

# Microbial ecology of activated sludge system to inform system operation and design

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- Context and study goals
- Lessons from just plant data
- Lessons including consideration of microbial ecology
- Key takeaways

## Context and Study Goals

Microbial  
Community

Operation

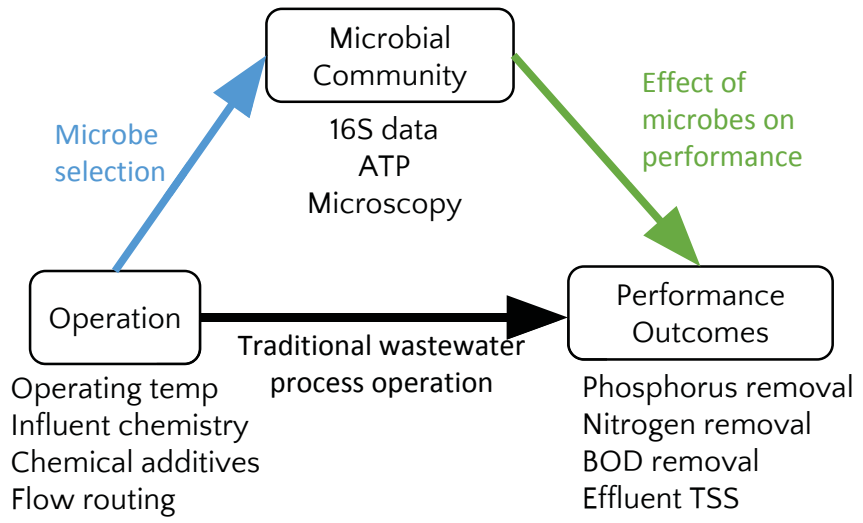
Traditional wastewater  
process operation

Performance  
Outcomes

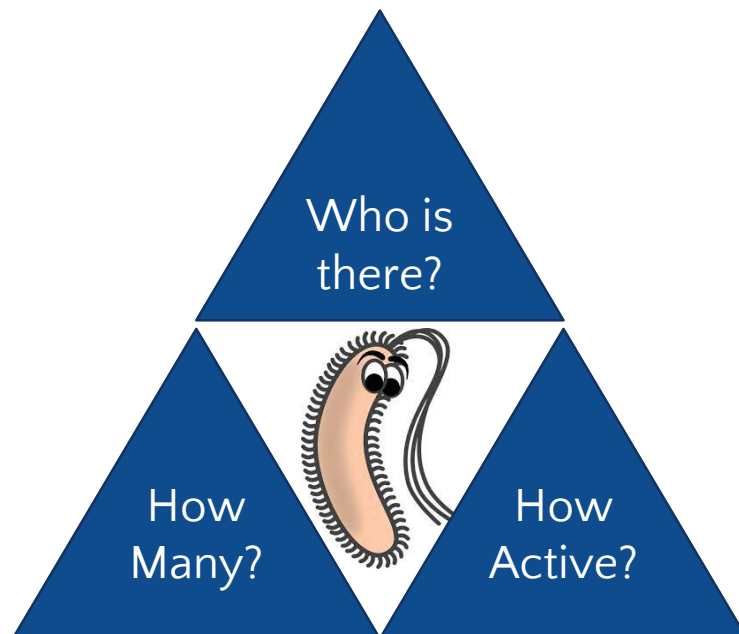
Operating temp  
Influent chemistry  
Chemical additives  
Flow routing

Phosphorus removal  
Nitrogen removal  
BOD removal  
Effluent TSS



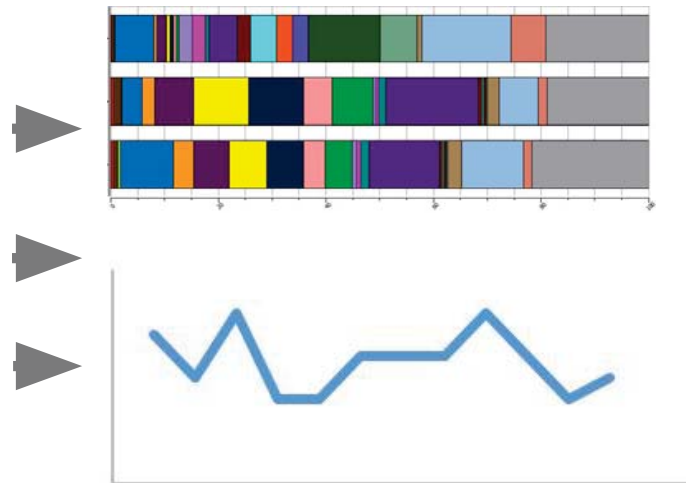


Tools for  
understanding  
microbes



## Other tools for understanding microbes

Question	Analysis	Method	Approx Cost/ Sample	Field/ Lab
<b>Who is there?</b>	Characterize entire microbial communities	16S microbiome analysis	\$300	Lab
<b>How many?</b>	Detect/quantitate specific genes of interest or total abundance	Quantitative PCR (qPCR)	\$150	Lab
<b>How active?</b>	Measure microbial activity	ATP analysis	\$20 + equipment	Lab or Field

