DNA-based real-time detection and quantification of aeromonads from fresh water beaches on Lake Ontario
Izhar U. H. Khan, Alyssa Loughborough and Thomas A. Edge

ABSTRACT

The present study was designed to develop a novel, rapid, direct DNA-based protocol to enumerate aeromonads in recreational waters. An Aeromonas genus-specific real-time quantitative polymerase chain reaction (Q-PCR) protocol was developed and optimized using newly designed genus-specific oligonucleotide primers derived from the gyrase B subunit (GyrB) gene. A standard curve was developed based on the PCR protocol with a minimum quantification limit of 10 cell equivalents ml$^{-1}$ achieved using an autoclaved water sample from recreational water spiked with known quantities of an Aeromonas ATCC strain. The Q-PCR protocol was validated and applied to detect and quantify the total number of aeromonads in water samples collected from two fresh water beaches on Lake Ontario. The Q-PCR protocol revealed significantly higher numbers of aeromonads in all water samples than a culture-based assay at both beaches. Foreshore sand was found to serve as a reservoir of high concentrations of Aeromonas similar to this phenomenon noted for enteric bacteria like Escherichia coli. The new real-time Q-PCR protocol facilitated the rapid quantification of total numbers of Aeromonas cells present in recreational water samples in $<3$ hours without culturing.

Key words | aeromonads, gyrase B subunit (GyrB) gene, real-time Q-PCR, recreational water

INTRODUCTION

Aeromonads are Gram-negative, non-spore forming, rod shaped waterborne bacteria that are ubiquitously found in environmental habitats such as soil, fresh and brackish water, sewage and wastewater, untreated and treated drinking water (Altwegg 1996; Brandi et al. 1996; Janda & Abbott 1998). Among 14 proposed species of Aeromonas, mesophilic and motile species such as A. hydrophila, A. veronii, A. caviae, A. jandaei and A. schubertii have been associated with human infections such as acute gastroenteritis, septicaemia, wound infections, endocarditis, meningitis and respiratory infections (Hanninen & Siitonen 1995; Janda & Abbott 1998; Isonhood & Drake 2002). In 1996, Aeromonas was included on the microbiological contaminant candidate list by the US Environmental Protection Agency (EPA 1998). The prevalence and distribution of Aeromonas in aquatic environments, its role as a contaminant of water, and the potential for pathogenicity mediated by mesophilic and psychrophilic Aeromonas spp. are all of public health concern (Borrell et al. 1998; Dumontet et al. 2000; Joseph & Carnahan 2000).

Accurate methods are needed to enumerate Aeromonas in aquatic ecosystems. Culture-based assays are recognized as only capable of enumerating cells that can be cultured under laboratory conditions. Viable cells that are injured, stressed or in a viable but non-culturable state might not be detected by culture-based methods (Pommepuy et al. 1996; Santo Domingo et al. 2003; Khan et al. 2007). Another disadvantage of culture-based methods is that they are not ideal for the rapid analysis of large numbers of samples in surveillance or outbreak investigations. In addition, the conventional biochemical and physical-based methods for the isolation and...
Identification of *Aeromonas* are generally time-consuming, labour intensive and often fail to identify cultured isolates to genus and species level.

In the last two decades, molecular methods based on polymerase chain reaction (PCR) or DNA-DNA hybridization have overcome many problems associated with culture-based techniques, enabling the detection of microorganisms in more rapid, accurate and robust fashion. A number of conventional PCR assays have been developed for the detection of *Aeromonas* spp. using 16S rRNA, 23S rRNA genes (Martinez-Murcia et al. 1992; Ash et al. 1993; East & Collins 1993; Dorsh et al. 1994; Borrell et al. 1997; Figueras et al. 2000; Morandi et al. 2005) and several virulence associated genes such as aerolysin (Husslein et al. 1992; Khan et al. 1999), lipases, amylase, chitinase, elastase, nuclease, gelatinase, lecithinase, protease and lateral flagella genes (Cascon et al. 1996; Pemberton et al. 1997; Kingombe et al. 1999; Nam & Joh 2007). However, recent advances in quantitative culture-independent DNA-based methods, such as the real-time PCR approach, offer a better measure for the quantification and monitoring of pathogens and microbial water quality indicators in various environmental sources including drinking water, agricultural water and wastewater as well as food and food products (Fukushima et al. 2003, 2007; Lee et al. 2006; Zucol et al. 2006; Khan et al. 2007; Wang et al. 2007).

