<table>
<thead>
<tr>
<th><strong>Title</strong></th>
<th>Distribution and abundance of human-specific bacteroides and relation to traditional indicators in an urban tropical catchment</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Author(s)</strong></td>
<td>Nshimyimana, J. P.; Ekklesia, Eveline; Shanahan, P.; Chua, L. H. C.; Thompson, J. R.</td>
</tr>
<tr>
<td><strong>Date</strong></td>
<td>2014</td>
</tr>
<tr>
<td><strong>URL</strong></td>
<td><a href="http://hdl.handle.net/10220/20970">http://hdl.handle.net/10220/20970</a></td>
</tr>
<tr>
<td><strong>Rights</strong></td>
<td>© 2014 The Authors. published by John Wiley &amp; Sons Ltd on behalf of Society for Applied Microbiology. This paper was published in Journal of Applied Microbiology and is made available as an electronic reprint (preprint) with permission of John Wiley &amp; Sons Ltd on behalf of Society for Applied Microbiology. The paper can be found at the following official DOI: [<a href="http://dx.doi.org/10.1111/jam.12455">http://dx.doi.org/10.1111/jam.12455</a>]. One print or electronic copy may be made for personal use only. Systematic or multiple reproduction, distribution to multiple locations via electronic or other means, duplication of any material in this paper for a fee or for commercial purposes, or modification of the content of the paper is prohibited and is subject to penalties under law.</td>
</tr>
</tbody>
</table>
Distribution and abundance of human-specific Bacteroides and relation to traditional indicators in an urban tropical catchment

J. P. Nshimyimana1,*, E. Ekklesia2, P. Shanahan1, L. H. C. Chua2 and J. R. Thompson1

1 Civil and Environmental Engineering, Massachusetts Institute of Technology, Cambridge, MA, USA
2 Civil and Environmental Engineering, National University of Singapore, Singapore

Abstract

Aims: The study goals were to determine the relationship between faecal indicator bacteria (FIB), the HF183 marker and land use, and the phylogenetic diversity of HF183 marker sequences in a tropical urban watershed.

Methods and Results: Total coliforms, Escherichia coli, and HF183 were quantified in 81 samples categorized as undeveloped, residential and horticultural from the Kranji Reservoir and Catchment in Singapore. Quantitative-PCR for HF183 followed by analysis of variance indicated that horticultural areas had significantly higher geometric means for marker levels ($4 \times 10^4$ HF183-GE 100 ml$^{-1}$) than nonhorticultural areas ($3 \times 10^3$ HF183-GE 100 ml$^{-1}$). E. coli and HF183 were moderately correlated in horticultural areas ($R = 0.59, P = 0.0077$), but not elsewhere in the catchment. Initial upstream surveys of candidate sources revealed elevated HF183 in a wastewater treatment effluent but not in aquaculture ponds. The HF183 marker was cloned, sequenced and determined by phylogenetic analysis to match the original marker description.

Conclusion: We show that quantification of the HF183 marker is a useful tool for mapping the spatial distribution and potential sources of human sewage contamination in tropical environments such as Singapore.

Significance and Impact: A major challenge for assessment of water quality in tropical environments is the natural occurrence and nonconservative behaviour of FIB. The HF183 marker has been employed in temperate environments as an alternative indicator for human sewage contamination. Our study supports the use of the HF183 marker as an indicator for human sewage in Singapore and motivates further work to determine HF183 marker levels that correspond to public health risk in tropical environments.

Introduction

Singapore is a highly urbanized island nation with limited freshwater resources. To protect urban catchments as water sources, the Public Utilities Board (PUB) of Singapore has embarked on the Active, Beautiful, Clean (ABC) Waters programme (PUB 2011). In this programme, green space and recreational infrastructure are brought together with stormwater management (PUB 2011) to both enhance public enjoyment and increase water security. In Singapore, reservoirs are the end-members of urban watersheds characterized by mixed land uses and extensive concrete-lined drainage systems. Water quality in these reservoirs is generally affected by nonpoint source pollution. Pollution of urban waters from human waste is one of the top concerns from a risk management perspective as numerous studies have established strong links between exposure to human waste and the spread of infectious disease (Pruss 1998). Faecal pollution is a major contributor to water quality degradation of urban...
beaches and water bodies worldwide (Pruss 1998; Johnson et al. 2003; Horman et al. 2004; Noble et al. 2006; USEPA 2009; Converse et al. 2011). Recent studies identify failing sewage infrastructure and a combination of sewage discharge, abundance of nutrients and favourable growth conditions as major factors influencing the persistence of faecal contamination in urban drainage systems (Field and O’Shea 1992; Rajal et al. 2007; Surbeck et al. 2010; Sauer et al. 2011). Tools to monitor and identify sources of human faecal contamination are critical for identifying and prioritizing management targets to improve urban water quality.

Faecal indicator bacteria (FIB), e.g. Enterococcus and Escherichia coli, are widely used as proxies for the estimation of faecal contamination, yet their accuracy is limited by the inability to differentiate human and wildlife sources (Layton et al. 2010), variable correlation with human pathogens (Noble and Fuhrman 2001; Boehm et al. 2003, 2009; Horman et al. 2004), growth or persistence in the environment (Hardina and Fujioka 1991; Anderson et al. 2005; Yamahara et al. 2009, 2012) and errors associated with culture-based quantification such as cells that are dormant or viable but not culturable (VBNC) (Rahman et al. 1996; Menon et al. 2003). A major factor affecting the use of FIB in tropical areas is the ability of some strains to grow in warm, high nutrient environments (Hazen 1988; Rivera et al. 1988).

