

# Pathogen Treatment Guidance and Monitoring Approaches for On-Site Non-Potable Water

**Jay Garland**<sup>1</sup>, Mary Schoen<sup>2</sup>, Brian Zimmerman<sup>1</sup>, Scott Keely<sup>1</sup>, **Nichole Brinkman**<sup>1</sup>, Susan De Long<sup>3</sup>, Sybil Sharvelle<sup>3</sup>, **Michael Jahne**<sup>1</sup>

<sup>1</sup>USEPA Office of Research & Development

<sup>2</sup>Soller Environmental

<sup>3</sup>Colorado State University





- Context
  - Increasing interest in fit for purpose water reuse
  - Limits of conventional indicator organism approaches
- Approach
  - Quantitative Microbial Risk Assessment (QMRA) to define treatment requirements
  - Performance monitoring approaches
    - Rationale for moving away from traditional microbiological indicators
    - On-line, non-biological surrogates linked to treatment requirements
    - Alternative microbiological targets (infrastructure microbiome?)

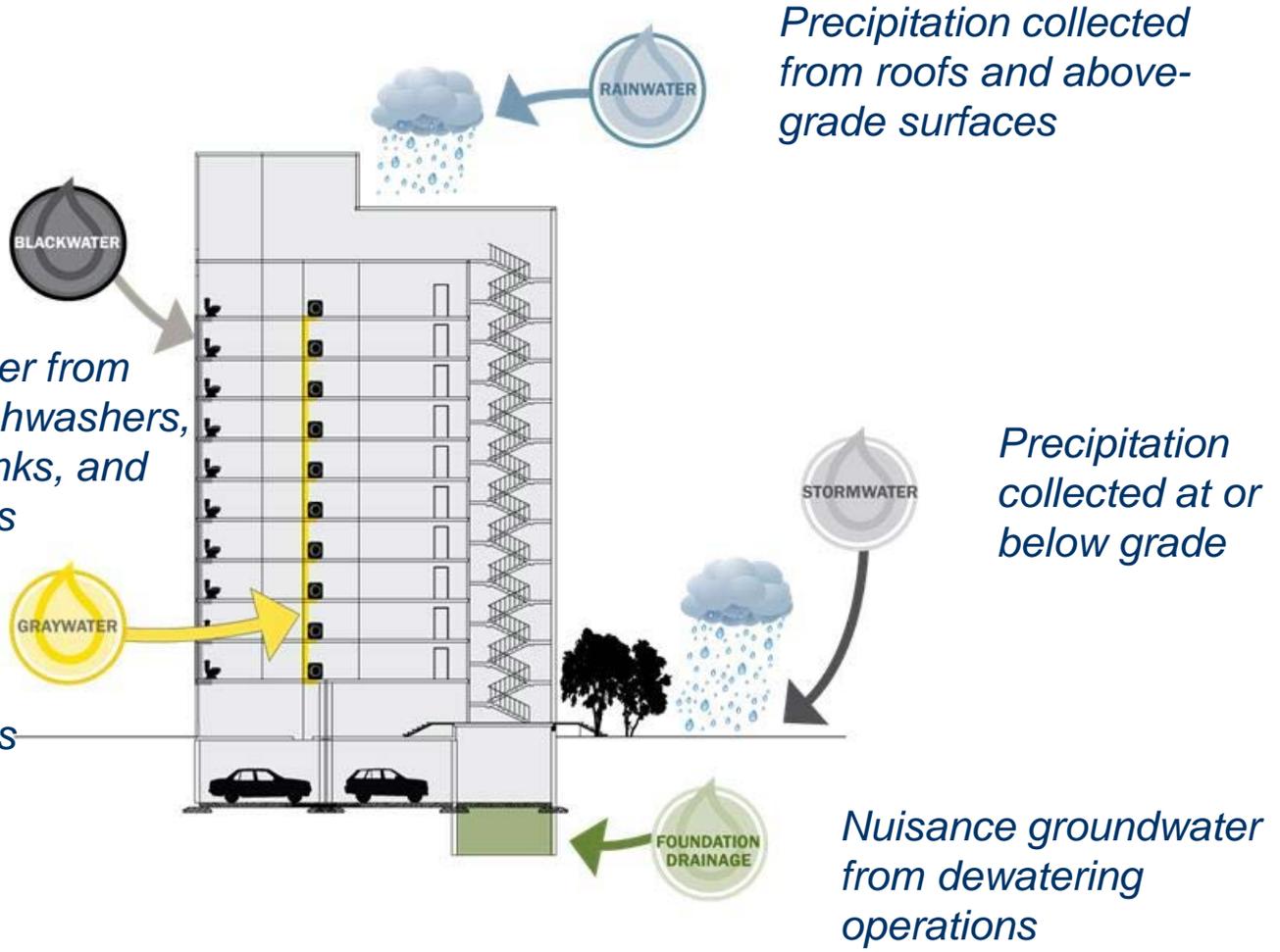


### San Francisco's Non-potable Water System Projects

San Francisco Public Utilities Commission  
April, 2014

*Wastewater from  
toilets, dishwashers,  
kitchen sinks, and  
utility sinks*

*Wastewater from  
clothes washers,  
bathtubs, showers,  
and bathroom sinks*



*Precipitation collected  
from roofs and above-  
grade surfaces*

*Precipitation  
collected at or  
below grade*

*Nuisance groundwater  
from dewatering  
operations*



# Traditional Indicators Are Not Predictive of Pathogen Levels in Alternative Waters

- **Graywater**

- O'Toole et al. (2012)

