



The impact of chlorine and chloramine on the detection and quantification of *Legionella pneumophila* and *Mycobacterium* spp.

Maura J. Donohue Ph.D.





Impact of Chlorine and Chloramine on the Detection and Quantification of *Legionella pneumophila* and *Mycobacterium* Species

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ABSTRACT Potable water can be a source of transmission for legionellosis and nontuberculous mycobacterium (NTM) infections and diseases. Legionellosis is caused largely by *Legionella pneumophila*, specifically serogroup 1 (Sg1). *Mycobacterium avium*, *Mycobacterium intracellulare*, and *Mycobacterium abscessus* are three leading species associated with pulmonary NTM disease. The estimated rates of these diseases are increasing in the United States, and the cost of treatment is high. Therefore, a national assessment of water disinfection efficacy for these pathogens was needed. The disinfectant type and total chlorine residual (TCR) were investigated to understand their influence on the detection and concentrations of the five pathogens in potable water. Samples ($n = 358$) were collected from point-of-use taps (cold or hot) from locations across the United States served by public water utilities that disinfected with chlorine or chloramine. The bacteria were detected and quantified using specific primer and probe quantitative-PCR (qPCR) methods. The total chlorine residual was measured spectrophotometrically. Chlorine was the more potent disinfectant for controlling the three mycobacterial species. Chloramine was effective at controlling *L. pneumophila* and Sg1. Plotting the TCR associated with positive microbial detection showed that an upward TCR adjustment could reduce the bacterial count in chlorinated water but was not as effective for chloramine. Each species of bacteria responded differently to the disinfection type, concentration, and temperature. There was no unifying condition among the water characteristics studied that achieved microbial control for all. This information will help guide disinfectant decisions aimed at reducing occurrences of these pathogens at consumer taps and as related to the disinfectant type and TCR.

IMPORTANCE The primary purpose of tap water disinfection is to control the presence of microbes. This study evaluated the role of disinfectant choice on the presence at the tap of *L. pneumophila*, its Sg1 serogroup, and three species of mycobacteria in tap water samples collected at points of human exposure at locations across the United States. The study demonstrates that microbial survival varies based on the microbial species, disinfectant, and TCR.

KEYWORDS chlorine, chloramine, drinking water, *Legionella*, *Mycobacterium*, total chlorine residual

Legionella and *Mycobacterium* are two genera of waterborne environmental bacteria that affect human health by causing the respiratory diseases legionellosis (Legionnaires' disease and Pontiac fever) (1) and nontuberculous mycobacterium (NTM) infections and diseases (2), respectively. Potable water is often suspected or identified as the cause of individual cases or a cluster of cases (an outbreak). Outbreaks for both genera



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A Tale of Two Bacterium...

Legionellaceae

- Legionella (Genus)
 - Gram negative bacteria (Gammaproteobacteria)
 - Flagella rod (2-20 μm)
 - Slow grower (3 to 10 days)
 - Majority of species will grow in free-living amoebae
 - Aerobic, L-cysteine and iron salts are required for in vitro growth, pH: 6.8 to 7, T: 25 to 43 $^{\circ}\text{C}$
 - ~65 species
 - Pathogenic or potentially pathogenic for human

Mycobacteriaceae

- Mycobacterium (Genus)
- Nontuberculous Mycobacterium (NTM)
- *M. avium-intracellulare* complex (MAC)
 - Gram positive bacteria
 - Rod shape (1-10 μm)
 - Non-motile, spore-forming, aerobic
 - Rapid to Slow grower (1 week to 8 weeks)
 - ~156 species
 - Some species capable of causing disease



NTM from Environmental Microorganism to Opportunistic Opponent

Genus

156 Species

Disease

NTM = Nontuberculous Mycobacteria

MAC = *M. avium* Complex

Clinically Relevant Species

Mycobacterium spp.

Mycobacterium
Mycobacterium abscessus
Mycobacterium africanum
Mycobacterium agri
Mycobacterium aichiense
Mycobacterium algericum
Mycobacterium alsense
Mycobacterium alvei
Mycobacterium angelicum
Mycobacterium anyangense
Mycobacterium arabicense
Mycobacterium aromaticivorans
Mycobacterium arosiense
Mycobacterium arupense
Mycobacterium asiaticum
Mycobacterium aurum
Mycobacterium austroafricanum
Mycobacterium avium
Mycobacterium bacteremicum
Mycobacterium boenickei
Mycobacterium botniense
Mycobacterium bouchedurhonense
Mycobacterium bourgelatii
Mycobacterium bovis
Mycobacterium brisbanense
Mycobacterium brumae
Mycobacterium canariense
Mycobacterium caprae
Mycobacterium celatum
Mycobacterium celeriflavum
Mycobacterium chelonae
Mycobacterium chitae
Mycobacterium chlorophenolicum
Mycobacterium chubuense
Mycobacterium colombiense
Mycobacterium conceptionense
Mycobacterium confluentis
Mycobacterium conspicuum
Mycobacterium cookii
Mycobacterium cosmeticum
Mycobacterium crocinum
Mycobacterium doricum

Mycobacterium duvalii
Mycobacterium elephantis
Mycobacterium europaeum
Mycobacterium fallax
Mycobacterium farcinogenes
Mycobacterium flavescens
Mycobacterium florentinum
Mycobacterium fluoranthenvorans
Mycobacterium fortuitum
Mycobacterium franklinii
Mycobacterium frederiksbergense
Mycobacterium gadium
Mycobacterium gastris
Mycobacterium genavense
Mycobacterium gilvum
Mycobacterium goodii
Mycobacterium gordonae
Mycobacterium haemophilum
Mycobacterium hassiacum
Mycobacterium heckeshornense
Mycobacterium heidelbergense
Mycobacterium hiberniae
Mycobacterium hippocampi
Mycobacterium hodleri
Mycobacterium holsaticum
Mycobacterium houstonense
Mycobacterium immunogenum
Mycobacterium insubricum
Mycobacterium interjectum
Mycobacterium intermedium
Mycobacterium intracellulare
Mycobacterium iranikum
Mycobacterium kansasii
Mycobacterium komossense
Mycobacterium koreense
Mycobacterium kubicae
Mycobacterium kumamotoense
Mycobacterium kyorinense
Mycobacterium lacus
Mycobacterium lentiflavum
Mycobacterium leprae
Mycobacterium lepraemurium

Mycobacterium litorale
Mycobacterium llutzerense
Mycobacterium madagascariense
Mycobacterium mageritense
Mycobacterium malmoense
Mycobacterium mantenii
Mycobacterium marinum
Mycobacterium massiliense
Mycobacterium microti
Mycobacterium minnesotense
Mycobacterium monacense
Mycobacterium montefiorensis
Mycobacterium morioakaense
Mycobacterium mucogenicum
Mycobacterium murale
Mycobacterium neoaurum
Mycobacterium nebraskense
Mycobacterium neworleansense
Mycobacterium nonchromogenicum
Mycobacterium noviomagense
Mycobacterium novocastrense
Mycobacterium pallens
Mycobacterium palustre
Mycobacterium paraense
Mycobacterium paraffinicum
Mycobacterium parafortuitum
Mycobacterium paragordoniae
Mycobacterium paraintracellulare
Mycobacterium parakoreense
Mycobacterium parascrofulaceum
Mycobacterium paraseoulense
Mycobacterium paratuberculosis
Mycobacterium parmensis
Mycobacterium peregrinum
Mycobacterium phlei
Mycobacterium phocaicum
Mycobacterium pinnipedii
Mycobacterium porcinum
Mycobacterium poriferae
Mycobacterium pseudoshottsii
Mycobacterium psychrotolerans