Nucleic acid-based techniques for detecting and enumerating FIB such as PCR and QPCR have been developed for emerging alternative indicators, circumventing biases associated with cultivation and allowing quantification of markers for which cultivation-based assays are not feasible (Bernhard and Field 2000a; Seurinck et al. 2005; Shanks et al. 2006; Bae and Wuertz 2009). The HF183 assay targeting the 16S rRNA gene of a human-associated Bacteroides strain has emerged as one of the most robust assays for identifying human sewage as this assay is highly specific for human faecal contamination (Bernhard and Field 2000a,b; Seurinck et al. 2005; Van De Werfhorst et al. 2011), with relatively few documented exceptions (McLain et al. 2009; Van De Werfhorst et al. 2011). The HF183 marker, originally described from a cultivation-independent study of microbial diversity in human faeces (Bernhard and Field 2000a), has since been detected in a cultivated bacterium, Bacteroides dorei. B. dorei is a strict anaerobe and is thus not expected to grow in oxic environments (Bakir et al. 2006). Thus, the HF183 marker, targeting B. dorei-like organisms, should qualify as a neutral tracer of human faecal contamination in surface waters (Bernhard and Field 2000a; Fogarty and Voytek 2005; Walters and Field 2009; Walters et al. 2009; Dick et al. 2010), and its use has been validated in various studies in temperate environments including in the United States (Bernhard and Field 2000b; Fogarty and Voytek 2005; Shanks et al. 2006; Santoro and Boehm 2007; Van De Werfhorst et al. 2011), Europe (Gawler et al. 2007), and Australia (Ahmed et al. 2008). Recent studies in Kenya (Jenkins et al. 2009), Tanzania (Pickering et al. 2010) and Bangladesh (Ahmed et al. 2010) have extended the use of the HF183 assay to tropical or semi-tropical conditions; however, the specificity of the marker for B. dorei-like organisms has not been confirmed by phylogenetic analysis nor has the marker abundance been compared to that of traditional indicators under tropical conditions. This study aims to address this research gap.

In this study, we have used detection and quantification of the HF183 marker for human-specific Bacteroides in parallel with E. coli and total coliforms to evaluate the potential distribution of sewage contamination in the watershed of Kranji Reservoir in Singapore. Previous work in the Kranji Reservoir Catchment has revealed high levels of FIB including E. coli and total coliforms, especially in the horticultural areas (NTU 2008); however, the distribution of human-specific Bacteroides is unknown. We have used cloning, sequencing and phylogenetic analysis to evaluate whether the HF183 marker recovered in Singapore matches the original marker description, and we provide a quantitative analysis of the correlation of HF183 abundance to that of E. coli, total coliforms and land-use characteristics in the reservoir. Our data support the use of HF183 marker quantification to improve the accuracy of human source identification in tropical environments; however, further work is needed to establish levels of the marker that correspond to sewage-associated risks in tropical environments such as Singapore.

Materials and methods

Site description

The Kranji Reservoir catchment (Fig. 1) located in the northwest of Singapore island (1°25’S, 103°43’E) drains 61 square kilometres (NTU 2008). The catchment is one of the most diversified watersheds in Singapore in terms of land use, containing areas designated as ‘residential’—dominated by high-density high-rise buildings, ‘undeveloped’—characterized by native vegetation and low population density and ‘farming/horticultural’—dominated by cultivation of flowers, vegetables, fish and chickens. The watershed is served by a system of concrete-lined drains that convey stormwater runoff from the watershed to the Kranji Reservoir. The residential sites are sewered, while horticultural sites are served by on-site treatment plants. The Kranji Reservoir is an impoundment reservoir with

Human Bacteroides in an urban tropical catchment

J. P. Nshimiyimana et al.
an estimated capacity of 16 million cubic metres based on area and mean depth. Drinking water is purified through Singapore’s advanced water treatment systems before distribution (NTU 2008). The climate in Singapore is tropical with temperatures ranging from diurnal highs of 29–31°C to lows of 23–24°C.

Sample collection and DNA extraction

Water samples were collected in the Kranji Reservoir and surrounding catchment (Fig. 1) during the months of January and July 2009. Water samples were collected from concrete-lined drainages near catchment monitoring stations of residential (R), farming/horticultural (F) and undeveloped (U) areas, which represent 19, 5 and 76% of catchment land use, respectively (Chassard et al. 2007). Samples were also collected from Kranji Reservoir (K) during January and July 2009. Samples were collected during dry weather, with the exception of seven samples from July 2009 that were collected from high water flows following a rain event (R1, R8, R12, F9, F10, F11 and U3). During January 2010, samples were collected from

Figure 1 HF183 marker distribution and abundance in Kranji Reservoir and catchment. (a) and (b) Abundance of the HF183 marker in Kranji Reservoir and catchment as determined by quantitative PCR. (c) HF183 marker abundance in each land-use category showing median, upper and lower quartiles spanning maximum and minimum observations. Bar width is proportional to the number of samples in each category. (△) Presence of total Bacteroides; (●) Inhibited Samples and (○) Presence of HF183. HF183—GE 100 ml⁻¹: (△) <150; (●) 151–1000; (○) 1001–10 000; (●) 10 001–100 000; (△) 100 001–1 000 000. (△) and Farming/Horticultural; (●) Recreational; (□) Undeveloped; (△) Residential; (●) Kranji Reservoir.
sites within the horticultural area suggested as potential sources of faecal contamination by local experts. Most of the horticultural areas are un-sewered and are served by on-site wastewater treatment plants and thus are potential sources of faecal contamination. Samples were collected from fish ponds (near F4 and F7) and effluents from several on-site wastewater treatment facilities (near F5, F7, F8 and F9/F10). Finally, a raw sewage sample from a sewer system in a high-density residential area was collected for comparison.

