Assessment of tap water quality in mobile homes in the Eastern Coachella Valley, California

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Abstract

Very few studies have been undertaken on water quality from mobile homes, with most information coming from press and policy reports suggesting that people living in mobile homes in the US have poor water quality. Our goal was to evaluate resident exposure to microbes at the point of use of tap water sourced from the Oasis Mobile Homes Park (OMHP), using physico-chemical parameters, concentrations of target cultivatable microbes, and quantitative polymerase chain reaction (qPCR) analyses. In this study, we sampled 15 mobile homes (MHs) and found arsenic concentrations to be 4–8 times above the acceptable EPA standard of 10 ppm. Our qPCR demonstrated high concentrations of gene targets for \textit{Salmonella} spp., \textit{L. monocytogenes}, \textit{P. aeruginosa}, \textit{C. jejuni}, \textit{E. faecalis}, and \textit{E. coli} in one or more of our sampled mobile homes. Except for MH4, which had the highest concentration of \textit{L. monocytogenes} and \textit{E. faecalis}, all MHs had different predominant microorganisms. Based on the physico-chemical parameters and our microbiological analysis, we conclude that drinking water from MH taps in the OMHP is unsafe for consumption.

1. Introduction

The United Nations (UN) has achieved considerable progresses in providing access to safer water, sanitation, and hygiene for most groups of people around the world [1]. In 2017, approximately 89.6% of the global population was estimated to have access to safe drinking water, and 73.5% to have access to basic sanitation [2]. However, despite significant achievements towards the UN Sustainable Development Goal 6 (to ensure access to clean drinking water and sanitation for all) [1], approximately 9 million people globally still lacked access to piped water in 2017, while 8.4 million more lacked access to basic sanitation, even in high-income countries [2]. Although drinking water contamination and deaths due to water borne diseases are mostly reported in low and middle income countries (LMICs) [3–5] some high-income countries (HICs) also experience issues of drinking water contamination. In New
Zealand, for example, a study of drinking water in campgrounds found *E. coli* and *Campylobacter jejuni* in more than 50% of samples [6]. A study in Canada [7] reported approximately 20% of the 600 First Nations’ reserves were under drinking water advisories, often due to unacceptable levels of bacteria. In the US, the well-publicized drinking water contamination in Flint, Michigan that exposed the community of Flint to lead and pathogenic bacteria in 2014 [8] is a reminder that HICs also suffer drinking water contamination, despite the commitment of HICs to provide access to safe drinking water. Water contamination with pathogenic microorganisms is a serious threat to human health, and may constitute a violation of the human right to access potable water [9]. The World Health Organization (WHO) estimated that approximately 829,000 people die each year globally from the consumption of unsafe drinking water, killing approximately 297,000 children under the age of five [4]. Similarly, the problem of poor water quality and unsafe waste management has continued among low-income communities in LMICs, as demonstrated among indigenous Canadian residents living on native reserves [10], or communities in the US living in mobile homes (MHs) [11]. In the US, water quality and sanitation inequality have been demonstrated in MHs [12, 13].

Mobile homes are considered affordable housing alternatives to traditional housing [14]. Mobile and manufactured homes are options that typically are of lower cost compared to buying a traditional wood-framed single-family dwelling. In the US, it is estimated that approximately 22 million people live in MHs [MHI 15], and that 56% of MH owners have lived in MHs for more than 10 years. In 2020, the State of Texas was reported to have the highest number of MHs in the United States, followed by Florida and Louisiana [16].

In California, there are approximately 4,800 mobile home parks (MHPs) [17] with more than 1 million MH residents that live in areas zoned for commercial or industrial purposes [11]. Nevertheless, MHs installed on native tribal lands are not governed by state laws or regulations, and problems arising between landlords and tenants, or which are due to park mismanagement, must be resolved in Federal Courts [18]. An article in the popular press [13] found MHPs more likely to have substandard drinking water quality, and more likely to incur health-related violations, with service shutoffs at higher rates than traditional housing.

An example of a MHP in California subject to water problems is the Oasis Mobile Home Park (OMHP) in the Eastern Coachella Valley (ECV). Due to past contamination with arsenic [19], and water odor and color changes, OMHP community members distrust their tap water and instead rely on bottled water and water from vending machines. However, Hile, Dunbar & Sinclair (2020) [20] demonstrated water vending machines (WVMs) in the community were also contaminated with pathogenic microorganisms. Moreover, there is a scarcity of published research on drinking water contamination in MHs [21]. Most issues in MHs are reported in grey literature sources, such as newspapers and reports by non-profit advocacy groups. To the best of our knowledge, there are no scientific publications on water quality and microbial contamination of tap water from the OMHP region.

