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RESEARCH ARTICLE

Rainwater harvesting in American Samoa: current practices and indicative health risks

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Abstract Roof-harvested rainwater (RHRW) is an important alternative source of water that many island communities can use for drinking and other domestic purposes when groundwater and/or surface water sources are contaminated, limited, or simply not available. The aim of this pilot-scale study was to investigate current RHRW practices in American Samoa (AS) and to evaluate and compare the quality of water from common potable water sources including RHRW stored in tanks, untreated stream water, untreated municipal well water, and treated municipal tap water samples. Samples were analyzed using culture-based methods, quantitative polymerase chain reaction (qPCR), and 16S amplicon sequencing-based methods. Based on indicator bacteria (total coliform and *Escherichia coli*) concentrations, the quality of RHRW was slightly lower than well and chlorinated tap water but exceeded that of untreated stream water. Although no *Giardia* or *Leptospira* spp. were detected in any of the RHRW samples, 86% of the samples were positive for *Cryptosporidium* spp. All stream water samples tested positive for *Cryptosporidium* spp. Opportunistic pathogens (*Pseudomonas aeruginosa* and *Mycobacterium intracellulare*) were also detected in the RHRW samples (71 and 21% positive samples, respectively). Several potentially pathogenic genera of bacteria were also detected in RHRW by amplicon sequencing. Each RHRW system was characterized by distinct microbial communities, 77% of operational taxonomic units (OTUs) were detected only in a single tank, and no OTU was shared by all the tanks. Risk of water-borne illness increased in the following order: chlorinated tap water/well water < RHRW < stream water. Frequent detection of opportunistic pathogens indicates that RHRW should be treated before use. Stakeholder education on RHRW system design options as well as on importance of regular cleaning and proper management techniques could improve the quality of the RHRW in AS.

Keywords Roof-harvested rainwater · Drinking water quality · Fecal indicator bacteria · Opportunistic pathogens · Microbial communities · Water resources

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Introduction

The demand for clean freshwater is outstripping surface and groundwater supplies worldwide. Potable water resources have diminished globally due to climate change and population growth (IPCC 2014). Even in areas of the world that

appear to have an adequate water supply, there is still a need to balance existing water supplies with ever growing demands and to augment current supplies through the use of more climate-resilient technologies (WHO 2011).

Island ecosystems have low buffering capacities and are therefore highly vulnerable to climate change and natural disasters. Extreme weather events, such as droughts and storms, appear to be increasing in frequency, and even greater extremes of climate are expected (WHO 2011). Sea level rise and related saltwater intrusion of groundwater are further compromising the sustainability of water resources (Unsal et al. 2014). These changes compromise drinking water as well as food security on Pacific Islands; ergo, a more responsive, resilient approach to water resource management is required to address these challenges.

Roof-harvested rainwater (RHRW) is an important alternative source of water that many island communities can use for drinking and other domestic purposes when groundwater and/or surface water sources are contaminated, limited, or simply not available. Since 1964, the US Virgin Islands has required most buildings to be constructed with a self-sustaining potable water system, such as a well or RHRW collection system (VIC 2016). It is estimated that roughly 30,000–60,000 people in Hawaii rely on RHRW (Macomber 2010). Governments across the world are beginning to introduce policies to promote the increased utilization of rainwater (Ahmed et al. 2014; Lye 2002). For example, in some areas of Australia, rainwater harvesting systems are mandated in all new buildings to alleviate pressure on the main water grid and provide an alternative water source in times of shortage and emergency (Mankad and Greenhill 2014).

The majority of the population in the US Territory of American Samoa (AS) is supplied with chlorinated drinking water obtained from groundwater sources by the AS Power Authority (Minshew et al. 2007). Many households also utilize stream water, often referred as village water, which is delivered to homes with a network of pipes and hoses. While many freshwater sources are available to American Samoans, just 28% of residents believe that their water is safe to drink, ranking lowest among six central Pacific Islands (Northern Mariana Islands, Republic of Marshall Islands, Guam, Palau, Federated States of Micronesia, and American Samoa) (CSREES 2005). Since 2009, a boil water notice has been issued for most parts of AS advising the population to boil municipal tap water due to the frequent detection of fecal indicator bacteria in the drinking water system (ASPA 2015). Furthermore, a significant amount of electricity, most of which is derived from imported fossil fuels, is used to pump, treat, and distribute drinking water (EIA 2016). Considering the current water quality issues and costs associated with drinking water delivery as well as maintenance of the current system, there is a need and an opportunity to explore more sustainable low-cost and low-energy alternatives.

