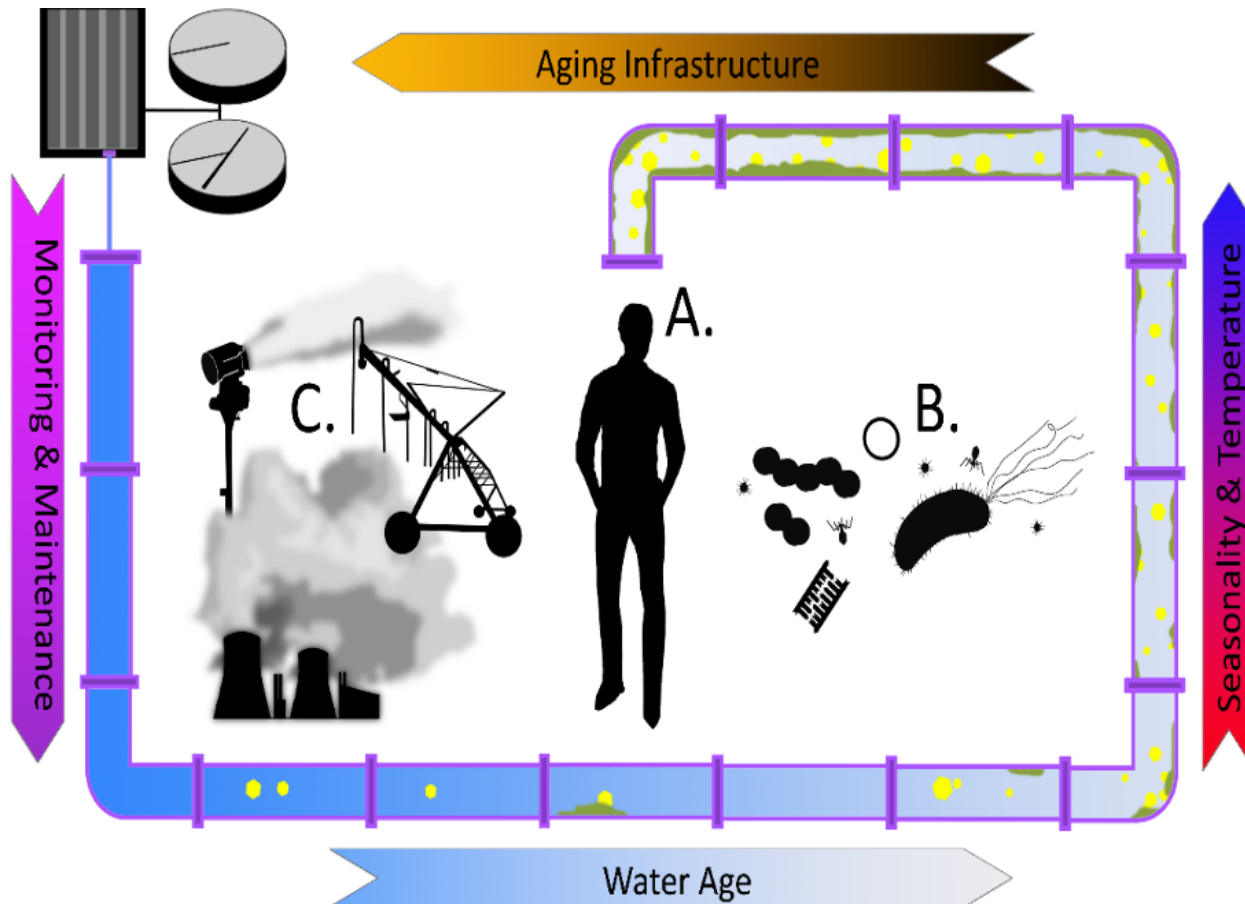


Microbial Contaminants & 'Omics



Tolulope Odimayomi
Presidential Postdoctoral Fellow
Via Department of Civil & Environmental Engineering

Thomas Byrne
Doctoral Student
Genetics, Bioinformatics, and Computational Biology

Summer, 2025

Garner et al. *Environ Sci: Water Res & Technol* 2015



Outline

1. Microbes in Wastewater and Drinking Water Systems
2. Pathogens: Past, Present, Future
3. Pathogen Testing: Past, Present, Future



Credit: Janice Haney
Carr, CDC

Microbes: Size Matters

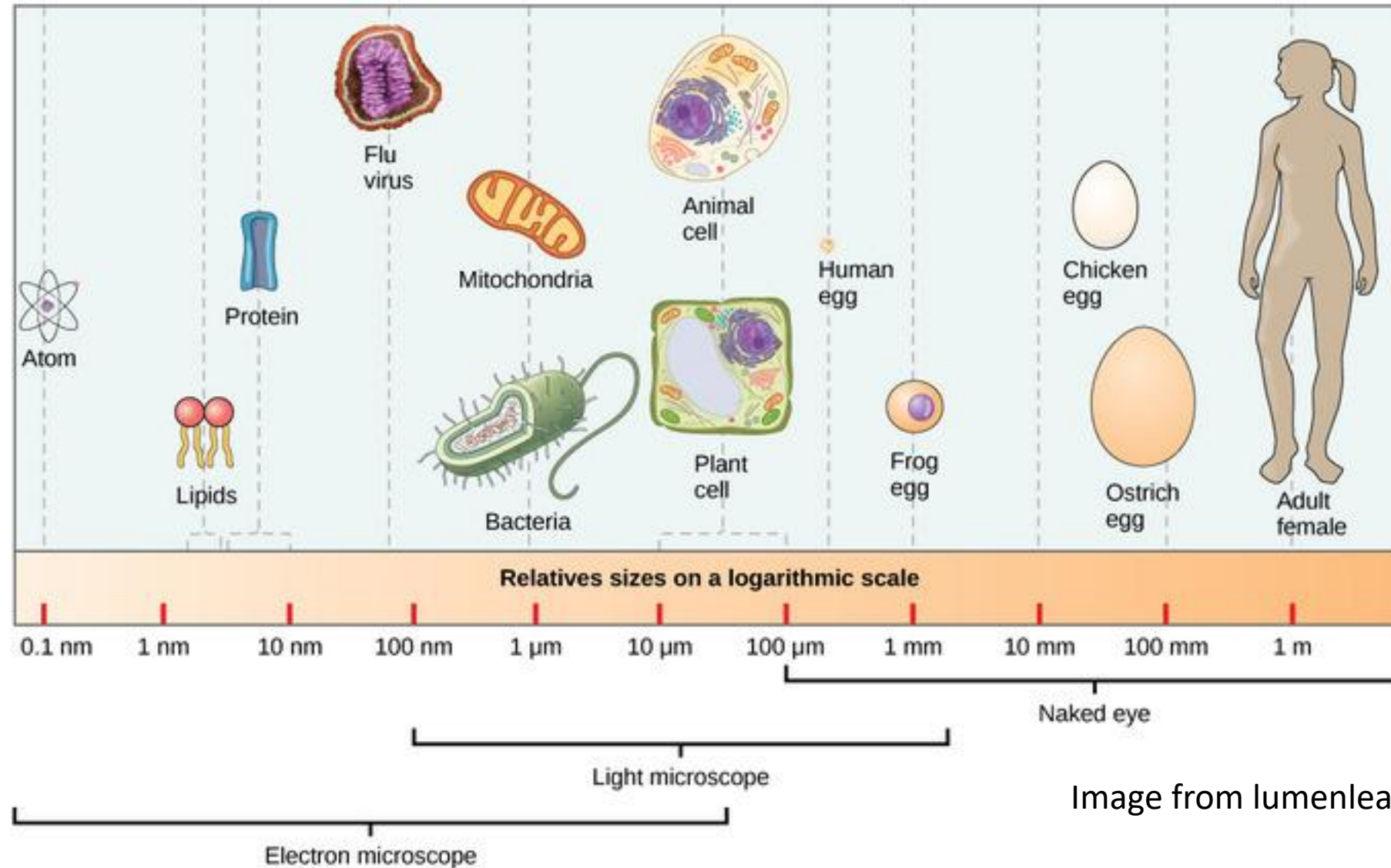
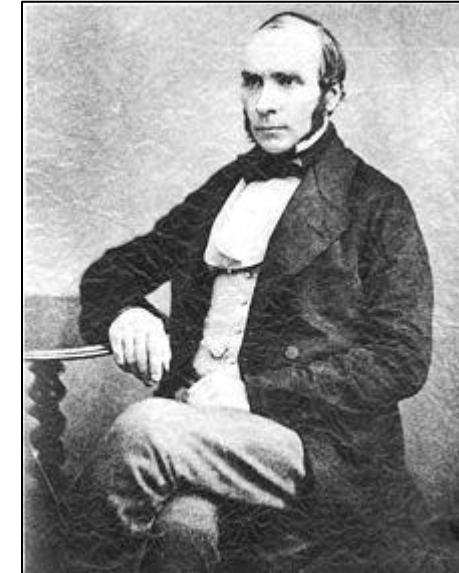
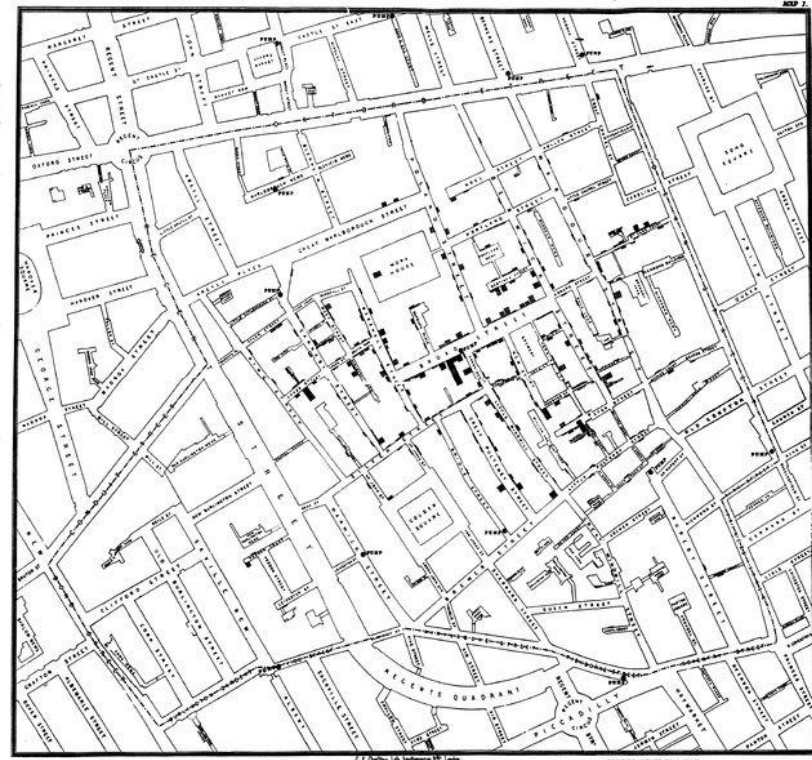


Image from lumenlearning.com

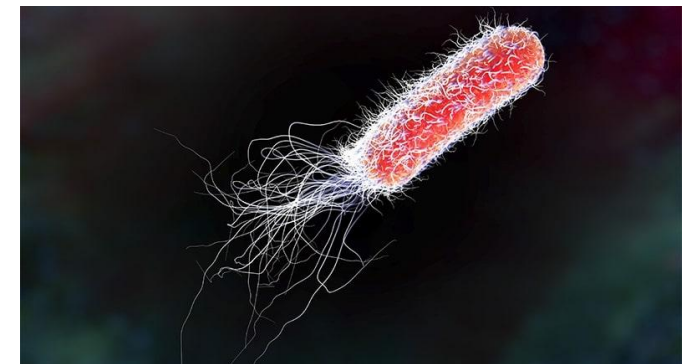
Back to the Future: The Ghost Map

- 1849 London
 - Epidemic began in Europe in 1840s
 - Golden Square- 500 people died in 10 days
- John Snow – Father of modern epidemiology
 - Drew connection between well water and cholera outbreaks



Pathogens

- **Pathogens**- disease carrying organisms that grow and multiply in host
 - **Waterborne** – spread by ingestion of contaminated water (e.g., hepatitis A, cholera)
 - **Water-washed** – associated with poor hygiene due to a lack of sufficient water (e.g., dysentery, trachoma)
 - **Water-based** – spread by mere contact with water; don't require ingestion (e.g., schistosomiasis)
 - **Water-related** – require water to survive, but aren't spread by contact or ingestion of water (e.g., malaria, West Nile virus)

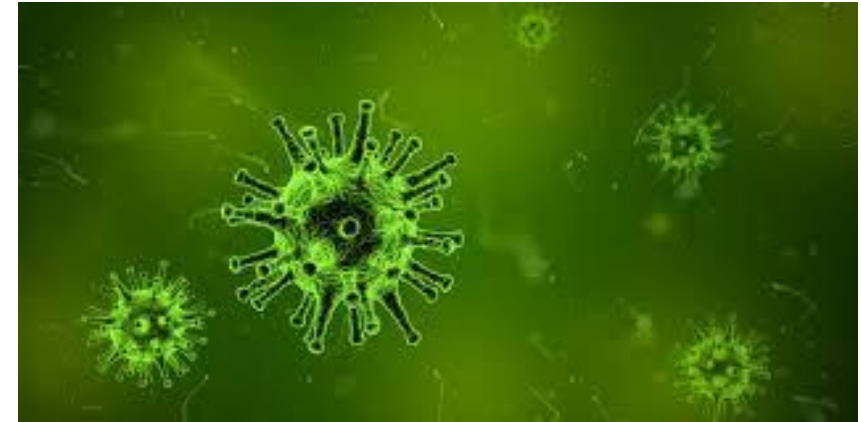


E. coli

Types of Pathogens

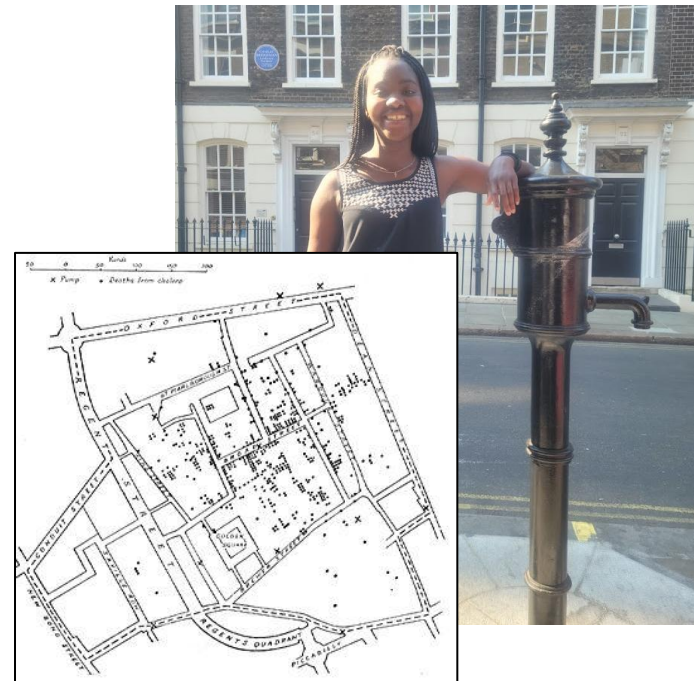
Virus

- Small infectious agent that replicates in living cells: genetic material surrounded with a protein coat ex. Polio, Hep A



Bacteria

- infectious microorganism ex. *Vibrio cholerae* - cholera, *Salmonella Typhi* – Typhoid fever



John Snow –
Father of modern
epidemiology.
Investigated
cholera epidemics
(London 1854)

Types of Pathogens (continued)



Protozoa

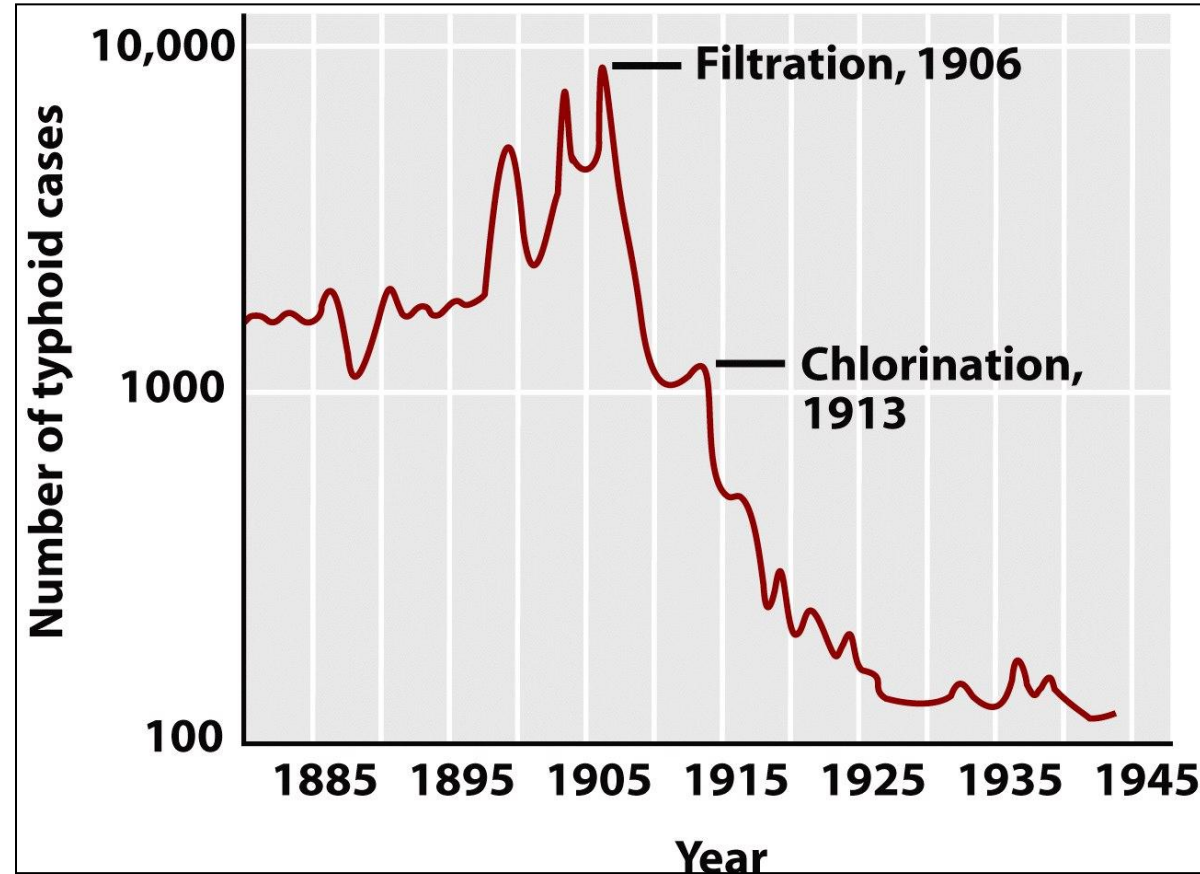
- Motile unicellular eukaryotes ex. Giardia lamblia, Cryptosporidium