- A total of 185 greywater samples (laundry, bath) from 93 households in Australia
- Analyzed for fecal indicator *E. coli*, pathogenic *E. coli*, and key viral pathogens (enterovirus, norovirus, rotavirus)
- No association between the presence of indicators and the presence of pathogens
- Norovirus was detected when the fecal indicator bacteria was not (7% of samples)
- ***Not surprising given the fact that pathogen shedding is highly variable***

- **Rainwater**

- Ahmed et al (2012)

- Event driven, non-human fecal sources –lead to highly variable pathogens detections

- Simmon et al. (2008)

- Legionella outbreak from rainwater drinking water system
- Importance of “environmental” pathogens (rather than host associated)
- To add to the complexity, source of the Legionella was linked to aerosols from a pressure washer at a nearby marina



So Need to Start By Defining the Necessary  
Treatment To Meet Acceptable Risk

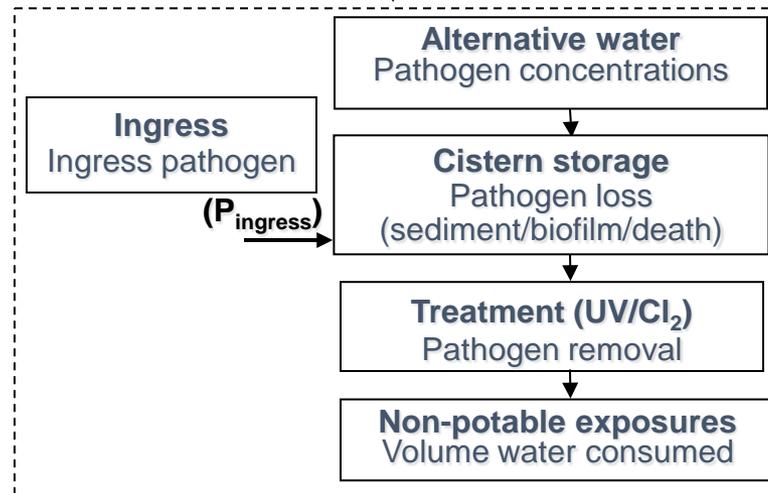


# Quantitative microbial risk assessment (QMRA)

## STEP 1 SETTING

**Problem formulation & Hazard identification**  
Describe physical system, selection of **reference pathogens** and **identification of hazardous events**

## STEP 2 EXPOSURE



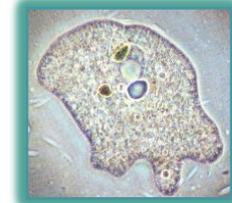
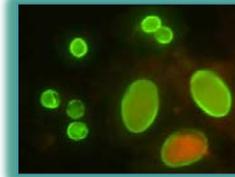
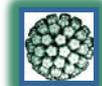
## STEP 3 HEALTH EFFECTS

**Dose-Response (P<sub>inf</sub>)**  
Selection of appropriate models for each pathogen and the population exposed

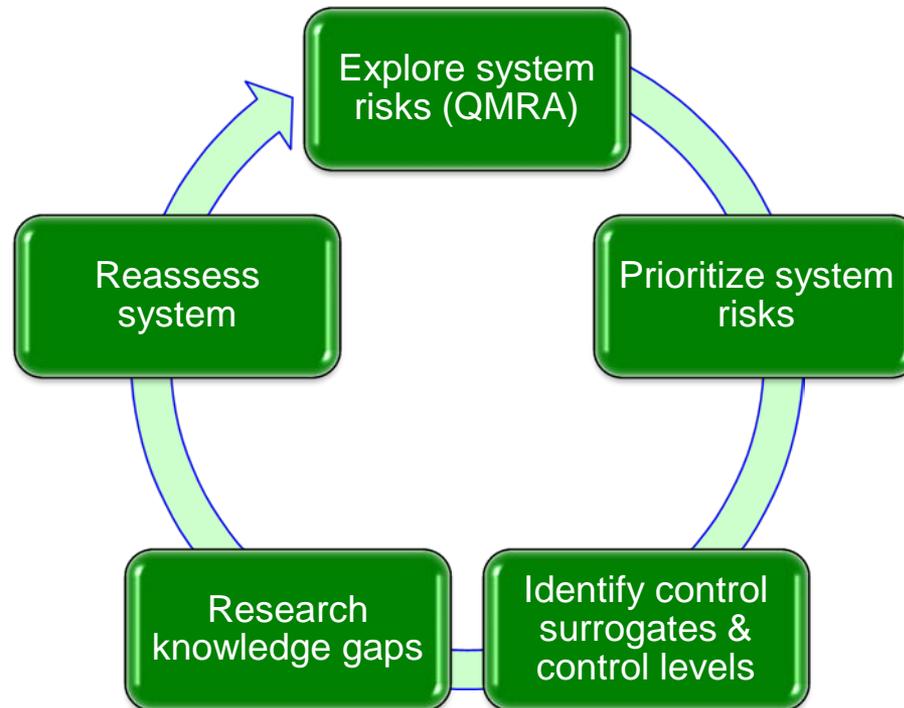
## STEP 4 RISK

**Risk Characterization**  
Simulations for each pathogen baseline and event infection risks with variability & uncertainty identified





# QMRA – Analytic Framework





# QMRA of Non-Potable Reuse of Alternative Water Sources: A Literature Review

- Focused on on-site domestic and commercial systems (not centralized systems)
- Review publications that a) recommended technology performance standards or b) estimated health risks from microbial exposures
- Evaluated graywater, rainwater, stormwater, foundation drainage, and blackwater (using SF PUC definitions)
- Focused on non-potable uses, but not agricultural production



