



Molecular detection of food-borne *Aeromonas* species

S GHATAK¹, R K AGARWAL², K N BHILEGAONKAR³ and J P S GILL⁴

Indian Veterinary Research Institute, Izatnagar, Uttar Pradesh 243 122 India

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ABSTRACT

The members of the genus *Aeromonas* have emerged as an important food-borne pathogen that pose many challenges to the scientific community. Difficulties regarding aeromonads involve its debated taxonomy, true role as pathogen and detection, particularly from foods. Various conventional techniques involving culture media and broths have been devised for identification from foods and immunological techniques viz. ELISA protocols have been standardized. Due to shortcomings of these methodologies molecular techniques were explored. These included nucleic acid hybridization probes, various formats of PCR, restriction fragment length polymorphism, amplified fragment length polymorphism, pulsed field gel electrophoresis, real time PCR, sequence analysis, DNA microarray technique, etc. Many of these modern assays have been promising, indicating that future detection paradigm for detection of *Aeromonas* will predominantly be based on molecular techniques. In this communication we have attempted to review these available molecular tools for detection of aeromonads from foods.

Key words: *Aeromonas*, Detection, Food, Molecular

Once considered an opportunistic pathogen, the organisms of the genus *Aeromonas* has emerged as an important food-borne pathogen for humans (Merino *et al.* 1995, Isonhood and Drake 2002, Pund and Theegarten 2008). Despite the discovery of these organisms dating more than a hundred years ago this collection of Gram negative, coccobacillary, oxidase and catalase positive organisms kept microbiologists busy debating its taxonomy, food-borne nature and clinical relevance (Janda and Abbott 1998). However, years of insightful research findings world wide have led to a better understanding of the aeromonal biology and recognition of this unique organism as an emerging food-borne pathogen.

Emergence of Aeromonas species as food-borne pathogen: Aeromonads are autochthonous inhabitants of aquatic environment (Schubert 1991). In addition various foods also act as important reservoir for these organisms. The foods include seafood, chicken and red meat, vegetables, raw milk and milk products (Isonhood and Drake 2002).

Among sea foods, aeromonads are reported in fish and fish-eggs, shrimp (Hanninen *et al.* 1997), prawn (Borch *et al.* 1996), finfish, shell fish (Palumbo *et al.* 1985, Tsai and Chen 1996). Among shellfishes, oyster had the highest incidence (Tsai and Chen 1996).

Aeromonas spp. has also been found in many types of meats including ground beef, chicken thigh meat, pork sausage, ground and unseasoned pork (Okrend *et al.* 1987). They are also found in high numbers in pig carcass processing equipment such as dehairing equipment, dehairing water, loin trimming belt and mesh gloves (Gill and Jones 1995). Keeping a view of endemicity of aeromonads in food processing lines in mind, Borch *et al.* (1996) proposed that *Aeromonas* spp. could be useful as an indicator of processing hygiene.

Reports on the prevalence of *Aeromonas* spp. in foods in India are far more limited. However, the organism has been isolated from variety of foods including fish, meat, milk, egg, tortoise and snail (Singh *et al.* 1997, Agarwal *et al.* 2000). Doke *et al.* (1994) isolated *Aeromonas* spp. from Indian mackerel. In 1997, a study by Khurana and Kumar in Haryana, showed distribution pattern of aeromonads to be 37.5% in sheep meat, 32.6% in edible organ of poultry, 28% in poultry meat, 24.2% in edible organs of sheep and 0.9% in poultry eggs. Agarwal *et al.* (2000) after investigating a wide range of foods found aeromonads in 22.22% of fish, 5% of tortoise, 6.25% of snail, 4.08% of other aquatic foods,

Present address: ¹ Senior Scientist (ghataksnd@rediffmail.com), Division of Animal Health, ICAR Research Complex for NEH Region, Umiam, Meghalaya 793103 India.

²Principal Scientist and Head (rajeshbly@ivri.res.in), Division of Bacteriology and Mycology; ³Principal Scientist (kiranvph@rediffmail.com), Division of Veterinary Public Health.

