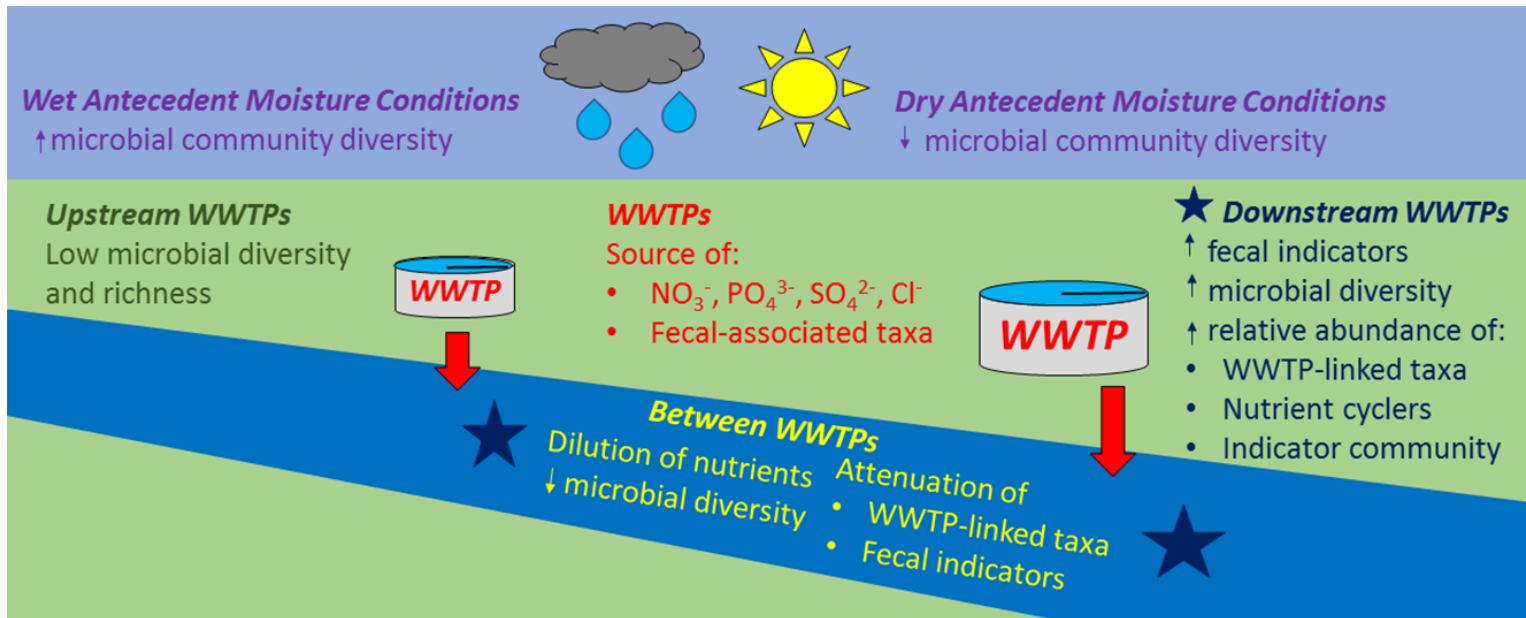


The impact of wastewater treatment plant effluent on the composition of microbial communities within receiving streams

Jacob Price^a, Sarah Ledford^b, Michael Ryan^a, Laura Toran^b, and Christopher Sales^a

