Water, Sanitation, and Hygiene (WASH) assessments two years after Nepal 2015 earthquake

2nd IDRC 2019, World Bosai Forum

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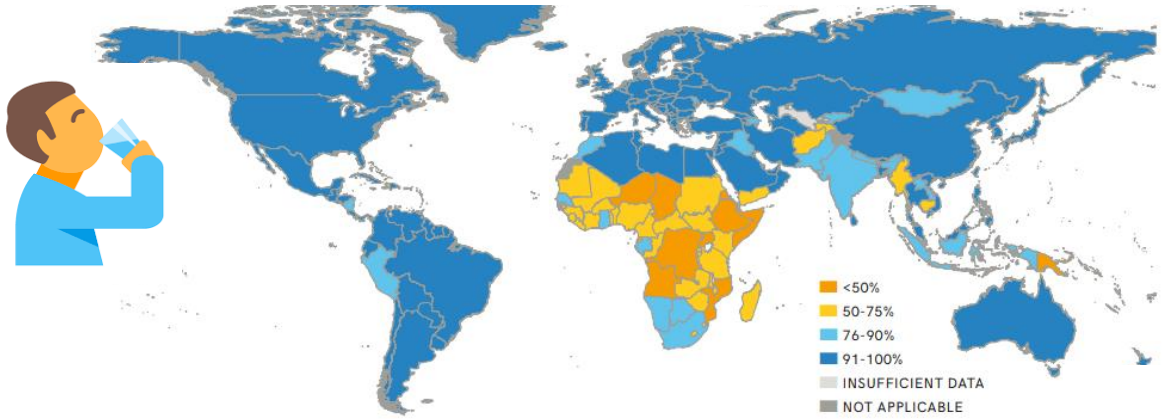
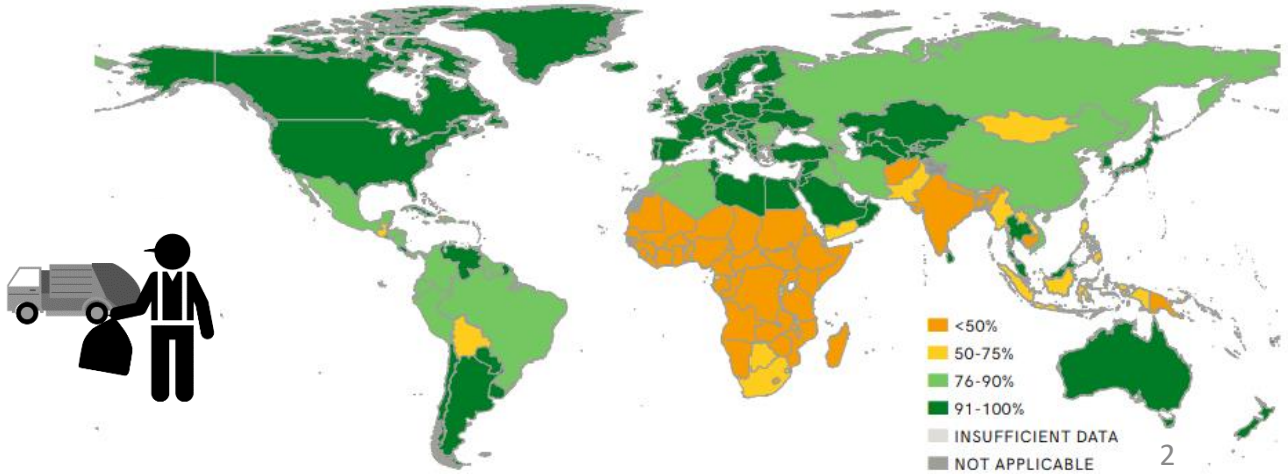
Less than 50% Basic Water and Sanitation Coverage in many places

Basic Drinking Water Coverage

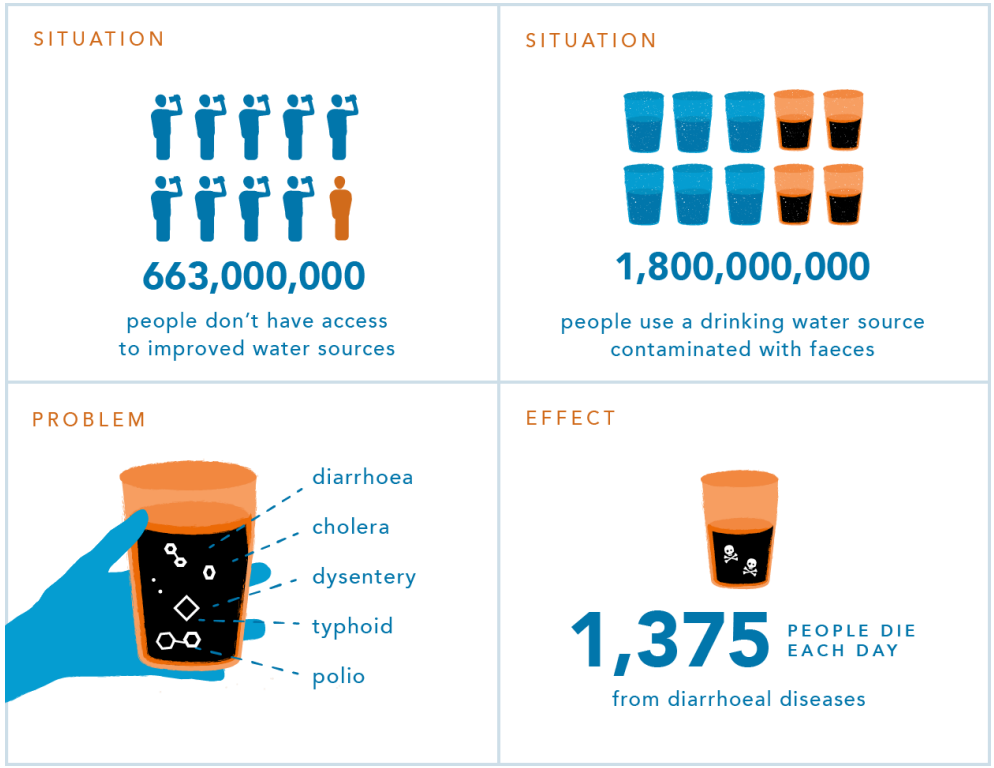


Basic Sanitation Coverage

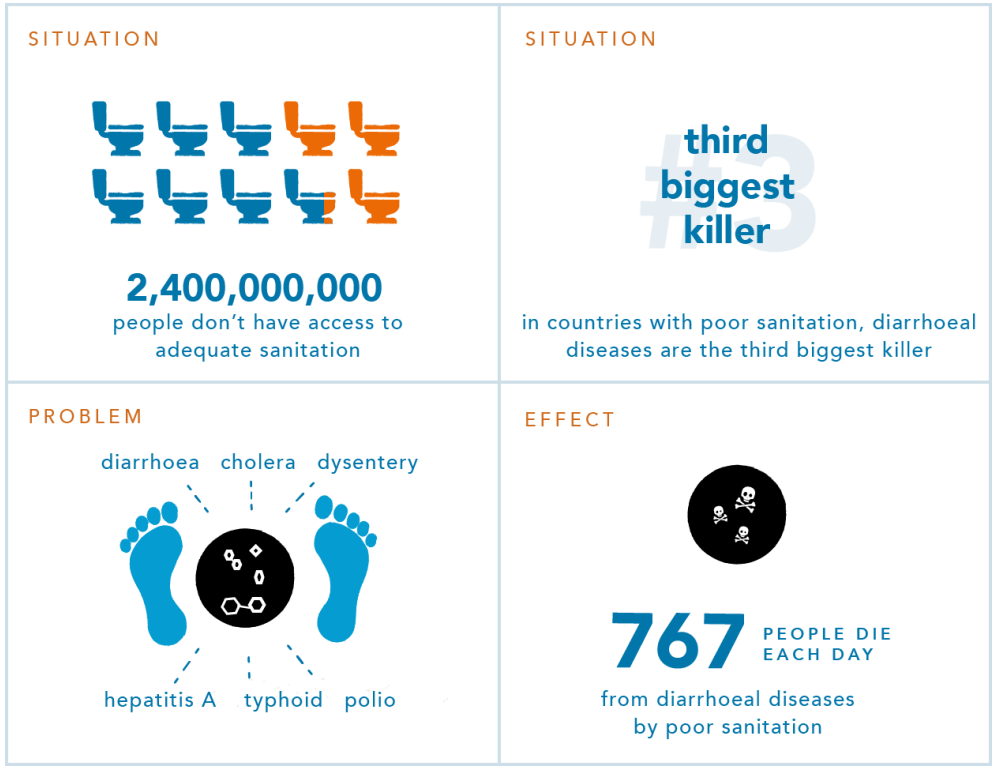


Source: WHO, 2015

Severity of the situation: Why we need more work?