As on many islands in the central Pacific region, AS receives generous amounts of rainfall; hence, RHRW has a high potential for augmenting the current water supply in the territory. Although rainwater in AS is plentiful (ranging 1780–5080 mm/year (Izuka et al. 2007)), rainwater harvesting and utilization for households use is limited. Roughly 5.3% of households supplement public or village water supply with RHRW, and only 1.1% of households rely solely on RHRW (Anon 2000; Crossett et al. 2008). The proportion of households utilizing RHRW as drinking water appears to be unknown. More extensive utilization of low-cost, low-energy RHRW systems would enhance the sustainability of AS by reducing pressure on the compromised central water network, limiting stormwater runoff and related environmental degradation, and increasing disaster readiness.

Well-designed and maintained RHRW systems can produce safe drinking water, while improperly designed and/or maintained systems can pose health risks (Abbott et al. 2007; Ahmed et al. 2011; Ahmed et al. 2017; Dobrowsky et al. 2014; Fujioka et al. 1991; Gwenzi et al. 2015; Hamilton et al. 2016; Kim and Han 2015; Kim et al. 2016; Lye 2009). Private RHRW systems are not regulated by state or federal guidelines in the USA and its territories; ergo, individual households rely on their own expertise when utilizing these catchments (Fujioka 1993). Systems can be poorly constructed and maintained (Abbott et al. 2007; Fujioka and Chinn 1987), and typically, the water is never tested for microbial and chemical contaminants. This is a concern as both microbial and chemical contaminants may compromise the quality of RHRW and pose a health risk if the water is consumed without a treatment (Simmons et al. 2001; Stewart et al. 2016).

While drinking water quality in AS is evaluated based on indicator bacteria, total coliform and fecal coliform bacteria or *Escherichia coli*, any of which should not be recurring in 100 ml water sample (ASEPA 2008), it is pathogenic microorganisms that cause illness. Opportunistic pathogens, which usually cause illness when the immune system is compromised, are an emerging concern as these pathogens are frequently detected in rainwater storage tanks (Ahmed et al. 2014; Ahmed et al. 2011; Dobrowsky et al. 2014; Hamilton et al. 2016), and the number of immunocompromised individuals is on rise worldwide (de Graaf et al. 2016; Gerba et al. 1996). To assess the health risk associated with microbial contaminants, this pilot study evaluated the microbial quality of RHRW collected in AS based on indicator bacteria, selected pathogens including those that are opportunistic in nature. Also, other potable water sources utilized in AS (untreated stream water, untreated municipal well water, and treated tap water) were tested and compared.

Materials and methods

Survey and sample collection

Overall, 14 RWRH catchments were examined in 2016 over a limited 3-day period available for a visit (Fig. 1a), all of which used harvested water for drinking among other household