To date, studies have been reported using real-time PCR assays for monitoring *Aeromonas* spp. in drinking water, stools and fish tissues (Fukushima et al. 2003; Balcázar et al. 2007; Yu et al. 2008). However, no studies have been reported for monitoring aeromonads in recreational waters. *Aeromonas* species occur at freshwater and marine beaches (Marino et al. 1995; Dickerman et al. 2006) and high numbers have been found in faecal pollution sources known to contaminate beaches such as gull faecal droppings (Levesque et al. 1993) and municipal wastewater (Ashbolt et al. 1995). *Aeromonas* species have been associated with a variety of human skin and wound infections in aquatic recreational environments (Hanson et al. 1977; Joseph et al. 1979; Vally et al. 2004). Considering the importance of *Aeromonas* spp. as a waterborne pathogen, the aim of this study was to develop a robust, rapid and reliable, culture-independent, DNA-based, real-time quantitative PCR (Q-PCR) protocol by designing *Aeromonas* genus-specific oligonucleotide primers using the GyrB gene. The protocol was then applied to validate this quantitative and sensitive molecular assay for the detection and quantification of total aeromonads at two fresh water beaches on Lake Ontario. The results from the culture and Q-PCR based assays were compared and used to determine the effectiveness of this protocol for recreational waters.

**MATERIALS AND METHODS**

**Reference strains and cultural conditions**

*Aeromonas hydrophila* ATCC 23123 was used as a reference strain for the development and optimization of the protocol. The specificity of the developed protocol including oligonucleotide primers, PCR conditions and optimization of the quantitative real-time assay was evaluated and validated using 17 *Aeromonas* and 35 reference strains of other bacterial species isolated from different sources to serve as positive and negative controls (Table 1). *Aeromonas* reference strains were grown aerobically in tryptic soy broth (Oxoid, Canada) with an overnight incubation at 30°C. The cell density (colony forming units (CFU) ml⁻¹) was measured after spread plating with an appropriate dilution on tryptic soy agar (TSA), and counting colonies per ml. The reference strains of different species used as negative controls were grown on selective growth media according to specified culture conditions.

**Collection of water samples**

A total of 96 water samples were collected over the 2006 bathing season from two fresh water beaches (Bayfront Park and Pier4 Park) in Hamilton Harbour at Lake Ontario. Sampling was conducted bi-weekly along a single transect at each beach at locations for sand pore water, ankle depth water and chest depth water. Sand pore water was collected by digging a hole in the wet foreshore sand about 1 metre inland from the water's edge, and collecting the water that seeped into the hole. All water samples were collected in 2-l sterile bottles and returned on ice to the laboratory for further analysis.
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Isolation and enumeration of culturable *Aeromonas*

One litre of each water sample was analysed by centrifugation at 12,800 g (Beckman, Fullerton, USA) for 20 min. For total number of culturable *Aeromonas* cells per 100 ml, the pellet was resuspended in 0.85% saline solution and spread plated on Ryan *Aeromonas*-selective growth media containing 5 mg l⁻¹ Ampicillin supplement (Oxoid) using a variable volume (range 10–100 μl). The plates were incubated overnight at 30°C. The putative *Aeromonas* isolates were initially confirmed by their growth characteristics, colony morphology and gram staining reaction. Putative culture isolates were confirmed as *Aeromonas* by the newly developed DNA-based PCR protocol.

