### Can stream microbial communities provide information about hydrology?

### The streamwater microbiome encodes hydrologic data across scales

**Citation** URycki, D. R., Bassiouni, M., Good, S. P., Crump, B. C., & Li, B. (2022). The streamwater microbiome encodes hydrologic data across scales. *Science of the Total Environment*, 849, 157911. http://dx.doi.org/10.1016/j.scitotenv.2022.157911

Can the microbiome of streamwater be used to investigate hydrology? Can studying microbial taxonomy and abundance provide insight into hydrologic characteristics of a watershed? Researchers investigated whether patterns in stream microbial communities can be used to investigate and understand stream hydrology. Microbial community composition has been associated with stream scale and landscape scale spatial characteristics and geomorphology, which are related to hydrologic function. To determine if microbiomes can be used to study open questions in hydrology, the scientists analyzed taxonomic composition of the microbial community along with hydrological metrics that are used to describe watershed hydrology and water balance characteristics.

#### What were the commonly identified microbial taxa?

• Across all samples, the most abundant microbial taxon was gammaproteobacteria and phylum Bacteroidota was also common. Although less abundant, Verrucomicrobiota, Actinobacteriota, Alphaproteobacteria, Cyanobacteria, and Planctomycetota were also commonly detected.

#### How many taxa were identified to have mutual information with hydrologic metrics?

- Out of 256 microbial taxa common among watersheds, 102 had statistically significant mutual information with at least one hydrologic metric. Likewise, each hydrologic metric shared mutual information with at least one microbial taxon.
- Across all hydrologic metrics, an average of 9.7% of taxa share information with each metric with a median reduction of uncertainty of 15.6%.

# Does the amount of shared information differ between the microbiome and hydrologic metrics at different spatial scales? What does this tell us?

- Absolute discharge metrics share more mutual information with microbial taxa and share information with a greater number of taxa than do specific (per unit area) discharge metrics.
- Patterns of mutual information between microbial taxa and absolute discharge and specific discharge indicate that distinct portions of the microbiome integrate information differently across the broad range of hydrologic processes.
- Summer microbial communities shared information with metrics related to the general hydrologic regime, indicating that the microbiome is shaped by catchment-level characteristics such as geomorphology and climate.

# Does the amount of information shared between the microbiome and discharge differ at different temporal scales?

• The amount of mutual information between microbial taxa and hydrological processes is significantly higher for mean monthly discharge and seasonal flow durations than for mean daily discharge. However, the mean number of informative taxa is similar across categories.

# Is the amount of mutual information related to the abundance of each microbial taxon or the number of sites at which it is identified?

- For each category of hydrologic metrics, the mutual information with microbial taxa increases linearly with the log of abundance a microbial taxon across all sites.
- The strongest correlation for mutual information is with the number of sites at which a microbial taxon is identified.

### What additional research areas would further our understanding of how streamwater microbial communities can provide information on hydrologic processes?

- The authors suggest seasonal sampling to investigate why there were a greater number of informative taxa for monthly discharge in winter months than in the summer months and whether the pattern holds across seasons.
- The researchers recommend sampling at a higher temporal resolution to investigate the timescales at which the microbiome responds to hydrologic conditions and the how the magnitude of responses differ with hydrologic metrics.
- The authors suggest analyzing which taxa share information with specific hydrologic metrics and determining whether and to what extent these sets of taxa overlap.
- The authors note that identifying the taxonomy, phylogeny, and functional roles of informative taxa will aid in understanding the complex relationships between hydrology and the microbiome.

#### **Research Approach/Methods**

- To sample the microbiome, the researchers collected water samples at summer baseflow levels from 81 sites near active stream gauges across three Oregon watersheds. Samples included microbes from subsurface and sediment areas and aquatic bacterioplankton.
- The researchers PCR-amplified the 16S rRNA gene and identified distinct amplified sequence variants (ASVs) that correspond to microbial taxa. The authors focused their subsequent analyses on the 256 ASVs that were common across the three watersheds.
- They excluded samples that amplified fewer than 1450 sequences, resulting in 64 sample sites for analysis. The sites were located on headwaters, tributaries, and outlets of all three watersheds.
- To characterize hydrology, specifically discharge dynamics, the researchers used mean daily discharge (m<sup>3</sup>/sec) measured by stream gauges at the 64 sites identified during microbiome collection to calculate 76 metrics in 3 categories: daily discharge, mean monthly discharge, and seasonal high and low flow.
- The authors used information theory to determine the mutual information shared between each microbial taxon and hydrologic metric, identify the statistically significant relationships, and calculate how much each microbial taxon reduced uncertainty for each hydrologic metric.

**Keywords** watershed hydrology, 16S metabarcoding, information theory, mutual information, Pacific Northwest

Images

RANK 1



**Figure 3 in URycki et al. 2022.** Heatmap illustrating the normalized mutual information ( $I(X;Y)_{norm}$  [bits/bit]) between streamwater microbial amplified sequence variants (X = ASVs) and absolute discharge (Y = Q; top), specific discharge (Y = q; bottom) hydrologic metrics, as well as basin drainage area (top, bottom line), for study streams in Oregon, USA. We collected microbial DNA samples in summer in the Willamette (2017), Deschutes (2017), and John Day (2018) basins. Hydrologic metrics include daily discharge at time lags *n* days prior to DNA sample day *t* ( $Q_{(t-n days)}, q_{(t-n days)}$ ), mean monthly discharge ( $\bar{Q}_{mon}, \bar{Q}_{mon}$ ) for months October to September, and seasonal high and low flow durations ( $Q_P$ ,

s,  $q_P$ , s for P = 5- and 95 % exceedance probability for seasons s = fall [OND], winter [JFM], spring [AMJ], summer [JAS], and annually [Ann]).





**Figure 7 in URycki et al. 2022**. Normalized mutual information ( $I(ASV;Y)_{norm}$  [bits/bit]) between hydrologic metrics and streamwater microbial taxa versus the log of abundance of taxa in streams across Oregon, USA. We collected microbial DNA samples in summer in the Willamette (2017), Deschutes (2017), and John Day (2018) basins. Hydrologic metrics include daily discharge at time lags up to n = 30 days prior to DNA sample collection ( $Q_{(t-n days)}$ ; green circles), mean monthly discharge ( $\bar{Q}_{mon}$ ; purple triangles), and seasonal high and low flow durations ( $Q_P$ , s; 5- and 95 % exceedence probability for all seasons and annually; blue squares). Legend shows Pearson's correlation (r) and p-value of the linear regression.

#### RANK 3



**Figure 1 in URycki et al. 2022**. Map of co-located stream gages and streamwater DNA sampling sites across Willamette (2017), Deschutes (2017), and John Day (2018) basins in Oregon, USA. Marker colors indicate mean annual precipitation in sample catchments (United States Geological Survey, 2017). Inset indicates number of unique and common microbial amplified sequence variants detected in *n* samples across each basin.