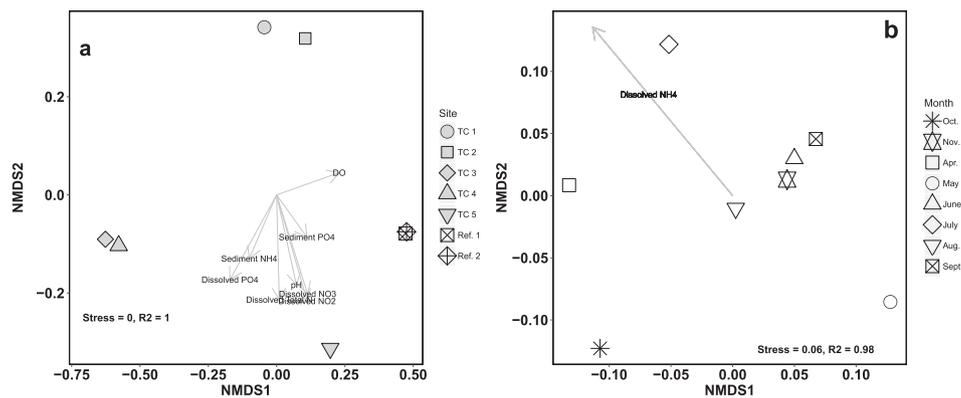


Fig. 4. NMDS plot of sampling location (a) and date (b) effect on family level OTU profiles of Tinkers Creek (sites 1–5), Yellow Creek (R1) and Furnace Run (R2). Each data point is the mean ($n = 7$; pooled across sampling location, and $n = 8$; pooled across sampling date). Physicochemical parameters influencing differences in 16S OTU profiles were determined via environmental fit ($\alpha \leq 0.05$). Arrows indicate the direction of the environmental gradient, and their lengths are proportional to their correlations with the ordination.

of the sequence reads) of the community. In July *Chitinopagaceae* was the most prevalent sediment community member, making up 8.2% of the sequence read. *Pirellulaceaea* taxa demonstrated a cyclic peaking pattern, with increases in abundance in October, May, and July followed by decreases in abundance in November, June, and August.

Less prominent families also demonstrated peaks in abundance over the course of the study. *Acidobacteria* peaked in abundance during April and July, making up 4.5% and 5.7% of sequencing reads, respectively (Fig. 6a). The *Bacteroidia*, *Cytophagales*, and *Deltaproteobacteria* taxa peaked in abundance in May, making up 8% and 4.7% of sequence reads. However, seasonal changes in community composition did not result in distinct changes in community function, as redundancy analysis of PICRUSt results showed no differences in major functional profiles over time (Fig. 7). The

majority (~51%) of functional genes were related to metabolic function, followed by genetic information processing (~20%).

4. Discussion

Urban discharge is a primary source of stream degradation in urban areas (Parr et al., 2015). Alterations in microbial-mediated nutrient cycling processes (Merbt et al., 2015) and increases in fecal bacterial indicator contamination (Baudart et al., 2000; Cha et al., 2010; Chigbu et al., 2004; Chu et al., 2014) as a result of urban discharge have been widely documented. However, there are few reports detailing spatiotemporal variations in bacterial sediment assemblages in streams dominated by urban discharge (Staley et al., 2013; Wang et al., 2011; Zhang et al., 2016). By analyzing the sediments of Tinkers Creek and two references

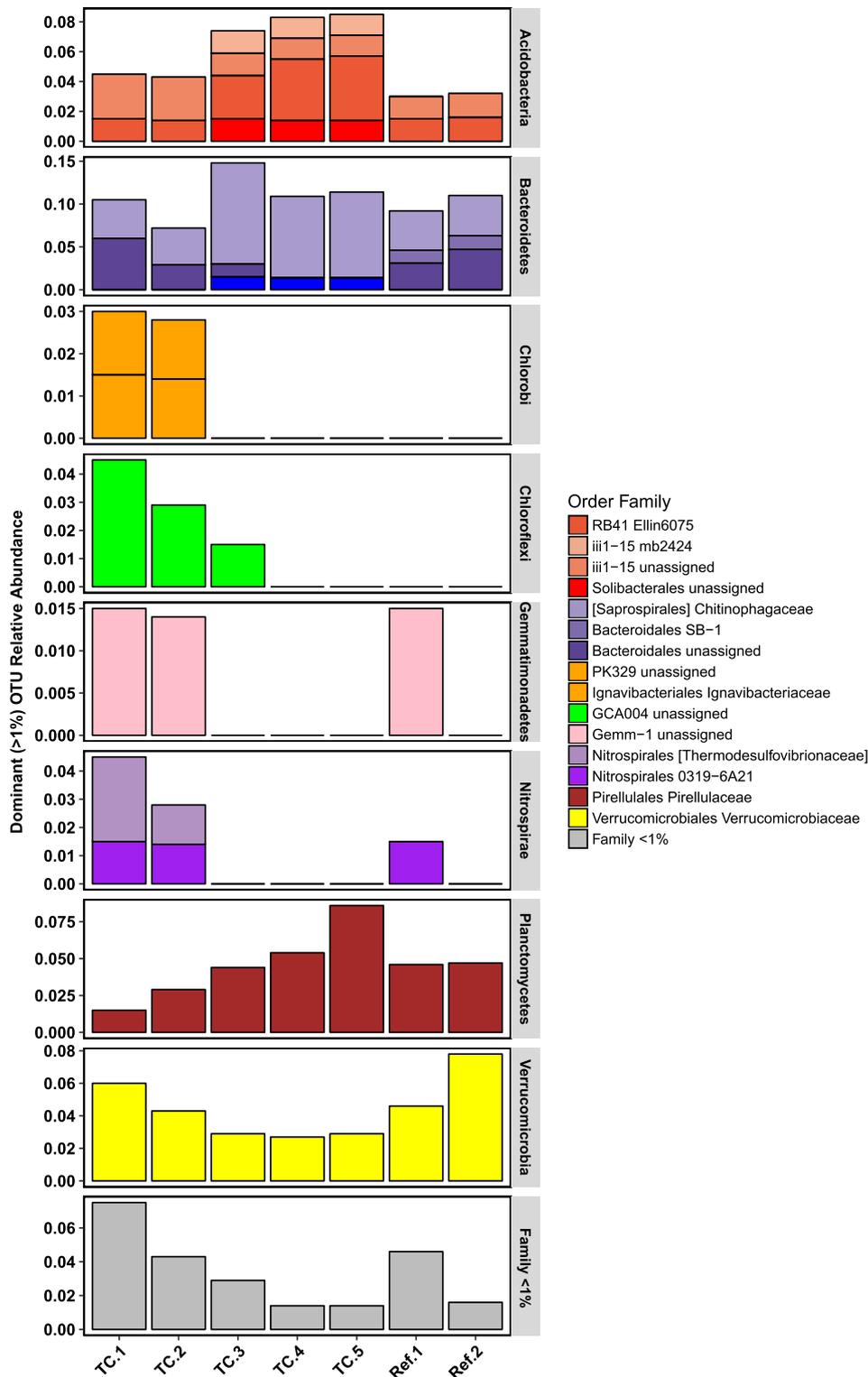


Fig. 5a. Relative abundance of non-proteobacterial taxa at family level sorted according to sampling location for Tinkers Creek (sites 1–5), Yellow Creek (R1) and Furnace Run (R2).

streams, we demonstrated that bacterial community composition was correlated with local environmental conditions (e.g., conductivity and nutrient concentrations), which were directly influenced by surrounding sub-watershed land use, suggesting that land use and local stream properties influence bacterial sediment communities.

The impacts of the urban discharge on physicochemical

variables were evident in downstream sites along Tinkers Creek and were hypothesized to result in a longitudinal decrease in bacterial species richness. However, despite large longitudinal differences in water and sediment physicochemical properties, bacterial communities exposed to higher urban drainage in Tinkers Creek did not differ in species richness or evenness relative to upstream and reference stream communities. These results are

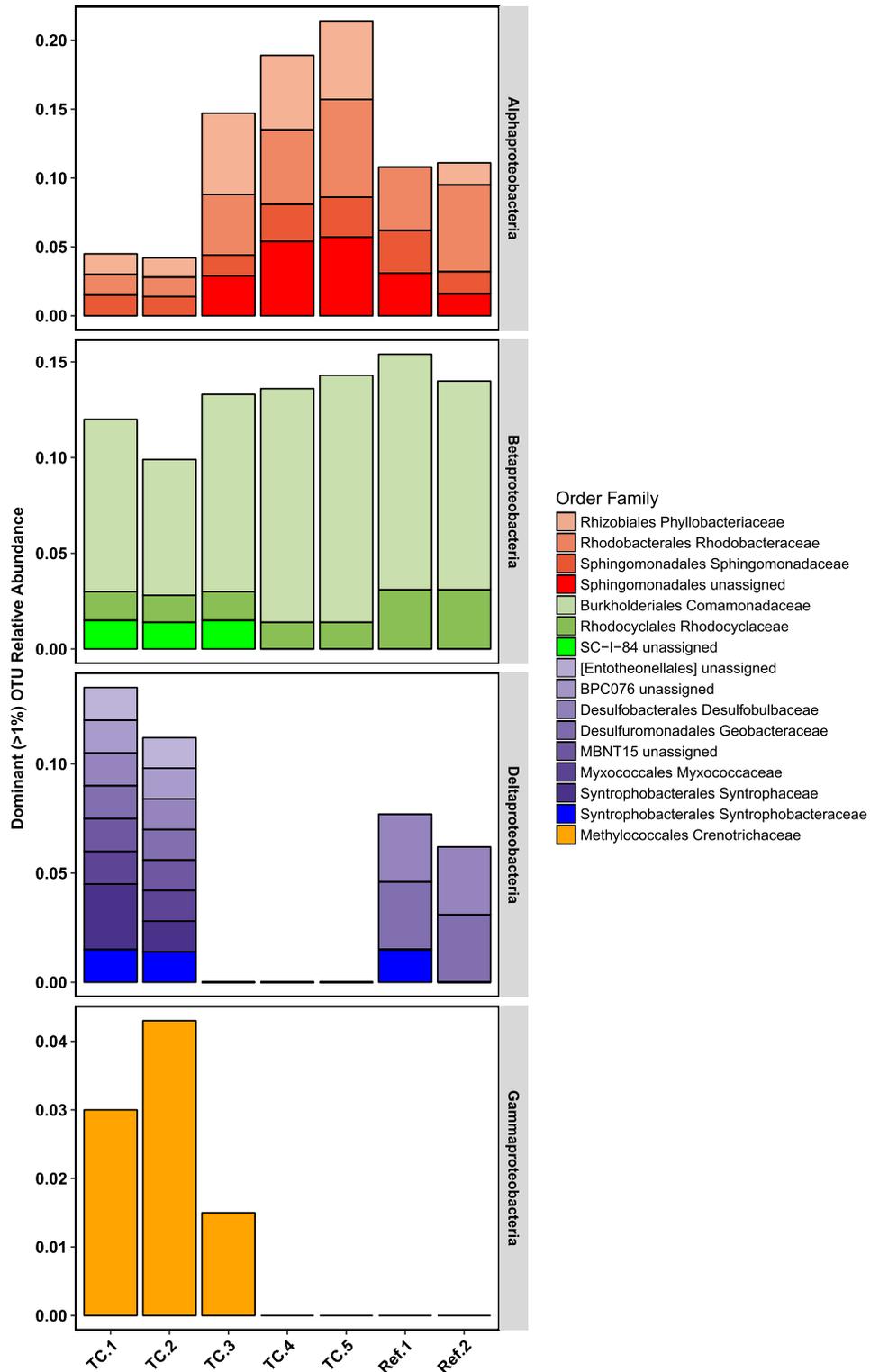


Fig. 5b. Relative abundance of proteobacterial taxa at family level sorted according to sampling location for Tinkers Creek (sites 1–5), Yellow Creek (R1) and Furnace Run (R2).

inconsistent with other studies that have shown that higher concentrations of organic and inorganic nutrients associated with anthropogenic activity may either increase (Staley et al., 2014; Marti and Balcázar, 2014; Wakelin et al., 2008) or decrease (Lu and Lu, 2014; Drury et al., 2013) species richness in stream sediment bacterial assemblages. The observed similarity in species richness and evenness may imply that many of the taxa are

generalists, capable of utilizing a wide variety of nutrients (Wittebolle et al., 2009), and/or capable of withstanding non-extreme environmental perturbations (Staley et al., 2014; Wittebolle et al., 2009). Along the same lines, Staley et al. (2014) observed a significant difference in diversity between forested and urban sites, but not between agricultural and urban sites, and suggested that the lack of differences was attributable to the

