

## **Pathogen flows from sanitation systems in Dhaka: A quantitative environmental assessment**

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**Keywords:** Pathogen contamination; Non-Sewered urban sanitation; Pathogen flow, SDG6, Dhaka

### **Abstract:**

There is limited field-based evidence on removal of pathogens from septic tanks and decentralised systems. In a low-income area in Dhaka, we investigated pathogen loads (*Shigella*, *S.Typhi*, *V.cholerae*, *Norovirus*, and *Giardia*) associated with sanitation systems using qPCR including in effluent, open-drains and waterways. These pathogens were detected with high frequency (particularly *Norovirus*, *V.cholerae* and *Shigella*), and at potentially unsafe concentrations of pathogens in most of the environmental samples except for *S.Typhi*. The exposure pathways to children and adults make these findings of high concern, and the results will be important to prompt rethinking in how to achieve safe sanitation solutions.

**Keywords:** Pathogen contamination; Non-Sewered urban sanitation; Pathogen flows, Dhaka

**Introduction:** Despite the recent success in reducing open defecation, environmental contamination with fecal pathogens still remain a widespread health and environmental hazard that needs to be addressed among many developing countries including Bangladesh. Recent evidence suggested that both urban and rural environments are contaminated; though use of Fecal Indicator Bacteria (FIB) as a reference [1] and detection of faecal pathogens. There is limited information available on the removal of pathogens from septic tanks and the faecal pathogen loads with septic tanks and Anaerobic Baffled Reactor (ABR). Detecting disease causing pathogens from environmental sources is also challenging and expensive [2]. To generate evidence, we conducted a cross-sectional study to explore pathogen loads from commonly used onsite sanitation systems (i.e., septic tank, ABR) and nearby drains and waterways in urban neighbourhoods of Dhaka.

**Methods:** We collected samples of drain water (400mL grab and 20L for ultrafiltration), drain sediment, canal water (400mL grab and 20L for ultrafiltration) and floodwater (400mL grab and 20L for ultrafiltration) from April-October 2019. Sludge, supernatant, and effluent samples were

also collected from septic tanks and anaerobic baffled reactor (ABR). We investigated the presence and concentration of *E. coli* [most probable number (MPN) using the IDEXX- Quantitray® 2000 technique with Colilert-24 media] [1,2] and selected enteric pathogens (*Shigella*, *Vibrio cholerae* (*V. cholerae*), *Salmonella* Typhi (S. Typhi), Norovirus Genogroup-II (NoV-GII), and *Giardia*) and presence of *Cryptosporidium* in these samples using quantitative polymerase chain reaction (qPCR). The equivalent genome copies (EGC) of individual pathogen were estimated in each sample by interpolation of the mean Ct value to the corresponding standard curve and the dilution factor for each sample type. Absolute quantification was expressed as  $\log_{10}$  EGC per 100mL for the water samples and  $\log_{10}$  EGC per gram for the sediment samples.

**Results and discussion:** All environmental samples (100%) were highly contaminated with *E. coli*. The highest *E. coli* concentrations were detected in canal ultrafiltration samples [ $8.79 \log_{10}$  MPN/100mL] and lowest detected in flood grab samples [ $5.23 \log_{10}$  MPN/100mL]. The concentration of *E. coli* was significantly higher in ABR samples compared to septic tanks [ $\log_{10}$  mean difference ABR minus septic tank samples for sludge=1.91 (95% CI: 1.19-2.65), supernatant=2.04 (95% CI: 1.54-2.54) and effluent=1.12 (95% CI: 0.39-1.86)], which may be due to significant overloading of the ABR systems. For pathogen analysis, the fieldworkers collected 40 grab samples, 37 ultrafiltration samples, 40 septic tank and 22 ABR samples. Among all samples tested (N=150), about 89% were contaminated with *Shigella*, 68% with *V. cholerae* and NoV-GII, 31% with *Giardia*, 17% with S. Typhi and 6% with *Cryptosporidium*. A wide range of concentration of pathogens [range: mean  $\log_{10}$  concentration of *Giardia*=0.74 EGC/100 mL in drain ultrafiltration samples to mean  $\log_{10}$  concentration of NoV-GII and *Giardia*=7.11 EGC/100mL in ABR sludge] was found in all environmental samples. Highest pathogen concentrations were detected in open drains [range: mean  $\log_{10}$  concentration=2.50-4.94 EGC/100mL], septic tank effluent [range: mean  $\log_{10}$  concentration=3.32-4.65 EGC/100mL] and ABR effluent [range: mean  $\log_{10}$  concentration=2.72-5.13 EGC/100mL].

**Conclusions and Implications:** In Dhaka, Bangladesh, we detected high frequency and concentrations of *V.cholerae*, *S.Typhi* and NoV-GII in effluent from community-scale ABRs and septic-tanks which subsequently entered open drains and waterways and may present a risk of exposure to children and adults in this and/or downstream communities. Given what is known about the infectivity of five target pathogens we examined, the concentrations of these pathogens detected in the environmental samples are of significant concern and raise questions about appropriate implementation of on-site sanitation systems in dense urban areas. Revised approaches to select and implement appropriate on-site sanitation technologies should take into account low-pathogen removal and potential exposure pathways through drains, groundwater, and surface water [4]. In addition, increased focus on appropriate management and maintenance of sanitation systems and appropriate behaviour change messages both for the community and implementers are crucial. Future studies should assess changes in pathogen exposure associated with specific sanitation interventions and consider the health-impacts of environmental contamination among high-income and low-income communities in Dhaka city. Further studies and guidance are needed to improve urban planning, current septic-tank and ABR design criteria, and operation and maintenance practices, to achieve safe and sustainable sanitation services [5].

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