Helminths

- parasitic worms ex. Schistosomiasis, dracunculiasis (guinea-worm disease)



Past: The Miracle of Drinking water Filtration and Disinfection



New Jersey begins routine disinfection of drinking water (1908), other states followed

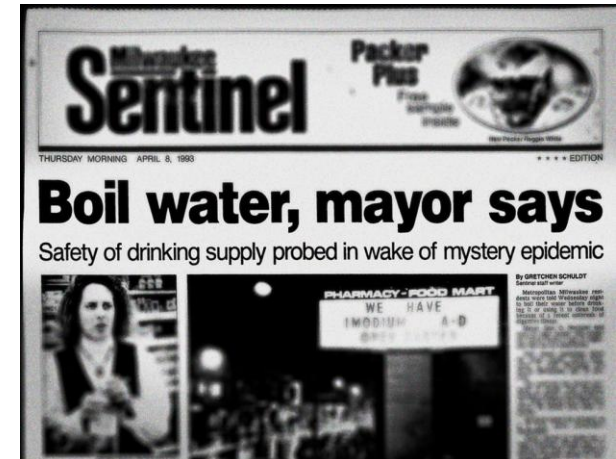
Fecal Pathogen Example: *Salmonella enterica*

- Rod-shaped, Gram-negative bacterium
 - Spreads rapidly among chicken
 - Waterborne Typhoid fever
- Pathogenic serovars:
 - Typhimorium, Typhi (Typhoid fever), and Enteritidis (Most common cause of food poisoning in US)
- First known asymptomatic carrier in US:
Typhoid Mary
 - 1869, Irish immigrant in New York
 - Infected up to 51 people (3 died)



Safe Drinking Water Act

- **1974 Act: federal responsibility for safe drinking water for >90% of population**
 - EPA established standards for systems serving ≥ 25 customers
 - Public water systems required to monitor and control water quality
 - EPA instituted primary and secondary standards
- **1986 Amendment**
 - Includes requiring EPA to use best available technology for regulated contaminants
 - All public water must be disinfected, all surface water must be filtered
- **1996 Amendment**
 - Annual customer confidence reports
 - More controls on pathogens and DBPs
 - Requires EPA to re-evaluate standards every 6 years
- **2002 Amendment - Water security**
 - Bioterrorism and emergency response preparedness



1993 Milwaukee Cryptosporidium Outbreak

Note: States can set stricter rules than the Federal Regulations

National Primary Drinking Water Regulations (NPDWRs)

Contaminant	MCLG	MCL	Health Effects	Source
<i>Cryptosporidium</i>	zero	TT, watershed control	Gastrointestinal illness	Fecal waste
<i>Giardia lamblia</i>	zero	TT, 99.9% removal	Gastrointestinal illness	Fecal waste
Heterotrophic plate count (HPC)	n/a	TT, 500 CFU/mL	None. Used to measure common bacteria in water.	Environment
<i>Legionella</i>	zero	TT, no specific limit	Legionnaire's Disease, a type of pneumonia	Naturally in water
Total Coliforms	zero	< 5% positive in a month	Not in itself; used as a presence indicator of harmful bacteria	Environment; fecal coliform
Turbidity	n/a	TT	Indicate water quality and filtration effectiveness	Soil runoff
Viruses (enteric)	zero	TT, 99.99% removal	Gastrointestinal illness	Fecal waste

Treatment technique (TT): A required process intended to reduce the level of a contaminant in drinking water (surface water treatment rules)

Maximum Contaminant Level (MCL)

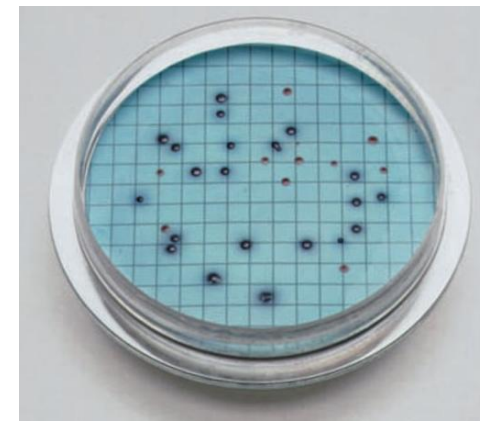
- **Enforceable** standards
- Treatment technique instead of MCL if pollutant is too difficult to detect and measure

Maximum Contaminant Level Goals (MCLG)

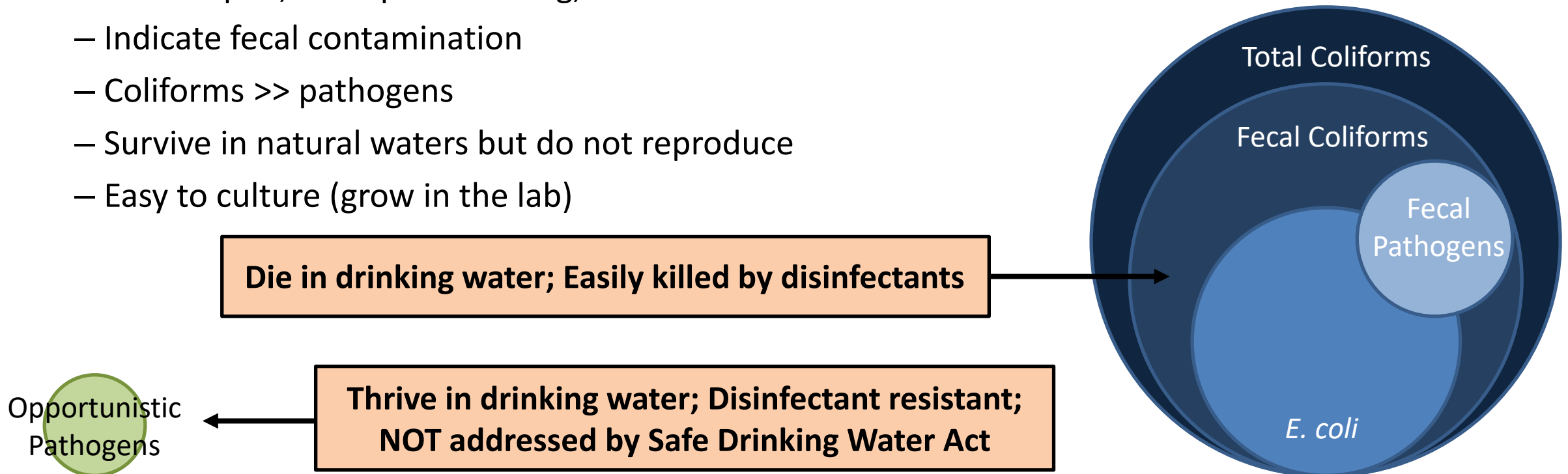
- **Unenforceable** goals
- Goal = no anticipated health effects plus safety margin

Total Coliform Bacteria

- Water should be free of pathogens (not sterile)
- Difficult to test for all pathogens so use indicator organisms
 - *Escherichia coli* and total coliform test
 - Rod-shaped, non-spore forming, can ferment lactose
 - Indicate fecal contamination
 - Coliforms >> pathogens
 - Survive in natural waters but do not reproduce
 - Easy to culture (grow in the lab)



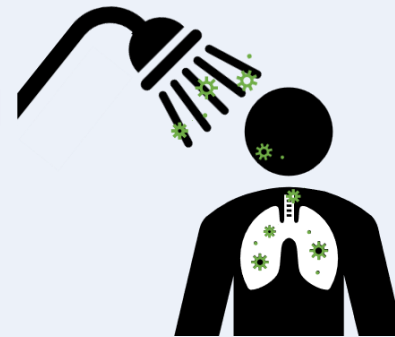
© Fisher Scientific



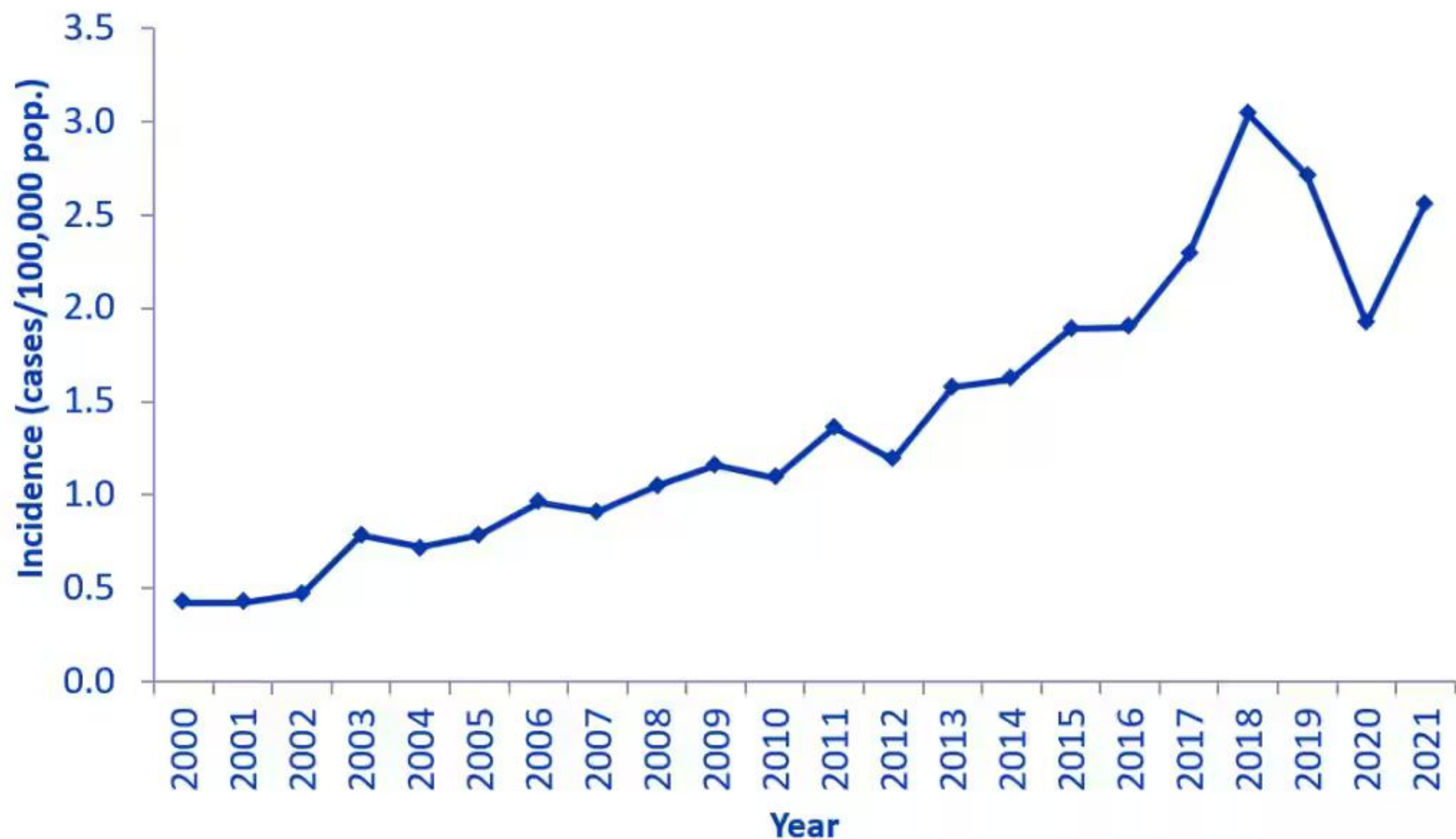
Background - Opportunistic Pathogens (OPs)

Importance of Monitoring OPs

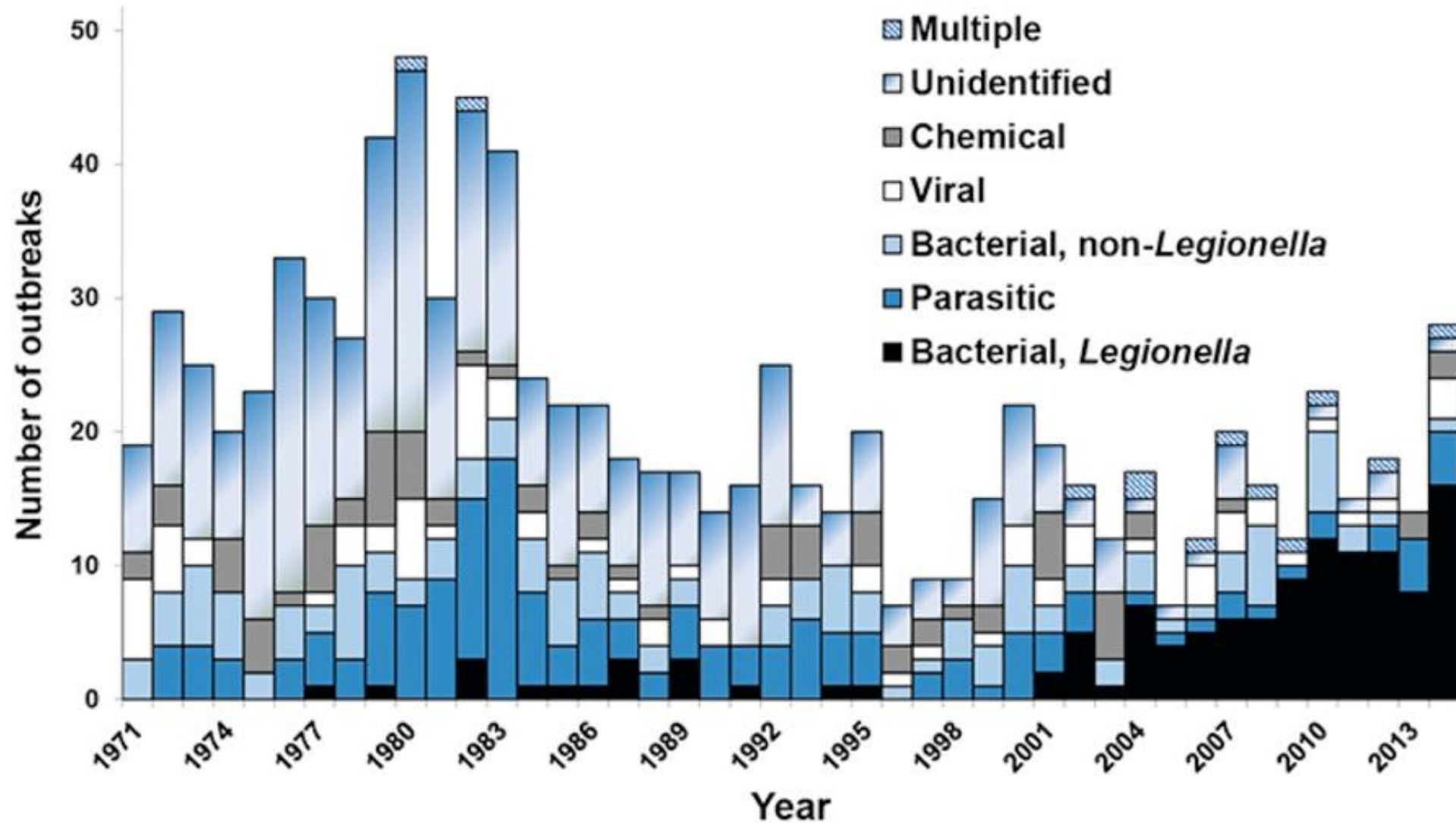
- Responsible for majority of tap water-associated hospitalizations and deaths in the US and many other countries
- Cost of at least \$2.39 billion annually
- Higher risk to older individuals, the immunocompromised, and those with other risk factors
- Non-ingestion exposure routes such as inhalation



Legionnaires' disease in the United States, 2000-2021



Legionella is now the primary source of drinking-water associated disease



Management of *Legionella* in Water Systems

Committee on Management of *Legionella* in Water Systems

Water Science and Technology Board

Board on Life Sciences

Board on Population Health and Public Health Practice

Division on Earth and Life Studies

Health and Medicine Division

A Consensus Study Report of
The National Academies of
SCIENCES • ENGINEERING • MEDICINE

THE NATIONAL ACADEMIES PRESS
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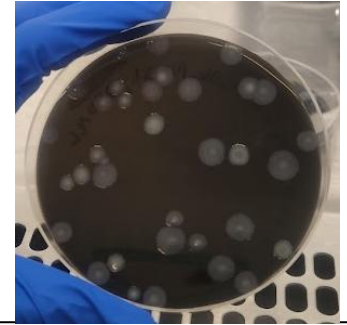
National Academies of Sciences Engineering and Medicine Report



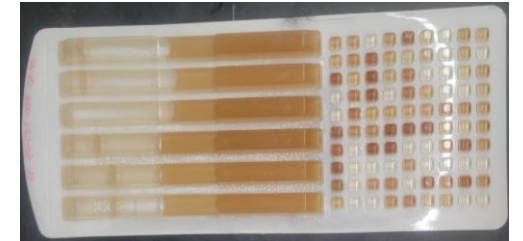
Present: Methods for Quantification of *Legionella* are evolving