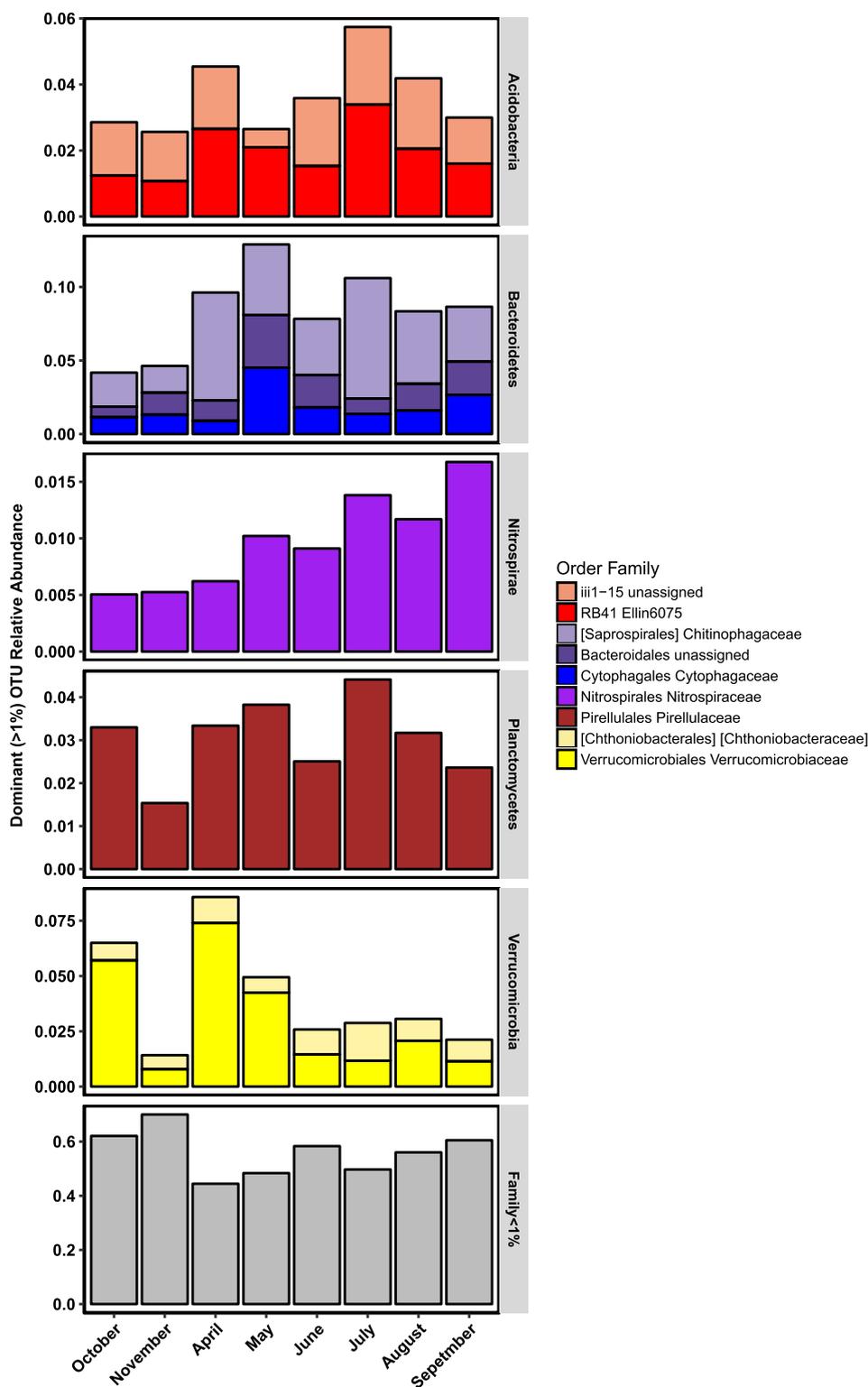


Fig. 6a. Relative abundance of non-proteobacterial taxa at family level by sampling date for Tinkers Creek (sites 1–5), Yellow Creek (R1) and Furnace Run (R2). (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)

similarity in anthropogenic disturbance between the sites (i.e., similar nutrient and contaminant loads). Alternatively, our results may reflect the large number of dormant cells within these communities, which has been documented to affect species richness, as dormant individuals are capable of withstanding environmental perturbations (Lennon and Jones, 2011).

In spite of similarities in species richness among sites, bacterial community composition differed among sites. Longitudinal differences in composition in Tinkers Creek were strongly connected to environmental conditions, including nutrient concentrations, DO, conductivity, redox, and discharge. This suggests that species sorting had a strong impact on sediment bacterial communities,

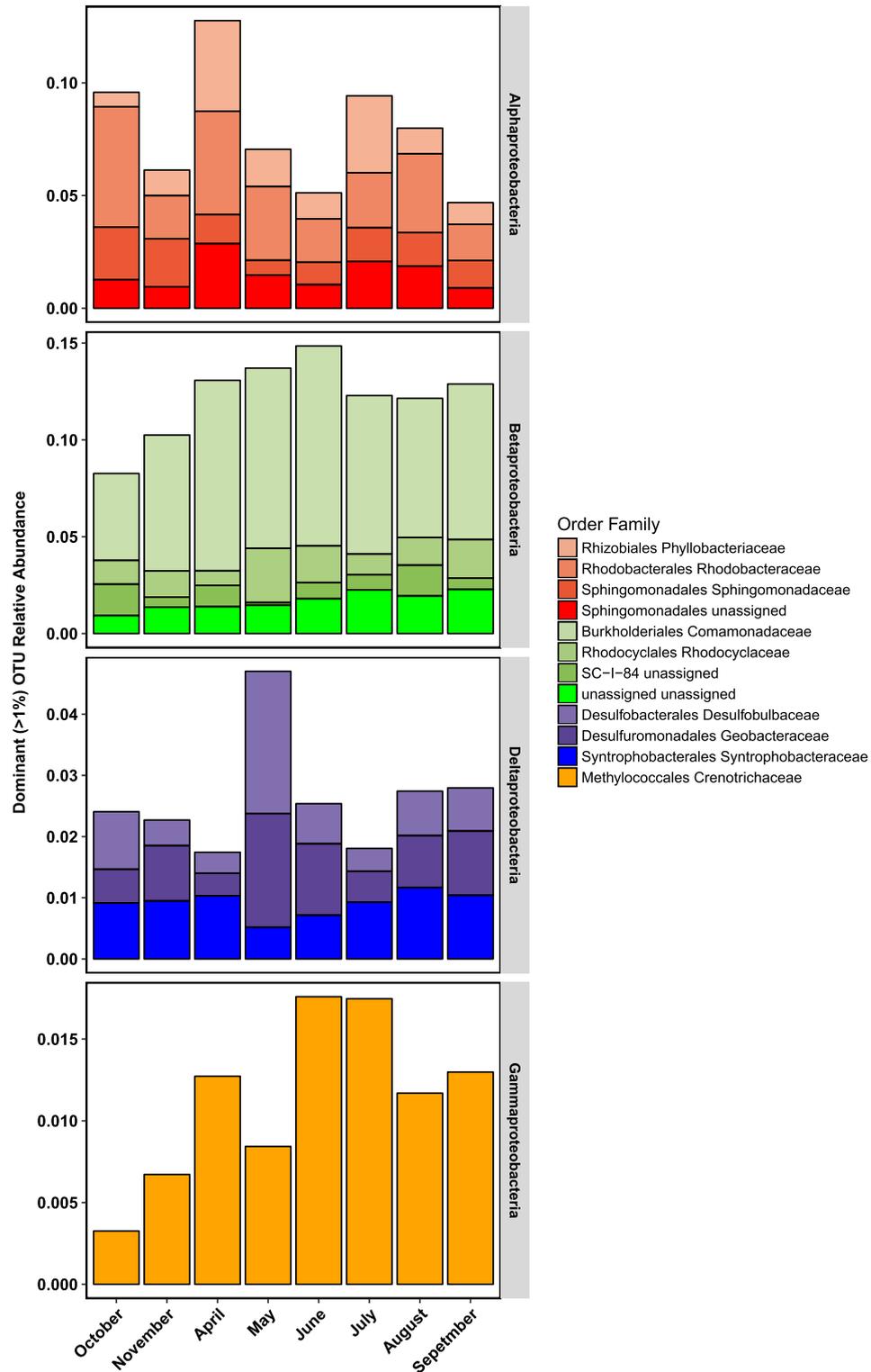


Fig. 6b. Relative abundance of proteobacterial taxa at family level by sampling date for Tinkers Creek (sites 1–5), Yellow Creek (R1) and Furnace Run (R2). (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)

with local habitat conditions selecting for specific groups of bacteria (Gibbons et al., 2014; Heino et al., 2014; Staley et al., 2013). The degree of connectivity between lotic systems and adjacent terrestrial systems are influenced by drainage density and hydrological exchange, which can have a direct impact on microbial communities in streams (Hullar et al., 2006). The bacterial communities in

our study encompassed microbes of terrestrial, aquatic, and human origins, with the mixture of bacteria from different putative sources varying among sampling locations.

More urbanized sites (TC 3–5) included taxa associated with nutrient pollution and other anthropogenic disturbance. The families *Comamonadaceae*, *Rhodobacteraceae*, and *Pirellulaceae* were

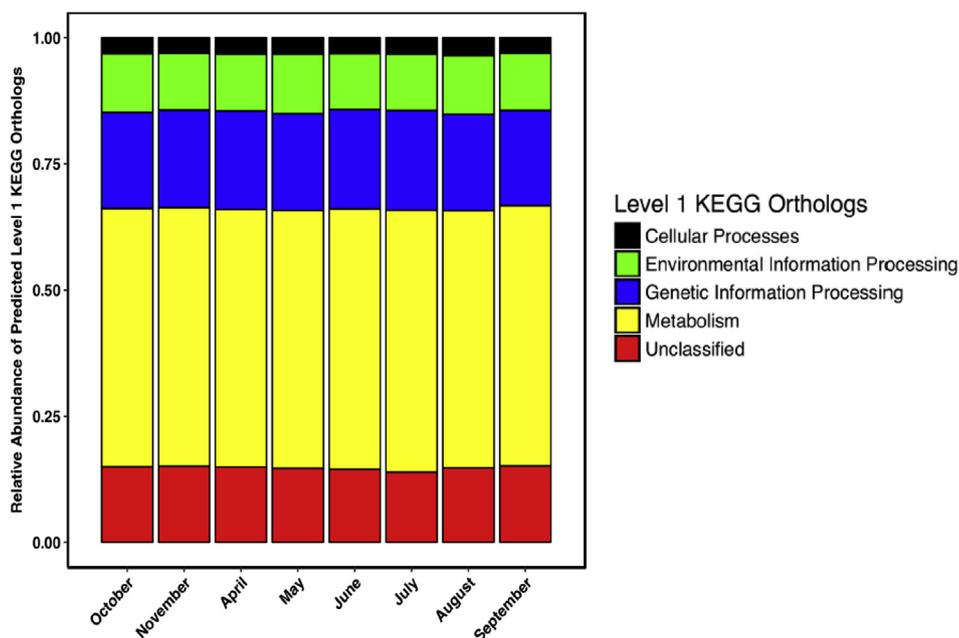


Fig. 7. Sampling time effects on predicted functional groups of OTUs in stream sediment bacteria based on KEGG database. Functional groups with less than 1% relative abundance are not included.

among the most dominant groups at downstream sites—accounting for up to 29% of sequence reads at these sites. Members of these families are commonly found in freshwater environments (Pujalte et al., 2014; Willems, 2014; Youssef and Elshahed, 2014), but are most known for being dominant groups in nutrient-rich environments (Rosenberg et al., 2013; Tang et al., 2017; Vetterli et al., 2015; Yu et al., 2017; Youssef and Elshahed, 2014). Other taxa with elevated abundance at sites with more urban impact included *Phyllobacteriaceae* (5.7% of sequences) and *Sphingomonadaceae* (6.13% of sequences). *Phyllobacteriaceae* taxa have most commonly been studied with regard to degradation of xenobiotic and recalcitrant compounds, such as thiophene (Bambauer et al., 1998), phenols (Fritsche et al., 1999), naphthalenesulfonates (Ghosh and Dam, 2009), ethylenediaminetetraacetic acid (Doronina et al., 2010), and thiophene-2-carboxylate (Bambauer et al., 1998). Likewise, *Sphingomonadaceae* are often found in high proportions in habitats contaminated with recalcitrant (poly) aromatic compounds of natural (Glaeser et al., 2010; Rosenberg et al., 2013) or anthropogenic origin (Basta et al., 2005; Romine et al., 1999; Sprenger, 1993; Rosenberg et al., 2013). The relative dominance of these two families in downstream sites may reflect increased industrial contaminants present in WWTP effluent, as the treatment facilities receive chemicals and other wastes from industrial sources. Alternatively, these taxa may serve as an indicator of the degree of urbanization occurring upstream of these sites as stormwater runoff from street drains enters this stream from a variety of locations.