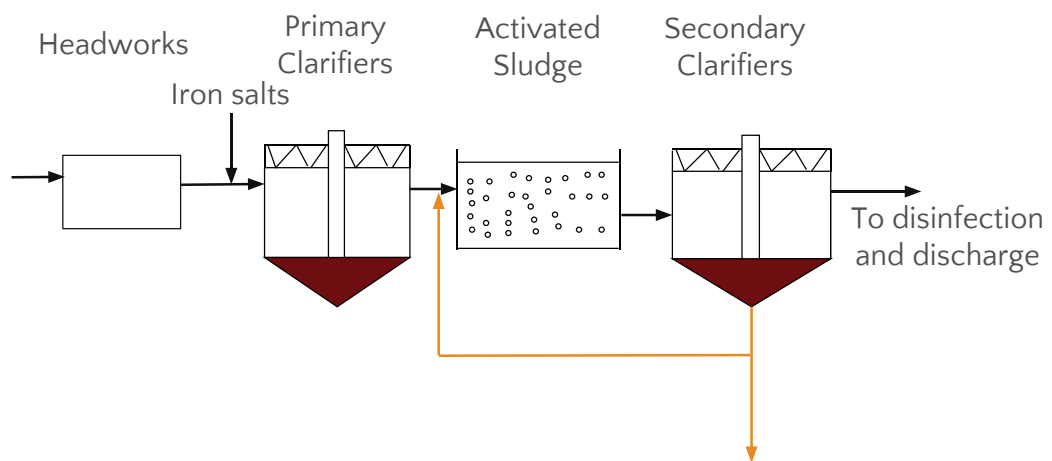


## Why use new methods?

- Microbiological methods typically applied in engineering systems are *centuries* old. Recent technology advances enable more reliable and detailed understanding of microbes and their activities
- Results enable optimization of design and operation practices
- Costs similar to advanced chemical analyses



## Process flow

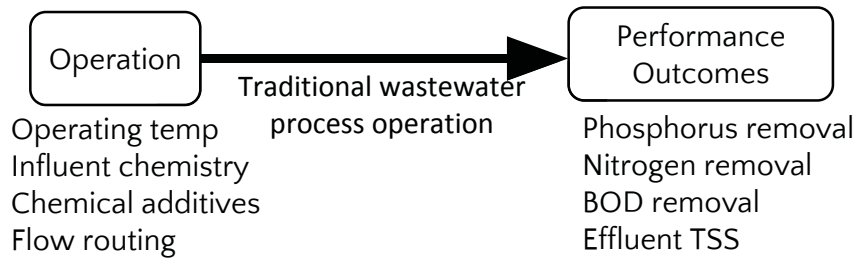


# Data used for this study

	Activated Sludge
<b>Operational/Influent Data</b>	<ul style="list-style-type: none"> <li>• Dissolved Oxygen (DO)</li> <li>• Temperature</li> <li>• Biochemical oxygen demand to ammonia ratio (BOD:NH<sub>3</sub>)</li> <li>• Mean cell residence time (MCRT)</li> <li>• Influent ammonia and total phosphorus</li> <li>• Influent flows</li> <li>• F:M and nutrient ratios</li> </ul>
<b>Microbial Community Data</b>	<ul style="list-style-type: none"> <li>• Microbial group abundances</li> </ul>
<b>Performance Data</b>	<ul style="list-style-type: none"> <li>• Effluent Biochemical Oxygen Demand (BOD)</li> <li>• Effluent Ammonia (NH<sub>3</sub>)</li> <li>• Effluent Phosphorus (P)</li> <li>• Effluent Total Suspended Solids (TSS)</li> <li>• Sludge volume index (SVI)</li> </ul>



## Analysis outcomes with just plant data



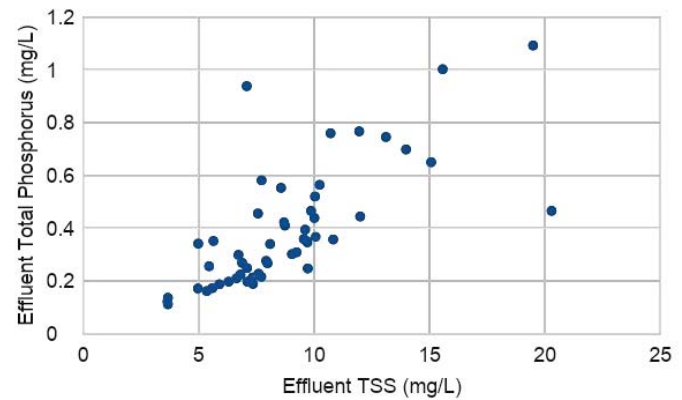
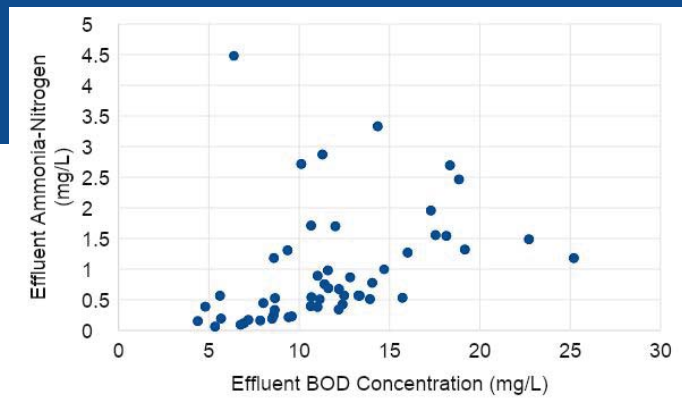
## Effluent water quality

