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Riverbank filtration for control of microorganisms: Results from field monitoring

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Abstract

Microbial monitoring was conducted over a period of more than 1 year at three full-scale riverbank filtration (RBF) facilities, located in the United States along the Ohio, Missouri, and Wabash Rivers. Results of this study demonstrated the potential for RBF to provide substantial reductions in microorganism concentrations relative to the raw water sources. *Cryptosporidium* and *Giardia* were detected occasionally in the river waters but never in any of the well waters. Average concentrations and log reductions of *Cryptosporidium* and *Giardia* could not be accurately determined due to the low and variable concentrations in the river waters and the lack of detectible concentrations in the well waters. Average concentrations of aerobic and anaerobic spore-forming bacteria, which have both been proposed as potential surrogates for the protozoans, were reduced at the three facilities by 0.8 to >3.1 logs and 0.4 to >4.9 logs, respectively. Average concentrations of male-specific and somatic bacteriophage were reduced by >2.1 logs and $\geqslant 3.2$ logs, respectively. Total coliforms were rarely detected in the well waters, with 5.5 and 6.1 log reductions in average concentrations at the two wells at one of the sites relative to the river water. Average turbidity reductions upon RBF at the three sites were between 2.2 and 3.3 logs. Turbidity and microbial concentrations in the river waters generally tracked the river discharge; a similar relationship between the well water concentrations and river discharge was not observed, due to the low, relatively constant well water turbidities and lack of a significant number of detections of microorganisms in the well waters. Further research is needed to better understand the relationships among transport of pathogens (e.g., *Cryptosporidium*, *Giardia*, viruses) and potential surrogate parameters (including bacterial spores and bacteriophage) during RBF and the effects of water and sediment characteristics on removal efficiency.

Keywords: Riverbank; Filtration; Microorganisms; *Cryptosporidium*; *Giardia*; Surrogates; Wells; Pumping; Drinking water

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1. Background

1.1. Riverbank filtration

In light of concerns over organic precursors to disinfection byproducts (DBPs) and microbial contaminants in drinking water, utilities have begun to consider riverbank filtration (RBF) as a means of improving water quality through natural physical, chemical, and biological processes that occur during ground passage. RBF has been shown in recent years to be very effective at controlling a variety of contaminants, most notably the reduction in concentrations of total and dissolved organic carbon, DBP precursors, turbidity, pesticides and other organic contaminants, and the mitigation of shock loadings of contaminants (Ray, 2004; Weiss et al., 2003a, b; Ray et al., 2002a, b; Hiscock and Grischek, 2002; Verstraeten et al., 2002; Kuehn and Mueller, 2000). The potential for RBF systems to provide a significant barrier to microorganisms has also been observed (Weiss et al., 2003a; Gollnitz et al., 2003; Schijven et al., 2003; Tufenkji et al., 2002; Irmscher and Teermann, 2002). However, little is known about the transport of microbial contaminants in a variety of RBF systems with different characteristics (including travel times, aquifer material, climate, water chemistry, and river flow conditions), and no standard protocol exists for evaluating and assigning natural filtration credit to water utilities employing RBF as one of the mechanisms to treat surface water (Berger, 2001).

As RBF becomes a more widely used "tool" for utilities to meet treatment requirements, regulators are beginning to consider the appropriate amount of credit to assign RBF for removal of microbial contaminants. Of particular concern are the protozoan pathogens *Giardia lamblia* and *Cryptosporidium parvum*, which are known to be extremely resistant to conventional means of disinfection (Solo-Gabriele and Neumeister, 1996; LeChevallier et al., 1991). In addition, there have been few studies on the transport of small pathogenic viruses through RBF systems. Under the Long Term 2 Enhanced Surface Water Treatment Rule (LT2ESWTR), utilities are allowed to choose from a "toolbox" of technologies in addition to existing treatment to comply with log treatment requirements for *Cryptosporidium* (USEPA, 2003). At present, bank filtration, as a pretreatment, is given the potential (based on proper design and implementation in accordance with EPA guidance) log credit of 0.5 for a well setback distance of 25 ft and 1.0 for a well setback distance of 50 ft. The aquifer must consist of unconsolidated sand with at least 10% fines, and average turbidities in the well water must be less than 1 nephelometric turbidity unit (NTU). The potential for the RBF process to reduce concentrations of precursors to potentially carcinogenic DBPs, the other major component of the LT2ESWTR, as well as to reduce the risk of waterborne disease makes it a very attractive additional treatment process for water utilities.

1.2. Study objectives

The purpose of this study was to document the reduction in concentrations of pathogenic microorganisms and commonly used or proposed microbial indicator/surrogate parameters at three full-scale RBF facilities. As regulators and utilities look more strongly at RBF as a potential treatment option, monitoring data from full-scale systems are important to help determine appropriate removal credit to assign such systems and to evaluate the important characteristics of such systems to achieve the desired removal efficiency. Data of this kind should be combined with the results from smaller-scale studies, such as column and aquifer transport experiments, to better understand the mechanisms for transport and removal; the effect of physical, chemical, and biological variables on RBF effectiveness; and the relationships among the pathogens and potential surrogate and indicator parameters during transport through the riverbank sediments.

2. Materials and methods

2.1. Study sites

The three study sites were the focus of a previous investigation into the merits of RBF at controlling DBP precursor concentrations and were described in detail elsewhere (Weiss et al., 2003a). At the Ohio River Indiana-American Water study site at Jeffersonville, IN, Well #9 (580 ft (177 m) from the river) and Well #2 (100 ft (30 m) from the river) were sampled for this study. At the Wabash River Indiana-American Water study site at Terre Haute, IN, the Collector Well (located 90 ft (27 m) from the Wabash River, with horizontal arms extending out from the center at a depth of approximately 80 ft (24 m) below the river bottom) and Well #3 (400 ft (122 m) from the river) were sampled for this study. Finally, at the Missouri River Missouri-American Water facility at Parkville, MO, Well #4 and Well #5 (both wells located approximately 120 ft (37 m) from the river) were sampled for this study.