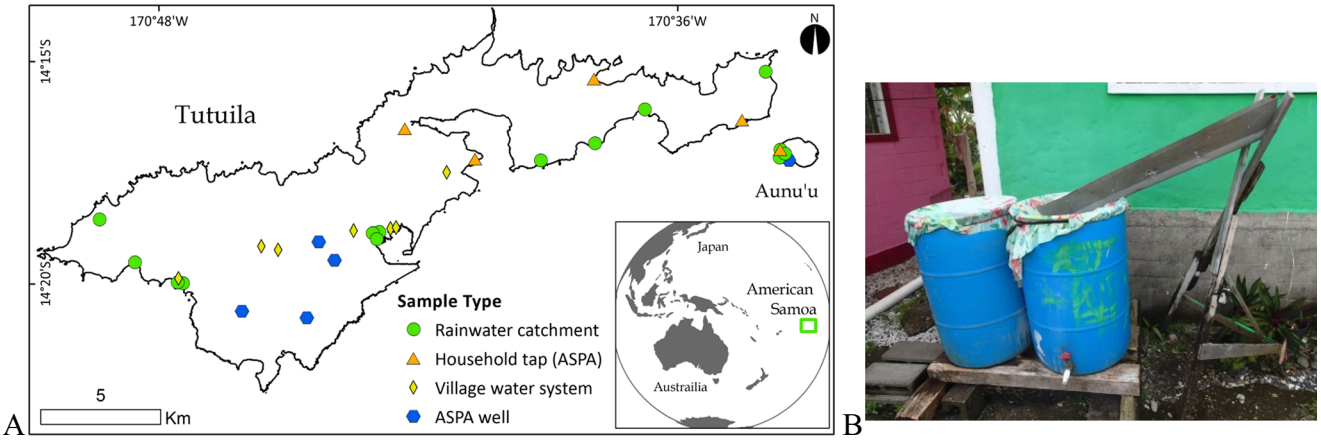

Fig. 1 Locations of the sampling sites (**a**) and a typical RHRW catchment in American Samoa (**b**)

uses. Eleven of the samples were collected on Tutuila Island (villages of Amaluia, Amanave, Avaio, Faga itua, Fagali i, Lauli i, Nu uuli, and Tula), and three samples were collected on the nearby islet Aunu u (village of Aunu u). A series of questions (Online Resource Table SI.pdf) was asked from an adult representative of each household by a native interpreter fluent in English and Samoan. Each catchment was photographed.

In addition, municipal tap water (n = 5), untreated well water (n = 5), and village (stream) water (n = 7) samples were collected. Note that the village (stream) water samples were collected from the taps within homes except for one, which was collected directly from the stream at the intake pipe. At each sampling site, separate 100 ml and a 1 l water samples were collected using sterilized plastic containers and cooled for transport to the laboratory at the American Samoa Community College (ASCC) for microbiological analyses. The time from sample collection to analysis did not exceed more than 6 h.

Analyses of indicator bacteria

In the ASCC laboratory, concentrations of total coliform bacteria and *E. coli* were determined in 100 ml sample aliquots using the Colilert®-18 Kit and Quanti-Tray®/2000 (IDEXX Laboratories Inc., Westbrook, ME) according to the manufacturer's protocol.

DNA extraction

In the ASCC laboratory, two sets of filters were obtained by filtering 500 ml of sample water through sterile hydrophilic polyethersulfone membrane filters (Supor®200, 0.2-μm pore size; Pall Corp., Ann Arbor, MI), except for stream water samples where filtration volume was 300 ml. Both sets of filters were transferred to PowerBead tubes from the PowerSoil® DNA Isolation Kit (MO BIO Laboratories Inc., Carlsbad, CA) submerged in a buffer and shipped to Water Resources Research Center's laboratory in Hawaii, where DNA was extracted using the PowerSoil® DNA Isolation Kit (MO BIO Laboratories Inc., Carlsbad, CA) according to the manufacturer's protocol, except that we incorporated 2 min of bead beating at maximum speed (3450 strokes/min) on a Mini Beadbeater™ (Biospec Products Inc., Bartlesville, OK) instead of the recommended vortexing for 10 min. All DNA samples were obtained using a final 100-μl elution buffer step.

Pathogen and avian GFD marker analyses

The DNA extracted from one set of filters was tested for selected human pathogens (*Cryptosporidium* and *Giardia* spp.), including opportunistic pathogens (*Pseudomonas aeruginosa* and *Mycobacterium intracellulare*), and for an avian-specific GFD marker, which is indicative of fecal contamination by birds. Concentrations of *Cryptosporidium* spp. (18S ribosomal ribonucleic acid (rRNA) gene), *Giardia* (giardin gene), *P. aeruginosa* (*regA* gene), *M. intracellulare* (16S rRNA gene), and GFD marker of unclassified *Helicobacter* spp. were determined by quantitative polymerase chain reaction (qPCR) as described in earlier studies (Ahmed et al. 2014; Ahmed et al. 2012; Green et al. 2012; Hamilton et al. 2016). The samples containing PCR inhibitors were determined by challenging PCR reactions containing equal concentrations of salmon testes DNA as exogenous control (Sigma-Aldrich, St. Louis, MO) with 5 μl of an unknown sample as described in an earlier study (Haugland et al. 2005). The samples did not need to be diluted to neutralize potential PCR inhibitors as the PCR threshold cycle (C_t) values determined for each sample seeded with this exogenous control did not exceed three standard deviations of the C_t determined for the seeded molecular grade water. The DNA extracted from the second set of filters was used to determine the concentrations of pathogenic *Leptospira* by qPCR assay (Ferreira et al. 2014). This assay

targets the *lipL32* gene, which is highly conserved among pathogenic *Leptospira* species (Haake et al. 2000). The limit of detection (LOD) for all the qPCR tests was 6.7 or 11 gene copies per 100 ml depending from the initial volume used for filtration (500 or 300 ml, respectively).