⁴Professor and Head (gilljps@yahoo.com), Department of Veterinary Public Health, Guru Angad Dev Veterinary and Animal Science University, Ludhiana, Punjab 141 004 India.

8.88% of goat meat, 2.85% of buffalo milk, 18% of quail eggs, whereas Kumar (1998) isolated aeromonads from fish (28.57%), poultry meat (16.67%), poultry eggs (12.50%), goat meat (12%), buffalo meat (7.69%) and cow milk (5.56%). *Aeromonas* spp. have also been isolated from about 12.5% of ice cream samples in Chennai (Shankar *et al.* 1994).

Besides foods, aeromonads have also been implicated in a number of food-borne outbreaks in various parts of the world including France, Japan, Norway and Sweden (Granum *et al.* 1998, Kingombe *et al.* 2004). Usually the food-borne aeromoniasis are now considered as emerging human pathogens as well as enterotoxigenic “neoenteropathogen” (Ljungh and Wadstrom 1985, Merino *et al.* 1995). Up to 13% of reported gastroenteritis cases in United States might be caused by *Aeromonas* spp. (Buchanan 1984). Gastroenteritis caused by *Aeromonas* spp. may assume either secretory (Gracey *et al.* 1982, Burke *et al.* 1983), dysenteric (Rahman and Willoughby 1980), chronic (for >10 days) (Gracey *et al.* 1982), choleraic (Gurwith *et al.* 1977, Champsaur *et al.* 1982, Swale *et al.* 1986) or traveller’s diarrhoea form (Echeverria *et al.* 1984, Gracey *et al.* 1984, Vila *et al.* 2003). Several outbreaks of gastroenteritis caused by *Aeromonas* spp. have also been documented (Bloom and Bottone 1990, de La Morena *et al.* 1993). In addition to these, a unique outbreak of toxi-infection caused by preformed toxin of *Aeromonas hydrophila* has been reported by Cantoni *et al.* (2002).

Common housefly (*Musca* sp.) is often termed the ‘porter of infection’ and is usually related to gastroenteritis in humans. Reports of isolation of *Aeromonas* spp. from housefly indicated the possible role of flies in spreading aeromonal gastroenteritis (Nayduch *et al.* 2001, 2002).

Aeromonads are able to grow in raw, cooked and processed foods that are stored under refrigeration or packaged under modified atmosphere (Kirov 1993, Merino *et al.* 1995). Under these conditions, aeromonads are also able to elaborate toxins, posing a serious public health threat to the consumers of refrigerated and / or packaged ready to eat foods (Callister and Agger 1987, Kirov 1993).

Troubled taxonomy: Following initial placement of these organisms clubbed within genus *Aeromonas* under the family *Vibrionaceae*, the taxonomic position for aeromonads were reviewed. Finally, the genus was positioned under family *Aeromonadaceae* under order *Aeromonadales* within the class gamma-proteobacteria (Garitty *et al.* 2001). One of the most important consideration behind forming a new order was the phylogenetic depth and diversity displayed by these organisms. This is evident from the discovery of new species within the genus as recent as in the year 2008 (Alperi *et al.* 2008). Now 19 species comprise the genus *Aeromonas* (Table 1).

Detection dilemma: Despite convincing scientific evidences in favour of *Aeromonas* spp. as an important and emerging food-borne pathogen, till date there are relatively few attempts to detect aeromonads routinely from suspected

Table 1. Members of the genus *Aeromonas*

<i>A. allosaccharophila</i>	<i>A. molluscorum</i>
<i>A. aquariorum</i>	<i>A. popoffi</i>
<i>A. bestiarum</i>	<i>A. salmonicida</i>
<i>A. bivalvium</i>	<i>A. schubertii</i>
<i>A. caviae</i>	<i>A. simiae</i>
<i>A. encheleia</i>	<i>A. sobria</i>
<i>A. eucrenophila</i>	<i>A. tecta</i>
<i>A. hydrophila</i>	<i>A. trota</i>
<i>A. jandaei</i>	<i>A. veronii</i> *
<i>A. media</i>	

* *A. veronii* has two distinct biogroups (bg.) – *A. veronii* bg. veronii and *A. veronii* bg. sobria

foods. This may perhaps be explained due to the inability of the conventional isolation methods (Sachan and Agarwal 2000), more demanding biochemical tests for speciation of the organisms (Abott *et al.* 2003) and inadequacy of the current biochemical tests to differentiate *Aeromonas* spp. (Ormen *et al.* 2005).