2.2. Monitoring schedule

Microbial monitoring at the three study sites was conducted from January 2002 through July 2003. River waters were sampled and analyzed monthly, while well samples were sampled less frequently. The closer wells at Jeffersonville (Well #9) and Terre Haute (Collector Well) were sampled more frequently than the distant

wells (Well #2 and Well #3, respectively). At Parkville, Well #4 was sampled more frequently than Well #5 (both wells located equidistant from the Missouri River). At the Jeffersonville site, data were collected over 18 sampling rounds for the Ohio River, nine sampling rounds for Well #9, and six sampling rounds for Well #2; at Terre Haute, data were collected over 19 sampling rounds for the Wabash River, nine sampling rounds for the Collector Well, and five sampling rounds for Well #3; at Parkville, data were collected over 18 sampling rounds for the Missouri River, nine sampling rounds for Well #4, and four sampling rounds for Well #5. For the Parkville site, additional monitoring data for total coliforms were available from Missouri-American Water over the time period of this study. Therefore, for Parkville total coliforms concentrations, data were collected over 31 sampling rounds (approximately twice per month) for the Missouri River, 15 sampling rounds for Well #4, and 14 sampling rounds for Well #5. River and well waters were collected on the same sampling dates. No attempt was made to stagger sampling to account for travel times. The travel times are highly uncertain, and the purpose of this study was to characterize the average concentrations over time, particularly for the rivers.

2.3. Protozoan sample collection and handling

River raw water samples (10-L) were collected in plastic disposable carboys and sent to the American Water Belleville Laboratory (Belleville, IL) for filtration and analysis. Raw well water samples (100-L) were collected according to Method 1623 (USEPA, 2001a) using the Envirochek™ sampling capsule (Pall Gelman Sciences, Ann Harbor, MI) at a flow rate of 2.0 L/min. All samples were kept at 4 °C and shipped by next day air to the Belleville Laboratory in coolers with cold packs. Upon arrival at the laboratory, all samples were checked for appropriate temperature and refrigerated at 4 °C until sample analysis within a holding time period less than 48 h.

2.4. Protozoan sample analysis

USEPA (2001a) Method 1623 was followed to detect *Cryptosporidium* and *Giardia* specimens. A wrist action shaker (Pall Gelman Sciences, Ann Harbor, MI) was set at 900 rpm, and the spiking procedure was performed using flow-cytometer-sorted suspensions of oocysts/cysts (Wisconsin State Laboratory of Hygiene, Flow Cytometry Unit, Madison, WI). A Dynabeads® GC Combo Kit (Dynal Biotech Inc., Brown Deer, WI) was used for the immunomagnetic separation (IMS) step.

The samples were dried onto Dynal® Spot-On poly lysine treated microscopy slides (Dynal Biotech Inc., Brown Deer, WI) and immunostained using Aqua-Glo G/C direct kit (Waterborne, Inc., New Orleans, LA). The nuclei were stained with 4″, 6 Diamino-2-phenylindole dihydrochloride, 1/5000 in phospate buffered saline (Sigma-Aldrich Corp., St. Louis, MO). Slide preparations were mounted using 2% 1,4-diazabicyclo [2,2,2] octane (pH 8.6)/glycerol mounting media (Sigma-Aldrich Corp., St. Louis, MO). Slides were kept in the dark at 4 °C until microscopic analysis was performed.

Epifluorescence and differential interference contrast microscopy at 100 × were carried out as recommended using either a BMAX 50 or a BH2 upright compound microscope (Olympus Optical Co., Ltd.). Microscopic images were documented using the PAX-IT™ Imaging System (MIS, Inc., Franklin Park, IL).

2.5. Oocyst and cyst recovery efficiencies

The recovery efficiency of Method 1623 was assessed using reverse osmosis water. The average recoveries for spiked QC samples were 58.5% and 40.6% for *Cryptosporidium* oocysts and *Giardia* cysts, respectively (Fig. 1). Matrix sample effects on *Cryptosporidium* and *Giardia* recoveries were analyzed during the study. For this purpose, personnel at each of the study sites collected one or two extra 10-L water samples in plastic carboys. Those samples were sent to the Belleville Laboratory and spiked with 100 *Cryptosporidium* oocysts and 100 *Giardia* cysts. A total of 12 spiked samples were processed, with recoveries ranging from 1% to 46% for the river water samples and from 1% to 18% for well water samples.

2.6. Microbial indicators sample collection

Several potential indicator or surrogate parameters were included in the monitoring campaign for this study. Aerobic and anaerobic bacterial spores have been proposed as potential surrogates for *Cryptosporidium* (Berger, 2001). Bacteriophages have been used as indicators of human viruses in drinking water systems

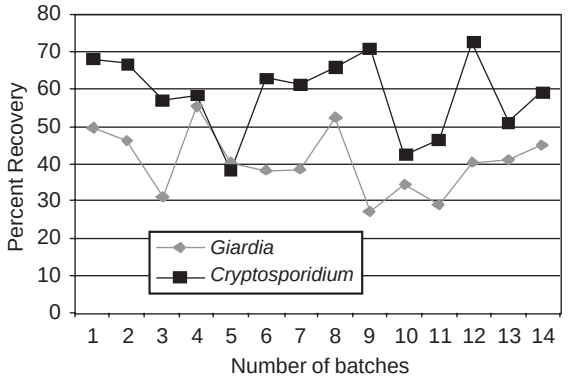

Fig. 1. Recovery efficiency for *Cryptosporidium* and *Giardia*.

(Azadpour-Keeley et al., 2003; Schijven et al., 2003; Sobsey et al., 1995). Turbidity has been used in drinking water treatment systems as an indicator of treatment performance, typically to signal breakthrough in treatment. Turbidity is not expected to be a quantitative surrogate for pathogens. Coliforms and coliphages are often used as an indicator of fecal contamination (Azadpour-Keeley et al., 2003). As part of the monthly sampling protocol, turbidity was measured in river and well waters at the beginning and at the end of sample collection. Two 1-L grab samples from the rivers were collected using sterilized 1-L plastic bottles (Nalgene). One grab sample was used for the *Bacillus* (aerobic spores), *Clostridium* (anaerobic spores), and phage assays, and the other for total coliform and *Escherichia coli* assays. Samples collected from the wells (10-L) for the *Clostridium* assay were collected using plastic disposable carboys.