Water samples were collected in sterile 500 ml WhirlPak® bags (Nasco, Fort Atkinson, WI, USA) or 1 L Nalgene bottles and immediately stored on ice. Reservoir water samples were collected at a depth of 1 m using an AquaStore Model 1010 Niskin water sampler (AquaStore, Aquatic Network, Miami, FL, USA). Microbiological analysis (total coliforms and E. coli) and filtration of water samples onto a Millipore Sterivex™-GS 0.22 µm Filter Unit (Millipore, Billerica, MA, USA) were accomplished within 6 h of sample collection. Filters containing biomass were stored at −80°C until further analysis.

For preparation of DNA from environmental samples, membranes were aseptically removed from Sterivex filter cartridges, split in half and sliced into 8–10 strips using a flame-sterilized blade and forceps. DNA for PCR and cloning were extracted from one half-filter with the UltraClean™ Soil Isolation Kit (MO BIO Laboratories, Carlsbad, CA, USA), and the remaining half-filter was stored frozen for future analyses. DNA for QPCR was subsequently extracted from the second half of the filter using the Ultraclean Plant DNA Kit (MO BIO Laboratories) that adds an additional reagent for removal of plant-based PCR inhibitors, such as may be associated with high algal biomass found at multiple sites in the catchment. Kits were used according to the manufacturer’s protocols that include a bead-beating step to remove biomass from the membrane and to mechanically lyse cells. DNA samples, eluted in 50 µl buffer, were electrophoresed on 1% agarose and quantified on a NanoDrop® ND-1000 Spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA) to validate their quality and purity. Environmental DNA samples were kept on ice during extraction procedures, and DNA samples were stored at −20°C.

**Detection of total and human Bacteroides by PCR**

Initial amplification of the HF183 marker by conventional PCR (Bernhard and Field 2000a,b) revealed a high percentage of PCR-inhibited samples and dilution of samples to relieve PCR inhibition resulted in a loss of sample signal and undetectable PCR yields. Successful and reproducible amplification was achieved with two modified approaches. First, cycling conditions adapted from Bernhard and Field (Bernhard and Field 2000a,b) were modified with an initial 10-cycle ‘touchdown’ annealing step (Fogarty and Voytek 2005). Amplification with HF183 marker primers HF183F and 708R (Table 1) was carried out in a volume of 50 µl with 15–275 ng DNA, 25 µM of each primer, 10 mM of deoxynucleoside triphosphate, 1-25 units of Taq DNA Polymerase, 10X ThermoPol Reaction Buffer and autoclaved Mill-Q-water. The PCR cycling conditions were as follows: 3 min at 95°C; followed by 10 cycles of 30 s at 95°C, 30 s at 63°C decreasing 1°C each cycle and 30 s at 72°C. This was followed by 40 cycles of 30 s at 95°C, 30 s at 53°C, then 90 s at 72°C; concluding with a final extension of 7 min at 72°C. Secondly, a semi-nested PCR protocol was used to detect both the Bacteroides-Prevotella group and the human-specific Bacteroides HF183 marker at a higher sensitivity (Shanks et al. 2006). PCR mixtures for the first and second stages of the semi-nested protocol contained 25 µM of each primer, 10 µM of dNTPs, 0-625 units of Taq DNA Polymerase, 10X ThermoPol Reaction Buffer and autoclaved Mill-Q-water. For the first stage, primers Bac32F and Bac708R (Table 1) were used to amplify Bacteroides-Prevotella using cycling conditions of 3 min at 95°C; followed by 35 cycles of 30 s at 95°C, 30 s at 53°C and 1 min at 72°C; followed by a final 3 min at 72°C. Positive amplicons were then purified (QIAquick® PCR Purification Kit, QIAGEN®, Valencia, CA, USA) and used as template for a second round of amplification with primers HF183F and Bac708R using the same cycling conditions with an annealing temperature of 63°C. Each PCR included a positive control plasmid (pHF183) containing an HF183 marker sequence (16S rRNA positions 183–708) from an uncultured Bacteroides cloned into a PCR2.1 TOPO plasmid (provided by A. Boehm). No template negative controls were propagated through all PCR steps and confirmed to be clean.

**Clone library preparation, sequencing and phylogenetic analysis**

PCR products from Kranji Reservoir (K6) (semi-nested protocol) and from farming/horticultural (F5) and residential areas (R15) (touchdown protocol) were gel-purified (QIAquick®; QIAGEN, Valencia, CA, USA) and cloned using the Zero Blunt® TOPO® kit (Invitrogen™, Grand Island, NY, USA). Sequencing was performed unidirectionally on an ABI3700 using HF183F as a sequencing primer. Sequences were assembled into operational taxonomic units (OTUs) at >99% identity using Sequencher 4.010.1 (Gene Codes, Ann Arbor, MI, USA). Closely related sequences from other studies were identified using NCBI-BLAST and were aligned to OTUs using ClustalX.
calculated based on propagation of error in the standard target concentrations based on measured Cp values were using a least-squares fit. Confidence intervals of predicted values versus target DNA concentration for each QPCR run marker were used to generate a standard curve of Cp values for serial dilutions of plasmid DNA containing the HF183 marker. Standards at concentrations exceeding 10^5 copies QPCR were confirmed to be within two standard deviations of the mean Tm associated with QPCR standards at concentrations exceeding 10^5 copies QPCR run calculated based on propagation of error in the standard curve (Harris 1995). The limit of detection (LOD) for each 96-well plate was determined based on uncertainty in the standard curve as the upper 99th per cent confidence interval of the Cp values of the negative controls or 50 cycles if no signal was apparent. For consistency in statistical analysis, the highest LOD used to indicate non-detect of the HF183 marker was selected as the study-wide LOD. The amplification efficiency (E) for each QPCR run was calculated from the slope of the standard curve and was consistently in the range of 99–100%.

