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Effects of Holding Time, Storage, and the Preservation of Samples on Sample Integrity for the Detection of Fecal Indicator Bacteria by Quantitative Polymerase Chain Reaction

RESEARCH AND DEVELOPMENT

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Effects of Holding Time, Storage, and the Preservation of Samples on Sample Integrity for the Detection of Fecal Indicator Bacteria by Quantitative Polymerase Chain Reaction (qPCR)-based Assays

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Executive Summary

The purpose of this project was to answer questions related to storage of samples to be analyzed by the quantitative polymerase chain reaction (qPCR)-based assays for fecal indicator bacteria. The report is divided into two parts. The first part describes studies that were performed to determine if filters that are used to collect fecal indicator bacteria can be stored frozen and analyzed at a later date. These studies were primarily directed at a specific, targeted question: can qPCR results from freezer archived samples be used to establish valid relationships between fecal indicator densities and health effects data collected from previous epidemiological studies. The second part describes studies that were performed to determine if refrigerated water samples can be held for 24 to 48 hours prior to analysis by qPCR. These studies addressed a question that may be relevant to the implementation of the qPCR method for water quality monitoring at remote locations where immediate analysis of the samples is not possible.

Part 1.
Archived Sample Stability Study and Long-Term Holding Time Study: Evaluation of effects of freezer-storage on the preservation of filter samples for qPCR analysis

The Beach Environmental Assessment and Coastal Health (BEACH) Act of 2000 directed the U.S. EPA to conduct studies concerning pathogen indicators in coastal recreation waters. The results of these studies are to be used by U.S. EPA to publish new or revised water quality criteria for the purpose of protecting human health in coastal recreational waters. U.S. EPA has conducted a number of studies pursuant to the BEACH Act including studies:

- To develop new rapid methods for measuring water quality
- To establish the relationship between water quality and health using the rapid methods
- To develop a system for monitoring water quality
- To provide guidance to states on the application of the new methods

The U.S. EPA has conducted the National Epidemiological and Environmental Assessment Research (NEEAR) Water Study at four beaches on the Great Lakes and three on the Atlantic and Gulf Coasts. Water quality at each of the beaches was impacted by point sources that

received combined treated sewage discharges from communities with populations of at least 15,000.

The NEEAR studies contained a health data collection component as described in Wade et al. (2006, 2008, 2010). The objective of the health portion of the studies was to quantify the symptomatological observations of illnesses in the swimmer vs. non-swimmer groups. The second component of the studies was to collect exposure data based on fecal indicator bacteria (FIB) densities in the water as determined by rapid methods such as quantitative polymerase chain reaction (qPCR) for *Enterococcus*. Data from the two components of the studies were compared to assess the relationships between risk of swimming-related illness and exposure (Wade et al. 2006, 2008, 2010).

As part of the NEEAR study design, additional replicate aliquots of each water sample were filtered and the filters were archived by freezing at -40 °C. The ultimate objective of the archived NEEAR sample stability study was to establish if the results of several more recently developed qPCR methods (e.g., for alternative indicators such as *Escherichia coli* and *Bacteroidales*) or method modifications might be suitable for generating meaningful health relationship assessments. If the archived sample results did not show a change with respect to the original sample results using the original qPCR methods, this would lend credibility to using the results of the newer qPCR methods employed in the analyses of the archived samples for also assessing health relationships using the health data collected from the original NEEAR studies. To address the question of archived sample stability, the analysis results from each of the qPCR methods that were performed from 2003–2007 on the original NEEAR study samples (*Enterococcus* for both fresh water and marine beach samples and *Bacteroidales* for marine beach samples only) were compared with corresponding results obtained two to six years later in 2009 from the archived samples.

To further evaluate the effects of filter freezer storage on qPCR analysis results, a supplemental long-term holding time study was also conducted by the U.S. EPA, Region 1 Research Laboratory in North Chelmsford, MA. In this study, replicate filters from 29 fresh water and 23 marine water samples from diverse non-recreational beach locations in the Boston, MA area

were held in freezer storage for varying lengths of time from 1 day up to 2 years prior to analysis. In addition to qPCR analysis for *Enterococcus*, this study also sought to provide data for some of the newer qPCR-based methods that were not included in the original NEEAR studies (specifically *Bacteroidales* in fresh water and *E. coli* in both fresh and marine waters). A demonstration that the filter analysis results in this study did not show a change over time, would lend further credibility to using the analysis results of the archived NEEAR study samples by these newer qPCR methods to assess health relationships.

Results from the NEEAR archived sample stability study showed, however, that substantial and statistically significant degradation of samples had occurred. The highly significant changes and low or absent correlation between archived and original sample analysis results indicate that the archived filters cannot be used in a credible manner to establish health relationships involving *Enterococcus* qPCR or, by extension, any other indicator, pathogen, or method. Any health relationships based on data derived from the archived samples is not useful because they do not reflect data that would have been obtained from the original samples in actual beach monitoring circumstances.

The results from the long-term holding time study, though of reduced importance due to the findings from the archived sample stability study, showed statistically significant decreases in qPCR estimates of *Bacteroidales* and *E. coli* after 2 years of freezer storage. These results complement the findings from the archived NEEAR study sample analyses for *Enterococcus* in indicating that archived sample analysis results for the two alternative indicator bacteria groups (*Bacteroidales* and *E. coli*) cannot be used in a credible manner to establish health relationships. It is noted that the holding temperature used in this study was -20 °C.

Part 2.
Short-Term Holding Time Study: Evaluation of holding refrigerated surface water samples for up to 48 h for qPCR analysis

The short-term holding time study was conducted to determine whether holding refrigerated surface water samples for 24 and 48 hours affects qPCR-determined density estimates of *Enterococcus*, *Escherichia coli*, and *Bacteroidales* bacteria as compared to results from samples

processed within the currently accepted holding time limit of six hours. Additional subsamples of the same water samples, collected in the Boston, Massachusetts area for the U.S. EPA Region 1 long term holding study, were held with refrigeration for 24 and 48 hours prior to the collection of target organisms by filtration and qPCR analysis. A supplemental study, motivated by ambiguous results from the main study of Boston area water samples, was also conducted using an Ohio River water sample.

Results from the short-term holding time study of Boston area water samples showed small but in some cases statistically significant changes in qPCR-estimated densities of the three different fecal indicator organism groups in subsamples of the water samples that were held for 24 and 48 hours prior to filtration compared to corresponding subsamples that were filtered within six hours. However, these changes were not consistent for the 24 and 48 hour holding times nor were they consistent between indicators. In comparisons with subsamples of the Ohio River water sample held for just one hour prior to filtration, statistically significant declines in density estimates of one of the indicator groups were observed in subsamples held for 24 hours and of all three indicator groups in subsamples held for 48 hours. Overall, the results of these studies were inconclusive and, as a result, **can neither support nor refute** recommendations to hold refrigerated water samples for 24 hours or longer prior to filtration and analysis.

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Introduction

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The NEEAR studies contained a health data collection component as described in Wade et al. (2006, 2008, 2010). The objective of the health portion of the studies was to quantify the symptomatological observations in the swimmer vs. non-swimmer groups. The second component of the studies was to collect water quality data on fecal indicator bacteria (FIB) using rapid methods such as quantitative polymerase chain reaction (qPCR) for *Enterococcus* and *Bacteroidales*.

As part of the NEEAR study design, additional replicate aliquots of each water sample were filtered and the filters were archived by freezing. The key objective of the archived NEEAR sample stability study was to establish if the results of several more recently developed qPCR methods (e.g., for alternative indicators such as *E. coli* and *Bacteroidales*) or using various method modifications might be suitable for generating meaningful health relationship assessments. If the archived sample results did not show a change with respect to the original sample results using the original qPCR methods, this would lend credibility to using the results of the newer qPCR methods that were employed in the analyses of the archived samples for also assessing health relationships. To address the question of archived sample stability, the analysis results from each of the qPCR methods that were performed from 2003–2007 on the original NEEAR study samples (*Enterococcus* for both fresh water and marine beach samples and *Bacteroidales* for marine beach samples only) were compared with corresponding results obtained two to six years later in 2009 from the archived samples.

To further evaluate the effects of filter freezer storage on qPCR analysis results, a supplemental long-term holding time study was also conducted by the U.S. EPA, Region 1 Research Laboratory in North Chelmsford, MA. In this study, replicate filters from 29 fresh water and 23 marine water samples from diverse non-recreational beach locations in the Boston, MA area were held in freezer storage for varying lengths of time from 24 hours up to2 years prior to analysis. In addition to qPCR analysis for *Enterococcus*, this study also sought to provide data for newer qPCR-based methods that were not included in the original NEEAR studies (specifically *Bacteroidales* in fresh water and *E. coli* in both fresh and marine waters). A demonstration that the filter analysis results in this study did not show a change over time, would lend further credibility to using the analysis results of the archived NEEAR study samples by these newer qPCR methods to assess health relationships.

Material and Methods

Materials and methods for archived sample stability study

Water samples. Water samples for the NEEAR study were collected over a four year period from 2003 to 2007. Sampling sites were West Beach at the Indiana Dunes National Lakeshore in

Porter, Indiana on Lake Michigan in 2003; Huntington Beach in Bay Village, Ohio on Lake Erie in 2003; Silver Beach, near St. Joseph, Michigan, and Washington Park Beach in Michigan City, Indiana on Lake Michigan in 2004; Edgewater Beach in Biloxi, MS on the Gulf of Mexico in 2005; Fairhope Municipal Beach in Fairhope, AL on the Gulf of Mexico in 2007; and Goddard State Memorial Park Beach in West Warwick, RI on Long Island Sound in 2007.

Sampling designs were similar at each of the sites. Sampling visits occurred on Saturdays, Sundays and holidays over time periods varying from approximately 10 to 12 weeks from either May through August or June through September. Sampling occurred three times daily, at 8 AM, 11 AM, and 3 PM in waist-level (1 m deep) and shin-level water (0.3 m deep) locations along three transects perpendicular to the shoreline. The sampling design at Huntington Beach included three additional shin-level locations.

Sample collection and distribution. One liter water samples were collected at each location by standard methods as recommended in Section 9060 of *Standard Methods for the Examination of Water and Wastewater*, American Public Health Association (1998). Following collection, all samples were placed in coolers and maintained on ice during transport to a local laboratory and at 1–4 °C during the time interval before they were processed. Processing of all samples by filtration was performed within six hours of collection.