Water

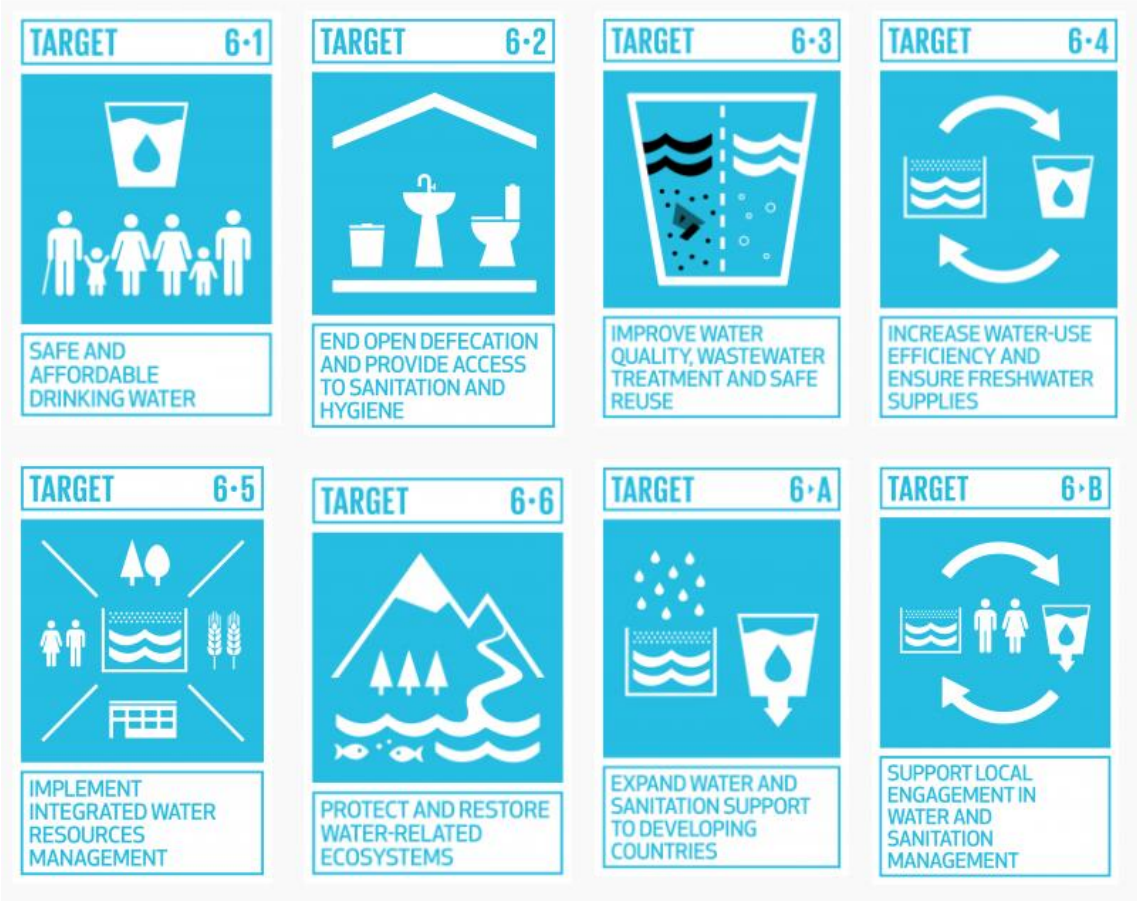


Sanitation

Source: UNICFE, 2015

What is being done? Sustainable Development Goal 6 (SDG 6)

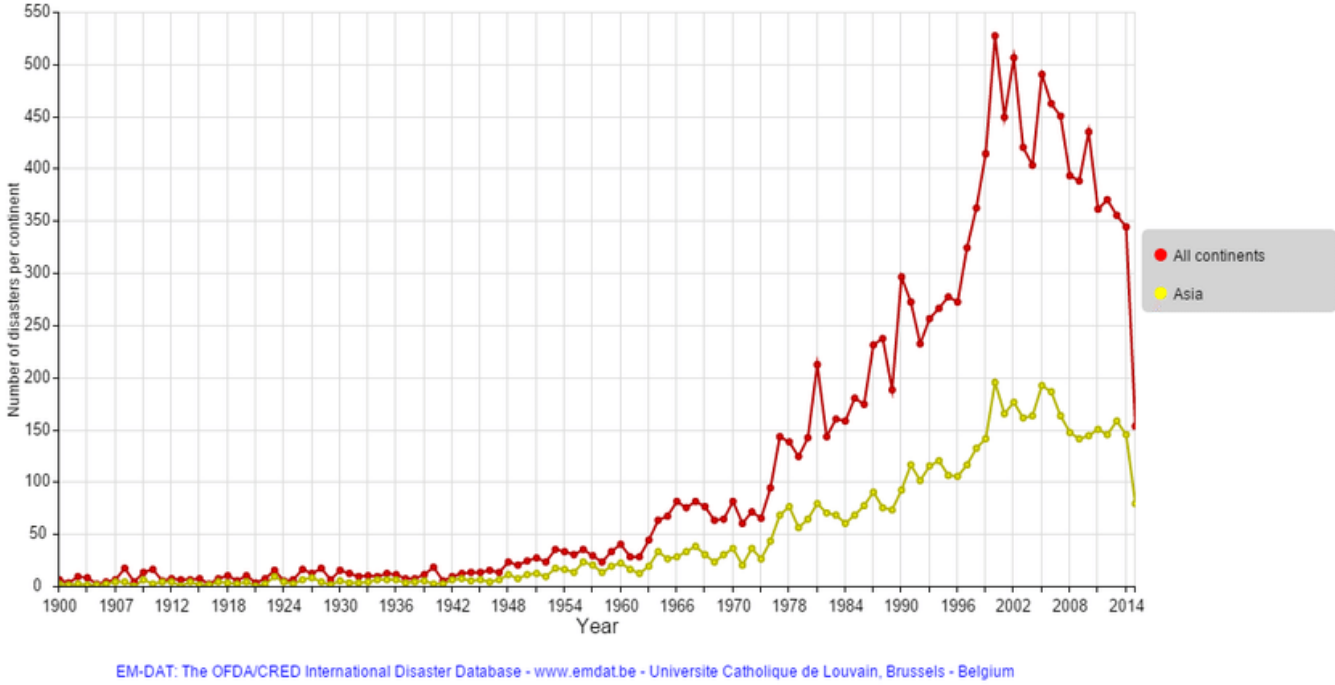
- Ensure availability and sustainable management of water and sanitation for all.
- Increase the investments in sanitation and drinking water to meet the sub-targets by 2030.



Source: UN Water, 2018

Challenges to meet SDGs?

- Increased number of natural disasters linked to climate change.[1]
- Complications to meet SDG 6 by 2030 with increased number of natural disasters, esp in Asia as Water and Sanitation issues are worsening after any natural disaster.

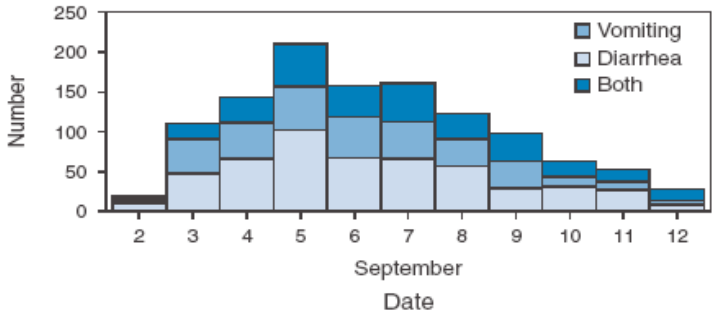


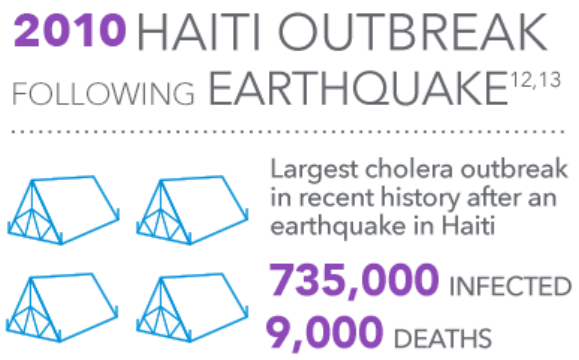
1: Natural Disasters and Climate Change (2017)
Image Source: IDD, Belgium

WASH Behavior and Diarrheal Diseases

- Because of limited resources and compromised living situation, natural disaster victims change their hygiene behaviors to meet the basic needs.[1]
- This can result in a diarrheal disease outbreak like in Haiti after 2010 Earthquake.

FIGURE. Number of persons reporting symptoms of acute gastroenteritis after Hurricane Katrina at an evacuee medical clinic, by symptom and date — Houston, Texas, September 2–12, 2005





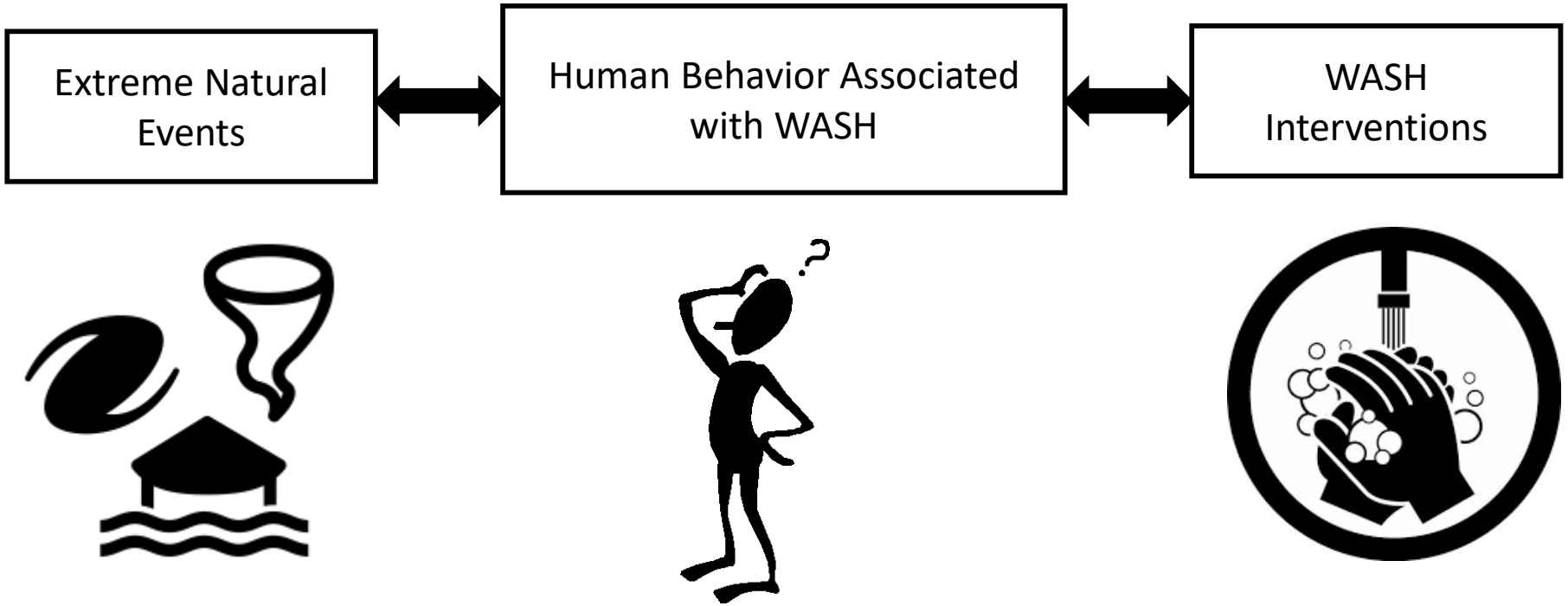
1: Uprety et al. (2017)
Image Source: RefliefWeb & CDC

Research Gap: What are we trying to address??