Other families that were prevalent at downstream sites are not well characterized in terms of their ecological role in aquatic systems, including *Ellin* 6077 RB411 (*Chloracidobacteria*), mb2424 (*Acidobacteria*-6 iii1-15), *Cryomorphaceae* and *Chitinophagaceae*. Taxa within the phylum *Acidobacteria* are known for their resistance to pollutants like petroleum compounds (Abed et al., 2002), *p*-nitrophenol (Paul et al., 2006), linear alkylbenzene sulfonate (Sánchez-Peinado et al., 2010), and uranium (Ellis et al., 2003; Gremion et al., 2003; Barns et al., 2007), whereas, *Bacteroidetes* are prevalent in organic-rich systems (Crump and Hobbie, 2005; Huang et al., 2008; Obernosterer et al., 2011; Wang et al., 2011).

Therefore, the dominance of *Acidobacteria* and *Bacteroidetes* in more urbanized sites may indicate the prevalence of organic wastewater compounds within Tinkers Creek (Tertuliani et al., 2008). In general, the variety of taxa found in high abundance in downstream sites of Tinkers Creek suggests that effluent from the WWTPs plays a strong role in shaping the stream bacterial communities, as different contaminants from these WWTPs may have different selective forces on community composition.

In contrast to the more urbanized sites, a large percentage (~32%) of the taxa prevalent in the less urbanized sites (Tinkers Creek 1 and 2, Ref 1 and 2) has syntrophic and fermentative lifestyles. Members of the family *Syntrophaceae* are commonly found in anaerobic freshwater sediments (Jackson et al., 1999; Shelton and Tiedje, 1984; Wallrabenstein and Schink, 1994), and are capable of fermenting substrates that are utilized by H_2 /formate-utilizing partners (Kuever et al., 2005; Schink, 1997). The *Desulfobulbaceae*, *Syntrophobacteraceae*, and *Geobacteraceae* are sulfate/sulfur-reducing bacteria (Kuever et al., 2005; Muyzer and Stams, 2008) and/or other metal-reducing bacteria (Holmes et al., 2004, 2004a, 2004b; Kuever, 2005; Röling, 2014), respectively. Although mostly known for their ability to utilize sulfur or other metal compounds as their terminal electron acceptors, genera in these families have an important role in the anaerobic fermentation oxidation of organic compounds (Aklujkar et al., 2012; reviewed in Muyzer and Stams, 2008; Röling, 2014). *Thermodesulfobivriaceae*, such as *Deltaproteobacteria* detected in this study, are sulfate reducers with chemoorganoheterotrophic or chemolithoheterotrophic lifestyles. During chemolithoheterotrophic growth, genera of this family use H_2 as electron donor and acetate as a carbon source (Henry et al., 1994). Additionally, *Crenotrichaceae* (Gammaproteobacteria), which was only found in upstream sites of Tinkers, is a type Ib methanotroph group. These organisms are facultative aerobes that utilize methane and methanol, or other C_1 compounds as substrates (Bowman, 2014; Stein et al., 2012; Stoecker et al., 2006). When considering the relatively high diversity of fermenters and sulfur/sulfate-reducing taxa found in the upstream sites and reference streams, the microbial communities may be structured by inputs from groundwater and the hyporheic zone (Griebler and

Lueders, 2009; Storey et al., 1999). Although we lack data on the source of water at the different sites, the difference in community composition and the differences in sediment composition (with fine sediment at upstream sites and pebbles/cobblestones at downstream sites) suggests a switch from deep to shallow water flow-paths longitudinally, thus supporting the notion that local sampling environment can influence the structure of the microbial community within the stream (Heino et al., 2014; Cloutier et al., 2015).

Overall, the dissimilarities in bacterial community composition among upstream, downstream, and reference sites reflect OTU-specific environmental tolerances to local conditions (Comte et al., 2014; Comte and Del Giorgio, 2009; Newton et al., 2011; Philippot et al., 2010; Wang et al., 2011). However, it is difficult to ascertain how much of these differences are due to site characteristics (land use and/or physical-chemical) that differ along the longitudinal gradients in and among these streams, and how much is due to dispersal limitations (Crump et al., 1999; Astorga et al., 2012; Lindström and Langenheder, 2012), interactions among species (Fortunato and Crump, 2011; Glibert et al., 2012), or some combination of the three (Astorga et al., 2012). Future work to tease apart the contributions of spatial proximity and shared environmental characteristics will be required. Nevertheless, these results suggest that differences in water chemistry attributable to urban discharge served as a selective force on bacterial taxa in these streams (Astorga et al., 2012; Beier et al., 2008; McArthur and Richardson, 2002).

Seasonal changes in the dominant sediment bacterial populations were correlated with changes in aqueous physicochemistry across all sites, as predicted. These results are consistent with previous studies that have discovered shifts in microbial composition linked to seasonal variation of water physicochemical properties (Duarte et al., 2016; Moss et al., 2006; Yannarell et al., 2003) and allochthonous inputs (Dann et al., 2017). Alterations in stream temperature, light penetration, organic and inorganic concentrations in the water column and sediments over the annual period may have shaped the changes observed in the community composition of sediment bacteria in these systems.

Distinct groupings of bacterial families became more prominent on particular dates, revealing the highly dynamic nature of the bacteria in these streams. Fall-dominant families contained known degraders of recalcitrant litter (*Verrucomicrobia*; Stevenson et al., 2004; Wymore et al., 2016) and humic substances (*Sphingomonadaceae*; Glaeser et al., 2010; Glaeser and Kämpfer, 2014). Specifically, these groups are important for their utilization of humic substances, and ability to degrade recalcitrant high-molecular weight compounds (Glaeser et al., 2010; Wymore et al., 2016), suggesting that these organisms play an important role in carbon cycling in our streams.

Spring-dominant families belonged to phyla that are often found associated with algae (*Planctomycetes*; Bengtsson and Øvreås, 2010; Bohórquez et al., 2017), and microbial mats (Allen et al., 2009; Baumgartner et al., 2009) or biofilms (*Bacteroidetes*; Bartrons et al., 2012; Bohórquez et al., 2017) during high levels of algal activity. Taxa within *Planctomycetes* have the ability to degrade sulfated polysaccharides of algal origin (Kim et al., 2016; Lage and Bondoso, 2014), whereas members of *Bacteroidetes* can degrade organic compounds that may be released from algae; thus suggesting that they have an ecological role in the degradation of polysaccharides produced by algae in streams. Alternatively, the high prevalence of *Bacteroidetes* and *Phyllobacteriaceae* may indicate a higher prevalence of discharge from WWTPs, or runoff during the rainy season (Bambauer et al., 1998; Drury et al., 2013; Doronina et al., 2010; Eichmiller et al., 2013; Fritsche et al., 1999;

Kämpfer, 1999). In comparison, summer was dominated by taxa in families that have wide genetic diversity, such as *Comamonadaceae*. Taxa within this group are known denitrifiers (Adav et al., 2010; Etchebehere et al., 2001; Khan et al., 2002; Wu et al., 2013), fermenters (Chen et al., 2013; Finneran et al., 2003; Kim et al., 2012), aerobic organotrophs (Kim et al., 2012; Liang et al., 2011), photoheterotrophs (Hiraishi et al., 1991; Madigan et al., 2000) and photoautotrophs (Zeng et al., 2012), which suggests that these organisms are involved in a variety of biogeochemical processes in aquatic ecosystems (reviewed by Willems, 2014). It should be noted, however, that more detailed phylogenetic work needs to be done to link function with phylogeny, especially with largely uncultured groups such as *Verrucomicrobia*, or for groups with unknown ecologies (i.e., *Chitinophagaceae*). However, our results suggest that in stream systems, seasonal changes allow for different and distinct combinations of bacterial populations to become prominent members of the community at different times of the year (Gilbert et al., 2012, 2009; Shade et al., 2013; Portillo et al., 2012).

Although site and date differences were observed in sediment bacterial community composition, we did not see any significant differences in functional profiles over space or time. Functional resilience to disturbance is possible if the microbial community contains individuals that have versatile physiologies (Evans and Hofmann, 2012). Core communities found in these systems were comprised of families that had a vast network of genera capable of performing a wide array of biogeochemical cycles. For example, genera in the family *Comamonadaceae* and *Rhodocateraceae* have metabolic capabilities that span a wide variety of cycles, such as organotrophs, denitrifiers, hydrogen oxidizers, photoheterotrophs, photoautotrophs, fermenters, Fe^{3+} -reducers (Baldani et al., 2014; Willems, 2014; Pujalte et al., 2014). Most genera in these families have an aerobic heterotrophic metabolism but are capable of switching to other metabolic forms depending on the substrate or electron acceptor availability (Willems, 2014). One such group, purple nonsulfur bacteria, can be heterotrophic under aerobic conditions and phototrophs under anoxic conditions (Hiraishi and Imhoff, 2005; Pujalte et al., 2014). Through altering metabolic capabilities (Meyer et al., 2004; Swingle et al., 2007) or genetic change (Evans and Hofmann, 2012; Lenski, 2017; De Meester et al., 2016), bacteria can often overcome detrimental environmental change by exploiting previously unavailable resources. Thus, changes in community composition may not correspond with the response, or the lack thereof, in community functional profiles (Allison and Martiny, 2008).

Alternatively, a large fraction of the community may be dormant (Lennon and Jones, 2011), which is common among communities living in temporally and spatially dynamic environments (Lennon and Jones, 2011; Pedrós-Alió, 2006; Rehman et al., 2010). In fact, dormant individuals of bacterial communities directly affect species diversity (Chesson, 2000) by acting as seed banks. Seed banks can contribute to the stability of ecosystem processes through the facilitation of niche complementation and/or functional redundancy (Loreau et al., 2001; Petchey and Gaston, 2002). This can occur as previously dormant groups become more prevalent under certain conditions while functionally complimentary groups or those functionally similar, but less tolerant to current environmental conditions revert to dormancy; however, compensatory growth of these groups may result in minimal change in ecological processes (Fernandez-Gonzalez et al., 2016; Frost et al., 1995; Schindler, 1990). In general, the functional attributes of stream sediment bacteria in this study appear to be similar across a broad range of land uses, suggesting that there is a high degree of functional gene redundancy (Qu et al., 2017) and a reduction of functional diversity (Cardinale et al., 2012; Elmquist et al., 2003; Jung

et al., 2016). As such, adaptation of local communities to changing environmental patterns can be independent of functional change in communities (Bier et al., 2015; Frost et al., 1995; Fernandez-Gonzalez et al., 2016; Östman et al., 2010; Reiss et al., 2009).

Overall, the predicted functional profile of the microbial community—as determined by PICRUSt's algorithm—provides a coarse overview of the functional potential present within the community; however, these results must be interpreted with caution. Rarefaction of pooled DNA samples fails to capture the full extent of diversity present within the system, which is likely reflected in the predicted functional profile. Additionally, individual functional genes may not necessarily be correlated with community structure (Fierer et al., 2012), as the placement of novel diversity cannot accurately be mapped into a phylogenetic context due to the fact that a large proportion of bacterial phylogeny is poorly identified (Harris et al., 2013). To adequately assess gene categories deeper sequencing would be required (Fierer et al., 2012). PICRUSt can neither preclude or outperform deep metagenomic sequencing (Langille et al., 2013); the algorithm is significantly affected by the phylogenetic dissimilarity among environmental samples and sequenced genomes (Langille et al., 2013). Thus, we suggest that further studies that utilize both metagenomic sequencing and marker gene studies are needed in this system and that more samples are required to adequately assess intra- and inter-stream variability.

5. Conclusion

Although α -diversity was relatively constant both spatially, we found that urban drainage impacts bacterial community structure in streams, with greater prevalence of bacteria associated with urban discharge in downstream sites in Tinkers Creek. Moreover, we found evidence for indirect seasonal effects, as nutrient and hydrologic characteristics influenced bacterial community assemblage within our streams. However, there were no spatial or temporal effects on the core community function. Our results suggest that deterministic forces are important for community assembly and that differences in β -diversity between sites and over time are predominantly due to changes in the relative abundance of a core community. This work demonstrates that urban drainage has a marked impact on shaping benthic bacterial communities; yet, these changes seem not to have an impact on sediment bacteria function. This suggests that communities in urban environments may be more resilient to disturbance via versatile physiologies and/or functional redundancy. Although there were no changes in the sediment bacteria functional profiles, changes in the composition of microbial communities may affect the energy requirements and expenditures of the communities (Bier et al., 2015; Cañedo-Argüelles et al., 2014; Nieuwdorp et al., 2014; de Ruiter et al., 1995), which in turn may affect the trophic transfer of energy in stream food webs.