The resultant scenario therefore is presence of a number of enrichment media (viz. alkaline peptone water, cephalothin alkaline peptone water, etc.), selective plating media (viz. rimler-shotts agar, ampicillin blood agar, ampicillin dextrin agar, UNISC agar etc.) and commercial identification systems with none winning universal acceptance across researchers and laboratories (Khan and Cerniglia 1997, Soler *et al.* 2003a, Kingombe *et al.* 2004, da Rocha *et al.* 2008).

In a bid to overcome detection limitations of conventional methods, immunological techniques were explored by various researchers. One of the prime targets for the development of immunoassays for aeromonads was the outer membrane proteins (OMPs) of the organism. OMPs were characterized and looked into for presence of homogeneity (Ghatak *et al.* 2001) and then the common fractions were used for standardization ELISA for detection of *Aeromonas* from foods (Merino *et al.* 1993, Sendra *et al.* 1997, Sachan and Agarwal 2002, Ghatak *et al.* 2003). However, the application of such immunoassay protocols remained somewhat limited.

Molecular tools - a way forward: The advent of molecular techniques in food microbiology has given a fillip for the detection of *Aeromonas* spp. from foods. These techniques not only circumvented the limitations faced by conventional as well as immunological techniques, they proved to be rapid, able to identify hitherto unsuspected aeromonads from foods and were robust in their applications (Kingombe *et al.* 2004).

Polymerase chain reaction (PCR): Two years after the first description of polymerase chain reaction by Saiki *et al.* (1988), Pollard *et al.* (1990) for the first time published a PCR methodology for *A. hydrophila*, targeting a well known virulence gene called aerolysin (*aer*). Inspired by the initial success the same target was employed for PCR detection of *Aeromonas* from foods, fishes and other sources (Baloda *et*

al. 1995). These early developments were followed by a number of PCR protocols optimized for detection of aeromonads involving various targets namely, haemolysin gene, enterotoxin gene, cytotoxin gene (Hirono *et al.* 1992, Chopra *et al.* 1993, Wang *et al.* 1996, Santos *et al.* 1999, Ormen and Ostenvik 2001, Sechi *et al.* 2002, Abdullah *et al.* 2003, Agarwal *et al.* 2003) (Table 2).

The common feature in these assays was that the targets for PCR amplification were various virulence genes, based on virulence assays. Once optimized, many of these assays found successful application in determining distribution of virulence genes among collections of *Aeromonas* isolates (Gonzalez-Serrano *et al.* 2002, Sechi *et al.* 2002, Abdullah *et al.* 2003, Chacon *et al.* 2003, Seethalakshmi *et al.* 2008).

A significant advancement of virulence based assays were reported which were able to standardize a multiplex-PCR protocol for simultaneous detection of one cytotoxic (*Act*), and two cytotoxic (*Alt*, *Ast*) enterotoxin gene for detection of *Aeromonas* spp. from food samples. The assay was applied to a relatively large number of suspected food poisoning samples and was reportedly rapid and specific (Chang *et al.* 2008).

Another class of PCR assays was also developed in parallel targeting housekeeping genes of aeromonads e.g. 16S rRNA, *gyr B*, *rpo D*, etc. These assays were employed for two main purposes, one for phylogenetic studies (Yanez *et al.* 2003) and the others for detection of aeromonads from various sources especially from food items like milk, chicken and fish samples (Porteen *et al.* 2006, 2007).