515F/806R amplicon sequencing

The DNA extracted from the second set of filters was also used to determine microbial community composition (Caporaso et al. 2011). Briefly, the variable V4 region of the 16S rRNA gene was amplified using primers 515F and 806R, both containing sequencing platform-specific (Illumina) adapter sequences. Primer 806R also contained specific 12-bp-sized bar codes to facilitate multiplexing of samples in a single sequencing run. Triplicate 25 μl PCR reactions for each sample contained 2 μl of DNA template, 0.5 μl of each forward and bar-coded reverse primer (1 mM final concentration), 10 μl 2.5× Prime HotMasterMix (5 Prime, Hamburg, Germany) (1× final concentration), and 12 μl of UltraClean PCR water (MO BIO Laboratories Inc., Carlsbad, CA). A negative control, containing no DNA template, was tested in parallel for each sample. After initial denaturation for 2 min at 94 °C, the reactions were cycled for 35 cycles (94 °C for 45 s, 50 °C for 30 s, and 65 °C for 90 s) on CFX 96 (Bio-Rad Laboratories Inc., Hercules, CA), followed by the final extension at 65 °C for 10 min. Triplicate PCR reactions were pooled, cleaned using a UltraClean® PCR Clean-Up Kit (MO BIO Laboratories Inc., Carlsbad, CA), visually examined on 2% agarose gel, and quantified using a Qubit® dsDNA HS Assay Kit (Life Technologies, Grand Island, NY) according to the manufacturer's protocols. All samples were pooled at equimolar ratio into a single DNA library and purified on 2% agarose gel using Wizard® VS Gel and PCR Clean-Up Kit (Promega, Madison, WI). The purified library was sequenced on a MiSeq sequencer (Illumina, San Diego, CA) using V3 chemistry at the Genetics Core Facility at the Hawaii Institute of Marine Biology (University of Hawaii). Demultiplexed sequences were filtered to remove low-quality reads and clustered to operational taxonomic units (OTUs) at 97% identity using CD_HIT-OUT (Li et al. 2012). Cluster sequences were aligned and compared to the reference database SSU Ref NR 119 (http://www.arb-silva.de/projects/ssu-ref-nr/) using the SINA aligner (Pruesse et al. 2012). A Python script, developed in-house, was used to generate diversity-abundance matrices of all identified OTUs for the analyses. Vegan software package (Oksanen et al. 2016) in R (R Core Team 2016) was used to evaluate alpha rarefaction (Online Resource Fig. S1.pdf).

Results and discussion

A survey of the RHRW practices in AS

The typical RHRW catchment in AS is simple (Fig. 1b). In most cases, catchments consist of a gutter, which directs rainwater from a roof into a repurposed 200-l plastic drum. Only three of the containers examined exceeded a 1000-l capacity, and only a single container was made from metal (Online Resource Table SI.pdf). Almost all the containers surveyed (79%) were covered with cloth, which was kept in place by a rope or a rubber band, while the larger containers (21%) had mosquito screens at the inlet. All of the 14 houses had roofs from unpainted corrugated steel panels, except one that had the steel panels painted. None of the systems had any first-flush diverters, nor was the water treated by filtration, UV light, or chemical disinfection before use. Four households (29%) reported regularly or occasionally boiling harvested rainwater before drinking, while the rest of the households did drink the harvested rainwater without any prior treatment. While the larger tanks (>1000 l) had spigots installed, only 3 out of 11 smaller systems had a spigot installed; hence, most of the users of smaller systems used a jug or cup to scoop rainwater directly from the barrel. Frequently, this involved direct hand-to-water or hand-to-jug-to-water contact. Typically, containers were cleaned from <1 to 8 times a month. Many households reported that containers are cleaned once the water level is low. Therefore, simple technical improvements, such as installation of a spigot or first flush diversion, would likely improve RHRW quality in AS. Stakeholder education, which should cover system design as well as the importance of proper regular system maintenance and utilization techniques, is needed.