BOD, Ammonia, Total P, TSS  
all strongly correlated

TSS contains

- Biomass
- Phosphorus precip

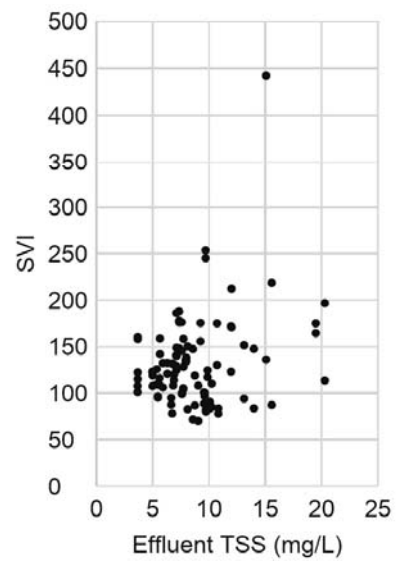
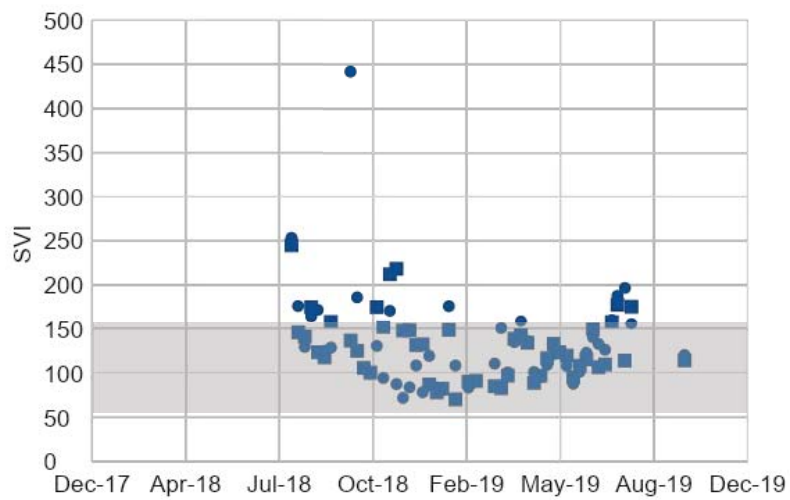
Treatment efficacy is primarily  
limited by settling



# Sludge settleability

## Higher SVI (poorly settling)

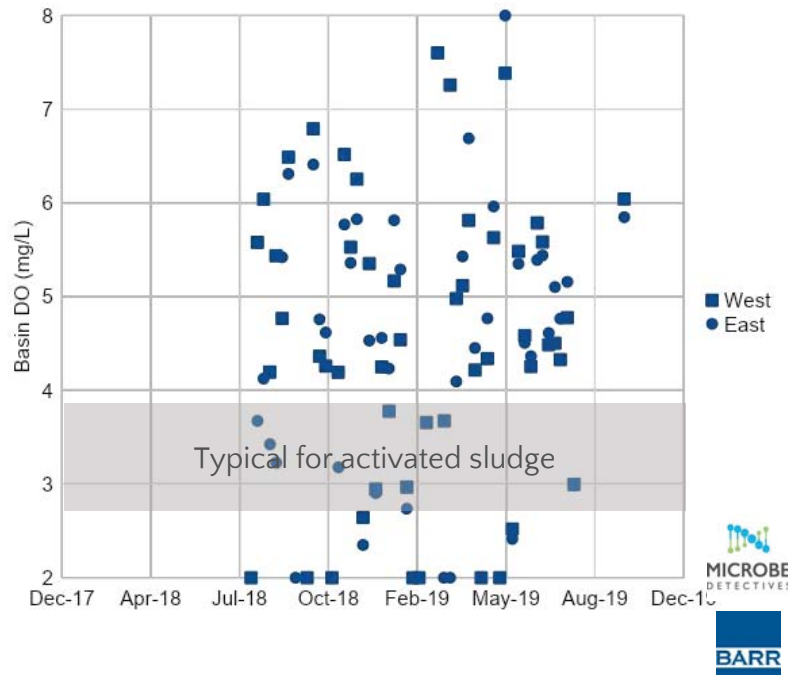
- Mostly during fall
- Correlated to high TSS



# Effect of dissolved oxygen

Dissolved oxygen (DO) concentrations higher than typically used in activated sludge.