- How people adapt their WASH behavior after natural disaster?
- Is the adapted behavior helping or hurting their risks of getting infected with diarrheal diseases?
- Although intervention works, how effective is it in removing pathogens from households (microbial analysis)?

Image Source: ENPHO

Interrelation: WASH Behavior and Other Factors



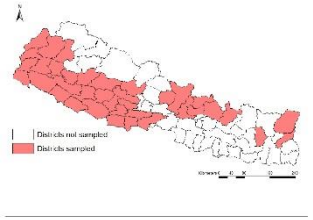
Timeline of the Study

2015

Nepal Earthquake

2015

WASH Relief immediately after the earthquake



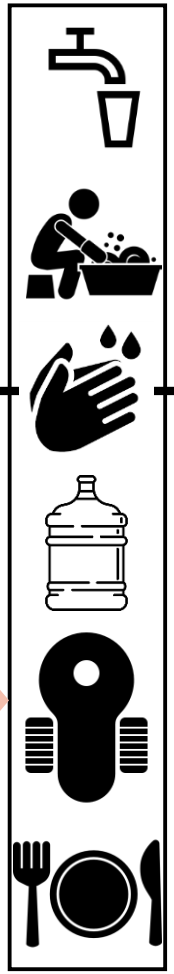
2017

E. coli testing in 2800 water samples throughout the country post earthquake

2017

Water Quality and Sanitation Study in Temporary and Permanent Settlements

WASH Intervention



2018 & 2019

Change in microbial water quality during and after intervention

Better understanding of immediate and prolonged effect of natural disasters on WASH behavior and its outcome

Pathogen exposure pathways at temporary and permanent settlements two years after the Nepal earthquake

Village 1: Permanent Settlements

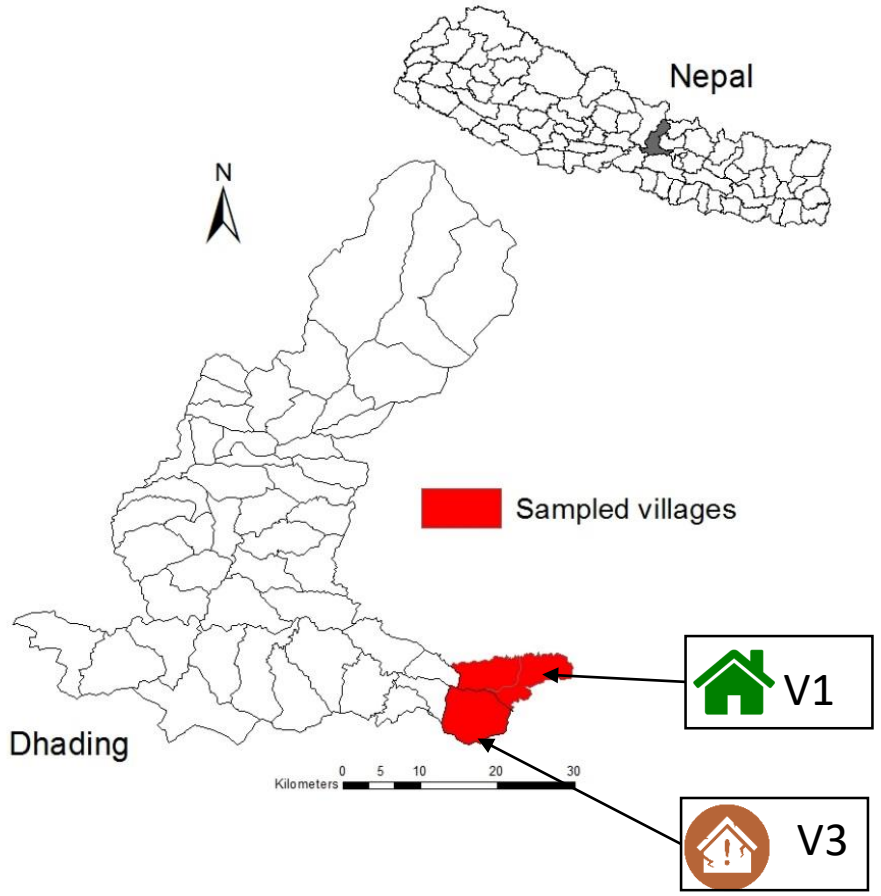
10 Houses

Village 3: Temporary Settlements

10 Houses

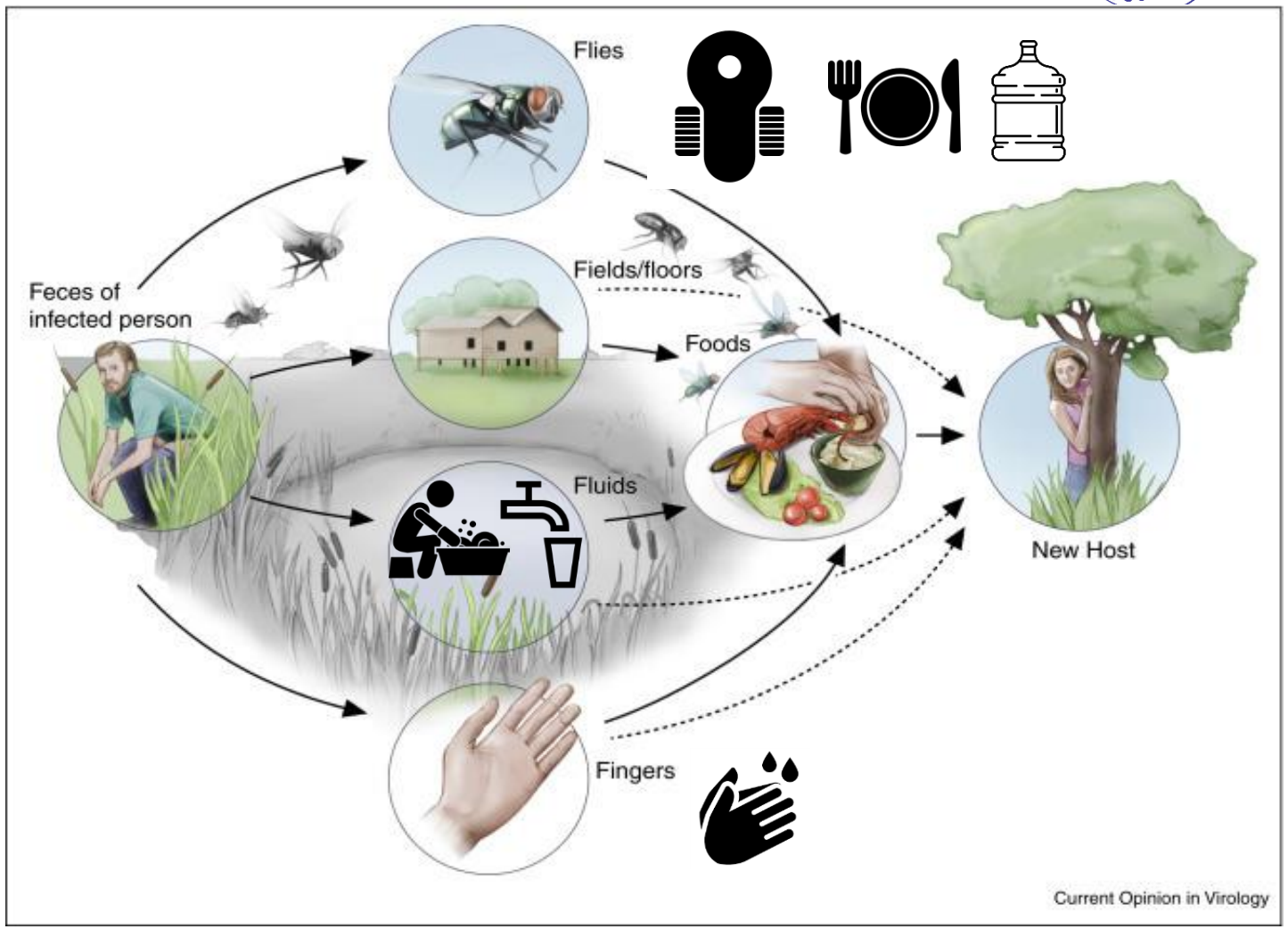
Sites: V1 and V3

- Both villages are located in one of the high risk districts for diarrheal diseases.
- They have similar population size and almost same hydroclimatic conditions.
- Water and sanitation samples were taken in 2017 from these two villages in triplicates for microbial quantification.
- Approximately 30 samples for each sample type for each village (V1 and V3) adding up to ~360 samples per sampling season.