Water	Scale <sup>a</sup>			Mis-use	Event	Pathogen <sup>c,d</sup>	Log Reductions											Ref	
	S	M	L				<1	1	2	3	4	5	6	7	8	9	10		>10
Wastewater			X	NA <sup>b</sup>		V, Cj, C											direct potable (dp)	1	
		X		NA		N,Cj											dp	25	
			X	X		R												agriculture	24
			X			R, Cj, C												agriculture	15
			X			R, Cj, C												home garden	15
			X			R, Cj, C												firefighting	15
			X			R, Cj, C												home use	15
Greywater			X	X		R												agriculture	13
		X				N,R,A,Cj,C												toilet flush and irrigation	16
		X			X	N,R,A,Cj,C												toilet flush and irrigation	16
Stormwater			NA			R,Cj, C												municipal	7
			NA			R,Cj, C												in/outdoor home	7
			NA			R,Cj, C												firefighting	7
			NA			R,Cj, C												agriculture	7
			NA			R,Cj, C												non-food crops	7
			NA			R,Cj, C												irrigation	29
Rainwater			NA			Cj												all uses <sup>e</sup>	7

a. Small (S) is single household, Medium (M) is multi-home systems, Large (L) is community-wide

b. NA is not applicable

c. V is enteric virus, C is Cryptosporidium, R is Rotavirus, N is Norovirus, A is Adenovirus. Cj is Campylobacter jejuni

d. Pathogens ordered from highest to lowest required log reduction

e. municipal, indoor and outdoor, firefighting, agriculture, non-food crops



# Conclusions of QMRA Literature Review

- Each water and use combination requires a unique pathogen reduction so that the water can be considered “safe”
- There are reuse applications for which the human health risk has not been characterized
  - On-site blackwater or mixed wastewater, Foundation drainage reuse, etc.
- Adoption of previously calculated pathogen reductions for on-site systems requires careful consideration so that waters can be considered safe
  - Differences in pathogen densities and occurrence between centralized and on-site systems
  - Need to account for sporadic nature of pathogen occurrences and treatment performance variation
- Review has been published (*Schoen and Garland 2015, Microbial Risk Analysis*)



# Current work on-going to refine models/estimates

- Characterize pathogen density in on-site collection systems
  - Distinction from municipal wastewater/failure of indicator paradigm
  - Direct monitoring data needed
- Incorporate pathogen intermittency
  - Important for small-scale systems where pathogens may not be routinely present
  - Implications for determination of annual risk
- Improve exposure models
  - Are people really exposed to 0.01 mL from toilet flushing? (NRMCC 2006)
  - Need realistic science-based assumptions, but also need to consider failure/accidental exposure
- Independent Advisory Panel: Technical Requirements for Public Health Standards for Onsite Water Systems
  - Working with the expert advisory group so that this information, contained in separate publication(s), will be referenced in the framework document





How do we quickly and effectively monitor the treatment performance of a system?

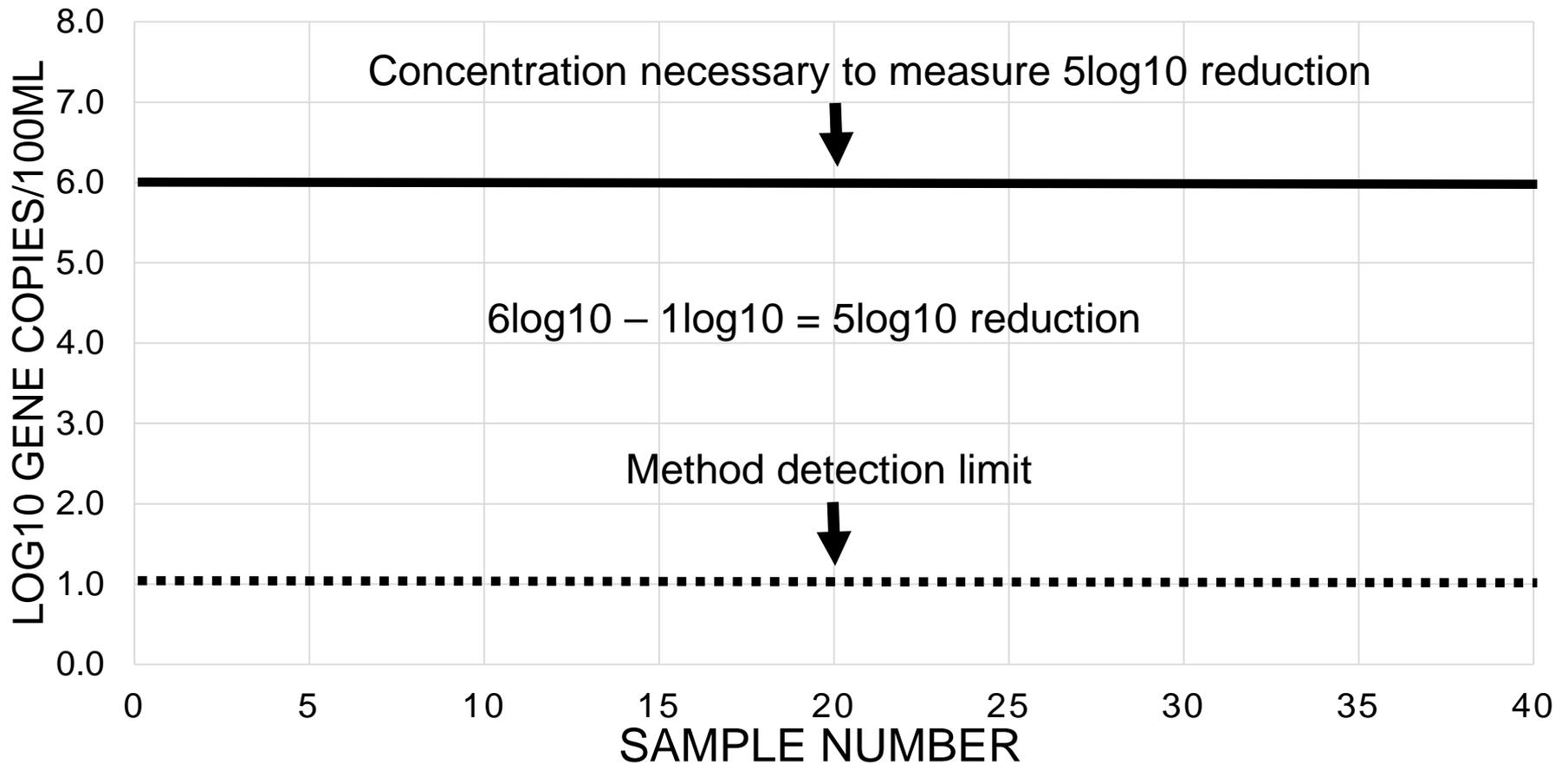
# What About Monitoring?