^a Drexel University, ^b Temple University



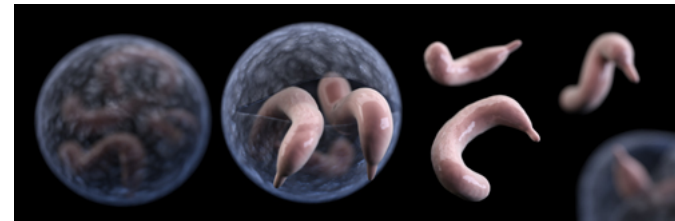
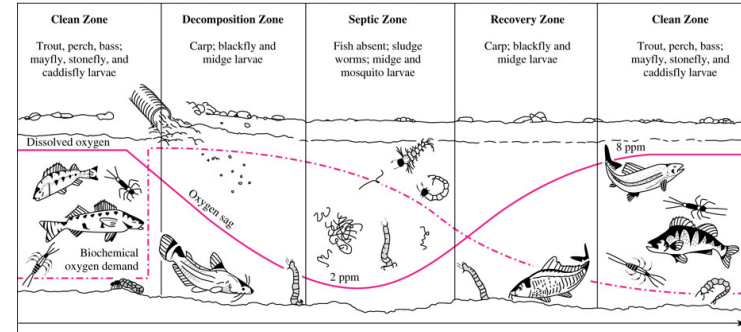
Delaware Watershed Research Conference

November 8th, 2017



Introduction

- BOD/COD
- Excess Nutrients
 - N, P
- Pathogens/Parasites
 - *Cryptosporidium*
 - *Giardia lamblia*





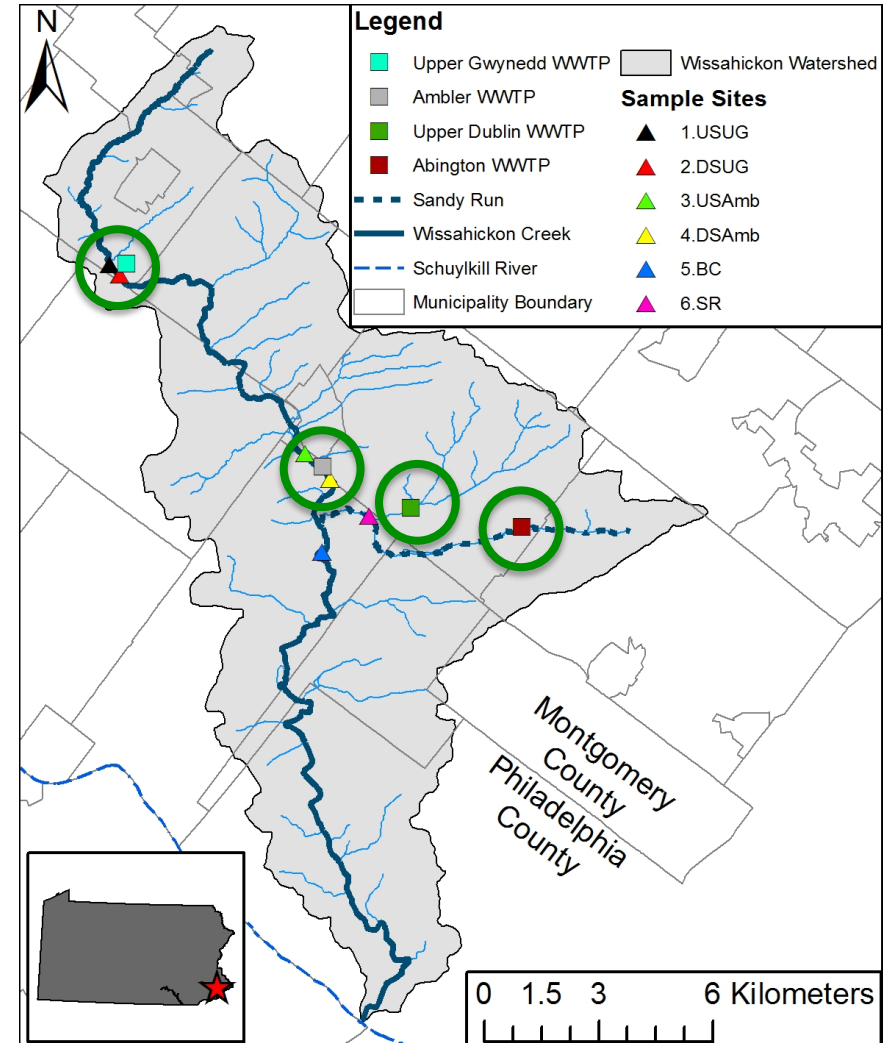
Methods

Sampling – 6 sites / 2 days

- Upstream/downstream
 - Upper Gwynedd WWTP
 - Ambler WWTP
- Sandy Run
- Below confluence Wissahickon Creek and Sandy Run