**DNA extraction and purification**

One litre of each water sample was centrifuged at 12,800 x g (Beckman) for 20 min. To test the specificity of primers and the PCR protocol as well as check for PCR inhibition, 1 ml of a previously grown pure culture of *Aeromonas* was spiked into 1 ml of an autoclaved (121°C, 15 min) sand pore water sample and processed with the above described protocol. The pellets obtained from centrifugation were washed in TE buffer and processed for an efficient nucleic acid extraction and purification to remove potential PCR inhibitors such as humic acid and debris of other compounds using the Qiagen Mini Stool DNA kit (Qiagen, USA) according to the procedure described by Khan et al. (2007). The purified DNA was further concentrated using the Pellet Paint kit as per the manufacturer’s instructions (Novagen, Madison, USA) and resuspended in 25 μl of TE buffer. The concentration, quality and purity of the total microbial genomic DNA extract was confirmed by agarose gel electrophoresis using 1x TAE buffer.

**Oligonucleotide primers**

An *Aeromonas* genus-specific PCR was developed based on a newly designed oligonucleotide primer pair selected from conserved flanking regions of the gyrase B subunit (*GyrB*) gene. The following primer sequences were used: IA- Forward 5'-CTG AAC CAG AAC AAG ACC CCG-3' and IA- Reverse 5'-ATG TTG TTG GTG AAG CAG TA-3'. The primer pair was used to amplify a *GyrB* fragment of an expected size of 130 bp. These primers were purchased from Integrated DNA Technologies (Coralville, USA). Initially the specificity of primers and optimization of the PCR protocol was carried out by a conventional Mastercycler Gradient PCR system (Eppendorf, Hamburg, Germany).

**Real-time PCR for detection of *Aeromonas***

The amplification reaction was performed using SYBR Green JumpStart Taq ReadyMix (Sigma, USA). The reaction mixture (25 μl) consisted of a varying amount of genomic DNA template, 10 μl of 10X master mix including buffer, MgCl₂, dNTPs, SYBR Green and DNA polymerase,
0.5X reference dye and 40 ng each of the forward and reverse primers. The PCR amplification programme comprising an initial melting cycle (94°C for 2 min) followed by 40 cycles of amplification each involving 94°C for 10 s (denaturation), 55°C for 10 s (annealing) and 72°C for 10 s (extension) was optimized for *Aeromonas*. The reaction was performed using the Chromo4 Real-Time PCR Detector system (Bio-Rad, USA). To check and confirm the quality of amplification, a melting profile was generated for the amplicon over a temperature range of 65°C to 95°C. Due to expected small amplicon fragment size, the PCR amplicons obtained from *Aeromonas* reference strains and field samples were confirmed by agarose electrophoresis using a 2% agarose gel matrix (Fisher Scientifics, California) with 1X TAE buffer containing ethidium bromide (0.5 μg ml⁻¹) using 100 bp DNA size marker (PGC Scientifics, USA). Gels were visualized on a UV transilluminator and photographed using the Ingenius Syngene Bioimaging gel documentation system (Perkin Elmer, USA).

**Real-time quantitative PCR for *Aeromonas***

**Development of standard curves**

Initially, a standard curve was prepared using a pure culture of the *A. hydrophila* reference strain as a template for real-time PCR amplification with varying number of cell equivalents per ml (10⁶ through 10⁰). In another set of reactions, the pure culture of *A. hydrophila* was spiked into an autoclaved (121°C, 15 min) sand pore water sample and a standard curve was developed with varying number of cell equivalents (10⁶ through 10⁴ per ml). The more turbid sand pore water sample represented the potential for more significant PCR inhibition and was used to validate the DNA purification procedure adopted. In order to obtain a standard curve, the threshold cycle (Ct) value for each set of reaction was plotted against each cell equivalent number.

**Validation of real-time assay and application to field samples**

Using the optimized real-time PCR amplification reaction and conditions, varying amounts of isolated total genomic DNA collected from the three different beach sampling zones were used for the detection of *Aeromonas* and quantification of their number per 100 ml based on the standard curve.