Duplicate 50 or 100 ml volumes of each water sample (either 50 or 100 ml was used consistently for all samples within a beach) were filtered through 47-mm, 0.4-µm pore size polycarbonate filters (catalog #K04CP04700, Osmonics Inc., Minnetonka, MN) and the sides of the funnels were rinsed twice with 20 ml of sterile, phosphate buffered saline. The filters were transferred to a Petri dish with the sample side facing up. Using sterile forceps, each filter was folded into a cylinder with the sample side facing inward, and then inserted into a 2 ml semiconical screw-cap microcentrifuge tube (extraction tube; catalog #506-636, PGC Scientific, Gaithersburg, MD) containing 0.3 g of acid-washed glass beads (catalog #G-1277, Sigma, St. Louis, MO). The filters were held at -20 °C for no more than three days until shipment to the analytical laboratories on dry ice. One filter from each water sample was shipped to EMSL Analytical,

Inc., Cinnaminson, NJ for analysis within seven days while the duplicate was shipped to the U.S. EPA's National Exposure Research Laboratory (NERL), Cincinnati, OH for archiving.

Sample archiving. Filters received by the U.S. EPA NERL laboratory were immediately transferred to a -40 °C, 25 cubic ft. capacity, 208V upright freezer (model A25-40T, So-Low Environmental Equipment Co., Cincinnati, OH) where they were stored continuously (except as noted below) until analysis in 2009. The freezer temperature was continuously monitored by a centralized monitoring system within the Cincinnati facility. On several occasions samples were briefly removed from the freezer for reorganization and/or while defrosting of the freezer and on one occasion they were temporarily transferred to other freezers due to a facility power outage. Possible temperature changes of the filters during these activities were not determined.

Sample analyses. Original filters sent to the EMSL lab and archived filters stored at the NERL laboratory were extracted to recover total DNA and the DNA extracts were subjected to qPCR analysis by the basic procedures described in Haugland et al. (2005). Briefly, cells were suspended from the filters and lysed in a bead mill for 60 seconds at maximum speed and the debris was removed by centrifugation. For all samples analyzed after 2004, including the archived samples, the published DNA extraction procedure was modified slightly by increasing the total volume of extraction buffer, containing 0.2 µg ml^{-1} salmon DNA in AE buffer (Qiagen, Valencia, CA), from 0.3 ml to 0.6 ml and decreasing the dilution of extracts prior to analysis from 10-fold to 5-fold. Calibrator samples (three to six replicates), consisting of clean polycarbonate filters amended with known cell quantities of *Enterococcus faecalis* (ATCC# 29212) and/or *Bacteroides thetaiotaomicron* (ATCC # 29741), and negative control samples (three to six replicates), consisting of clean filters only, were extracted in the same manner with each batch of test samples. Cells used by EMSL in the calibrator samples originated from laboratory grown cultures and were enumerated as previously described (Haugland et al. 2005, Siefring et al. 2008). Cells used by U.S. EPA NERL were enumerated by flow cytometry and were acquired in the form of commercially available, lyophilized pellets (Bioballs™, BTF, Sydney Australia). QPCR analyses were performed using previously described primer and TaqMan™ hybridization probe assays for *Enterococcus* and *Oncorhynchus keta* (salmon) DNA target sequences (Haugland et al. 2005) on all samples (Great Lakes and marine) and a

previously described primer and TaqMan™ hybridization probe assay for total *Bacteroidales* target sequences (Siefring et al. 2008) were performed on marine samples only. Primer and probe characteristics of each of these assays are listed in part II of this report. QPCR amplification of water sample and calibrator sample DNA extracts, and negative control samples, was performed by using 5 µL of equally diluted extracts in a total reaction volume of 25 µL. Reagent mixes were prepared by combining 12.5 µL of TaqMan® Universal Master Mix (Applied Biosystems, Foster City, CA), 2.5 µL of 2 mg/ml bovine serum albumin, 1 µM of each primer, and 80 nM of probe for each reaction. Amplification occurred with an initial start at 50 °C for 2 min followed by 95 °C for 10 min, then forty PCR cycles of 95 °C for 15 s and 60 °C for 1 min. All analyses of the fresh samples were performed by EMSL Analytical Inc., Cherry Hill, NJ in a Cepheid SmartCycler® II (Cepheid, Sunnyvale, CA). All analyses of the archived samples were performed in the U.S. EPA NERL laboratory in either a Cepheid SmartCycler® II (freshwater samples) or in an Applied Biosystems StepOnePlus® (marine samples). Results obtained on these two instruments have been previously compared in simultaneous analyses of DNA extracts from multiple, replicate filter retentates of 12 marine and 12 freshwater samples from diverse locations. No significant difference ($p > .05$) in log10 target sequence copy recovery estimates, based on three-way ANOVA with fixed factors: instrument, matrix, instrument*matrix; and random factors: sample (nested in matrix) and inst*sample (nested in matrix), nor in precision among these estimates ($p > .05$), based on the one-way ANOVA of Levene's Test for Homogeneity of Variance was observed in the results from the two instruments (unpublished data). For this reason results from the present study treated results from both instruments as equivalent or interchangeable.

Materials and methods for long-term holding time study

Water samples. Water samples analyzed in this study were collected from 29 freshwater sites and 23 marine water sites in the Boston, MA area. Different subsamples of the same water samples used in this study were used for the short term holding study, presented in part II of this report. Sampling locations and considerations in the selection of these locations are described in part II of this report. Although 25 samples from both marine and freshwater sites were planned for, some sites thought to be saltwater were later reclassified after measurements revealed low levels of salinity.

Sample collection and archiving. Either three or four water samples were simultaneously collected in 1 liter bottles at each site by standard methods as recommended in Section 9060 of *Standard Methods for the Examination of Water and Wastewater*, American Public Health Association (1998). Following collection, all samples were placed in coolers and maintained on ice during transport to the U.S. EPA Region 1 laboratory and at 1–4 °C during the time interval before they were processed.

Upon arrival to the laboratory, and within six hours of collection, the contents of the individual 1 liter collection bottles for each sampling site were combined in a carboy and mixed. A total of eight 50 ml, or for some samples 100 ml, volume aliquots of each composite water sample were filtered through 47-mm, 0.4-μm pore size polycarbonate filters (catalog #K04CP04700, Osmonics Inc., Minnetonka, MN) and the sides of the funnels were rinsed twice with 20 ml of sterile, phosphate buffered saline. The filters were then transferred to a Petri dish with the sample side facing up. Using sterile forceps, each filter was folded in half three times to form an umbrella and then inserted into a 2 ml semiconical screw-cap extraction tubes, containing 0.3 g of siliconized ceramic beads (Roche MagNA Lyser Green Beads™). All filter samples were flash frozen by placing the tubes in a cooling block, pre-chilled to -20 °C for 1 hour, and then held in a -20 °C freezer until they were extracted and analyzed. Duplicate filter samples from each site were extracted and analyzed after being held for 1 day, and 6, 12, and 24 months. Multiple replicate calibrator sample filters were prepared just prior to the study by placing aliquots of a single mixed cell suspension containing pre-determined cell quantities of laboratory-grown, representative target strains of each of the assays (*E. faecalis, B. thetaiotaomicron* and *E. coli*) on clean filters. These calibrator filter samples were held at -20 °C and replicate filters were extracted and analyzed in parallel with each batch of test samples at each time point in the holding study. Since the calibrator sample filters were held in freezer storage for the same lengths of time as the water sample filters, the holding time effects presented in this report are specific to the water samples and do not take into account any potential holding time effects on the cultured calibrator cells. However, target sequence recoveries from the calibrator samples were also assessed independently at each time point based

on comparisons of raw CT values and after calibration of the CT results with standard curve data.

Sample analyses. Filter samples were extracted to recover total DNA and the DNA extracts were subjected to qPCR analysis as described for the NEEAR study samples. Duplicate analyses were performed on each filter sample extract. In addition, analyses for *E. coli* 23S rRNA gene target sequences were performed in the same manner except using Gene Expression PCR Master Mix (Applied Biosystems) and an unpublished TaqMan® probe and primer set (Primer and probe characteristics of this assay are listed in part II of this report). All of the qPCR analyses were conducted by the U.S. EPA Region 1 laboratory in a Cepheid SmartCycler® II.

Computational methods

Analysis data consisted of paired observations of filters from each sample: (1) a qPCR measurement soon after the sample had been collected and (2) a qPCR measurement after archival and storage over a six month to two year period (long-term holding time study) or a two to six year period (archived sample stability study). Statistical analysis was performed on log transformed calibrator cell equivalents (CCE) estimated by qPCR using the "ΔΔCT" approach as previously described (Haugland et al. 2005) and as used in the NEEAR study analysis of swimmers' risk-exposure relationship (Wade et al. 2006, 2008, 2010).

The ΔΔCT computational approach, which is derived from the comparative cycle threshold (CT) method (Applied Biosystems 1997), employs an arithmetic formula to determine the ratio of target sequence quantities in DNA extracts from test sample filters relative to those in similarly-prepared DNA extracts from calibrator sample filters containing a known quantity of target organism cells based on the difference in CT values obtained from qPCR analyses of these samples. Similar comparisons of CT values from qPCR assays for an exogenous target sequence from salmon sperm DNA, added in equal quantities to both the test and calibrator sample filters before DNA extraction, were used both as a reference to normalize results for differences in the amount of total DNA recovered from each sample (e.g., caused by test sample effects on DNA recovery) and as a sample processing control (SPC) to signal potentially non-quantifiable test sample results caused by PCR inhibition or low DNA recoveries (Haugland et al. 2005). The calculation can be expressed by the following equations:

$$\Delta\Delta C_T = \Delta C_{T,target} - \Delta C_{T,reference} \quad (1)$$

$$CCE = N_{Calibrator} \cdot A^{-\Delta\Delta CT} \quad (2)$$

in which $\Delta C_{T,target}$ represents $C_{T,sample}$ - Mean $C_{T,calibrator}$ for the target sequence (e.g., enterococci) and $\Delta C_{T,reference}$ represents the corresponding difference for the salmon sperm reference sequence. $N_{calibrator}$ is the known number of cells in the calibrator sample and A is the amplification factor for the assay. Ideally, A=2 but typically it is in the range 1.9 – 2.0 with values less than 2 resulting from less than 100% replication of the target sequence at each cycle. In practice, A is either assumed to be 2 or is calculated based on the slope of a standard curve (Applied Biosystems 1997). The calculation can be expressed by the following equation:

$$A = 10\text{^}(1/\text{-stand curve slope}) \quad (3)$$

For both the archived sample stability and the long-term holding time studies, slope values were obtained from standard curves generated by each of the laboratories from pooled results of repeated qPCR analyses of serially diluted DNA standards nominally containing target sequences in a range from 10 to 4 x 10^4 copies per analysis. Table 1-1 shows the Y-intercept, slope and amplification factors calculated by each of the laboratories from their respective master standard curves from each of the qPCR assays.