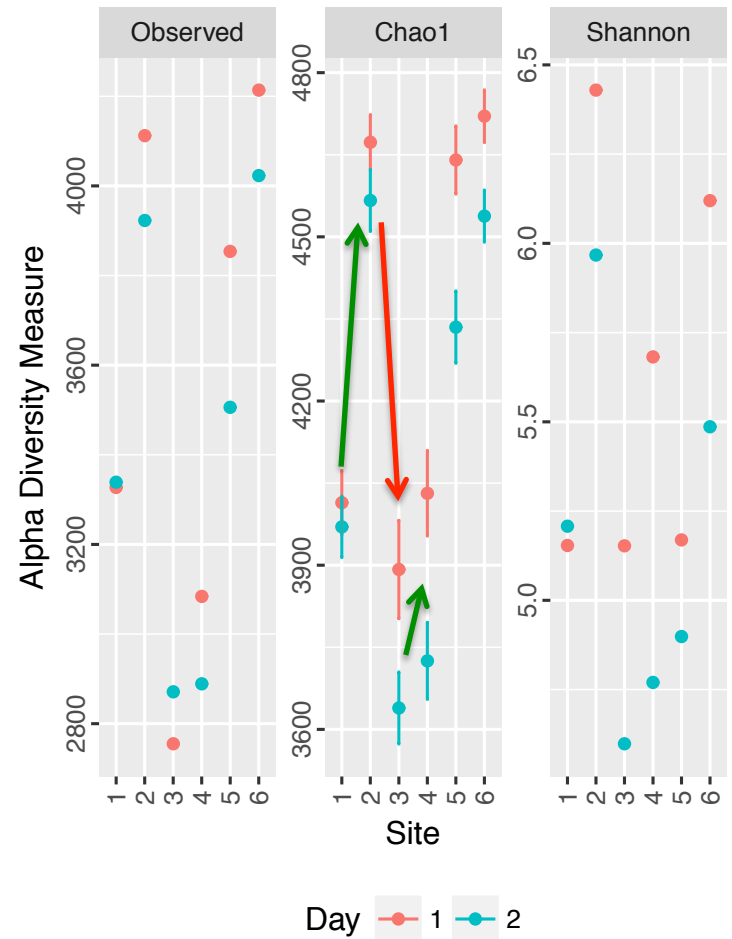
Analysis

- **Water chemistry**
- qPCR – fecal-associated taxa
 - *B. dorei* - Human-specific
 - *Bacteroides spp.* – non-specific
- 16s rDNA amp seq
 - Full community
 - **Indicator subset** (McLellan et al, 2010)
 - Bifidobacteriales,
 - Bacteroidales, and
 - Clostridiales