- Process indicator
  - Demonstrates efficacy of a process (treatment)
- Could use common water quality parameters
  - Preferably using real or near real-time sensors
  - Need to be validated as an accurate predictor of treatment performance
- But what about biologically based process indicators?
  - Consistently present in sufficiently high numbers to measure necessary dynamic range required by log removal estimates



## MEASURING A 5LOG<sub>10</sub> REDUCTION





## Indicator Organisms (IO) in Graywater

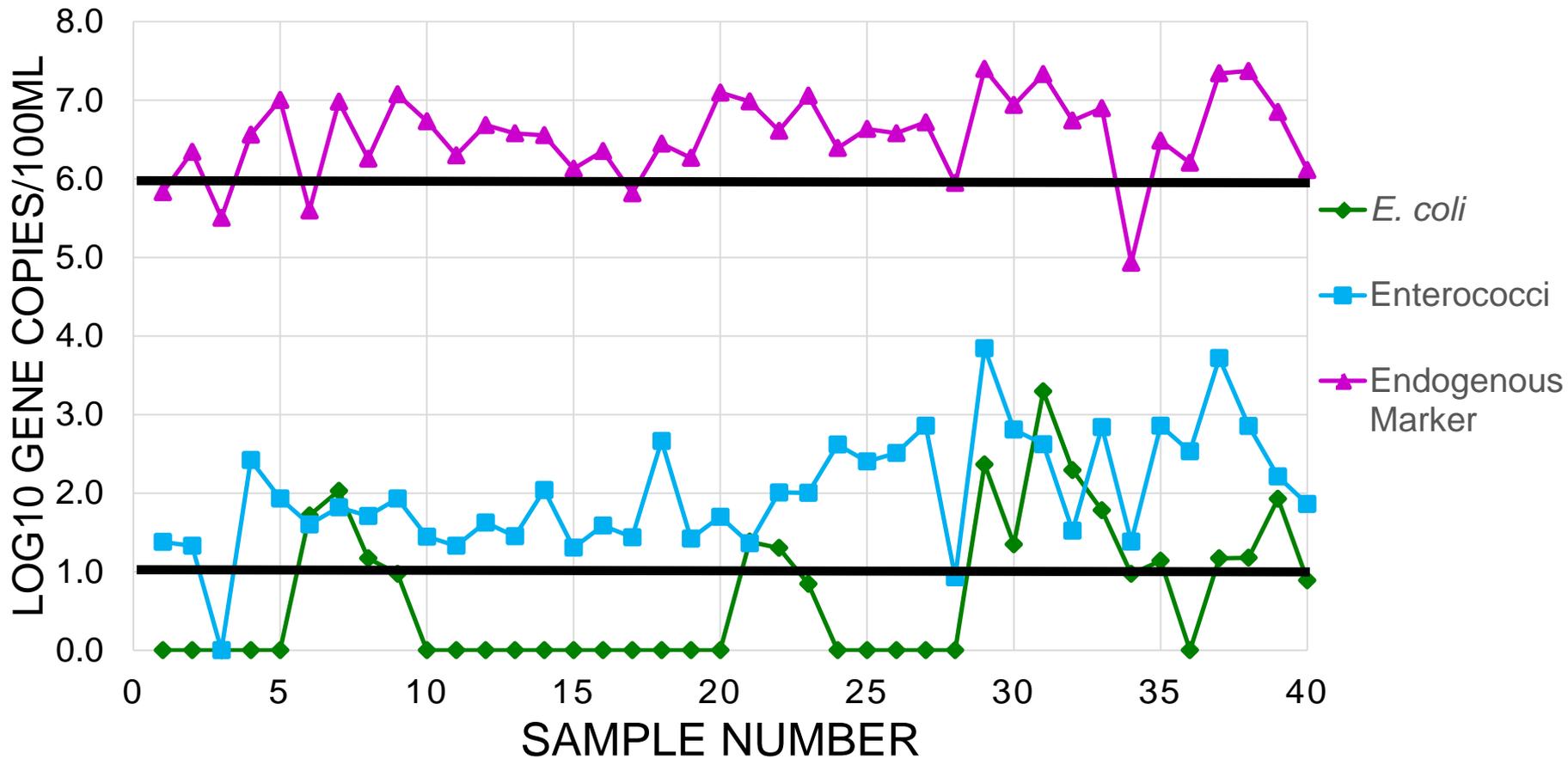
Indicator	Graywater $\log_{10}/100\text{mL}$	Wastewater $\log_{10}/100\text{mL}$
<i>E. coli</i>	0 - 6	4 - 6
Enterococci	0 - 4	4 - 6
Sulfite-reducing clostridia	0 - 3	3 - 6
Coliphage (Somatic and F-RNA)	0 - 3	6 - 7