2.7. Bacillus (aerobic spores) assay

Bacillus subtilis (ATCC 6633) was used for seeding positive controls and spiking experiments to calculate the method recovery efficiency. After rehydration, the spore stock was grown in nutrient broth (Difco Laboratories), 1/10 strength, supplemented with 0.1 mM $MnSO_4 \cdot 4H_2O$ at 37 °C, for 96 h. The working stocks were adjusted to 80–100 colony forming units (CFU)/mL. Modified starch agar (MSA) containing 15 g agar, 1 g soluble starch, 8 g nutrient broth, and 3.75 mL trypan blue stain (0.4%) per liter of Milli-Q water with a final pH of 6.8 ± 0.2 was used to enumerate indigenous *Bacillus* spores.

Bacillus assays were carried out by the membrane filtration method. Water samples were processed using modifications of the methods of Nieminski et al. (2000) and Rice et al. (1996). Twenty-milliliters of each sample were aseptically transferred to sterile, heat-resistant, glass storage bottles; samples, along with positive and negative controls, were heat-treated in a water bath at 60 °C for 20 min. A blank water sample with a thermometer was used to verify the temperature and timing was begun when the blank sample reached 60 °C. After heat treatment, samples were placed on ice. Duplicates of 100 mL of each sample were filtered using 47 mm, 0.45-μm porosity membrane filters, type HC (Millipore). Filters were placed on MSA plates (60×15 mm Petri dishes) and incubated for 20–24 h at 37 °C. After incubation, filter membranes were removed, placed in the Petri dish lids and covered with Lugol's iodine solution to visualize zones of clearing due to starch hydrolysis. Zones of clearing and the presence of colonies on filters were scored as *Bacillus*. A set of duplicate samples from each designated sampling point was spiked to analyze sample matrix effects for each designated sampling point.

2.8. Clostridium (anaerobic spores) assay

Clostridium perfringens (ATCC 3626) was used for seeding positive controls. *Clostridium* assays were carried out using the membrane filter method as described in section XI of the ICR Microbial Laboratory Manual (USEPA, 1996) with selective mCP media; anaerobic conditions were provided by using a GasPak® Jar (GasPak® System, BBL, BD, Franklin Lakes, NJ) and the AnaeroPack™ system (Mitsubishi Gas Chemical Co., Inc., Tokyo, Japan). The cultures were incubated at 44.5 °C in a bacteriological incubator (Gallenkamp, Plus Series, Sanyo Gallenkamp, Sanyo Scientific, Chicago, IL) for 24 h. After incubation, the yellow straw-colored colonies were exposed to ammonium hydroxide fumes in a chemical extraction hood (Classical Modular Systems, Inc.). Colonies that turned pink or magenta were scored as *C. perfringens*.

2.9. Coliphage assay

To isolate male-specific (F^+) coliphage and somatic coliphage, *E. coli* strains Famp (ATCC 15597) and CN-13 served as host cells, respectively. Phage stocks MS2 (ATCC 15597-B1) and PhiX174 (ATCC 13706-B1) served as positive controls. Phage assays were carried out using the single agar layer method. The procedure used 100 mL of water sample and 100 mL of 2 × molten TSA as described in Method 1602 (USEPA, 2001b).

2.10. Total coliform and E. coli analyses

Coliform analyses were carried out using the EC-MUG method (Method 9221 B/F, Standard Methods for the Examination of Water and Wastewater, 1998). Method 9221 B is known as the standard coliform fermentation technique and uses lauryl tryptose broth. The fermentation tubes were arranged in sets of five or ten tubes per sample. After incubating the samples for a period of 24 ± 2 h to 48 ± 3 h at 35 ± 0.5 °C, growth with gas and acid reaction (yellow color) was considered as presumptive positive. Positive samples were tested following method 9221 F *E. coli* using EC-MUG broth and incubation at 44.5 °C in a water bath for a period of 24 ± 2 h. Bright blue fluorescence after exposure to long-wave UV lamp was read as confirmation for *E. coli*.

2.11. Matrix sample effect on microbial indicators recovery

One set of duplicated samples from each designated sampling point was spiked to analyze sample matrix effects in duplicate for each designated sampling point.

3. Results

3.1. Microbial monitoring

The data in Table 1 were collected at the three study sites between January 2002 and July 2003. Average concentrations were calculated as the sum of the counts over all sampling rounds divided by the sum of the sample volumes, with non-detects treated as zeroes (Parkhurst and Stern, 1998). For some wells in which there were no counts over all sampling rounds, the average was represented by a detection limit, calculated as 1 divided by the sum of the sample volumes over all sampling rounds. Log reductions in the well water concentrations relative to the river water concentrations were calculated based on these average concentrations and detection limits, where appropriate. Log reductions calculated for wells where there were no detects represent a lower bound, as indicated in Table 1 by "greater than" signs.

Average bacterial spore concentrations in the Ohio, Wabash, and Missouri River waters ranged from 8.1×10^4 to 3.9×10^5 CFU/L for the aerobic spores (*Bacillus*) and from 7.6×10^2 to 3.1×10^3 CFU/L for the anaerobic spores (*Clostridium*) (Table 1). Reductions in *Bacillus* concentrations in the Jeffersonville and Terre Haute wells relative to the Ohio and Wabash Rivers were all greater than 2 logs. At Parkville, the average *Bacillus* concentration in Well #4 was less than one order of magnitude smaller than that in the Missouri River, yielding the lowest reduction observed for the aerobic spores (0.8 log). In Well #5, a 2.6 log reduction in average *Bacillus* concentration was observed relative to the Missouri River water. For *Clostridium* (anaerobic spores) greater than 4.5 log reductions were observed in both wells at two of the sites (Jeffersonville and Parkville). At Terre Haute, less than a one-half log reduction was observed in the Collector Well, while a 2.3 log reduction was observed in the distant well (Well #3). *Bacillus* concentrations were often observed in the well waters, while *Clostridium* concentrations for the wells at two of the three sites (Jeffersonville and Parkville) were below the detection limit for all sampling rounds.

Average concentrations of total coliforms ranged from 7.5×10^5 to 4.6×10^6 MPN/L at the three sites, with average concentrations of *E. coli* between 1.5×10^4 and 4.6×10^4 MPN/L (Table 1). The number of sampling events for total coliforms for the Missouri River was greater than that for the other two sites (31 compared to 18 and 19 for Jeffersonville and Terre Haute, respectively). Total coliform average concentrations in Well #4 and Well #5 at Parkville were 0.7 and 2.1 MPN/L, respectively, corresponding to reductions of 6.1 and 5.5 log relative to the Missouri River water. While coliform concentrations in the Jeffersonville and Terre Haute wells were not available, presence/absence tests indicate only limited breakthrough of coliforms in the wells (Table 2). At Jeffersonville, three out of 54 sampling events for Well #9 and seven out of 55 sampling events for Well #2 indicated the presence of total coliforms. At Terre Haute, two out of 62 sampling events in the Collector Well indicated the presence of coliforms, while all of the 13 sampling events for Well #3 were negative for coliforms. At Parkville, one out of 15 sampling events for Well #4 and one out of 14 sampling events for Well #5 showed positive results for coliforms.