Alpha Diversity

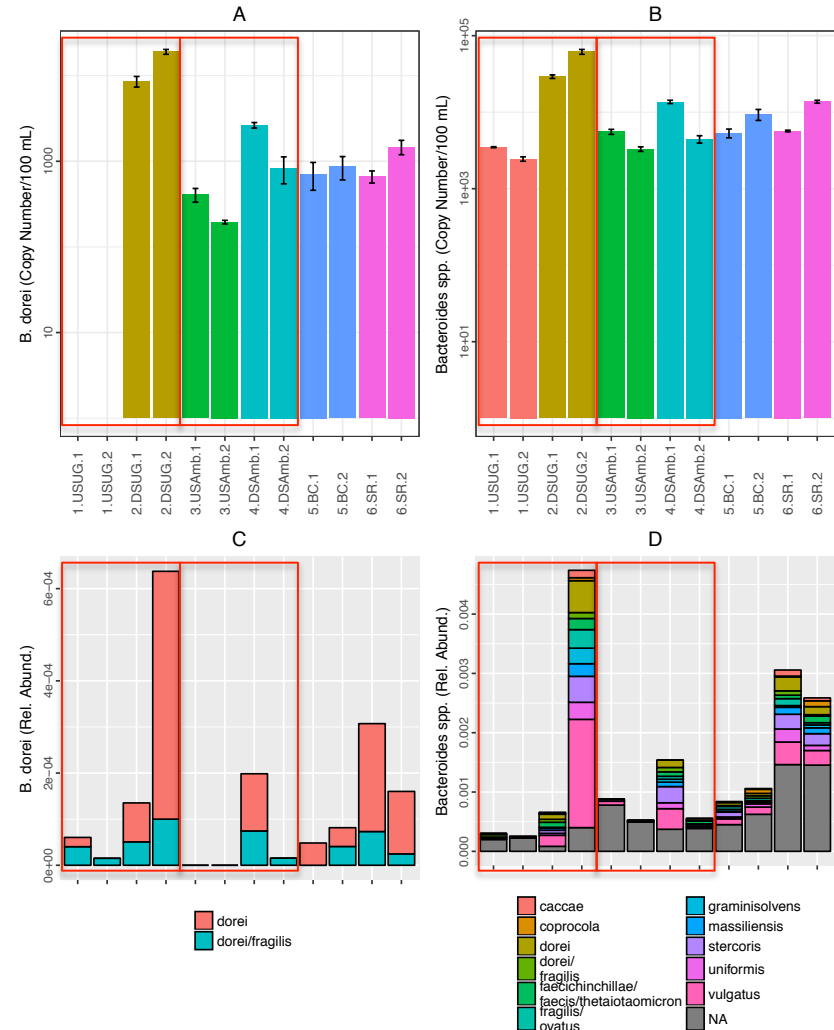
- Effluent sources increased species richness
 - Upper Gwynedd: ~ 630
 - Ambler: ~ 110
- Richness decreased between the two plants
 - ~ 850 taxa
- Effluent source appears to result in a net loss of diversity





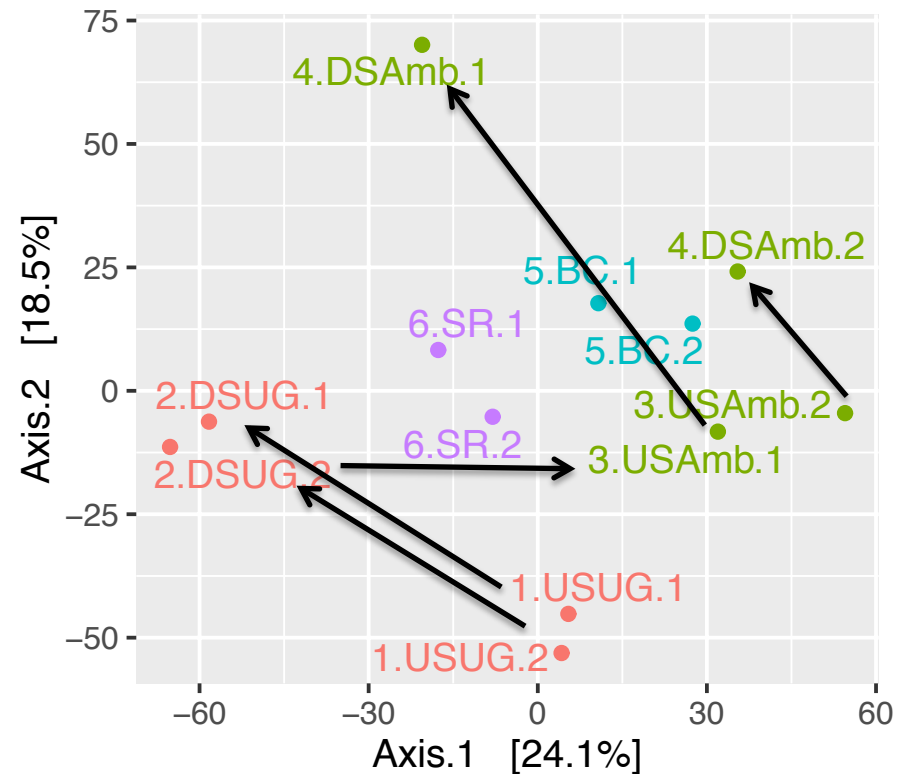
Fecal Indicators: qPCR vs Amp Seq

- Effluent outflows significant sources
 - *B. dorei*
 - *Bacteroides* spp.
- (Abs & Rel) Abundances decreased between the two WWTP