**Sequencing of Q-PCR amplicons of field samples**

The oligonucleotide primers and real-time Q-PCR protocol were evaluated to determine the specificity of amplified products for aeromonads. Eighteen of 96 positive real-time PCR amplicons representing water samples from each sampling location were arbitrarily selected and purified using a QIAquick gel extraction kit (Qiagen Sciences, Maryland, USA). The purified amplicons were sequenced at McMaster University (Hamilton, Ontario, Canada). The sequence data were further analysed using a BLAST search against the global database to identify that sample at the genus and species level. The sequences for all samples were further analysed and compared by multiple alignment with the *Aeromonas* reference strain using MegAlign 1993–2006 (DNASTAR Inc., Madison, Wisconsin).

**Nucleotide sequence accession numbers**

Sequences for the 18 *Aeromonas* Q-PCR positive amplicons were submitted to GenBank with the following accession numbers: EU369396 to EU369413, respectively.

**Data analysis**

Statistical analysis to compare culturable and total numbers of *Aeromonas* (viable but non-culturable cells) per 100 ml was performed by a paired t-test using JMP® 7.0.1 (SAS Institute Inc., Cary, North Carolina). In addition, the coefficient of variation (CV) was used for comparison of the variability between conventional culture and Q-PCR-based approaches.

**RESULTS**

**Detection and enumeration of aeromonads**

Occurrence patterns for *Aeromonas* at both beaches were very similar, so results were combined. All water samples
collected from sand pore water at both beaches showed the highest culturable *Aeromonas* numbers (ranging from 18 to $1.8 \times 10^5$ CFU 100 ml$^{-1}$), followed by ankle depth water (ranging from 15 to $5.9 \times 10^3$ CFU 100 ml$^{-1}$) and chest depth water (ranging from 9 to $9.5 \times 10^3$ CFU 100 ml$^{-1}$). Putative *Aeromonas* isolates from water samples routinely showed typical growth patterns and colony morphology on selective growth media. PCR assays have confirmed these growth and colony characteristics are reliable for identifying *Aeromonas* spp. isolates (data not shown).

**PCR optimization and amplification**

The newly designed gyrase B subunit (*GyrB*) gene primer pair successfully yielded a typical amplicon with a predicted size of 130 bp and detected all reference strains of *Aeromonas* species chosen for the study. The specificity of the primers was also tested on DNA templates prepared from the 35 different bacterial reference strains serving as negative controls, and did not show any cross-reaction (Table 1). The results indicated that the primer pair showed specificities only for all *Aeromonas* species (data not shown).

**Quantitative real-time PCR and development of standard curve**

Based on the conventional PCR results, standard curves for quantitation were generated using the optimized Q-PCR amplification assay conditions based on cell equivalent numbers ranging from $10^0$ to $10^6$ per ml for laboratory water and $10^1$ to $10^6$ per ml for spiked autoclaved sand pore water, respectively. The standard curves showed correlation coefficients ($R^2$) of 0.999 and 0.998, and the quantification detection limits were 1 and 10 cell equivalents per ml, respectively (Figures 1(a) and 2(a)). Typical amplification curves for the amplicons were also detected based on the fluorescent signals measured by the Chromo4 detection system following the annealing step at 55°C (Figures 1(b) and 2(b)). The melting curve analysis of the PCR products showed typical melt profiles at 85°C (Figures 1(c) and 2(c)), while the negative control did not show any melting curve.