Table 1-1. Master standard curve variables for qPCR assays

Laboratory (instrument)	Indicator qPCR Assay	Y-intercept	Slope	A
EMSL (Smart Cycler)	*Enterococcus*	38.32	-3.42	1.96
	Bacteroidales	38.61	-3.34	1.99
NERL (Smart Cycler)	*Enterococcus*	38.16	-3.62	1.89
NERL (StepOnePlus))	*Enterococcus*	38.94	-3.50	1.95
	Bacteroidales	39.19	-3.62	1.89
U.S. EPA Region 1 (Smart Cycler)	*Enterococcus*	37.01	-3.24	2.05
	Bacteroidales	37.41	-3.22	2.05
	E. coli	39.62	-3.45	1.95

Statistical analyses

For both the archived sample stability and the long-term holding time studies, the analyses were conceptually the same, although differences in the designs of the respective studies necessitated slightly different treatment of the data. In the long-term holding time study, duplicate filters were analyzed for each sample and the extract from each filter was analyzed by qPCR in duplicate reactions at each time point. All of the results were well above the detection limit, this having been a criterion of sample selection in the first place. Therefore, for each water type, a nesting sampling scheme was present (duplicate analysis nested within filter and filter nested within sample). A mixed model was used to account for these as nested random effects. Data from the Frozen Storage study were analyzed using the MIXED procedure in SAS v. 9 for Windows (SAS Institute, Cary, NC 2009). Explicitly, the model used was:

$$\Delta\Delta C_T = W + T + WT + Sample(W) + S*T(W) + Filter(W*T*S) + \varepsilon(0,\sigma^2) \qquad (4)$$

in which W represents water type (fresh, marine), T represents time (0, 6 m, 12 m, 24 m), S uniquely identifies an individual random sample within each water type, and F is a uniquely identified filter (filter 1 or 2) within each sample. Within filter, there is random variability represented by $\varepsilon(0,\sigma^2)$, which is assumed normal with mean zero and variance σ^2 of the duplicate runs performed on each filter.

In the archived sample stability study, a single analysis of a single filter of each sample was performed shortly after collection and again for an archived filter two to six years later. The samples were not collected with the intention that they would necessarily all contain sufficiently high densities of the target fecal indicator organisms to allow their detection and, in fact, many samples were non-detects (up to 20% depending on beach). Data from the archived sample stability study could thus be analyzed for differences (archived result minus original result), but it was necessary to consider the non-detects as censored results. If the censored result was the original analysis, the difference was right censored, that is representing a lower bound on the actual difference since the original result could be lower than the stated value. Similarly, if the censored result was the archived analysis, the difference was left-censored, that is, likely to be smaller than the stated value. Sufficient statistics comprised the set of samples for which one or

both results were quantifiable so that samples for which both analyses yielded non-quantifiable results were ignored.

Maximum likelihood estimation ("Tobit analysis") was used for the archived sample stability study analysis where the difference in log (base 10) between the qPCR results before and after archival were censored as above. Monte Carlo Markov Chain (MCMC) estimation using WinBUGS v. 1.4 (Lunn et al. 2000, Ntzoufras 2009) with diffuse priors was employed for this purpose because of the software's ability to capture estimates of individual differences. These estimates were useful for evaluating the reasonableness of the normality model used and for further evaluating paired observations, particularly in terms of prediction of archived results based on the original results.

Other data analyses and summaries were performed in R v. 2.8 (2008) and Excel 2003 for Windows. An alpha level of 0.05 is used to determine statistical significance of differences or effects.

Quality control/ Quality assurance

Laboratory

General guidance for overall laboratory quality assurance for environmental PCR analyses have been developed (U.S. EPA 2004) and was followed in this project.

Cultures

Culture collection strains of representative target species *E. faecalis, B. thetaiotaomicron,* and *E .coli* were maintained as cell suspension freezer stocks. Fresh cultures of these strains were prepared as described in the qPCR methods (U.S. EPA 2010a, 2010b, Chern et al. 2010) and routinely checked for evidence of contamination by microscopic examination of cell morphology and by examination of colony morphology on the appropriate agar plates. Freezer stocks were maintained at -80 °C. For NERL Cincinnati analyses, lyophilized Bioball^{TM} cell preparations were used to prepare positive control (calibrator) samples rather than lab-grown cell preparations.

Water samples

Collection and storage of water samples were conducted following general quality control guidelines described in sections 9060 A and B of Standard Methods for the Examination of Water and Wastewater (1998) and specific guidelines for the qPCR methods (U.S. EPA 2010a, 2010b).

Instruments

Microscopes and general laboratory equipment. General guidelines described in section 9030 of Standard Methods for the Examination of Water and Wastewater (1998) were followed for the maintenance of microscopes and general laboratory equipment.

Real-time sequence detection instruments. Calibrations of instruments were performed on-site or off-site as specified by the instrument manufacturers. Potential instrument performance problems were identified from positive control QC sample results. Service contracts for the instruments were maintained which included telephone troubleshooting support and on-site or off-site instrument service by a factory trained technician when required.

Data

qPCR data. Raw fluorescence growth curve data and other diagnostic information generated by the sequence detectors (run files) were archived on compact disks or flash drives that were specifically designated for this purpose. Run files were labeled with the date of the analysis and the analyst's initials. C_T results tables from each instrument run were exported and saved as Excel files. Data from analyses performed by the sequence detectors consisted of C_T values from the different assays for positive control (calibrator), negative control, and test samples. The C_T data were copied into Excel template worksheets that were custom designed for performing comparative cycle threshold analysis and simple descriptive statistics tests (e.g., means and standard deviations of replicate samples).

Quality controls, QC acceptance criteria and responses

CFU enumeration. Quality controls for *Enterococcus, B. thetaiotaomicron* and *E. coli* cultured cell enumeration were performed as described in the qPCR methods (U.S. EPA 2010a, 2010b, Chern et al. 2010). Certificates of analyses indicating mean and standard deviations of cell quantities per Bioball^{TM} for each lot were either provided directly by the manufacturer or are available online at: http://www.btfbio.com/cofa.php?nav=BioBall.

qPCR analyses. Quality controls and QC acceptance criteria used in the *Enterococcus* and *Bacteroidales* qPCR methods have been reported (U.S. EPA 2010a, 2010b). The same quality controls and QC acceptance criteria were employed in qPCR analyses for *E. coli.* These QC acceptance criteria are identified in Table 1-2.

QC failures and responses. Frequencies of samples that failed the QC acceptance criterion for the salmon DNA SPC in the archived sample stability study are indicated in Table 1-3. These samples were excluded from further analyses. All other QC acceptance criteria for sample analyses by qPCR were consistently met.

Table 1-2. QC acceptance criteria for current U.S. EPA *Enterococcus* and *Bacteroidales* qPCR methods[1]

Control	Method	QC acceptance criteria
Negative controls	qPCR assay for target sequences in no template controls	At least 66% of analyses yield no logarithmic amplification traces. All analyses yield C_T values >35.
	qPCR assay for target sequences in method blanks	At least 66% of analyses yield no logarithmic amplification traces. All analyses yield C_T values >35.
Positive controls	qPCR assay for SPC sequences	Test sample analyses are within 3 C_T units of mean value from daily analyses of at least 3 equally diluted calibrator samples.
	qPCR assay for target sequences in calibrator samples	Baseline mean C_T value and standard deviation are determined from analyses of a minimum of 9 calibrator samples. Mean C_T values from daily analyses of calibrator samples from same source are within 3 standard deviations of the laboratory's baseline mean C_T value.
	Standard Curves	Baseline slope values are determined from linear regression analysis of C_T values from a minimum of three separate analyses (performed in duplicate) of DNA standards. Slope values determined from subsequent analyses are within 95% confidence range of baseline values.

[1] Unless otherwise specified, same QC acceptance criteria are applied to methods for alternative indicators.

Table 1-3. NEEAR study archived sample characteristics

	West Beach	Huntington Beach	Silver Beach	Washington Park Beach	Edgewater Beach	Fairhope Beach	Goddard Beach
Years stored	6	6	5	5	4	2	2
			Enterococcus qPCR-CCE				
Total Samples	294	420	423	421	396	438	426
- Failed QC[1]	11	5	16	19	29	36	8
- Both times < DL[2]	8	10	18	7	9	49	35
Samples Used	275	405	389	395	358	353	383
# samples							
- Original < DL	5	7	38	23	38	74	24
- Archived < DL	102	111	105	113	46	85	109
- Neither < DL	168	287	246	259	274	194	250
% < DL before or after archival[3]	38.9	29.1	36.8	34.4	23.5	45.0	34.7
			Bacteroidales qPCR-CCE				
Total Samples	-[4]	-	-	-	396	438	426
- Failed QC	-	-	-	-	16	5	12
- Both times < DL	-	-	-	-	26	36	5
Samples Used	-	-	-	-	354	397	409
# samples	-	-	-	-			
- Original < DL	-	-	-	-	14	36	29
- Archived < DL	-	-	-	-	33	14	20
- Never < DL	-	-	-	-	307	347	360
% < DL before or after archival	-	-	-	-	13.3	12.6	12.0

[1] Sample Processing Control out of range of ±3 cycle thresholds from mean.

[2] Detection limit (DL) of 40 cycles reached without a positive signal in analyses for both the initial and archive sample.

[3] Among samples used.

[4] *Bacteroidales* qPCR was not performed at the 4 freshwater beaches.

Results

Archived sample stability study

Table 1-3 summarizes sample characteristics from the NEEAR original and archived data analyses. A total of 2818 samples were collected at the four fresh water and three marine water beach sites. An average of 4% and 5% of these samples did not meet quality control standards or gave assay values below the detection limit for both the original and archived samples, analyzed by EMSL Analytical Inc. and U.S. EPA, respectively. These samples were excluded from further analyses. Quality control failure and unusable data rates were similar for both fresh and marine samples (Table 1-3).

Of particular note is the relative number of sample data that were below the detection limit ("censored") in the original analysis vs. when they were reanalyzed after a period of archival. For the *Enterococcus* assay, 24 to 45% of the samples from the different beaches yielded at least one qPCR result that was below the limit of detection. Among the Great Lakes samples, as well as Goddard Beach, non-detects were much more frequent after archival than before. This is as expected if there is a decline in the qPCR signal as a result of archival. However, at the other two marine beaches, non-detects were about as likely to occur after as they were before being archived. The imbalance in results below the limit of detection in original vs. archived samples was one more impetus to incorporate the non-detects in the analysis. Otherwise, results would be biased by discarding more samples that had declined than those that had increased.

Non-detect results for *Bacteroidales* were considerably less prevalent because of the larger number of these organisms, generally amounting to about an order-of-magnitude. Assays for *Bacteroidales* were performed at only the three marine beaches, where non-detect results amounted to only about 13% of all usable samples. While the percentage of non-detects may be small in comparison to those for *Enterococcus*, a 13% non-detect rate is still substantial. Note that samples with non-detects both before and after archival do not inform the estimation of an archival effect. We may infer that where this occurred, there was increased likelihood that that particular sample was devoid of the target DNA for the respective qPCR assay.