Our study sought to determine the quality of tap water from the OMHP and its safety for consumption in relation to OMHP resident health concerns. We investigated whether water from the OMHP met the requirements of water quality based on US standards and hypothesized that water from the OMHP was contaminated with microbes due to open septic tanks found in proximity to tap water pipes. We also hypothesized that arsenic remains a problem in the OMHP due to its prevalence in the Oasis area. Our goal was to evaluate resident exposure to microbes at the point of use of tap water sourced from the OMHP, using physico-chemical parameters, concentrations of target cultivatable microbes, and quantitative polymerase chain reaction (qPCR) analyses.
2. Materials and methods

2.1. Study site

The present study was carried out in the Eastern Coachella Valley (ECV), a desert area situated in southern California (33°7′N116.2′W). It extends southeast into Riverside County for approximately 72.4 km, from the San Bernardino Mountains to the northern shore of the Salton Sea. It is limited on the West by the San Jacinto mountains and the Santa Rosa Mountains, and on the North and East by the Little San Bernardino Mountains (Fig 1). The ECV is made up of the four unincorporated rural communities of Thermal, Oasis, Mecca, and North Shore. These communities are populated by Latino service industry and agricultural-worker families that contribute approximately 430 million dollars per annum to the Gross Domestic Product of the USA [22]. The OMHP in the ECV, Riverside County, California is mostly located on allotted land owned by a tribal member of the Torres Martinez Desert Cahuilla Indians, while the remainder of the park is on free land within the Torres Martinez reservation [23]. The community of the OMHP is made up of approximately 1,900 people, most of whom are LMIC immigrants, and agricultural workers [22].

2.2. Sample collection

Prior to sampling, our collaborators at the Leadership Counsel for Justice and Accountability (LCJA) in Coachella Valley contacted OMHP residents to obtain consent for water sampling in their homes. Sampling dates and times were based on resident availability.

In the laboratory, prior to sampling, we sterilized sampling bottles (1L glass bottles) by washing them with soap and bleach, rinsing with deionized water, then autoclaving at 121°C for 15 min and allowing them to cool to room temperature. We aseptically added 1 mg of sodium thiosulfate to each bottle to neutralize the chlorine (Cl2) in the sampled water, then added the screw-on bottle tops, ready for sampling.

The LCJA recruited participants in the Oasis Mobile Home Park through a list of residents that had contacted them for assistance in testing their drinking water, as well as for several other related issues over the previous five years. The LCJA decided on the sample number and locations because this sampling represented a good geographical spread of mobile homes throughout the park.

For arsenic samples, after sampling bottle sterilization as described above, we added hydrochloric acid (3 mL 6M HCl•L⁻¹ sample) as described by the U.S. Environmental Protection Agency (EPA) method 1632 [24]. In the field, verbal consent was collected from MH owners before water collection. Since our goal was to evaluate resident exposure to microbes at the point of use, rather than to test water from the well source to which all MHs are connected (Fig 1), we collected 2 L of water from OMHP MH taps without a prior flushing. The 2 L of water from each MH was from kitchen taps. An additional 1 L was collected for arsenic testing.

Each bottle was labelled with the house number, date, and sampling time. Collected water samples were immediately placed on ice in a cooler ready for transportation. We measured physico-chemical parameters onsite with three portable meters and kits. We used the HM digital TDS-4 meter (HM digital, Redondo Beach, California, USA) to measure total dissolved solids (TDS) in mg•L⁻¹ and electrical conductivity (EC) in μS•cm⁻¹. We measured temperature (°C) and pH using a portable Omega meter (Connecticut, USA), and free Cl₂ (mg•L⁻¹ Cl₂) using the HACH Pocket Colorimeter LR kit (HACH # 5870000) LR-0.02 to 2.00 mg/L method (Hach, Loveland, Colorado, USA) with a lower limit of 0.02. Instruments used for physico-chemical parameters were all calibrated in the laboratory prior to sampling according to manufacturer instructions. Arsenic was measured in the laboratory immediately upon arrival,
Fig 1. Map featuring California State, San Bernardino County, the Eastern Coachella Valley and the Oasis Mobile Home Park. MH3 and MH7 GPS locations were missing and consequently removed from the map [61]. U.S. Geological Service National Map. https://apps.nationalmap.gov/services/.
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approximately 4 hours after sampling. We prepared 100 mm plates for heterotrophic bacteria plate counts using BD™ Difco™ R2A Agar (Fisher Scientific, Ontario, California, USA) a day before sampling, according to the manufacturer’s recommendations. We discarded samples that were potentially contaminated as evidenced by a finger or spigot touching the inside of the bottle cap, or the mouth of the sampling bottle.

To test for arsenic in tap water from the OMHP, we used the Hach arsenic low-range test kit 280000 (Hach, Loveland, Colorado, USA). We confirmed our results by sending three of our samples to a third-party laboratory that used the USEPA ICP/MS Method 200.8 (Babcock Laboratory, Riverside, California, USA). In our laboratory, samples were processed within 24 hr of arrival and arsenic was tested according to the manufacturer’s recommendation [25].

2.3. Heterotrophic plate counts (HPCs)

To test for heterotrophic bacteria in our samples, 1 mL of water sample was diluted 1:10 with sterile PBS in 3 tubes. We then streaked 100 μL of sample on labelled R2A agar plates in duplicate and incubated them at 35˚C for 48 hrs. Colonies were counted afterward, and results expressed as colony-forming units per milliliter (CFU•mL⁻¹).