Average concentrations of male-specific bacteriophage (*E. coli Famp* as the host bacterium) in the Ohio, Wabash, and Missouri River waters were 43, 36, and 34 PFU/L, respectively (Table 1). Average concentrations of somatic bacteriophage (*E. coli C* as the host bacterium) in the river waters were between 1.7×10^3 and 2.6×10^3 PFU/L. Reductions of male-specific bacteriophage in the well waters relative to the river waters were greater than 2 logs for all wells, while reductions of somatic bacteriophage average concentrations were greater than 4 logs for all wells. With the exception of Well #9 at Jeffersonville, where somatic bacteriophage were observed at an average concentration of 1.1 PFU/L (one sampling round yielding a concentration of 10 PFU/L), bacteriophage were not detected in the well waters.

Calculations of average concentrations and log reductions for the protozoans, *Cryptosporidium* and *Giardia*, were limited by low and variable concentrations (with frequent non-detects) in the river waters and non-detects in the well waters. Calculated reductions of *Cryptosporidium* in the well waters relative to the river waters ranged from >0.9 to >1.5 log, based on river average concentrations of 2.2×10^{-2}, 3.5×10^{-2}, and 1.9×10^{-2} oocysts/L for Jeffersonville, Terre Haute, and Parkville, respectively (Table 1). Reductions in *Giardia* concentrations in the well waters relative to the river waters ranged from >1.3 to >1.9 log, based on average river concentrations of 6.0×10^{-2}, 8.5×10^{-2}, and 5.1×10^{-2} cysts/L for Jeffersonville, Terre Haute, and Parkville, respectively.

The total volumes sampled and protozoan counts in the river waters for all sampling events for Jeffersonville, Terre Haute, and Parkville are given in Table 3. For the well waters, 100 L of water were assayed during each sampling event; river water assay volumes were much smaller due to clogging of the filters by suspended material. *Cryptosporidium* oocysts and *Giardia* cysts were occasionally detected in the river waters, while all well water samples from the three sites assayed were negative for *Cryptosporidium* oocysts and *Giardia* cysts.

Turbidity monitoring results for the three study sites are presented in Table 4. Average turbidities in the Ohio, Wabash, and Missouri River waters were 60.1, 190.3, and 78.6 NTU, respectively. Reductions in average turbidity concentrations upon bank filtration at the

Table 1
Field monitoring summary: January 2002 through July 2003; Average concentrations[a] and log reductions[b] in well waters relative to the river waters

	Bacillus [CFU/L]	*Clostridium* [CFU/L]	Total coliforms [MPN/L]	*E. coli* [MPN/L]	Male-specific Bacterio phage [PFU/L]	Somatic Bacterio-phage [PFU/L]	*Cryptosporidium* [oocysts/L]	*Giardia* [cysts/L]
Indiana–American Water Company at Jeffersonville, IN								
Ohio river [$n = 18$]	8.1×10^4	7.6×10^2	1.3×10^6	1.5×10^4	4.3×10^1	1.7×10^3	2.2×10^{-2}	6.0×10^{-2}
Well #9 [$n = 9$]	1.7×10^2 [2.7]	$<1.1 \times 10^{-2}$ [>4.8]	—	—	<0.11 [>2.6]	1.1[3.2]	$<1.1 \times 10^{-3}$ [>1.3]	$<1.1 \times 10^{-3}$ [>1.7]
Well #2 [$n = 6$]	6.7×10^2 [2.1]	$<1.7 \times 10^{-2}$ [>4.7]	—	—	<0.17 [>2.4]	<0.17 [>4.0]	$<2.0 \times 10^{-3}$ [>1.0]	$<2.0 \times 10^{-3}$ [>1.5]
Indiana–American Water Company at Terre Haute, IN								
Wabash river [$n = 19$]	2.6×10^5	3.1×10^3	4.6×10^6	4.6×10^4	3.6×10^1	2.4×10^3	3.5×10^{-2}	8.5×10^{-2}
Collector well [$n = 9$]	1.8×10^3 [2.2]	1.1×10^3 [0.4]	—	—	<0.11 [>2.5]	<0.11 [>4.3]	$<1.2 \times 10^{-3}$ [>1.5]	$<1.2 \times 10^{-3}$ [>1.9]
Well #3 [$n = 5$]	$<2.0 \times 10^2$ [>3.1]	1.6×10^1 [2.3]	—	—	<0.20 [>2.3]	<0.20 [>4.1]	$<2.0 \times 10^{-3}$ [>1.2]	$<2.0 \times 10^{-3}$ [>1.6]
Missouri–American Water Company at Parkville, MO								
Missouri river [$n = 18$]	3.9×10^5	8.9×10^2	7.5×10^{5c}	3.1×10^4	3.4×10^1	2.6×10^3	1.9×10^{-2}	5.1×10^{-2}
Well #4 [$n = 9$]	6.2×10^4[0.8]	$<1.1 \times 10^{-2}$ [>4.9]	0.7[c] [6.1]	—	<0.11 [>2.5]	<0.11 [>4.4]	$<1.1 \times 10^{-3}$ [>1.2]	$<1.1 \times 10^{-3}$ [>1.7]
Well #5 [$n = 4$]	1.0×10^3 [2.6]	$<2.5 \times 10^{-2}$ [>4.6]	2.1[c] [5.5]	—	<0.25 [>2.1]	<0.25 [>4.0]	$<2.5 \times 10^{-3}$ [>0.9]	$<2.5 \times 10^{-3}$ [>1.3]

[a]Averages calculated as sum of counts divided by sum of volumes; detection limit calculated as 1 divided by sum of the volumes. Number of samples indicated in parentheses.
[b]Log reductions indicated in brackets.
[c]For Parkville total coliforms: Missouri River—$n = 31$, Well #4—$n = 15$, Well #5—$n = 14$.

three sites ranged from 2.2 to 3.3 log units. The maximum turbidity concentrations measured in the well waters during the study period ranged from 0.27 NTU in the Collector Well at Terre Haute to 3.8 NTU in Well #4 at Parkville, while maximum turbidity concentrations in the river waters ranged from 661 NTU in the Ohio River water to 1761 NTU in the Wabash River water.