Using one-half the detection limit for non-detect results, Table 1-4 shows that when qPCR-CCE are calculated for the fresh and archived samples at each beach, the mean values for archived samples are consistently lower than those of fresh samples, although this decline was relatively small at Edgewater and Fairhope compared to the other beaches. These mean differences by beach, as well as a pooled precision parameter based on substituting one-half of the detection limit for censored data, were used as initial values in the MCMC estimation procedure.

Table 1-4. NEEAR study mean log10(qPCR calibrator cell equivalents) based on qPCR calibrator cell equivalents ÷ 2 for non-detects

	West Beach	Huntington Beach	Silver Beach	Washington Park Beach	Edgewater Beach	Fairhope Beach	Goddard Beach
				Enterococcus qPCR-CCE			
Original	2.201	2.244	1.696	1.746	2.062	1.847	2.239
Archived	0.831	1.246	1.098	0.965	1.935	1.670	1.451
Change	-1.370	-0.998	-0.598	-0.781	-0.128	-0.178	-0.788
				Bacteroidales qPCR-CCE			
Original	-[1]	-	-	-	2.999	3.050	3.120
Archived	-	-	-	-	2.494	2.862	2.807
Change	-	-	-	-	-0.505	-0.187	-0.313

[1] *Bacteroidales* qPCR was not performed at the 4 freshwater beaches.

A probability plot of the residuals from the MCMC estimation procedure, that is, $\log_{10}(\Delta\Delta C_{T,\,archived}) - \log_{10}(\Delta\Delta C_{T,\,fresh})$ less it's respective MCMC mean, is given in Figure 1-1. The plot justifies using the Normal model for these data.

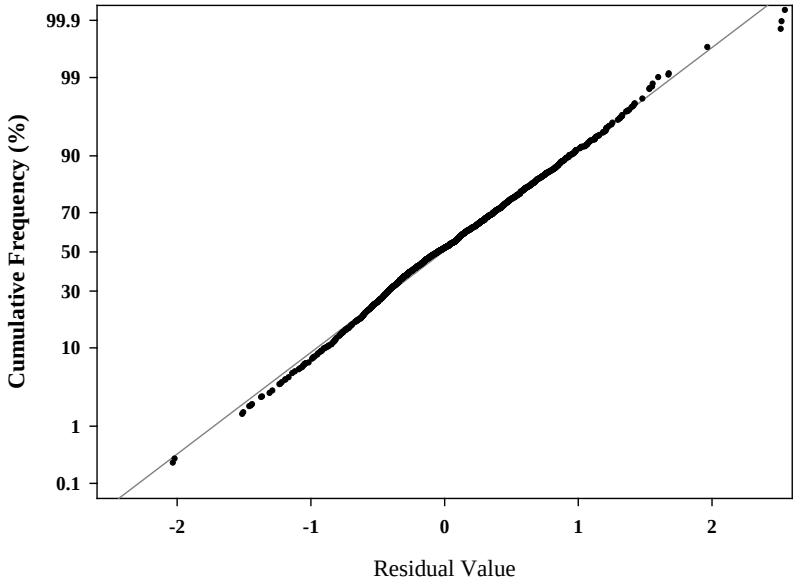

Figure 1-1. Probability plot of residuals from the MCMC model for differences in observed log10 qPCR analysis between archived and original samples

Final analytical results from MCMC estimation that explicitly accounted for values below their respective limits of detection (Table 1-5) indicated strong, statistically significant declines in qPCR-CCE yields from the archived NEEAR samples from most beaches. Samples from all but Edgewater Beach in Biloxi and Fairhope Beach exhibited highly significant declines with respect to *Enterococcus* recoveries. With respect to *Bacteroidales* qPCR-CCE, Edgewater and Goddard Beach samples exhibited highly significant changes. The analysis was performed on logarithm-transformed qPCR-CCE. To put these numbers in perspective, Table 1-5 also shows the equivalent percent declines that corresponded to the differences in geometric means (the antilogarithms of the mean log differences). In many cases, these declines imply that only 10% or less of the original DNA remained in the archived samples.

Pearson product moment correlations based on the MCMC estimates are given in the last column of Table 1-5. For enterococci, the correlations were particularly low where there was any correlation whatsoever. A common measure of predictability in regression analysis is R^2, which is equal to the square of the Pearson correlation. Multiplied by 100, an R^2 indicates the percent

Table 1-5. Maximum likelihood estimates of difference between archived and original samples

	Log10 change	P-value[1]	Equivalent % change	Pearson correlation
		Enterococcus qPCR-CCE		
West Beach	-1.65	< **0.001**	-98%	0.36
Huntington Beach	-1.19	< **0.001**	-94%	0.39
Silver Beach	-0.70	< **0.001**	-81%	-0.01
Washington Park Beach	-0.94	< **0.001**	-89%	-0.04
Edgewater Beach	-0.14	0.195	-28%	0.11
Fairhope Beach	-0.21	0.113	-38%	-0.04
Goddard Beach	-1.00	< **0.001**	-90%	0.11
		Bacteroidales qPCR-CCE		
Edgewater Beach	-0.51	< **0.001**	-69%	0.52
Fairhope Beach	-0.06	0.255	-12%	0.46
Goddard Beach	-0.28	< **0.001**	-47%	0.48

[1] P-values in **bold-face** indicate statistically significant differences.

of variation explained by the independent variable. In this study, the independent variable would be regarded as the initial qPCR-CCE result, and knowing this value was seen to account for only 10% or less in the variation among archived sample qPCR results. Scatter plots of archived vs. original $\log_{10}$(qPCR-CCE) results for *Enterococcus* are shown by beach in Figure 1-2.

Bacteroidales qPCR-CCE results from the archived samples show much better correlation with their respective initial analyses compared to the *Enterococcus* analyses. These correlations still are not substantial, however, and amount to R^2 values on the order of 0.25, thus explaining only 25% of the variation among archived sample analyses for *Bacteroidales*. We show the scatter of archived vs. original $\log_{10}$ qPCR-CCE results for *Bacteroidales* in Figure 1-3.

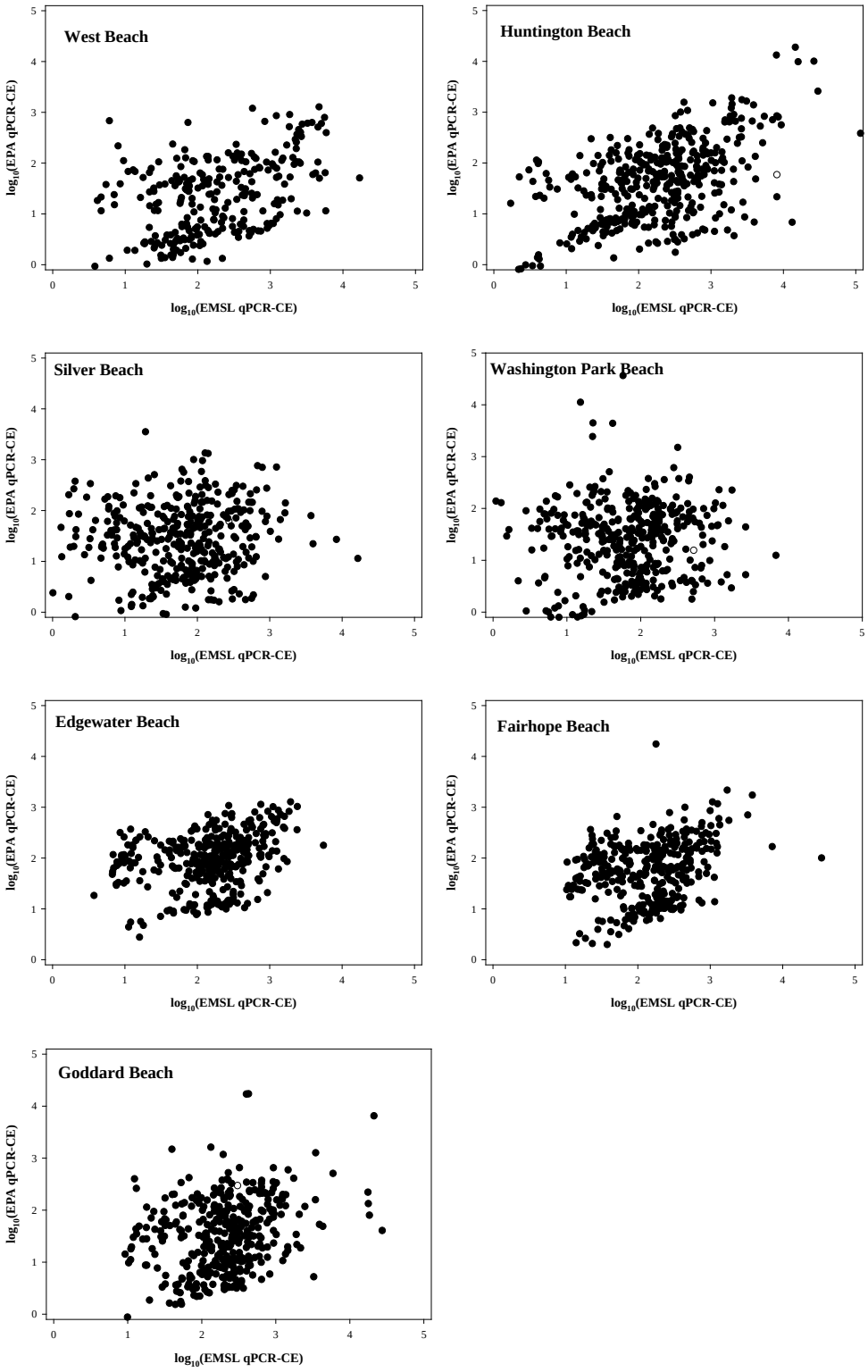

Figure 1-2. Scatter plots of archived sample stability study samples, *Enterococcus* qPCR archived ("EPA") vs. initial ("EMSL") value