From: Ottosson (2003), Gilboa (2008), Winward (2008)

- No correlation between *E. coli* and gastroenteritis or *E. coli* and Norovirus occurrence (O'Toole, 2012)
- IO can grow  $\sim 1-2\log_{10}$  in graywater (Ottosson, 2003)

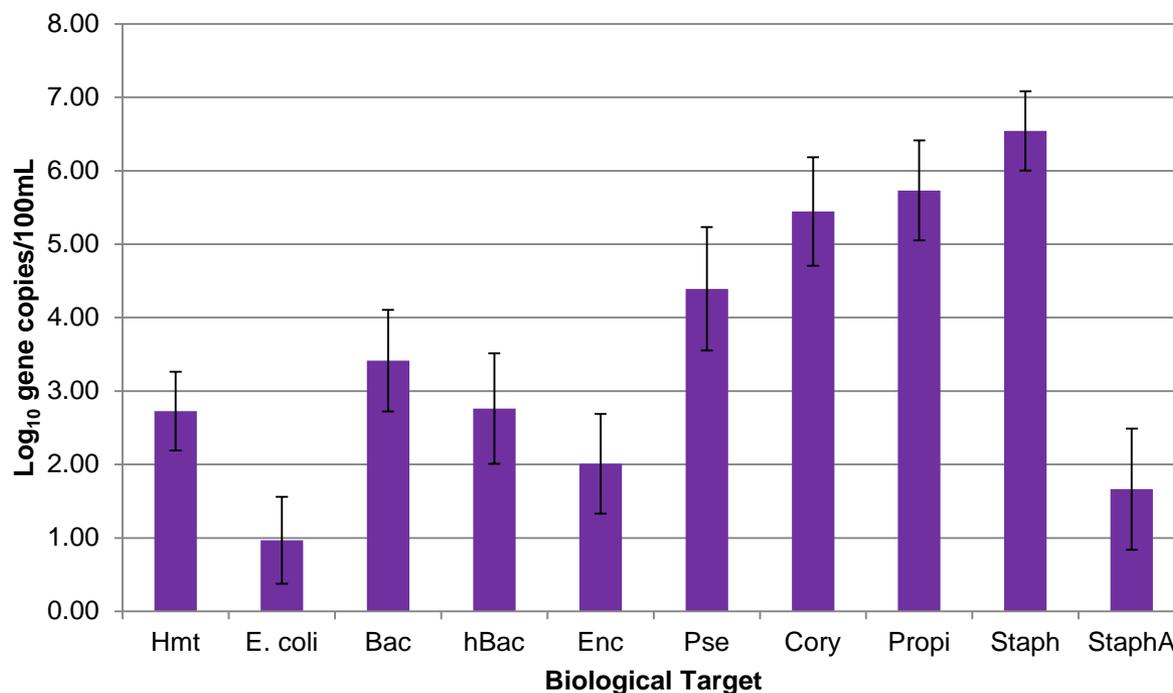


# INDICATOR BACTERIA IN GRAYWATER





# Quantification of Select Targets In Laundry Water



Mean  $\log_{10}$  copies  $\pm$  SD of qPCR targets (Hmt = HmtDNA, Bac = *Bacteroides* spp., hBac = human-specific *Bacteroides*, Enc = *Enterococcus* spp., Pse = *Pseudomonas* spp., Cory = *Corynebacterium*, Propi = *Propionibacterium*, Staph = *Staphylococcus* spp., StaphA = *S. aureus*) in laundry graywater.  
Adenovirus not found in any sample