3.2. Comparison with river discharge data

River discharge data from United States Geological Survey (USGS) gaging stations located on the Ohio, Wabash, and Missouri Rivers near the study sites were available from the USGS NWISWeb online database (http://waterdata.usgs.gov/nwis/). During high flow events, there is greater opportunity for contaminants to be washed into the river. This presents an opportunity for increased concentrations of microbial contaminants in the rivers (Atherholt et al., 1998). Therefore, flow data for the rivers were compared with the monitoring data obtained during this study to evaluate the effect of changing river water flow on the concentrations of the various microbes.

Turbidity concentrations in the river and well waters at each of the three sites were plotted with the USGS flow data (Figs. 2–4). At Jeffersonville, the Ohio River turbidity concentrations varied over a range of approximately three log units, increasing with increasing mean daily gage height in the river (Fig. 2). In the well waters, turbidity concentrations remained relatively constant, ranging from approximately 0.05–0.5 with the exception of two sampling events (late December 2002), in which the well turbidity concentrations were slightly above 1 NTU. Turbidity data for the Ohio River were not available prior to August 2002. At Terre Haute, the turbidity concentrations in the Wabash River varied greatly, over approximately 4 log units (Fig. 3). Concentrations in the well waters were very constant, within the range given in Table 4. Turbidity concentrations in the Missouri River water at Parkville varied over approximately 3 log units and tracked the mean daily discharge (Fig. 4). Turbidity concentrations in the well waters at Parkville varied over a larger range than those at the other two sites, but generally fell between 0.1 and 1 NTU with some exceptions. Turbidity concentrations in the well waters at the three sites generally did not follow the trends of the river flow data, indicating that the aquifer provides an adequate barrier to dampen changes in river water turbidity with changing flow conditions. However, the late December 2002 data at Jeffersonville indicate a spike in the well water turbidity concentrations that may correspond to increased mean daily gage height in the Ohio River that immediately precedes the spike. Similarly, several sharp

Table 2
Coliform monitoring results for the wells [number of samples positive for total coliforms]

	No. positive sampling events for total coliforms
Indiana–American Water at Jeffersonville, IN	
Well #9 [$n = 54$]	3
Well #2 [$n = 55$]	7
Indiana–American Water at Terre Haute, IN	
Collector Well [$n = 62$]	2
Well #3 [$n = 13$]	0
Missouri–American Water at Parkville, MO	
Well #4 [$n = 15$]	1
Well #5 [$n = 14$]	1

Table 3
Summary of protozoan sampling at the three study sites [January 2002–July 2003]

	Total volume assayed [L]	Total No. *Cryptosporidium* Oocysts	Total No. *Giardia* Cysts
Indiana–American Water at Jeffersonville, IN			
Ohio river	182.2 [$n = 18$]	4 [2 of 18][a]	11 [2 of 18]
Well #9	900 [$n = 9$]	0	0
Well #2	500 [$n = 5$]	0	0
Indiana–American Water at Terre Haute, IN			
Wabash river	142.0 [$n = 18$]	5 [3 of 18]	12 [6 of 18]
Collector well	866 [$n = 9$]	0	0
Well #3	500 [$n = 5$]	0	0
Missouri–American Water at Parkville, MO			
Missouri river	156.0 [$n = 18$]	3 [3 of 18]	8 [6 of 18]
Well #4	900 [$n = 9$]	0	0
Well #5	400 [$n = 4$]	0	0

[a]Number of samples with detects out of the total number of sampling rounds.

Table 4
Summary of turbidity monitoring [January 2002–July 2003]; log reductions of average turbidity concentrations in well waters relative to river waters indicated in brackets

	Average turbidity [NTU]	Min. turbidity [NTU]	Max. turbidity [NTU]
Indiana–American Water at Jeffersonville, IN			
Ohio river [$n = 40$]	60.1	1.9	661
Well #9 [$n = 51$]	0.1 [2.8]	0.07	1.1
Well #2 [$n = 52$]	0.2 [2.5]	0.07	1.5
Indiana–American Water at Terre Haute, IN			
Wabash river [$n = 75$]	190.3	0.5	1761
Collector well [$n = 75$]	0.1 [3.3]	0.05	0.27
Well #3 [$n = 74$]	0.1 [3.3]	0.08	0.41
Missouri–American Water at Parkville, MO			
Missouri river [$n = 71$]	78.6	0.8	1521
Well #4 [$n = 68$]	0.5 [2.2]	0.1	3.8
Well #5 [$n = 65$]	0.5 [2.2]	0.1	2.7

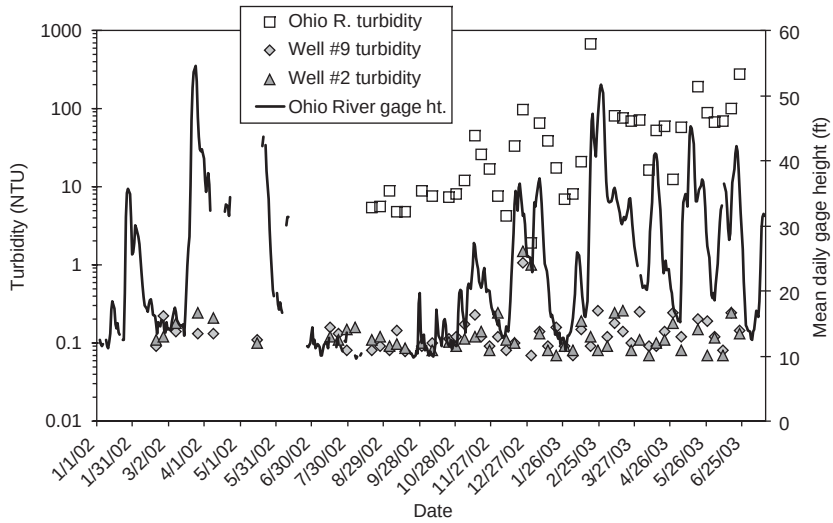

Fig. 2. Jeffersonville turbidity concentrations for all sampling events and mean daily gage height in the Ohio River (from USGS gaging station 03294500 Ohio River at Louisville, KY).

increases in well water turbidity concentrations at Parkville between January and June 2002 appear to correspond to the increasing and fluctuating mean daily discharge in the Missouri River over that time period.