2.4. Coliforms / E. coli

We used the Colilert reagent test (IDEXX, Maine, USA) to detect and count total coliform and E. coli cells in water samples. We mixed 100 mL of water samples with Colilert reagent in a sterile 100 mL bottle that was later sealed and shaken thoroughly to mix. That solution was poured into a Quanti-Tray labelled with the sample identification number and sealed with the IDEXX Quanti-Tray Sealer. Quanti-Trays were incubated at 35˚C for 24 hr, and the presence of total coliform was confirmed by a yellow color in Quanti-Tray wells. We determined the presence of E. coli by fluorescence emitted when Quanti-Trays were exposed to long wave (365 nm) UV light.

2.5. Filtration

After physico-chemical and Quanti-Tray measurements, we assembled a Whatman vacuum filtration system (Ohio, Cleves, USA) to filter approximately 1,750 mL of water sample from each household visited through a 0.45 μm MF Millipore™ membrane (Millipore Sigma, USA). All glass funnels and filter frit were sterilized by bleaching, rinsing with deionized water, then autoclaving. We further sterilized the glassware using a benchtop U.V. sterilizer (Millipore, Sigma, USA) for approximately 5 minutes. After the vacuum and filter were assembled, each water sample was poured in and filtered. Each filter was aseptically removed after filtration and placed in a labelled sterile 50 mL microcentrifuge tube containing 10 μL of sterile PBS. A water bath sonicator was used for 5 min at 37˚C to remove bacteria from the filters. Samples were further centrifuged at 12,000 RPM for 5 min for DNA extraction.

2.6. In-house standard curves

The quantitative analyses from qPCR were completed by creating standard curves with the reference microbes. Tenfold serial dilutions of genomic DNA extracted from stock solutions were prepared. In this study, we used stock solutions of Salmonella typhimurium (ENVH Carolina 155351A), Listeria monocytogenes (ATCC 7644), Pseudomonas aeruginosa (ATCC 27853), Enterococcus faecalis (ATCC 29212), Campylobacter jejuni (ATCC 33291), and Escherichia coli (ATCC 25922). Selected microorganisms were enriched overnight as indicated in Table 1. We counted colonies and calculated the concentration of the original suspension in
CFU•mL⁻¹, from which DNA was simultaneously extracted for the standards. To estimate CFU•mL⁻¹, plate colonies were counted the next day and averaged to determine the original suspension. Suspensions were serially diluted 1:10 in PBS, and 100 μL of the last three dilutions were plated in duplicate on selective media, as indicated in Table 1, then incubated overnight at 35°C. In addition, 1.5 mL of the suspension was used for immediate DNA extraction. A 10-fold dilution series was then created from each template and assayed in duplicate using a SYBR Green I assay (Sigma-Aldrich, St. Louis, Missouri, USA). Regression lines from the dilution curve with R² > 0.95 were used to determine the concentration of unknown samples.

### 2.7. Ethics and IRB

Ethics were considered in the conduct of this study with regard to tap water sampling in MHs in the ECV. The Loma Linda University Institutional Review Board considered this study exempt from IRB review (approval number IRB# 5220100), because it did not obtain or receive private individually identifiable data and there was no intervention or interaction with community members.

### 2.8. DNA extraction

To extract DNA from environmental microorganisms, we used GenElute Bacterial Genomic DNA KIT (Sigma-Aldrich, Missouri, USA). For field samples, we used the modified gram-positive extraction procedure described by Sigma-Aldrich. After filtration and sonication, we centrifuged samples for 2 min at 12,000 RPM without the overnight enrichment step recommended by the manufacturer, to preserve original concentrations. Pelleted cells were resuspended in 200 mL of lysozyme solution and incubated for 30 min at 37°C. We then added 20 μL of Proteinase K solution to the sample, followed by 200 μL of lysis solution, then incubated at 55°C for 10 min after thorough vortexing. Columns were prepared by adding 500 μL of the column preparation solution to each pre-assembled GenElute Miniprep Binding Column and centrifuging for 1 min at 12,000 RPM. We then added 200 μL of 95% ethanol to the lysate and mixed thoroughly. The entire lysate was transferred into the binding column and centrifuged at 12,000 RPM for 1 min, after which the column was placed in a new collection tube and 500 μL of wash solution # 1 was added to the column and centrifuged for 1 min at 12,000 RPM. After discarding the eluate, we placed 500 μL of wash solution # 2 into the binding column and centrifuged for 3 min at 12,000 RPM. For DNA elution, we poured 200 μL of elution solution onto the column and allowed it to incubate for 5 min at room temperature then centrifuged it for 1 min at 8,000 × g. DNA concentration was estimated using a Nanodrop 1000 (Thermo-Scientific, Ramsey, Minnesota).