Purpose: Diagnosis, Outbreak investigation, Routine monitoring, Mitigation assessment, and Research

- Urinary antigen test (UAT) which detects only *Lp1*
- Certified standard culture methods vs. New culture methods
- Quantitative PCR/droplet digital PCR
(*L. spp.*, *Lp*, *Lp1*, *L. anisa*, *L. micdadei*, *L. longbeachae*, *L. bozemanii*)
- DNA Sequencing
- Co-culture with amoeba hosts



Culture *Legionella* on Buffered Charcoal Yeast Extract (BCYE) agar



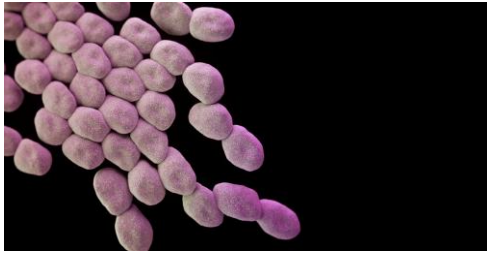
Detect *Legionella pneumophila* using IDEXX Legiolert kit

- ✓ The diagnosis of LD caused by *Legionella* spp. other than *Lp1* is very difficult with the current routine approaches
- ✓ Need evaluation, training, proficiency testing, national approaches for surveillance
- ✓ New investment in modified culture and molecular tools is needed

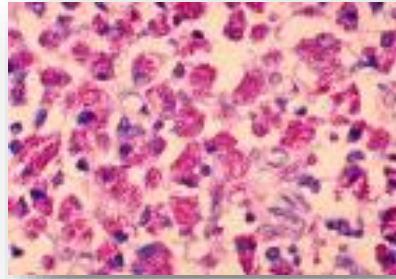
Legionella and other opportunistic pathogens in premise plumbing (OPPPs):



Legionella pneumophila



Acinetobacter baumannii



Mycobacterium avium
complex (MAC)



Pseudomonas aeruginosa



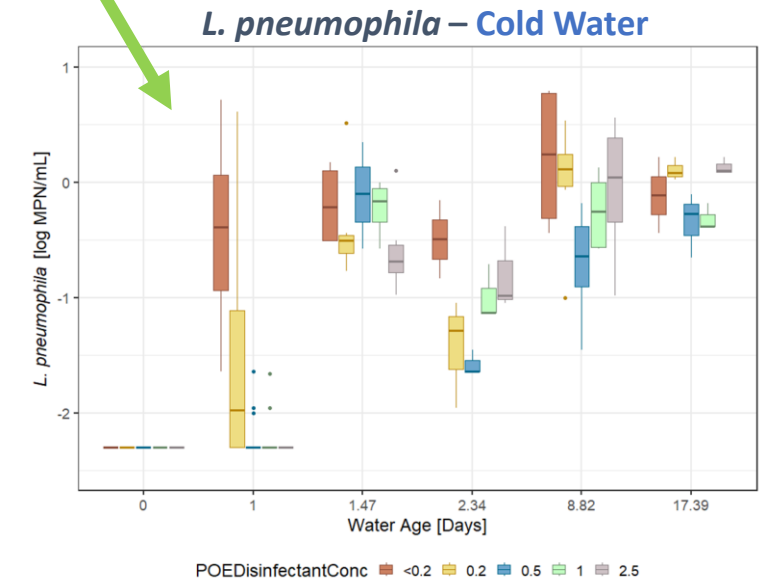
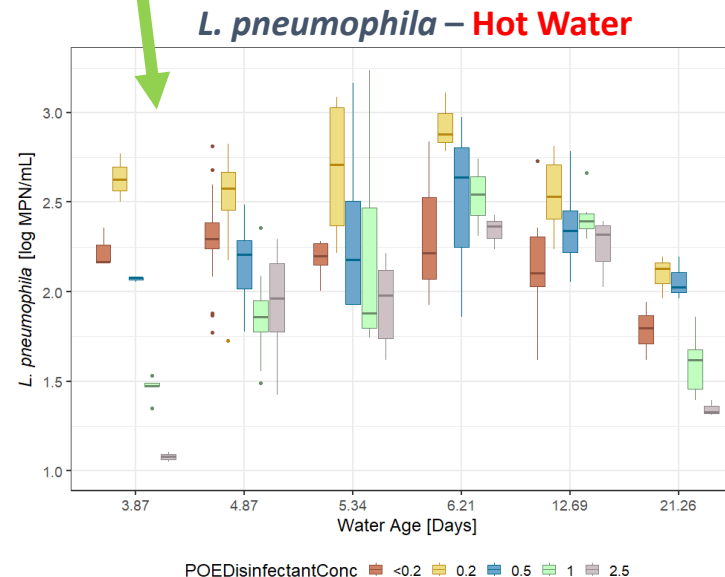
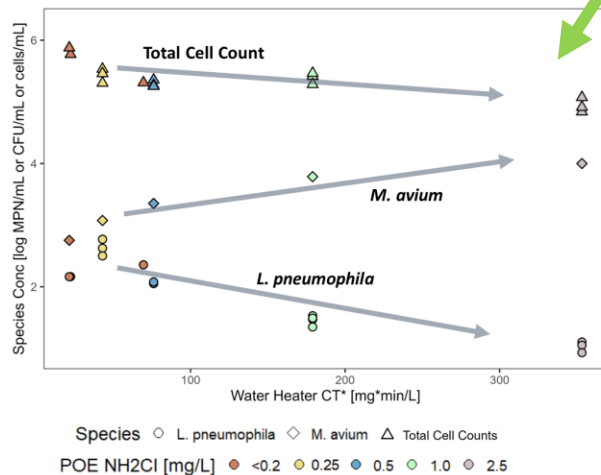
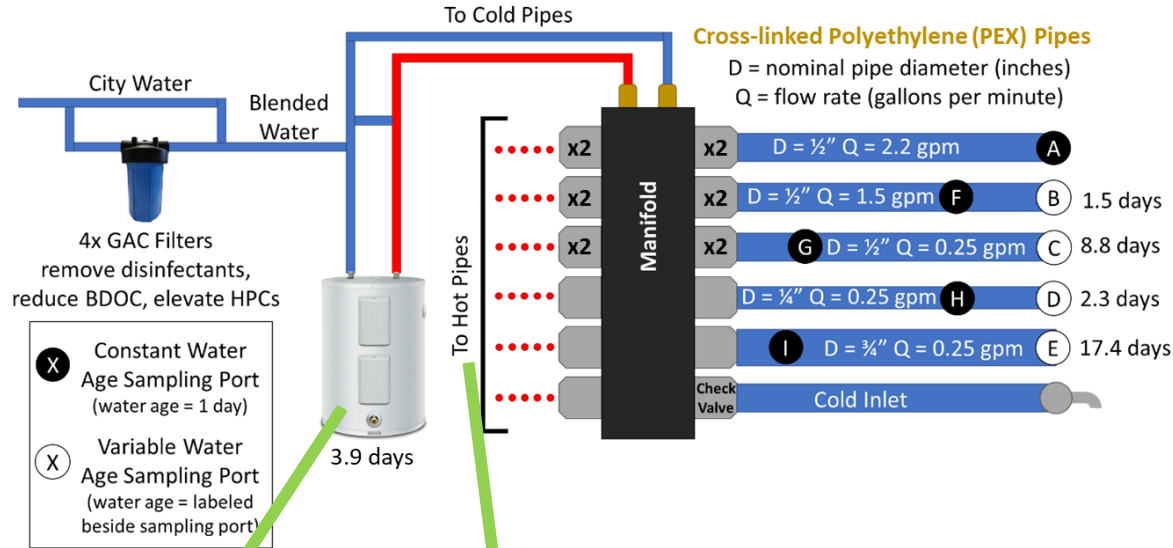
Acanthamoeba
and *Naegleria*

- Thomas and Ashbolt, *ES&T* 2011: Tendency of OPPPs to be “amoebae-resisting microorganisms” (ARMs)
 - Increases *Legionella* virulence (i.e., more invasive of host tissue) (Garduño et al. 2002)
 - Increases *Legionella* tolerance to disinfectants, heat-shock, etc. (Kwaik et al. 1997; Flynn and Swanson, 2014)
- Falkinham, *Pathogens* 2015: Tend to be biofilm formers, tend to be disinfectant tolerant/resistant.

Present: Culturable *Legionella pneumophila* in Building Plumbing Systems



Tolulope
Odimegwe



Present: qPCR of *Legionella* DNA at different Water Heater Set Points

Rhoads et al.
Microbiome
2015

A *L. pneumophila* concentration (log gene copies/mL)

Control System (39° C)	Water Use Frequency			Experimental System	Water Use Frequency		
	Low	Medium	High		Low	Medium	High
5 months	4.2	4.2	4.1	Baseline (39° C)	4.3	4.3	4.2
8 months	4.2	3.4	3.9	Exp.1 (42° C)	3.5	3.1	3.0
13 months	4.3	4.7	4.3	Exp. 2 (51° C)	4.3	2.3	2.2
15 months	5.1	4.8	4.3	Exp. 3 (58° C)	3.4	3.2	2.7

B *L. pneumophila* regrowth factor (distal taps/recirculating lines)

Control System (39° C)	Water Use Frequency			Experimental System	Water Use Frequency		
	Low	Medium	High		Low	Medium	High
5 months	0.8	0.9	0.7	Baseline (39° C)	0.3	0.4	0.3
8 months	4.2	0.7	2.1	Exp.1 (42° C)	1.5	0.5	0.5
13 months	1.9	5.6	1.9	Exp. 2 (51° C)	68.2	0.7	0.6
15 months	5.5	3.2	1.0	Exp. 3 (58° C)	2.7	1.6	0.5

C Total *L. pneumophila* yield per week (log gene copies)

Control System (39° C)	Water Use Frequency			Experimental System	Water Use Frequency		
	Low	Medium	High		Low	Medium	High
5 months	6.9	7.4	8.1	Baseline (39° C)	7.0	7.5	8.2
8 months	6.9	6.6	7.9	Exp.1 (42° C)	6.2	6.2	7.0
13 months	7.0	7.9	8.3	Exp. 2 (51° C)	7.0	5.5	6.3
15 months	7.8	8.0	8.4	Exp. 3 (58° C)	6.1	6.4	6.7

Candidate Contaminant List (CCL)

- A list of drinking water contaminants that are **NOT** currently regulated but are known or anticipated to occur in public water systems.
- These contaminants may require future regulation under SDWA.
- SDWA requires EPA to publish CCL every 5 years
 - CCL1 (1998)
 - CCL2 (2005)
 - CCL3 (2009)
 - CCL4 (2016)
 - CCL5 (2021)
- Regulatory determinations: EPA is required to make formal decision for at least five contaminants on whether to develop a national primary regulation.

CCL 5 Microbial Contaminants

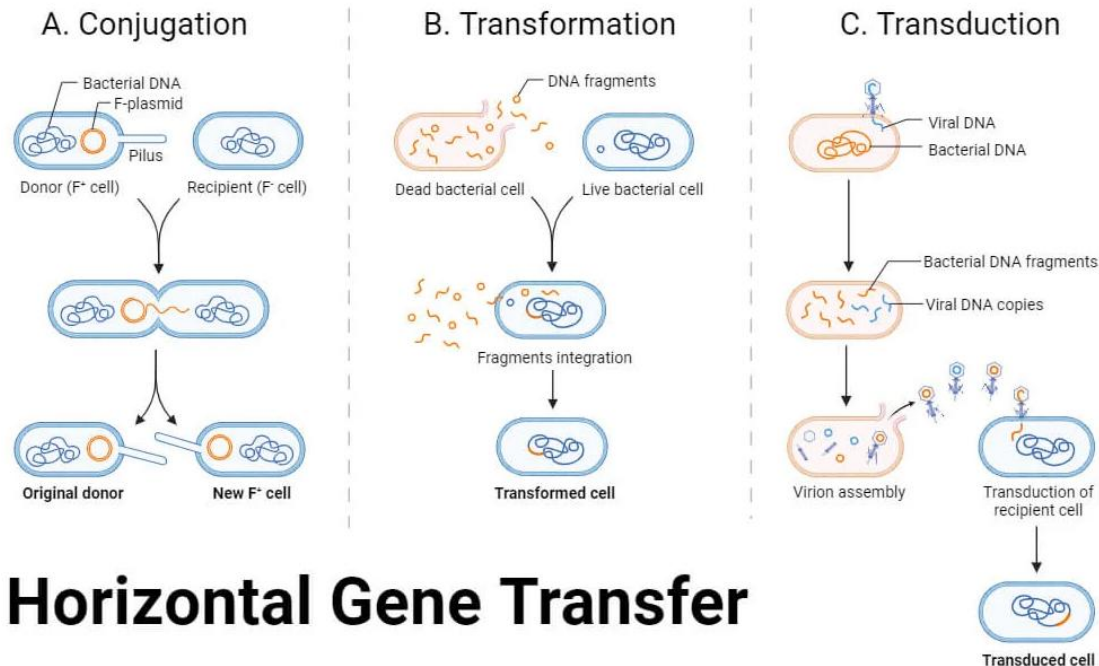
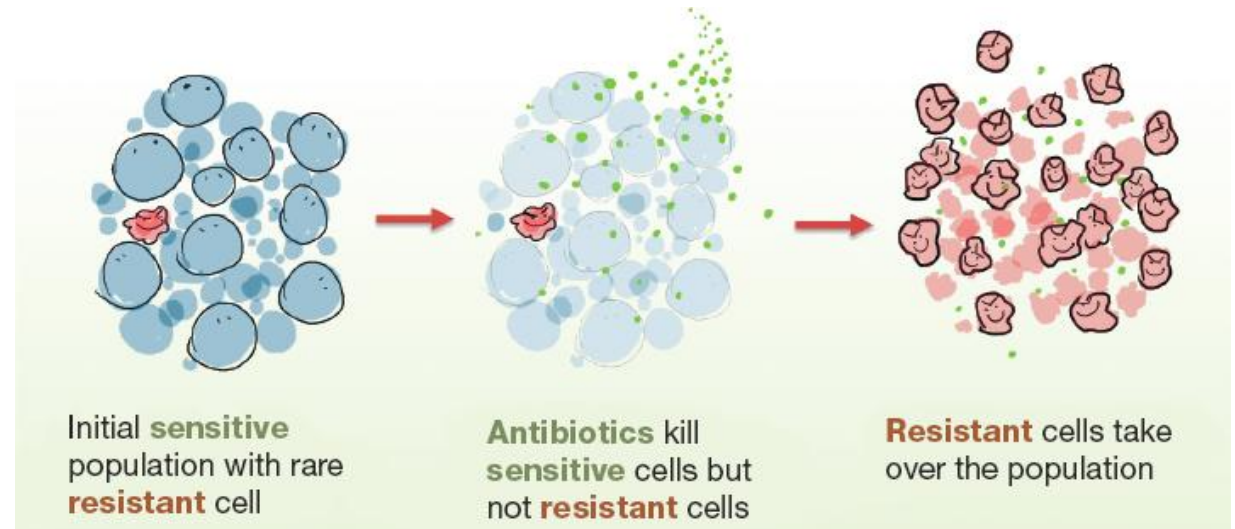
Contaminant	Disease and infections
Adenovirus	Virus most commonly causing respiratory illness, and occasionally gastrointestinal illness
Caliciviruses	Virus (includes Norovirus) causing mild self-limiting gastrointestinal illness
<i>Campylobacter jejuni</i>	Bacterium causing mild self-limiting gastroentestinal illness
<i>Enteroviruses</i>	Group of viruses including polioviruses, coxsackieviruses and echoviruses that can cause mild respiratory illness
<i>Escherichia coli (0157)</i>	Toxin-producing bacterium causing gastrointestinal illness and kidney failure
<i>Helicobacter pylori</i>	Bacterium sometimes found in the environment capable of colonizing human gut that can cause ulcers and cancer

CCL 5 Microbial Contaminants (Continued)

Contaminant	Disease and infections
<i>Legionella pneumophila</i>	Bacterium found in the environment including hot water systems causing lung diseases when inhaled
<i>Mycobacterium avium</i> , <i>Mycobacterium abscessus</i>	Bacterium causing lung infection in those with underlying lung disease, and disseminated infection in the severely immunocompromised
<i>Naegleria fowleri</i>	Protozoan parasite found in shallow, warm surface and ground water causing primary amebic meningoencephalitis
<i>Pseudomonas aeruginosa</i>	Bacterium that is often multi-drug resistant and causes skin, blood, and ear infections
<i>Shigella sonnei</i>	Bacterium causing mild self-limiting gastrointestinal illness and bloody diarrhea

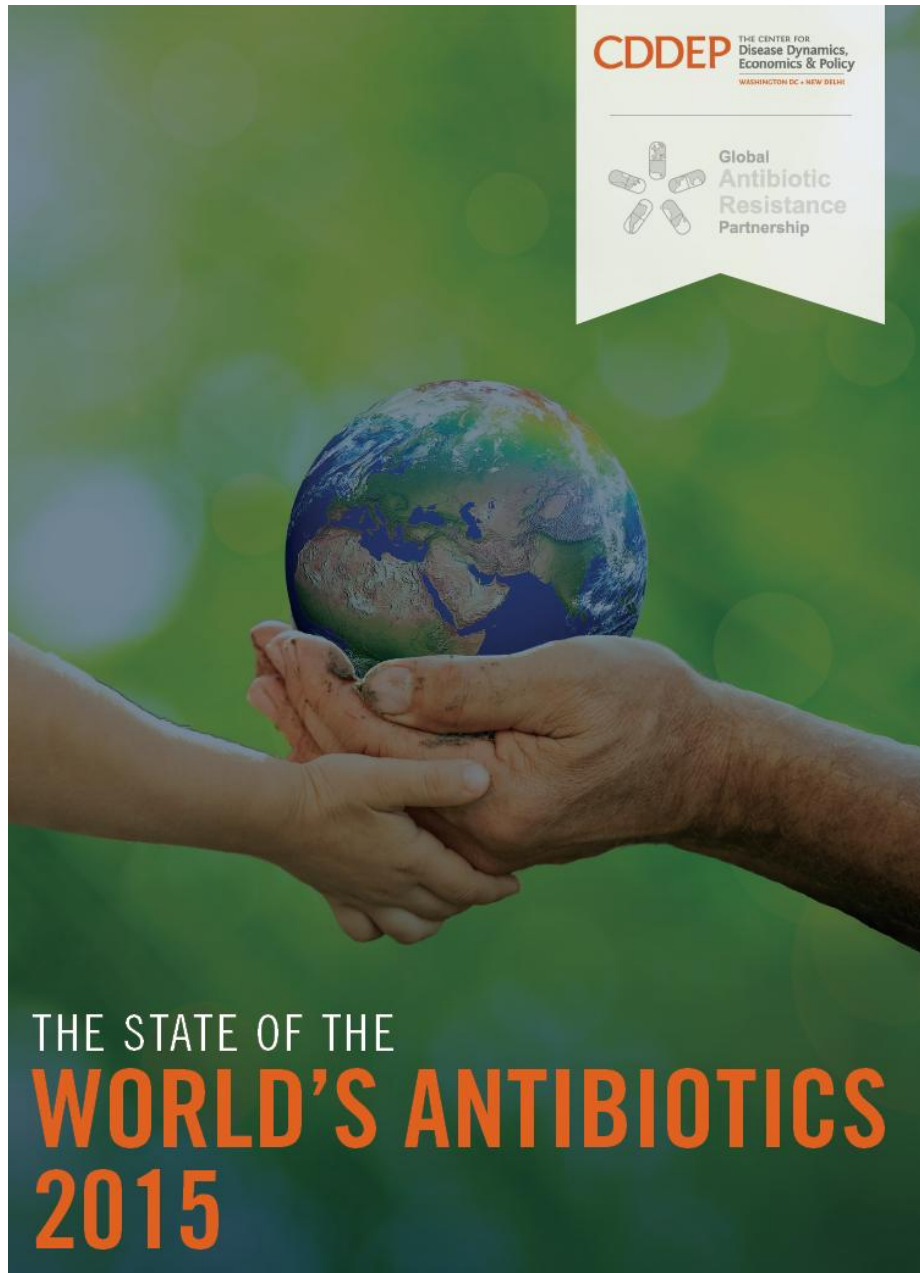
What is Antibiotic Resistance (AR)?