Mycobacterium pulveris
Mycobacterium pyrenivorans
Mycobacterium rhodesiae
Mycobacterium riyadhense
Mycobacterium rufum
Mycobacterium rutilum
Mycobacterium salmoniphilum
Mycobacterium saopaulense
Mycobacterium saskatchewanense
Mycobacterium scrofulaceum
Mycobacterium sediminis
Mycobacterium senegalense
Mycobacterium senuense
Mycobacterium seoulense
Mycobacterium septicum
Mycobacterium setense
Mycobacterium sherrisii
Mycobacterium shimoidei
Mycobacterium shinjukuense
Mycobacterium shottsii
Mycobacterium simiae
Mycobacterium smegmatis
Mycobacterium sphagni
Mycobacterium stomatopiae
Mycobacterium szulgai
Mycobacterium terrae
Mycobacterium thermoresistibile
Mycobacterium timonense
Mycobacterium tokaiense
Mycobacterium triplex
Mycobacterium triviale
Mycobacterium tuberculosis
Mycobacterium tusciae
Mycobacterium ulcerans
Mycobacterium vaccae
Mycobacterium vanbaalenii
Mycobacterium vulneris
Mycobacterium wolinskyi
Mycobacterium xenopi
Mycobacterium yongonense

M. avium, *M. intracellulare*,
M. fortuitum, *M. chelonae*,
M. kansasii, *M. abscessus*,
 etc.

- Pulmonary NTM lung disease
- Chronic bronchopulmonary disease
- Cervical or other lymphadenitis
- Skin and soft tissue diseases
- Disseminated infections
- Catheter-related infections



Legionellosis: Respiratory Disease

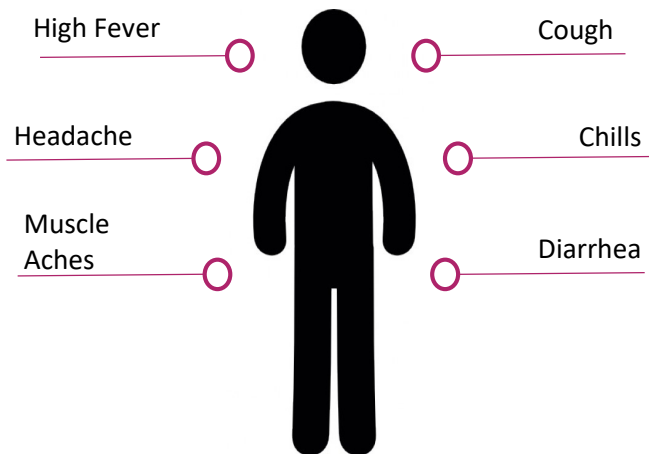
Disease

Legionellosis = **pneumonia**

- Legionnaires' Disease (severe)
- Pontiac Fever (mild)

Signs/Symptoms

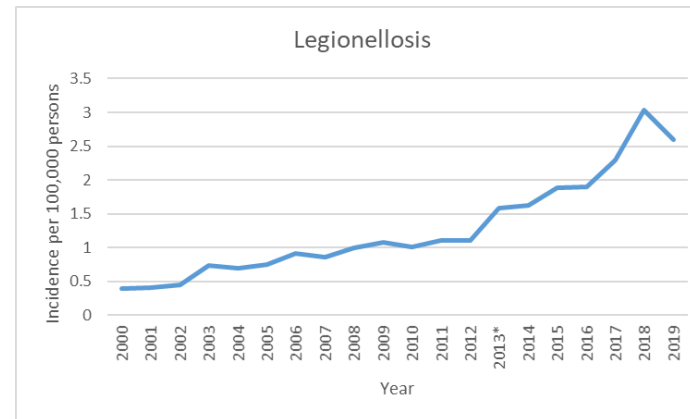
Pneumonia
(Signs/Symptoms)



National Notifiable Disease Surveillance System (NNDSS)

2019 National Reportable Disease List: contained the names of over 110 Diseases/Microorganisms

Number of Cases Reported in 2019:
7,802 cases



LEGIONELLOSIS.

Incidence,* by year — United States, 2000–2019, Source NNDSS



Annual Cost of Treatment in the U.S.

Number of Hospitalization/year



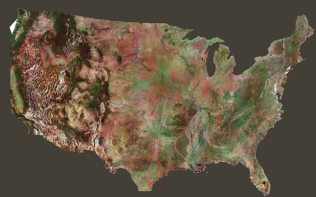
8,000-18,000 cases

avg(13,000) Marston, (1997)

Total Hospitalization Cost:
\$433,758,000

Collier, S.A. et al 2012:

Direct healthcare costs of selected disease primarily or partially transmitted by water. Epidemiology Infection, 140, p2003-2013

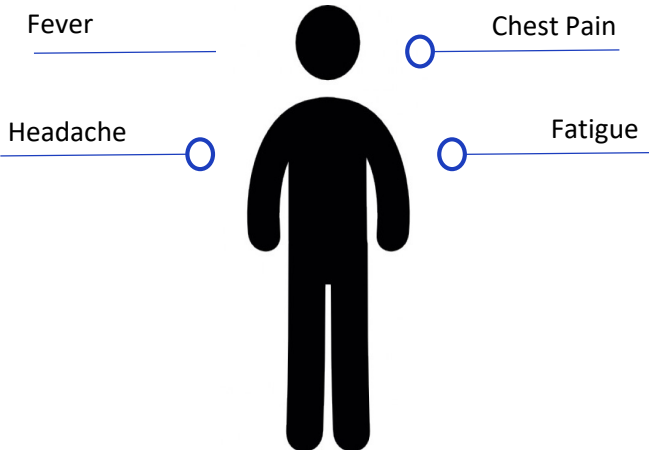


Nontuberculous Mycobacteria Infection/Disease: Primarily Respiratory Diseases

Infection/Disease

- Pulmonary NTM lung disease
- Chronic bronchopulmonary disease
- Cervical or other lymphadenitis
- Skin and soft tissue diseases
- Disseminated infections
- Catheter-related infections

Signs/Symptoms



State Health Departments

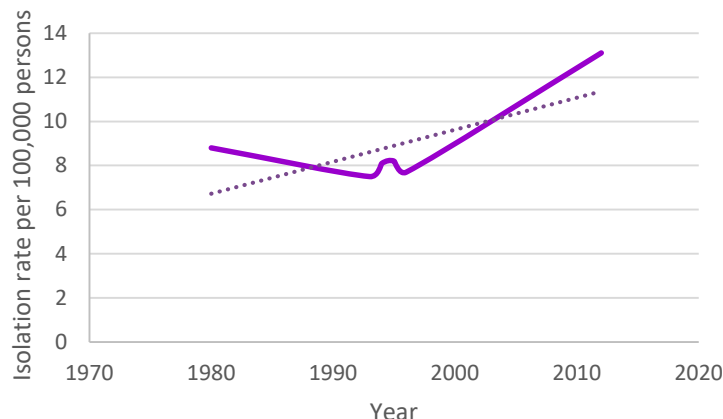
Laboratory Reports

*Report is defined as the presence of culturable NTM from a human specimen (Lavage, Sputum, Blood, and/or Tissue)

Number of Cases Reported in 2010:

Est 86,244 cases

Nontuberculous Mycobacteria



NONTUBERCULOUS MYCOBACTERIA.

Isolation Rate,* by year — United States, 1980–2013,

Sources: Good et al. (1980), CDC, NTM 1993-1996 report (1999), Donohue et al. (2016)



Annual Cost of Treatment in the U.S.