### Table 1. Culture base conditions for selected microorganisms used to generate the standard curves and their counts on respective media in CFU•mL⁻¹.

| Microorganism         | Enrichment media                                      | Agar plate                                      | Incubation parameters         | CFU•mL⁻¹  |
|-----------------------|-------------------------------------------------------|-------------------------------------------------|-------------------------------|-----------|
| Salmonella spp.       | Rappaport-Vassiladi Soya Peptide (RVS) broth (OXIOD)  | Salmonella shigella agar BBL                     | 35°C overnight aerobic        | 8.90E+07  |
| Listeria monocytogenes| Listeria enrichment broth (Alpha biosciences)         | PALCAM (Difco)                                  | 35°C overnight aerobic        | 1.55E+08  |
| Campylobacter jejuni  | Campylobacter enrichment broth (OXOID)                | Campylobacter blood-free selective agar base     | 35°C overnight Anaerobic chamber | 2.13E+07  |
| Pseudomonas aeruginosa| Heart Infusion broth (RPI)                            | Brain Heart Infusion Agar (RPI)                  | 35°C overnight aerobic        | 1.41E+08  |
| Enterococcus faecalis | Trypticase soy broth (BBL)                            | Tryptic soy agar (Difco)                        | 35°C overnight aerobic        | 1.60E+08  |
| E. coli               | Trypticase soy broth (BBL)                            | Tryptic soy agar (Difco)                        | 35°C overnight aerobic        | 8.60E+07  |

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2.9. Primer design

Primer sets used in this study were designed using the SILVA database [26]. We also cross-checked all primers in the literature, and list source references in Table 2. We selected primers based on annealing temperature, small amplicon size, and specificity to the selected microorganisms. Specificity of each primer was tested using Primer-Blast-NCBI [27].

2.10. Quantitative PCR

Quantitative PCR (qPCR) was performed using a C1000 Touch Thermal Cycler CFX 96 (Bio-Rad, Hercules, USA). Each 96-well plate reaction mixture (20 μL) contained 10 μL iTaq Universal SYBR Green Supermix (Bio-Rad, California), 7 μL Nanopure distilled water, 1 μL of forward primers, 1 μL of reverse primers, and 1 μL of the extracted sample’s genomic deoxyribonucleic acid (gDNA). In the 96-well plate set-up, we had positive control wells with gDNA from target microorganisms, negative controls with only de-ionized water, and a common mix without the sample gDNA as our no-template control (NTC). This NTC allowed quality control for contamination, and any plate with compromised NTCs were not used. The thermocycling program was 40 cycles at 95˚C for 3 min for the initial cycle, 95˚C for 10 s, and 55˚C for 30 s. All amplifications and standards were run on the same CFX 96 qPCR instrument.

3. Results

3.1. Physico-chemical parameters

The physico-chemical parameters analyzed in this study were limited to temperature, EC, TDS, pH, free chlorine, and arsenic. Results of all physico-chemical analyses are provided in Table 3. Most water samples from the OMHP had a pH lower than 7 and ranged from 6.2 for MH3 to 9.04 for MH12. We found EC in this study ranged from 0.3 to 2.4 μS•cm⁻¹ and were therefore well below the WHO guidelines [34]. Our study demonstrated that TDS in water samples collected from OMHP ranged from 146 mg•mL⁻¹ for MH9 to 1,225 mg•mL⁻¹ for MH6. Except for MH6, OMHP TDS were within WHO guidelines. Arsenic concentrations in this study varied, ranging from 50 ppm to 86 ppm. We had samples MH13–MH15 tested by an external, third-party laboratory which demonstrated arsenic ranging from 84 ppm to 86 ppm (see Fig 2). In this study, we found arsenic concentrations to be 4 to 8 times above the acceptable EPA standard of 10 ppm. We found that Cl₂ ranged from a maximum of 1.5 down

Table 2. Primer sets of selected microorganisms with their various amplicon size and justification references used in qPCR.

| Target microorganisms | Primer sets (5'-3') | Size | Justification |
|-----------------------|--------------------|------|--------------|
| Salmonella spp.       | F GGGGAAACGCTGGCTAATACC | 103  | [28]         |
|                       | R CCTCACCAACAAGCTAAATCC |      |              |
| Listeria monocyto genes | F GATGATCAAGCTAGATAGTTGG | 119  | [29]         |
|                       | R CTCAGACTGCCCCCTTCTTC |      |              |
| Campylobacter         | F CCGTATCACAATCGAGATACC | 93   | [30]         |
| Jejuni                | R TGTATCTCAGGGTGCCTTCC  |      |              |
| Pseudomonas           | F GACGAGCTTAAGGTTAGG    | 111  | [31]         |
|                       | R GCTTAATCAAGCTCGGAGATAG|      |              |
| Enterococcus          | F TGTGGTTAGCAACCCTCAAACC| 124  | [32]         |
| E. coli spp.          | R GTTCCCCTCGAAATTGGTG   |      |              |
|                       | F CTATGTGGTGTTGGGTAGGG  | 423  | [33]         |

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During sample collection, members of all households mentioned an intermittent strong Cl₂ smell. Three of the households had Cl₂ levels greater than 1.2 mg•L⁻¹. We also observed brown colored water coming from the sink tap of MH4 (S1 Fig) and two households had saved a 300 ml bottle of discolored yellow tap water to demonstrate the intermittent appearance.

### 3.2. Microbiological analysis

We present results from our microbial analyses in Table 4. We found 26% of samples had HPC above 500 CFU•mL⁻¹. HPCs ranged from $5.6 \times 10^3$ CFU•mL⁻¹ for MH11 to $1.1 \times 10^8$.