- Bacteria adapt to survive our methods of killing them
 - We are losing the ability to treat infections



- Bacteria can give their genes to one another
 - AR can develop in non-pathogenic bacteria and be passed to pathogens
 - Its hard to study all bacteria for AR when our tools were meant for specific pathogens

Horizontal Gene Transfer

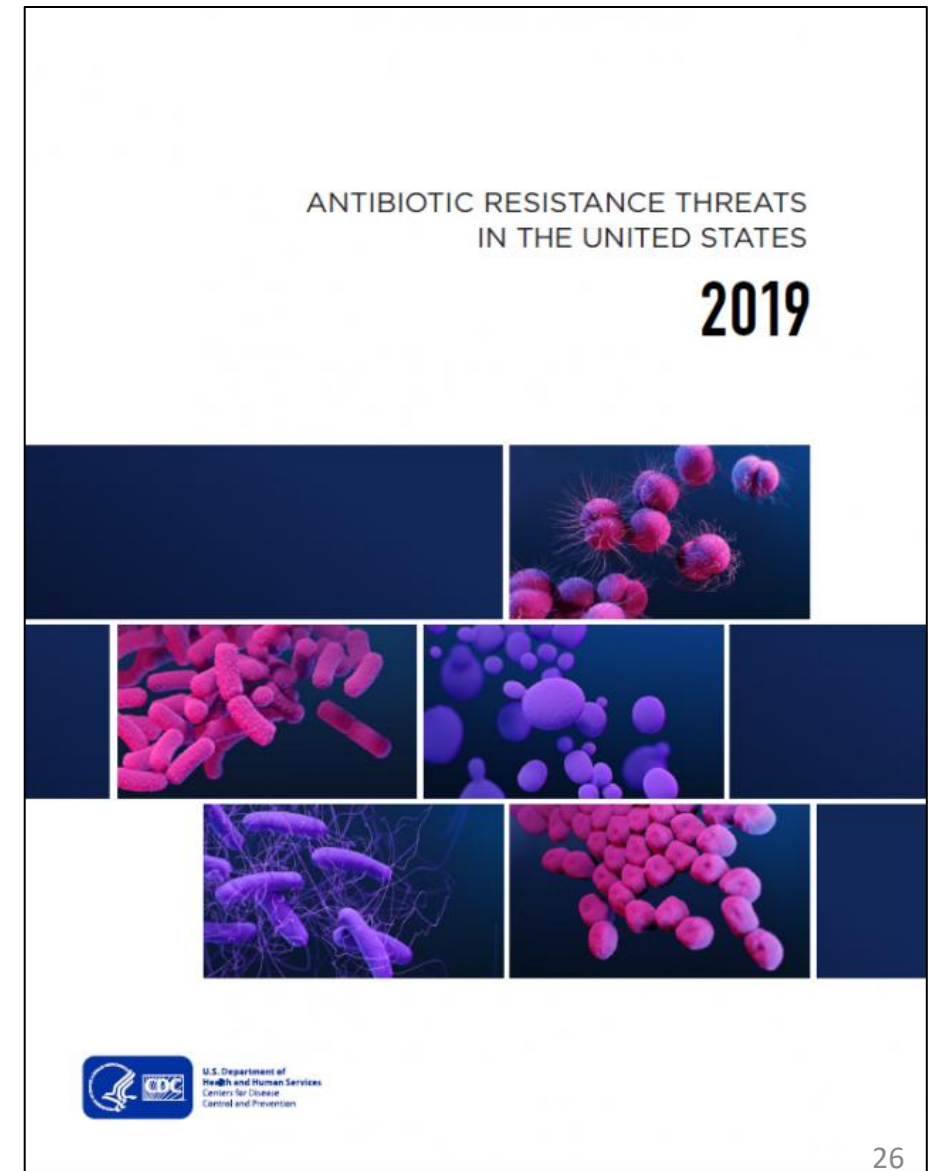


- **CDDEP: US-India Global Antibiotic Resistance Partnership:**
 - In Europe, 25,000 deaths are attributable to antibiotic-resistant infections, with cost of €1.5 billion annually (EMA, ECDC 2009).
 - In India, 58,000 neonatal sepsis deaths are attributable to drug resistant infections (Laxminarayan et al. 2013)

Antibiotic Resistance as an Emerging “Pathogen” in Water

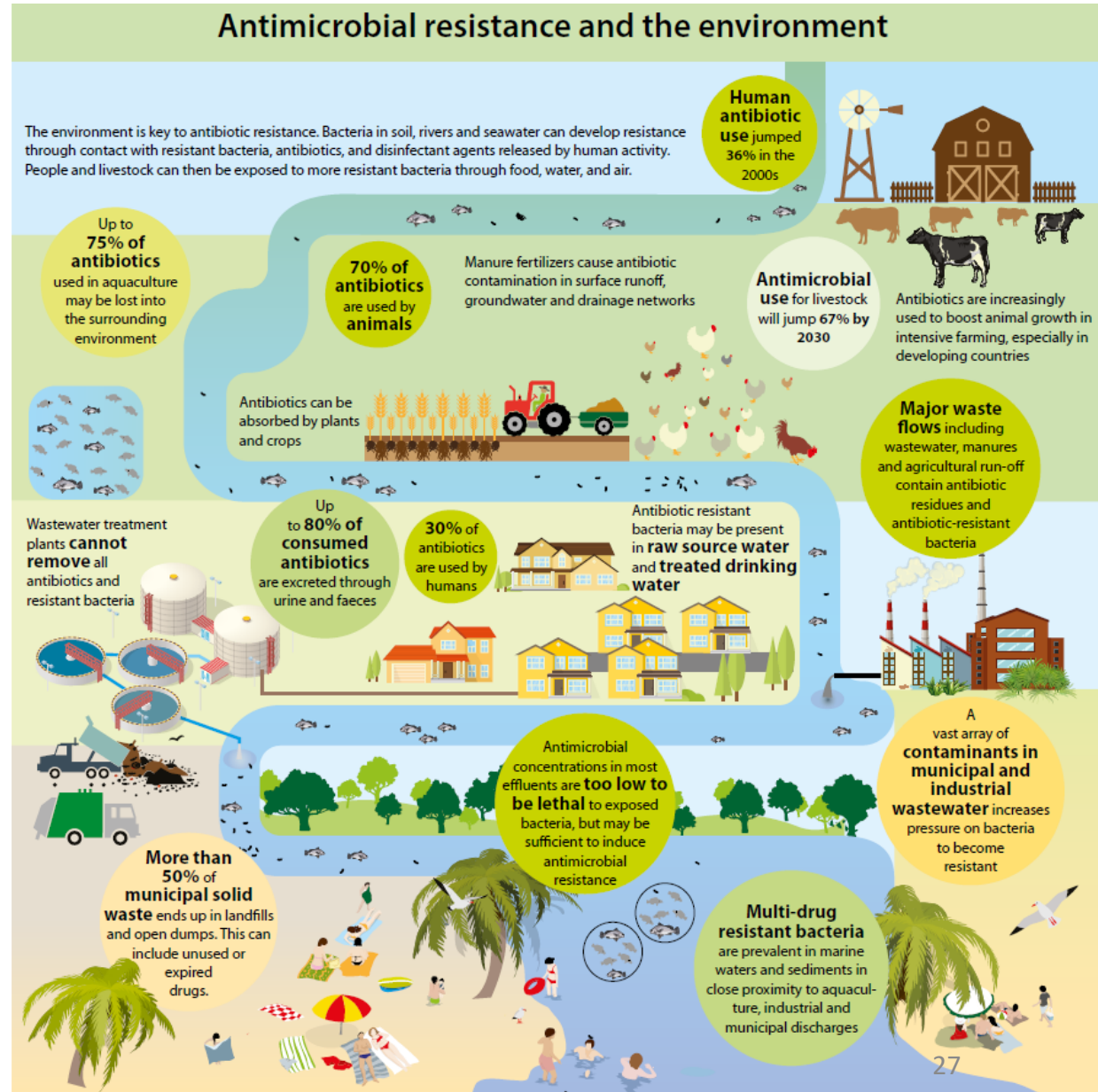
- 2019 CDC Report:
 - 2.8 million Americans fall ill from antibiotic-resistant bacteria
 - At least 35,000 die as a result (many more if count complications)
 - \$55 billion annual cost

“Antibiotic-resistant infections can happen anywhere. Data show that most happen in the general community”



Antimicrobial Resistance and the Water Environment: What to Monitor?

- Most AR infections are acquired in the community as opposed to in hospitals
 - Where are AR infections being acquired?
 - Where is AR developing?



How can we Measure Antibiotic Resistance?

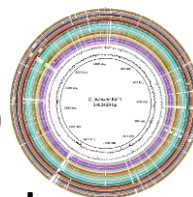
Culture

By culturing organisms, we can:

- Quantify live cells
- Quantify rate of resistance
- Assess what antibiotics the organism is resistant to
- Isolate colonies
- **Whole Genome Sequence the isolates**



Whole Genome Sequencing (WGS)

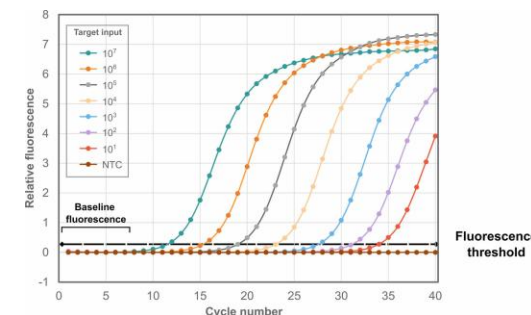


By sequencing isolates, we can:

- Find the genes responsible for antibiotic resistance
- Compare bacterial strains with high resolution

Quantitative Polymerase Chain Reaction (qPCR)

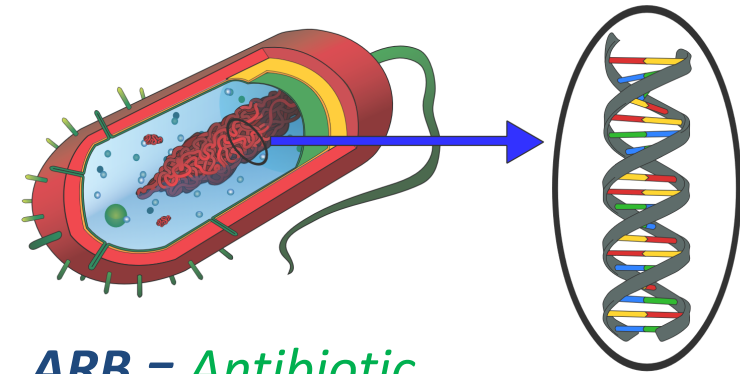
- A single gene is copied over and over and back calculated to the original concentration
- Can quantify specific AR genes



Tracking Antibiotic Resistance Genes (ARGs) as Environmental “Contaminants”

Poudre River Colorado, USA 2005-2012

- Primary water source is snowmelt from the Rocky Mountains
- qPCR and culture used
- *su1* ARGs (sulfonamide resistance) strongly correlated with upstream WWTPs and animal feeding operations (AFOs)



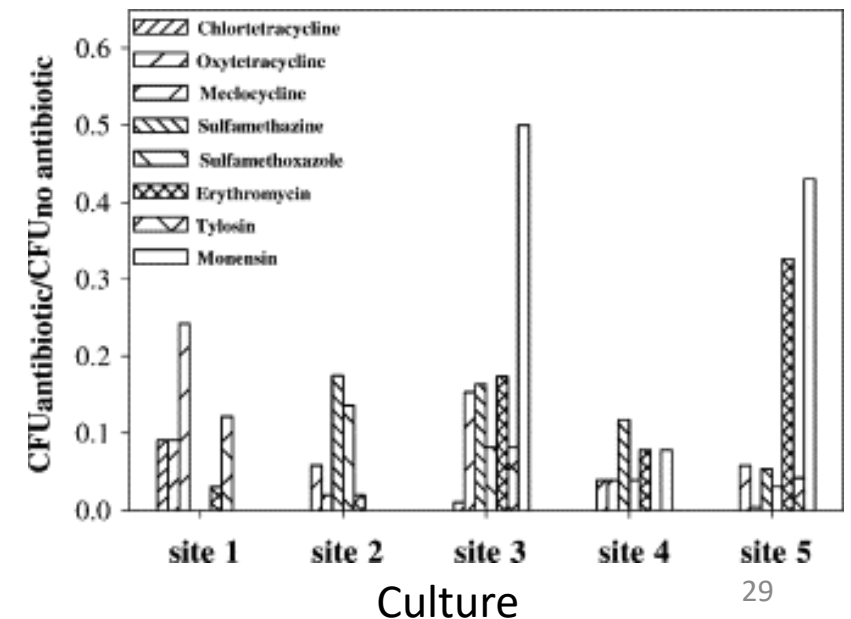
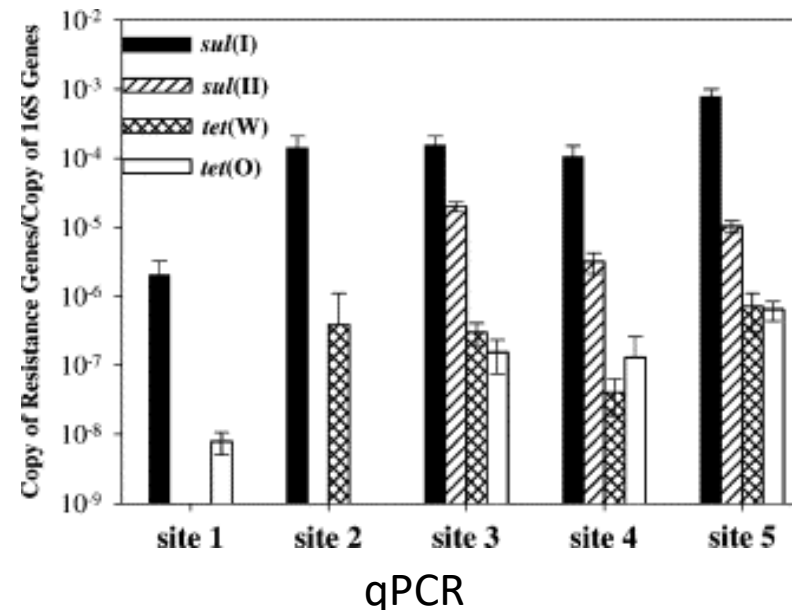
ARB = Antibiotic