**Protocol validation and quantification of total aeromonads in field water samples**

The optimized real-time PCR protocol for detecting and quantifying total number of aeromonads in water samples was robustly validated. All 96 water samples yielded culturable counts on *Aeromonas* selective growth media, and showed positive real-time PCR amplification signals with specific melting profiles comparable to the standards (Figure 3(a) and (b)). Agarose gel electrophoresis confirmed the size and quality of the amplified products for all samples.
Total *Aeromonas* numbers in sand pore water samples ranged from $1.1 \times 10^3$ to $9.3 \times 10^5$ cell equivalents $100$ ml$^{-1}$ compared with ankle depth water (ranging from $1.0 \times 10^3$ to $1.3 \times 10^5$ cell equivalents $100$ ml$^{-1}$) and chest depth water (ranging from $3.2 \times 10^2$ to $1.7 \times 10^4$ cell equivalents $100$ ml$^{-1}$). Even the water samples with the lowest culturable *Aeromonas* counts (as low as 9 cells $100$ ml$^{-1}$) in chest depth water showed higher total counts ($1.225 \times 10^4$ total cell equivalents $100$ ml$^{-1}$) and ankle depth ($15$ culturable cells $100$ ml$^{-1}$ vs. $4.6 \times 10^5$ total cell equivalents $100$ ml$^{-1}$) water samples. The results revealed that the total cell equivalent numbers per $100$ ml (including viable but non-culturable and dead cells) of aeromonads were significantly higher (paired $t$-test; $P < 0.05$) than the culturable cell numbers per $100$ ml in each water sample collected from each sample location (Figure 4(a) and (b)). The coefficient of variation for the culture-independent Q-PCR protocol indicated less variability for enumerating *Aeromonas* than the culture-based method (Figure 4(c)). Across all 96 water samples, the Q-PCR protocol also
detected significantly greater numbers (>16%) of cells than the conventional culture-based approach.

Nucleotide sequence-based identification

All 18 Q-PCR positive amplicons selected for sequencing were confirmed as Aeromonas to genus level by available GenBank sequence data analysis and showed >98% sequence homology with Aeromonas spp. by multiple sequence alignment results (data not shown).

**DISCUSSION**

Traditional and novel DNA-based molecular methods are improving knowledge about the occurrence of Aeromonas spp. in aquatic ecosystems. Unlike conventional PCR assays, real-time PCR uses short fragments that can be amplified efficiently. In addition, detection is based on hybridization to specific sequences rather than amplicon product length; hence time consuming blot and probe techniques are not necessary to confirm product identity. However, the use of PCR assays as a diagnostic tool depends on a high quality purified nucleic acid template. The present study adopted the previously optimized protocol using centrifugation concentration and rigorous DNA purification approach for PCR amplification of templates naturally contaminated with PCR inhibitors such as humic acids, and debris of other compounds (Khan et al. 2007). The success of this quantitative real-time Q-PCR assay was, in part, based on direct and efficient DNA recovery using a centrifugation procedure as well as the efficient purification of a high quality DNA template for sensitive PCR amplification. Our data on cell equivalents and colony forming units are presented as minimum detectable numbers given some possibility of less than 100% DNA extraction efficiency and less than 100% cell recovery. The present Q-PCR protocol was successfully developed and optimized for quantifying the total number of aeromonads in recreational water samples. The protocol was validated and applied to water samples collected from two Lake Ontario beaches.

Several genes have been used for the molecular detection and confirmation of Aeromonas. However, the selection of the GyrB gene (encoding the B-subunit of DNA gyrase, a type-II DNA topoisomerase) in this study was based on its suitability as a phylogenetic marker for bacterial systematics (Kasai et al. 1998; Yamamoto et al. 1999; Yáñez et al. 2003). This protein plays a crucial role in the DNA replication process, and its gene has a mean synonymous substitution rate that is almost four times that
of the 16S rDNA gene (Yamamoto & Harayama 1996). Although the GyrB gene is ubiquitously distributed among bacterial species, it is rarely transmitted horizontally (Kasai et al. 1998). Recently this gene has been characterized in 53 Aeromonas strains (Yáñez et al. 2003). Therefore, the gene provided valuable conserved sites for designing Aeromonas genus-specific primers.

Following the development and optimization of the assay targeting the GyrB gene, it was applied to the field samples for validation purposes. The developed protocol can be used to detect a minimum of 10 cells per ml of Aeromonas in environmental samples. A significant difference between the results obtained from culture-based and real-time Q-PCR assays was observed. On average, the Q-PCR protocol detected >16% more cells than culture-based techniques. It is possible that viable but non-cultururable Aeromonas spp., which may potentially be infectious, might not be detected by culture-based methods but could be detected by Q-PCR assay. A more accurate enumeration of Aeromonas in water samples may allow a better assessment of the likelihood that high numbers of Aeromonas may interfere with existing methods for enumerating coliform bacteria in water samples. Conventional cultural-based assays have shown that lactose-fermenting aeromonads can interfere with counts of total coliform bacteria in environmental and drinking water samples by yielding false positive results based on their β-galactosidase activity (Leclerc et al. 1977; Freier & Hartman 1987). β-galactosidase can be used in rapid and simple methods that differentiate lactose-utilizing from non-lactose-utilizing members of the family Enterobacteriaceae (Edberg et al. 1988; Rambach 1990); however, most Aeromonas spp. also showed β-galactosidase activity (Sakazaki & Balows 1981). Ciebin et al. (1995) reported false-positive β-glucuronidase Aeromonas spp. with the isolates of E. coli, Klebsiella pneumoniae, Citrobacter freundii and Enterobacter species at specific thermophilic cultural conditions.