### Table 3. Physico-chemical parameters including temperature, electrical conductivity, total dissolved solids, pH, free chlorine, and arsenic measured from MHs of the OMHP in the ECV.

| Home ID | Temp ˚C | Conductivity µS.cm⁻¹ | TDS mg. L⁻¹ | pH | Free Chlorine mg. L⁻¹ | Arsenic ppb |
|---------|---------|----------------------|-------------|----|----------------------|------------|
| MH1     | 25.3    | 1.1                  | 509         | 7.2 | 0.1                  | 80         |
| MH2     | 28.6    | 0.8                  | 384         | 6.69| 0.91                 | 60         |
| MH3     | 29.8    | 0.8                  | 376         | 6.2 | 1.5                  | 60         |
| MH4     | 28.2    | 0.8                  | 788         | 6.7 | 0.9                  | 70         |
| MH5     | 29.7    | 0.8                  | 397         | 6.46| 1.21                 | 70         |
| MH6     | 28.8    | 2.4                  | 1225        | 6.97| 0.06                 | /          |
| MH7     | 27.5    | 0.8                  | 392         | 6.55| 1.24                 | /          |
| MH8     | 29.4    | 0.3                  | 147         | 7.86| 0.14                 | /          |
| MH9     | 31.1    | 0.3                  | 163         | 8.47| 0.18                 | /          |
| MH10    | 29.3    | 0.3                  | 147         | 8.73| 0.28                 | 50         |
| MH11    | 28.9    | 0.3                  | 146         | 8.9 | 0.13                 | /          |
| MH12    | 32.2    | 0.3                  | 148         | 9.04| 0.11                 | /          |
| MH13    | 23.3    | 0.3                  | 150         | 8.18| 0.28                 | 84         |
| MH14    | 29.8    | 0.8                  | 148         | 8.95| 0.4                  | 83         |
| MH15    | 29.5    | 0.3                  | 152         | 9   | 0.3                  | 86         |
| EPA     |         |                      | 6.5 to 8.5  | 0.02|                      | 10         |

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Fig 2. Arsenic concentrations in mobile homes of the Oasis Mobile Home Park. MH13, MH14, MH15, arsenic results from a third-party laboratory. The presence of arsenic in the Oasis Mobile Home Park was measured in some mobile homes. We had MH13, MH14, MH15 tested for arsenic at an external laboratory (a). MH6, MH7, MH8, MH9, MH11, MH12 were not measured.

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CFU•mL$^{-1}$ for MH7. Our results also showed that 20% of samples had total coliforms ranging from 4.1 to 5.2 CFU•mL$^{-1}$, with the highest count found in MH9.

Our quantitative qPCR results interpolated from our standard curves are presented in Table 5. We found high levels of *Salmonella* spp. in MH15, *L. monocytogenes* in MH4, *P. aeruginosa* in MH10, *C. jejuni* in MH9, *E. faecalis* in MH4, and *E. coli* in MH3. Except for MH4, which had the highest concentration of *L. monocytogenes* and *E. faecalis*, all MHs had different predominant microorganisms. Our results indicate that all selected microorganisms were identified in at least one OMHP tap water sample (see Fig 3).

We found six MHs out of 15 to have contamination with *Salmonella* spp., with MH15 having the highest contamination level, followed by MH9, MH3, MH11, MH1, and MH10.

### Table 4. Biological characteristics of tap water in mobile homes in the ECV, including HPCs.

| Samples | HPCs (CFU•mL$^{-1}$) | Total coliforms (MPN • 100 mL$^{-1}$) |
|---------|----------------------|-------------------------------------|
| H1      | <1                   | <1                                  |
| H2      | <1                   | <1                                  |
| H3      | <1                   | <1                                  |
| H4      | <1                   | <1                                  |
| H5      | 4.05E+04             | <1                                  |
| H6      | 2.08E+03             | <1                                  |
| H7      | 1.16E+05             | <1                                  |
| H8      | <1                   | 4.1                                 |
| H9      | <1                   | 5.2                                 |
| H10     | <1                   | <1                                  |
| H11     | 5.60E+03             | 2                                   |
| H12     | <1                   | <1                                  |
| H13     | <1                   | <1                                  |
| H14     | <1                   | <1                                  |
| H15     | <1                   | <1                                  |
| EPA     | < 500                | 0                                   |

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### Table 5. Copy number of selected microorganisms from the Oasis Mobile Home Park based on calculated standard curves and qPCR products.