Resistant Bacteria

ARG = Antibiotic
Resistance Gene



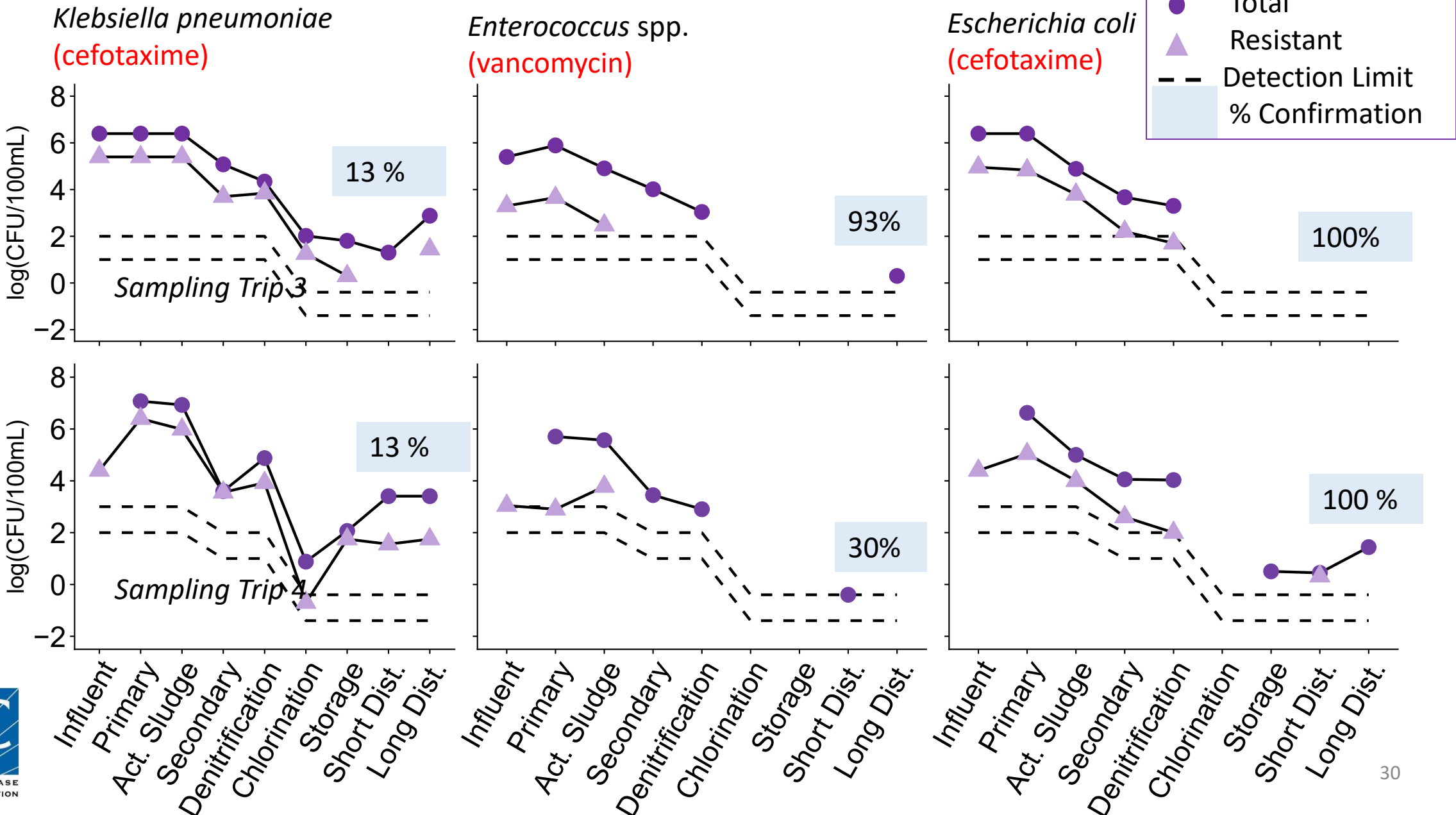
Amy Pruden,
VT



Water Reuse: Culturing ARB



Key Collaborator:
Jody Harwood,
USF



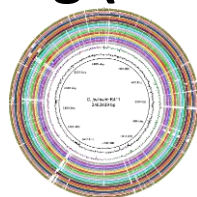
Digital Droplet PCR (ddPCR) vs qPCR

Culture



- Quantify live cells
- Quantify rate of resistance
- Assess what antibiotics the organism is resistant to
- Isolate colonies
- **Whole Genome Sequence the isolates**

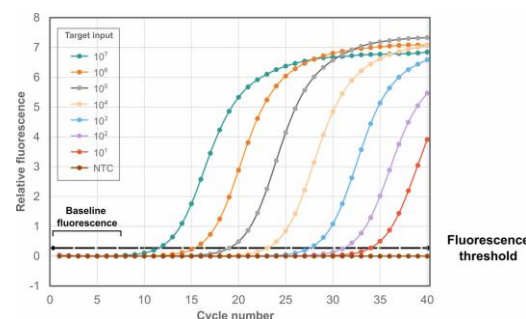
Whole Genome Sequencing (WGS)



- Find the genes responsible for antibiotic resistance
- Compare bacterial strains with high resolution

Quantitative Polymerase Chain Reaction (qPCR)

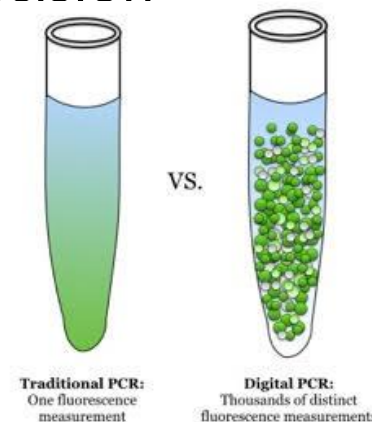
- Can quantify specific AR genes
- Requires a standard curve each run



Droplet Digital Polymerase Chain Reaction (ddPCR)

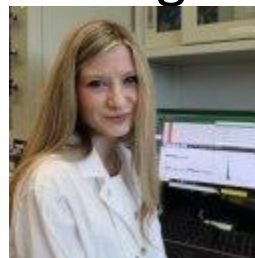
Can quantify specific AR genes

- At a lower concentration
- Without a standard curve
- With less inhibition
- More precision than qPCR

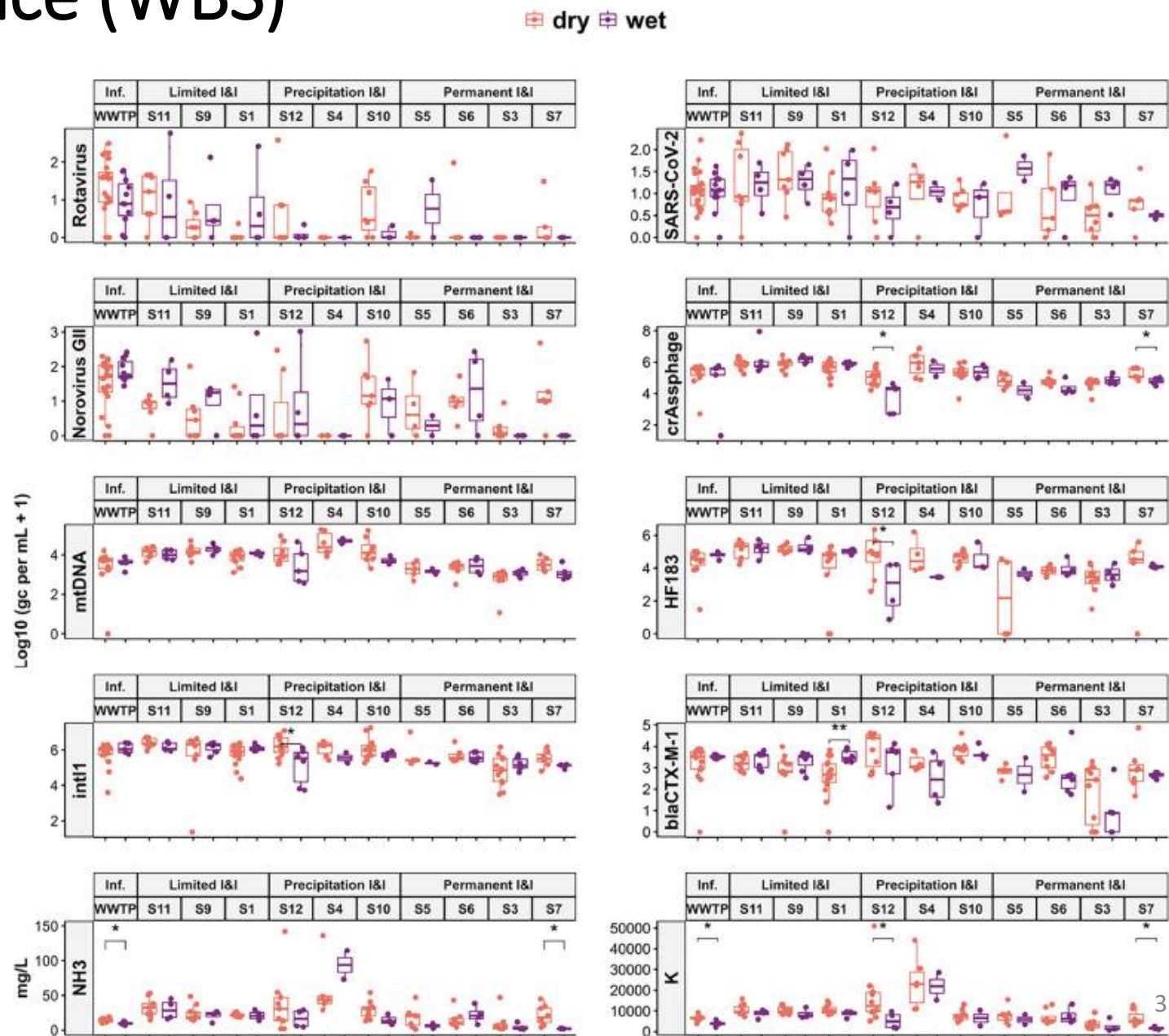


Wastewater-Based Surveillance (WBS)

- Using wastewater to assess population health and levels of AR
- Poor infrastructure makes WBS challenging to conduct
 - Stormwater infiltration changes ARG and ARB signal



Amanda Darling, PhD at VT, now at Harvard



16S rRNA Amplicon Sequencing

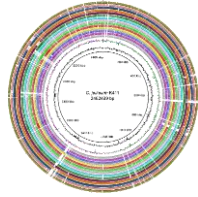
Culture

- Quantify live cells
- Quantify rate of resistance
- Assess antibiotics the organism resists



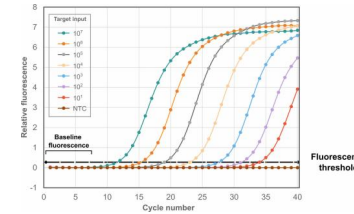
Whole Genome Sequencing (WGS)

- Find the ARGs
- Compare strains



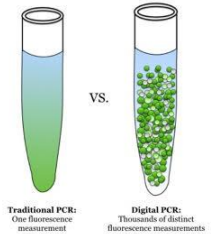
Quantitative Polymerase Chain Reaction (qPCR)

- Can quantify specific AR genes



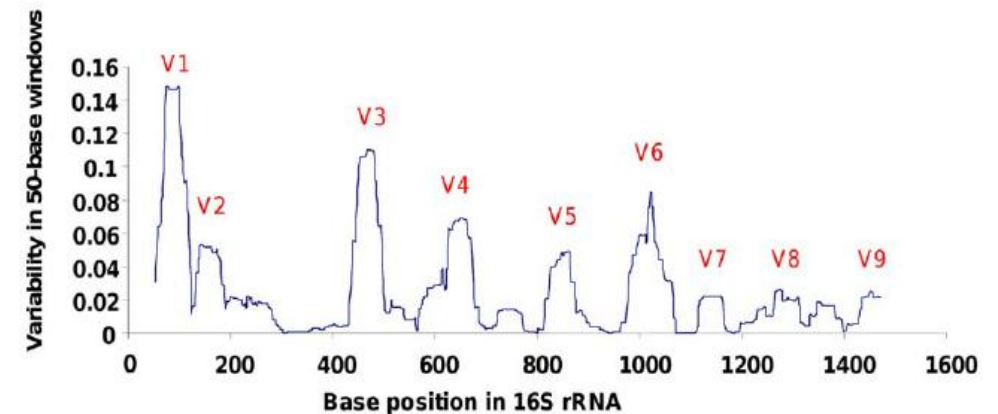
Droplet Digital Polymerase Chain Reaction (ddPCR)

- More precision than qPCR



16S rRNA Amplicon Sequencing

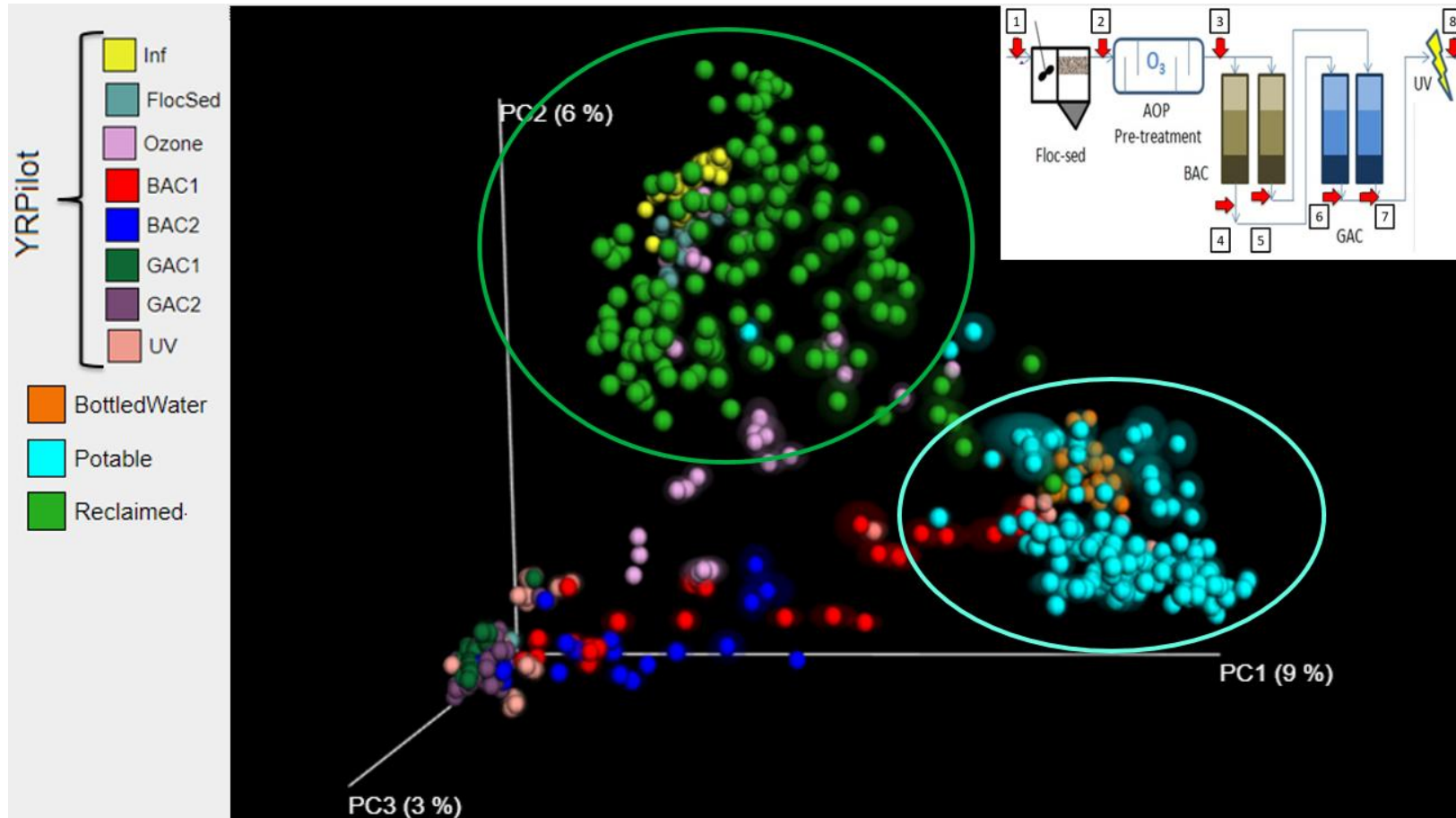
- Every bacteria has a 16S gene
- Amplify all 16S genes in a sample, then sequence
- Able to analyze all of the bacteria in your sample
- Hard to differentiate some bacteria's 16S genes



Microbiome as a “Fingerprint”: Wastewater, Recycled Water, Bottled Water



Matt Blair,
Post-Doc,
EAWAG,
Switzerland



Principle Coordinate Analysis: 16S rRNA gene Amplicon Sequences

Metagenomic Sequencing

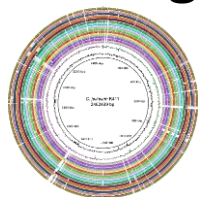
Culture

- Quantify live cells
- Quantify rate of resistance
- Assess antibiotics the organism resists



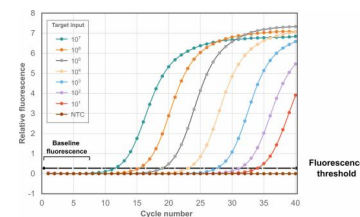
Whole Genome Sequencing (WGS)

- Find the ARGs
- Compare strains



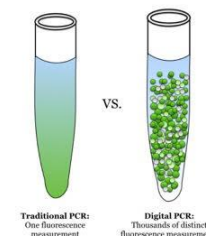
Quantitative Polymerase Chain Reaction (qPCR)

- Can quantify specific ARG genes



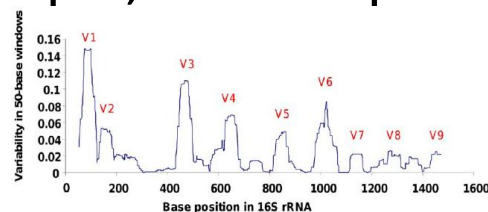
Droplet Digital Polymerase Chain Reaction (ddPCR)