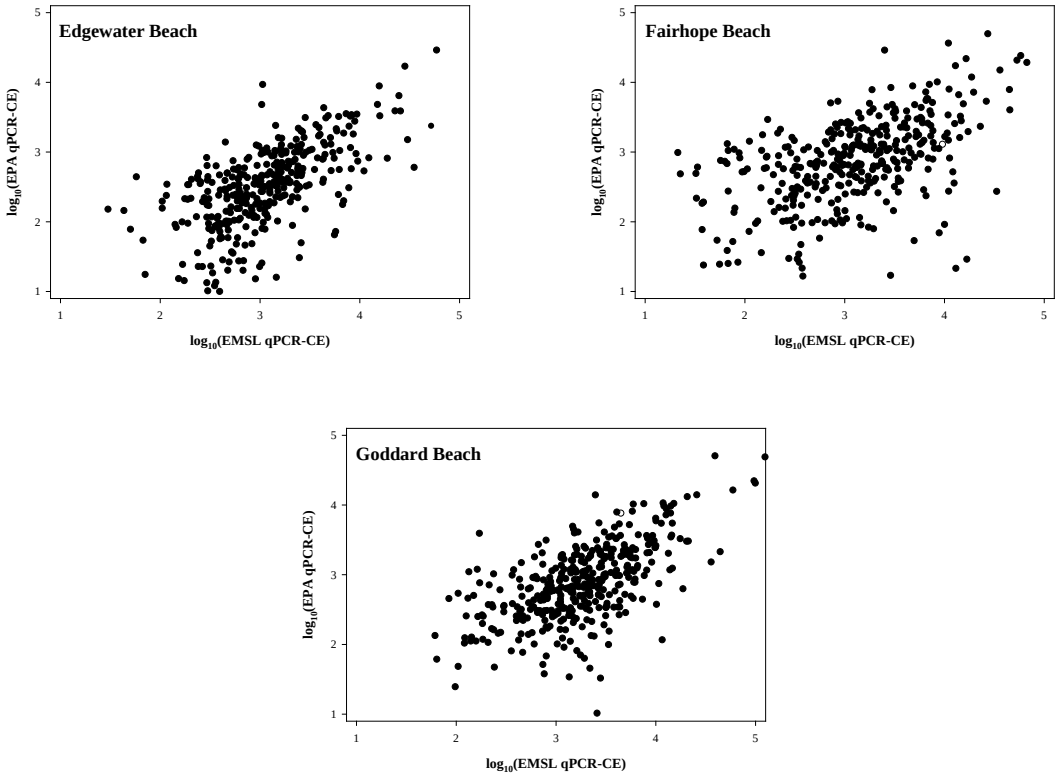

Figure 1-3. Scatter plots of archived sample stability study samples, *Bacteroidales* qPCR archived ("EPA") vs. original ("EMSL") values

Long-term holding time study

Some significant changes in qPCR-CCE results for the long-term holding time study samples between their initial analysis and their reanalysis two years later were observed (Table 1-6). Marine water *Enterococcus* assay results actually showed a statistically significant *increase* of 0.16 logs (44%) over this period (p=0.002). Mean log qPCR-CCE in this case rose between the initial analysis and the reanalysis at six months and stayed more or less constant at that level at the one and two year marks. Meanwhile, *Enterococcus* qPCR-CCE results from freshwater samples exhibited a small "marginally significant" (p=0.063) *decline*. Among the other assays, both *Bacteroidales* (p<0.001) and *E. coli* (p=0.022) re-analyses indicated significant declines in the PCR target in freshwater samples after two years amounting to 40% and 21% of their initial values (0.22 and 0.10 logs), respectively. The decrease in *Bacteroidales* signal was already evident at six months, but *E. coli* declined incrementally. Another decrease in qPCR results over the two year period was for *Bacteroidales* from marine water samples where the change was

Table 1-6. Long-term holding time study samples mean log10(qPCR calibrator cell equivalents) and change from initial results (24 hr) for samples held for two years

	Mean $\log_{10}$(qPCR-CCE)				2 yr net		Equivalent	Pearson
	24 h	6 mo	1 yr	2 yr	change[1]	P-value[2]	% change	correlation
				Enterococcus qPCR-CCE				
Freshwater[3]	3.82	3.93	3.77	3.73	-0.08	0.063	-17	0.94
Marine[4]	3.34	3.61	3.45	3.50	0.16	**0.002**	44	0.92
				Bacteroidales qPCR-CCE				
Freshwater	6.49	6.23	6.32	6.27	-0.22	< **0.001**	-40	0.96
Marine	6.10	6.30	5.98	6.00	-0.10	0.056	-20	0.96
				E. coli qPCR-CCE				
Freshwater	4.65	4.64	4.58	4.55	-0.10	**0.022**	-21	0.95
Marine	3.99	4.02	3.98	4.01	0.02	0.658	5	0.95

[1] Difference from 24 h to 2 yr mean $\log_{10}$(qPCR-CCE).

[2] P-values in **bold-face** indicate statistically significant differences.

[3] N=29.

[4] N=23.

only marginally significant (p=0.056). Target sequence recoveries from the calibrator samples showed no decreases over this time period for any of the indicator organisms.

Pearson correlations between initial and two-year $\log_{10}$(qPCR-CCE) values were all above 0.9, being in all but one case about 0.95 (Table 1-6). Correspondingly, R^2 values were all 0.84 or higher. This fact is reflected in the plots of two-year vs. initial $\log_{10}$(qPCR-CCE) values in Figure 1-3.

Discussion

The primary purpose of the present analysis is to evaluate the feasibility of using the archived NEEAR study samples as surrogates for fresh samples in determining relationships between results of new or revised methods for potential indicator bacteria of fecal pollution and swimmers' health risks. New methods that were examined in the analyses of the archived

samples included qPCR assays for *E. coli* and total *Bacteroidales* (the former assay being of interest due to the widespread acceptance of *E. coli* as an indicator of fecal pollution in fresh waters and the latter assay being of interest due to its use in the original analyses of marine samples only). Modified methods included purification and concentration of DNA in the filter extracts as well as the incorporation of additional and/or improved positive controls for the detection of PCR inhibition. For the archived data to be used in this manner, the most desirable outcome would be for there to be no change between the original analyses and the archived sample analyses two to six years later. In addition there should be a relatively high correlation between the two sets of results (the latter implying a low variance of the difference). Lacking this, at least a high correlation between the two sets of results might allow some adjustment to be made to the archived data so that they would reliably reflect the fresh sample data. Devising an adjustment factor would necessarily involve non-provable, critical assumptions, such as that other qPCR assays would follow the predictive model established by the results that were available. Results from analyses of the archived samples by the new or revised methods may at least be more readily accepted if one or both of the conditions described above are indicated by the available data.

The analysis of the previous section shows, however, that suitability of the archived samples as surrogates for original samples is contraindicated by comparisons between archived and original sample results with respect to the available data, i.e., qPCR results for *Enterococcus* and marine *Bacteroidales*. Not only are large, highly significant declines in qPCR-CCE recoveries observed, but the differences are largely unpredictable from sample to sample as evidenced by the low correlation between results of archived and original sample analyses. This precludes the possibility of using any sort of "adjustment factor" to rectify this change.

A short-coming of the archived sample data from the archived sample stability study, with respect to the interpretation of their change, is that the initial analysis of original samples and analysis of archived samples two to six years later were performed by different laboratories. Thus, the effects of change over time may be confounded with effects of different analysts and equipment. However, even for the long-term holding time study data, time effects are confounded with any potential changes that may have occurred within the single laboratory that

performed all of the qPCR analyses. An experiment designed to properly capture all of the between lab and between time variation would have to involve several labs performing both the original and archived sample qPCR analysis. The cost of doing so would be prohibitive and even then, one would have to assume that there were no systematic changes in labs and/or qPCR quality over time. By way of a rough comparison of the changes observed among the archived samples over time and the magnitude of changes that may be expected from lab-to-lab variation, some preliminary data on qPCR inter-laboratory variance are available (U.S. EPA Office of Water 2008, unpublished data; *Ad Hoc* multi-laboratory study 2010, unpublished data). These data indicate that a two standard deviation (i.e., 95% confidence level) difference on the order of about 0.5–0.7 logs might be expected between two labs analyzing the identical sample. Most of the significant changes observed in the archived samples are outside this range. Therefore, it does not seem likely that inter-laboratory differences themselves could have accounted for all of the observed changes.

Given the negative results for the archived sample stability study data, results from long-term holding time study have a greatly reduced relevance. The value of the long-term holding time information would have been in supporting the inference that the equivalency or predictability of the NEEAR archived sample data could be extrapolated to other qPCR targets (most notably *E. coli* and fresh water *Bacteroidales*), but neither equivalency nor predictability were observed for any of the NEEAR study results that could be directly compared. Even if one or both of these conditions had been met, there would have been additional challenges in making such extrapolations. Results from the long-term holding time study, particularly the high correlations between held and initial sample qPCR-CCE values, indicate that archived samples may be capable of serving as surrogates for fresh samples under some circumstances, at least with a statistical correction. However, the predictive relationship observed in the long-term holding time study would need to have been extrapolated from two years out to as long as six years in order to be applicable to the archived sample stability study samples. The length of time that samples are held would logically seem to be an important factor, as is borne out by the archived data, except for enterococci results at Goddard Beach. The Goddard Beach data showed a 90% 2-year decline in mean $\log_{10}$ (qPCR-CCE) that was more in line with the five and six year declines seen for the fresh water beaches (Table 1-5). However, the long-term holding time

study data themselves, which were designed to track change over time, were not consistent among the different indicator and water matrix combinations with respect to showing progressive declines, if any at all, over time, nor were they consistent with the changes seen in the archived sample stability study Fairhope, and particularly Goddard marine beach, samples that were held for the same total amount of time of two years.

The finding of a lack of stability in the archived samples in this study does not preclude the possibility that more favorable results might have been achieved using alternative storage conditions. The conditions used for storing the archived NEEAR study samples were adopted primarily for practical reasons, such as the availability of freezer space in the NERL Cincinnati laboratory, rather than on the basis of what might have been the optimal storage conditions. Because of our intention of being able to link the results of the two studies, the storage conditions used in the long-term holding study were also dictated in large part by the storage conditions used for the archived NEEAR study samples.

It was difficult to interpret results in the literature for their relevance to the specific questions posed in this study. Particularly important studies to consider would be those involving similar types of cells, similar influences of organic, chemical and other constituents in water samples, low copy numbers of the target of interest, and similarities in the conditions and duration of storage. However, no studies meeting all of these conditions were identified.

Recovery of DNA standards after storage under various conditions has been reported. Storage conditions that appeared to give the greatest recoveries included storage at -20 °C in buffer or glycerol or lyophilized at +4 or -20 °C (Podivinsky et al. 2009, Roder et al. 2010). A number of studies have characterized DNA recovery from cells that were in high abundance and not from environmental samples (Cannas et al. 2009, King et al. 2009, Rohland and Hofreiter 2007, Smith and Morin 2005, Wallenius et al. 2010, Wong et al. 2008). Some of these studies indicate better recovery at -80 °C compared to -20 °C. A number of additives have been studied however there is generally mixed results with some reporting that the recovery was just as efficient with no additives (Smith and Morin 2005). Recovery of DNA from urine samples stored for up to 28 days indicated a log or more loss of signal from storage at temperatures ranging for 4 °C to -80

°C (Cannas et al. 2009). Another study indicated more efficient recovery at -20 °C over -80 °C for DNA samples analyzed by RFLP from stomach tissue (Molbak et al. 2006). Recovery of DNA from ancient and forensic samples has also been studied (King et al. 2009, Rohland and Hofreiter 2007, Wallenius et al. 2010, Wong et al. 2008). However, the relevance of these studies is also questionable since the recovery efficiency requirements were generally not as great and the duration of storage was not comparable. Efficient recovery of viral DNA by qPCR was observed from clinical samples after storage of 16 months at -20 °C (Jerome et al. 2002).