A valuable extension of application of PCR technology on housekeeping genes (16S rRNA and *gyr B*) of *Aeromonas* spp. was optimization of typing scheme for aeromonads based on PCR-denaturing gradient gel electrophoresis (PCR-DGGE). *gyr B* gene based PCR-DGGE was reportedly a powerful detection tool for aeromonads in complex samples (Tacao *et al.* 2005b). This technology is relatively new to food microbiology and promising for culture-independent food quality assessment (Ercolini 2004). Therefore it is expected and would be interesting to see the application of PCR-DGGE for monitoring and diversity evaluation of

aeromonads in food.

As PCR technology kept evolving and found many new applications *Aeromonas* researchers experimented with newer technologies and reported many different PCR formats for diverse objectives. Among them notable are RAPD, ERIC and BOX-PCR techniques.

Randomly amplified polymorphic DNA (RAPD) – PCR: RAPD-PCR methodology comprises use of arbitrary primers to enable random priming at various locations of the target genome which is followed by low stringency amplification generating PCR products of varying sizes that are indicative of the nucleotide polymorphisms in the genomes under study. Since the technique is poised for delineating polymorphisms, it has been employed for strain differentiation and source discrimination among isolates of *Aeromonas* spp. (Oakey *et al.* 1996, Davin Regli *et al.* 1998, Talon *et al.* 1998, Alavandi *et al.* 2001, Aguilera-Arreola *et al.* 2005, Korbsrisate *et al.* 2007).

Enterobacterial repetitive intergenic consensus (ERIC) – PCR: Despite aeromonads not being members of *Enterobacteriaceae* family, ERIC-PCR technique has been employed by many researchers to gain insight into the differences among strains and to achieve other typing goals (Davin Regli *et al.* 1998, Soler *et al.* 2003, Aguilera-Arreola *et al.* 2005). ERIC elements comprise repetitive sequences in bacterial genomes not restricted only to enterobacterial genomes, which are targeted to produce unique fingerprint for target bacteria based on the relative abundance of the repeats within the bacterial genome. The discriminatory power of ERIC-PCR have been claimed to be at par or more than the RAPD-PCR for *Aeromonas* spp. (Soler *et al.* 2003b, Aguilera-Arreola *et al.* 2005).

BOX-PCR: Like ERIC elements, BOX elements too are repetitive sequences of 154 bp length found within the bacterial genome. PCR amplifying these repeats can be useful for fingerprinting and typing of bacteria. Based on this principle, Tacao *et al.* (2005a) successfully optimized a BOX-PCR protocol yielding fingerprints applicable for typing and epidemiological studies of *Aeromonas* spp.

Nucleic acid probes: Probes are usually short stretches (15 – 30 bp) of nucleic acid that are labeled with radio tracer or fluorogenic tracer. Probe assays utilize the binding ability of denatured nucleic acid strands between a target organisms' DNA/RNA and a complementary sequence bearing labeled probe. In case of binding or hybridization target DNA/RNA will emit signal which can be detected by suitable sensor.

As a downstream study to characterize RAPD band by cloning and sequencing, Okay *et al.* (1999) developed a digoxigenin (DIG) labeled probe for *A. hydrophila*. However, this probe was specific for only hybridization group 1 (HG1) of *Aeromonas* spp. and have not been reported to be applicable for detection of *Aeromonas* from foods. While, a labeled DNA probe based on the highly conserved outer membrane protein of *Aeromonas* spp. specifically detected

Table 2. Common targets for PCR detection of *Aeromonas* spp.*

Virulence genes	Housekeeping genes
Aerolysin	16S rRNA
Cytotoxic enterotoxin	<i>rpo D</i>
Cytolytic enterotoxin	<i>gyr B</i>
Haemolysin	Type III secretion systems
Lipase	" <i>asc V</i>
Protease	" <i>aex T</i>
Histone like protein	" <i>asc F</i>
Elastase	" <i>asc G</i>
AHCYTOEN	

*This list is indicative only.

aeromonads in dot-blot assay, and was claimed to be suitable as rapid diagnostic tool for *Aeromonas* from foods (Khusiramani *et al.* 2009).