Sample Types: F- Diagram

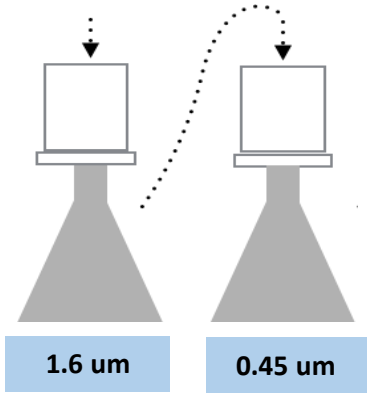
- 6 sample type collected from each house in each sampling round (3 sampling rounds)
  - Drinking Water (DW)
  - Cleaning Water (CW)
  - Handwash Water (HW)
  - Swab - Toilet Handle (TH)
  - Swab - Utensils (U)
  - Swab – Water Vessel (WV)



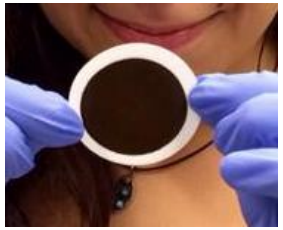
Graaf et al., 2017

Experimental Method

2 L Water



2 filters per sample



DNA Extraction

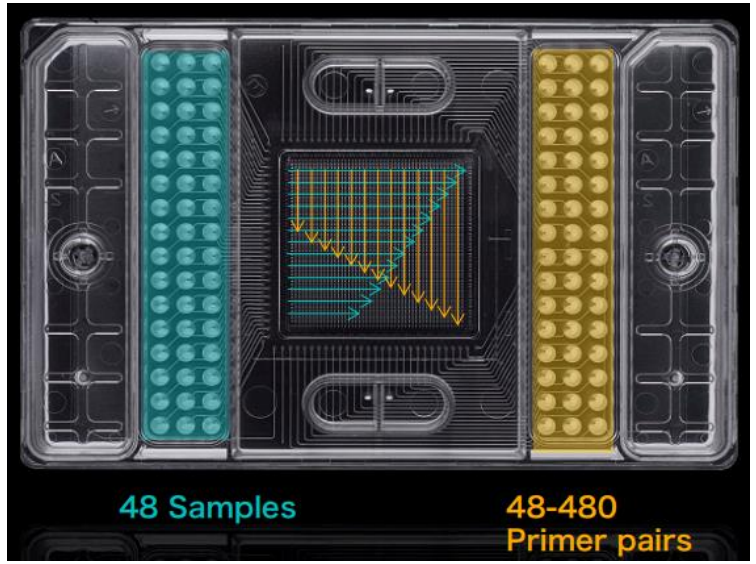
Swab

DNA Extraction

Biomark

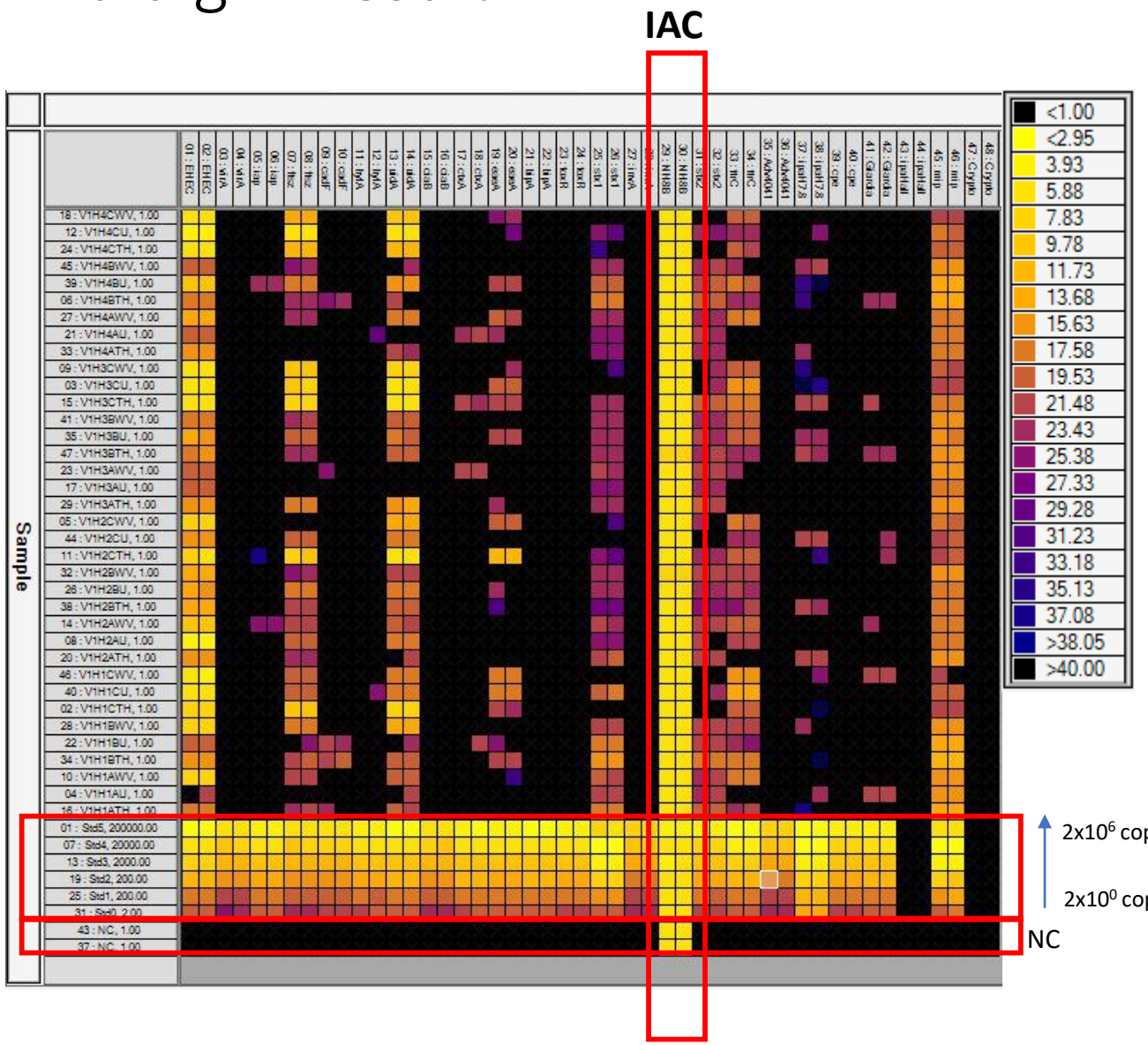
Biomark System

- Can simultaneously quantify up to 48 pathogens in the same sample.
- Faster, efficient and reliable quantification as conventional qPCR.
- 24 assays (bacterial pathogenic genes) were selected based on the primer validity and disease incidences in Nepal.
- 10 plates ran for total >300 samples collected in 2017.



48x48 plate = 2,304 reactions
Less labor and less time than conventional qPCR

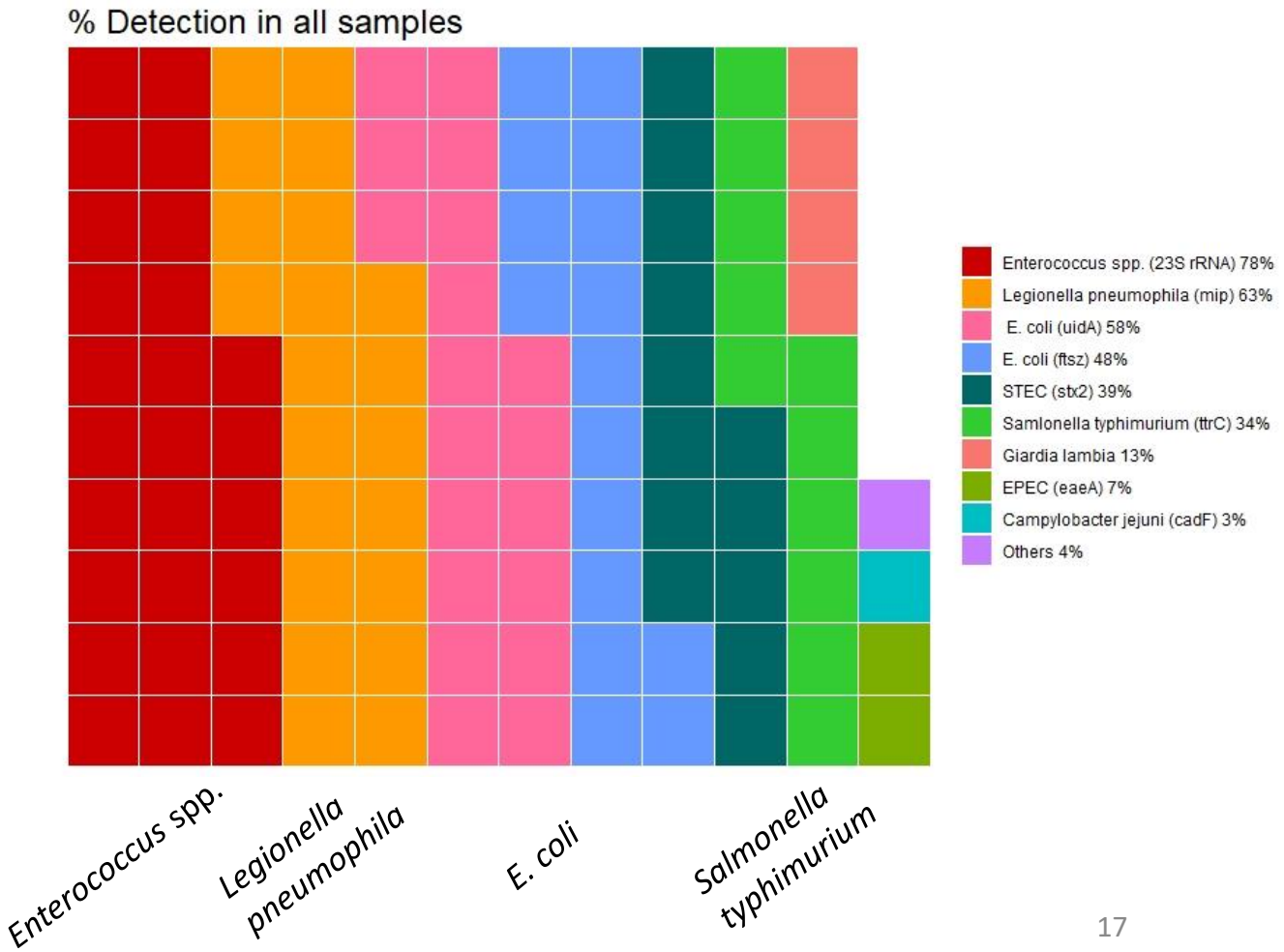
Results: Fluidigm Result



- Average assay efficiency = 93.4%
- Only assays greater than 90% and less than 110% are considered for the analysis.