High DO concentrations were correlated to growth of filaments

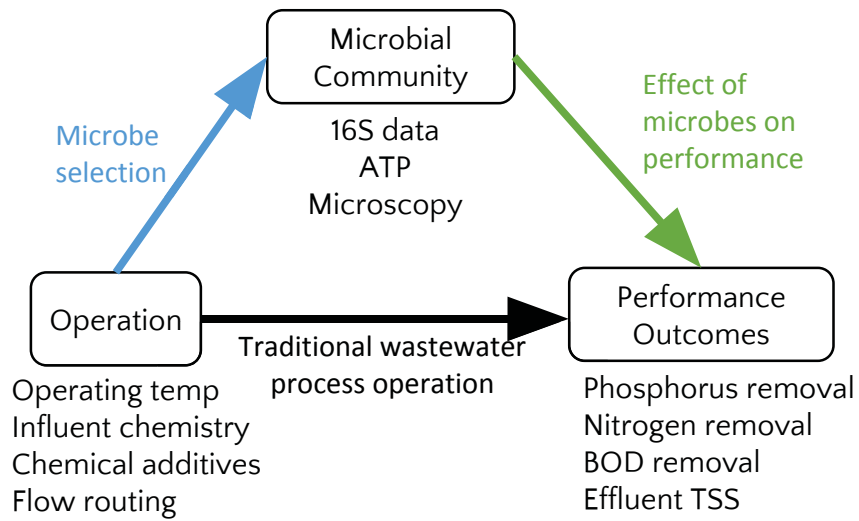


## Potential operational changes

Upgrade blowers to provide more targeted oxygen supply to aeration basin

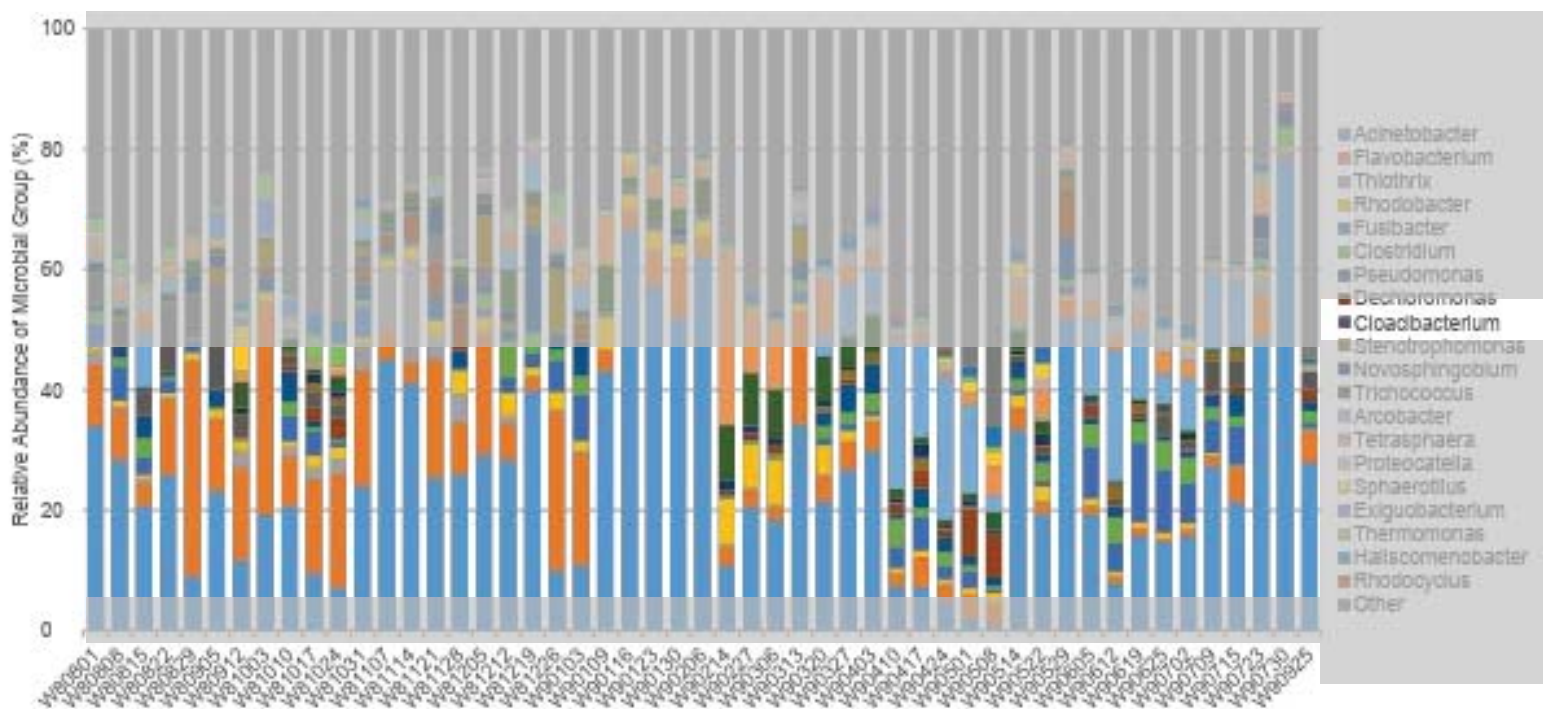
-> expected to save energy costs and improve settling characteristics