- More precision than qPCR



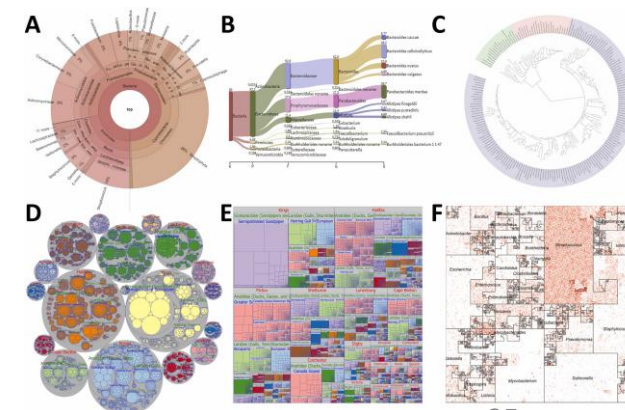
16S rRNA Amplicon Sequencing

- Amplify all 16S genes in a sample, then sequence



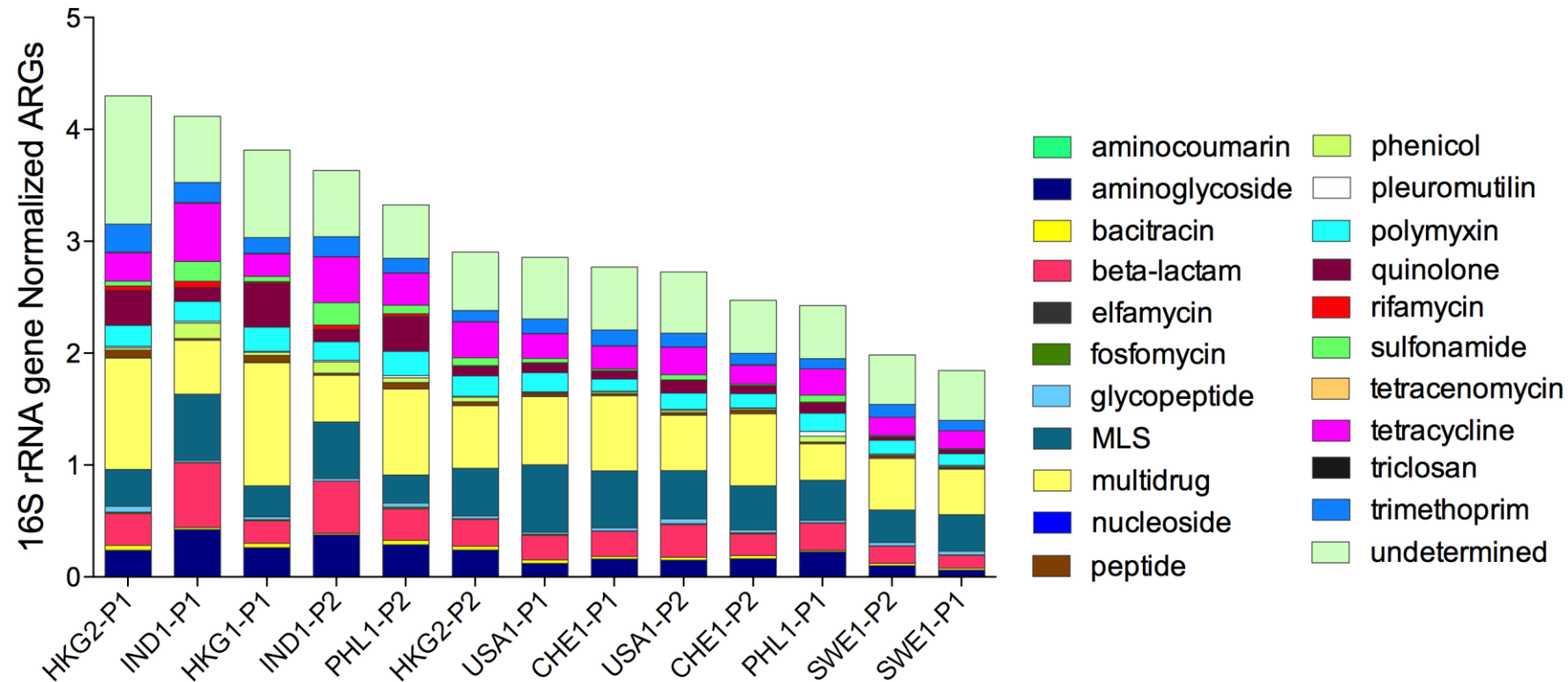
Metagenomic Sequencing

- Sequence all genes in a sample
- Allows semi-quantitative measure of all genes and bacteria in a sample



Global Metagenomic ARG Survey

INFLUENT Sewage: Ranked “Total ARG” Abundance



Locations:

CHE – Switzerland
HKG – Hong Kong
IND – India
PHL - Philippines
SWE – Sweden
USA – United States

Riquelme et al.
ES&T 2022

-Highest in Hong Kong and India
-Lowest in Sweden

CARD

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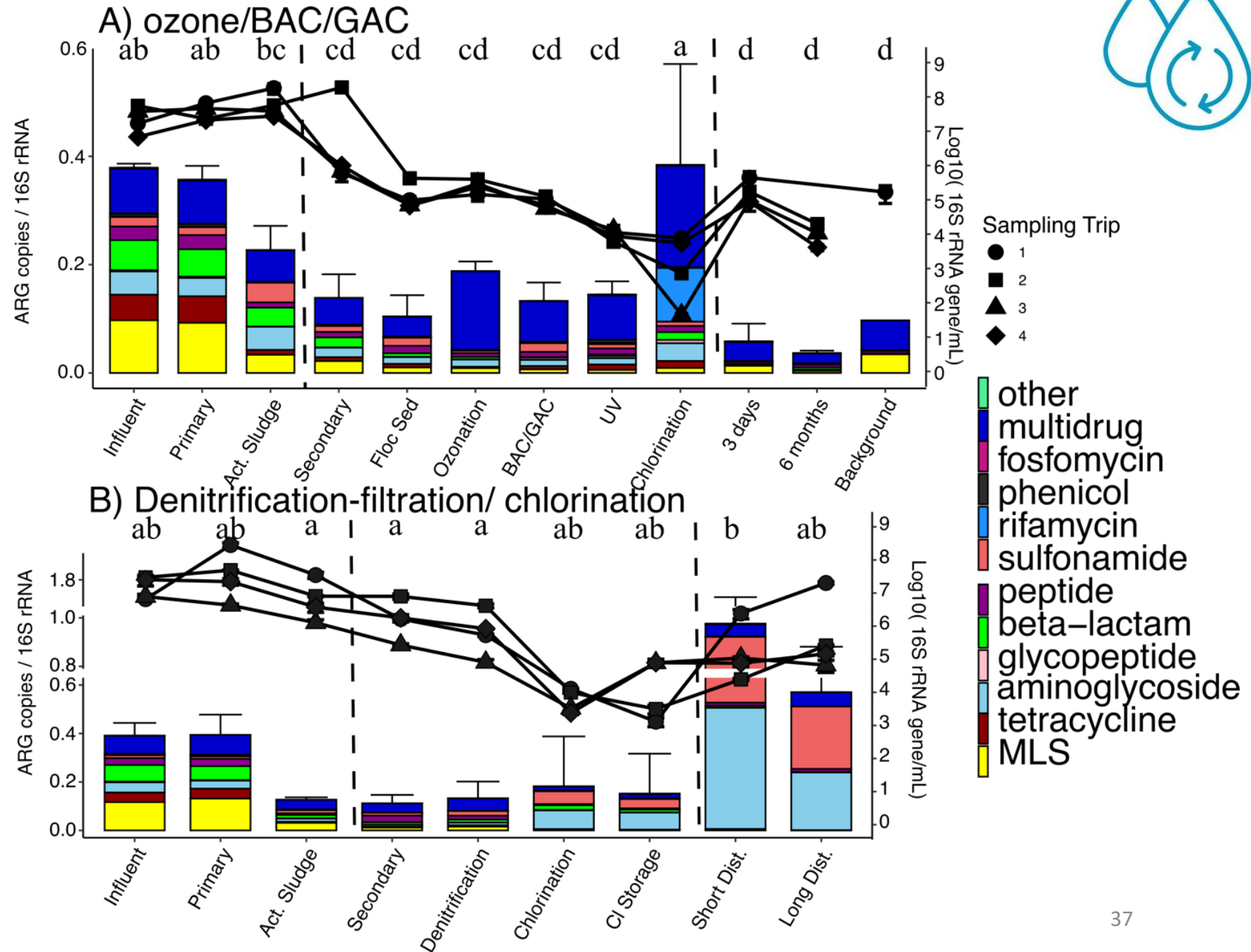


Key Collaborator:
Peter Vikesland, VTech³⁶

Metagenomic Profiling of ARGs in Reuse Systems



Ishi Keenum,
PhD at VT, now
at Michigan



Long-read Metagenomic Sequencing

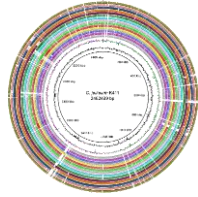
Culture

- Quantify live cells
- Quantify rate of resistance
- Assess antibiotics the organism resists



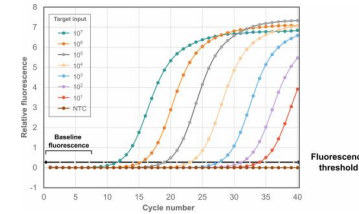
Whole Genome Sequencing (WGS)

- Find the ARGs
- Compare strains



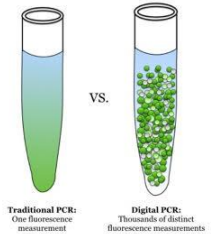
Quantitative Polymerase Chain Reaction (qPCR)

- Can quantify specific ARG genes



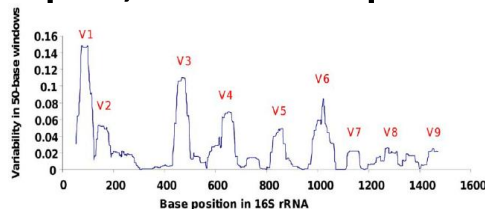
Droplet Digital Polymerase Chain Reaction (ddPCR)

- More precision than qPCR



16S rRNA Sequencing

- Amplify all 16S genes in a sample, then sequence



Metagenomic Sequencing

- Semi-quantitative measure of all genes and bacteria in a sample

Long-read Metagenomic Sequencing

- Longer sequences at a time
- Allows us to see what genes are next to one another

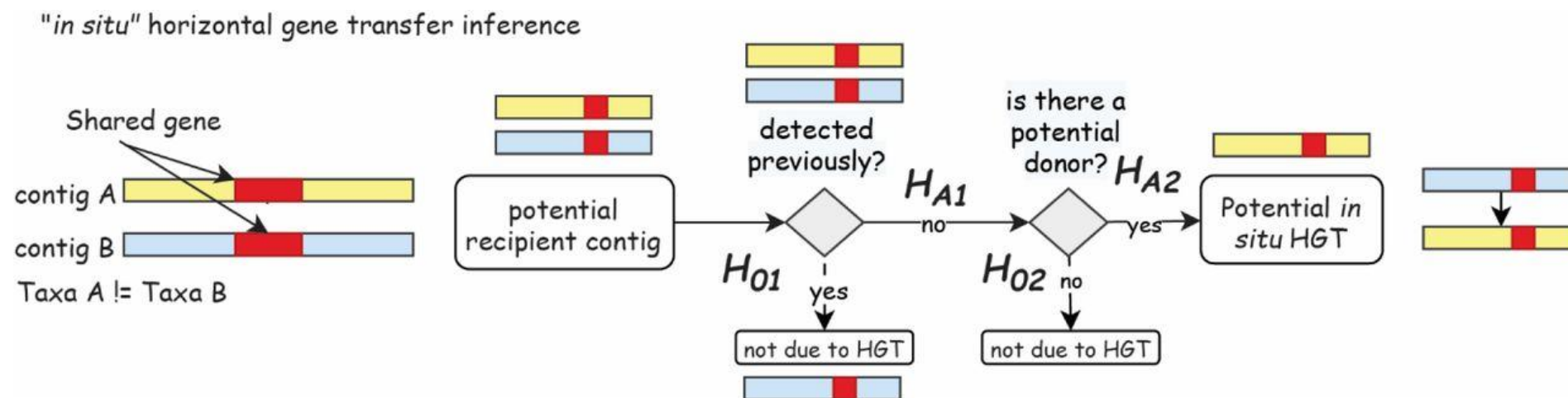
Finding Horizontal Gene Transfer Events

Finding who passes what ARG to whom, when it happens, and seeing what caused

- Long reads allow context of ARGs in longitudinal datasets to predict horizontal gene transfer events

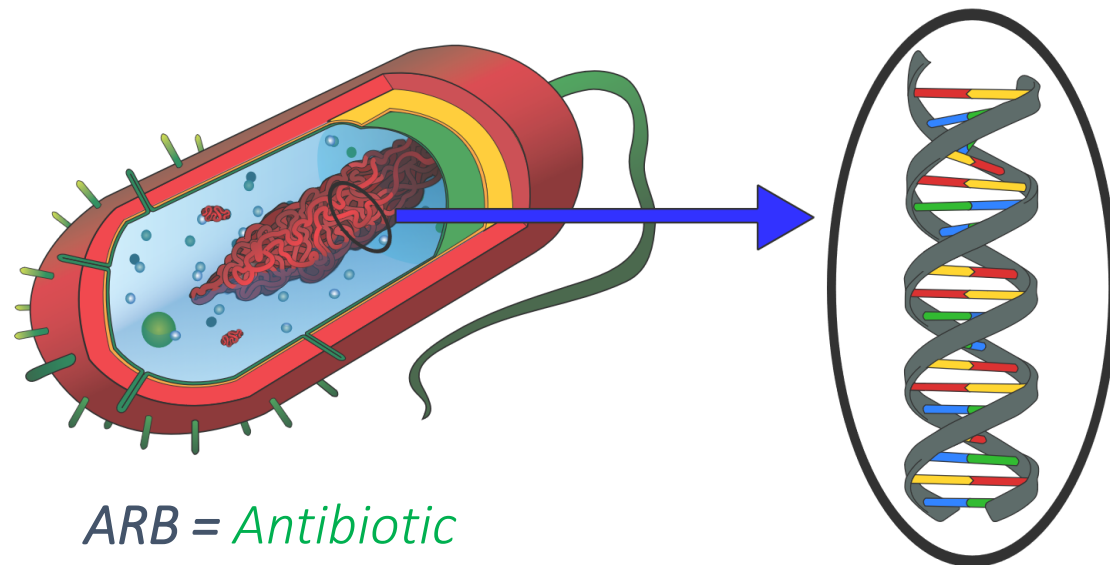


Connor Brown,
PhD at VT, now
at Aalborg
University,
Denmark



uture: What to Monitor and *Why*?

- ARBs (*which ARBs?*)
- ARPs (*which ARPs?*)
- ARGs (*which ARGs?*)
- Mobile genetic elements
(MGEs- *plasmids, transposons, integrons*)
- *Imminent public health risk?*
- *Potential for new strains of ARBs/ARPs to develop*



ARB = *Antibiotic
Resistant Bacteria*

ARG= *Antibiotic Resistance
Gene*

Mariana Ruiz Villarreal-
Wikimedia Commons

Environment International 130 (2019) 104880



Contents lists available at ScienceDirect

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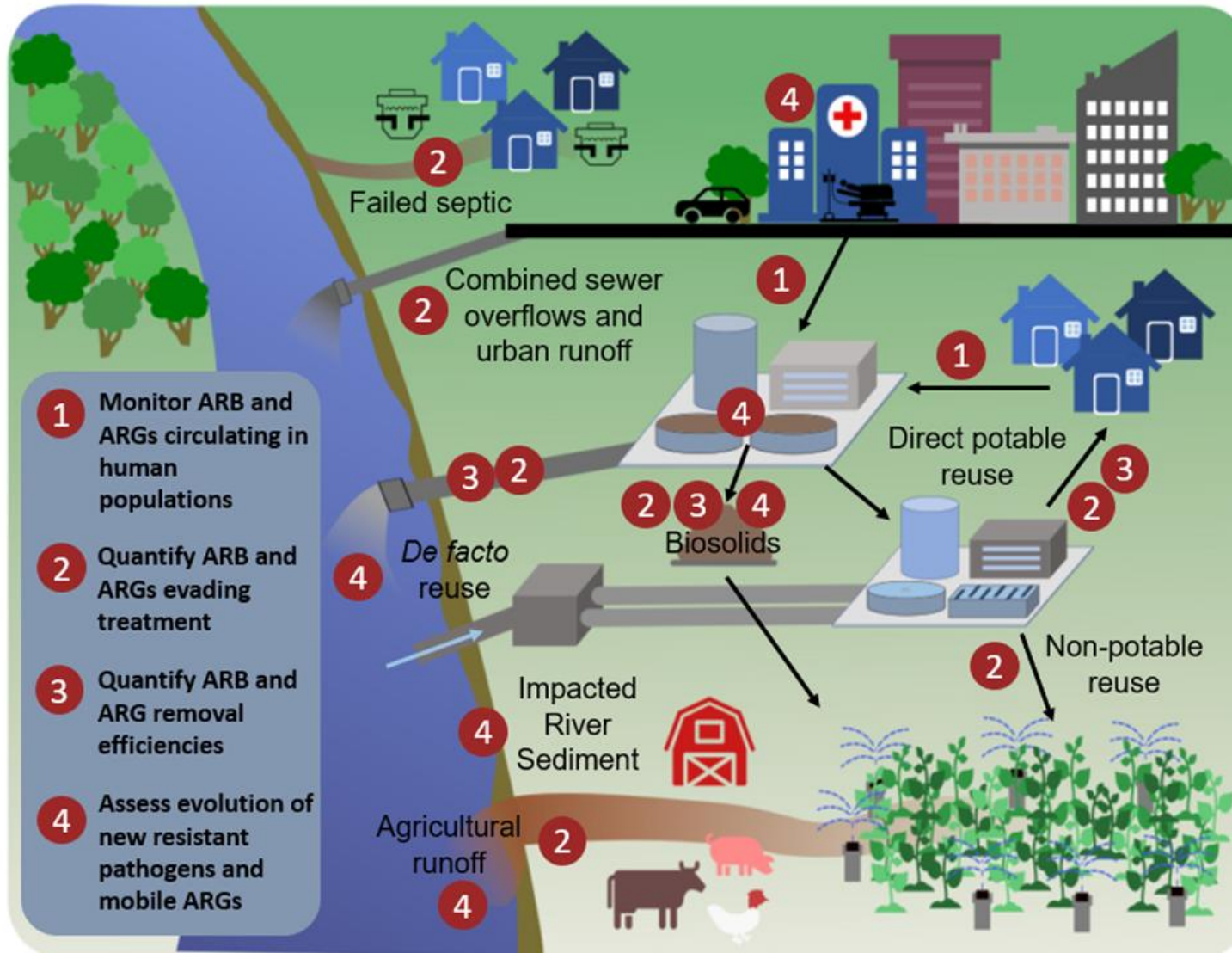