Number of Hospitalization/year
16,386 cases: 2007

Total Hospitalization Cost:
\$425,788,469

Collier, S.A. et al 2012:

Direct healthcare costs of selected disease primarily or partially transmitted by water. *Epidemiology Infection*, **140**, p2003-2013

Number of NTM Cases
est 86,244 cases: 2010

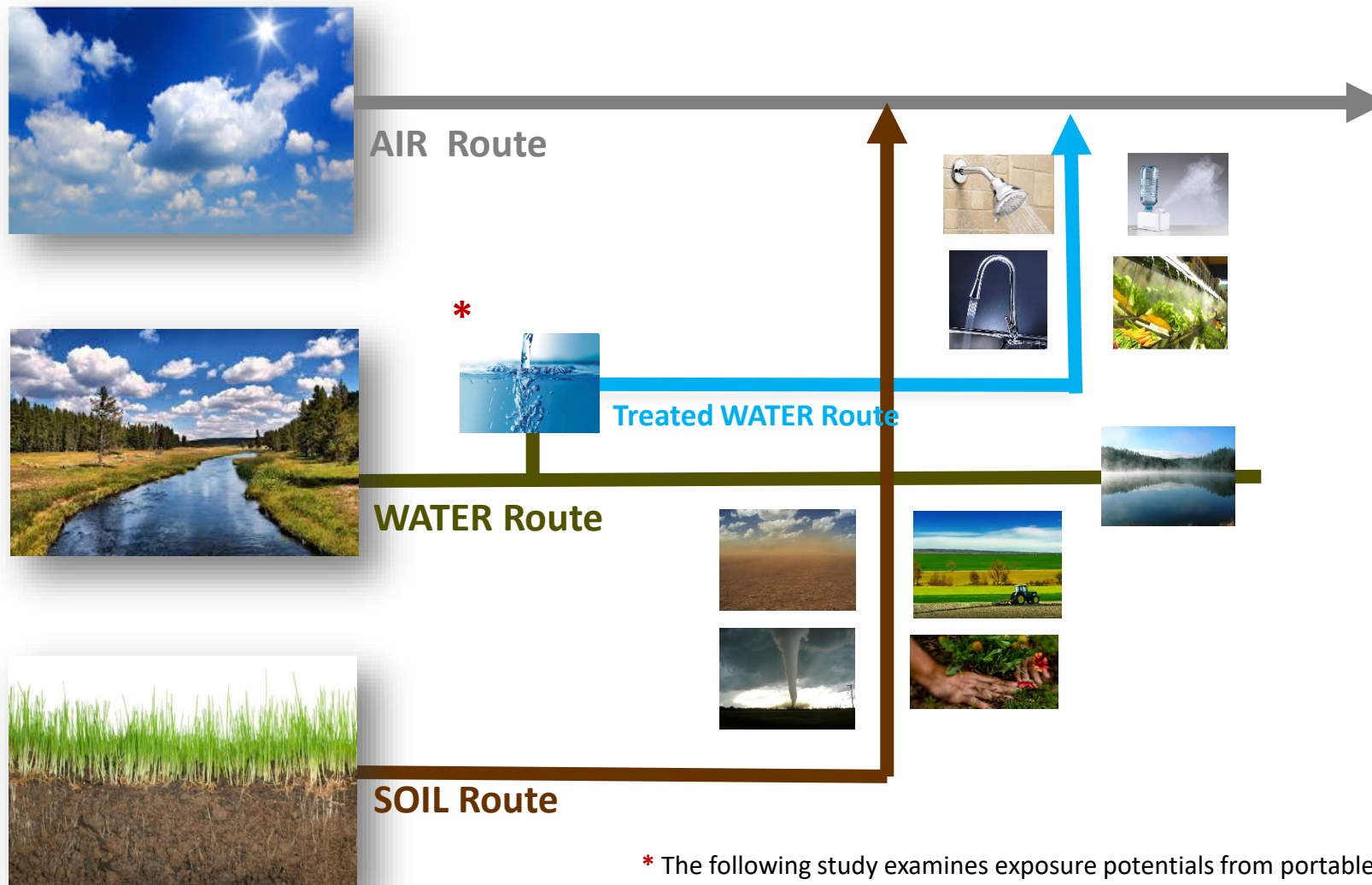
Total Hospitalization Cost:
\$815,098,690

Strollo S.E. et al 2015: The Burden of Pulmonary Nontuberculous Mycobacterial Disease in the United States. *AnnalsATS*, **12**, p1458-1464



Exposure Routes: Environmental Sources

Legionella pneumophila and *Mycobacterium avium* are microorganisms of the natural environment found in soil and water.



* The following study examines exposure potentials from portable water

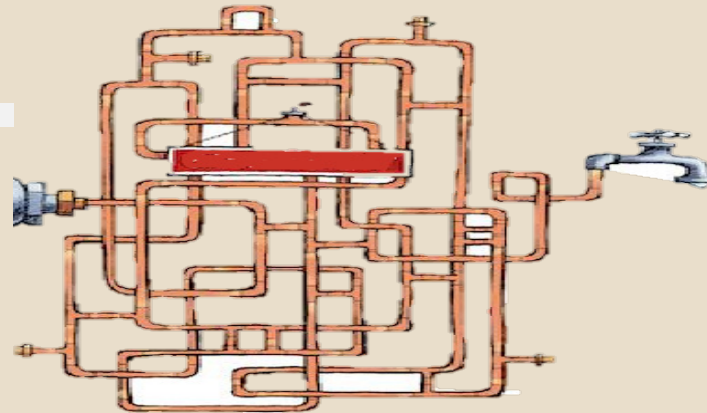
What Is the Purpose of this Study?



Source Water



Waterworks



Distribution



Houses/Building

Point of Use

$L_p = 25\%$ (6/24)

$MA = 25\%$ (6/24)

$MI = 25\%$ (6/24)

King et al 2016: SOTEN

$L_p = 4\%$ (1/24)

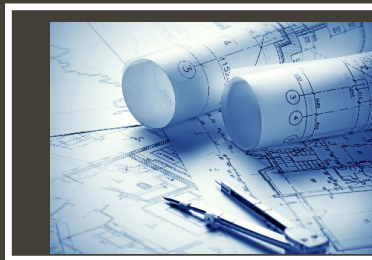
$MA = 25\%$ (6/25)

$MI = 25\%$ (6/25)

Y

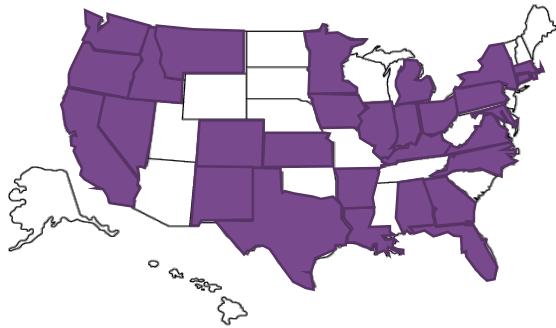
X

Donohue et al 2019: JAM & AEM



Study Design

46 States and Territories



Structure/ Point of Use 358 Samples



Houses



Buildings



5 qPCR Assays

- *Legionella pneumophila*
Donohue et al. 2014
- *L. pneumophila* Sg1
Merault et al 2011
- *Mycobacterium avium*
Chen et al. 2015
- *Mycobacterium intracellulare*
Chen et al. 2015
- *Mycobacterium abscessus*
Steindor M. et al. 2015