Similar comparisons were made between the river flow data and the microorganism concentrations in the river and well waters. Bacteria concentrations in the river and well waters at Terre Haute, plotted with river discharge, are given in Figs. 5 and 6, respectively. Coliform and spore concentrations in the Wabash River water generally tracked the river discharge, with increased concentrations of bacteria occurring during periods of high discharge (Fig. 5). Because of the lack of a significant number of microbe detections in the well waters, no firm relationship between breakthrough in the well waters and river flow could be established (Fig. 6). Similar conclusions were drawn for the other microorganisms and study sites.

4. Discussion

Prior to this study, results from the few studies of pathogen removal that have been carried out at full-scale RBF facilities have been positive. Gollnitz et al. (2003) monitored *Giardia* cysts and *Cryptosporidium* oocysts in the Great Miami River at the Greater Cincinnati Water Works in Cincinnati, OH from 1991

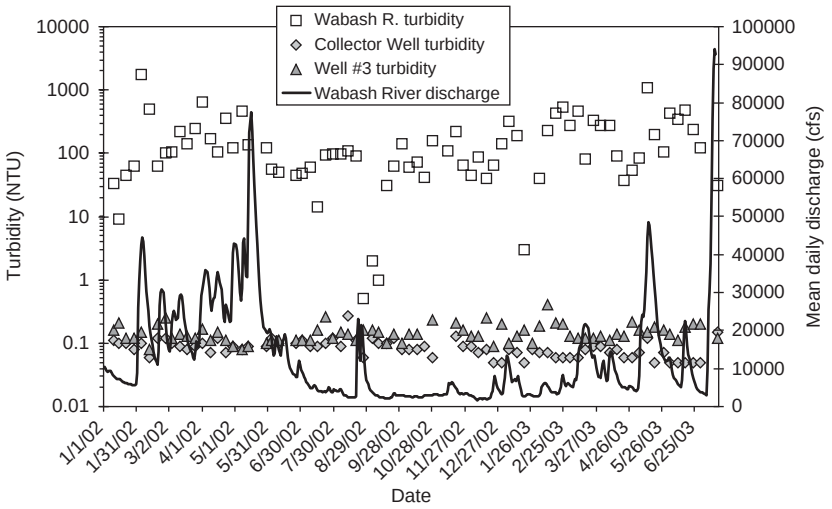

Fig. 3. Terre Haute turbidity concentrations for all sampling events and mean daily discharge in the Wabash River (from USGS gaging station 03341500 Wabash River at Terre Haute, IN).

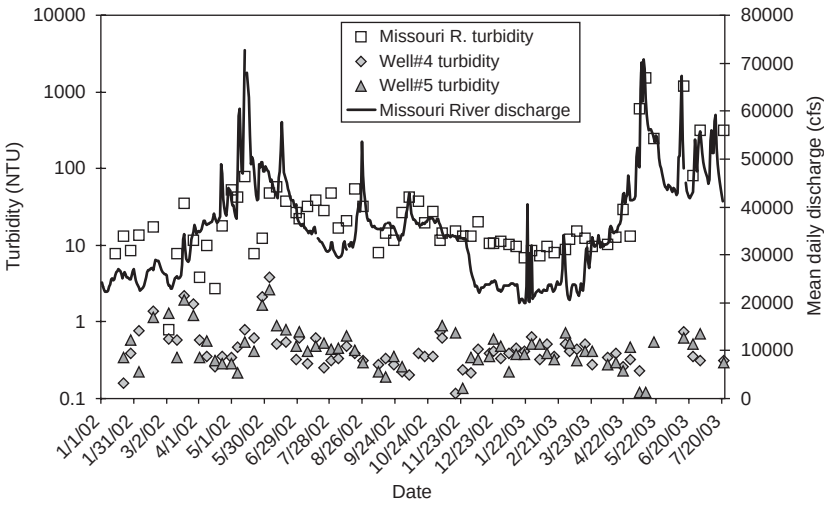

Fig. 4. Parkville turbidity concentrations for all sampling events and mean daily discharge in the Missouri River (from USGS gaging station 06893000 Missouri River at Kansas City, MO).

to 1999 using the Information Collection Rule method (USEPA, 1996), finding cysts in 14 of 43 samples and oocysts in seven of 43 samples, and from 1999 to 2002 using Method 1623 (USEPA, 2001a), finding cysts in 12 of 36 samples and oocysts in four of 36 samples. More than 200 samples taken from production wells and monitoring wells located along the flowpath between the riverbed and the production wells were negative for cysts and oocysts. Reductions of potential surrogates for the protozoans (algae, aerobic bacterial spores, and particle counts in the 3–5- and 7–10-μm size ranges) in two production wells relative to the river concentrations were greater than 3 log units. Weiss et al. (2003a) reported greater than 3 log reductions in average anaerobic *Clostridium* spore concentrations and greater than 1.9 log reductions of average bacteriophage concentrations at the three sites monitored in the current study. Ray et al. (2002a) noted a 3 log reduction in average aerobic bacterial spore concentrations and greater than 6 log reduction in average algal concentrations for a travel distance of 50 ft near a collector well at the Louisville Water Company in Louisville, KY. Despite these positive results, the validity of using particle counts, bacterial spores, algae, or bacteriophage as surrogates for pathogenic microorganisms in RBF systems has not been established.