Declaration of interest

All authors have seen and approved the final version of the manuscript, and warrant that the article is the author's original work, is not considered for publication elsewhere, and has not received the prior publication. Additionally, authors declare no conflicts of interest.

Contributors

The study was conceived of and designed by AR and LL. Samples were collected by AR and JVG and processed by AR. Statistical analysis was done by AR and JVG. Interpretation of data and writing

of the manuscript was done by AR, JVG, and LL.

Acknowledgments

This work was supported by Kent State's Graduate Student Senate Research Award, the Art and Margaret Herrick Aquatic Ecology Research Award, and the Department of Biological Sciences at Kent State University (101347)

Appendix A. Supplementary data

Supplementary data related to this article can be found at <https://doi.org/10.1016/j.watres.2018.01.045>.

References

- Abed, R.M.M., Safi, N.M.D., Köster, J., de Beer, D., El-Nahhal, Y., Rullkötter, J., Garcia-Pichel, F., 2002. Microbial diversity of a heavily polluted microbial mat and its community changes following degradation of petroleum compounds. *Appl. Environ. Microbiol.* 68, 1674–1683. <https://doi.org/10.1128/AEM.68.4.1674-1683.2002>.
- Adav, S.S., Lee, D.-J., Lai, J.Y., 2010. Microbial community of acetate utilizing denitrifiers in aerobic granules. *Appl. Microbiol. Biotechnol.* 85, 753–762. <https://doi.org/10.1007/s00253-009-2263-6>.
- Aklujkar, M., Haveman, S.A., DiDonato, R., Chertkov, O., Han, C.S., Land, M.L., Brown, P., Lovley, D.R., 2012. The genome of *Pelobacter carbinolicus* reveals surprising metabolic capabilities and physiological features. *BMC Genomics* 13, 690. <https://doi.org/10.1186/1471-2164-13-690>.
- Allen, M.A., Goh, F., Burns, B.P., Neilan, B.A., 2009. Bacterial, archaeal and eukaryotic diversity of smooth and pustular microbial mat communities in the hypersaline lagoon of Shark Bay. *Geobiology* 7, 82–96. <https://doi.org/10.1111/j.1472-4669.2008.00187.x>.
- Allison, S.D., Martiny, J.B.H., 2008. Colloquium paper: resistance, resilience, and redundancy in microbial communities. *Proc. Natl. Acad. Sci. U. S. A.* 105 (Suppl. 1), 11512–11519. <https://doi.org/10.1073/pnas.0801925105>.
- Ancion, P.-Y., Lear, G., Lewis, G.D., 2010. Three common metal contaminants of urban runoff (Zn, Cu & Pb) accumulate in freshwater biofilm and modify embedded bacterial communities. *Environ. Pollut.* 158, 2738–2745. <https://doi.org/10.1016/j.envpol.2010.04.013>.
- Astorga, A., Oksanen, J., Luoto, M., Soininen, J., Virtanen, R., Muotka, T., 2012. Distance decay of similarity in freshwater communities: do macro- and microorganisms follow the same rules? *Glob. Ecol. Biogeogr.* 21, 365–375. <https://doi.org/10.1111/j.1466-8238.2011.00681.x>.
- Baldani, J.L., Videira, S.S., dos Santos Teixeira, K.R., Reis, V.M., de Oliveira, A.L.M., Schwab, S., de Souza, E.M., Pedraza, R.O., Baldani, V.L.D., Hartmann, A., 2014. The family rhodospirillaceae BT - the prokaryotes: Alphaproteobacteria and Betaproteobacteria. In: Rosenberg, E., DeLong, E.F., Lory, S., Stackebrandt, E., Thompson, F. (Eds.), *The Prokaryotes*. Springer Berlin Heidelberg, Berlin, Heidelberg, pp. 533–618. https://doi.org/10.1007/978-3-642-30197-1_300.
- Bambauer, A., Rainey, F.A., Stackebrandt, E., Winter, J., 1998. Characterization of *Aquamicrobium defluvii* gen. nov. sp. nov., a thiophene-2-carboxylate-metabolizing bacterium from activated sludge. *Arch. Microbiol.* 169, 293–302. <https://doi.org/10.1007/s002030050575>.
- Barns, S.M., Cain, E.C., Sommerville, L., Kuske, C.R., 2007. Acidobacteria phylum sequences in uranium-contaminated subsurface sediments greatly expand the known diversity within the phylum. *Appl. Environ. Microbiol.* 73, 3113–3116. <https://doi.org/10.1128/AEM.02012-06>.
- Bartrons, M., Catalan, J., Casamayor, E.O., 2012. High bacterial diversity in epilithic biofilms of oligotrophic mountain lakes. *Microb. Ecol.* 64, 860–869. <https://doi.org/10.1007/s00248-012-0072-4>.
- Basta, T., Buerger, S., Stolz, A., 2005. Structural and replicative diversity of large plasmids from sphingomonads that degrade polycyclic aromatic compounds and xenobiotics. *Microbiology* 151, 2025–2037.
- Baudart, J., Grabulos, J., Barusseau, J.-P., Lebaron, P., 2000. Salmonella spp. and fecal coliform loads in coastal waters from a point vs. Nonpoint source of pollution. *J. Environ. Qual.* 29, 241. <https://doi.org/10.2134/jeq2000.00472425002900010031x>.
- Baumgartner, L.K., Dupraz, C., Buckley, D.H., Spear, J.R., Pace, N.R., Visscher, P.T., 2009. Microbial species richness and metabolic activities in hypersaline microbial mats: insight into biosignature formation through lithification. *Astrobiology* 9, 861–874. <https://doi.org/10.1089/ast.2008.0329>.
- Beaulieu, J.J., Mayer, P.M., Kaushal, S.S., Pennino, M.J., Arango, C.P., Balz, D.A., Canfield, T.J., Elonen, C.M., Fritz, K.M., Hill, B.H., Ryu, H., Domingo, J.W.S., 2014. Effects of urban stream burial on organic matter dynamics and reach scale nitrate retention. *Biogeochemistry* 121, 107–126. <https://doi.org/10.1007/s10533-014-9971-4>.
- Beier, S., Witzel, K.-P., Marxsen, J., 2008. Bacterial community composition in central European running waters examined by temperature gradient gel electrophoresis and sequence analysis of 16S rRNA genes. *Appl. Environ. Microbiol.* 74, 188–199. <https://doi.org/10.1128/AEM.00327-07>.