Ordination - PCA

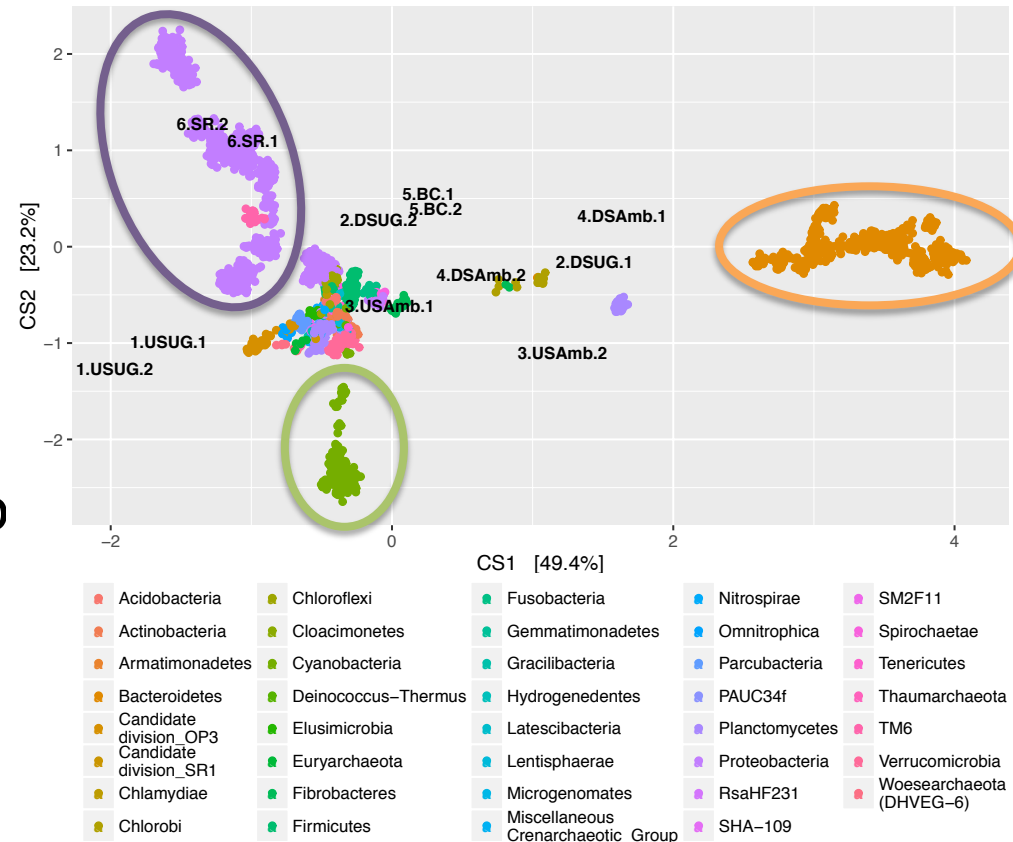
- Effluent sources result in repeatable shifts in community composition
- Major changes in community structure also occur between Upper Gwynedd and Ambler WWTP





Ordination - DPCoA

- Effluent sources result in repeatable shifts in community composition
 - Bacteroidetes increase
 - Cyanobacteria decrease
- Major changes in community structure also occur between Upper Gwynedd and Ambler WWTP
 - Proteobacteria increase
 - Bacteroidetes decrease