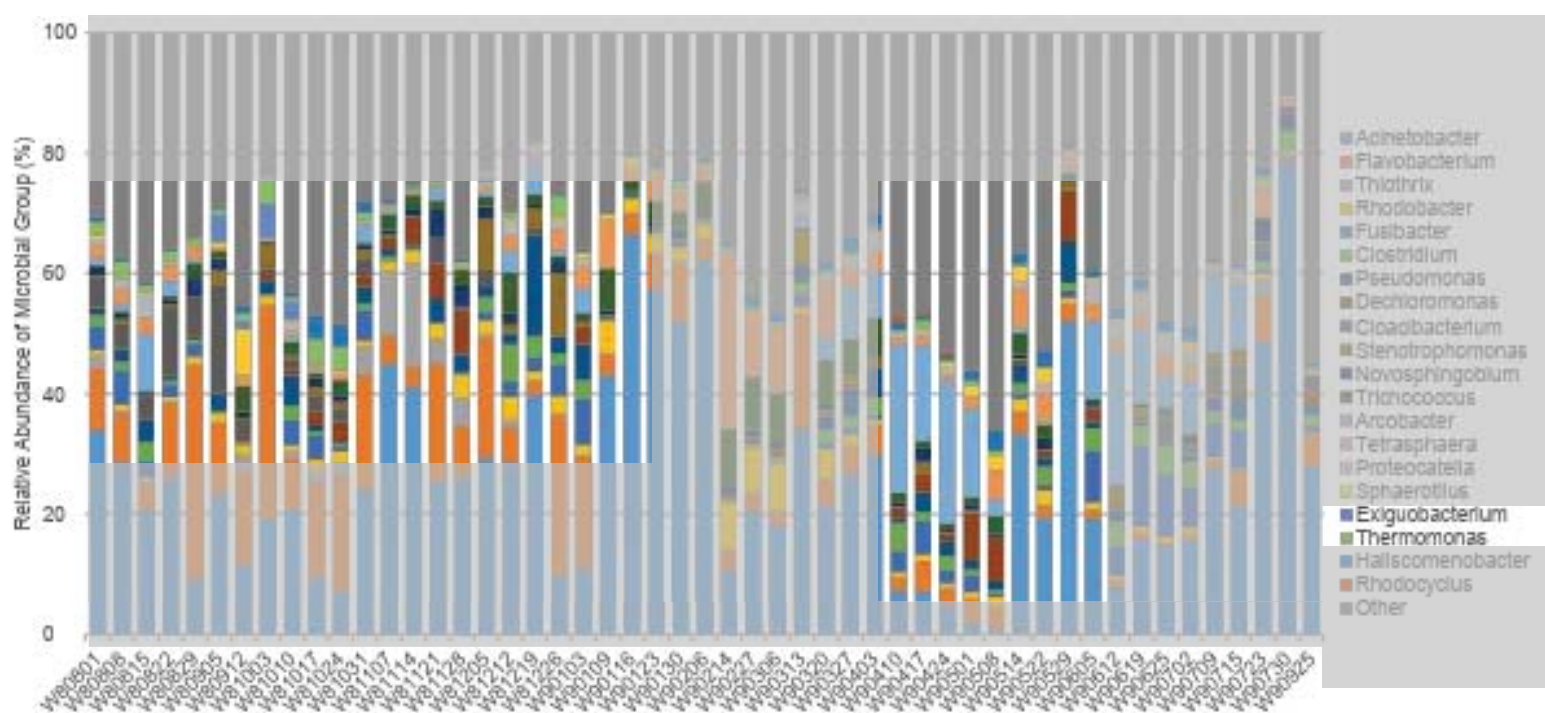
# Analysis outcomes with microbial ecology