- Bengtsson, M.M., Øvreås, L., 2010. Planctomycetes dominate biofilms on surfaces of the kelp *Laminaria hyperborea*. *BMC Microbiol.* 10, 261. <https://doi.org/10.1186/1471-2180-10-261>.
- Bier, R.L., Voss, K.A., Bernhardt, E.S., 2015. Bacterial community responses to a gradient of alkaline mountaintop mine drainage in Central Appalachian streams. *ISME J.* 9, 1378–1390. <https://doi.org/10.1038/ismej.2014.222>.
- Blackwood, C.B., Marsh, T., Kim, S.-H., Paul, E.A., 2003. Terminal restriction fragment length polymorphism data analysis for quantitative comparison of microbial communities. *Appl. Environ. Microbiol.* 69, 926–932.
- Bohórquez, J., McGenity, T.J., Papaspyrou, S., García-Robledo, E., Corzo, A., Underwood, G.J.C., 2017. Different types of diatom-derived extracellular polymeric substances drive changes in heterotrophic bacterial communities from intertidal sediments. *Front. Microbiol.* 8, 245. <https://doi.org/10.3389/fmicb.2017.00245>.
- Bowman, J.P., 2014. The family methylcocccaceae. In: Rosenberg, Eugene, DeLong, Edward F., Lory, Stephen, Stackebrandt, Erko, Thompson, Fabiano (Eds.), *The Prokaryotes – Gammaproteobacteria*. Springer-Verlag, Berlin Heidelberg, pp. 411–442. https://doi.org/10.1007/978-3-642-38922-1_237.
- Boyer, L., Pearson, R.G., Gessner, M.O., Barmuta, L.A., Ferreira, V., Graça, M.A.S., Dudgeon, D., Boulton, A.J., Callisto, M., Chauvet, E., Helson, J.E., Bruder, A., Albariño, R.J., Yule, C.M., Arunachalam, M., Davies, J.N., Figueroa, R., Flecker, A.S., Ramirez, A., Death, R.G., Iwata, T., Mathooko, J.M., Mathuriau, C., Gonçalves, J.F., Moretti, M.S., Jinggut, T., Lamothe, S., M'Erimba, C., Ratnarajah, L., Schindler, M.H., Castela, J., Buria, L.M., Cornejo, A., Villanueva, V.D., West, D.C., 2011. A global experiment suggests climate warming will not accelerate litter decomposition in streams but might reduce carbon sequestration. *Ecol. Lett.* 14, 289–294. <https://doi.org/10.1111/j.1461-0248.2010.01578.x>.
- Bryant, W.L., Carlisle, D.M., 2012. The relative importance of physicochemical factors to stream biological condition in urbanizing basins: evidence from multimodel inference. *Freshw. Sci.* 31, 154–166. <https://doi.org/10.1899/10-131.1>.
- Cañedo-Argüelles, M., Bundschuh, M., Gutiérrez-Cánovas, C., Kefford, B.J., Prat, N., Trobajo, R., Schäfer, R.B., 2014. Effects of repeated salt pulses on ecosystem structure and functions in a stream mesocosm. *Sci. Total Environ.* 476–477, 634–642. <https://doi.org/10.1016/j.scitotenv.2013.12.067>.
- Caporaso, J.G., Kuczynski, J., Stombaugh, J., Bittinger, K., Bushman, F.D., Costello, E.K., Fierer, N., Peña, A.G., Goodrich, J.K., Gordon, J.I., Huttley, G.A., Kelley, S.T., Knights, D., Koenig, J.E., Ley, R.E., Lozupone, C.A., McDonald, D., Muegge, B.D., Pirrung, M., Reeder, J., Sevinsky, J.R., Turnbaugh, P.J., Walters, W.A., Widmann, J., Yatsunenko, T., Zaneveld, J., Knight, R., 2010. QIIME allows analysis of high-throughput community sequencing data. *Nat. Methods* 7, 335–336. <https://doi.org/10.1038/nmeth.f.303>.
- Cardinale, B.J., Duffy, J.E., Gonzalez, A., Hooper, D.U., Perrings, C., Venail, P., Narwani, A., Mace, G.M., Tilman, D., Wardle, D.A., Kinzig, A.P., Daily, G.C., Loreau, M., Grace, J.B., Larigauderie, A., Srivastava, D.S., Naeem, S., 2012. Biodiversity loss and its impact on humanity. *Nature* 486, 59–67. <https://doi.org/10.1038/nature11148>.
- Carey, R.O., Migliaccio, K.W., 2009. Contribution of wastewater treatment plant effluents to nutrient dynamics in aquatic systems: a review. *Environ. Manage.* 44, 205–217. <https://doi.org/10.1007/s00267-009-9309-5>.
- Cha, S.M., Lee, S.W., Park, Y.E., Cho, K.H., Lee, S., Kim, J.H., 2010. Spatial and temporal variability of fecal indicator bacteria in an urban stream under different meteorological regimes. *Water Sci. Technol.* 61, 3102–3108. <https://doi.org/10.2166/wst.2010.261>.
- Chen, W.-M., Lin, Y.-S., Young, C.-C., Sheu, S.-Y., 2013. *Pseudorhodofera aquiterra* sp. nov., isolated from groundwater. *Int. J. Syst. Evol. Microbiol.* 63, 169–174.
- Chesson, P., 2000. Mechanisms of maintenance of species diversity. *Annu. Rev. Ecol. Syst.* 31, 343–366.
- Chiaramonte, J.B., Roberto, M. do C., Pagioro, T.A., 2013. Seasonal dynamics and community structure of bacterioplankton in upper paraná river floodplain. *Microb. Ecol.* 66, 773–783. <https://doi.org/10.1007/s00248-013-0292-2>.
- Chigbu, P., Gordon, S., Strange, T., 2004. Influence of inter-annual variations in climatic factors on fecal coliform levels in Mississippi Sound. *Water Res.* 38, 4341–4352. <https://doi.org/10.1016/j.watres.2004.08.019>.
- Chu, Y., Tournoud, M.G., Salles, C., Got, P., Perrin, J.L., Rodier, C., Caro, A., Troussellier, M., 2014. Spatial and temporal dynamics of bacterial contamination in South France coastal rivers: focus on in-stream processes during low flows and floods. *Hydrol. Process* 28, 3300–3313. <https://doi.org/10.1002/hyp.9900>.
- Claessens, L., Tague, C.L., Groffman, P.M., Melack, J.M., 2010. Longitudinal assessment of the effect of concentration on stream N uptake rates in an urbanizing watershed. *Biogeochemistry* 98, 63–74. <https://doi.org/10.1007/s10533-009-9376-y>.
- Cloutier, D.D., Alm, E.W., McLellan, S.L., 2015. Influence of land use, nutrients, and geography on microbial communities and fecal indicator abundance at lake Michigan beaches. *Appl. Environ. Microbiol.* 81, 4904–4913. <https://doi.org/10.1128/AEM.00233-15>.
- Coles, J., Cuffney, T., McMahon, G., Beaulieu, K., 2004. *The Effects of Urbanization on the Biological, Physical, and Chemical Characteristics of Coastal New England Streams*, 1695th ed. US Geological Survey, Denver.
- Comte, J., Del Giorgio, P.A., 2009. Links between resources, C metabolism and the major components of bacterioplankton community structure across a range of freshwater ecosystems. *Environ. Microbiol.* 11, 1704–1716. <https://doi.org/10.1111/j.1462-2920.2009.01897.x>.
- Comte, J., Lindstrom, E.S., Eiler, A., Langenheder, S., 2014. Can marine bacteria be recruited from freshwater sources and the air? *ISME J.* 8, 2423–2430. <https://doi.org/10.1038/ismej.2014.89>.
- Crump, B.C., Armbrust, E.V., Baross, J.A., 1999. Phylogenetic analysis of particle-attached and free-living bacterial communities in the Columbia river, its estuary, and the adjacent coastal ocean. *Appl. Environ. Microbiol.* 65, 3192–3204.
- Crump, B.C., Hobbie, J.E., 2005. Synchrony and seasonality in bacterioplankton communities of two temperate rivers. *Limnol. Oceanogr.* 50, 1718–1729. <https://doi.org/10.4319/lo.2005.50.6.1718>.
- Cuffney, T.F., Zappia, H., Giddings, E.M.P., Coles, J.F., 2005. Effects of urbanization on benthic macroinvertebrate assemblages in contrasting environmental settings: boston, Massachusetts; Birmingham, Alabama; and Salt Lake City, Utah. In: Brown, L.R., Gray, R.H., Hughes, R.M., Meador, M.R. (Eds.), *Effects of Urbanization on Stream Ecosystems*, American Fisheries Society Symposium. Amer Fisheries Soc, 5410 Grosvenor Lane, STE 110, Bethesda, MD 20814-2199 USA, pp. 361–407.
- Culman, S.W., Bukowski, R., Gauch, H.G., Cadillo-Quiroz, H., Buckley, D.H., 2009. T-REX: software for the processing and analysis of T-RFLP data. *BMC Bioinformatics* 10, 171. <https://doi.org/10.1186/1471-2105-10-171>.
- Dann, L.M., Smith, R.J., Jeffries, T.C., McKerral, J.C., Fairweather, P.G., Oliver, R.L., Mitchell, J.G., 2017. Persistence, loss and appearance of bacteria upstream and downstream of a river system. *Mar. Freshw. Res.* 68, 851–862.
- De Meester, L., Vanoverbeke, J., Kilsdonk, L.J., Urban, M.C., 2016. Evolving perspectives on monopolization and priority effects. *Trends Ecol. Evol.* <https://doi.org/10.1016/j.tree.2015.12.009>.
- de Ruiter, P.C., Neutel, A.-M., Moore, J.C., 1995. Energetics, patterns of interaction strengths, and stability in real ecosystems. *Science* 80 (269), 1257 LP-1260.
- Dodds, W.K., Smith, V.H., Lohman, K., 2002. Nitrogen and phosphorus relationships to benthic algal biomass in temperate streams. *Can. J. Fish. Aquat. Sci.* 59, 865–874. <https://doi.org/10.1139/f02-063>.
- Doronina, N.V., Kaporullina, E.N., Trotsenko, Y.A., Nörtemann, B., Bucheli-Witschel, M., Weilenmann, H.-U., Egli, T., 2010. Chelatorans multitrophicus sp. nov., sp. nov. and Chelatorans oligotrophicus sp. nov., aerobic EDTA-degrading bacteria. *Int. J. Syst. Evol. Microbiol.* 60, 1044–1051.
- Drury, B., Rosi-Marshall, E., Kelly, J.J., 2013. Wastewater treatment effluent reduces the abundance and diversity of benthic bacterial communities in urban and suburban rivers. *Appl. Environ. Microbiol.* 79, 1897–1905. <https://doi.org/10.1128/AEM.03527-12>.
- Duarte, S., Cássio, F., Ferreira, V., Canhoto, C., Pascoal, C., 2016. Seasonal variability may affect microbial decomposers and leaf decomposition more than warming in streams. *Microb. Ecol.* 72, 263–276. <https://doi.org/10.1007/s00248-016-0780-2>.
- Eaton, A.D., Franson, M.A.H., Association, A.P.H., Association, A.W.W., Federation, W.E., 2005. *Standard Methods for the Examination of Water & Wastewater*, Standard Methods for the Examination of Water and Wastewater. American Public Health Association.
- Edgar, R.C., 2010. Search and clustering orders of magnitude faster than BLAST. *Bioinformatics* 26, 2460–2461. <https://doi.org/10.1093/bioinformatics/btq461>.
- Eichmiller, J.J., Hicks, R.E., Sadowsky, M.J., 2013. Distribution of genetic markers of fecal pollution on a freshwater sandy shoreline in proximity to wastewater effluent. *Environ. Sci. Technol.* 47, 3395–3402. <https://doi.org/10.1021/es305116c>.
- Ellis, R.J., Morgan, P., Weightman, A.J., Fry, J.C., 2003. Cultivation-dependent and -independent approaches for determining bacterial diversity in heavy-metal-contaminated soil. *Appl. Environ. Microbiol.* 69, 3223–3230. <https://doi.org/10.1128/AEM.69.6.3223-3230.2003>.
- Elmqvist, T., Folke, C., Nyström, M., Peterson, G., Bengtsson, J., Walker, B., Norberg, J., 2003. Response diversity, ecosystem change, and resilience. *Front. Ecol. Environ.* 1, 488–494. [https://doi.org/10.1890/1540-9295\(2003\)001\[0488:RDECAR\]2.0.CO;2](https://doi.org/10.1890/1540-9295(2003)001[0488:RDECAR]2.0.CO;2).
- Etchebehere, C., Errazquin, M.J., Dabert, P., Moletta, R., Muxí, L., 2001. *Comamonas nitratorans* sp. nov., a novel denitrifier isolated from a denitrifying reactor treating landfill leachate. *Int. J. Syst. Evol. Microbiol.* 51, 977–983.
- Ettema, C.H., Lowrance, R., Coleman, D.C., 1999. Riparian soil response to surface nitrogen input: temporal changes in denitrification, labile and microbial C and N pools, and bacterial and fungal respiration. *Soil Biol. Biochem.* 31, 1609–1624. [https://doi.org/10.1016/S0038-0717\(99\)00071-1](https://doi.org/10.1016/S0038-0717(99)00071-1).
- Evans, T.G., Hofmann, G.E., 2012. Defining the limits of physiological plasticity: how gene expression can assess and predict the consequences of ocean change. *Philos. Trans. R. Soc. Lond. B. Biol. Sci.* 367, 1733–1745. <https://doi.org/10.1098/rstb.2012.0019>.
- Fazi, S., Vázquez, E., Casamayor, E.O., Amalfitano, S., Butturini, A., 2013. Stream hydrological fragmentation drives bacterioplankton community composition. *PLoS One* 8, 1–10. <https://doi.org/10.1371/journal.pone.0064109>.
- Fernandez-Gonzalez, N., Huber, J.A., Vallino, J.J., 2016. Microbial communities are well adapted to disturbances in energy input. *bioRxiv* 1, 66050. <https://doi.org/10.1101/066050>.
- Fierer, N., Leff, J.W., Adams, B.J., Nielsen, U.N., Bates, S.T., Lauber, C.L., Owens, S., Gilbert, J.A., Wall, D.H., Caporaso, J.G., 2012. Cross-biome metagenomic analyses of soil microbial communities and their functional attributes. *Proc. Natl. Acad. Sci.* 109, 21390–21395. <https://doi.org/10.1073/pnas.1215210110>.
- Findlay, S.E.G., Sinsabaugh, R.L., 2003. Response of hyporheic biofilm bacterial metabolism and community structure to nitrogen amendments. *Aquat. Microb. Ecol.* 33, 127–136.
- Finneran, K.T., Johnsen, C.V., Lovley, D.R., 2003. *Rhodofera ferrireducens* sp. nov., a psychrotolerant, facultatively anaerobic bacterium that oxidizes acetate with the reduction of Fe(III). *Int. J. Syst. Evol. Microbiol.* 53, 669–673.