Although chlorinated water was available through the centralized system to most of the households utilizing RHRW catchments, the rainwater was preferred by 80% of households over the chlorinated tap water due to poor taste and high costs associated with the latter. None of the surveyed RHRW catchments had previously been tested for microbial or chemical water quality. While chemical contaminants, such as lead, zinc, copper, and others typically attributed to the input from catchment components, is a concern, this paper focuses on health risks associated with microbial contaminants.

Microbial water quality

Indicator bacteria

The majority of the RHRW samples were not suitable for potable use as all samples were positive for total coliforms and 60% of collected samples were positive for *E. coli* and, therefore, violated AS water quality standards (<1 CFU of total coliforms/100 ml and <1 CFU of fecal coliforms or

E. coli/100 ml). Concentrations of total coliforms ranged over three orders of magnitude and frequently exceeded the upper quantification limit of the test (2420 MPN/100 ml), while *E. coli* concentrations were relatively low, reaching a maximum of 20 MPN/100 ml (Table 1). Percentages of positive samples and concentrations of both indicator bacteria were comparable to concentrations observed in the RHRWs elsewhere in tropical and subtropical regions (Ahmed et al. 2012; Fujioka et al. 1991; Levesque et al. 2008). The microbial quality of RHRW was slightly inferior when compared to the collected well and chlorinated tap water but exceeded the quality of the untreated stream water (Table 1). Presence of both *E. coli* and total coliforms in RHRW, untreated well water, and water from the treated tap water is not unexpected, as both types of bacteria grow in moist tropical and subtropical environments and do not necessarily indicate sewage contamination (Fujioka and Byappanahalli 2003; Hardina and Fujioka 1991). Therefore, use of alternative RHRW quality indicator organisms has been advocated (Rijal and Fujioka 1995). Nevertheless, presence of these indicator bacteria indicates that microbial contaminants from some sources do reach the system, and treatment is warranted.

Sources of indicator bacteria-avian GFD marker

Indicator bacteria in the RHRW can originate from various animals, which have access to rooftops. While birds are the most likely source of indicator bacteria as they have easy access to rooftops, no avian GFD markers were detected in any of the RHRW samples. Other sources such as bats, rodents, lizards, and other organisms as well as soils, adjacent vegetation, and humans themselves can all contribute indicator bacteria into the RHRW. It is also possible that the GFD marker tested in this study is not frequent or not present in birds in AS region. The marker was also not detected in any of the stream, well, or chlorinated tap water samples.

Pathogens in rainwater

Because indicator bacteria can grow in extra-enteric environments, and therefore do not necessarily represent risk from fecal contaminants, RHRW was evaluated for selected pathogens. Although no *Giardia* spp. or *Leptospira* spp. were detected in any of the RHRW samples, 86% of samples were positive for *Cryptosporidium* spp. Concentrations of *Cryptosporidium* spp. varied from below level of detection up to 500 gene copies/100 ml (geometric mean 107 gene copies/100 ml), which translates to roughly 5.35 *Cryptosporidium* spp. oocycts/100 ml (as there are 20 copies per oocyst; Jothikumar et al. 2008). The percentage of *Cryptosporidium* spp. positive samples in RHRW systems was elevated compared to those found in other studies conducted in Australia, Denmark, New Zealand, and the US Virgin Islands (Ahmed et al. 2010; Ahmed et al. 2012; Albrechtsen 2002; Crabtree et al. 1996; Simmons et al. 2001). All stream water samples tested positive for *Cryptosporidium* spp. While resistance of *Cryptosporidium* oocycts to different water disinfection techniques such as chlorination or ozonation is known (Chauret et al. 2001; Peeters et al. 1989), it is concerning that this potential pathogen was also detected in one of the chlorinated tap water samples. *Cryptosporidium* ssp. is shed in the excreta of birds, rodents, lizards, and other animals (Ahmed et al. 2014; Casemore 1990). It remains unclear which of the sources contributed to the high prevalence in Samoan RHRW. It has to be noted that there are over 20 valid species of *Cryptosporidium* but not all of them are pathogenic to humans (Smith and Nichols 2010; Staggs et al. 2013). In humans, the main causes of disease are *C. parvum* and *C. hominis* (Fayer 2010; Xiao 2010). *C. canis*, *C. felis*, *C. meleagridis*, and *C. muris* can also cause disease in humans (Fayer 2010; Xiao 2010).