We determined the impact of inhibition on QPCR by spiking 1·2 × 10^5 copies of the positive control plasmid (pHF183) bearing the HF183 marker into an aliquot from each sample before QPCR amplification and comparing the results measured by QPCR with and without spike addition. If the spiked sample was quantified as having less than 65% of the added amount of HF183 marker (corresponding to both the 95% confidence interval for quantification of the QPCR standard curve and observed variability between technical replicates), then the sample was diluted tenfold and re-analysed.

**Estimation of HF183 marker genome equivalents (GE) in natural waters**

To convert from QPCR-detected HF183 marker copies to units of genome equivalents (GE), the efficiency of DNA extraction from water-borne biomass concentrated onto filters was determined. *Bacteroides dorei* strain DSM 17855, which contains a single-copy 16S rRNA gene sequence (Bakir et al. 2006) matching the HF183 marker, was obtained from the German Collection of Microorganisms and Cells (DSMZ, Braunschweig, Germany) and grown to stationary phase in a modified PYG-Medium at 37°C under anaerobic conditions for 4 days. Cells were pelleted from 1 ml aliquots of *B. dorei* culture (7000 g for 10 min) and washed in phosphate-buffered saline (PBS) to reduce cell-free DNA. Replicate cell pellets were either resuspended in DNA extraction buffer and subjected to the extraction protocol directly or were resuspended with or without 100-fold dilution into natural water samples (200 ml) obtained from the Charles River, MA, which is adjacent to the laboratory where the sample analysis was performed. River water samples with and without spiked cells were then concentrated by filtration

<table>
<thead>
<tr>
<th>Primer</th>
<th>Target</th>
<th>Sequences (5‘–3‘)</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bac32F</td>
<td>Bacteroides-Prevotella group</td>
<td>AACGGTAGCTACACGCTTT</td>
<td>Bernhard and Field (2000a)</td>
</tr>
<tr>
<td>Bac708R</td>
<td>Bacteroides-Prevotella group</td>
<td>CAATCGAGATCTTCTCGTG</td>
<td>Bernhard and Field (2000a)</td>
</tr>
<tr>
<td>HF183F</td>
<td>HF183 marker</td>
<td>ATCATGACATCATGTCG</td>
<td>Bernhard and Field (2000a)</td>
</tr>
<tr>
<td>Bac242R</td>
<td>Bacteroidales 16S rRNA</td>
<td>TACCCGCCTACTATCTAAATG</td>
<td>Seurinck et al. (2005)</td>
</tr>
</tbody>
</table>

(Thompson et al. 1997). Phylogenetic relationships between sequences were reconstructed ClustalX implementing the neighbour-joining method. Nucleotide sequences have been deposited at NCBI with accession numbers KC492830–KC492832.

**QPCR and quantification of DNA extraction efficiency and PCR inhibition**

**Quantitative polymerase chain reaction**

The human-specific HF183 marker was quantified by QPCR using primers HF183F and 242R (Table 1) (Seurinck et al. 2005) using the LightCycler® 480 Real-Time PCR system and software v. 1.5.0 (Roche Applied Sciences, Indianapolis, IN, USA) for calculation of crossing point (Cp) values and melting temperature (Tm) analysis. The reverse primer for QPCR described by (Seurinck et al. 2005) allowed formation of a 83-bp amplicon compatible with QPCR and was confirmed to match HF183 marker sequences recovered using the HF183F 708R primer pair from clone libraries in this and other studies. QPCR reaction mixtures consisted of 10 μl of KAPA SYBR® FAST 2X Master Mix (KAPABIOSYSTEMS, Woburn, MA, USA), 10 μM of each primer and 1 μl DNA template. Amplification followed the manufacturer’s instructions; briefly, reactions were subjected to a pre-incubation step of 95°C for 3 min, followed by 50 cycles of 95°C for 10 s, 53°C for 20 s and 72°C for 1 s. Each sample was analysed in triplicate, and Cp values were examined after amplification to verify consistency (i.e. coefficient of variation ≤3%). To confirm the specificity of amplification, melting temperatures (Tm) of sample amplicons were confirmed to be within two standard deviations of the mean Tm associated with QPCR standards at concentrations of 10^5–10^6 copies per QPCR (78-93°C ± SD 0-15), while late-stage PCR artefacts were associated with standards at concentrations exceeding >10^7 copies QPCR^-1 (Tm 80-01°C ± SD 1-92). Tenfold serial dilutions of plasmid DNA containing the HF183 marker were used to generate a standard curve of Cp values versus target DNA concentration for each QPCR run using a least-squares fit. Confidence intervals of predicted target concentrations based on measured Cp values were calculated based on propagation of error in the standard curve (Harris 1995). The limit of detection (LOD) for each 96-well plate was determined based on uncertainty in the standard curve as the upper 99th per cent confidence interval of the Cp values of the negative controls or 50 cycles if no signal was apparent. For consistency in statistical analysis, the highest LOD used to indicate non-detect of the HF183 marker was selected as the study-wide LOD. The amplification efficiency (E) for each QPCR run was calculated from the slope of the standard curve and was consistently in the range of 99–100%.