- Fisher, J.C., Newton, R.J., Dila, D.K., McLellan, S.L., 2015. Urban Microbial Ecology of a Freshwater Estuary of Lake Michigan, vol. 3. Elem, Washington, D.C., p. 64. <https://doi.org/10.12952/journal.elementa.000064>
- Fitzpatrick, F.A., Peppler, M.C., 2010. Relation of Urbanization to Stream Habitat and Geomorphic Characteristics in Nine Metropolitan Areas of the United States (Scientific Investigations Report).
- Fortunato, C.S., Crump, B.C., 2011. Bacterioplankton community variation across river to ocean environmental gradients. *Microb. Ecol.* 62, 374–382. <https://doi.org/10.1007/s00248-011-9805-z>.
- Fritsche, K., Auling, G., Andreesen, J.R., Lechner, U., 1999. *Defluviobacter lusitiae* gen. nov., sp. nov., a new chlorohexol-degrading member of the alpha-2 subgroup of proteobacteria. *Syst. Appl. Microbiol.* 22, 197–204.
- Frost, T.M., Carpenter, S.R., Ives, A.R., Kratz, T.K., 1995. Species compensation and complementarity in ecosystem function. In: *Linking Species & Ecosystems*. Springer US, Boston, MA, pp. 224–239. https://doi.org/10.1007/978-1-4615-1773-3_22.
- Gessner, M.O., Chauvet, E., 1994. Importance of stream microfungi in controlling breakdown rates of leaf litter. *Ecology* 75, 1807–1817. <https://doi.org/10.2307/1939639>.
- Ghosh, W., Dam, B., 2009. Biochemistry and molecular biology of lithotrophic sulfur oxidation by taxonomically and ecologically diverse bacteria and archaea. *FEMS Microbiol. Rev.* 33, 999–1043. <https://doi.org/10.1111/j.1574-6976.2009.00187.x>.
- Gibbons, S.M., Jones, E., Bearquiver, A., Blackwolf, F., Roundstone, W., Scott, N., Hooker, J., Madsen, R., Coleman, M.L., Gilbert, J.A., 2014. Human and environmental impacts on river sediment microbial communities. *PLoS One* 9, e97435. <https://doi.org/10.1371/journal.pone.0097435>.
- Gilbert, J.A., Field, D., Swift, P., Newbold, L., Oliver, A., Smyth, T., Somerfield, P.J., Huse, S., Joint, I., 2009. The seasonal structure of microbial communities in the Western English Channel. *Environ. Microbiol.* 11, 3132–3139. <https://doi.org/10.1111/j.1462-2920.2009.02017.x>.
- Gilbert, J.A., Steele, J.A., Caporaso, J.G., Steinbrück, L., Reeder, J., Temperton, B., Huse, S., McHardy, A.C., Knight, R., Joint, I., Somerfield, P., Fuhrman, J.A., Field, D., 2012. Defining seasonal marine microbial community dynamics. *ISME J.* 6, 298–308. <https://doi.org/10.1038/ismej.2011.107>.
- Gilliom, R.J., E.J., G.C., Hamilton, P.A., Martin, J.D., Nakagaki, N., Nowell, L.H., Scott, J.C., Stackelberg, P.E., Thelin, G.P., Wolock, D.M., 2006. *Pesticides in the Nation's Streams and Ground Water, 1992–2001*, (No. 1291). Reston, Virginia.
- Glaeser, S.P., Grossart, H.-P., Glaeser, J., 2010. Singlet oxygen, a neglected but important environmental factor: short-term and long-term effects on bacterioplankton composition in a humic lake. *Environ. Microbiol.* 12, 3124–3136. <https://doi.org/10.1111/j.1462-2920.2010.02285.x>.
- Glaeser, S., Kämpfer, P., 2014. The family Sphingomonadaceae. In: *Rosenberg, Eugene, DeLong, Edward F., Lory, Stephen, Stackebrandt, Erko, Thompson, Fabiano* (Eds.), *The Prokaryotes – Alphaproteobacteria and Betaproteobacteria*. Springer-Verlag Berlin Heidelberg, Berlin, pp. 643–707. https://doi.org/10.1007/978-3-642-30197-1_302.
- Glibert, P.M., Burkholder, J.M., Kana, T.M., 2012. Recent insights about relationships between nutrient availability, forms, and stoichiometry, and the distribution, ecophysiology, and food web effects of pelagic and benthic. *Harmful Algae* 14, 231–259. <https://doi.org/10.1016/j.hal.2011.10.023>.
- Gosset, A., Ferro, Y., Durrieu, C., 2016. Methods for evaluating the pollution impact of urban wet weather discharges on biocenosis: a review. *Water Res.* 89, 330–354. <https://doi.org/10.1016/j.watres.2015.11.020>.
- Gremion, F., Chatzinotas, A., Harms, H., 2003. Comparative 16S rDNA and 16S rRNA sequence analysis indicates that Actinobacteria might be a dominant part of the metabolically active bacteria in heavy metal-contaminated bulk and rhizosphere soil. *Environ. Microbiol.* 5, 896–907. <https://doi.org/10.1046/j.1462-2920.2003.00484.x>.
- Griebler, C., Lueders, T., 2009. Microbial biodiversity in groundwater ecosystems. *Freshw. Biol.* 54, 649–677. <https://doi.org/10.1111/j.1365-2427.2008.02013.x>.
- Groffman, P.M., Law, N.L., Belt, K.T., Band, L.E., Fisher, G.T., 2004. Nitrogen fluxes and retention in urban watershed ecosystems. *Ecosystems* 7, 393–403. <https://doi.org/10.1007/s10021-003-0039-x>.
- Harbott, E.L., Grace, M.R., 2005. Extracellular enzyme response to bioavailability of dissolved organic C in streams of varying catchment urbanization. *J. North Am. Benthol. Soc.* 24, 588–601. <https://doi.org/10.1899/04-023.1>.
- Heino, J., Tolkkinen, M., Pirttilä, A.M., Aisala, H., Mykka, H., 2014. Microbial diversity and community-environment relationships in boreal streams. *J. Biogeogr.* 41, 2234–2244. <https://doi.org/10.1111/jbi.12369>.
- Henry, E.A., Devereux, R., Maki, J.S., Gilmour, C.C., Woese, C.R., Mandelco, L., Schauder, R., Remsen, C.C., Mitchell, R., 1994. Characterization of a new thermophilic sulfate-reducing bacterium. *Arch. Microbiol.* 161, 62–69. <https://doi.org/10.1007/BF00248894>.
- Hiraishi, A., Hoshino, Y., Satoh, T., 1991. *Rhodoferrax fermentans* gen. nov., sp. nov., a phototrophic purple nonsulfur bacterium previously referred to as the “Rhodocyclus gelatinosus-like” group. *Arch. Microbiol.* 155, 330–336. <https://doi.org/10.1007/BF00243451>.
- Hiraishi, A., Imhoff, J., 2005. *Roseateles Suyama, Shigematsu, Takaichi, Nodasaka, Fujikawa, Hosoya, Tokiwa, Kanagawa and Hanada 1999, 455 VP*. In: *Bergey's Manual® of Systematic Bacteriology*. Springer, pp. 746–748.
- Hochberg, Y., Benjamini, Y., 1995. Controlling the false discovery rate: a practical and powerful approach to multiple testing. *Source J. R. Stat. Soc. Ser. B* 57, 289–300. <https://doi.org/10.2307/2346101>.
- Holmes, D.E., Bond, D.R., Lovley, D.R., 2004a. Electron transfer by desulfobulbus propionicus to Fe(III) and graphite electrodes. *Appl. Environ. Microbiol.* 70, 1234–1237. <https://doi.org/10.1128/AEM.70.2.1234-1237.2004>.
- Holmes, D.E., Bond, D.R., O'Neil, R.A., Reimers, C.E., Tender, L.R., Lovley, D.R., 2004. Microbial communities associated with electrodes harvesting electricity from a variety of aquatic sediments. *Microb. Ecol.* 48, 178–190. <https://doi.org/10.1007/s00248-003-0004-4>.
- Holmes, D.E., Nevin, K.P., Lovley, D.R., 2004b. Comparison of 16S rRNA, *nifD*, *recA*, *gyrB*, *rpoB* and *fusA* genes within the family Geobacteraceae fam. nov. *Int. J. Syst. Evol. Microbiol.* 54, 1591–1599.
- Hood-Nowotny, R., Umana, N.H.-N., Inselbacher, E., Oswald- Lachouani, P., Wanek, W., 2010. Alternative methods for measuring inorganic, organic, and total dissolved nitrogen in soil. *Soil Sci. Soc. Am. J.* 74, 1018–1027. <https://doi.org/10.2136/sssaj2009.0389>.
- Hothorn, T., Hornik, K., van de Wiel, M., Zeileis, A., 2008. Implementing a class of permutation tests: the coin package. *J. Stat. Softw.* 28, 1–23. <https://doi.org/10.18637/jss.v028.i08>.
- House, M., Ellis, J., Herricks, E.E., Hvidtvej-Jacobsen, T., Seager, J., Lijklema, L., Alderink, H., Clifford, I.T., 1993. Urban drainage-impacts on receiving water quality. *Water Sci. Technol.* 27, 117–158.
- Huang, L.-N., Wever, H. De, Diels, L., 2008. Diverse and distinct bacterial communities induced biofilm fouling in membrane bioreactors operated under different condition. *Environ. Sci. Technol.* 42, 8360–8366. <https://doi.org/10.1021/ES801283Q>.
- Hullar, M.A.J., Kaplan, L.A., Stahl, D.A., 2006. Recurring seasonal dynamics of microbial communities in stream habitats. *Appl. Environ. Microbiol.* 72, 713–722. <https://doi.org/10.1128/AEM.72.1.713-722.2006>.
- Imberger, S.J., Walsh, C.J., Grace, M.R., 2008. More microbial activity, not abrasive flow or shredder abundance, accelerates breakdown of labile leaf litter in urban streams. *J. North Am. Benthol. Soc.* 27, 549–561. <https://doi.org/10.1899/07-123.1>.
- Jackson, B.E., Bhupathiraju, V.K., Tanner, R.S., Woese, C.R., McInerney, M.J., 1999. *Syntrophus aciditrophicus* sp. nov., a new anaerobic bacterium that degrades fatty acids and benzoate in syntrophic association with hydrogen-using microorganisms. *Arch. Microbiol.* 171, 107–114. <https://doi.org/10.1007/s002030050685>.
- Jung, J., Philippot, L., Park, W., 2016. Metagenomic and functional analyses of the consequences of reduction of bacterial diversity on soil functions and bioremediation in diesel-contaminated microcosms. *Sci. Rep.* 6, 23012. <https://doi.org/10.1038/srep23012>.
- Kämpfer, P.A.M.M., 1999. Description of *Pseudaminobacter* gen. nov. with two new species. *Pseudaminobacter. Int. J. Syst. Bacteriol.* 6, 887–897.
- Khan, S.T., Horiba, Y., Yamamoto, M., Hiraishi, A., 2002. Members of the family Comamonadaceae as primary poly(3-hydroxybutyrate-co-3-hydroxyvalerate)-degrading denitrifiers in activated sludge as revealed by a polyphasic approach. *Appl. Environ. Microbiol.* 68, 3206–3214. <https://doi.org/10.1128/AEM.68.7.3206-3214.2002>.
- Kim, J.W., Brawley, S.H., Prochnik, S., Chovatia, M., Grimwood, J., Jenkins, J., LaButti, K., Mavromatis, K., Nolan, M., Zane, M., Schmutz, J., Stiller, J.W., Grossman, A.R., 2016. Genome analysis of Planctomycetes inhabiting blades of the red alga porphyra umbilicalis. *PLoS One* 11, 1–22. <https://doi.org/10.1371/journal.pone.0151883>.
- Kim, S.-J., Weon, H.-Y., Kim, Y.-S., Moon, J.Y., Seok, S.J., Hong, S.-B., Kwon, S.-W., 2012. *Caenimonas terrae* sp. nov., isolated from a soil sample in Korea, and emended description of the genus *Caenimonas* Ryu et al. 2008. *J. Microbiol.* 50, 864–868. <https://doi.org/10.1007/s12275-012-1587-6>.
- Harris, J.K., Gregory Caporaso, J., Walker, J.J., Spear, J.R., Gold, N.J., Robertson, C.E., Hugenholtz, P., Goodrich, J., McDonald, D., Knights, D., Marshall, P., Tufo, H., Knight, R., Pace, N.R., 2013. Phylogenetic stratigraphy in the Guerrero Negro hypersaline microbial mat. *ISME J.* 7, 50–60. <https://doi.org/10.1038/ismej.2012.79>.
- Konrad, C.P., Booth, D.B., Burges, S.J., 2005. Effects of urban development in the Puget Lowland, Washington, on interannual streamflow patterns: consequences for channel form and streambed disturbance. *Water Resour. Res.* 41. <https://doi.org/10.1029/2005WR004097>.
- Kuever, J., 2005. Family I. *Syntrophobacteraceae* fam. nov. In: *Brenner, D.J., Krieg, N.R., Staley, J.T.G.G.M.* (Eds.), *Bergey's Manual of Systematic Bacteriology*. John Wiley & Sons, Springer, New York, p. 1021.
- Kuever, J., Rainey, F.A., Widdel, F., 2005. Class IV. *Deltaproteobacteria* class nov. In: *Brenner, D.J., Krieg, N.R., Staley, J.T.* (Eds.), *Bergey's Manual® of Systematic Bacteriology: Volume Two the Proteobacteria Part C the Alpha-, Beta-, Delta-, and Epsilonproteobacteria*. Springer US, Boston, MA, pp. 922–1144. https://doi.org/10.1007/0-387-29298-5_3.
- Lage, O.M., Bondoso, J., 2014. Planctomycetes and macroalgae, a striking association. *Front. Microbiol.* 5, 267. <https://doi.org/10.3389/fmicb.2014.00267>.
- Langille, M.G.I., Zaneveld, J., Caporaso, J.G., McDonald, D., Knights, D., Reyes, J.A., Clemente, J.C., Burkpile, D.E., Vega Thurber, R.L., Knight, R., Beiko, R.G., Huttenhower, C., 2013. Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. *Nat. Biotechnol.* 31, 814–821. <https://doi.org/10.1038/nbt.2676>.
- Lear, G., Boothroyd, I.K.G., Turner, S.J., Roberts, K., Lewis, G.D., 2009. A comparison of bacteria and benthic invertebrates as indicators of ecological health in streams. *Freshw. Biol.* 54, 1532–1543. <https://doi.org/10.1111/j.1365-2427.2009.02190.x>.
- Lennon, J.T., Jones, S.E., 2011. Microbial seed banks: the ecological and evolutionary implications of dormancy. *Nat. Rev. Microbiol.* 9, 119–130. <https://doi.org/>