Several other studies have also observed a significant difference between Q-PCR and culture-based methods investigating microbial pathogens and water quality indicators in various environmental and food matrices (Ibekwe & Grieve 2003; Khan & Yadav 2004; Bohaychuk et al. 2007; Khan et al. 2007). Several factors might contribute to the difference in detection between culture-based and real-time Q-PCR assays. First, injured or stressed cells which had lost their viability and/or culturability would not be detected by a culture-based method. Second, the culture-based method might underestimate the concentration of Aeromonas because only green centred with opaque margin colonies on Aeromonas selective agar plates were considered as presumptive Aeromonas. However, some strains of Aeromonas could possibly be Ampicillin-sensitive, an antimicrobial agent that was used in our media to suppress the growth of background bacteria. Previous studies have reported the presence of atypical colonies on selective growth media as Aeromonas as well as the occurrence of Ampicillin-sensitive Aeromonas strains (Havelaar et al. 1987; Holmes & Sartory 1993; EPA 2001). Third, after prolonged incubation of cultures, the colonies can diffuse and merge, which may lead to lower colony counts (Havelaar et al. 1987). On the other hand, real-time PCR may overestimate the number of viable cells due to the detection of dead cells. To estimate the number of target genes in viable cells, there is need to first quantify the live cells and dead cells in a sample before applying the developed Q-PCR assays. In a recent study, Nocker et al. (2006) reported the use of propidium monoazide (PMA) in combination with Q-PCR, which can quantify viable and dead cells over a wide range of bacterial pathogens. Moreover, several studies have been conducted on the use of ethidium monoazide (EMA) to quantify viable cells. However, a disadvantage of EMA is that it can penetrate into live cells of some bacterial species (Novga et al. 2003; Rudi et al. 2005; Wang & Levin 2006). It is possible our real-time Q-PCR assay could be used in combination with either PMA or EMA in future studies to quantify the number of viable Aeromonas in recreational waters and other environmental matrices.

The Q-PCR protocol developed in this study can also contribute to gaining a better understanding of the prevalence and ecology of aeromonads in recreational waters. The two beaches we studied have been frequently closed in recent years due to high levels of E. coli (O’Connor 2003). A microbial source tracking study found that beach sand was serving as an important secondary source of E. coli contamination of the adjacent beach water at BayFront Beach, and that there was a significant concentration gradient of declining E. coli concentrations moving offshore
from the beach (Edge & Hill 2007). Our current study found a similar concentration gradient of high Aeromonas numbers in foreshore sand, with declining concentrations in water samples collected while wading offshore from the beach. This suggests that foreshore sand can also serve as a reservoir of high concentrations of ubiquitous bacteria such as Aeromonas similar to the phenomenon noted for enteric bacteria such as E. coli. Further research is warranted in order to better understand the relationship between Q-PCR results, Aeromonas health risks to humans and the ecology of Aeromonas in beach sand.

CONCLUSIONS

A Q-PCR protocol was developed to allow a rapid detection and quantification of the total number of aeromonad cells in water. This protocol can contribute to better understanding of various ecological factors involved in the prevalence, survival and human health risks of Aeromonas in recreational waters. Application of the Q-PCR protocol at two Lake Ontario beaches found that foreshore sand can serve as a reservoir of high concentrations of Aeromonas similar to the phenomenon noted for enteric bacteria such as E. coli.

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