- Detection Frequency (FD)
- Persistence
- Concentration

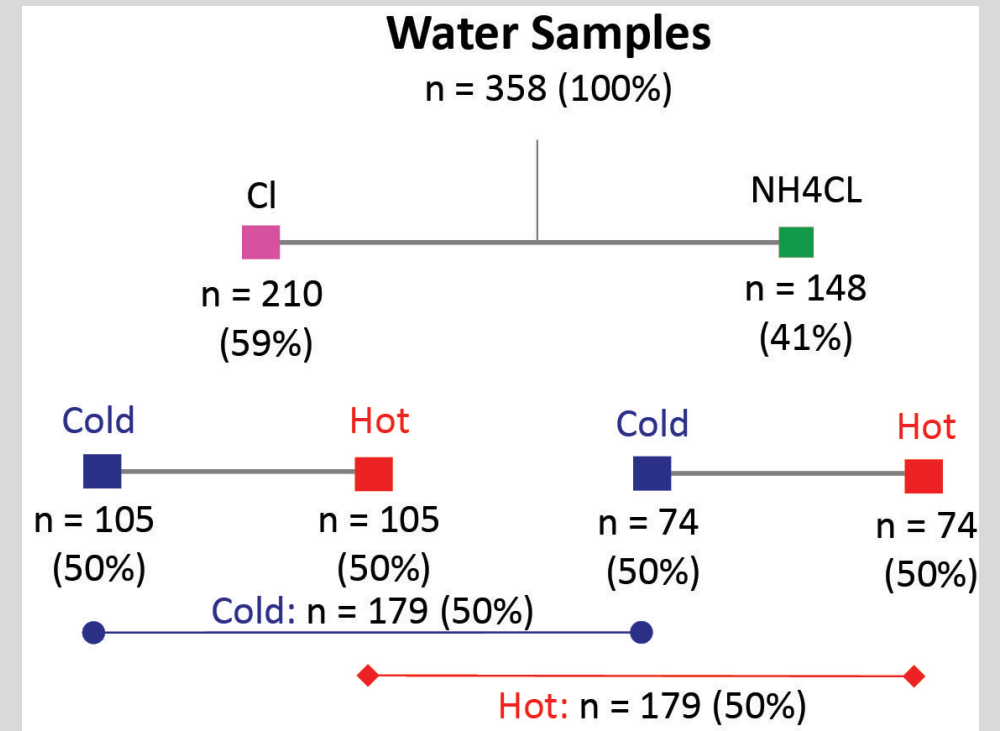
Water Quality Testing

- Total Chlorine
DPD Total Chlorine Test
- Monochloramine
Monochlor F Test
- Temperature
Cold water line
Hot water line
- Heterotrophic Plate
Counts (HPC)
Standard Method 9215

Sampling Time Frame : 2011 – 2017

Scope and Sample Design

- Chlorine (Cl) - Chloramine (CLM)
- Residual (Total Chlorine Test) – Temperature (Cold vs Hot)
- *L. pneumophila* (Lp) – *Mycobacterium* spp.(Myco)





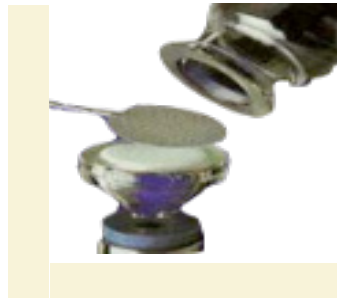
Molecular Testing: qPCR

Method

Water



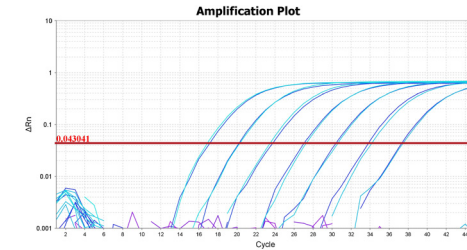
Membrane Filtration
Polycarbonate 0.4 µm



DNA Extraction
Bead Beating
DNA precipitation

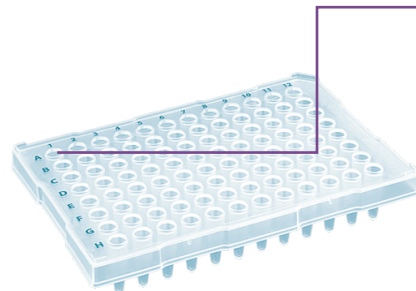


qPCR
40 cycles
1hr 45 min



Assays

1. Genus: Gen-L (16S)
2. Species: Lp-16S (16S)
3. Species: Lp-Mip (Mip)



1 Well = 1 Reaction

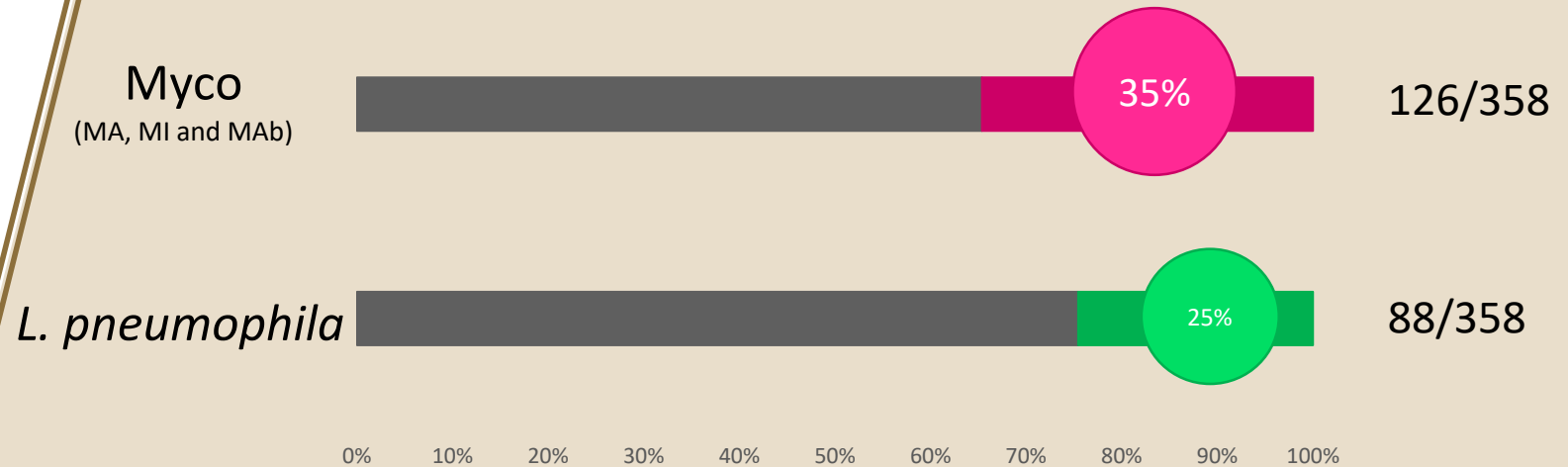
96 plate well: Well Format

- Assay/Mastermix
- Primer/Probes
- Template(DNA/ddH₂O) 10 µL reaction ~ 200mL
- Internal Control

Overview Of Occurrence (DF)

Point of Use

Houses/Building



Is
L. pneumophila
Mycobacterium
spp.
 Occurrence
 Influenced by
 Residual
 Choice?