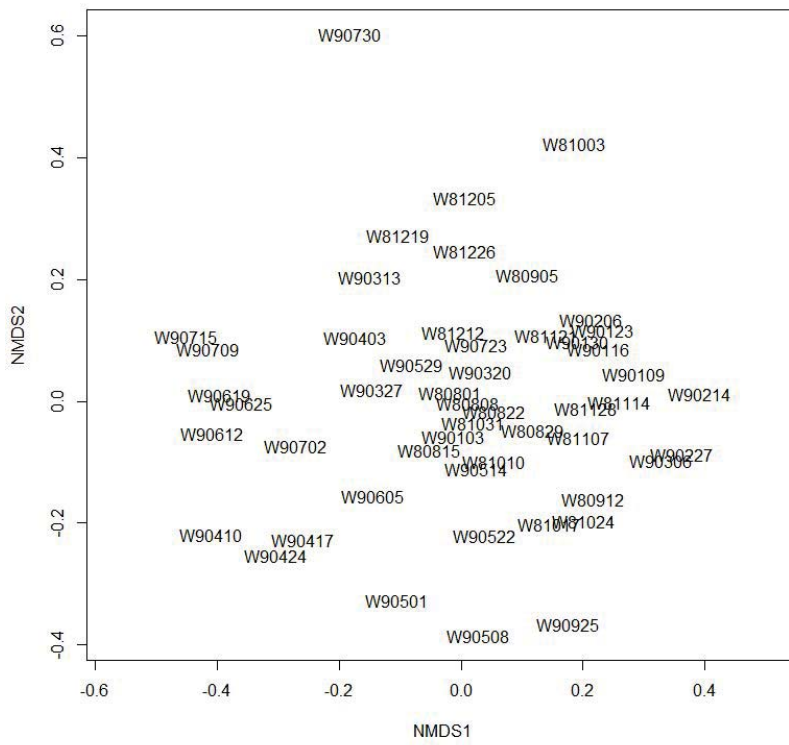




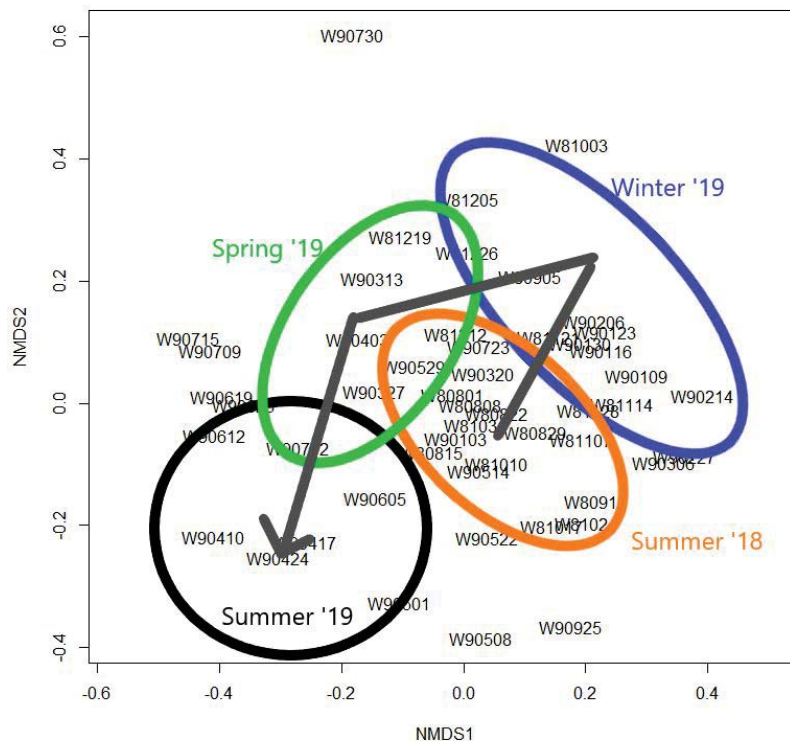








# Community changes seasonally, but not identical between years



## Hypotheses from Microbial Data

- Similar community members over time, but abundances vary on a weekly basis.
- 10–70% *Acinetobacter* spp.
  - No significant correlations to outcomes or influent/operation conditions
  - This one microbial group has a significant effect on microbial diversity and evenness

## More trends seen through microbial groups

What microbes are good versus bad?

	Microbial Group (Genus)	Likely Role in Community	Outcomes				
			BOD	NH3	SVI	P	TSS
<b>Good - Microbes correlated to higher performance</b>	<i>Haliscomenobacter</i>	Filamentous	X		X	X	X
	<i>Proteocatella</i>					X	
	<i>Fusibacter</i>				X	X	
	<i>Arcobactor</i>				X	X	
	<i>Clostridium</i>	Varied				X	X
	<i>Cloacibacterium</i>	Anaerobe		X			
<b>Bad - Microbes correlated to lower performance</b>	<i>Flavobacterium</i>	Varied				X	X
	<i>Thermomonas</i>	Not Identified					X
	<i>Thiothrix</i>	Filamentous			X		X
	<i>Cloacibacterium</i>			X			
	<i>Novosphingobium</i>	Aromatic degrader	X			X	X

## More trends seen through microbial groups

What microbes are good versus bad?

How to select for the right microbes?

	Microbial Group (Genus)	Likely Role in Community	Outcomes					Operation/influent			
			BOD	NH3	SVI	P	TSS	RAS Cl	MLSS	DO	Temp
Good - Microbes correlated to higher performance	<i>Haliscomenobacter</i>	Filamentous	X		X	X	X				
	<i>Proteocatella</i>					X					
	<i>Fusibacter</i>				X	X					
	<i>Arcobactor</i>				X	X	↑	↑			↓
	<i>Clostridium</i>	Varied				X	X			↓	
	<i>Cloacibacterium</i>	Anaerobe		X						↓	
Bad - Microbes correlated to lower performance	<i>Flavobacterium</i>	Varied				X	X				↓
	<i>Thermomonas</i>	Not Identified					X				↓
	<i>Thiothrix</i>	Filamentous			X		X		↑		↓
	<i>Cloacibacterium</i>			X							↓
	<i>Novosphingobium</i>	Aromatic degrader		X			X	X			



## Again, lower DO is beneficial

What microbes are good versus bad?

How to select for the right microbes?

	Microbial Group (Genus)	Likely Role in Community	Outcomes					Operation/influent			
			BOD	NH3	SVI	P	TSS	RAS Cl	MLSS	DO	Temp
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	<i>Proteocatella</i>					X					
	<i>Fusibacter</i>				X	X					
	<i>Arcobactor</i>				X	X	↑	↑		↓	
	<i>Clostridium</i>	Varied				X	X			↓	
	<i>Cloacibacterium</i>	Anaerobe		X						↓	
Bad - Microbes correlated to lower performance	<i>Flavobacterium</i>	Varied				X	X			↓	
	<i>Thermomonas</i>	Not Identified					X			↓	
	<i>Thiothrix</i>	Filamentous			X		X		↑	↓	
	<i>Cloacibacterium</i>			X						↓	
	<i>Novosphingobium</i>	Aromatic degrader	X			X	X				

## Increasing RAS chlorination selects for good microbes

What microbes are good versus bad?

How to select for the right microbes?