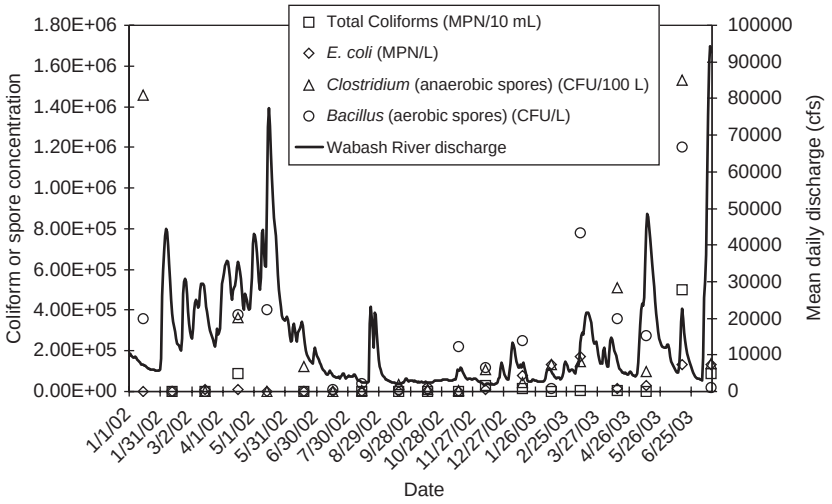

Fig. 5. Terre Haute coliform and bacterial spore concentrations in the Wabash River for all sampling events and mean daily discharge in the Wabash River (from USGS gaging station 03341500 Wabash River at Terre Haute, IN).

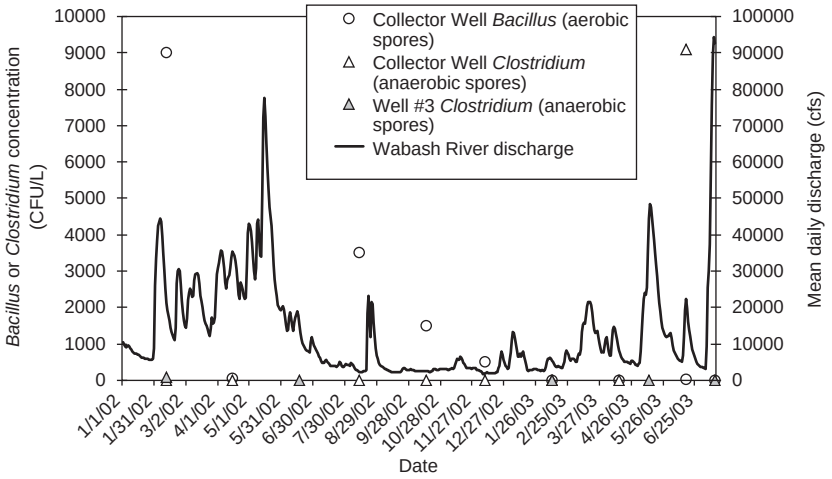

Fig. 6. Terre Haute bacterial spore concentrations in the Collector Well and Well #3 for all sampling events and mean daily discharge in the Wabash River (from USGS gaging station 03341500 Wabash River at Terre Haute, IN).

The data collected during this study show no breakthrough of *Cryptosporidium* and *Giardia* in the well waters, and limited detection of coliforms, aerobic and anaerobic bacterial spores, and bacteriophage in the well waters during RBF at three full-scale facilities. The data illustrate the difficulty involved in accurately evaluating the actual *Cryptosporidium* oocyst and *Giardia* cyst (which are potentially the pathogens of most concern in RBF systems due to their high resistance to conventional means of disinfection) removals within a RBF system. Due to the low and variable concentrations of protozoans in the river waters during the monitoring campaign and their complete absence in the well waters, the data collected were able to provide only a minimum estimate of log removals during RBF at these systems. Although all efforts were made to provide enough sampling events for an accurate evaluation of the input (river) concentrations over a period of more than a year, there is no way to determine from these data the ultimate potential of these systems to provide an adequate barrier to higher concentrations of protozoans entering the system, such as during a heavy rain event. Further, because the protozoan methods involve filtering the water samples, only a limited volume of the river waters could be filtered without clogging the filters with suspended material, resulting in high detection limits for the river waters. In addition, protozoa recovery efficiencies using the best available published methods approved by the EPA were variable and low. It is because of these difficulties inherent in monitoring for

the protozoans that much attention has been focused on potential indicator or surrogate parameters to evaluate pathogen reduction potential in RBF systems.

Because of the variable nature of microorganism concentrations, these field monitoring results were intended to provide an average characterization of river and well water concentrations over a period of more than a year. The method for calculating average microbial concentrations for the data was carefully chosen to provide statistically significant averages. The Parkhurst and Stern (1998) method for calculating average concentrations based on counting non-detects as zeroes was used because the authors found that this method provided the least biased average both at low and high pathogen concentrations.

Aerobic spores (*Bacillus*) were present in the river waters at all three study sites at average concentrations approximately two orders of magnitude higher than that of the anaerobic spores (*Clostridium*) (Table 1). At two of the sites (Jeffersonville and Parkville), calculated log reductions in the well waters relative to the rivers for the aerobic spores were 2–4 logs lower than the corresponding reductions for the anaerobic spores, which were not detected in the wells at either of these two sites. At the third site (Terre Haute), log reductions of average aerobic spore concentrations in the wells relative to the Wabash River water were greater than the corresponding reductions of anaerobic spores, which were detected in both wells. It is not clear whether these log reduction differences were a result of different transport and survival behavior in the subsurface or a result of the different river concentrations of the aerobic and anaerobic spores. Since both types of spores are of interest as potential surrogates for the protozoal pathogens, their relative transport behavior should be the focus of further study.

Total coliforms were occasionally detected in the well waters (Table 2), although average concentrations in the wells at Parkville (the only site for which actual concentrations of total coliforms for the well waters were available) indicated $\geqslant 5.5$ log reductions relative to the Missouri River water. For this site, among the coliforms and spores, the total coliforms data provided the least conservative indicator of RBF performance. In particular, it is noteworthy to compare log reductions of total coliforms for Parkville with the corresponding *Bacillus* data (Table 1). These potential surrogates were present in similar concentrations in the Missouri River water, while average *Bacillus* concentrations in the well waters were significantly higher than the corresponding average total coliforms concentrations.

The results of this study, while positive in regard to the potential for RBF to provide significant reductions in microbial concentrations, illustrate the need for a better understanding of the mobility of pathogens of interest (particularly *Cryptosporidium* and *Giardia*) in comparison to the mobility of potential surrogate and indicator parameters in RBF systems. The potential surrogate/indicator parameters measured here were present in the river waters in significantly higher concentrations and occurred more frequently during the monthly sampling campaign than the protozoan pathogens, providing a better characterization of the input concentrations to the system. However, the parameters measured also exhibited a large range of reductions in the well waters relative to the river waters (from less than 1 log to more than 6 logs). While there is not likely to be one perfect surrogate for pathogen transport in all RBF systems, a better understanding of how such parameters behave during RBF relative to the pathogens is essential as the industry moves toward a protocol to assign treatment credits for utilities that provide adequate protection against waterborne disease using RBF.