Recovery and qPCR amplification of DNA from stored bacterial cells have been reported, however, there were still significant differences in the types of cells, samples and storage conditions examined in these studies as compared to those examined in the present study. Efficient recoveries have been reported from *Bacillus anthraces* spores stored at 4 °C for 182 days (Alemeida et al. 2007). However spores may be more stable to environmental influences and the duration of storage was much shorter. Studies on the recovery of bacterial DNA from stored soil samples reported efficient recoveries in samples stored at -20 or -80 °C with (phenol–chloroform–isoamyl alcohol) or without additives for storage for 14–30 days (Lauber et al. 2010, Rissenen et al. 2010).

As a final point in the comparison of original and archived sample results from the NEEAR study, we note that *Enterococcus* and *Bacteroides* target organism cells used for the preparation of calibrator sample filters by the two laboratories came from different sources. Cells used by EMSL originated from laboratory grown cultures and were enumerated as previously described (Haugland et al. 2005, Siefring et al. 2008). Cells used by U.S. EPA NERL were enumerated by flow cytometry and were acquired in the form of commercially available, lyophilized pellets (Bioballs™, BTF, Sydney Australia). To evaluate the comparability of target organism CCE estimates in the test samples using calibrator samples prepared from these two cell sources, target sequence recoveries from calibrator sample DNA extracts prepared by each of the laboratories were examined. Quantitative estimates of target sequence recoveries per calibrator cell were obtained by interpolating qPCR CT values from analyses of the calibrator extracts on master standard curves generated by each of the laboratories from pooled results of repeated qPCR analyses of DNA standards nominally containing from 10^1 to $4x10^4$ target sequence copies

per analysis. Results from these analyses indicated that the mean target sequence recoveries from the laboratory grown *Enterococcus* cells used by EMSL were approximately two-fold higher than those from the Bioball™ *Enterococcus* cells used by U.S. EPA NERL. This apparent difference may have been related to uncertainty in the applicability of the EMSL standard curves. Uncertainty in the EMSL recovery estimates was associated with the fact that known concentration DNA standards were only analyzed by this lab during one year of the study. In other years only slope (amplification efficiency) values were determined from serial dilutions of the calibrator sample extracts. The slope values from this laboratory were not considered to be different from year to year as indicated by overlapping 95% confidence ranges. If real, the observed difference in target sequence recovery estimates from the two sources of cells would result in a systematic bias towards relatively high CCE estimates for the archived U.S. EPA NERL test samples compared to those obtained for the original EMSL samples implying that, if anything, the actual difference between initial and archived data were even greater than the differences in enterococci results of Table 1-5. In contrast, the mean target sequence recoveries from the laboratory grown *Bacteriodes* calibrator cells used by EMSL were nearly identical to those from the Bioball™ cells used by U.S. EPA NERL as determined from the master standard curves generated by the respective laboratories, a condition that does not lead to change in Table 1-5 for *Bacteroidales*.

Conclusions

The archived sample stability study results from Great Lakes and marine beaches indicate that significant degradation of samples had occurred. The highly significant changes and low or absent correlation between archived and original sample analyses indicate that the archived filters cannot be used in a credible manner to establish health relationships involving *Enterococcus* qPCR or, by extension, any other indicator, pathogen, or method. Any health relationship based on data derived from the archived samples is not useful because these do not reflect data that would have been obtained from fresh samples in actual beach monitoring circumstances.

The results from the long-term holding time study, though minor in importance compared to the analysis of the archived sample stability study samples, showed small but significant differences

in the 24-month holding time study for *Bacteroidales* and *E. coli* that further complement the findings of the archived sample stability study samples that differences are observed between the original and archived samples.

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Part 2. Short-Term Holding Study: Evaluation of holding refrigerated water samples for up to 48 hours for qPCR analysis.

Introduction

This study was conducted to determine whether holding surface water samples under refrigeration for 24 and 48 hours affects qPCR-estimated recoveries of DNA target sequences from *Enterococcus*, *Escherichia coli*, and *Bacteroidales* bacteria as compared to samples held for no more than the currently accepted time limit of six hours. While the qPCR method is normally intended to provide rapid determinations of fecal indicator bacteria densities in surface or recreational waters, which is contrary to the holding of water samples, instances could arise where temporary holding of water samples would be beneficial or necessary. Such instances might include when water samples are collected at remote locations where it is not possible to transport them to an analytical laboratory immediately after collection. Another example might be where it is desired to transport samples to several different laboratories for round-robin testing. The current recommended limit on water sample holding time is six hours for microbiological culture methods (U.S. EPA 2000). This time limit imposes constraints on the applicability of the culture methods for reasons such as those mentioned above. Previous studies have suggested that the DNA target sequences of the qPCR method may be more stable than cultivability of the respective target organisms (Duprey et al. 1997, Walters et al. 2009, Wery et al. 2008). Thus water samples might be held longer than the 6 hour microbiological culture method time limit without significant effects on quantitative density estimates of these organisms as determined by qPCR. The objective of the current study was to provide additional data to support this hypothesis.

Sample size (the number of different fresh water and marine water samples) used in this study was based on results from a U.S. EPA study in which filter retentates of replicate water samples with greater than 100 enterococci cells were distributed to multiple laboratories (U.S. EPA Office of Water 2008, unpublished data). A design of approximately 25 samples per water matrix (fresh or marine water), with 2 subsamples (filters) per sample was estimated as the

required number to enable detection of a decline in target recovery by qPCR of 36% at the 0.05 critical level (alpha=0.05).

Material and Methods

Water samples

Water samples from 29 freshwater and 23 marine locations in the Boston, MA area were collected from July through October, 2008 (Table 2-1). Selection of freshwater and marine sampling sites was based on their ambient levels of fecal indicator bacteria (FIB) and their proximity to the laboratory that conducted the study. All locations had to be close enough to the laboratory to allow collection, transport to the laboratory and filtration of the samples within the currently recommended time limit of six hours for microbiological culture methods. A further consideration in the selection of the sampling sites was that historic data gathered by the laboratory and various collaborators indicated that the water samples could reasonably be expected to contain more than the estimated 95% confidence detection limit of the qPCR method of approximately 100 target organism cells per sample (unpublished data). Actual samples giving lower mean results than 100 enterococci in initial 24 hour analyses were excluded from the study to eliminate the possibility of having subsequent results below the detection limit of the qPCR methods.

Sample treatments

In most studies of this nature, samples would be analyzed as soon as possible (within six hours) to establish the initial concentration against which samples that have been held for 24 or 48 hours would be compared. Complete analysis of the samples within six hours was not possible in the present study because of the amount of time necessary to collect samples from diverse locations during the day and transport them to the laboratory as well as the amount of time necessary to filter multiple aliquots of each water sample to support both this study and the parallel long-term holding time study. Instead, within six hours of collection aliquots of each sample was filtered in the lab and the filters were stored in a freezer at -20 °C to serve as recovery standards as described below.

Table 2-1. Boston, MA area sample locations and descriptions

ID	Date Collected	Source
Freshwater samples		
1–5	08/05/08	Charles River, Stony Brook Tributary
6–8	08/11/08	Charles River, Boston Water & Sewer Outfalls
9–11	08/13/08	Charles River, Muddy River Outfalls
22, 24–26	08/25/08	Winns Brook
30	08/27/08	Newtown
36	09/03/08	Salem Sound
37	09/08/08	Ell Pond, Melrose
38	09/08/08	Mill Brook, Melrose
39, 40	09/08/08	Lower Mystic Lake, Arlington
41	09/08/08	Spy Pond, Arlington
52, 53	09/22/08	York Beach, ME, River Rd, Sewage Spiked
58	09/25/08	Concord, NH WWTF, pre-UV
59	09/25/08	Concord, NH WWTF, post-UV
61	09/25/08	Outfall at Wollaston Beach, Sewage Spiked
62	09/25/08	Furnace Brook, Sewage Spiked
63	10/08/08	Lowell WWTF (chlorinated)
Marine samples		
14–15	08/18/08	Mystic River, Marine Side of Dam
17–21	08/20/08	Mill Creek, Chelsea
27, 28	08/27/08	E. Boston
29	08/27/08	Revere
32–36	09/03/08	Salem Sound
43, 44	09/15/08	Kings Beach, Lynn
45	09/15/08	Fisheries Beach, Lynn
54–57	09/22/08	York Beach, ME, Clark Rd
60	09/25/08	Wollaston Beach, Sewage Spiked

The different treatments to which subsamples of each water sample were subjected are described below and in Table 2-2.

- Recovery Standard: Multiple 50 or 100 ml aliquots of each water sample were filtered within six hours of collection. Replicate filters from each water sample were held at -20 °C until 24 and 48 hours after collection and then extracted for DNA and analyzed by qPCR.
- Refrigerated Water: The remainder of each of the water samples was refrigerated and then equivalent aliquot volumes to those used to prepare each of the respective recovery standard filters were filtered at 24 and 48 hours after collection. After filtration, the filters were immediately flash frozen in a -20 °C cooling block for 1 hour and then thawed, extracted for DNA and analyzed by qPCR. A freeze/thaw cycle was important in order to be consistent with the also frozen and thawed recovery standard filters.

Table 2-2. Description of sample treatments

Treatment	Treatment description	Extraction and analysis
Recovery Standard	Water samples filtered within six hours of collection, filters immediately stored at –20 °C until extraction and analysis	24 and 48 hours after sample collection
Refrigerated Water	Refrigerated water samples filtered 24 and 48 hours after sample collection, filters immediately frozen and thawed and then extracted and analyzed	24 and 48 hours after sample collection

The purpose of the recovery standard filters was to establish standards representing the initial densities of indicator organisms that could be recovered by the qPCR method when the water samples were filtered within six hours of collection. This study design assumed that results from samples held for 6 hour or less prior to filtration could be considered to be representative of freshly collected samples. This assumption was based on previous holding time studies that have shown no significant losses of culturable bacteria counts over this time period (The Public Health Laboratory Service Water Sub-Committee 1953). The recovery standard filters were frozen and stored instead of processing and analyzing the water samples on the same day that they were collected (e.g., within six hours) in part because of the logistical and time challenges associated with collecting, transporting and filtering multiple water samples, as indicated above. A second

important consideration in the decision to use frozen recovery standard filters was that this procedure enabled side-by-side extraction and analysis of these filters under the same conditions as the refrigerated water samples at each holding time. Freezing the recovery standard filters assumed that the DNA targets of the qPCR method would be preserved in this manner and thus allowed these filters to be used as a basis for comparing target organism density estimates in the original samples with those in the samples that had been refrigerated. By using this approach, run to run variation (batch effects) was eliminated from the analysis.