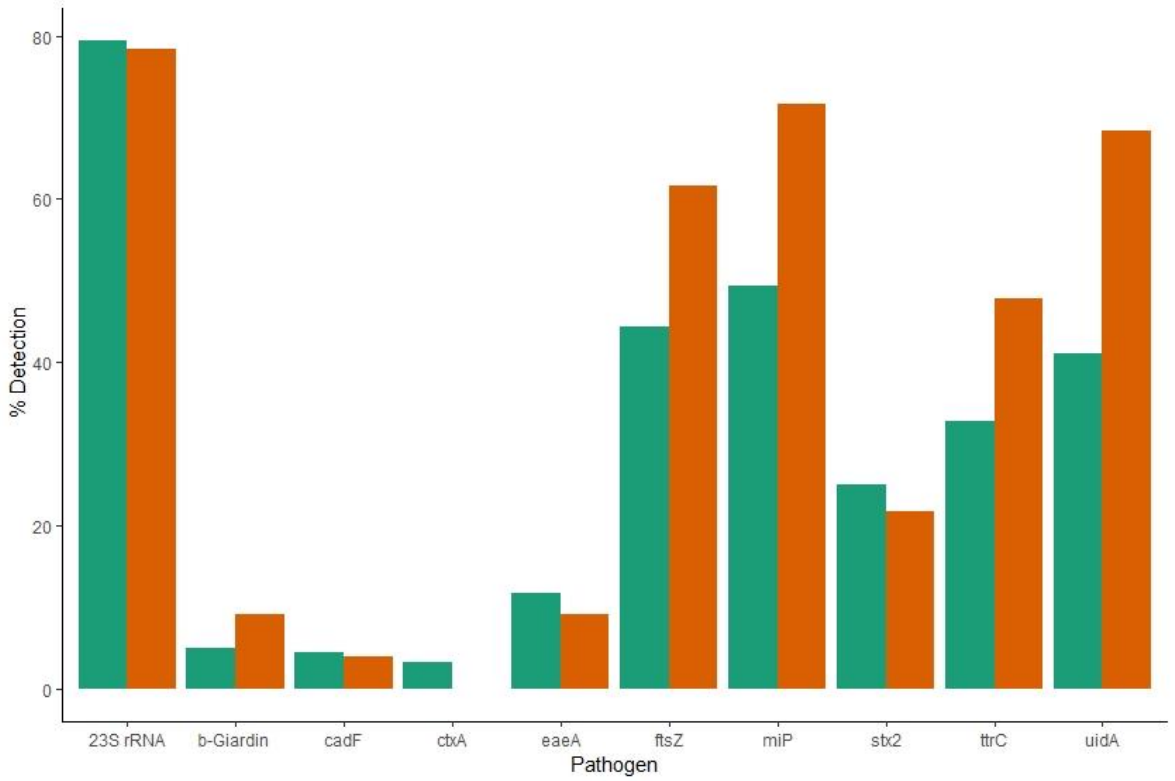
Results: Overall detection in all samples

- Highest detection of *Enterococcus spp.* in ~78% of the samples.
- 63% of samples were positive for *Legionella pneumphila.*
- *34%* of total samples had one gene of *Salmonella typhimurium*.

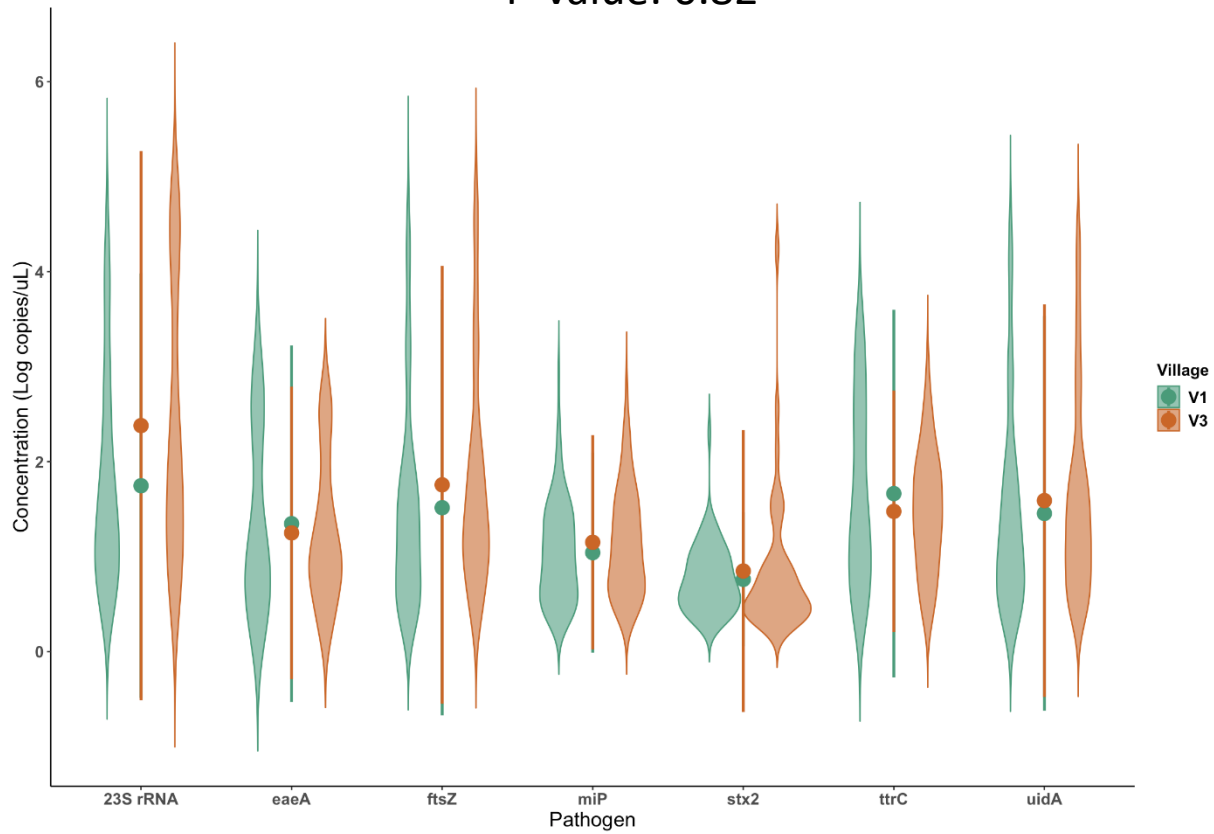


Higher detection of pathogens **from all sources** in V3 compared to V1 but not statistically significant