| House ID | *Salmonella* spp. CFU•mL$^{-1}$ | *L. monocytogenes* CFU•mL$^{-1}$ | *P. aeruginosa* CFU•mL$^{-1}$ | *C. jejuni* CFU•mL$^{-1}$ | *E. faecalis* CFU•mL$^{-1}$ | *E. coli* CFU•mL$^{-1}$ |
|----------|----------------------------------|----------------------------------|-------------------------------|---------------------------|---------------------------|--------------------------|
| MH1      | 2.00E+04                         | <1                               | 2.40E+06                      | <1                        | <1                        | <1                       |
| MH2      | <1                               | <1                               | <1                            | <1                        | <1                        | <1                       |
| MH3      | 7.43E+05                         | 9.81E+01                         | <1                            | 1.69E+07                  | <1                        | 7.34E+07                 |
| MH4      | 8.56E+02                         | 4.42E+02                         | 2.75E+03                      | 1.47E+02                  | 1.26E+04                  | 1.27E+04                 |
| MH5      | 8.56E+02                         | <1                               | <1                            | 1.24E+04                  | <1                        | 5.59E+05                 |
| MH6      | <1                               | <1                               | 6.12E+03                      | <1                        | <1                        | 2.27E+04                 |
| MH7      | 3.30E+03                         | <1                               | <1                            | 2.64E+05                  | 3.06E+02                  | 1.33E+03                 |
| MH8      | <1                               | <1                               | <1                            | <1                        | <1                        | 1.33E+03                 |
| MH9      | 2.63E+06                         | 4.49E+01                         | 4.25E+01                      | 3.35E+08                  | <1                        | 3.69E+07                 |
| MH10     | 7.79E+00                         | 3.17E+02                         | 1.69E+10                      | <1                        | <1                        | 1.49E+03                 |
| MH11     | 3.05E+05                         | <1                               | <1                            | 8.92E+06                  | <1                        | 4.70E+07                 |
| MH12     | 1.96E+01                         | 2.64E+02                         | 3.09E+04                      | 2.68E+02                  | <1                        | 3.97E+03                 |
| MH13     | <1                               | <1                               | <1                            | <1                        | <1                        | <1                       |
| MH14     | <1                               | <1                               | <1                            | <1                        | <1                        | <1                       |
| MH15     | 5.62E+06                         | <1                               | 5.70E+07                      | 1.04E+03                  | 1.51E+02                  | <1                       |

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respectively. We also found many sampled MHs contaminated with *L. monocytogenes*, with MH4 ranking as the highest contamination followed by MH10, MH12, MH3, and MH9.

Although we were unable to detect the presence of *E. coli* in the MHP using Quanti-Trays, we were able to identify genetic material from this species in water samples via the use of qPCR. We found MH3 to have the highest concentration of *E. coli*, followed by MH11, MH9, and MH5. We also found that MH1, MH2, MH13, MH14 and MH15 were below detection for both cultivable coliforms and qPCR.

We compared arsenic concentrations from this study to a study conducted by the EPA region IX [35], and a study by Ying & Monica [36] from UC Riverside. We found that arsenic concentrations in the OMHP remained relatively elevated from July 2020 to August 2021, as shown in Fig 4.

We noticed during our sampling that MHs are old, with frequent water leaks. Additionally, we found evidence of breaks to the sewage system throughout the park, as demonstrated in S2 Fig.

**4. Discussion**

We found water contaminated with arsenic and bacteria in the OMHP by measuring physicochemical and microbial parameters. Many of the tap water samples we tested had physicochemical parameters, such as EC, TDS, pH, and free Cl\textsubscript{2}, which do not necessarily affect health, yet hinder consumers from using these water sources. Very few studies have been done on tap water conditions in MHs, with most information coming from press and policy reports, suggesting that people living in MHs in the US have poor water quality [12, 13, 11]. Scholarly studies on water quality in MHs are lacking.

We found 46% of OMHP tap water samples fell outside of the pH Secondary Maximum Contaminant Levels of 6.5 to 8.5, as established by the EPA [37]. The pH measurement of

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Fig 3. qPCR percent positive of indicated microorganisms in drinking water tested from mobile homes in the Oasis Mobile Home Park. A list of selected pathogenic microorganisms was used, and percent positive of each microorganism was determined for mobile homes in the park. Results represent the percentage positive of each microorganism in the fifteen mobile homes studied.

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Acidity and basicity is important because it influences other physico-chemical parameters and the presence of metal ions [38]. Groundwaters are known to typically be acidic [39]. Our results clearly indicated that more than half of OMHP water samples had pH values that fell well within the range recommended by the EPA. Although drinking water pH does not necessarily impact human health directly, it has been demonstrated that high pH values (above 7.5) cause pipes to be encrusted with deposits, while low-pH water may cause corrosion of pipe metals [40]. The pH variation among MHs at our study site may be explained by recurrent water shut-offs in the park, as well as pipe breaks and repairs. Samples MH3 and MH5 had pH values below 6.2, which could cause pipe corrosion and increase metal leaching, especially from copper and lead pipes, which could subsequently affect human health [41, 42].

Electrical conductivity measures the capacity of water to transmit an electrical current, and although there are no WHO guidelines for EC ranges in drinking water, that organization recommends an EC for drinking water below 300 μS•cm⁻¹. Our results indicated that OMHs have EC far below WHO recommend levels. Electrical conductivity is used to determine the suitability of drinking water in many parts of the world.

Although no guidelines have been established for drinking water TDS limits, WHO recommends 600 mg•L⁻¹ or less for aesthetic reasons [34]. The high TDS value in MH4 was expected because muddy water (S1 Fig) was first collected during our sampling from this home. Colored water from some OMHs may be explained by pipe breaks or repairs, with soil infiltration into the water system. A recent report from the USEPA Region 9 septic inspection of the OMHP [19] found open sewage was in proximity to water lines that supply the OMHP. They found pipe ruptures allowed sewage water to infiltrate water lines, posing potentially serious health concerns. Our results showed that OMHPs TDS varied considerably among MHs, considering water comes from the same source. We can infer that the concentration of TDS in the OMHP is influenced by individual MH plumbing conditions, water lines, and water usage.