A conceptual framework for the **environmental surveillance of antibiotics
and antibiotic resistance**

Patricia M.C. Huijbers, Carl-Fredrik Flach, D.G. Joakim Larsson*



Linking Sampling Location and Analysis with Monitoring Objective



Antimicrobial Resistance Monitoring of Water Environments: A Framework for Standardized Methods and Quality Control

Krista Liguori, Ishi Keenum, Benjamin C. Davis, Jeanette Calarco, Erin Milligan, Valerie J. Harwood, and Amy Pruden*

Cite This: *Environ. Sci. Technol.* 2022, 56, 9149–9160

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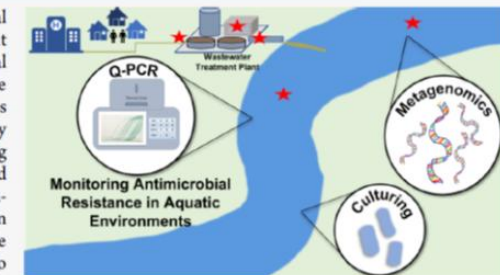
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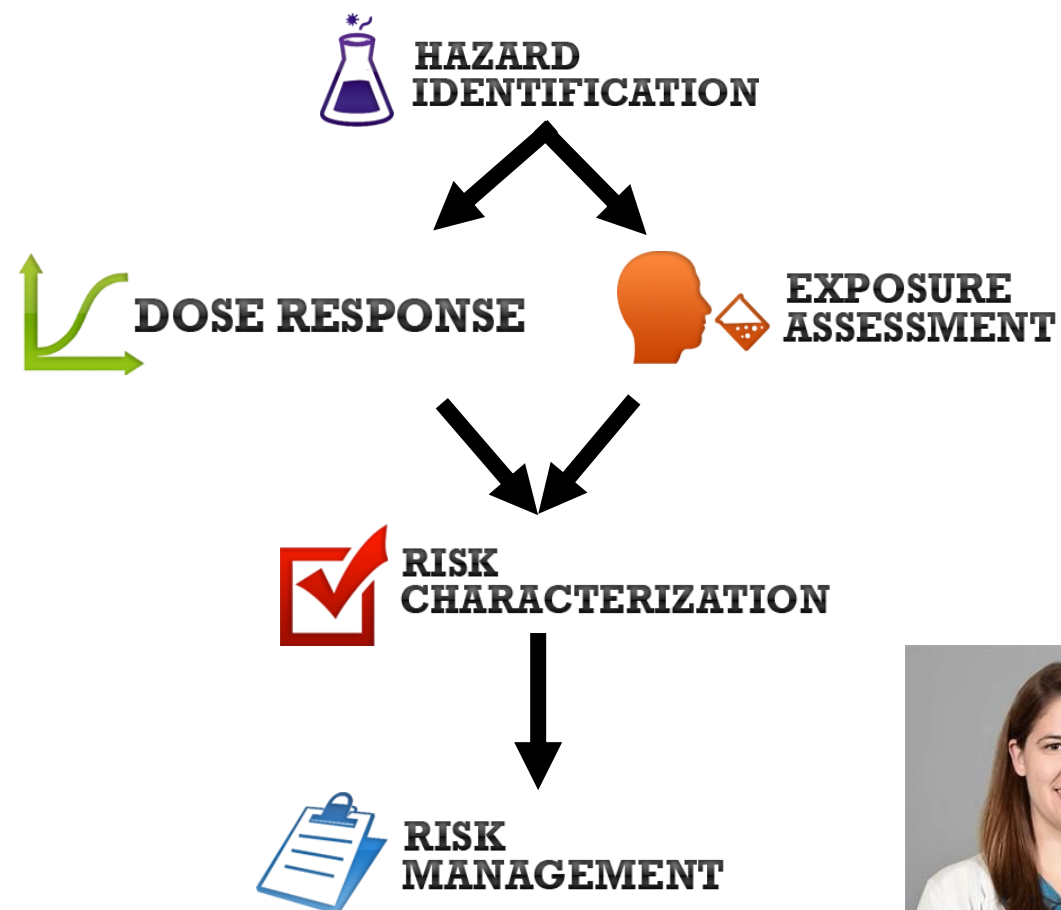
ABSTRACT: Antimicrobial resistance (AMR) is a grand societal challenge with important dimensions in the water environment that contribute to its evolution and spread. Environmental monitoring could provide vital information for mitigating the spread of AMR; this includes assessing antibiotic resistance genes (ARGs) circulating among human populations, identifying key hotspots for evolution and dissemination of resistance, informing epidemiological and human health risk assessment models, and quantifying removal efficiencies by domestic wastewater infrastructure. However, standardized methods for monitoring AMR in the water environment will be vital to producing the comparable data sets needed to address such questions. Here we sought to establish scientific consensus on a framework for such standardization, evaluating the state of the science and practice of AMR monitoring of wastewater, recycled water, and surface water, through a literature review, survey, and workshop leveraging the expertise of academic, governmental, consulting, and water utility professionals.

KEYWORDS: antibiotic resistance, surveillance, standardization, wastewater, recycled water, surface water



Liguori et al. *ES&T* 2022

Quantitative Microbial Risk Assessment



- Excellent framework for established pathogens, e.g., *E. coli*
- Challenging framework for antibiotic resistance:
 - Colonization, delayed onset, morbidity versus mortality
 - Overall “risk” of new resistant strain emerging versus traditional human health risk



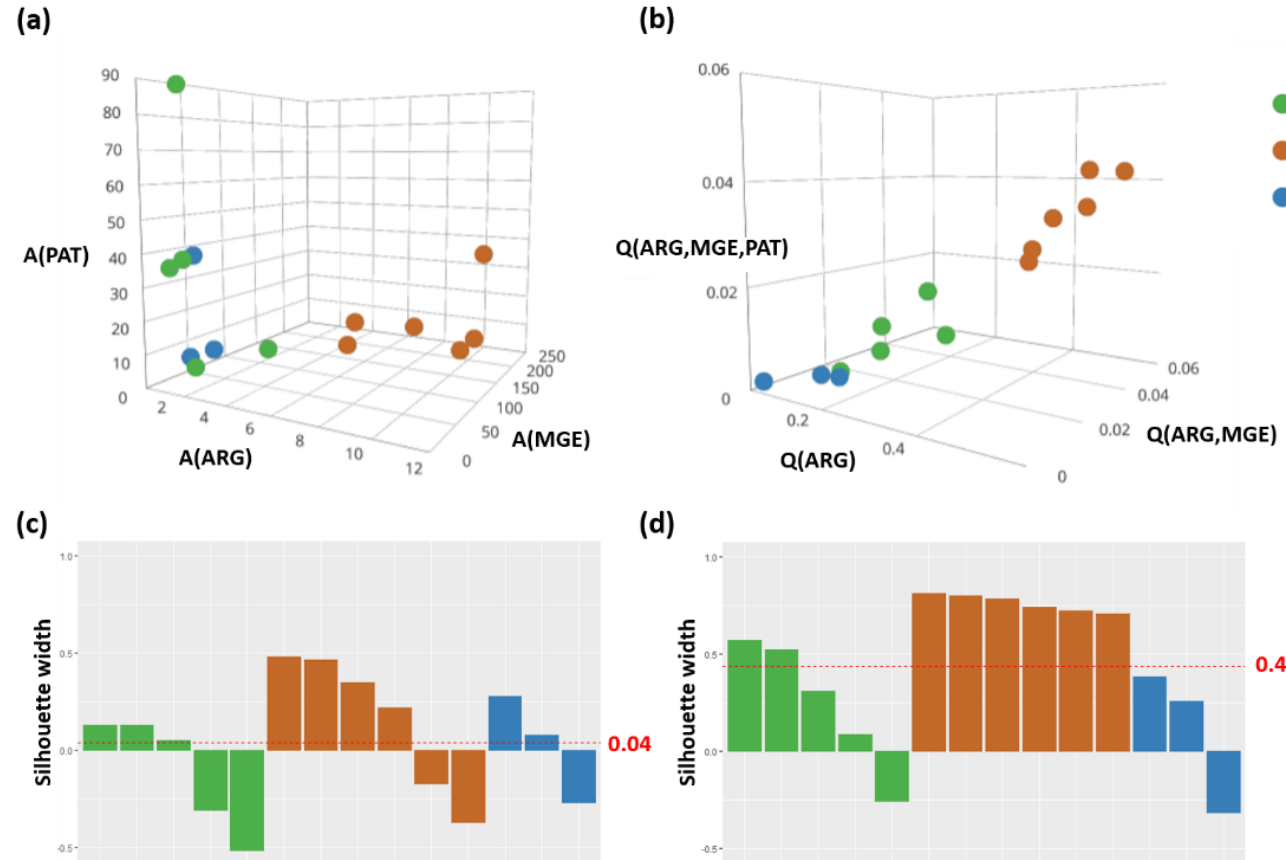
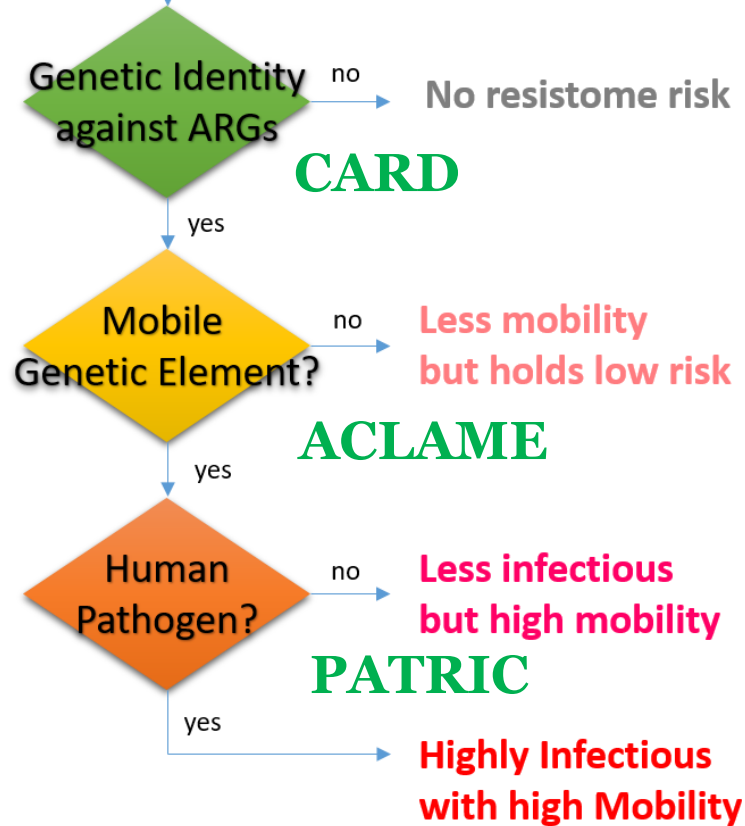
Key Collaborator:
Kerry Hamilton,
ASU

WRF Project 4961

MetaCompare: A Computational Pipeline for Ranking “Relative Resistome Risk” in Various Environmental Compartments

An assembled Contig

Oh et al. 2018. *FEMS Microbiol. Ecol.*



● Farm Effluent
● Hospital Effluent
● WWTP



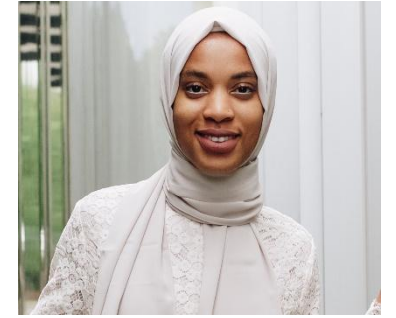
Liqing Zhang



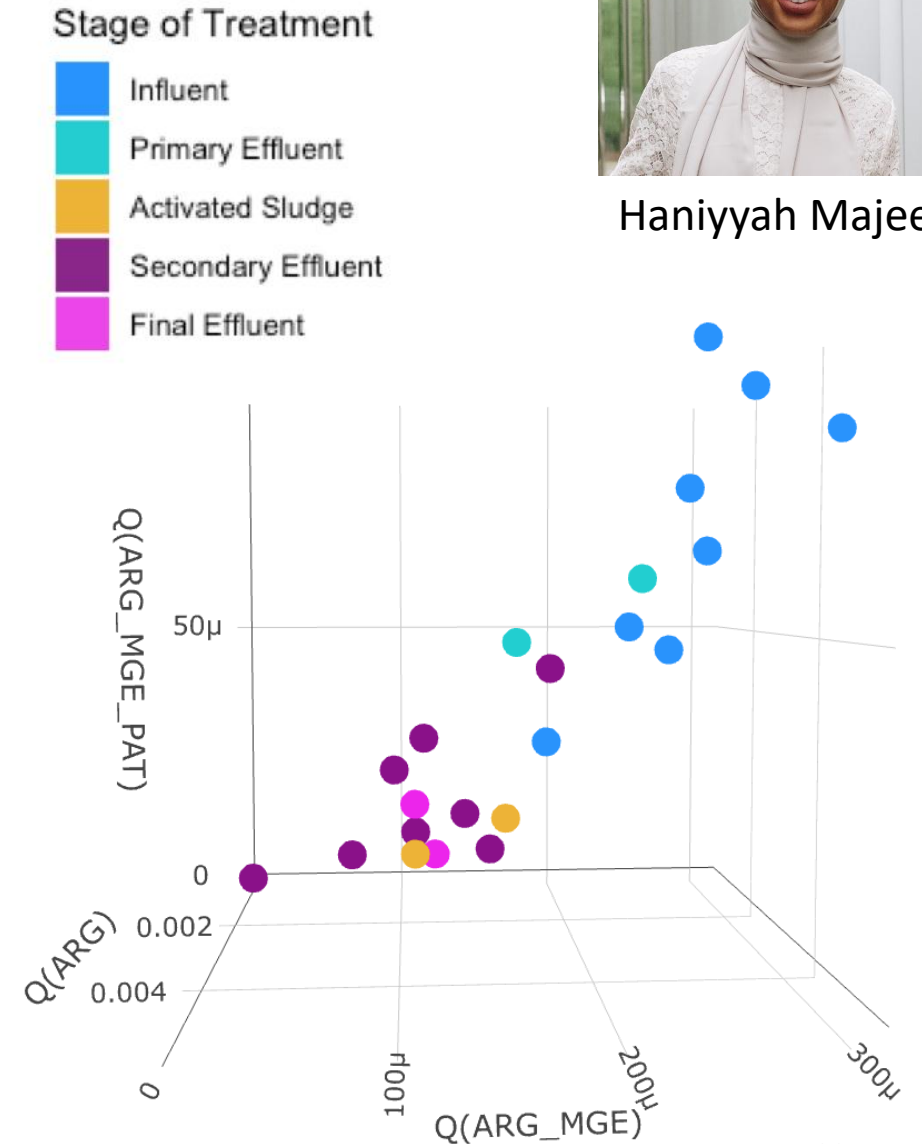
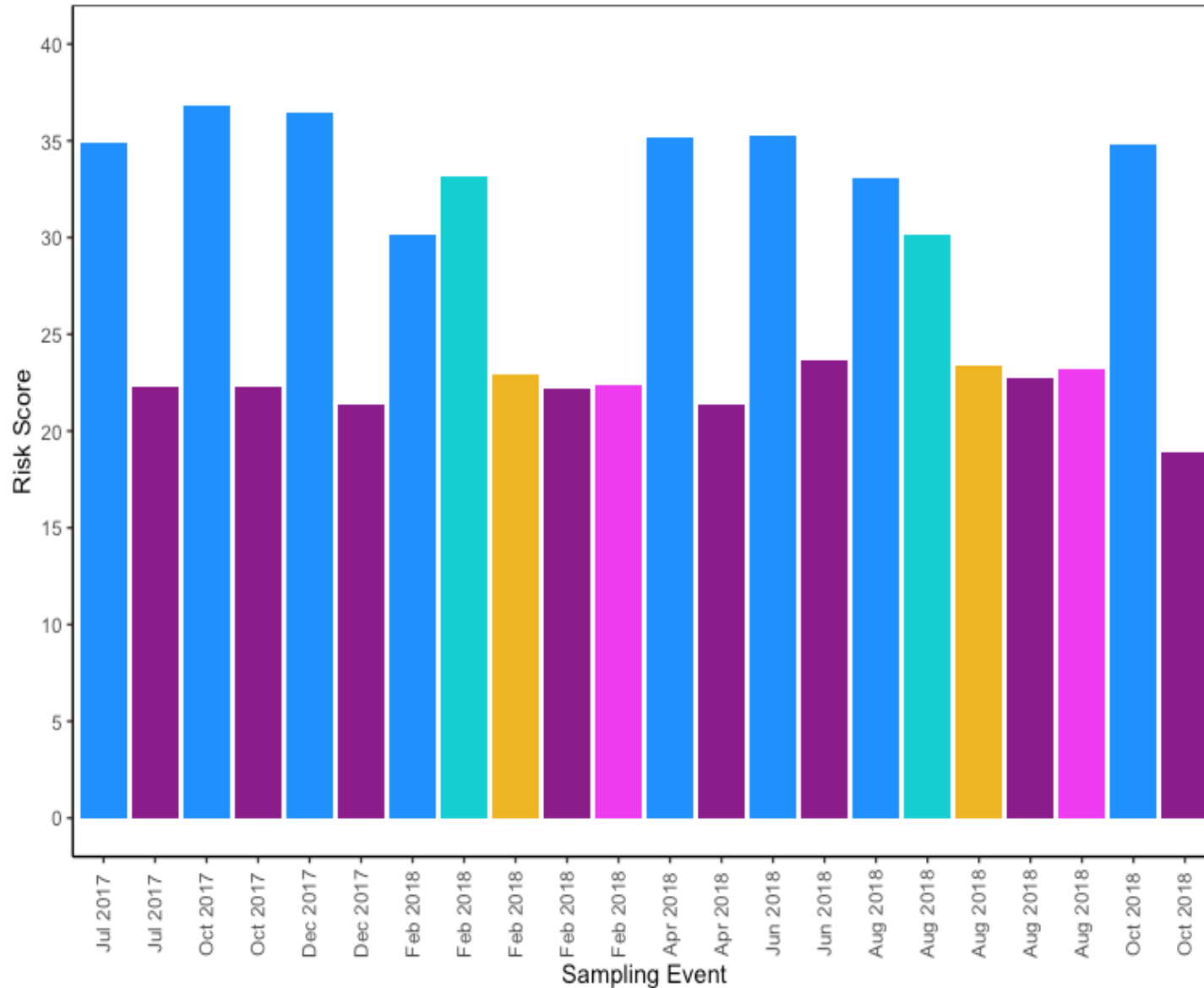
Min Oh

Adapted from: Martínez, Coque, and Baquero. "What is a resistance gene? Ranking risk in resistomes." *Nature Reviews Microbiology* 13.2 (2015): 116-123.