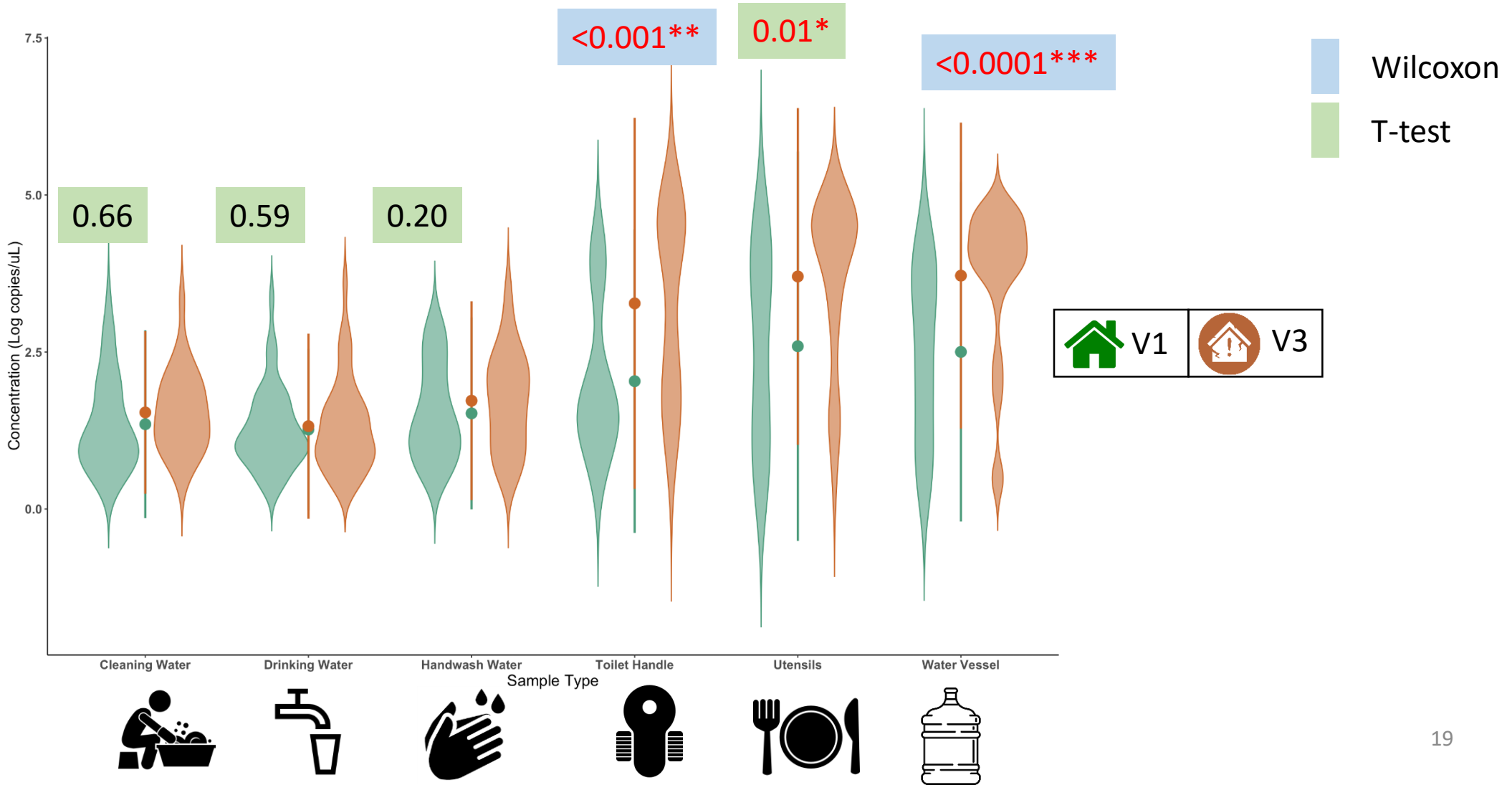
V1 V3



P-value: 0.82



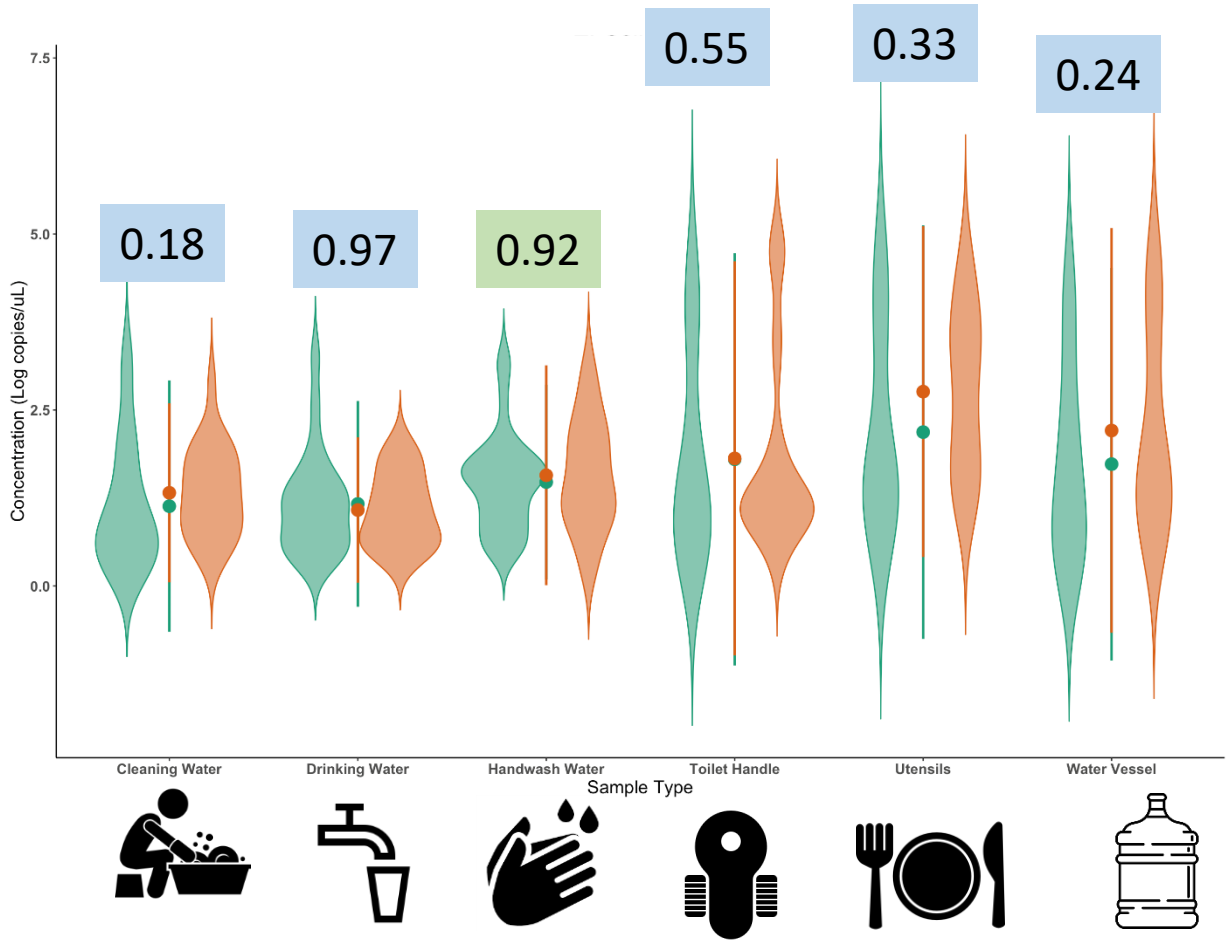
Enterococcus spp. significantly higher in toilet handle, utensils and water vessels in V3 compared to V1



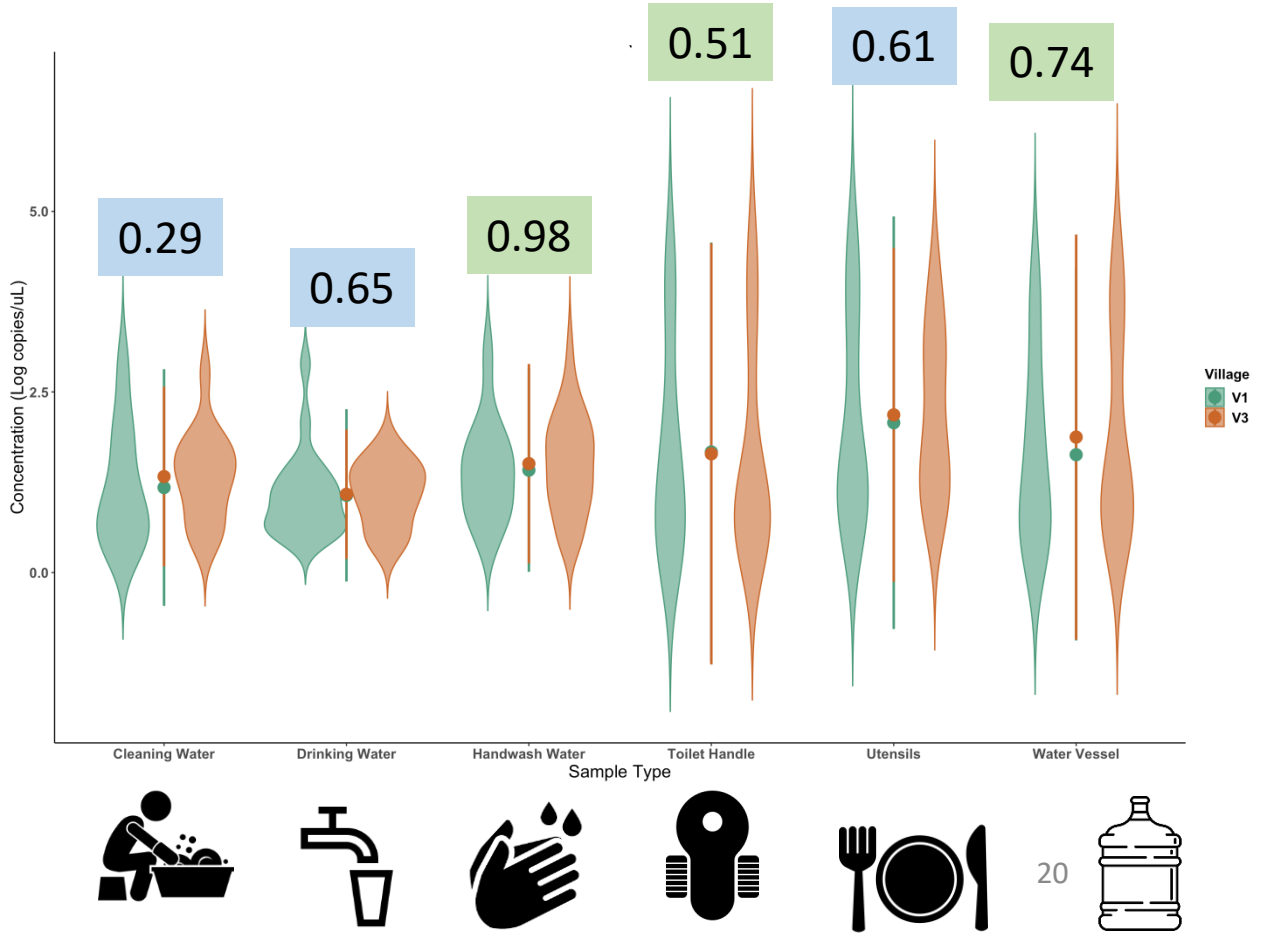
No statistical difference in detection of *E. coli* in different samples between V1 and V3