Each water sample was subjected to both of the treatments (recovery standard and refrigerated water) described above and each treatment was analyzed at 24 and 48 hours. Each of the 4 combinations of treatment and holding time (recovery standard and refrigerated water at 24 and 48 hours) was performed on duplicate filters and the DNA extracts from each filter were analyzed via qPCR in duplicate, giving a total of 8 subsamples and 16 qPCR analyses for each sample.

Sample analyses

Sample analyses were performed as described for the long-term holding time study in part I of this report. QPCR assays for *Enterococcus* (Entero1), general *Bacteroidales* (GenBac3), *E. coli* (EC23S857), and spiked salmon sperm as sample processing controls (Sketa2) were performed on each subsample. Primer and probe characteristics of each of these assays are listed below in Table 2-3.

Computational methods

Quantitative estimates of target organism calibrator cell equivalents (CCE) in the test samples were obtained as described in part I of this report. Multiple replicate calibrator sample filters were prepared from a single mixed suspension containing pre-determined cell quantities of representative target strains of each of the assays (*E. faecalis*, *B. thetaiotaomicron* and *E. coli*) just prior to the study. It is noted that while quantitative estimates of target organism densities in the samples were calculated by the comparative cycle threshold method and are reported as CCE as described above, the role of the calibrator sample CT measurements had no influence on the comparisons between recovery standard and refrigerated water samples in this study. Common

Table 2-3. Primers and probes for qPCR assays

Assay Name	Target Species and (Gene)	Sequences (5' to 3')*	GenBank Reference (Base Positions)
Entero1	*Enterococcus*	F: AGAAATTCCAAACGAACTTG	AJ295306 (818-837)
	(23S rRNA)	R: CAGTGCTCTACCTCCATCATT	AJ295306 (889-909)
		P: TGGTTCTCTCCGAAATAGCTTTAGGGCTA	AJ295306 (846-874)
GenBac3	*Bacteroidales*	F: GGGGTTCTGAGAGGAAGGT	M58763 (299-318)
	(16S rRNA)	R: CcGTCATCCTTCACGCTACT†	M58763 (409-428)
		P: CAATATTCCTCACTGCTGCCTCCCGTA	M58763 (354-380)
EC23S857	*E. coli*	F: GGTAGAGCACTGTTTtGGCA†	DQ682619 (857-876)
	(23S rRNA)	R: TGTCTCCCGTGATAACtTTCTC†	DQ682619 (923-944)
		P: TCATCCCGACTTACCAACCCG	DQ682619 (883-903)
Sketa2	*Oncorhynchus*	F: GGTTTCCGCAGCTGGG	AF170538 (23-38)
	keta (rRNA	R: CCGAGCCGTCCTGGTCTA	AF170538 (82-99)
	ITS region 2)	P: AGTCGCAGGCGGCCACCGT	AF170538 (41-59)

* F = Forward primer, R = reverse primer, P = probe

† Lower case denotes deliberately mismatched base

calibrator sample CT measurements were used in the calculations for the two sets of samples in all instances.

Statistical analyses

Statistical analysis was performed using a linear mixed model on logarithm (base 10) of the number of CCE as calculated by ΔΔCT. Samples were treated as random. Filters, which were performed in duplicate for each sample, were treated as another random factor. Holding time (24 and 48 hours), water type (freshwater and marine water), and treatment (recovery standard, refrigerated water) comprise fixed, controllable, effects. Of particular interest are comparisons between recovery standard and refrigerated water at each holding time as the estimator of the respective holding time effect.

Ohio River water holding time study

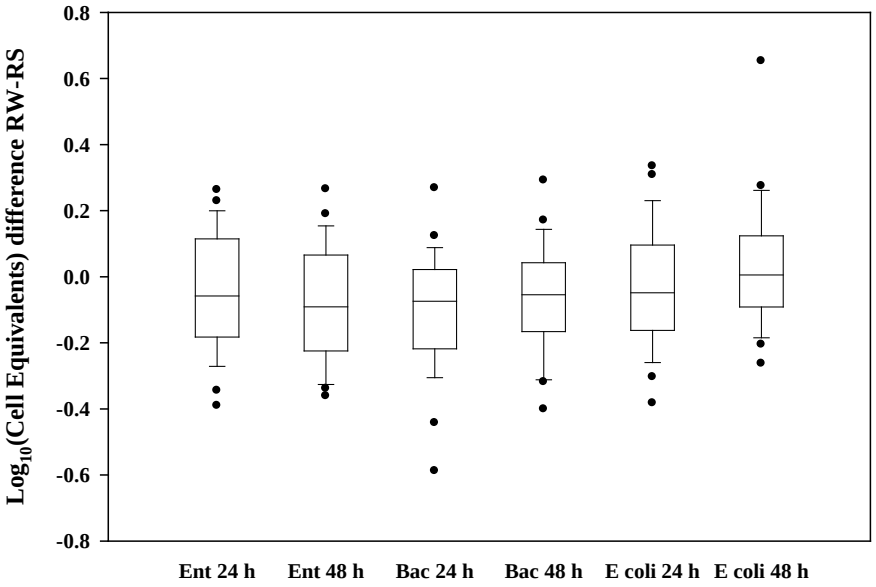
Given that it was not possible to complete analyses of samples described above within six hours, a supplemental study was conducted for the purpose of obtaining data from a more traditional design in which a sample was analyzed immediately after holding times of 1, 24 and 48 hours without freezing. In February, 2009, a sample of Ohio River water was collected in Cincinnati. The sample was refrigerated and subsequently 12 aliquots were filtered each at 1 hour, 24 hours and 48 hours. All filters were extracted immediately and the DNA extracts from each filter were immediately analyzed in duplicate. Identical assays, methods and calculations to those described above were performed and used in evaluating the results. This portion of the study also provided data on variability among replicate aliquots from the same sample that were used in evaluating the importance of any variability introduced by sample holding time, but does not account for run to run or "batch" variation in the analysis. Rather than comparison with a parallel recovery standard as was necessary in the case of the Boston area samples, 24 and 48 hour holding time results from the Ohio River water sample were compared back to the one hour recovery values.

Quality control/ Quality assurance

Quality control and quality assurance measures described in Part I of this report were also applied in this project. All QC acceptance criteria were consistently met.

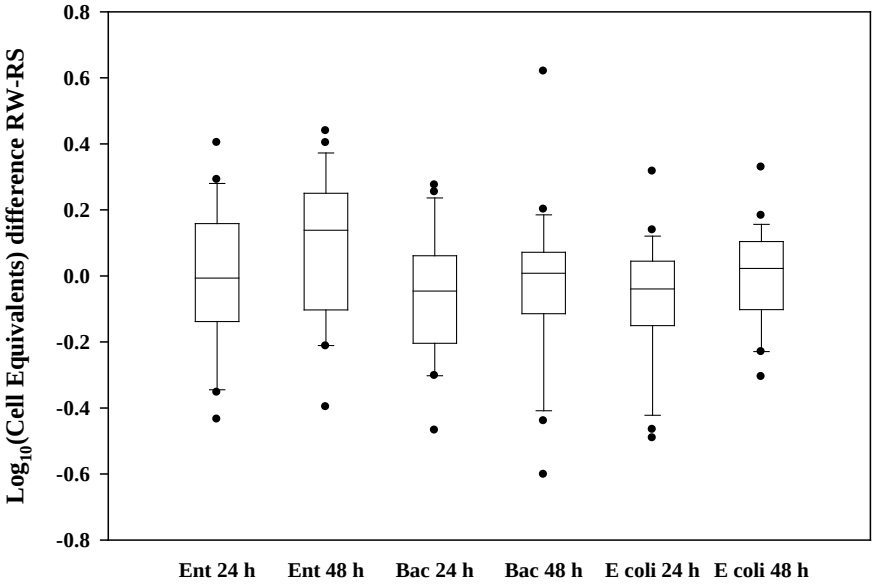
Results

The samples described in Table 2-1 were analyzed by the three qPCR assays and the results are given in Figures 2-1 and 2-2 and Table 2-4. Figures 2-1 and 2-2 show box and whisker plots of the *difference* in $\log_{10}$(qPCR calibrator cell equivalents per 100 ml) between refrigerated water and their respective recovery standards at 24 and 48 hours for freshwater and marine samples, respectively. The box indicates the interquartile range, wherein 50% of the samples lie, and the horizontal line indicates the median value for the respective difference. "Whiskers" indicate the range of the 90^{th} percentile. Data lying outside the 90^{th} percentile range are individually plotted.



[1] Box shows 50% range, "whiskers" show 90% range, individual points shown outside this range. Median value is indicated within each box.

Figure 2-1. Fresh water box and whisker plot1 of differences in log10(calibrator cell equivalents per 100 ml): refrigerated water – recovery standards



[1] Box shows 50% range, "whiskers" show 90% range, individual points shown outside this range. Median value is indicated within each box.

Figure 2-2. Marine water box and whisker plot1 of differences in log10(calibrator cell equivalents per 100 ml): refrigerated water – recovery standards

Table 2-4 shows that there are small but statistically significant mean differences in enterococci and *Bacteroidales* assay results for 24 hr refrigerated fresh water samples compared to the corresponding recovery standards. No significant differences were found for 24 hr refrigerated marine water samples or for 48 hour refrigerated fresh or marine water samples with their corresponding recovery standards.

Table 2-4. Holding time effects: qPCR recovery comparisons between refrigerated water (RW) and the recovery standards (RS)

		Mean log Calibrator Cell Equivalents			
Fresh/ Marine	Holding time (h)	RS[1]	RW[2]	Difference	P-value
		Entero1			
Combined	24	3.58	3.52	-0.06	**0.042**
	48	3.51	3.53	0.02	0.457
F	24	3.82	3.74	-0.08	**0.028**
	48	3.75	3.71	-0.03	0.356
M	24	3.34	3.31	-0.03	0.460
	48	3.28	3.35	0.07	0.132
		GenBac3			
Combined	24	6.29	6.23	-0.06	**0.023**
	48	6.23	6.26	0.02	0.380
F	24	6.49	6.38	-0.11	**0.001**
	48	6.41	6.41	0.00	0.892
M	24	6.10	6.09	-0.01	0.887
	48	6.06	6.10	0.04	0.289
		EC23S857			
Combined	24	4.32	4.31	-0.01	0.577
	48	4.32	4.36	0.03	0.159
F	24	4.65	4.62	-0.03	0.276
	48	4.60	4.65	0.05	0.111
M	24	3.98	3.99	0.01	0.823
	48	4.04	4.06	0.02	0.641

[1] Recovery Standards: filtrates taken within six hours of sample collection and representing the initial densities of indicator organisms that could be recovered by the qPCR method.
[2] Refrigerated Water: water held for 24 or 48 hours prior to filtration and analysis by qPCR.