Opportunistic human pathogens (*P. aeruginosa* and *M. intracellulare*) were also detected in the RHRW samples, although at lower frequency than in tap water samples. *P. aeruginosa* concentrations varied from below level of detection to 1540 gene copies/100 ml (geometric mean 540 gene copies/100 ml), and *M. intracellulare* was detected in a single sample (157 gene copies/100 ml). *P. aeruginosa* was detected frequently in stream water samples as well, but only a single tap and well water sample was positive (Table 2). *M. intracellulare* was more frequently detected in stream water when compared to RHRW. As *P. aeruginosa*, it was detected only in a single tap and well water sample. Frequent detection of pathogens including opportunistic pathogens

Table 1 Geometric mean of indicator bacteria concentrations and range (in parenthesis) in different water samples collected in American Samoa

Sample type	Number of samples	Total coliforms		*E. coli*	
		% positive	(MPN 100 ml^{-1})	% positive	(MPN 100 ml^{-1})
Treated tap water (ASPA)	5	60	27 (<1–1300)	40	2 (<1–6)
Groundwater well (ASPA)	5	60	5 (<1–59)	40	2 (<1–8)
Rainwater (RHRW)	14	100	259 (43–>2420)	64	2 (<1–20)
Stream water	7	100	574 (60–>2420)	100	57 (1–792)

Percentage of positive samples is also indicated

Table 2 Distribution of selected pathogens (*Cryptosporidium* spp., *Giardia* spp., *Leptospira* spp.) and opportunistic human pathogens (*P. aeruginosa*, *M. intracellulare*) in different types of water samples collected in AS

Water sources	No. of samples	*Cryptosporidium* spp.	*Giardia* spp.	*Leptospira* spp.	*P. aeruginosa*	*M. intracellulare*
Treated tap water (ASPA)	4	25	0	0	25	25
Groundwater well (ASPA)	5	0	0	0	20	20
Rainwater (RHRW)	14	86	0	0	71	21
Stream water	7	100	0	0	71	57

Percent of positive samples is indicated

indicates that RHRW in AS should be treated before it is used for drinking or other household purposes. Based on the microorganisms studied, risk of water-borne illness increases in the following order: well/tap water < RHRW < stream water.

515F/806R amplicon sequencing

Our sequencing effort of RHRW samples yielded 1780,331 sequences, which were assigned to 356 OTUs. The majority of the OTUs clustered within Bacteroidetes and Alphaproteobacteria and Betaproteobacteria (Fig. 2). OTUs belonging to families of Commamonadaceae and Chitinophagaceae, which include many common soil bacteria, were dominant in the RHRW systems (Table 3). Several potential opportunistic pathogenic genera were detected in the rainwater samples, which are *Pseudomonas* (29% of samples), *Acinetobacter* (21% of samples), *Sphingomonas* (21% of samples), *Legionella* (14% of samples), *Brevundimonas* (7% of samples), *Burkholderia* (7% of samples), *Enterococcus* (7% of samples), *Mycobacterium* (7% of samples), and *Staphylococcus* (7% of samples). Several of those genera (*Acinetobacter*, *Burkholderia*, *Legionella*, *Mycobacterium*, *Pseudomonas*, and *Staphylococcus*) have also been detected in the RHRW in Australia (Ahmed et al. 2017) using similar sequencing-based techniques. The taxonomic resolution of the current partial 16S RNA amplicon sequencing is not sufficient to identify pathogens as it rarely provides resolution below the genus level. Nevertheless, our data indicate that some potentially pathogenic taxa were present, further emphasizing the need to treat RHRW. Various sources contribute microbial contaminants into RHRW. While the dominant bacterial families were identical in all rainwater samples, no OTU was present in all the catchments and 77% of the OTUs were detected in only a single RHRW catchment. This indicates that each RHRW catchment harbors distinct microbial communities.