V1 V3

E. Coli (ftsz)

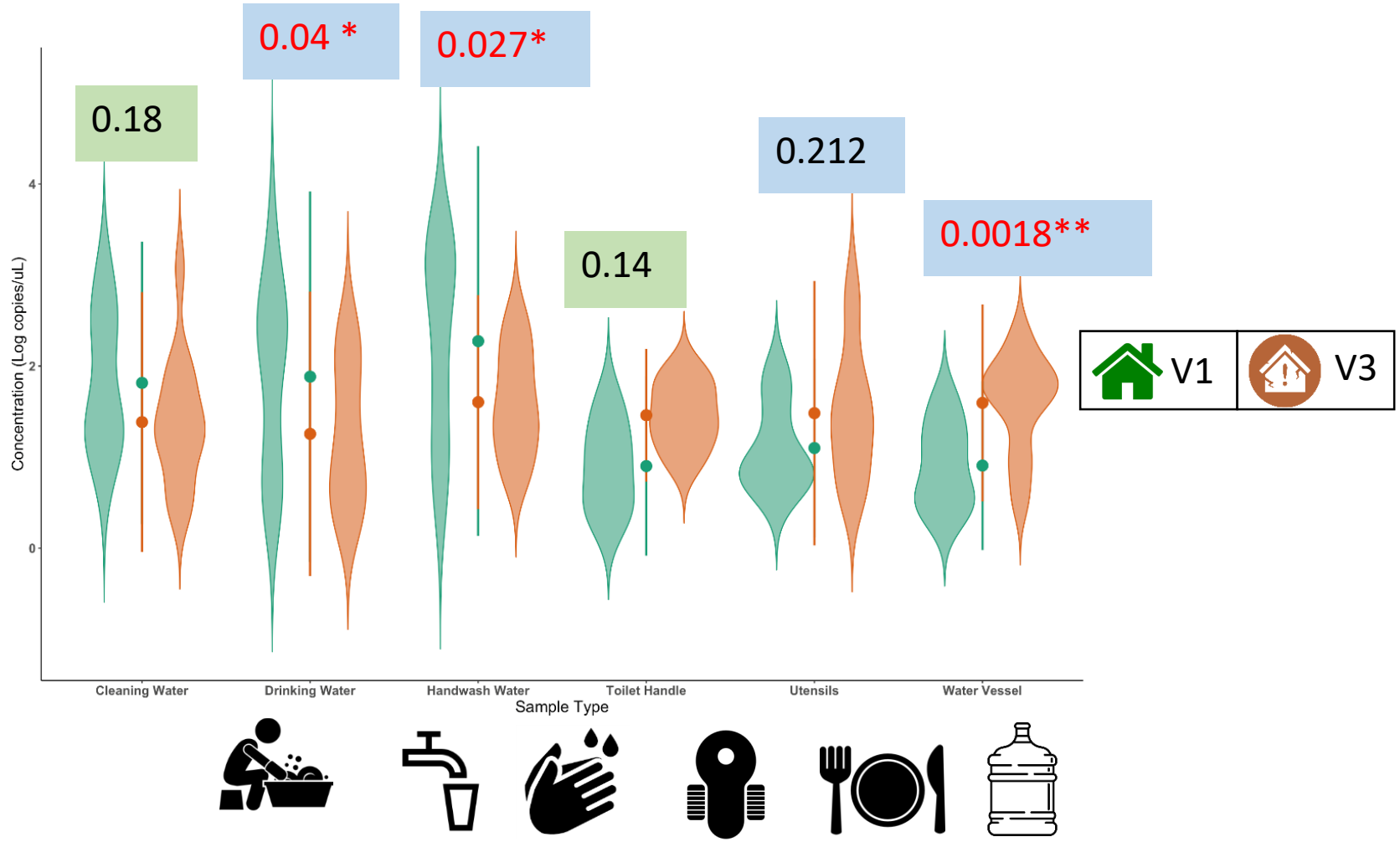


E. Coli (uidA)

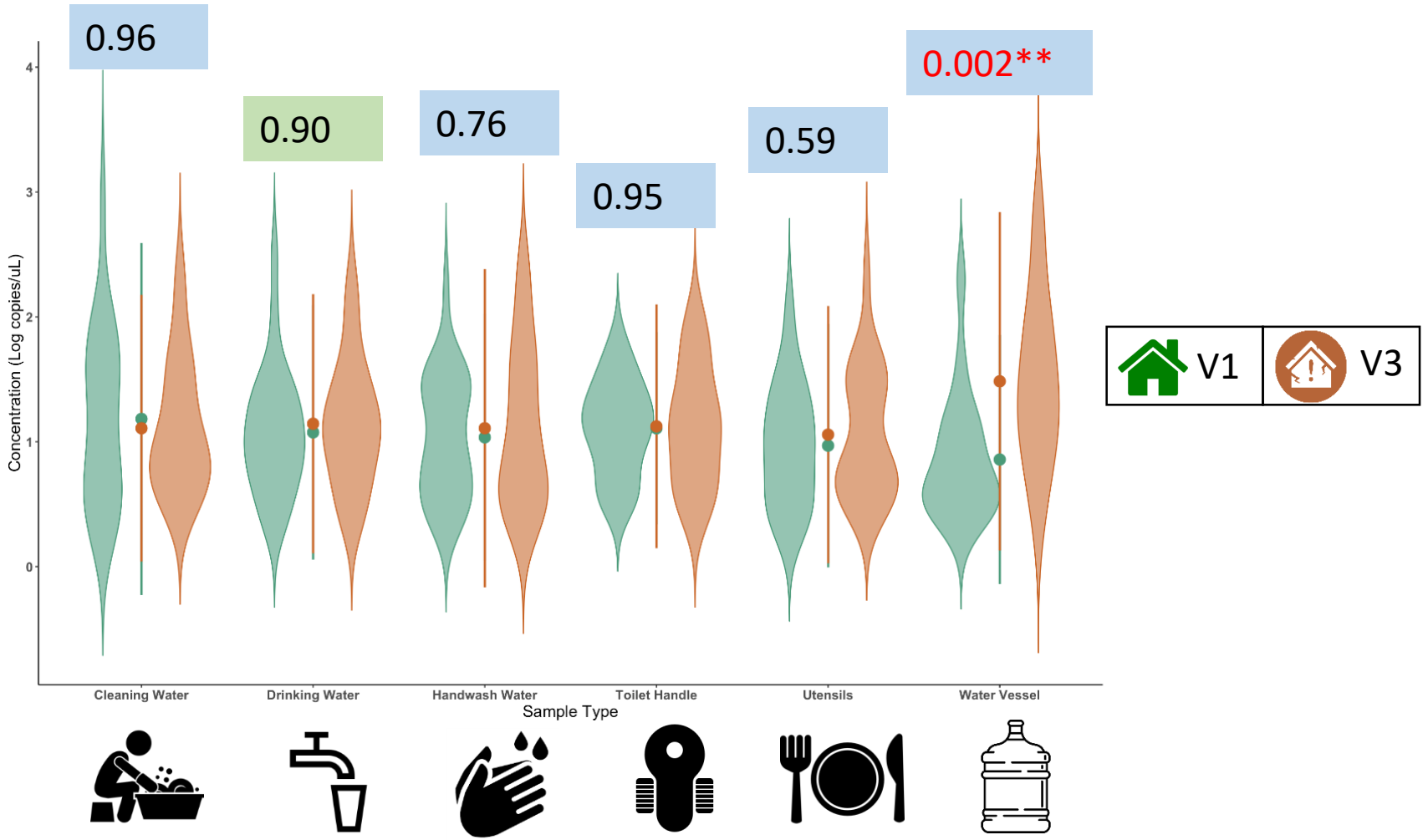


Higher concentration of *Salmonella* was observed in V1 for water samples

Salmonella typhimirium (ttrC)



Difference in *Legionella pneumophila* (miP) was only observed in water vessel



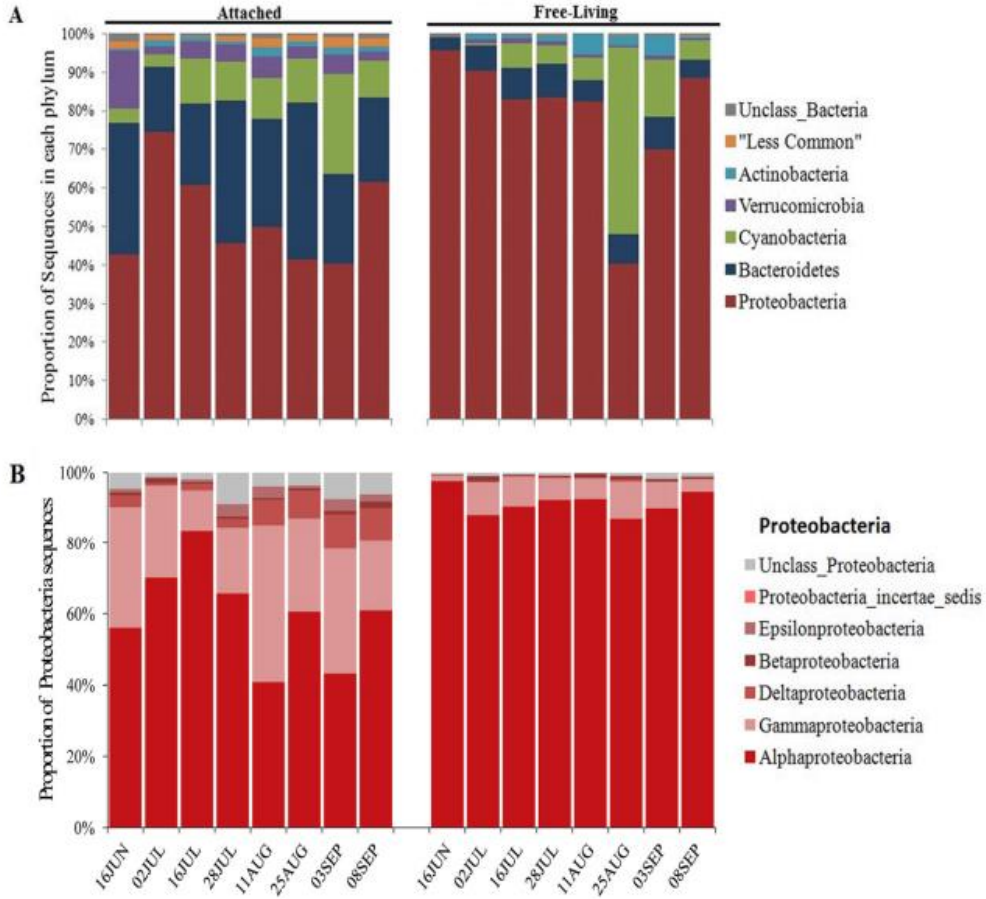
Statistical data between V1 and V3

Stat Summary: V1 | V3

	Enterococcus spp.	*E. coli* (uidA)	*Salmonella* (ttrC)	STEC (stx2)	*E. coli* (*f*tsZ)	*Legionella* (mip)
CW	0.66	0.29	0.18	0.63	0.18	0.96
DW	0.59	0.65	0.042*	0.91	0.97	0.90
HW	0.20	0.98	0.027*	0.30	0.92	0.76
TH	<0.001***	0.51	0.14	0.19	0.55	0.95
U	0.013**	0.61	0.21	0.66	0.33	0.59
WV	<0.001***	0.74	0.0018**	0.43	0.24	0.002**

Can microbial composition help us understand this in a better way?

- 85 samples from both villages were randomly selected for 16S rRNA sequencing using MiSeq platform.
- Possible difference in bacterial profile between different villages and different samples were sought.
- Investigate the 16S profile to see if we missed any important bacteria.
- Investigate whether or not, there is a transfer between water samples and hygiene samples.