We determined the impact of inhibition on QPCR by spiking 1·2 × 10^5 copies of the positive control plasmid (pHF183) bearing the HF183 marker into an aliquot from each sample before QPCR amplification and comparing the results measured by QPCR with and without spike addition. If the spiked sample was quantified as having less than 65% of the added amount of HF183 marker (corresponding to both the 95% confidence interval for quantification of the QPCR standard curve and observed variability between technical replicates), then the sample was diluted tenfold and re-analysed.

**Estimation of HF183 marker genome equivalents (GE) in natural waters**

To convert from QPCR-detected HF183 marker copies to units of genome equivalents (GE), the efficiency of DNA extraction from water-borne biomass concentrated onto filters was determined. *Bacteroides dorei* strain DSM 17855, which contains a single-copy 16S rRNA gene sequence (Bakir et al. 2006) matching the HF183 marker, was obtained from the German Collection of Microorganisms and Cells (DSMZ, Braunschweig, Germany) and grown to stationary phase in a modified PYG-Medium at 37°C under anaerobic conditions for 4 days. Cells were pelleted from 1 ml aliquots of *B. dorei* culture (7000 g for 10 min) and washed in phosphate-buffered saline (PBS) to reduce cell-free DNA. Replicate cell pellets were either resuspended in DNA extraction buffer and subjected to the extraction protocol directly or were resuspended with or without 100-fold dilution into natural water samples (200 ml) obtained from the Charles River, MA, which is adjacent to the laboratory where the sample analysis was performed. River water samples with and without spiked cells were then concentrated by filtration...
onto Millipore Sterivex™-GS 0.22 μm Filter Units (Millipore, Billerica, MA, USA). Nucleic acids were extracted from cell pellets and filters with or without spiked cells using the UltraClean Plant DNA Isolation Kit (MO BIO Laboratories Inc., Carlsbad, CA, USA). Extracted samples were subjected to analysis by QPCR to determine the extraction efficiency (E) calculated as the ratio of HF183 marker recovered from filters relative to the values obtained from quantification of HF183 marker copies in B. dorei cell pellets subjected to direct extraction. After determination of DNA extraction efficiencies, genome equivalents (GE) of the B. dorei HF183 marker in environmental samples were determined as:

$$GE_{mL} = \frac{C_{HF} \times V_{Elute}}{V_{Template} \times V_{Sample} \times F_{Elute} \times E}$$

where $C_{HF}$ is the number of HF183 marker copies detected by the QPCR (copies QPCR$^{-1}$); $V_{Elute}$ is the volume of buffer in which DNA extracts are suspended following purification (μl); $V_{Template}$ is the volume of DNA extract added to the QPCR (μl); $V_{Sample}$ is the volume of environmental sample subjected to DNA extraction (μl); $F_{Elute}$ is the fraction of sample DNA that is eluted, accounting for known volumetric losses in the extraction protocol (=0.75); and E is the efficiency of HF183 marker recovery from B. dorei cells suspended in river water and accounts for the use of half-filters in DNA extraction. Error associated with estimation of genome equivalents (GE) was determined by propagation of random error through multiplicative expressions based on standard methods (Harris 1995). Error tolerance for volumetric measurement was ±1%, while relative errors for $C_{HF}$ and E were determined using measured standard deviations.

Enumeration of total coliforms and E. coli

Total coliforms (TC) and E. coli bacteria in Kranji Reservoir and catchment were enumerated in January and July 2009, and January 2010 using the Hach m-ColiBlue24™ method (Hach Company, Loveland, CO, USA) and Colilert Quanti-Trap™/2000 (IDEXX Laboratories, Westbrook, ME, USA), respectively. Sample dilution was performed to increase the range of E. coli and TC abundances quantified.

Statistical analysis of the distribution of human Bacteroides, E. coli, and TC

Sampling sites, land-use categories and abundance of bacterial markers were mapped with ArcGIS version 10.1 software (ESRI®, Redlands, CA, USA). Abundance data for E. coli and TC (CFU 100 ml$^{-1}$ or MPN 100 ml$^{-1}$) and the HF183 marker (GE 100 ml$^{-1}$) were log$_{10}$-transformed to achieve normal distributions and meet the assumptions of a parametric test (Srinivasan et al. 2011). Two-way analysis of variance (ANOVA) followed by post hoc Tukey’s HSD tests was calculated in JMP Pro v.10 (SAS Institute Inc., Cary, NC, USA) to determine whether indicator abundance varied across sampling dates and land-use categories. The relationship between log$_{10}$-transformed indicator bacteria (E. coli and total coliforms) and HF183 marker levels across land-use categories was examined by Pearson’s correlation and hierarchical clustering using Ward’s method on standardized data (JMP Pro v.10). Samples harbouring the HF183 marker (HF), E. coli (EC) or total coliforms (TC) at or below the detection limit (i.e. <150 HF GE 100 ml$^{-1}$; <1 CFU or MPN 100 ml$^{-1}$ for EC and TC) were represented in correlation and clustering analyses as the detection limit. To avoid biases associated with sampling method, samples with indicator levels above the detection maxima (i.e. TC $>4 \times 10^7$ CFU 100 ml$^{-1}$ or EC $>4 \times 10^6$ CFU 100 ml$^{-1}$ in January 2009 and TC $>1.3 \times 10^6$ MPN 100 ml$^{-1}$ or EC $>1.55 \times 10^5$ MPN 100 ml$^{-1}$ in July 2009) were represented by the lower MPN-based detection maximum.