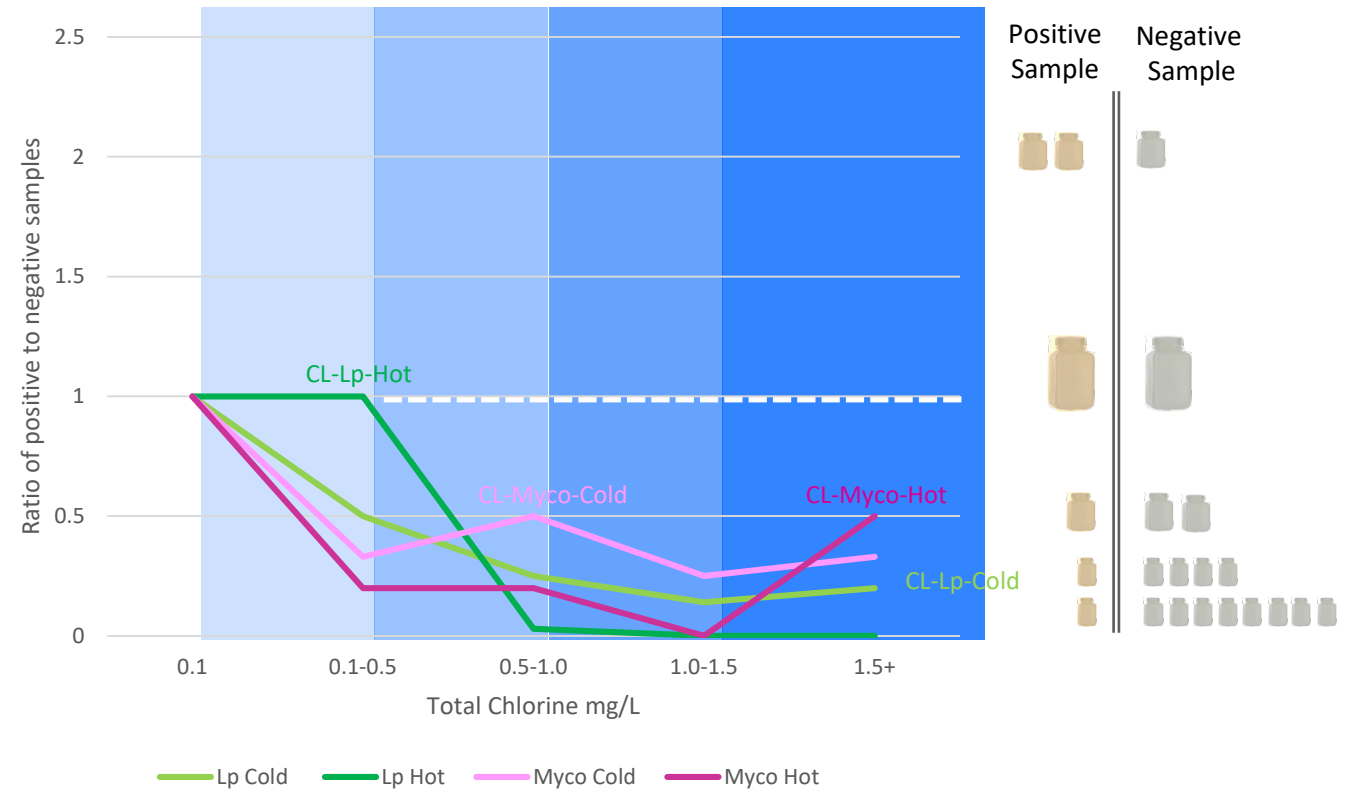
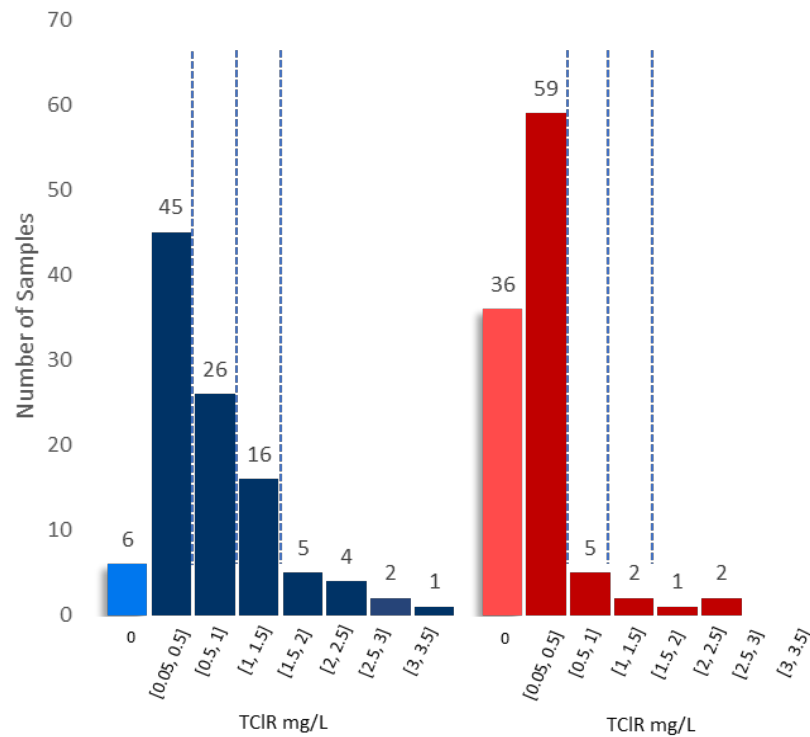
Detection Frequency



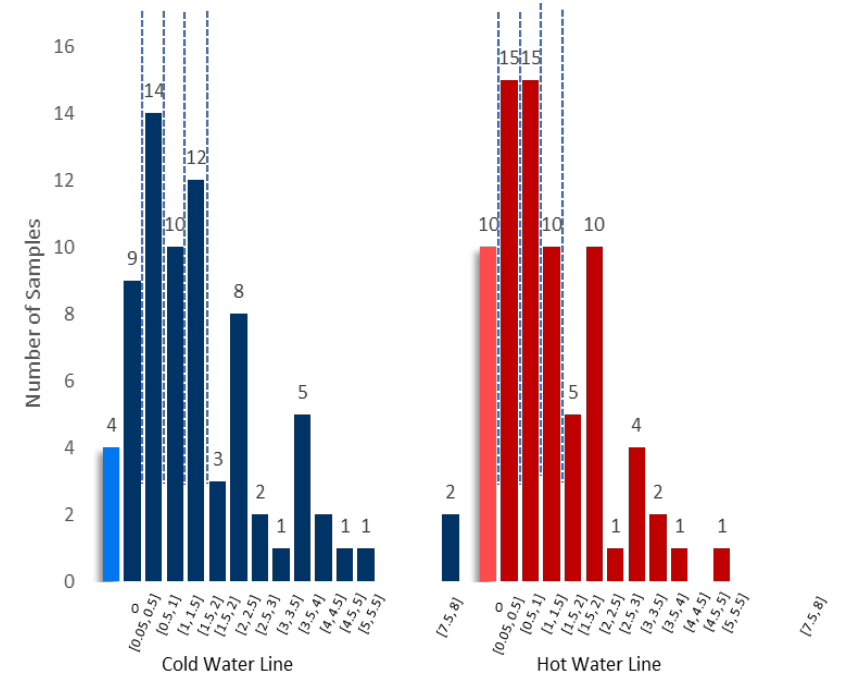
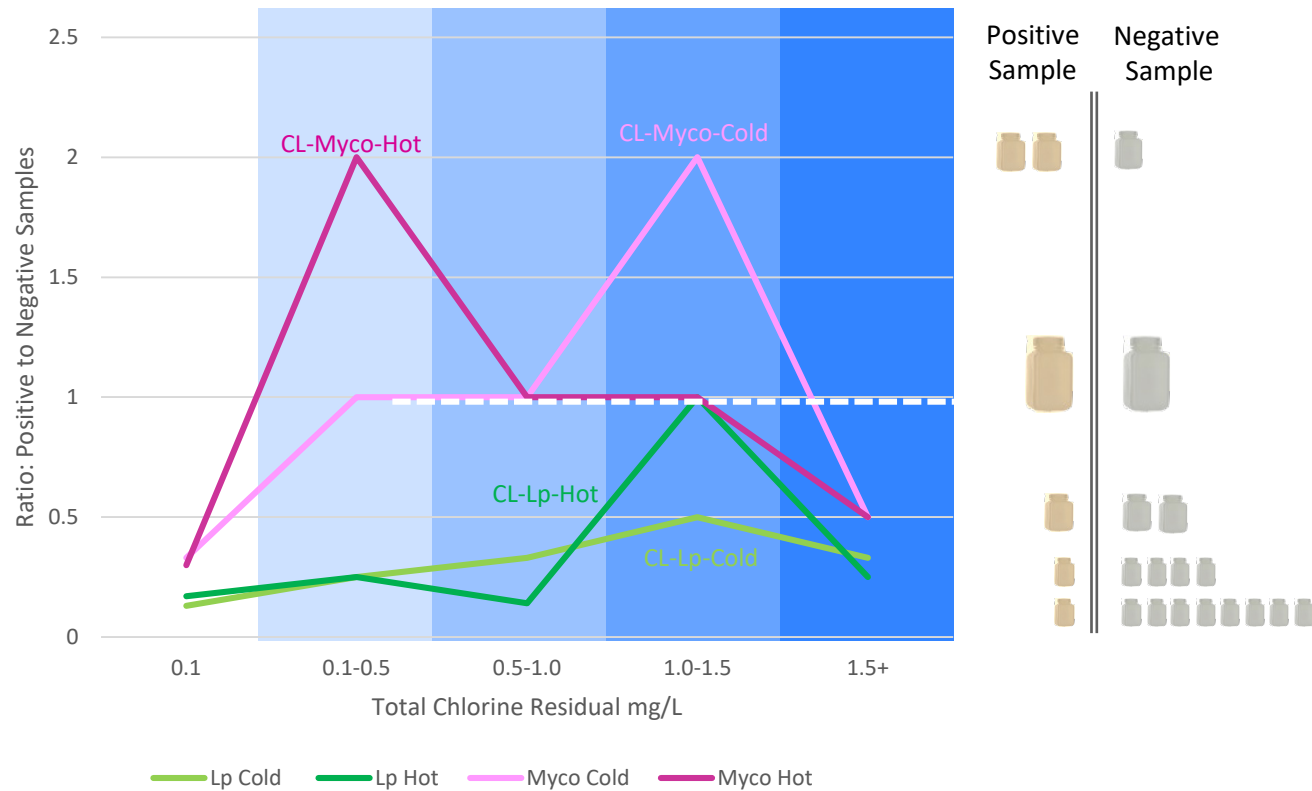
Species-Serogroup	Chlorine	Chloramine	Chi-Square p-value
	Number of Positive Samples (Percent)	Number of Positive Samples (Percent)	
All Samples	N = 210	N = 148	
<i>L. pneumophila</i>	55 (26)	32 (22)	NS
<i>L. pneumophila Sg1</i>	18 (9)	7 (5)	NS
<i>M. avium</i>	26 (12)	32 (22)	P = 0.02
<i>M. intracellulare</i>	44 (21)	29 (20)	NS
<i>M. abscessus</i>	19 (9)	25 (17)	P = 0.03
Cold Water Line	N = 105	N = 74	
<i>L. pneumophila</i>	29 (28)	17 (24)	NS
<i>L. pneumophila Sg1</i>	8 (8)	4 (6)	NS
<i>M. avium</i>	15 (14)	16 (22)	NS
<i>M. intracellulare</i>	21 (20)	16 (22)	NS
<i>M. abscessus</i>	11 (10)	13 (18)	NS
Hot Water Line	N = 105	N = 74	
<i>L. pneumophila</i>	27 (26)	16 (22)	NS
<i>L. pneumophila Sg1</i>	10 (9)	3 (4)	NS
<i>M. avium</i>	11 (10)	16 (22)	NS
<i>M. intracellulare</i>	23 (22)	13 (19)	NS
<i>M. abscessus</i>	8 (8)	12 (17)	NS