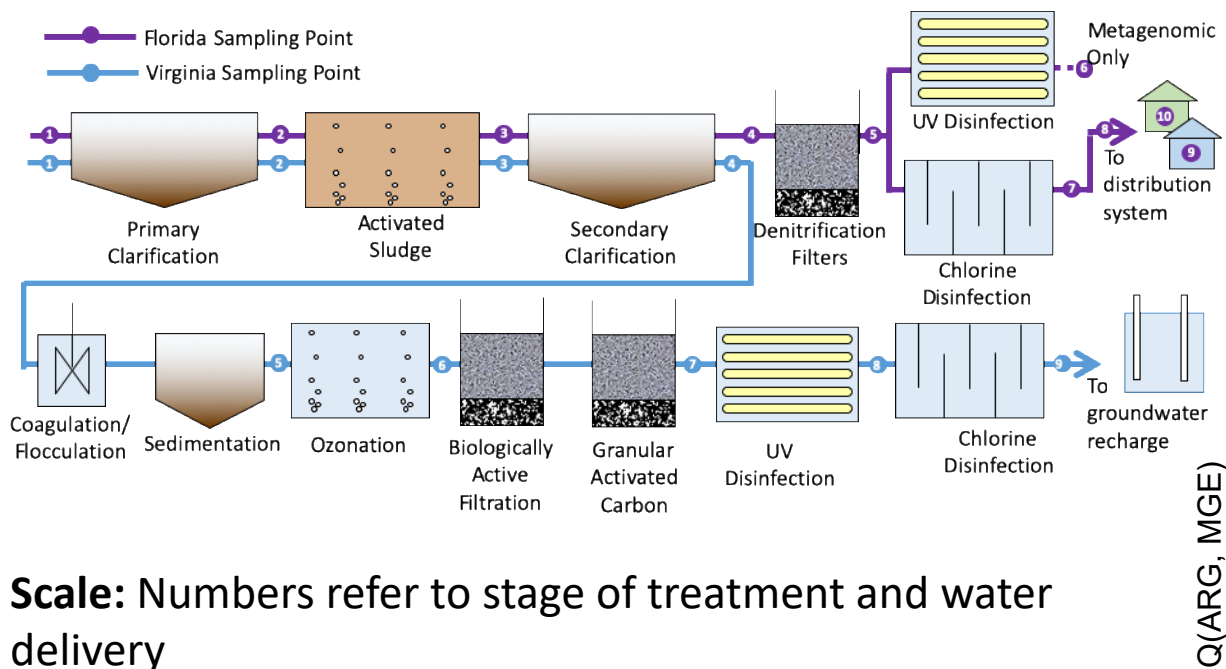
Relative Resistome Risk Score through a WWTP



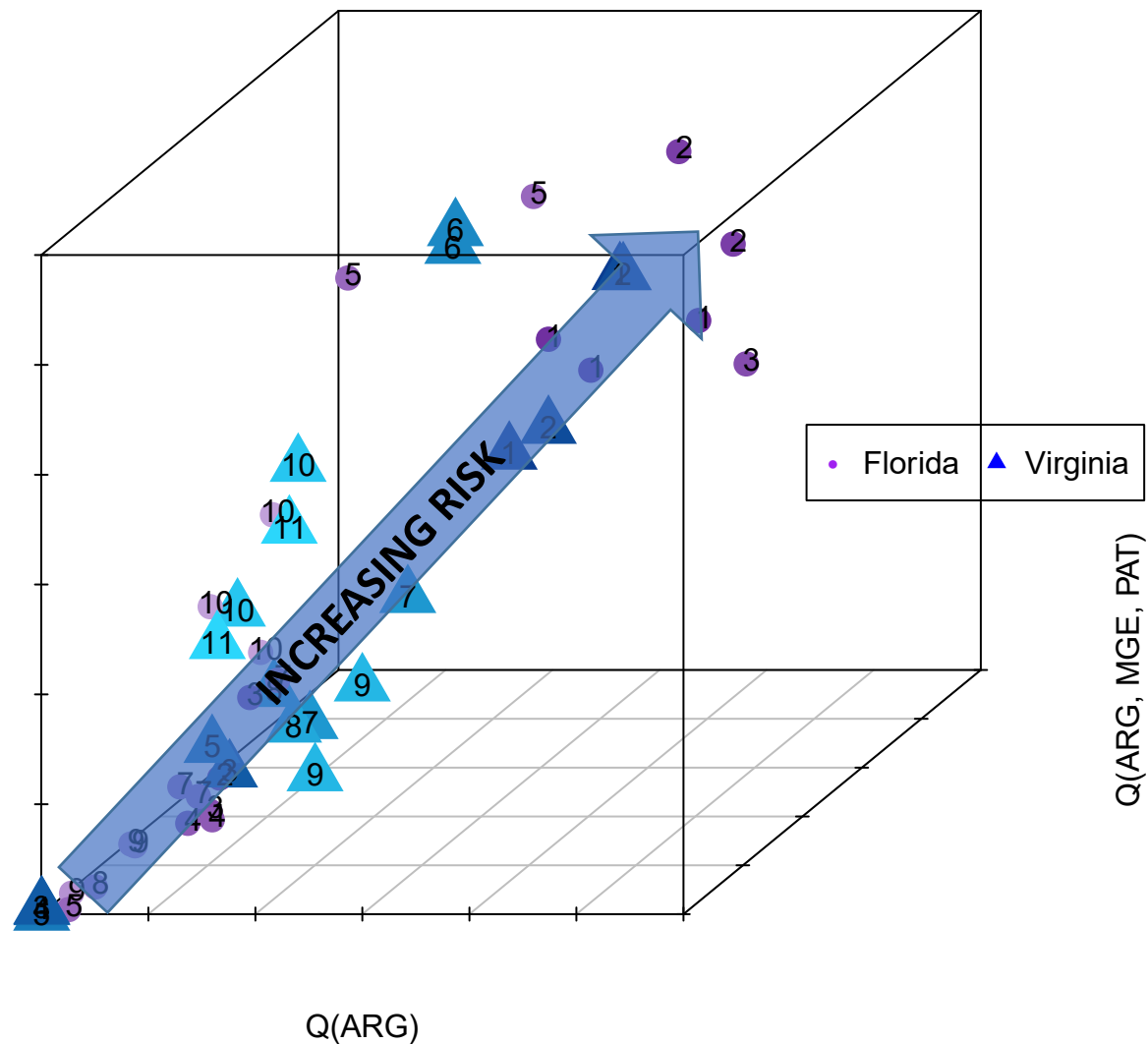
Haniyyah Majeed



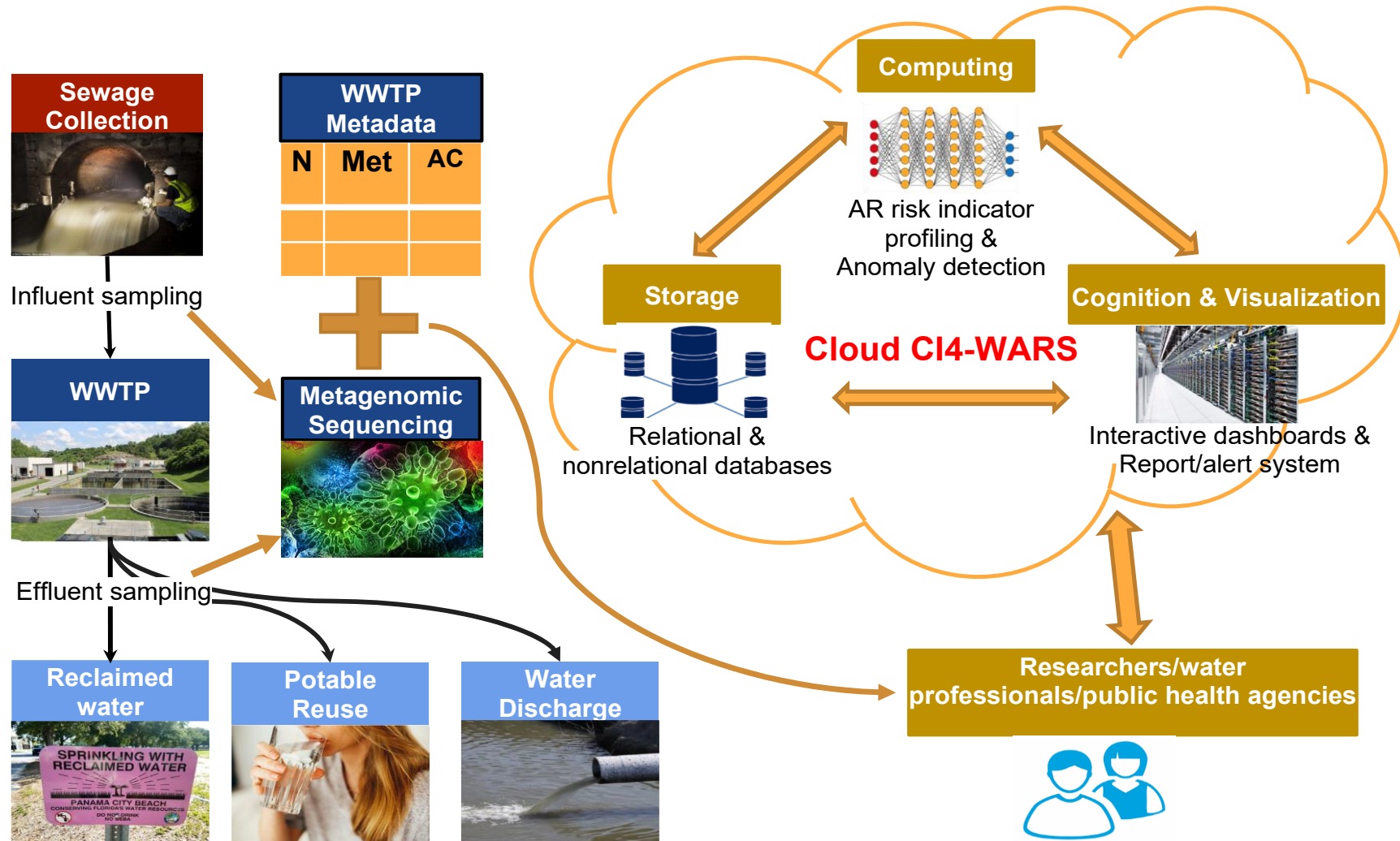
Recycled Water: MetaCompare



Ishi Keenum

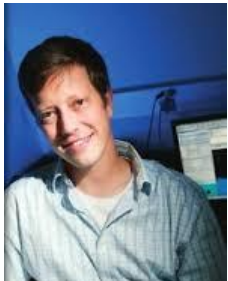


Future: Cyberinfrastructure-Enabled Monitoring of Antibiotic Resistance and Pathogens



Key Collaborator:
Liqing Zhang, VTech

Antibiotic Rx Before/During/After Pandemic: SW Virginia



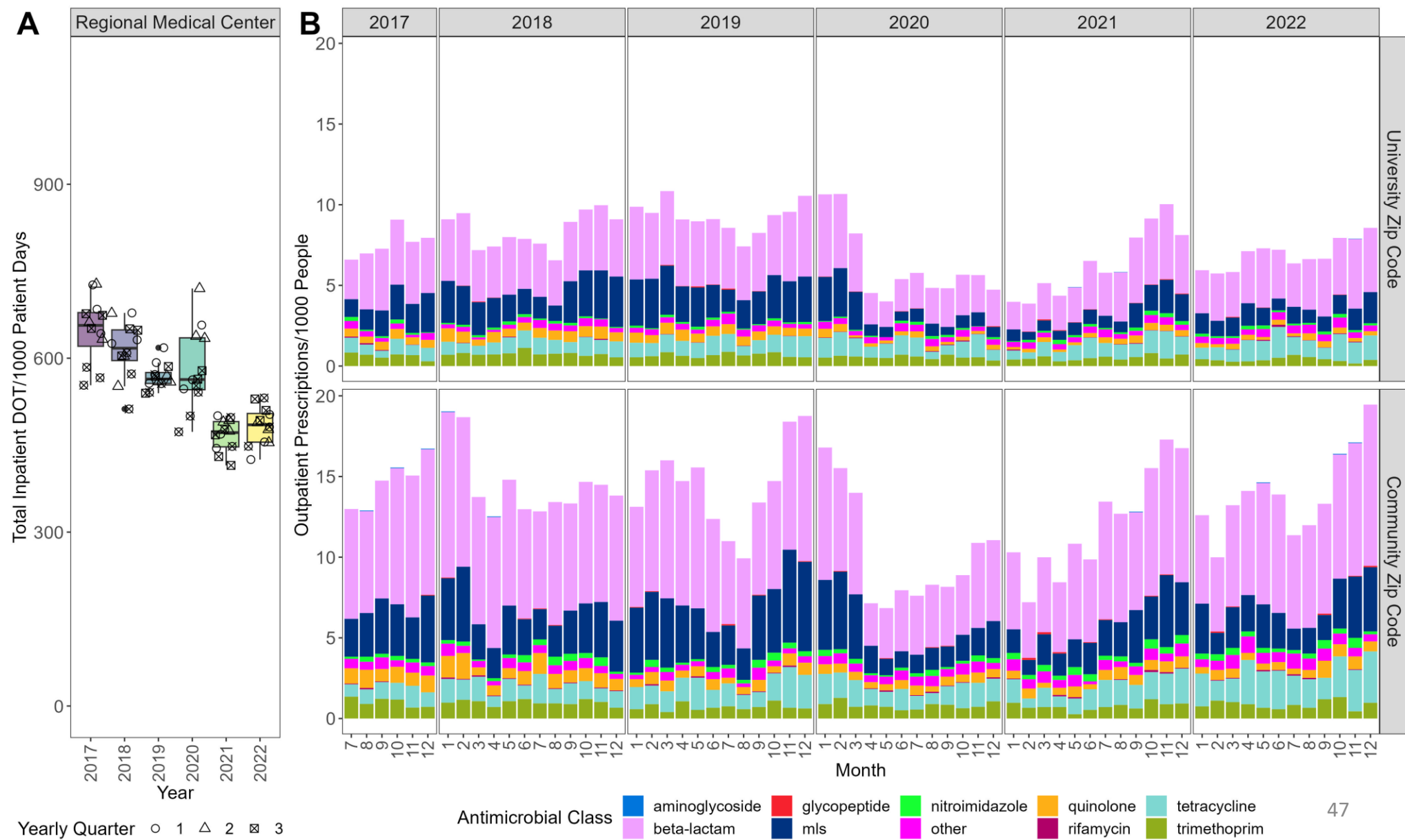
Co-PI: Peter Vikesland



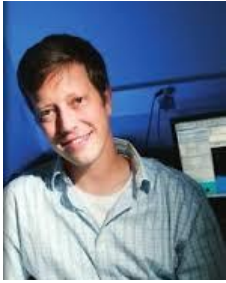
Connor Brown



Ayella Maile-Moskowitz et al. in review



Unique ARGs to two Neighboring WWTPs *circa* Pandemic



Co-PI: Peter Vikesland



Co-PI: Liqing Zhang



Connor Brown



Ayella Maile-Moskowitz et al. in review



Metagenomics, Pathogens, and ARGs in the Water Industry- Final Reports

- Water, Environment, and Public Health Agencies Interested in Monitoring:
 - *What do we tell them to monitor and where?*
- Water Research Foundation Project 4813
 - *Critical Evaluation and Assessment of Health and Environmental Risks from Antibiotic Resistance in Reuse and Wastewater Applications (PI Hamilton)*
- Water Research Foundation Project 4961
 - *The Use of Next Generation Sequencing (NGS) Technologies and Metagenomics Approaches to Evaluate Water and Wastewater Quality Monitoring and Treatment Technologies (PI Pruden)*
- Water Research Foundation Project 5052
 - *Standardizing Methods with QA/QC Standards for Investigating the Occurrence and Removal of Antibiotic Resistant Bacteria/Antibiotic Resistance Genes (ARB/ARGs) in Surface Water, Wastewater, and Recycled Water (PI Pruden)*



Pathogen Monitoring in Water and Wastewater: Past, Present, Future

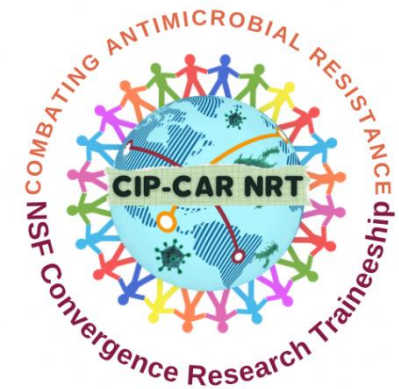
- Past/Present: Fecal indicators (total coliforms, fecal coliforms, *E. coli*)
- Present/Future: Molecular (i.e., DNA/RNA-based monitoring) as a screen, coupled with culture to confirm viable pathogens
- Future: DNA sequencing coupled with cyberinfrastructure to tackle new pathogens and public health concerns (e.g., COVID and antibiotic resistance)
 - Not just monitoring drinking water for removal, but also sewage as a public health surveillance resource.

Acknowledgements



CENTERS FOR DISEASE
CONTROL AND PREVENTION

Contract #
75D35118C02904



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