The presence of residual Cl₂ in drinking water is an indicator of potability, while a lack of Cl₂ represents potential for bacterial contamination. Free Cl₂ indicates the water source has...
been treated to kill disease-causing microorganisms. The Centers for Disease Control and Prevention (CDC) recommends a range of 0.2 to 2 mg•L$^{-1}$ of Cl$_2$ in tap water, while the WHO maximum allowable value for Cl$_2$ in drinking water is 5 mg•L$^{-1}$. Our results indicated that Cl$_2$ measurements obtained from these MHs fall within the recommended CDC and WHO requirements. The spatial (GIS), cultivatable and qPCR data, did not show any relationship to Cl$_2$ distribution in the OMHP.

Our results also demonstrated that Cl$_2$ concentration in the OMHP varies extensively among MHs. We found that some MHs (MH3, MH5, MH7) had higher concentrations of Cl$_2$ compared to the remainder of MHs studied. Although these concentrations were within the acceptable range of Cl$_2$ recommended by the CDC, this may be of concern, since it may be due to short contact times of disinfecting Cl$_2$ with the water prior to use. Brief contact times may allow some pathogenic microorganisms to remain viable in the water system and consequently expose the community to potentially pathogenic microorganisms [43, 44]. The variable free Cl$_2$ concentrations may be a result of high Cl$_2$ demands throughout the system, which has several potential sites where chlorinated water is exposed to untreated sewage.

Residents may be exposed to elevated arsenic through drinking water in the OMHP. Long-term exposure to inorganic arsenic through drinking water and food can lead to chronic arsenic poisoning. In 2001, the EPA adopted a maximum safe arsenic intake concentration of 0.01mg•mL$^{-1}$ or 10 parts per billion (ppb) [45]. In the current study, we found arsenic levels ranged from 50 ppm to 86 ppm. As shown in Fig 2, arsenic concentrations tested by an external third-party laboratory were within the same range and slightly higher from what we reported with the portable semi-quantitative test kit.

Arsenic contamination in the OMHP is persistent (Fig 4), seriously endangering the health of residents. Although in May, 2020, the EPA found the OMHP water system complied with the arsenic maximum contaminant level running annual average (MCL RAA), our study demonstrated the presence of elevated concentrations of arsenic. This triggered the EPA to test the OMHP for arsenic concentration, and later issue an emergency order to the OMHP, requiring changes to the drinking water system, and provision of water bottles to residents [19].

Arsenic contamination of groundwater is a widespread global challenge. India, for example, is reported to have the highest groundwater fluoride and arsenic concentrations in the world [46]. A study in Bangladesh on arsenic exposure from drinking found that 39 million people were exposed to arsenic concentrations above the 0.01mg •mL$^{-1}$ recommended by the WHO [47]. Although the study in Bangladesh was a longitudinal study on the health effects of arsenic intake through drinking water in 11,746 people visiting hospitals, and not a study of arsenic contamination in MHs, the study demonstrated a common mechanism through which people are contaminated with arsenic.

As a result of poverty and lack of awareness, some residents of the OMHP may continue to consume water contaminated with arsenic from their taps. Arsenic exposure has been linked with several illnesses, including cancer of the bladder and lungs, diabetes, pulmonary disease, and cardiovascular disease, among others [48]. Although evaluating the health effect of arsenic in the OMHP was beyond the scope of the current study, the importance of resolving arsenic contamination in the OMHP cannot be overemphasized.

Located in the desert, the ECV consistently breaks records for extreme heat conditions in California, at times reaching 50˚C [49]. This may be a reason why our findings of water temperatures had an average of 28.7˚C, which is suitable for the growth of many microorganisms. Notwithstanding the fact that water temperature does not directly affect water potability, it may induce bacterial growth and biofilm formation. Water temperature is an influencing factor for bacterial growth kinetics and competition processes. An increase in bacterial production could be expected with a temperature rise in the Southern Ocean [50]. A drinking water
distribution system biofilm study demonstrated that temperature is a key factor for the regrowth of microorganisms in drinking water distribution systems [51].

Heterotrophs are defined as microorganisms that require organic carbon for growth. However, only a small proportion of microorganisms present in water are able to grow and become detectable in HPC test conditions [52]. Our results indicated 73% of OMHs did not have detectable heterotrophic bacteria. We can infer that these results may be influenced by physico-chemical factors, such as OMHP water chlorination, pH, and temperature. However, the absence of heterotrophic bacteria on R2A plates does not indicate that the water is safe for consumption, or free from pathogenic microorganisms. Time and temperature of incubation are important conditions for heterotrophic microorganismal growth [53]. Growing microorganisms on R2A plates at 35˚C for 48 hours, we found that MH5, MH6, MH7, and MH11 all had elevated concentrations of heterotrophic bacteria, indicating a potential failure of OMHP groundwater treatments, despite the incidence of treatment with Cl₂.

The EPA sets the maximum permissible level of heterotrophic bacteria in drinking water at 500 CFU•mL⁻¹ [54]. Our results indicated that MH5, MH6, MH7, and MH11 had HPC above the recommended 500 CFU•mL⁻¹. Although HPC does not have a direct impact on human health, it indicates that a water source may be a source of bacterial risk to human health, and that the presence of pathogenic microorganisms may occur.