Yes, detection frequency for *M. avium* and *M. abscessus* were found to be significantly different between residual type.

Chlorine: Does the Residual (TCLR) Concentration Influence *L. pneumophila* / *Mycobacterium* spp. Detection Frequency?



Chloramine: Does the Residual (TCLR) Concentration Influenced *L. pneumophila*/*Mycobacterium* spp. Detection Frequency?



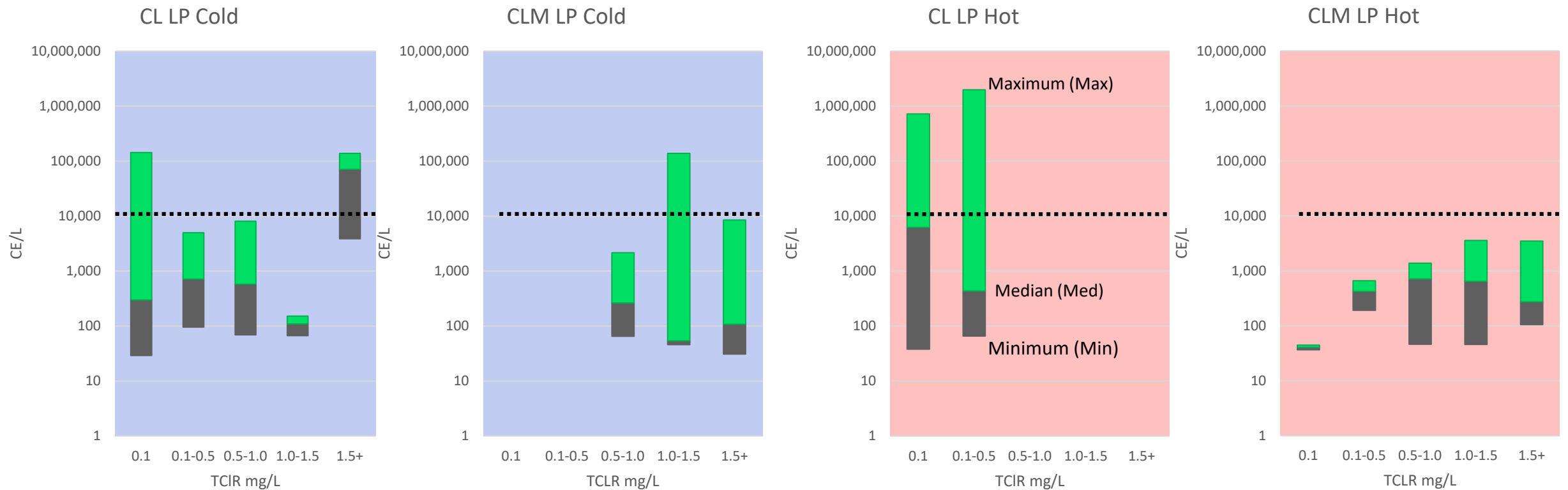
Does *L. pneumophila*/ *Mycobacterium* spp. Concentration Differ by Residual Choice?

Species-Serogroup	Chlorine	Chloramine	Mann-Whitney U
	Median (CE/L)	Median (CE/L)	p-value
All samples	N = 210	N=148	NS
<i>L. pneumophila</i>	581	132	P = <0.001
<i>L. pneumophila</i> Sg1	15,721	863	NS
<i>M. avium</i>	603	1,243	NS
<i>M. intracellulare</i>	487	661	NS
<i>M. abscessus</i>	1,339	2,157	NS
Cold Water Line	N = 105	N = 74	
<i>L. pneumophila</i>	341	82	P = 0.04
<i>L. pneumophila</i> Sg1	938	570	P = 0.05
<i>M. avium</i>	616	1,880	NS
<i>M. intracellulare</i>	359	928	P = 0.02
<i>M. abscessus</i>	1,113	834	NS
Hot Water Line	N = 105	N = 74	
<i>L. pneumophila</i>	4,201	187	P = 0.01
<i>L. pneumophila</i> Sg1	85,316	942	NS
<i>M. avium</i>	425	761	NS
<i>M. intracellulare</i>	542	602	NS
<i>M. abscessus</i>	9,048	17,304	NS