- 10.1038/nrmicro2504.
- Lenski, R.E., 2017. Experimental evolution and the dynamics of adaptation and genome evolution in microbial populations. *ISME J.* 11, 2181–2194. <https://doi.org/10.1038/ismej.2017.69>.
- Lewis, G.P., Mitchell, J.D., Andersen, C.B., Haney, D.C., Liao, M.K., Sargent, K.A., 2007. Urban influences on stream chemistry and biology in the Big Brushy Creek watershed, South Carolina. *Water. Air. Soil Pollut.* 182, 303–323. <https://doi.org/10.1007/s11270-007-9340-1>.
- Liang, B., Yang, C., Gong, M., Zhao, Y., Zhang, J., Zhu, C., Jiang, J., Li, S., 2011. Adsorption and degradation of triazophos, chlorpyrifos and their main hydrolytic metabolites in paddy soil from Chaohu Lake, China. *J. Environ. Manage* 92, 2229–2234. <https://doi.org/10.1016/j.jenvman.2011.04.009>.
- Lindström, E.S., Langenheder, S., 2012. Local and regional factors influencing bacterial community assembly. *Environ. Microbiol. Rep.* 4, 1–9. <https://doi.org/10.1111/j.1758-2229.2011.00257.x>.
- Loreau, M., Naeem, S., Inchausti, P., Bengtsson, J., Grime, J.P., Hector, A., Hooper, D.U., Huston, M.A., Raffaelli, D., Schmid, B., Tilman, D., Wardle, D.A., 2001. Biodiversity and ecosystem functioning: current knowledge and future challenges. *Science* (80-.) 294, 804–808. <https://doi.org/10.1126/science.1064088>.
- Lu, X.-M., Lu, P.-Z., 2014. Characterization of bacterial communities in sediments receiving various wastewater effluents with high-throughput sequencing analysis. *Microb. Ecol.* 67, 612–623. <https://doi.org/10.1007/s00248-014-0370-0>.
- Lukasz, K., 2015. Package “outliers”.
- Madigan, M.T., Jung, D.O., Woese, C.R., Achenbach, L.A., 2000. *Rhodiferax antarcticus* sp. nov., a moderately psychrophilic purple nonsulfur bacterium isolated from an Antarctic microbial mat. *Arch. Microbiol.* 173, 269–277. <https://doi.org/10.1007/s002030000140>.
- Maintainer, F.K., Konietzschke, F., 2015. Package “nparcomp” Title Multiple Comparisons and Simultaneous Confidence Intervals.
- Marti, E., Balczár, J.L., 2014. Use of pyrosequencing to explore the benthic bacterial community structure in a river impacted by wastewater treatment plant discharges. *Res. Microbiol.* 165, 468–471. <https://doi.org/10.1016/j.resmic.2014.04.002>.
- Masella, A.P., Bartram, A.K., Truszkowski, J.M., Brown, D.G., Neufeld, J.D., Bartram, A., Lynch, M., Stearns, J., Moreno-Hagelsieb, G., Neufeld, J., Gloor, G., Hummel, R., Macklaim, J., Dickson, J., Fernandes, A., MacPhee, R., Reid, G., Degnan, P., Ochman, H., Caporaso, J., Lauber, C., Walters, W., Berg-lyons, D., Lozupone, C., Turnbaugh, P., Fierer, N., Knight, R., Needleman, S., Wunsch, C., Zhou, H., Li, D., Tam, N., Jiang, X., Zhang, H., Sheng, H., Qin, J., Liu, X., Zou, F., Cock, P., Fields, C., Goto, N., Heuer, M., Rice, P., Muzer, G., Waal, E. de, Uitterlinden, A., Rodrigue, S., Materna, A., Timberlake, S., Blackburn, M., Malmstrom, R., Alm, E., Chisholm, S., Li, W., Godzik, A., Cole, J., Wang, Q., Cardenas, E., Fish, J., Chai, B., Farris, R., Kalam-Syed-Mohideen, A., McGarrell, D., Marsh, T., Garrity, G., Tiedje, J., Cole, J., Chai, B., Farris, R., Wang, Q., Kalam-Syed-Mohideen, A., McGarrell, D., Bandela, A., Cardenas, E., Garrity, G., Tiedje, J., 2012. PANDaseq: paired-end assembler for illumina sequences. *BMC Bioinformatics* 13, 31. <https://doi.org/10.1186/1471-2105-13-31>.
- McArthur, M.D., Richardson, J.S., 2002. Microbial utilization of dissolved organic carbon leached from riparian litterfall. *Can. J. Fish. Aquat. Sci.* 59, 1668–1676. <https://doi.org/10.1139/f02-135>.
- Merbt, S.N., Auguet, J.-C., Blesa, A., Martí, E., Casamayor, E.O., 2015. Wastewater treatment plant effluents change abundance and composition of ammonia-oxidizing microorganisms in mediterranean urban stream biofilms. *Microb. Ecol.* 69, 66–74. <https://doi.org/10.1007/s00248-014-0464-8>.
- Meyer, A.F., Lipson, D.A., Martin, A.P., Schadt, C.W., Schmidt, S.K., 2004. Molecular and metabolic characterization of cold-tolerant alpine soil *Pseudomonas sensu stricto*. *Appl. Environ. Microbiol.* 70, 483–489. <https://doi.org/10.1128/AEM.70.1.483-489.2004>.
- Moss, J.A., Nocker, A., Lepo, J.E., Snyder, R.A., 2006. Stability and change in estuarine biofilm bacterial community diversity. *Appl. Environ. Microbiol.* 72, 5679–5688. <https://doi.org/10.1128/AEM.02773-05>.
- Muzer, G., Stams, A.J.M., 2008. The ecology and biotechnology of sulphate-reducing bacteria. *Nat. Rev. Microbiol.* 6, 441–454.
- Newton, R.J., Bootsma, M.J., Morrison, H.G., Sogin, M.L., McLellan, S.L., 2013. A microbial signature approach to identify fecal pollution in the waters off an urbanized coast of lake Michigan. *Microb. Ecol.* 65, 1011–1023. <https://doi.org/10.1007/s00248-013-0200-9>.
- Newton, R.J., Jones, S.E., Eiler, A., McMahon, K.D., Bertilsson, S., 2011. A guide to the natural history of freshwater lake bacteria. *Microbiol. Mol. Biol. Rev.* 75, 14–49. <https://doi.org/10.1128/MMBR.00028-10>.
- Nieuwdorp, M., Giljijamse, P.W., Pai, N., Kaplan, L.M., 2014. Role of the microbiome in energy regulation and metabolism. *Gastroenterology* 146, 1525–1533. <https://doi.org/10.1053/j.gastro.2014.02.008>.
- Obernosterer, I., Catala, P., Lebaron, P., West, N.J., 2011. Distinct bacterial groups contribute to carbon cycling during a naturally iron fertilized phytoplankton bloom in the Southern Ocean. *Limnol. Oceanogr.* 56, 2391–2401. <https://doi.org/10.4319/lo.2011.56.6.2391>.
- Ohio Environmental Protection Agency, Division of Surface Water, 2003. Total Maximum Daily Loads for the Lower Cuyahoga River.
- Oksanen, J., Blanchet, F., Guillaume Friendly, M., Kindt, R., Legendre, P., McGlenn, D., Minchin, P.R., O'Hara, R.B., Simpson, G.L., Solymos, P., Stevens, M.H., Szoecs, E., Wagner, H., 2007. The Vegan Package. *Community Ecology Package*.
- Östman, Ö., Drakare, S., Kritzberg, E.S., Langenheder, S., Logue, J.B., Lindström, E.S., 2010. Regional invariance among microbial communities. *Ecol. Lett.* 13, 118–127. <https://doi.org/10.1111/j.1461-0248.2009.01413.x>.
- Paerl, H.W., Hall, N.S., Peierls, B.L., Rossignol, K.L., Joyner, A.R., 2014. Hydrologic variability and its control of phytoplankton community structure and function in two shallow, coastal, lagoonal ecosystems: the neuse and new river estuaries, North. *Estuar. Coasts* 37, 31–45. <https://doi.org/10.1007/S12237-013-9686-0>.
- Parent-Raoult, C., Volatier, L., Boisson, J.-C., 2005. Response of periphytic communities to simulated thunderstorm discharge in artificial channels: influence of duration of exposure. *La Houille Blanche* 84–90. <https://doi.org/10.1051/lhb:200506007>.
- Parent-Raoult, Charlotte, Boisson, J.-C., 2007. Impacts of urban rainfall discharges (RUTP) on aquatic environments: state of knowledge. *J. Water Sci.* 20, 229–239.
- Parr, T.B., Smucker, N.J., Bentsen, C.N., Neale, M.W., 2015. Potential roles of past, present, and future urbanization characteristics in producing varied stream responses Potential roles of past, present, and future urbanization characteristics in producing varied stream responses. *Freshw. Sci.* 35, 436–443. <https://doi.org/10.1086/685030>.
- Paul, D., Pandey, G., Meier, C., van der Meer, J., Jain, R.K., 2006. Bacterial community structure of a pesticide-contaminated site and assessment of changes induced in community structure during bioremediation. *FEMS Microbiol. Ecol.* 57, 116–127. <https://doi.org/10.1111/j.1574-6941.2006.00103.x>.
- Paul, M.J., Meyer, J.L., 2001. Streams in the urban landscape. *Annu. Rev. Ecol. Syst.* 33, 333–365.
- Pedros-Alió, C., 2006. Marine microbial diversity: can it be determined? *Trends Microbiol.* 14, 257–263. <https://doi.org/10.1016/j.TIM.2006.04.007>.
- Perryman, S.E., Rees, G.N., Walsh, C.J., 2008. Analysis of denitrifying communities in streams from an urban and non-urban catchment. *Aquat. Ecol.* 42, 95–101. <https://doi.org/10.1007/s10452-007-9085-3>.
- Perryman, S.E., Rees, G.N., Walsh, C.J., Grace, M.R., 2011. Urban stormwater runoff drives denitrifying community composition through changes in sediment texture and carbon content. *Microb. Ecol.* 61, 932–940. <https://doi.org/10.1007/s00248-011-9833-8>.
- Petchey, O.L., Gaston, K.J., 2002. Functional diversity (FD), species richness and community composition. *Ecol. Lett.* 5, 402–411. <https://doi.org/10.1046/j.1461-0248.2002.00339.x>.
- Philippot, L., Andersson, S.G.E., Battin, T.J., Prosser, J.L., Schimel, J.P., Whitman, W.B., Hallin, S., 2010. The ecological coherence of high bacterial taxonomic ranks. *Nat. Rev. Microbiol.* 8, 523–529. <https://doi.org/10.1038/nrmicro2367>.
- Poff, N.L., Bledsoe, B.P., Cuhaciyan, C.O., 2006. Hydrologic variation with land use across the contiguous United States: geomorphic and ecological consequences for stream ecosystems. *Geomorphology* 79, 264–285. <https://doi.org/10.1016/j.geomorph.2006.06.032>.
- Portillo, M.C., Anderson, S.P., Fierer, N., 2012. Temporal variability in the diversity and composition of stream bacterioplankton communities. *Environ. Microbiol.* 14, 2417–2428. <https://doi.org/10.1111/j.1462-2920.2012.02785.x>.
- Pujalte, M.J., Lucena, T., Ruvira, M.A., Ruiz Arahál, D., Carmen Macián, M., 2014. The family rhodobacteraceae. In: Rosenberg, E., et al. (Eds.), *The Prokaryotes*. Springer Berlin Heidelberg, Berlin, Heidelberg, pp. 439–512. https://doi.org/10.1007/978-3-642-30197-1_377.
- Qu, X., Ren, Z., Zhang, H., Zhang, M., Zhang, Y., Liu, X., Peng, W., 2017. Influences of anthropogenic land use on microbial community structure and functional potentials of stream benthic biofilms. *Sci. Rep.* 7, 15117. <https://doi.org/10.1038/s41598-017-15624-x>.
- R Development Core Team, 2014. R: A Language and Environment for Statistical Computing.
- Rehman, A., Lepage, P., Nolte, A., Hellmig, S., Schreiber, S., Ott, S.J., 2010. Transcriptional activity of the dominant gut mucosal microbiota in chronic inflammatory bowel disease patients. *J. Med. Microbiol.* 59, 1114–1122. <https://doi.org/10.1099/jmm.0.021170-0>.
- Reiss, J., Bridle, J.R., Montoya, J.M., Woodward, G., 2009. Emerging horizons in biodiversity and ecosystem functioning research. *Trends Ecol. Evol.* 24, 505–514. <https://doi.org/10.1016/j.TREE.2009.03.018>.
- Röling, W.F.M., 2014. The family Geobacteraceae. In: Rosenberg, E., DeLong, E.F., Lory, S., Stackebrandt, E., Thompson, F. (Eds.), *The Prokaryotes: Deltaproteobacteria and Epsilonproteobacteria*. Springer Berlin Heidelberg, Berlin, Heidelberg, pp. 157–172. https://doi.org/10.1007/978-3-642-39044-9_381.
- Romine, M.F., Fredrickson, J.K., Li, S.-M.W., 1999. Induction of aromatic catabolic activity in *Sphingomonas aromaticivorans* strain F19. *J. Ind. Microbiol. Biotechnol.* 23, 303–313.
- Rosa, J., Ferreira, V., Canhoto, C., Graca, M.A.S., 2013. Combined effects of water temperature and nutrients concentration on periphyton respiration—implications of global change. *Int. Rev. 98*, 14–23. <https://doi.org/10.1002/iroh.201201510>.
- Rosenberg, E., Edward, E.-I.-C., DeLong, F., Lory, S., Stackebrandt, E., Thompson, F., 2013. *The Prokaryotes*. Springer Berlin Heidelberg, Berlin, Heidelberg. <https://doi.org/10.1007/978-3-642-31331-8>.
- Roy, A.H., Rhea, L.K., Mayer, A.L., Shuster, W.D., Beaulieu, J.J., Hopton, M.E., Morrison, M.A., St Amand, A., 2014. How much is enough? Minimal responses of water quality and stream biota to partial retrofit stormwater management in a suburban neighborhood. *PLoS One* 9, e85011. <https://doi.org/10.1371/journal.pone.0085011>.
- Roy, A.H., Wenger, S.J., Fletcher, T.D., Walsh, C.J., Ladson, A.R., Shuster, W.D., Thurston, H.W., Brown, R.R., 2008. Impediments and solutions to sustainable, watershed-scale urban stormwater management: lessons from Australia and the United States. *Environ. Manage* 42, 344–359. <https://doi.org/10.1007/s00267-008-9119-1>.