	Microbial Group (Genus)	Likely Role in Community	Outcomes					Operation/influent			
			BOD	NH3	SVI	P	TSS	RAS Cl	MLSS	DO	Temp
Good - Microbes correlated to higher performance	<i>Haliscomenobacter</i>	Filamentous	X		X	X	X				
	<i>Proteocatella</i>					X					
	<i>Fusibacter</i>				X	X					
	<i>Arcobactor</i>				X	X	↑	↑		↓	
	<i>Clostridium</i>	Varied				X	X			↓	
	<i>Cloacibacterium</i>	Anaerobe		X						↓	
Bad - Microbes correlated to lower performance	<i>Flavobacterium</i>	Varied				X	X				↓
	<i>Thermomonas</i>	Not Identified					X				↓
	<i>Thiothrix</i>	Filamentous			X		X		↑		↓
	<i>Cloacibacterium</i>			X							↓
	<i>Novosphingobium</i>	Aromatic degrader	X			X	X				

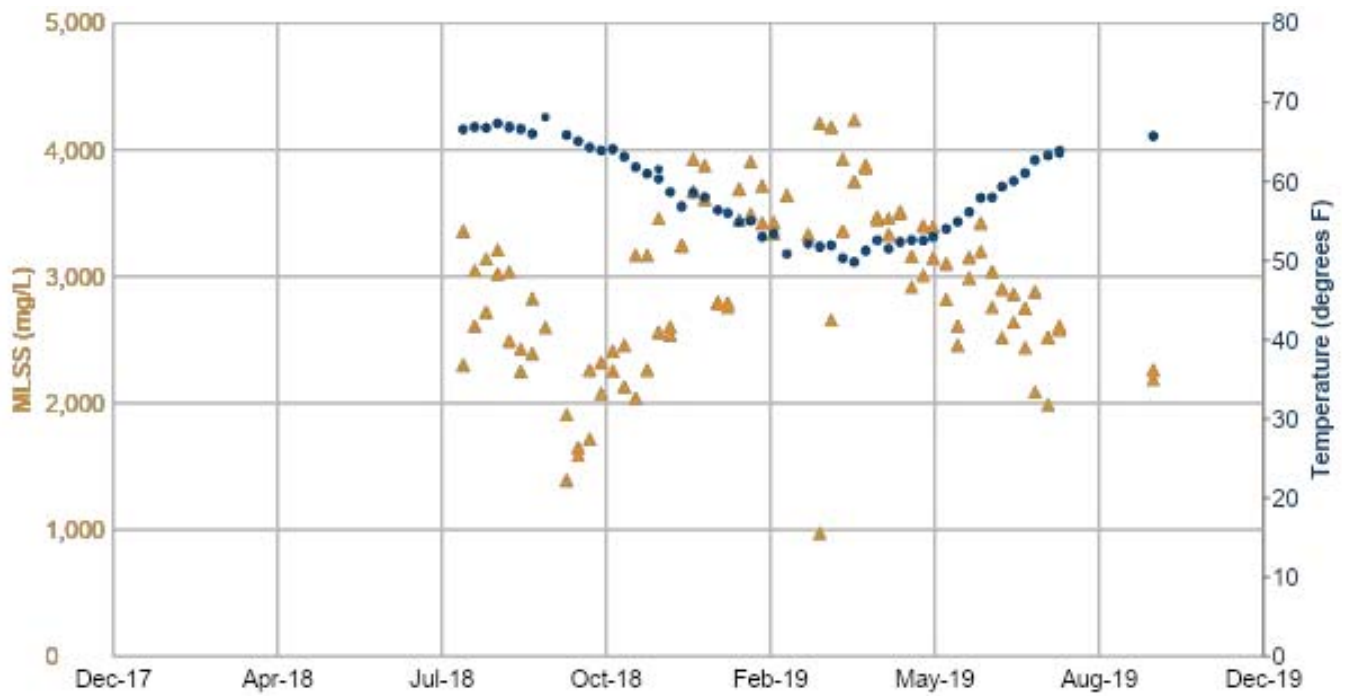
## Winter conditions (lower wasting) saw better performance

What microbes are good versus bad?

How to select for the right microbes?

	Microbial Group (Genus)	Likely Role in Community	Outcomes					Operation/influent			
			BOD	NH3	SVI	P	TSS	RAS Cl	MLSS	DO	Temp
Good - Microbes correlated to higher performance	<i>Haliscomenobacter</i>	Filamentous	X		X	X	X				
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	<i>Fusibacter</i>				X	X					
	<i>Arcobactor</i>				X	X	↑	↑		↓	
	<i>Clostridium</i>	Varied				X	X			↓	
	<i>Cloacibacterium</i>	Anaerobe		X						↓	
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	<i>Thermomonas</i>	Not Identified					X			↓	
	<i>Thiothrix</i>	Filamentous			X		X	↑		↓	
	<i>Cloacibacterium</i>			X						↓	
	<i>Novosphingobium</i>	Aromatic degrader	X			X	X				