These data showed a lack of significant "interaction effects" between water type (freshwater/marine water) and treatment (recovery standard / refrigerated water) regardless of organism or holding time as shown in Table 2-5. This suggests that the effect of holding a sample on qPCR results may be the same regardless of whether it is a freshwater or marine water sample. Comparing data combined from both water types continued to show small but statistically significantly lower recoveries in refrigerated water samples held for 24 hours for the Entero1 and GenBac3 assays (Table 2-4). After 48 hours holding time, on the other hand, none of refrigerated water samples, using combined freshwater and marine results, were seen to be significantly different from the frozen and presumably fixed, recovery standard samples. As Table 2-4 shows, Entero1 and GenBac3 recoveries among recovery standards were slightly lower at 48 hours compared to the 24 hour analyses, while refrigerated water samples remained fairly constant.

Table 2-5. Evaluation of difference in holding time effects between fresh and marine waters

	"Interaction" P-value[1]	
	24 hours	48 hours
Entero1	0.53	0.08
GenBac3	0.06	0.65
EC23S857	0.57	0.25

[1] Test of difference between fresh and marine waters with respect to holding time effect on recovery.

Table 2-6 shows the data from the Ohio River sample. These data show holding time effects at 48 hours for all assays and at 24 hours for the GenBac3 assay (Table 2-6).

Table 2-6. Ohio River holding time effects: qPCR recovery comparisons

Holding time (h)	Mean log CCE	Difference from 1 hour	P-value
		Entero1	
1	2.98	-	
24	2.79	-0.19	0.073
48	2.74	-0.24	**0.029**
		GenBac3	
1	4.59	-	
24	4.32	-0.27	**0.024**
48	4.26	-0.33	**0.007**
		EC23S857	
1	3.12	-	
24	2.87	-0.25	0.080
48	2.69	-0.43	**0.004**

Discussion

The results from the samples described in Table 2-1 indicated small but statistically significant lower recoveries of qPCR targets from two of the three target organism groups among refrigerated water samples held for 24 hours based on comparison with their respective recovery standards. Ninety five percent confidence intervals for these differences between the held refrigerated water and their recovery standards among both freshwater and marine water samples combined are shown in Table 2-7. These are further interpreted in terms of equivalent percentage differences simply by taking the antilogarithms of the differences in $\log_{10}$(cell equivalents per 100 ml). This is the corresponding percentage change in average (*geometric* mean) recovery by qPCR over 24 or 48 hours of holding time.

Table 2-7. Holding time effects: qPCR recovery comparisons between refrigerated water (RW) held for 24 or 48 hours and respective recovery standards (RS)

	24 hours		48 hours	
	RW-RS	95% CI	RW-RS	95% CI
	Difference in log10(CCE)			
Entero1	-0.06	(-0.11, -0.00)	0.02	(-0.03, +0.07)
GenBac3	-0.06	(-0.11, -0.01)	0.02	(-0.03, +0.07)
EC23S857	-0.01	(-0.06, +0.03)	0.03	(-0.01, +0.08)
	Difference as a percent of geometric means			
Entero1	-12%	(-22%, -0%)	+5%	(-7%, +18%)
GenBac3	-13%	(-22%, -2%)	+5%	(-6%, +18%)
EC23S857	-3%	(-13%, +8%)	+8%	(-3%, +21%)
	Relative increase in root mean square error			
Entero1	1%	(< 5%)	0.2%	(< 2%)
GenBac3	3%	(< 10%)	0.4%	(< 5%)
EC23S857	0%	(< 2%)	0.6%	(< 4%)

RW-RS: refrigerated water minus recovery standard (log_{10} difference)

At 24 hours, geometric mean recoveries for both the Entero1 and GenBac3 assays were 12–13% lower in the refrigerated water samples than in the recovery standards, with a potential range of up to 28% lower. For EC23S857 the difference amounted to 3%, possibly as high as 13%. Near parity between refrigerated water and their recovery standards for EC23S857 was indicated by the low percent differences and the fact that their respective 95% confidence intervals bracket zero.

The use of recovery standards for these samples was an approach to evaluating holding time effects on microorganisms in water samples that would not be available for culture based methods because samples for culture cannot be preserved through freezing like DNA. By controlling predation, chemical reactions, or other factors that might degrade DNA in a water sample, the target DNA in organisms deposited on a filter and subsequently frozen were assumed to persist without any losses for at least the short holding times involved in this investigation.

Thus, the recovery standards acted as a control group against which the refrigerated water analyses were compared in a side-by-side manner for the 24 and 48 hour time points. Differences in the qPCR results of the two sets of samples using this side-by-side analysis approach was anticipated to minimize any potential influences of method-related "batch" effects, i.e., variability between the results of two sets of samples associated with their being extracted and analyzed at different times. A potential illustration of this benefit can be seen in comparisons of the mean CCE densities estimated in the recovery standards at 24 and 48 hours in Table 2-4. Although the overall mean CCE estimates obtained by the *E. coli* EC23S857 assay remained constant, the overall mean CCE estimates obtained by the Entero1 and GenBac3 assays differed appreciably between 24 and 48 hours. While not found to be statistically significant, the latter differences may be indicative of the aforementioned "batch" effects. A similar difference was observed in the 24 and 48 hour refrigerated water results obtained by the *E. coli* EC23S857 assay. In this instance an unexpected increase in the 48 hour CCE densities was observed. Although the possibility of growth by these indicator organisms in stored water samples can not be completely ruled out, we are not aware of any published results demonstrating growth of these organisms in refrigerated surface water samples.

Despite the efforts taken to eliminate as many method-related variables as possible that might confound the results of this water sample holding time study, the observation of going from a significant difference between refrigerated water and recovery standard results at 24 hours to no significant difference at 48 hours was unexpected. It is noted that the net change in recovery standards between 24 and 48 hours was not significant, even though the differences themselves go from being significant at 24 hours to non-significance at 48 hours. As always, lack of statistical significance is not convincing evidence for no difference, but only lack of convincing evidence for a difference.

Nevertheless, it is possible that there are variables still unaccounted for in this study. An effect associated with the freezing of the recovery standard samples could be such a variable. While an attempt was made to control for the potential influence of sample freezing on target DNA recovery in the qPCR method by also flash-freezing the refrigerated water filters prior to extraction, it could only be assumed that these two freezing methods had the same net effects on

DNA recovery. It was also necessary to assume that there were no differential effects of holding frozen recovery standard samples for 24 vs. 48 hours. This uncertainty associated with the potential effects of sample freezing in this portion of the study was part of the rationale for also conducting the supplemental Ohio River water portion of the study where no freezing of the samples was involved. It is noted, however, that while the Ohio River water portion eliminated freezing effects as a variable, it reintroduced the method-related variables indicated above.

The experimental design used in the Ohio River sample allowed for the comparison of recoveries for 24 and 48 hours based on recoveries at 1 hour which may be a more standard approach for comparing recoveries over time. However this analysis approach created the potential to introduce greater uncertainties in comparing time point results than with the samples from Massachusetts. The uncertainties are associated with extracting and analyzing the different holding time samples in different batches. The results from the Massachusetts samples indicate that there was run to run or batch effects but they were accounted for in the study design. These effects were not considered in the Ohio River sample analysis. The Ohio River results indicate that different conclusions may be reached if run to run or batch effects are not a component of the analysis.

To put the results of this study in further perspective, any bias as a result of holding a sample should be compared to the difference that might be expected among different aliquots from that sample. In practice only a single aliquot most likely would be drawn from the sample for analysis. A 12% difference in recovery, such as shown in Table 2-7 for the Entero1 and Genbac3 assays at 24 hours, might be important if the range of results that could be reasonably expected from the "luck of the draw" is, for example, ±10%, but of little importance if the range is more like ±50%. Representative data that could be used for determining such differences in the analyses of a single aliquot were available from the Ohio River study, where twelve aliquots were taken for analysis at each time point. The variances in the indicator density estimates from the twelve aliquots that were taken just one hour after collection were used as a basis for comparisons with the potential biases that could be attributable to holding time effects.

To use the Ohio River data for evaluating a holding-time bias, the concept of mean square error (MSE) can be used (Cochran 1963). MSE is the average of the squared deviations of "all possible" results from the "true" value of what is being measured (the overall mean log qPCR-CE of the water sample at or near the time of collection). If there is no bias (i.e., the sample is analyzed immediately), the MSE is obviously the same as the variance of $\log_{10}$(qPCR-CE). If there is a bias (e.g., due to holding time degradation) the MSE is equal to this variance plus the square of the bias. The square root of the MSE is the root mean square error (RMSE), the same as the standard deviation for the unbiased result, and larger than this, influenced by the size of the bias, for a biased result. Dividing MSE by variance gives the MSE relative to pure variance, and the square root of this (minus 1), the relative increase in RMSE due to bias. Based on the observed sample aliquots variances for the respective targets from the 1-hour $\log_{10}$ variances pooled over subsamples of Ohio River water, the last section of Table 2-7 shows the relative increase in RMSE corresponding to biases represented by the refrigerated water minus respective recovery standard $\log_{10}$ differences after 24 and 48 hours of holding time. These range from nil up to an 8% increase in RMSE. At the 95% confidence level, the increase in RMSE amounts to less than 17%.

This indicates that the potential difference in mean log recovery of enterococci and *Bacteroidales* in held samples may not be an important factor in relation to normal sampling variation. The existence of a "statistically significant" difference in recovery (i.e., bias) simply means that we are fairly certain that holding affects recovery, not that the bias would be considered substantial, and evaluating the magnitude of the estimate bias or potential range of this bias in terms of normal sampling variability is one way to evaluate how important the bias might be. Note, however, that while sample variability can be compensated for by the collection and analysis of additional sample replicates, bias cannot.

Conclusions

There were small, and in some cases statistically significant changes in qPCR-estimated fecal indicator densities in subsamples of refrigerated water samples that were held for 24 and 48 hours prior to filtration compared to recovery standards consisting of additional subsamples of

the corresponding water samples that were filtered within six hours. However, these changes were neither consistent for the 24- and 48-hour holding times nor were they consistent among different indicator groups. In comparisons with subsamples of the Ohio River water sample held for just one hour prior to filtration, statistically significant declines in density estimates of one of the three indicator groups were observed in subsamples held for 24 hours and of all three indicator groups in subsamples held for 48 hours with refrigeration, Taken together, the results of the two studies were inconclusive and, as a result, **can neither support nor refute** recommendations to hold refrigerated water samples for 24 hours or longer prior to filtration and analysis.

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