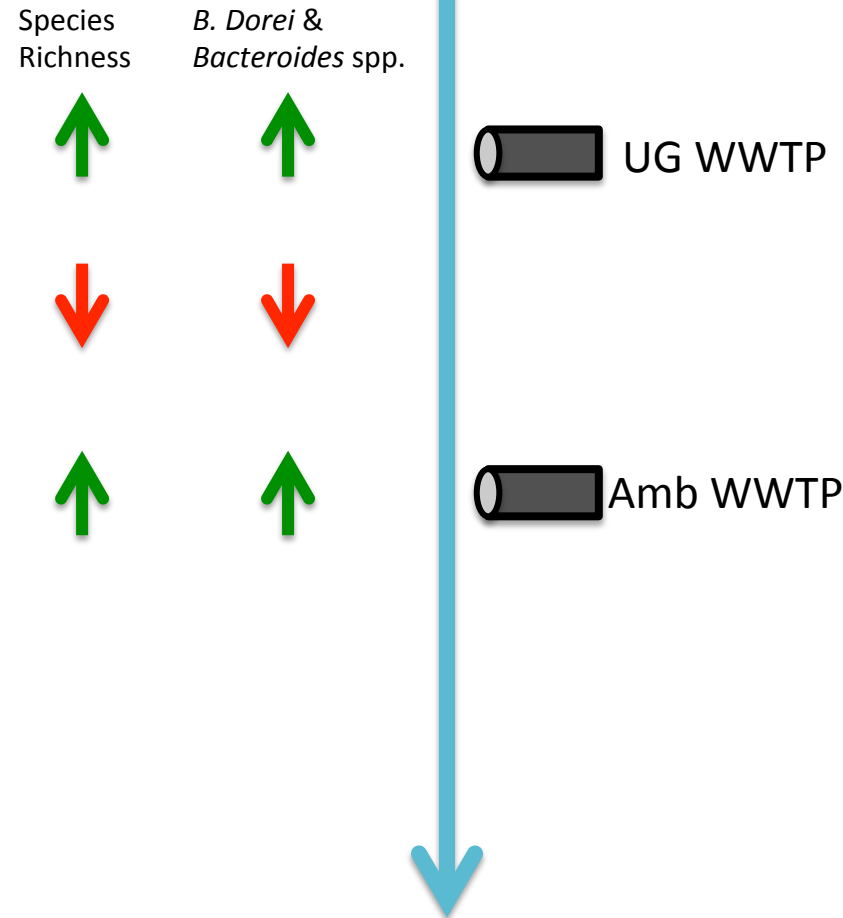
Differential Abundance

Two patterns

- At effluent source
 - Richness
 - Fecal-associated taxa
- Between WWTP
 - Richness
 - Fecal-associated taxa

Test for Diff. Abund.