Results

Distribution and phylogenetic analysis of human Bacteroides in the Kranji Reservoir and catchment

The HF183 assay was used to detect the human Bacteroides marker throughout the Kranji Reservoir and catchment. Due to the need to dilute samples to reduce PCR inhibition, Touchdown PCR (detection limit 1000 copies per PCR) was unreliable for quantitative assessment of presence/absence. When the semi-nested PCR protocol was applied (detection limit 10 copies per PCR), a high proportion of samples was found to be positive for the Bacteroides-Prevotella group (96% in January 2009 and 100% in July 2009) and the HF183 marker (83% in January 2009 [n = 20/24] and 100% in July 2009 [n = 30/30]) (Table 2).

Clone libraries of HF183 marker sequences (16S rRNA gene positions 183–708) were prepared from three samples obtained from sites with different land-use designations: Farming/horticultural (F5—1/2009), residential (R15—1/2009) and reservoir (K6—7/2009). Sequencing 36 clones per library yielded a total of 93 good quality sequences. Clustering analysis revealed three closely related operational taxonomic units (OTUs) defined as a set of sequences with >99% nonambiguous nucleotide sequence identity. One sequence type (JPA05) was observed in the majority at all three sites and corresponded to the nucleotide sequence of the B. dorei-type strain. A second sequence type (JPH08) was observed at
two sites (R9, n = 4; F5, n = 4). The third sequence type (JPH04) was detected once (R15, n = 1). Phylogenetic analysis of the HF183 marker sequences (Fig. 2) revealed that HF183 marker sequences obtained from this study were closely related to those from various other studies (Paster et al. 1994; Ruimy et al. 1996; Bernhard and Field 2000b; Miyamoto et al. 2000; Bower et al. 2005; Cerdeno-Tarraga et al. 2005; Bakir et al. 2006; Chassard et al. 2007; Santoro and Boehm 2007).

Validation of QPCR assay for determination of HF183 marker genome equivalents

Genome equivalents of the HF183 marker were determined in samples from the Kranji Reservoir and catchment by QPCR. Quantification of the HF183 marker by QPCR was linear over the range of 10^3–10^8 HF183 marker copies per QPCR (R^2 > 0.99). HF183 marker copies detected by QPCR were converted to genome equivalents (GE) based on a measured DNA extraction efficiency of 58% ± 24% for B. dorei suspended in natural freshwater (Table 2). Detection limits for the HF183 marker were determined for each 96-well QPCR run based on error from the respective run’s standard curve. Single-run detection limits varied from <10 to 19 copies per QPCR (P < 0.01) which, after adjustment for sample volumes, corresponded to a conservative detection limit of 150 GE 100 ml⁻¹ which was set as the study-wide LOD for subsequent statistical analyses.

HF183 marker in the Kranji Reservoir and catchment

Quantification of HF183 marker genome equivalents in samples from the Kranji Reservoir and catchment revealed a wide range of abundance from <150 GE 100 ml⁻¹ to 9.7 × 10^7 GE 100 ml⁻¹ (Fig. 1a,b, and S1). Sites within the designated horticultural areas were associated with the highest levels of HF183 marker with a geometric mean of 6.0 × 10^4 GE 100 ml⁻¹ and 3.2 × 10^4 GE 100 ml⁻¹ for January and July 2009, respectively (Fig. 1c, S1). Significantly lower levels of the HF183 marker were observed in the nonhorticultural areas (geometric mean 3.1 × 10^3 GE 100 ml⁻¹) where geometric means for residential, undeveloped and reservoir were 2.5 × 10^3 GE 100 ml⁻¹, 2.7 × 10^3 GE 100 ml⁻¹, and 5.2 × 10^3 GE 100 ml⁻¹, respectively (Fig. 1c). Two-way analysis of variance (ANOVA) revealed differences in mean log-transformed HF183 levels with land-use category (F = 8.80; P < 0.0001) but not sample date or the interaction of date and land use (F = 0.699; P = 0.41 and F = 1.32; P = 0.27, respectively). Farming/horticultural areas had significantly elevated HF183 levels relative to residential and undeveloped areas and the reservoir (Tukey’s HSD α < 0.05) (Table 3).

Correlation between human Bacteroides, total coliforms, and E. coli

To examine the hypothesis that E. coli and the HF183 marker were both predictive for the presence of human sewage, we tested the relationship between E. coli, total coliforms and land use/sample date and compared log-transformed concentrations of HF183, E. coli, and total coliforms across the dataset with the expectation that positive correlations would be consistent with prediction of the same property. Similar to the ANOVA results obtained for the HF183 marker, two-way analysis of variance revealed differences in mean log-transformed E. coli levels with land-use category (F = 26.3; P < 0.0001) but not sample date or the interaction of land use and sample date (F = 2.86; P = 0.09 and F = 0.701; P = 0.55, respectively), while total coliform levels varied with land-use category (F = 15.73; P < 0.0001), sample date (F = 5.48; P = 0.0220) and the interaction of land use and sample date (F = 3.65; P = 0.0164) (Table 3). Farming/horticultural areas had significantly elevated E. coli and total coliform levels relative to undeveloped areas and the reservoir (Tukey’s HSD alpha < 0.05). In contrast to the HF183 marker and E. coli, total coliform levels in the farming/horticultural areas were not significantly different from levels in the residential areas.
We observed a weak but significantly positive correlation in the total dataset between HF183 marker levels and *E. coli* (*R* = 0.34; *P* = 0.0014) that was driven by moderate correlation of these indicators within the farming/horticultural areas (*R* = 0.59; *P* = 0.0007). The majority of samples collected from the farming/horticultural areas had elevated levels of all indicators and emerged as a distinct cluster in hierarchical clustering analysis of indicator profiles (Fig. 3, cluster 6). In the nonhorticultural areas (residential, undeveloped and within the reservoir), correlation between HF183 and *E. coli* or total coliforms was weak and not significant (*P* > 0.05) (Table 4). Some samples with *E. coli* levels exceeding the USEPA single-sample limit had below study median or nondetected HF183 levels (Fig. 3, clusters 4 and 5), while in several samples near-median to