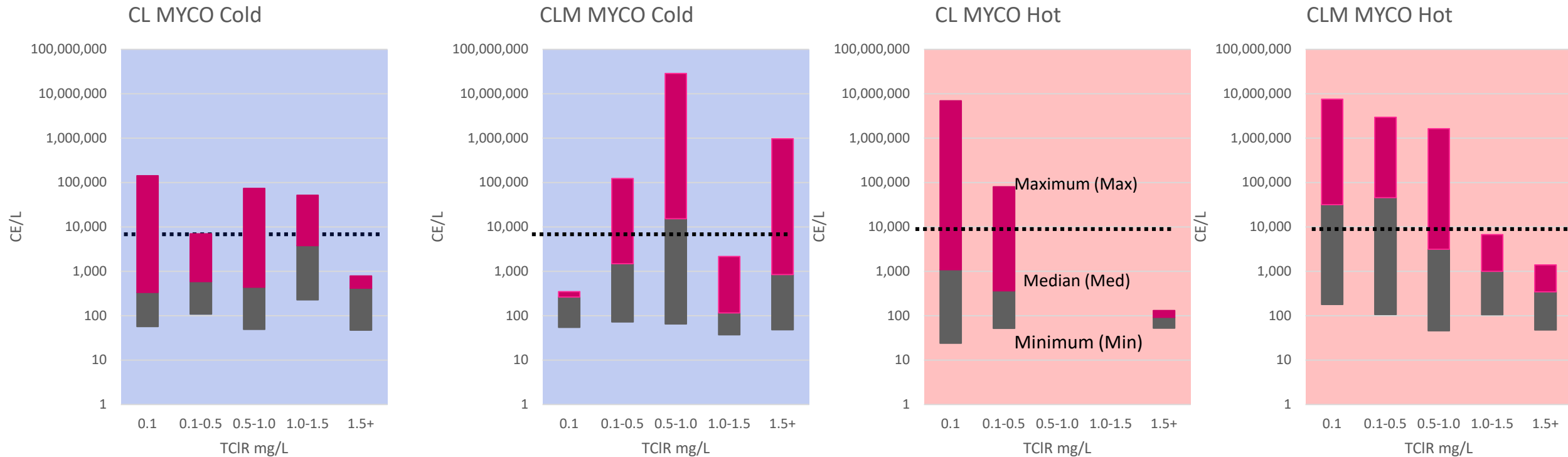
Yes, significant differences in concentrations were observed for *L. pneumophila* in both cold and hot water line samples and for *M. intracellulare* (cold water line samples).

Does Residual Concentration Influence *L. pneumophila* Concentration?



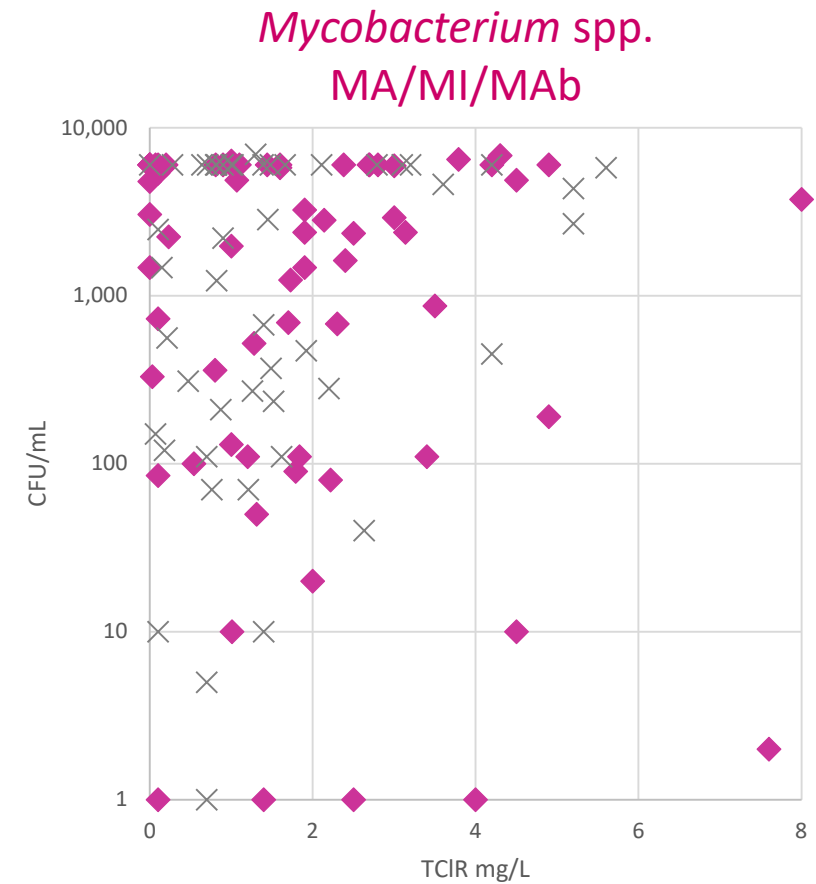
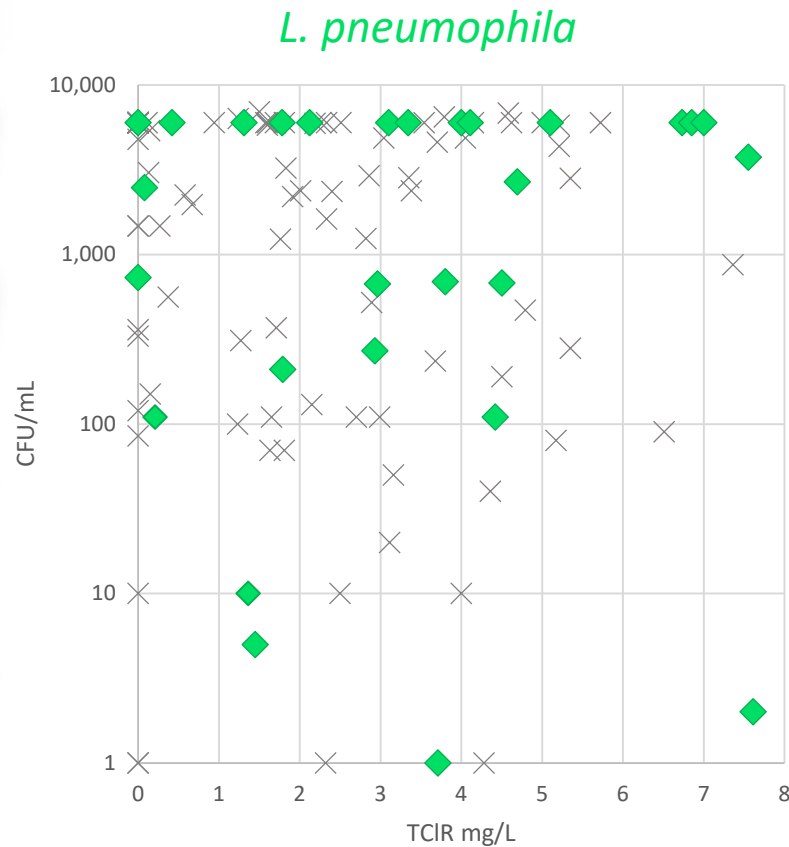
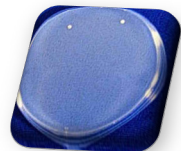
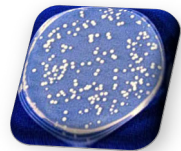
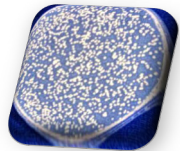
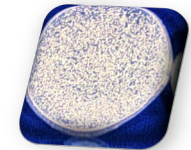
Each, residual type has its own impact on *L. pneumophila*. Chlorine (CL) impact on *L. pneumophila* concentrations is in a dose dependent manor. CLM impact on *L. pneumophila* isn't as does dependent.

Does Residual Concentration Influence *Mycobacterium* spp. Concentration?