## Log<sub>10</sub> Reduction In Graywater Summary

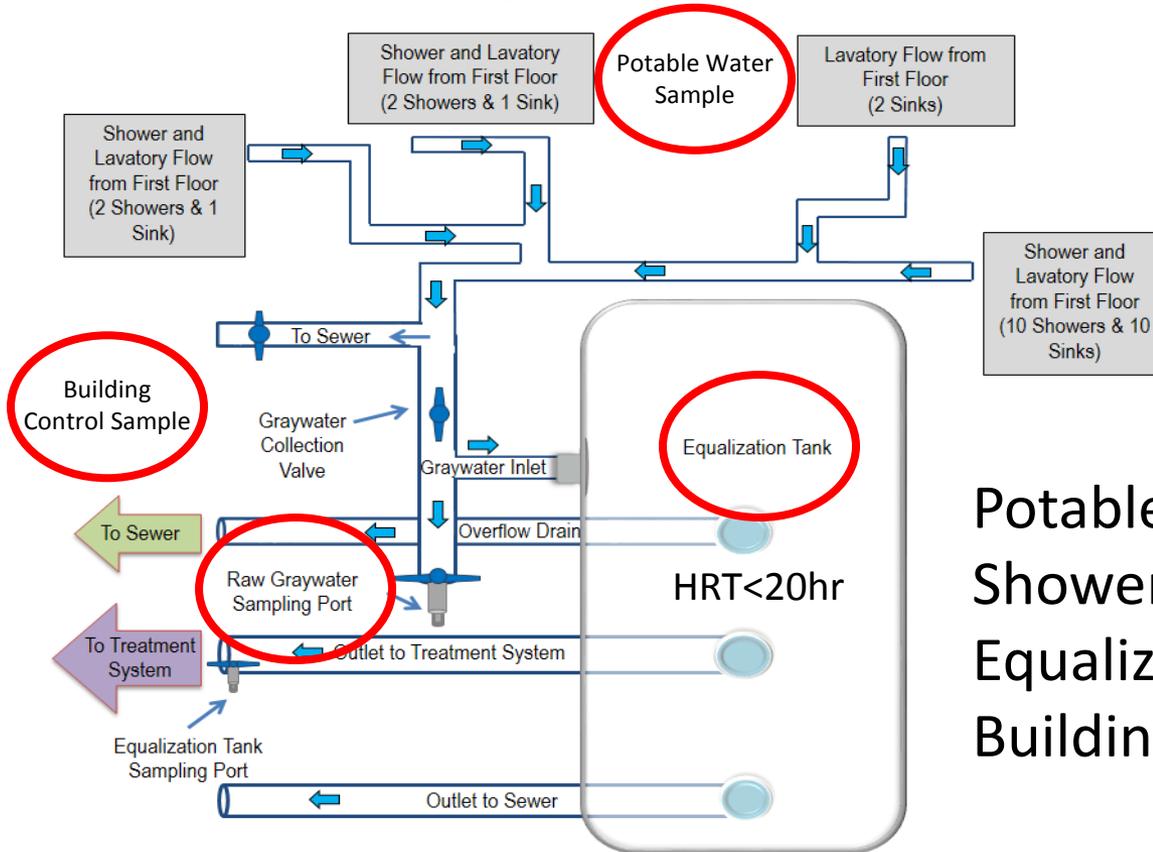
- Enterococci and *E. coli* levels not sufficiently high to quantify 5log<sub>10</sub> reduction
  - Can only measure average of 1-2log<sub>10</sub> reduction
  - Measure 0log<sub>10</sub> reduction 30% of the time
- Endogenous marker can measure up to 6.4log<sub>10</sub> reduction
  - Can measure ≥5log<sub>10</sub> reduction 85% of the time
  - Can measure average of 5.5log<sub>10</sub> reduction



## In Search of Endogenous Bacterial Markers in Graywater

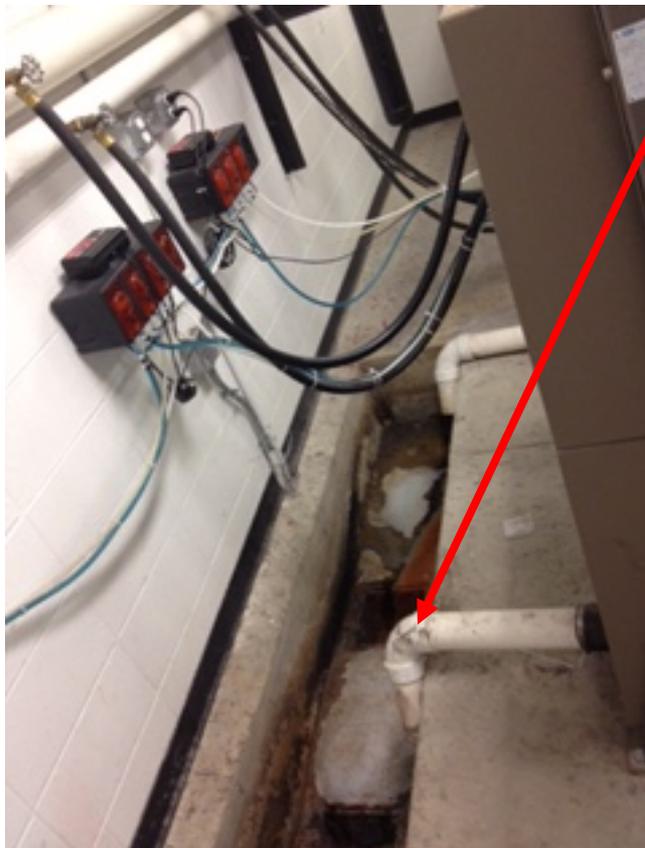
- 52 graywater samples from two distinct graywater sources
  - Colorado State University (CSU) system (Ft. Collins, CO)
    - Dormitory including 14 residence halls
    - 14 showers and 14 sinks (28 person capacity)
    - Composited in 946L equalization tank
  - University of Cincinnati (UC) athletic department's commercial washing machine (Cincinnati, OH)
    - Launder ~10-30 garments per wash
- Analyzed by pyrosequencing 16S rRNA gene
  - Classification to genus level of characterized bacteria

# CSU Recycling System Schematic



Potable Water (PW): n=1  
 Shower/Handwash (SH): n=18  
 Equalization Tank (ET): n=6  
 Building Control (BC): n=3

# UC Commercial Washer



Laundry (LA): n=24





# Conclusions from Bacterial Metagenomics of Graywater

- Infrastructure-associated bacteria are the most abundant bacteria in graywater recycling systems
  - Suspended/attached growth or persistence of organisms in plumbing drain lines/equalization tank
- Skin-associated bacteria are the most abundant bacteria shed from humans
  - Most abundant in laundry
  - Present but variable in graywater recycling system