Restriction fragment length polymorphisms (RFLP): RFLP techniques involving endonuclease digestion of DNA segment offer valuable tool for detection, confirmation and speciation of food-borne pathogens. For aeromonads, RFLP assays developed, have however mostly been directed towards non-food applications including detection of clinical isolates (Borrell *et al.* 1997, Ghatak *et al.* 2006), for taxonomic inference (Figuears *et al.* 2000, Martinez-Murcia *et al.* 2005), for species identification (Iganowska and Kaznowski 2004, Kaznowski and Konecka 2005). These studies involved PCR amplification of a target piece of DNA within *Aeromonas* genome and then looking for enzyme specific restriction sites by digesting the amplicon with a selected enzyme(s). Polymorphisms were revealed by the differing banding patterns among isolates or strains or species when digested amplicon were analyzed by gel electrophoresis. Most of these above mentioned studies looked for polymorphism within 16S rRNA gene or in the 16S – 23S rRNA intergenic spacer region of *Aeromonas* spp. and, Kingombe *et al.* (2004) successfully employed RFLP technique on PCR amplicons for detection and speciation of aeromonads from foods. Moreover, this technique has also been utilized to detect and characterize *Aeromonas* isolates from chicken carcasses and in fish farm (Lee *et al.* 2002, Abdullah *et al.* 2003). One limitation that most of these studies suffered from is apparent similarity among RFLP fingerprints of various strains and isolates. Only close examination could reveal the true identity of the isolates. To circumvent this limitation Ghatak *et al.* (2006) devised a stepwise RFLP protocol that was based on either presence or absence of fragmentation of the 16S rDNA amplicon or highly discernible banding profile among more important of the *Aeromonas* species. The protocol was developed in such a fashion that once the identity of an isolate was established, there was no need to go through the further steps thus saving valuable time and costly chemicals.

Amplified fragment length polymorphism (AFLP): AFLP technique is similar to RFLP with difference being in the use of specific adapter molecules to detect and amplify polymorphisms within a set of DNA molecules. This unique technique has been widely used for the detection and species identification of *Aeromonas* spp. (Huys *et al.* 1996, Lund *et al.* 2002) and also for molecular epidemiological studies of aeromonads (Kuhn *et al.* 1997, Rahman *et al.* 2007). Moreover, AFLP has also been employed for the detection of *Aeromonas* spp. from foods (Kingombe *et al.* 2004).

Pulsed field gel electrophoresis (PFGE): When it comes to discriminatory ability of typing technique there are only a few tests that may equal PFGE. The technique essentially involves restriction enzyme digestion of carefully extracted intact genomic DNA of bacteria followed by electrophoresis

on agarose gel under the influence of an alternating field of electric current, so that the large DNA fragments can wriggle through the pores of the gel without being stuck up (Jay *et al.* 2005). Early experimentation on aeromonads started with application of this technique to construct physical and genetic map of *A. hydrophila* (Dodd and Pemberton 1998). Subsequently, PFGE was employed to study and characterize genetic diversity of *Aeromonas* isolates from diverse sources including food isolates (Hanninen and Hirvela-Koski 1999, Villari *et al.* 2000, Bonadonna *et al.* 2002).

Real time PCR: Extension of PCR, especially the quantitative (q-PCR) technology to combine with advances in fluorescence optics yielded the intelligently conceived technology of real time PCR. This technique is regarded truly revolutionary in that it has catapulted traditional analytical goal of end point analysis to dynamic detection ability during exponential amplification phase of PCR in real time (hence the name is) (Espy *et al.* 2006).