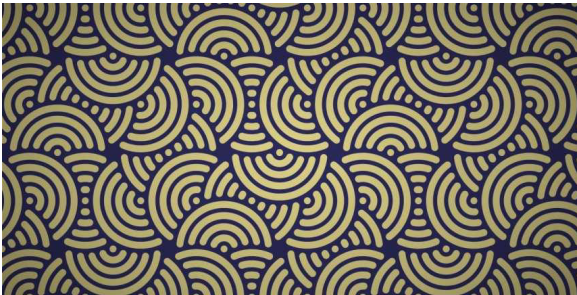
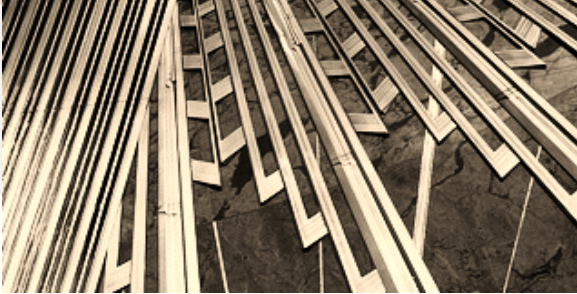
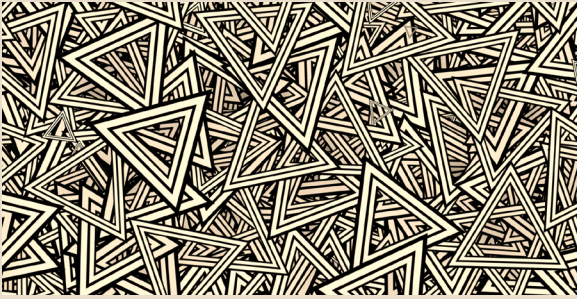


Each, residual type has its own impact on the *Mycobacterium* spp. Chlorine (CL) in cold water impact the *Mycobacterium* spp isn't does dependent. However CL+hot water does have a dose dependent impact on *Mycobacterium* spp. concentrations. CLM in cold water doesn't appear to impact on the *Mycobacterium* spp. species concentration. CLM+heat does impact *Mycobacterium* spp. in a does dependent manor.

Chloramine: HPC

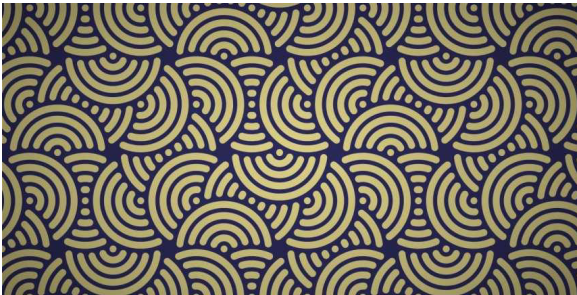
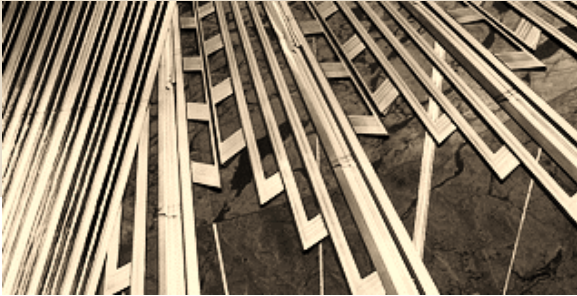
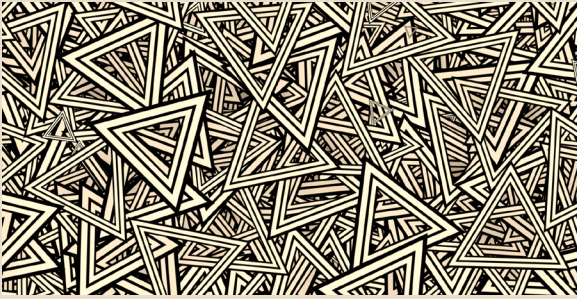


Lp/Myco positive Samples ◆ Negative samples X



Conclusions

- Residual type (CI/CLM) does significantly influence MA and MAb occurrence patterns.
- Residual type (CI/CLM) does significantly influence *L. pneumophila* and MI concentration.
- CLM is effective for controlling LP, but not MA/MI/Mab
- CL is relatively more effective at controlling MA/MI/Mab, than CLM.
- Temperature is both a stimulant for microbial growth but acts as a deterrent, especially if a residual is maintained in the hot water.



In the Larger Context

- JUST because your system uses CLM. Does NOT mean your water has MA/MI/Mab issues.
- JUST because your system uses CL doesn't mean you have Lp issues.
- If you do have Lp issues and you're a CL system is it most likely do to the lack of a active residual.
- A residual correction is not available for CLM systems.
- REMEMBER these observations are broad brush strokes which may or may not be applicable to your specific water system.
- Also REMEMBER, I talked today about just two water-borne bacteria and these observations do NOT take into account how other water pathogens will responds to our treatment and practices with.

Collaborators

- Jatin Mistry
- Stacy Pfaller
- Dawn King
- Steve Vesper



Dr. Betsy Hilborn



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Draft Genome Sequences of Seven *Legionella pneumophila* Isolates from a Hot Water System of a Large Building

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ABSTRACT Public health data show that a significant fraction of the nation's waterborne disease outbreaks are attributable to premise plumbing. We report the draft genome sequences of seven *Legionella pneumophila* serogroup 1 isolates from hot water lines of a large building. Genomic analysis identified the isolates as belonging to sequence type 1.

Legionella pneumophila is a Gram-negative bacterium and is the major causative agent of Legionnaires' disease (1). Serogroup 1 has been implicated in most cases associated with built environments (2). *Legionella* spp. colonize and persist in building water systems despite disinfection strategies that aim to mitigate their presence (3), due to the complexity of the pipe network (4). Regardless of the public health relevance of *Legionella* spp., very little information is available about their occurrence in large buildings (5).

Strains were isolated from drinking water obtained from branch lines serving a hot water system in a large occupational building. A 100-ml aliquot of each sample was concentrated by membrane filtration (0.2-µm pore size) and resuspended in 5 ml of Butterfield's phosphate buffer, and 100 µl was cultured on buffered charcoal-yeast extract (BCYE) selective agar (catalog number R110107; Remel, Lenexa, KS) for 5 days at 35°C. The agar is used for the selective recovery of *L. pneumophila* from potable water samples and contains vancomycin and anisomycin to suppress contaminating flora. A single colony was transferred to Remel BCYE agar (catalog number R01334), incubated for 2 days at 35°C, and screened with the *Legionella pneumophila* latex agglutination kit (Dioxid Ltd., Basingstoke, UK). Latex agglutination confirmed the identification of the seven isolates as *L. pneumophila* serogroup 1. DNA was extracted using the UltraClean DNA microbial isolation kit, following the manufacturer's instructions (Mo Bio Laboratories, Solana Beach, CA). Genomic libraries were prepared using the Nextera XT index kit 2 set A and sequenced on the HiSeq 4000 platform (Illumina, Inc., San Diego, CA) with a 150bp paired-end (PE) cluster kit (2 × 150bp).

A total of 197,184,931 reads were generated. Prior to assembly, libraries were cleaned from adapters and phx artifacts, error corrected, normalized (≤100×), and filtered to a minimum length of 100 nucleotides (nt) using the software package BBMap v37.100 (BBtools v3.8.2) (6). The total size of the assembly was 1.1 Gb. A reference-assisted *de novo* assembly approach was used to assemble the processed reads using Unicycler v0.4.4 (7). Average nucleotide identity (ANI) was calculated using the ANI calculator (8). ANI, an index of similarity between two genomes (9), was used to verify the taxonomic affiliation of the isolates (10). The *in silico* multisequence type (IMST) based on seven alleles (11, 12) was obtained using Multist v0.2.3 (13). Default

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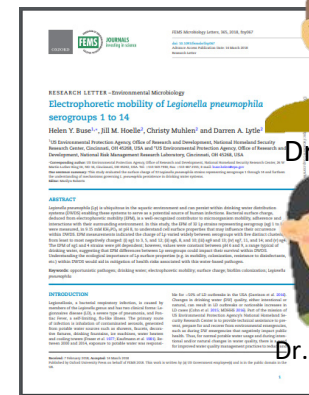
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