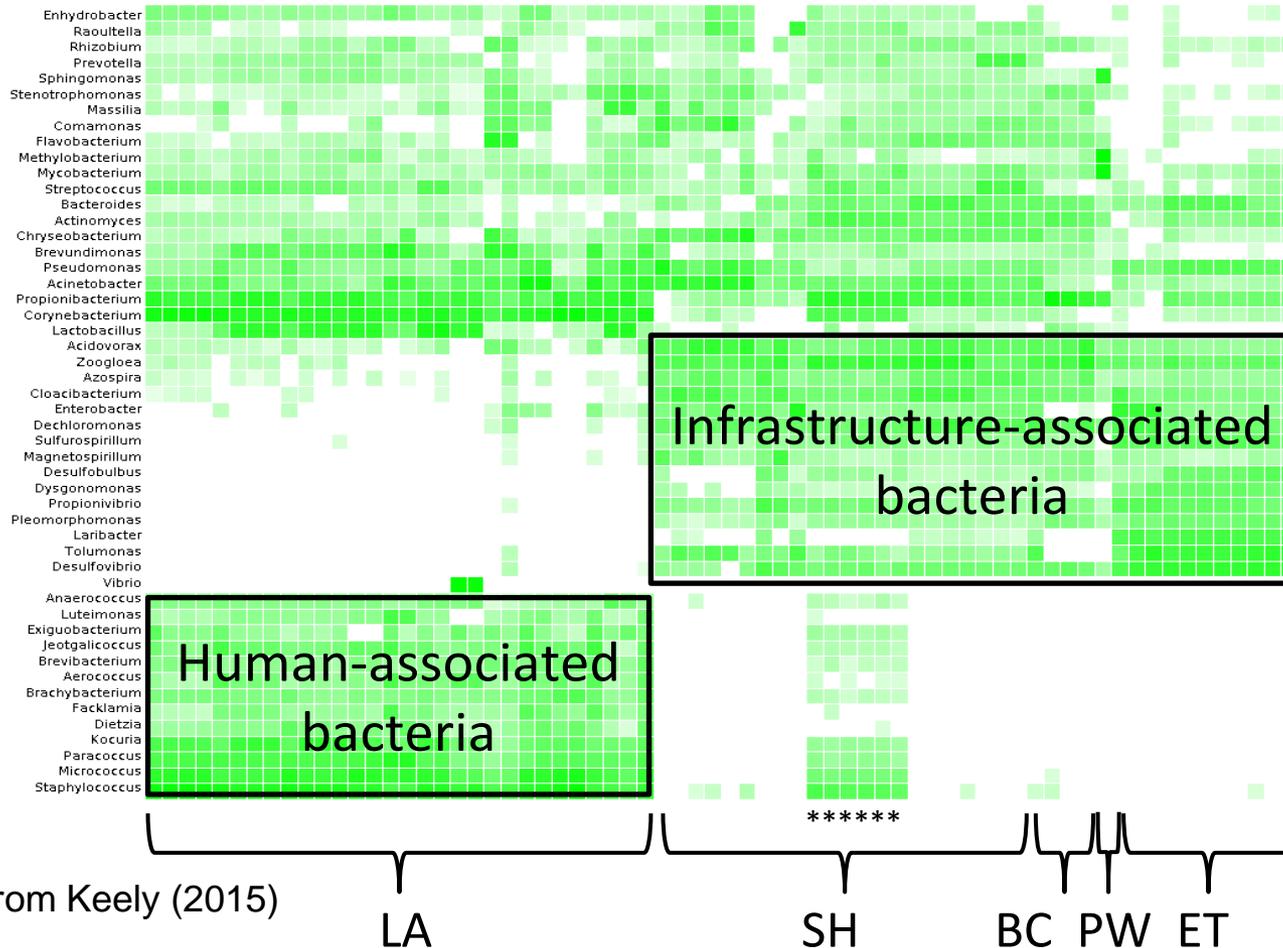
## Sequence Statistics

- Over 1.8 million raw reads generated
  - Average over 35,000 raw reads per sample

Sample Type	Number of Samples	Average Number of Genera Detected	Total Number of Genera Detected
SH	18	86	191
ET	6	53	90
BC	3	82	107
PW	1	37	37
LA	24	105	295



# Log<sub>10</sub>-scale Heat Map of Genera Detected



Adapted from Keely (2015)