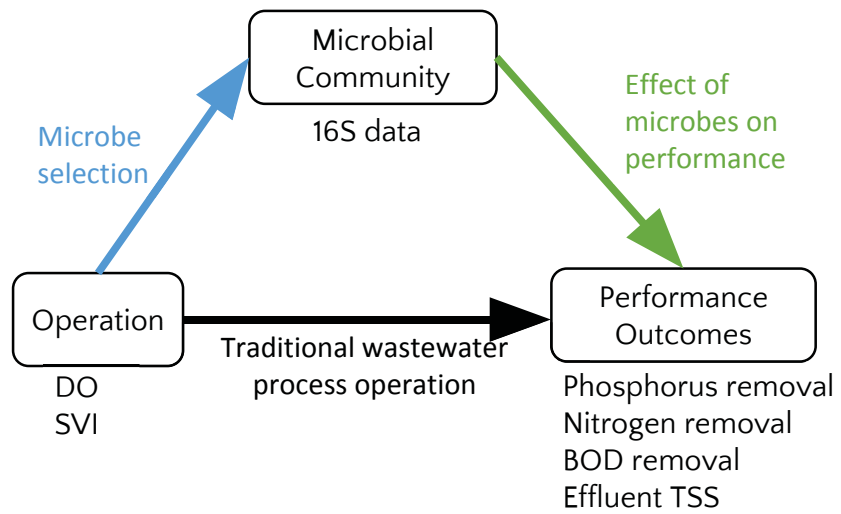
## Winter and summer conditions

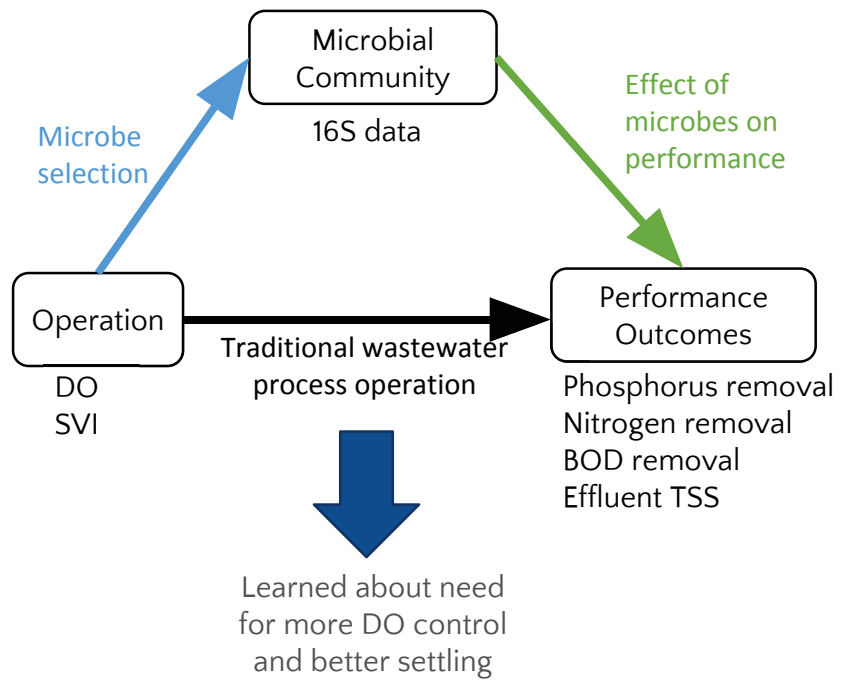


## Hypotheses from Microbial Data

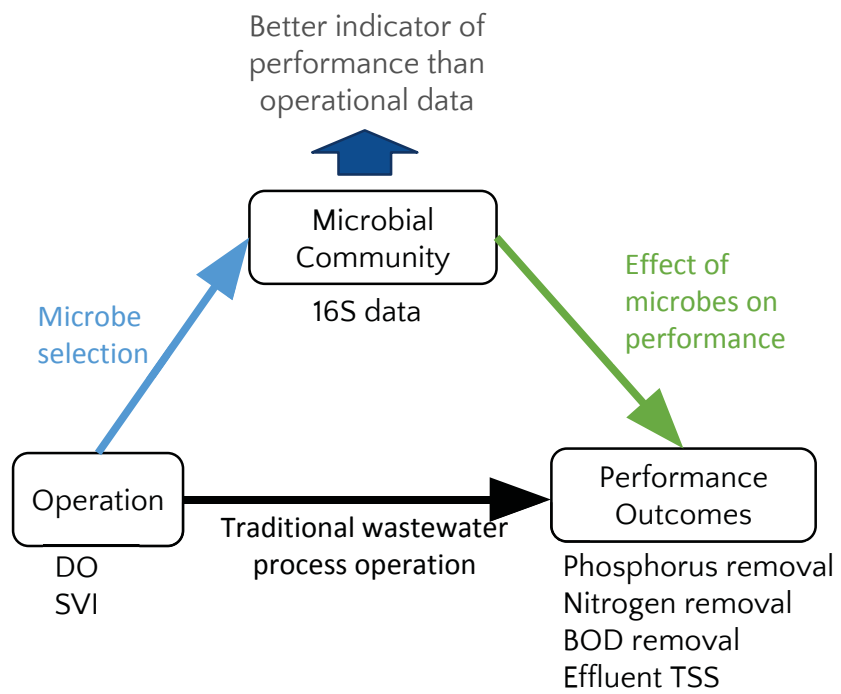
- Better indicator of effluent TSS than SVI, DO or any other parameter traditionally measured
- No trends observed relating F:M ratio or MCRT directly to specific microbe abundances.
- Winter conditions grow more favorable microbes, and are reflected by low temperatures and high MLSS and MCRT
  - Methods to retain MLSS during summer months has the potential to improve treatment

## Key Takeaways









## Takeaways

- Can learn useful trends and insight from more detailed analysis of plant data
- **Microbial community data can identify additional correlations**

## Use of Microbial Methods

- System Understanding
  - Provide an **operational baseline** and to help understand potential causes of system upsets
  - Specific growth preferences of **microbial groups** can be used to select or inhibit targeted abundant microbial groups
- Operational Input
  - **Real-time measurement (ATP or cell count)** data may be a useful of to understand microbial activity and reactor performance.
  - Upcoming advances in qPCR and 16S turnaround times

Thanks to

## Microbe Detectives

- Trevor Ghylin
- John Tillotson



## Barr

- Becca Vermace
- Don Richard