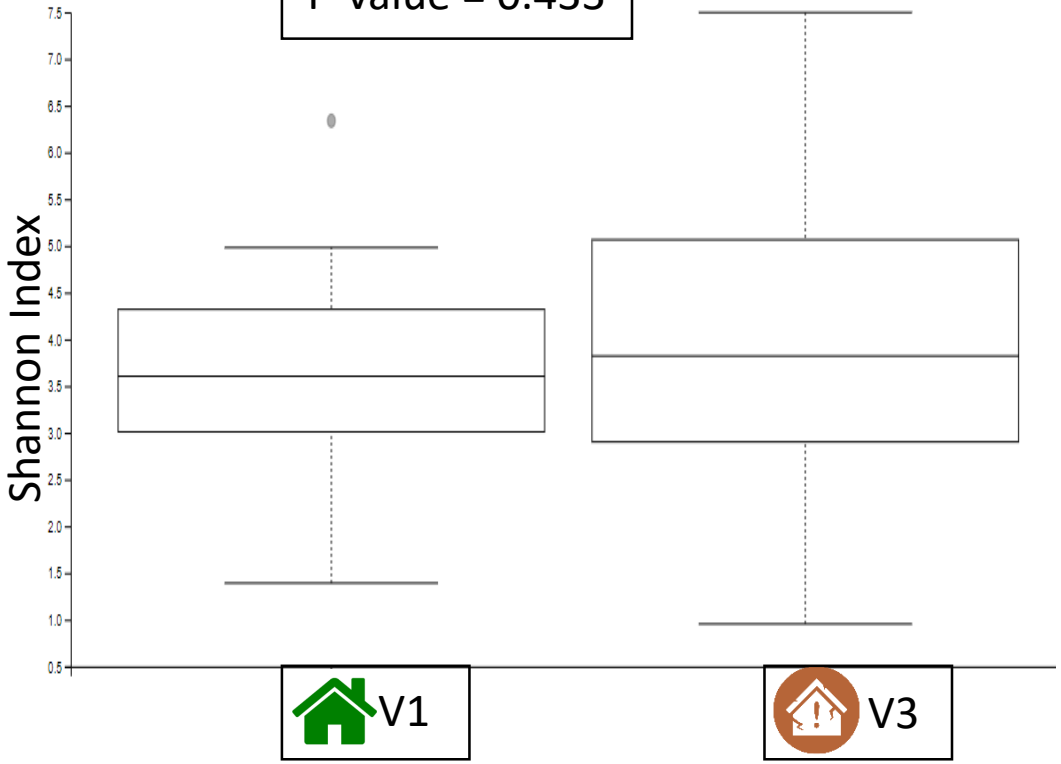


Previous studies have also shown different between attached and free-living bacterial profile

Mohit et. al (2014)

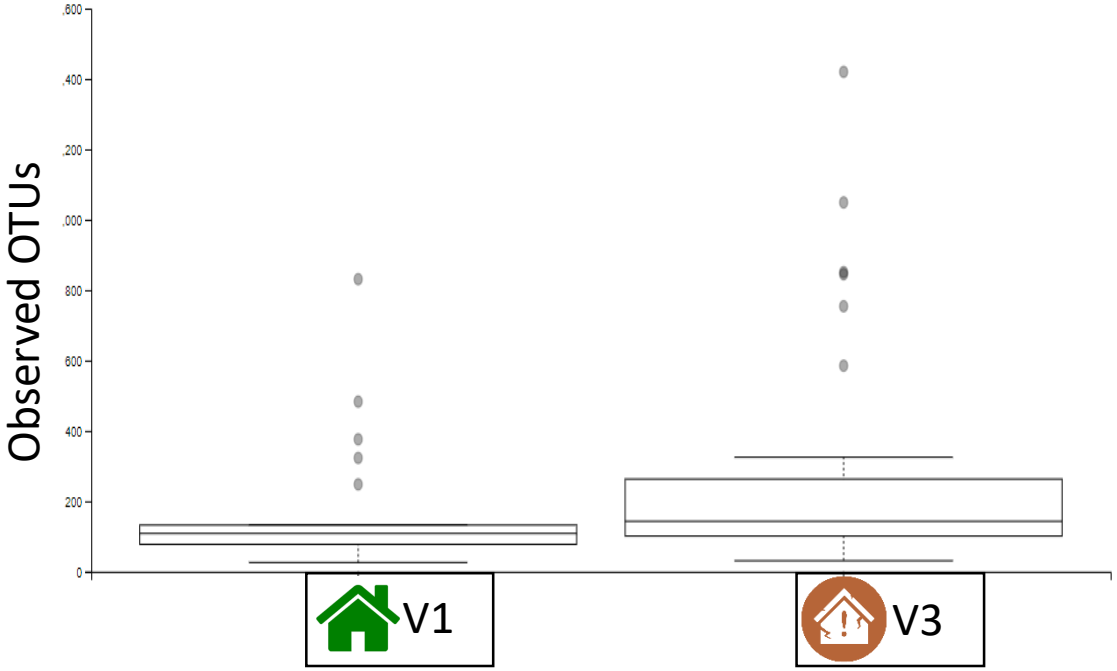
Microbes were evenly distributed between V1 and V3

P-value = 0.433



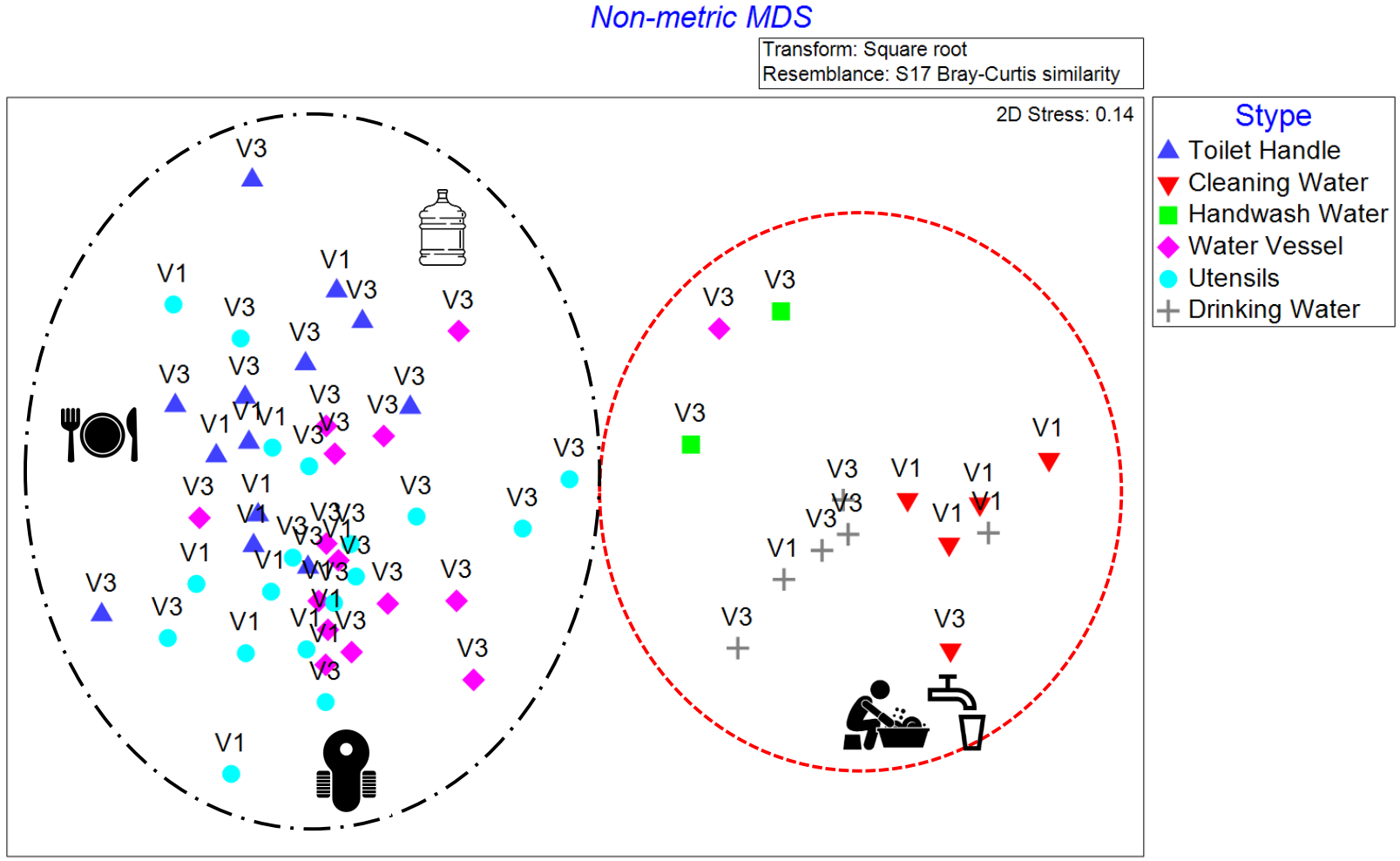
Species Diversity
(How different?)

P-value = 0.103



Species Richness
(How many?)

Microbial composition different between sample type



Relative Abundance: Class level

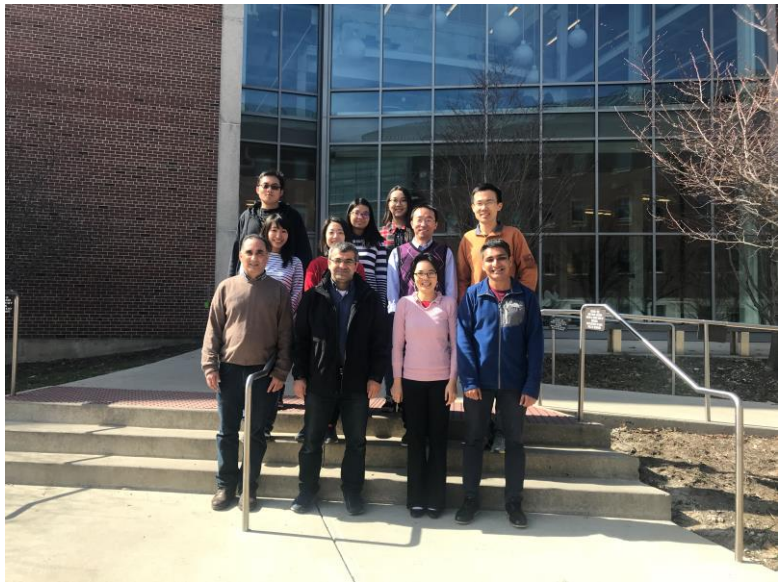
Conclusions

- *Enterococcus* spp. indicated a possible higher risk in the village with temporary settlements compared to the village with permanent settlements.
- Possible high risk of infection by *Salmonella typhirimium* and *Legionella penumophila* from water vessel. QMRA will make this more clear.
- Sequencing results showed a very different bacterial profile for sanitation samples compared to water samples. Pathogenic family more dominant in swab samples compared to water samples.
- Recovery affects microbial contamination.

Side note: Undergrads contributed a lot to this project

Image Source: ENPHO, Nepal

Thank you!



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