- Sánchez-Peinado, M. del M., González-López, J., Martínez-Toledo, M.V., Pozo, C., Rodelas, B., 2010. Influence of linear alkylbenzene sulfonate (LAS) on the structure of Alphaproteobacteria, Actinobacteria, and Acidobacteria communities in a soil microcosm. *Environ. Sci. Pollut. Res.* 17, 779–790. <https://doi.org/10.1007/s11356-009-0180-y>.
- Schindler, D.W., 1990. Experimental perturbations of whole lakes as tests of hypotheses concerning ecosystem structure and function. *Oikos* 57, 25. <https://doi.org/10.2307/3565733>.
- Schink, B., 1997. Energetics of syntrophic cooperation in methanogenic degradation. *Microbiol. Mol. Biol. Rev.* 61, 262–280.
- Schwermer, C.U., Lavič, G., Abed, R.M.M., Dunsmore, B., Ferdelman, T.G., Stoodley, P., Gieseke, A., de Beer, D., 2008. Impact of nitrate on the structure and function of bacterial biofilm communities in pipelines used for injection of seawater into oil fields. *Appl. Environ. Microbiol.* 74, 2841–2851. <https://doi.org/10.1128/AEM.02027-07>.
- Shade, A., Caporaso, J.G., Handelsman, J., Knight, R., Fierer, N., 2013. A meta-analysis of changes in bacterial and archaeal communities with time. *ISME J.* 7, 1493–1506. <https://doi.org/10.1038/ismej.2013.54>.
- Shelton, D.R., Tiedje, J.M., 1984. Isolation and partial characterization of bacteria in an anaerobic consortium that mineralizes 3-chlorobenzoic acid. *Appl. Environ. Microbiol.* 48, 840–848.
- Sliva, L., Williams, D.D., 2005. Exploration of riffle-scale interactions between abiotic variables and microbial assemblages in the hyporheic zone. *Can. J. Fish. Aquat. Sci.* 62, 276–290. <https://doi.org/10.1139/f04-190>.
- Sprenger, G.A., 1993. Approaches to broaden the substrate and product range of the ethanologenic bacterium *Zymomonas mobilis* by genetic engineering. *J. Biotechnol.* [https://doi.org/10.1016/0168-1656\(93\)90087-4](https://doi.org/10.1016/0168-1656(93)90087-4).
- Staley, C., Gould, T.J., Wang, P., Phillips, J., Cotner, J.B., Sadowsky, M.J., 2014. Bacterial community structure is indicative of chemical inputs in the Upper Mississippi River. *Front. Microbiol.* 5, 524. <https://doi.org/10.3389/fmicb.2014.00524>.
- Staley, C., Unno, T., Gould, T.J., Jarvis, B., Phillips, J., Cotner, J.B., Sadowsky, M.J., 2013. Application of Illumina next-generation sequencing to characterize the bacterial community of the Upper Mississippi River. *J. Appl. Microbiol.* 115, 1147–1158. <https://doi.org/10.1111/jam.12323>.
- Stein, L.Y., Roy, R., Dunfield, P.F., 2012. Aerobic Methanotrophy and Nitrification: Processes and Connections. *eLs.* <https://doi.org/10.1002/9780470015902.a0022213>.
- Stevenson, B.S., Eichorst, S.A., Wertz, J.T., Schmidt, T.M., Breznak, J.A., 2004. New strategies for cultivation and detection of previously uncultured microbes. *Appl. Environ. Microbiol.* 70, 4748–4755. <https://doi.org/10.1128/AEM.70.8.4748-4755.2004>.
- Stoecker, K., Bendinger, B., Schöning, B., Nielsen, P.H., Nielsen, J.L., Baranyi, C., Toenshoff, E.R., Daims, H., Wagner, M., 2006. Cohn's crenothrix is a filamentous methane oxidizer with an unusual methane monooxygenase. *Proc. Natl. Acad. Sci. U. S. A.* 103, 2363–2367.
- Storey, R.G., Fulthorpe, R.R., Williams, D.D., 1999. Perspectives and predictions on the microbial ecology of the hyporheic zone. *Freshw. Biol.* 41, 119–130. <https://doi.org/10.1046/j.1365-2427.1999.00377.x>.
- Swingle, W.D., Sadekar, S., Mastrian, S.D., Matthies, H.J., Hao, J., Ramos, H., Acharya, C.R., Conrad, A.L., Taylor, H.L., Dejesa, L.C., Shah, M.K., O'hualachain, M.E., Lince, M.T., Blankenship, R.E., Beatty, J.T., Touchman, J.W., 2007. The complete genome sequence of *Roseobacter denitrificans* reveals a mixotrophic rather than photosynthetic metabolism. *J. Bacteriol.* 189, 683–690. <https://doi.org/10.1128/JB.01390-06>.
- Tang, X., Chao, J., Gong, Y., Wang, Y., Wilhelm, S.W., Gao, G., 2017. Spatiotemporal dynamics of bacterial community composition in large shallow eutrophic Lake Taihu: high overlap between free-living and particle-attached assemblages. *Limnol. Oceanogr.* 62, 1366–1382. <https://doi.org/10.1002/lno.10502>.
- Tertuliani, J.S., Alvarez, D.A., Furlong, E.T., Meyer, M.T., Zaugg, S.D., Koltun, G.F., 2008. Occurrence of Organic Wastewater Compounds in the Tinkers Creek Watershed and Two Other Tributaries to the Cuyahoga River, Northeast Ohio (Scientific Investigations Report).
- Valet, H.M., Dahm, C.N., Campana, M.E., Morrice, J.A., Baker, M.A., Fellows, C.S., 1997. Hydrologic influences on groundwater-surface water ecotones: heterogeneity in nutrient composition and retention. *J. North Am. Benthol. Soc.* 16, 239–247. <https://doi.org/10.2307/1468254>.
- Vetterli, A., Hyytiäinen, K., Ahjos, M., Auvinen, P., Paulin, L., Hietanen, S., Leskinen, E., 2015. Seasonal patterns of bacterial communities in the coastal brackish sediments of the Gulf of Finland, Baltic Sea. *Estuar. Coast. Shelf Sci.* 165, 86–96. <https://doi.org/10.1016/j.ecss.2015.07.049>.
- Wagner, R.J., Boulger, R.W.J., Oblinger, C.J., Smith, B.A., Wagner, R.J., Boulger Jr., R.W., Oblinger, C.J., Smith, B., 2006. Guidelines and Standard Procedures for Continuous Water-quality Monitors: Station Operation, Record Computation, and Data Reporting. USGS Tech. Methods 1–D3, 96.
- Wakelin, S.A., Colloff, M.J., Kookana, R.S., 2008. Effect of wastewater treatment plant effluent on microbial function and community structure in the sediment of a freshwater stream with variable seasonal flow. *Appl. Environ. Microbiol.* 74, 2659–2668. <https://doi.org/10.1128/AEM.02348-07>.
- Walker, C.E., Pan, Y., 2006. Using diatom assemblages to assess urban stream conditions. In: *Advances in Algal Biology: a Commemoration of the Work of Rex Lowe*. Springer Netherlands, Dordrecht, pp. 179–189. https://doi.org/10.1007/1-4020-5070-4_13.
- Wallrabenstein, C., Schink, B., 1994. Evidence of reversed electron transport in syntrophic butyrate or benzoate oxidation by *Syntrophomonas wolfei* and *Syntrophus buswellii*. *Arch. Microbiol.* 162, 136–142. <https://doi.org/10.1007/BF00264387>.
- Walsh, C.J., Fletcher, T.D., Ladson, A.R., 2005. Stream restoration in urban catchments redesigning stormwater systems: looking to the catchment to save the stream. *J. North Am. Benthol. Soc.* 24, 690–705. <https://doi.org/10.1899/04-020.1>.
- Wang, S.-Y., Sudduth, E.B., Wallenstein, M.D., Wright, J.P., Bernhardt, E.S., 2011. Watershed urbanization alters the composition and function of stream bacterial communities. *PLoS One* 6, e22972. <https://doi.org/10.1371/journal.pone.0022972>.
- Weatherburn, M.W., 1967. Phenol-hypochlorite reaction for determination of ammonia. *Anal. Chem.* 39, 971–974. <https://doi.org/10.1021/AC60252A045>.
- Wenger, S.J., Roy, A.H., Jackson, C.R., Bernhardt, E.S., Carter, T.L., Filoso, S., Gibson, C.A., Hession, W.C., Kaushal, S.S., Martí, E., Meyer, J.L., Palmer, M.A., Paul, M.J., Purcell, A.H., Ramírez, A., Rosemond, A.D., Schofield, K.A., Sudduth, E.B., Walsh, C.J., 2009. Twenty-six key research questions in urban stream ecology: an assessment of the state of the science. *J. North Am. Benthol. Soc.* 28, 1080–1098. <https://doi.org/10.1899/08-186.1>.
- Wickham, H., Winston, C., RStudio, 2016. ggplot2: Create Elegant Data Visualisations Using the Grammar of Graphics. CRAN.
- Willems, A., 2014. The family Comamonadaceae. In: Rosenberg, Eugene, DeLong, Edward F., Lory, Stephen, Stackebrandt, Erko, Thompson, Fabiano (Eds.), *The Prokaryotes – Alphaproteobacteria and Betaproteobacteria*. Springer Berlin Heidelberg, Berlin, pp. 777–851. https://doi.org/10.1007/978-3-642-30197-1_238.
- Wittebolle, L., Marzorati, M., Clement, L., Balloi, A., Daffonchio, D., Heylen, K., De Vos, P., Verstraete, W., Boon, N., 2009. LETTERS Initial community evenness favours functionality under selective stress. *Nature* 458. <https://doi.org/10.1038/nature07840>.
- Wu, W., Yang, L., Wang, J., 2013. Denitrification using PBS as carbon source and biofilm support in a packed-bed bioreactor. *Environ. Sci. Pollut. Res.* 20, 333–339. <https://doi.org/10.1007/s11356-012-0926-9>.
- Wymore, A.S., Liu, C.M., Hungate, B.A., Schwartz, E., Price, L.B., Whitham, T.G., Marks, J.C., 2016. The influence of time and plant species on the composition of the decomposing bacterial community in a stream ecosystem. *Microb. Ecol.* 71, 825–834. <https://doi.org/10.1007/s00248-016-0735-7>.
- Yannarell, A.C., Kent, A.D., Lauster, G.H., Kratz, T.K., Triplett, E.W., 2003. Temporal patterns in bacterial communities in three temperate lakes of different trophic statu. *Microb. Ecol.* 46, 391–405.
- Youssef, N.H., Elshahed, M.S., 2014. The phylum Planctomycetes. In: Rosenberg, E., DeLong, E.F., Lory, S., Stackebrandt, E., Thompson, F. (Eds.), *The Prokaryotes: Other Major Lineages of Bacteria and the Archaea*. Springer Berlin Heidelberg, Berlin, Heidelberg, pp. 759–810. https://doi.org/10.1007/978-3-642-38954-2_155.
- Yu, S.-X., Pang, Y.-L., Wang, Y.-C., Li, J.-L., Qin, S., 2017. Spatial variation of microbial communities in sediments along the environmental gradients from Xiaqing River to Laizhou Bay. *Mar. Pollut. Bull.* 120, 90–98. <https://doi.org/10.1016/j.marpolbul.2017.04.059>.
- Zeglin, L.H., 2015. Stream microbial diversity in response to environmental changes: review and synthesis of existing research. *Front. Microbiol.* 6, 454. <https://doi.org/10.3389/fmicb.2015.00454>.
- Zeng, Y., Kasalický, V., Šimek, K., Koblížek, M., 2012. Genome sequences of two freshwater betaproteobacterial isolates, limnophilic species strains Rim28 and Rim47, indicate their capabilities as both photoautotrophs and ammonia oxidizers. *J. Bacteriol.* 194, 6302–6303. <https://doi.org/10.1128/JB.01481-12>.
- Zhang, M., Yu, N., Chen, L., Jiang, C., Tao, Y., Zhang, T., Chen, J., Xue, D., 2012. Structure and seasonal dynamics of bacterial communities in three urban rivers in China. *Aquat. Sci.* 74, 113–120. <https://doi.org/10.1007/s00027-011-0201-z>.
- Zhang, X., Gu, Q., Long, X.-E., Li, Z.-L., Liu, D.-X., Ye, D.-H., He, C.-Q., Liu, X.-Y., Väänänen, K., Chen, X.-P., 2016. Anthropogenic activities drive the microbial community and its function in urban river sediment. *J. Soils Sediments* 16, 716–725. <https://doi.org/10.1007/s11368-015-1246-8>.
- Zoppini, A., Amalfitano, S., Fazi, S., Puddu, A., 2010. Dynamics of a benthic microbial community in a riverine environment subject to hydrological fluctuations (Mulargia River, Italy). *Hydrobiologia* 657, 37–51. <https://doi.org/10.1007/s10750-010-0199-6>.