- Identify taxa that significantly increase or decrease

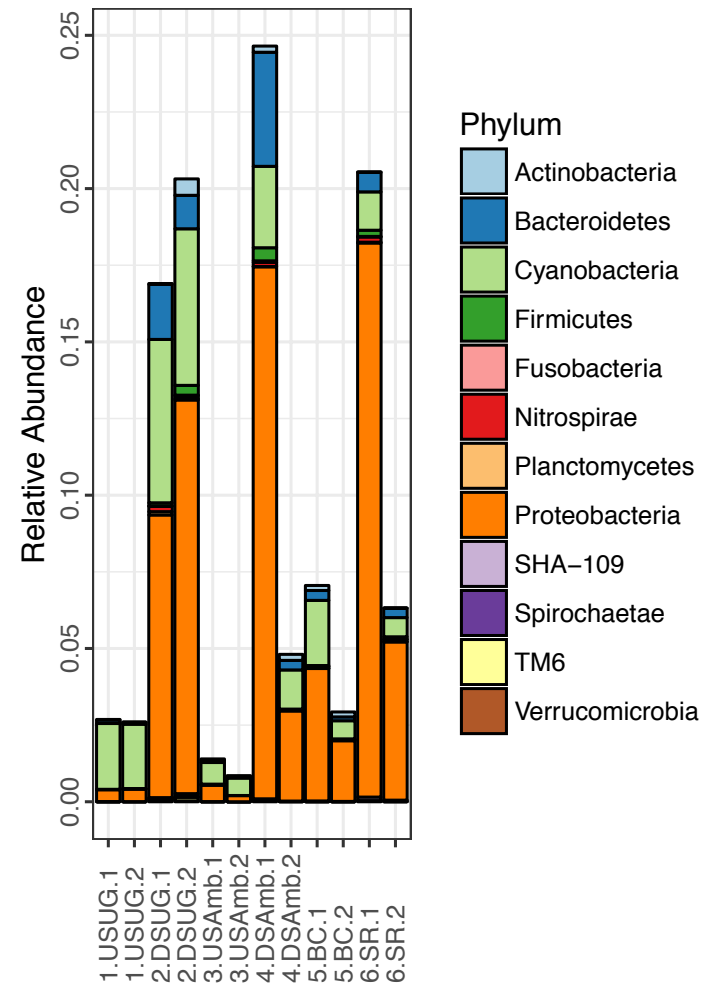




Differential Abundance

At effluent source

- 137 taxa differentially abundant
 - 7 to 11.6 times more abundant
- Largest increases
 - WWTP-associated
 - Nutrient cyclers
 - AOB / NOB
 - denitrifiers
 - Indicator subset Orders
 - Bifidobacteriales,
 - Bacteroidales, and
 - Clostridiales



Differential Abundance

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Between WWTP

- 205 taxa
 - 102 increased
 - 103 decreased
 - WWTP-associated
 - Nutrient cyclers
 - Indicator Orders

Comparison

- 53 taxa in common
- All 53
 - Increased at effluent source
 - Decreased downstream

Conclusions

- Effluent outflows
 - Increase species richness
 - Sources of
 - WWTP-associated taxa
 - Nutrient cycling bacteria
 - Fecal-associated / indicator organisms
- Partial attenuation
 - Taxa sourced from effluent decreased severely downstream
 - Effluent-sourced taxa do not persist downstream
- More work is needed
 - Limited dataset → limited generalizability

Other Themes:

- Antecedent moisture conditions
- N & P did not control community structure
- Use of indicator subsets may be feasible

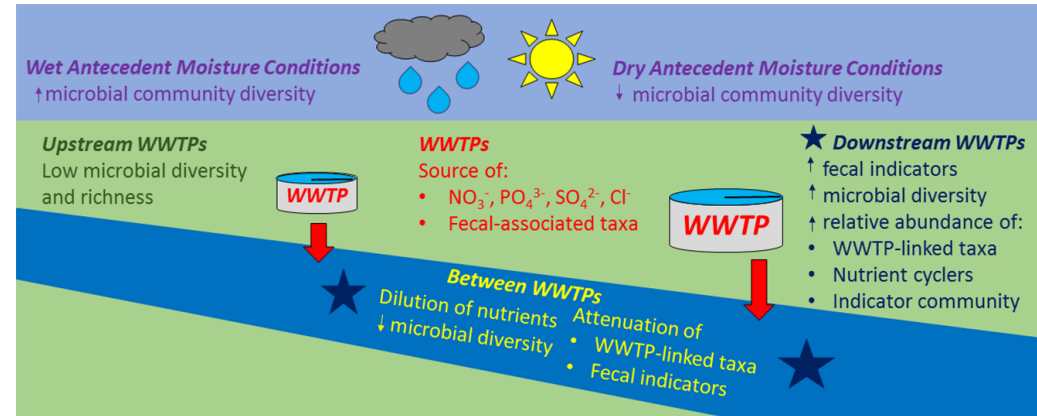
Wastewater treatment plant effluent introduces recoverable shifts in microbial community composition in receiving streams

Price, J.R., Ledford, S.H., Ryan, M.O., Toran, L., and C.M. Sales. 2017.
Sci. Total Environ. doi:10.1016/j.scitotenv.2017.09.162.



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- Delaware River Watershed Initiative



microbes.cae.drexel.edu

@SalesLaboratory

[jacobrprice.github.io](https://github.com/jacobrprice)

@Jake_in_the_Lab