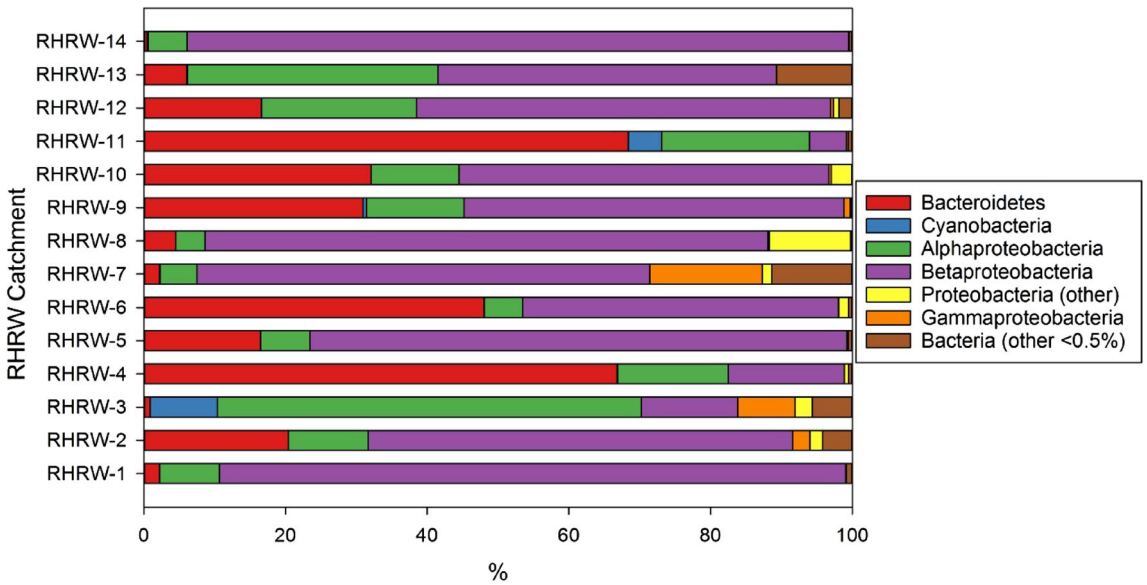

Fig. 2 Dominant groups of bacteria in the RHRW catchments at the phylum level. Sequences of *Proteobacteria* are represented at class rank, and sequences that could not be assigned to any of the classes of *Proteobacteria* are grouped as *Proteobacteria* (other). Groups that represent less than 0.5% of total sequences were combined into the *Bacteria* (other <0.5%) group. *X* axis represents the relative abundance of sequences in a given sample (*Y* axis) as percentage

Table 3 Top five most abundant OTUs in the RHWS in AS

Sequence accession number	Family	Genus	Number of sequences	Percentage of sequence (%)
JX133439	*Comamonadaceae*	Unassigned	558,637	32.1
FN984878	*Chitinophagaceae*	Unassigned	167,287	9.61
FJ936936	*Chitinophagaceae*	*Sediminibacterium*	146,494	8.42
JF113631	*Comamonadaceae*	Unassigned	108,213	6.22
HM314246	*Comamonadaceae*	Unassigned	88,640	5.09

Limitation of the study

This was a pilot-scale study. Although just a snapshot based on the 14 RHRW catchments, we believe that it provides a meaningful representation of the RHRW quality and indicates a need for further studies and stakeholder education. Also importantly, chemical hazards can be associated with RHRW but were not studied. Chemical contaminants, such as lead, zinc, copper, and others, can leach into harvested rainwater from the catchment components and pose a health risk (Mendez et al. 2011; Simmons et al. 2001; Stewart et al. 2016). The health effects of those chemicals may be manifested after years of consumption, and the toxicity of many chemical contaminants cannot be removed by simple filtration or boiling. Therefore, evaluation of chemical contaminants in the RHRW catchments in AS is warranted.

Conclusions

To our knowledge, this is the first study that investigated the microbiological quality of roof-harvested rainwater in AS. Currently, only a limited number of households in AS rely on rainwater collection. Current RHRW catchments in AS are not fitted with water quality improvement devices that are commonly used in other areas of the world such as first flush devices. However, feasible design changes, such as installation of spigots, as well as education of the tank/barrel owners on the importance of regular cleaning and proper management techniques would minimize health risks associated with the use of private RHRW catchments in AS. Based on the microorganisms studied, risk of water-borne illness increases in the following order: chlorinated tap water/well water < RHRW < stream water. While broader utilization of RHRW in AS is warranted, frequent detection of potential pathogens in harvested rainwater indicates that it needs to be treated before it can be used for drinking or other household purposes. More comprehensive evaluation of microbial as well as chemical contaminants in the RHRW catchments and surveillance of the population for waterborne illnesses in AS is warranted.

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Compliance with ethical standards

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Conflict of interest The authors declare that there is no conflict of interest.

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