Anthropogenically Driven Changes to Shallow Groundwater in southeastern Wisconsin and its Effects on the Aquifer Metagenome

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#### OVERVIEW

- Waukesha water use
- Previous studies
- Current study
  - Geochemistry data
  - Microbial data
- Future work



#### HISTORY OF THE CITY OF WAUKESHA WATER USE

- Regional drawdown of 500ft had developed within the deep aquifer of southeastern Wisconsin
- By 2006 the deepest cone of depression in the region lay under Waukesha
- City of Waukesha has high radium concentrations in the deep aquifer it uses for municipal drinking water
- Waukesha approved for diversion under Great Lakes Compact
- Currently using shallow wells that have been placed close to rivers with the intention of inducing water to flow from the river to the aquifer

#### **RBI WELLS**

- Riverbank Inducement wells
- More sustainable water supply



### PROJECT OBJECTIVE

- This study investigates if, and to what extent the microbial community present in the shallow groundwater of southeastern Wisconsin is affected by the influx of treated municipal wastewater effluent.
- Characterize the change in microbial community composition and genetic functional potential between pristine and impacted groundwater sites to better understand the impact of anthropogenic activities on native microbial communities.

WAUKESHA WELLFIELD



(Fields-Sommers, 2015)



SAMPLING NETWORK

#### PREVIOUS STUDIES



#### PREVIOUS STUDIES CONTINUED



--Cl ---Na ---Ca ---Mg -->-Pumpage



# **CURRENT STUDY**









## DISSOLVED GASES AND NUTRIENTS

	RBI	RBI	Pristine
	RL255	RL256	WK947
CH <sub>4</sub> (nM)	5 - 9	250 - 550	15-65
$H_2(nM)$	2 - 2.6	2.3 - 7.0	3.6 - 4.2
O <sub>2</sub> (μM)	0 - 22	0 - 11	0 - 12
CO <sub>2</sub> (µM)	945	760 - 810	622 - 724
NO <sub>3</sub> (μM)	2.8 - 4.7	0 - 3	2.9 - 5.9
NO <sub>2</sub> (μM)	0.43 - 1.7	0.09	0.87
$NH_4 (\mu M)$	0 - 0.38	3.1 - 4	0.33 - 2.2
TDP (nM)	9.6 – 151	55 - 235	55 - 161
DOC (mg/L)	0-0.96	0.4 - 1.26	0.14 – 1.21

#### MICROBIAL DATA

- 16S rRNA Gene Community Composition ("who is there")
- 16S rRNA Activity ("who is active and in what ratio to 16S genetic abundance")
- Metagenomic techniques provide deeper analysis of microbial populations in an ecosystem ("what is the genetic potential")
- Metagenomics techniques and analyses will allow for better understanding of the genetic functional potential in the Waukesha wellfield



### 16S rRNA GENE COMPOSITION WITH NCBI BLAST

Top 10 Averages	Taxon	Sample Source	Seq. % ID
1	Uncultured Acidithiobacillus sp.	Environmental, sediment	96
2	Uncultured bacterium	Environmental, sub surface	99
3	Uncultured Bacteria	Environment, polluted waste dump	99
4	Uncultured Bacterium	Environmental, carbonate cave New Mexico	99
5	Uncultured Bacteria	Environmental, soil uranium waste dump	98
6	Uncultured Bacteria	Environmental, acid mine drainage Tongling pyrite mine	93
7	Uncultured Bacteria	Environmental, deep-sea hydrothermal vent sediments of the East Pacific Ocean	95
8	Uncultured Bacteria	Environmental, spring	96
9	Uncultured Bacterium	Environmental, water	97
10	Uncultured Gamma Proteobacterium	Environmental, ultramific rock	100

## 16S rRNA GENE COMPOSITION WITH NCBI BLAST

Top 10 Average	Isolate Name (16S)	Sample Source	Seq. % ID
1	Sulfuricaulis limicola	Lake	95
2	Desulfatiglans parachlorophenolica	NA	88
3	Chlorobium chlorovibrioides	NA	84
4	Sulfuricaulis limicola	Lake	93
5	Desulfatiglans parachlorophenolica	NA	89
6	Sulfuricaulis limicola	Lake	92
7	Pelobacter acetylenicus	NA	88
8	Hydrogenispora ethanolica	Sludge	88
9	Mogibacterium neglectum	Human oral cavities	83
10	Acidiferrobacter thiooxydans	NA	94

#### CONCLUSIONS

- Based on our initial results there is no obvious nutrient flow from the Fox River to the Waukesha wellfield
- Nitrogen couples are being processed
- Most likely below iron reduction on redox ladder
- We have targeted the 16S rRNA gene region to identify which bacteria are present in the wells
- Currently the results show unknown novel taxa

#### FUTURE WORK

- Further characterize microbial community composition and microbial activity from all of our samples to identify patterns correlated to river water infiltration
- Metagenomic sequencing (shotgun, whole genome sequencing)
- Calculate free energy yields in order to determine energetically favorable reactions present in the system
- Assess differences in the metagenomes and geochemical reactivities of the pristine and impacted locations
- Characterize the change in aquifer bacterial community composition following the addition of varied concentrations of WWTP effluent

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