LA

SH

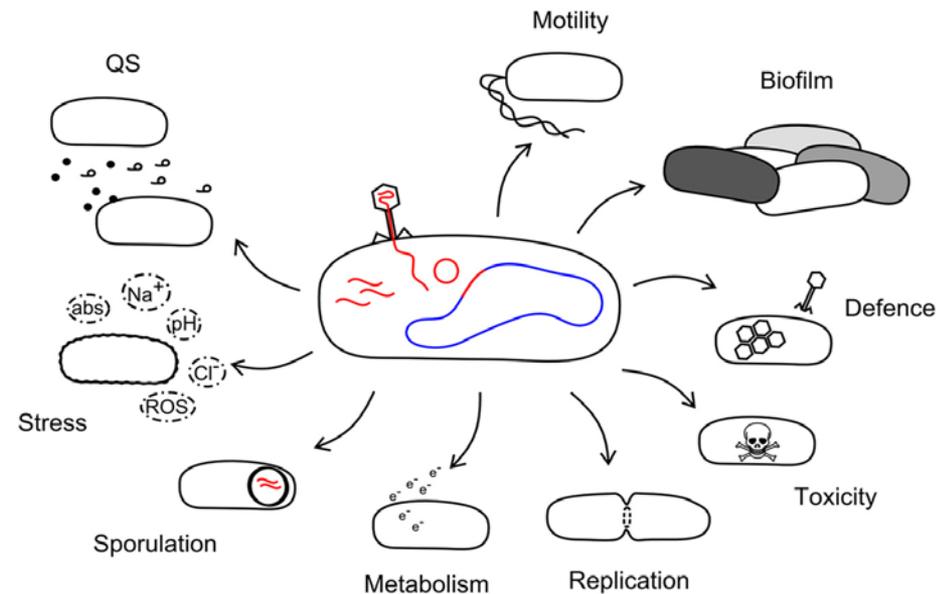
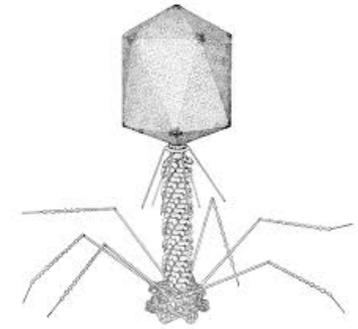
BC

PW

ET

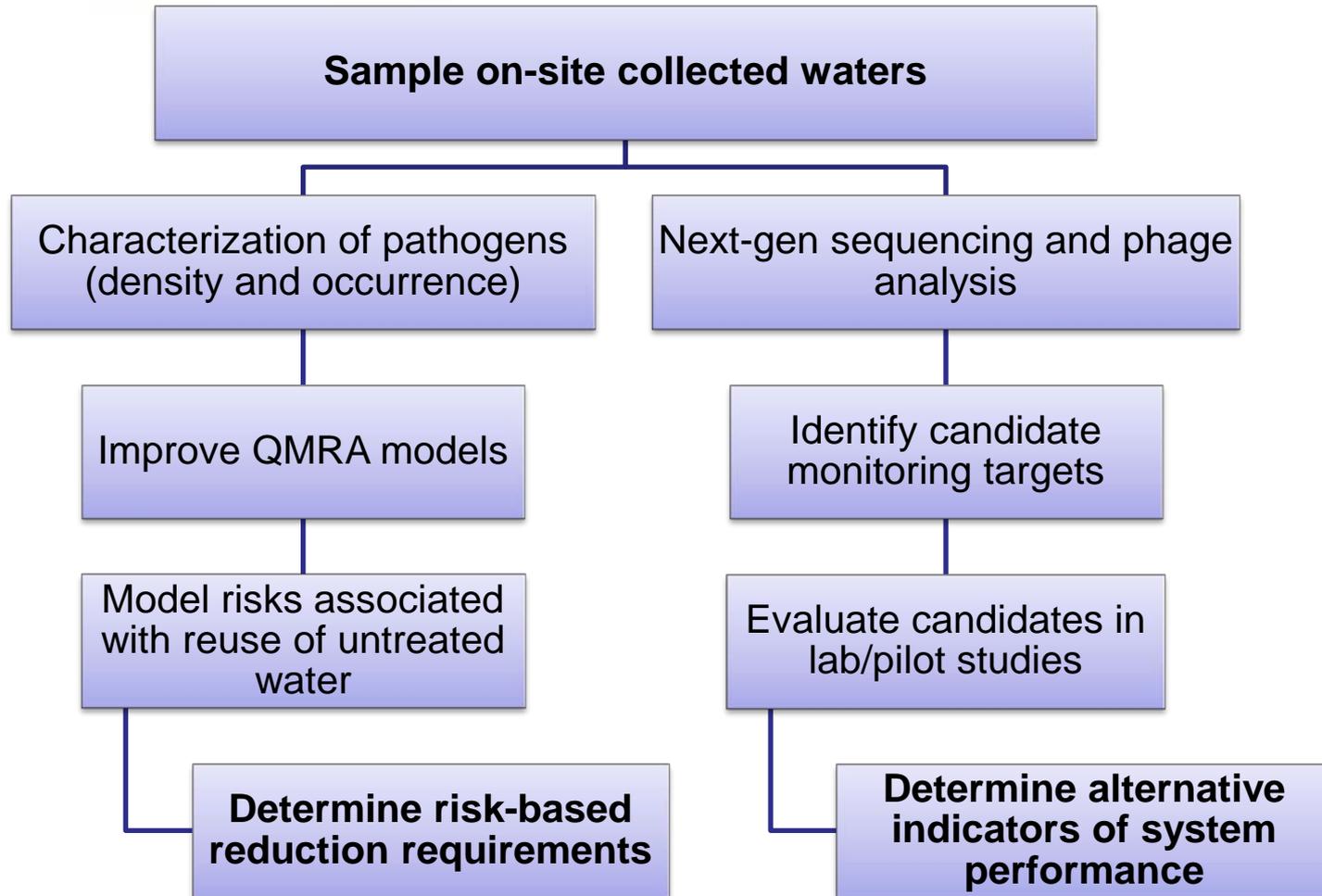
# Are Bacteriophage Better Targets?

- Viruses that infect bacteria
- Abundant – 10x more than bacteria
- Relevant – biologically similar to viral pathogens
- Challenges for Characterizing “Phageome”
  - No universal gene
  - Need to remove prokaryotes, archaea and eukaryotes



From Hargreaves et al. 2014. Bacteriophage 4:e29866, doi:  
[10.4161/bact.29866](https://doi.org/10.4161/bact.29866)

# Working With Partners





So....

Putting this all together