![Figure 2](https://example.com/figure2.png)

**Figure 2** Neighbour-joining tree of cloned sequences recovered from Kranji Reservoir and catchment samples using the human *Bacteroides*-specific HF183F and 708R primer pair. For each representative sequence, the number of sequences sharing >99% nucleotide identity from each of the three field sites is provided in brackets. Field sites are: R15—Residential Area, Bukit Panjang; F5—Farm Area in Tengah; K6—Kranji Reservoir at branch point between catchment and open water. The most closely related reference sequences included in the phylogenetic analysis were downloaded from the NCBI database (9/16/10—12/15/2009) and correspond to the following studies: EF215526, EF215460, EF215509, EF215464, EF215518, EF215511, EF215512 from Santoro and Boehm (2007); AF233408 and AF294909 from Bernhard and Field (2000a,b).
above-median HF183 levels were found in samples that had compliant *E. coli* levels (Fig. 3, clusters 3 and 7). The majority of samples collected from the reservoir were characterized by low levels or nondetection of all indica-
tors (Fig. 3, cluster 9). HF183 marker levels at 21 sites sampled during both January 2009 and July 2009 showed consistency across sampling dates (R = 0.62; P = 0.0025).

**Investigation of potential sources**

To gain preliminary insight into potential sources of human faecal contamination in the horticultural areas, we analysed effluent samples from four on-site wastewater treatment systems (near sites F8, F7 and F5, and between F9 and F10), from two fish ponds (near sites F7 and F4) and a sample of raw sewage from the sanitary sewer of a residential area. The raw sewage sample contained the HF183 marker at an abundance of \(3.1 \times 10^7\) GE 100 ml\(^{-1}\) which is similar to the range of levels observed associated with sewage in other studies (i.e. \(4.0 \times 10^6\) to \(2.5 \times 10^8\) HF183 marker copies 100 ml\(^{-1}\)) (Van De Werfhorst et al. 2011). Samples of effluent from the fish ponds and three of four on-site wastewater treatment systems revealed HF183 marker concentrations within the range of variability observed in the catchment (Fig. 4). However, one effluent (Effluent–F8) connected to farming/horticultural site F8 had elevated HF183 marker levels similar to that observed in the raw sewage sample and was identified as a concentrated source of sewage contamination (Fig. 4).

**Discussion**

Maintenance of high water quality is necessary to enable recreational activities such as fishing and boating and to protect drinking water resources. However, identifying the primary mechanisms that introduce human sewage into reservoirs and drainage systems is a challenge,
especially in tropical systems where the conservative behaviour of sewage indicators has not been well established. In this study, we compared the abundance and
distribution of FIB (E. coli and total coliforms) with the
distribution and abundance of an alternative DNA-based human faecal indicator, the HF183 marker, to evaluate
the distribution of human sewage contamination in the Kranji Reservoir and catchment. Semi-nested PCR revealed that the human-specific HF183 marker was widespread in the Kranji Reservoir and its catchment (Table 2), however, did not provide information regarding the relative abundance of the marker across different sites or potential existence of a low, but nonzero, environmental-baseline abundance. Analysis of sequences recovered with the HF183F 708R primer pair confirmed that the HF183 assay was specific for *Bacteroides dorei*–like organisms in Singapore and similar to sequences recovered from previous studies designed to validate the assay (Fig. 2). Although we cannot rule out contribution of HF183 marker from alternate sources in this environment, previous studies have revealed low cross-reactivity of the HF183 marker, as amplified with the 183F-708R primer pair, with nonhuman sources (Bernhard and Field 2000a; McLain *et al.* 2009; Van De Werfhorst *et al.* 2011).

The use of the Sybr HF183 QPCR assay which relies on primer pair 183F-242R to generate a suitable sized amplicon for QPCR subsequently revealed differences in HF183 marker abundance among sites that were correlated with land use (Fig. 1a–c) and pointed to on-site treatment plants within horticultural areas as potential contributors to elevated levels of human faecal contamination. Melting temperature profiles of QPCR amplicons in our study supports amplification of a single 16S rRNA sequence type, corresponding to sequenced clones and supporting the specificity of the QPCR assay for quantification of the same bacterial group as detected with the 183F-708R primer pair. *E. coli* and total coliforms were also elevated in the horticultural areas and were correlated with HF183 marker levels (Fig. 3, cluster 6). In contrast, in the nonhorticultural areas, high *E. coli* concentrations were not well correlated with the HF183 marker, possibly due to nonconservative behaviour of *E. coli* as a tracer for human sewage (Fig. 3, clusters 1, 4, 5). The single-sample threshold recommended by the USEPA for *E. coli* in freshwater used for water-contact recreation is 235 100 ml$^{-1}$ (USEPA 1986, 2002a, 2012). A similar threshold has not been established for the HF183 marker (Ashbolt *et al.* 2010); however, for this specific environment, we sought to identify potential sources for human sewage contamination by identifying samples with HF183 levels above baseline levels observed in the reservoir and catchment. In the farming/horticultural areas, 18 of 19 samples had *E. coli* levels above the USEPA single-sample limit and of these 72% (13/18) also had HF183 levels higher than the study median (i.e. >4.16 $\times$ 10$^3$ GE 100 ml$^{-1}$). In contrast, in the nonhorticultural areas, 30 samples (of 62 total) exceeded the USEPA single-sample threshold for *E. coli*, but only 7/30 (23%) of these also had HF183 levels above the study median. This raises the possibility that many of the nonhorticultural sites with elevated *E. coli* levels may not be appreciably contaminated by human sewage.