The presence of total coliform in drinking water indicates that environmental infiltration of biological matter into drinking water systems requires investigation [55]. The EPA considers total coliform to be an important indicator of other pathogens in drinking water, and as such, is used to determine the competence of water treatment [56]. In our study, the presence of total coliforms in MH8, MH9, and MH11 indicates that a problem occurred with well water treatment, or a break in the water distribution system occurred in proximity to contaminated soil. The low concentration of HPC and coliforms may be due to the elevated free Cl₂ concentration and potential odor that residents reported. During our visits to the MHs, we measured free Cl₂, which diminishes over time. In Speegleville, Texas, the odor of free Cl₂ from showers and taps resulted in residents buying bottled water [57].

No *E. coli* was detected using the Quanti-Tray method, indicating that no viable *E. coli* was present in our samples. Since the method we used only identifies live *E. coli* in water samples, we can infer that no live *E. coli* occurred in the OMHPs during our study. Despite our diligent use of sodium thiosulfate as a chlorine neutralizer, the high and variable concentrations of free chlorine in the household samples may have prevented the cultivable microbial growth that we were expecting to see with the IDEXX and HPC methods. This could also explain the high concentrations of microbial genetic material that was detected using the qPCR methods.

These findings demonstrated that qPCR is a high yield technique that can identify the presence of the target microorganism even at low concentrations, and even if the microorganisms are no longer viable.

In our study, we found that five out of 15 water samples from MHs had *L. monocytogenes* present. We also found that MH9 had the highest concentration of *C. jejuni* followed by MH3 and MH11. *Campylobacter* is a common cause of bacterial gastroenteritis in LMIC [58]. According to the CDC, 1.5 million people in the U.S. become ill from *Campylobacter* every year [59]. We found qPCR techniques to be more sensitive compared to culture methods and recommend that qPCR should be promoted for routine analyses of drinking water quality. A study comparing culture-based methods with qPCR in the detection of mycobacteria, found that qPCR identified bacteria 5–34 times better than cultivable methods [60]. In our study, we found that no single microorganism was predominant in all MHs (Table 5).

It is important that disadvantaged communities have their drinking water tested regularly. Testing may require the use of qPCR methods for identification of pathogenic microorganisms.
in their water to reduce the risk of ingesting microbially contaminated water. Installation of personal reverse osmosis filters in homes would greatly increase the safety of tap water. However, filters require regular maintenance as indicated by the manufacturers to sustain adequate water in MHs. Communities with poor infrastructure, and suffering from microbial contaminations, arsenic contamination, and soil contamination from overflowing septic tanks need immediate assistance from lawmakers and stakeholders, regardless of their location and socio-economic status. Additional studies using microbial source tracking techniques may be useful in the OMHP to determine the origin and relationship of detected microbes in relation to breaks in the on-site sewage system.

5. Conclusion

Microbial contamination of water in the OMHP revealed that variable concentrations of selected microorganisms were found in MHs in addition to high arsenic concentrations. Based on the physico-chemical parameters and our microbial analyses, we conclude that drinking water from MH taps in the OMHP is unsafe for consumption. To address the recurrent arsenic presence in the OMHP, it would be advantageous to install point-of-use reverse osmosis filters in every MH. This process is likely to ensure that community members can safely use their tap water (for which they pay), in addition to eliminating arsenic from their water. This process will also reduce economic hardship caused by securing water from vending machines, which may also be contaminated. Further studies, such as those using microbial source tracking, are necessary to determine the source of the microbial contamination.

Supporting information

S1 Fig. Muddy tap water collected from a kitchen tap in the Oasis Mobile Home Park in California. The muddy tap water in the violet cup was collected from the sink of a mobile home. According to the resident, tap water comes out muddy after a period of 2 to 4 hours of inactivity. The cuvette (A) used to measure chlorine concentration in water, held by the sampler, contains tap water from the sink after running the tap for approximately one minute. (TIF)

S2 Fig. Images of wastewater from broken septic systems from different locations (A-D) in the Oasis Mobile Home Park in Coachella Valley, California. (TIF)

S3 Fig. The Standard curve of 10-fold dilutions of DNA of known concentration of *L. monocytogenes* plotted against qPCR amplification nucleic acid and a linear regression line fitted to generate the calibration curve. (TIF)

S4 Fig. The Standard curve of 10-fold dilutions of DNA of known concentration of *Salmonella* spp. plotted against qPCR amplification nucleic acid and a linear regression line fitted to generate the calibration curve. (TIF)

S5 Fig. The Standard curve of 10-fold dilutions of DNA of known concentration of *E. coli* plotted against qPCR amplification nucleic acid and a linear regression line fitted to generate the calibration curve. (TIF)

S6 Fig. The Standard curve of 10-fold dilutions of DNA of known concentration of *C. jejuni* plotted against qPCR amplification nucleic acid and a linear regression line fitted to
generate the calibration curve.
(TIF)

S7 Fig. The Standard curve of 10-fold dilutions of DNA of known concentration of P. aeruginosa plotted against qPCR amplification nucleic acid and a linear regression line fitted to generate the calibration curve.
(TIF)

S8 Fig. The Standard curve of 10-fold dilutions of DNA of known concentration of E. faecalis plotted against qPCR amplification nucleic acid and a linear regression line fitted to generate the calibration curve.
(TIF)

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