5. Conclusions

The results of this study demonstrate the potential for RBF systems to provide a significant barrier to the transport of microorganisms from surface water sources to the extraction wells. The data presented here support the application of treatment credits to utilities using RBF, as proposed by the USEPA as part of the LT2ESWTR microbial toolbox; however, due to the low and variable concentrations of *Cryptosporidium* and *Giardia* present in the river waters, accurate log reductions for these pathogens could not directly be determined. The data indicate the potential for these systems to provide log reductions in several potential surrogate or indicator parameters that exceed the 0.5–1.0 log credits given for *Cryptosporidium* removal by the LT2ESWTR. Further research is necessary to evaluate whether the transport behavior of any of the potential surrogate/indicator parameters measured here would be representative of the behavior of the pathogens. The results obtained during this field monitoring study demonstrate the value of RBF as a treatment technology, especially when considered along with previous work showing the ability of RBF to reduce the concentrations of potentially carcinogenic DBPs and other contaminants in finished drinking water.

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therefore do not necessarily reflect the views of the agency, and no official endorsement should be inferred.

References

Atherholt, T.B., LeChevallier, M.W., Norton, W.D., Rosen, J.S., 1998. Effect of rainfall on Giardia and Crypto. J. Am. Water Works Assoc. 90 (9), 66–80.

Azadpour-Keeley, A., Faulkner, B.R., Chen, J.-S., 2003. Movement and Longevity of Viruses in the Subsurface. EPA/540/S-03/500, Washington.

Berger, P., 2001. Removal of *Cryptosporidium* using bank filtration. In: Laszlo, F., Bourg, A. (Eds.), Riverbank Filtration: Understanding Contaminant Biogeochemistry and Pathogen Removal. Kluwer Academic Publishers, Tihany, Hungary.

Gollnitz, W.D., Clancy, J.L., Whitteberry, B.L., Vogt, J.A., 2003. RBF as a microbial treatment process. J. Am. Water Works Assoc. 95 (12), 56–66.

Hiscock, K.M., Grischek, T., 2002. Attenuation of groundwater pollution by bank filtration. J. Hydrol. 266 (3/4), 139–144.

Irmscher, R., Teermann, I., 2002. Riverbank filtration for drinking water supply—a proven method, perfect to face today's challenges. Water Sci. Technol.: Water Supply 2 (5/6), 1–8.

Kuehn, W., Mueller, U., 2000. Riverbank filtration: an overview. J. Am. Water Works Assoc. 92 (12), 60–69.

LeChevallier, M.W., Norton, W.D., Lee, R.G., 1991. *Giardia* and *Cryptosporidium* spp. In filtered drinking water supplies. Appl. Environ. Microbiol. 57 (9), 2617–2621.

Nieminski, E.C., Bellamy, W.D., Moss, L.R., 2000. Using surrogates to improve plant performance. J. Am. Water Works Assoc. 92 (3), 67–78.

Parkhurst, D.F., Stern, D.A., 1998. Determining average concentrations of *Cryptosporidium* and other pathogens in water. Environ. Sci. Technol. 32 (21), 3424–3429.

Ray, C., 2004. Modeling RBF efficacy for mitigating chemical shock loads. J. Am. Water Works Assoc. 96 (5), 114–128.

Ray, C., Grischek, T., Schubert, J., Wang, J.Z., Speth, T.F., 2002a. A perspective of riverbank filtration. J. Am. Water Works Assoc. 94 (4), 149–160.

Ray, C., Melin, G., Linsky, R.B., 2002b. Riverbank Filtration: Improving Source-Water Quality. Kluwer Academic Publishers, Dordrecht, The Netherlands.

Rice, E.W., Fox, K.R., Miltner, R.J., Lytle, D.A., Johnson, C.H., 1996. Evaluating plant performance with endospores. J. Am. Water Works Assoc. 88 (9), 122–130.

Schijven, J.F., de Bruin, H.A.M., Hassanizadeh, S.M., de Roda Husman, A.M., 2003. Bacteriophages and clostridium spores as indicator organisms for removal of pathogens by passage through saturated Dune sand. Water Res. 37 (9), 2186–2194.

Sobsey, M.D., Battigelli, D.A., Handzel, T.R., Schwab, K.J., 1995. Male-specific Coliphages as Indicators of Viral Contamination of Drinking Water. American Water Works Research Foundation, Denver, CO 150pp.

Solo-Gabriele, H., Neumeister, S., 1996. US outbreaks of cryptosporidiosis. J. Am. Water Works Assoc. 88 (9), 76–86.

Standard Methods for the Examination of Water and Wastewater, 1998. 20th ed., APHA, AWWA, and WEF, Washington.

Tufenkji, N., Ryan, J.N., Elimelech, M., 2002. The promise of bank filtration. Environ. Sci. Technol. 36 (11), 422A–428A.

USEPA, 1996. ICR Microbial Laboratory Manual. EPA/600/R-95/178, Washington.

USEPA, 2001a. Method 1623: *Cryptosporidium* and *Giardia* in Water by Filtration/IMS/FA. EPA/821/R-01/025, Washington.

USEPA, 2001b. Method 1602: male-specific (F^+) and somatic coliphage in water by single agar layer (SAL) procedure. EPA/821/R-01/029, Washington.

USEPA, 2003. National primary drinking water regulations: long term 2 enhanced surface water treatment rule. Fed. Register 68 (154).

Verstraeten, I.M., Thurman, E.M., Lindsey, M.E., Lee, E.C., Smith, R.D., 2002. Changes in concentrations of Triazine and Acetamide Herbicides by Bank filtration, ozonation, and chlorination in a public water supply. J. Hydrol. 266 (3/4), 190–208.

Weiss, W.J., Bouwer, E.J., Ball, W.P., O'Melia, C.R., LeChevallier, M.W., Arora, H., Speth, T.F., 2003a. Riverbank filtration—fate of DBP precursors and selected microorganisms. J. Am. Water Works Assoc. 95 (10), 68–81.

Weiss, W.J., Bouwer, E.J., Ball, W.P., O'Melia, C.R., Arora, H., Speth, T.F., 2003b. Comparing RBF with bench-scale conventional treatment for precursor reduction. J. Am. Water Works Assoc. 95 (12), 67–80.