Previous studies of waterways in temperate urban environments suggest an absence of correlation between HF183 marker and other indicator bacteria (Converse *et al.* 2011; Sauer *et al.* 2011). These earlier results are consistent with our observations of poor correlation between *E. coli* and HF183 marker in the nonhorticultural areas of the Kranji catchment. *E. coli*’s ability to serve as a FIB is hampered by the potential for environmental growth (Hazen 1988; Rivera *et al.* 1988; Hardina and Fujioka 1991), especially in warm tropical areas. Thus, the HF183 marker, which is not expected to grow under oxic conditions, may act as a more specific marker for human sewage in this catchment. However, it is not known if HF183 marker-bearing organisms can proliferate in environmental microhabitats that mimic the gut—i.e. are warm, anoxic and nutrient-rich. Such microhabitats may be present in the Kranji catchment and proliferation of HF183-marker-bearing organisms under
eutrophic tropical conditions needs to be better constrained before the HF183 marker is adopted as a reliable standard in tropical areas (Balleste and Blanch 2010; Surbeck et al. 2010).

Agricultural areas in the United States and elsewhere are frequently associated with water quality impairments due to nutrient loading and agricultural wastes (USGS 1999). In Singapore, where farming activities are dominated by vegetable and flower horticulture, aquaculture and a very limited amount of chicken farming, combined drainage systems that merge sanitary wastewater with farm wastewater, and stormwater into the same discharge drain may contribute to impaired water quality (Chua et al. 2010). Indeed, our partial survey of potential sources of contamination in the farming/horticultural area pointed to a wastewater effluent as a source of human faecal contamination. In addition, direct discharge of septic tanks into the main drainage was observed at sites F8 and F7, and a make-shift toilet in use by farm workers and discharging into a surface-water drain was observed at site F6. These observations provide additional ground truthing of the utility of the HF183 marker assay to identify sources of human wastes in a complex environmental background.

The farming/horticultural areas in the Kranji catchment are located close to the reservoir and many farm drains almost directly into the reservoir. Although not necessarily producing high-volume flows, the drains exhibit very high coliform bacteria concentrations (Bossis 2011) and thus deliver a significant bacterial load to the reservoir. The effects on the reservoir were observed in water-quality samples collected on a north–south transect along the reservoir (Zhang 2011). These showed E. coli concentrations in excess of 100 MPN 100 ml$^{-1}$ and as high as 5,000 MPN 100 ml$^{-1}$ in the middle upstream arm of the reservoir adjacent to the horticultural areas as compared to single-digit E. coli concentrations in the main body of the reservoir. This is consistent with our results, in which reservoir sites K2 and K5 were associated with above-median levels of the HF183 marker in January 2009 (but not July 2009).

This study was carried out to determine the distribution of HF183 marker in a mixed tropical urban environment, to identify potential sources of human faecal contamination to the Kranji Reservoir and to phylogenetically validate the use of the HF183 marker in Singapore and similar tropical urban environments. Based on a synthesis of these results, we conclude that quantification of the HF183 marker targeting bacteria closely related to B. dorei can be a useful tool for mapping the spatial distribution of human sewage contamination and identifying potential sources of human sewage contamination in tropical environments such as Singapore. However, further studies are needed to understand the ecology of organisms bearing the HF183 marker in tropical environments, to confirm that they act as conservative tracers of human faecal contamination and to relate these levels to human health risks.

**Acknowledgements**

This research was supported by the National Research Foundation Singapore through the Singapore MIT Alliance for Research and Technology’s Center for Environmental Sensing and Modeling research programme. Substantial assistance was provided by Dr. Hans Eikaas and others at the Public Utilities Board of Singapore. We thank MIT students Cameron Dixon, Kevin Foley, Erika Granger, Kathleen Kerigan, Adriana Mendez-Sagel, Shammai Quddus, Amruta Sudhalkar and Jessica Yeager, NTU students Li-Jun Lee and Yu-Ling Por, and Syed Alwi Bin Sheikh Bin Hussien Alkaff of NTU for their contributions to the completion of this study.

**Conflict of interest**

No conflict of interest declared.

**References**


Human Bacteroides in an urban tropical catchment

J. P. Nshimyimana et al.


Supporting Information

Additional Supporting Information may be found in the online version of this article.
**Figure S1** HF183 marker genome equivalents (GE 100 ml⁻¹) in Kranji Reservoir and catchment samples collected in January 2009 (a) and July 2009 (b). *denotes samples with HF levels below detection (i.e. <150 GE 100 ml⁻¹). Sample and colour codes: undeveloped area (U) (purple bars), farming/horticultural area (F) (green bars), residential area (R) (orange bars), Kranji Reservoir (K) (blue bars). Error bars correspond to standard deviations calculated through uncertainty propagation.

**Table S1** Quantification of Indicator Bacteria in Samples from Kranji Reservoir Catchment, Singapore.