One of the first reports of application of real time PCR for aeromonads was by Fukushima *et al.* (2003) who reported standardization of a duplex real time SYBR green PCR assay, wherein the researchers were able to detect *Aeromonas* spp. along with 16 other food and waterborne pathogens. Since one of the principal advantages of real time PCR has been the ability to measure the target (bacteria), a number of researchers reported real time assays for detection and quantification of aeromonads (Balcazar *et al.* 2007, Ahmed *et al.* 2008, Yu *et al.* 2008, Khan *et al.* 2009, Trakhna *et al.* 2009). These assays were reportedly rapid (Fukushima *et al.* 2003, Khan *et al.* 2009), sensitive (Balcazar *et al.* 2007) and were culture independent (Khan *et al.* 2009). However, the assays suffered the weakness in detecting aeromonads chiefly from water. As the sensitivity of real time PCR is of many orders higher than conventional one (Espy *et al.* 2006), it is expected that many assays will come up for *Aeromonas* spp. for detection from foods.

DNA microarray: DNA microarrays are systematic collection of discretely immobilized oligonucleotides on a solid matrix that can produce a signal pattern upon hybridization with labeled target DNA (Rasooly and Herold 2008). DNA microarrays have found wide range of application including gene expression studies, genotyping and detection of pathogens important in food safety, medicine, and others (Kostrzynska and Bachand 2006). This novel technology is particularly capable in parallel identification of multiple targets (much higher than conventional multiplex PCR) (Rasooly and Herold 2008). Several researchers, therefore, attempted development of assays for multiple food-borne pathogens that included *Aeromonas* spp. also. (Kostic *et al.* 2007, Lee *et al.* 2008). As microarray technology enjoys diversified applications, many workers employed this technology for non-food studies on aeromonads including elucidation of toxin induced gene expression (Galindo *et al.* 2003, 2005) comparative genomic

profiling (Nash *et al.* 2006), comparison between virulence assay models (Hayes *et al.* 2006), detection of fish pathogens (Gonzalez *et al.* 2004). The array technology is especially suitable for food-borne pathogens when foods normally harbour numbers of harmless and innocuous organisms. Moreover, sensitivity and rapidity of this technology have been reported to be comparable or more than the conventional detection protocols (Hong *et al.* 2004, Wang *et al.* 2007)

Sequence analysis: Sequence analysis is one of the most convincing tools in modern molecular biology for the detection and confirmation of identity of food-borne pathogens. The technique involves chemical determination of nucleotide sequence of a desired segment of genome of the suspected pathogen and then comparing the same with available sequences for that particular segment of the same organism from computerized database(s). Sequence analyses for aeromonads have chiefly been utilized for phylogenetic and taxonomic studies (Yanez *et al.* 2003). Nevertheless, amplicon sequence analysis (ASA) of PCR amplified genome segments has been found to be particularly useful for detection and species determination of *Aeromonas* spp. from foods (Kingombe *et al.* 2004).

Conclusion and future trends: Detection of *Aeromonas* spp. from foods poses many challenges. For decades, researchers all over the world had to rely on conventional detection methodologies despite their documented limitations. These bottlenecks ironically prompted next-in-the-line researchers to explore and apply the benefits of molecular techniques for *Aeromonas* research in general detection in food in particular. Result is a smorgasbord of molecular techniques that were innovatively experimented upon, painstakingly optimized, rigorously evaluated and ready to use.

However, the true test of a technique lies with its ability to cope with changing demands of researchers, industry and law enforcers over time. Amongst molecular tools, PCR appear to possess this rare quality, that for last two decades its applications for detection of aeromonads have been steady. Although traditional culture based assays are considered natural reference test to compare molecular assays, it has been convincingly documented that many a times rapid molecular assays outperform the former detecting additional 'truly' positive cases (Abubakar *et al.* 2007).

Another concern that haunts molecular techniques is the inability to differentiate live and dead cells (Ghatak and Gill 2009). However, newer protocols have been reported that incorporated azide dyes in the PCR cycles to effectively rule out amplification of DNA from dead cells (Soejima *et al.* 2007, Brescia *et al.* 2009). These newer PCR protocols are yet to be reported for *Aeromonas* spp., but may be expected ahead in time.

The future holds many promises for *Aeromonas* researchers particularly engaged in detection from foods and perhaps we will see many new assays, innovative

modification of existing ones, especially, of PCR, real time PCR and microarray technology.

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