***Review Article***

The Genus *Aeromonas*: Taxonomy and Diseases in fish and humans

ABSTRACT:

Aeromonads are Gram-negative bacteria that naturally inhabit aquatic environments. Species of *Aeromonas* are opportunistic pathogens affecting both aquatic animals and humans, often causing septicemic diseases. In fishes, Aeromonads causes hemorrhagic septicemia, dropsy, and tail and fin rot. Similarly, certain species of *Aeromonas* are responsible for human diseases, including gastroenteritis, eye infections, peritonitis, and urinary tract infections. These bacteria can be isolated from diverse habitats, including water, fish, shrimp, poultry, milk, and other food products. The taxonomy of the *Aeromonas* genus is highly complex due to its phenotypic variability. To date, 41 species have been identified, of which at least 19 are recognized as major human pathogens. Literature suggests that pathogenic *Aeromonas* species pose significant health risks to both fish and humans. Given their potential for causing infections, these bacteria are likely to remain a major public health concern in the future.

Keywords: *Aeromonas*, Fish, Taxonomy, Distribution, Diseases

Introcudtion

The genus [Aeromonas](https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/aeromonas) comprises more than thirty Gram-negative bacterial species which mostly act as opportunistic microorganisms. These bacteria are distributed naturally in diverse [aquatic ecosystems](https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/aquatic-ecosystem), where they are easily isolated from animals such as fish and crustaceans (Bhowmick and Bhattacharjee, 2018). A capacity for adaptation also makes [Aeromonas](https://www.sciencedirect.com/topics/immunology-and-microbiology/aeromonas) able to colonize terrestrial environments and their inhabitants, so these microorganisms can be identified from different sources, such as soils, plants, fruits, vegetables, birds, reptiles, amphibians, among others. Infectious processes usually develop in immunocompromised humans; in fish and other marine animals this process occurs under conditions of stress. Such events are most often associated with incorrect practices in aquaculture. Aeromonas has element diverse ranges, denominated [virulence factors](https://www.sciencedirect.com/topics/medicine-and-dentistry/virulence-factor), which promote adhesion, colonization and invasion into host cells. These [virulence factors](https://www.sciencedirect.com/topics/immunology-and-microbiology/virulence-factor), such as membrane components, enzymes and toxins, for example, are differentially expressed among species, making some strains more virulent than others (Pessoa et al., 2019).

2.1. Taxonomic classification of *Aeromonas* species

 The order Aeromonadales comprises a single family of bacteria
Aeromonadaceae, where the genus *Aeromonas* resides (Martin-Carnahan and
Joseph, 2005). They are natural inhabitants of aquatic environment causing diseases
in aquatic animals and as opportunistic pathogens in humans, other warm-blooded
and cold-blooded animals and invertebrates.

 The *Aeromonas* spp. are Gram-negative non spore-forming rods, facultative anaerobes, oxidase- and catalase positive, able to reduce nitrates to nitrites and resistant to the vibriostat O/129 (2,4-diamino-6,7-diisopropylpteridine). Motile species possess a single polar flagellum (Martin-Carnahan and Joseph, 2005). Zimmerman (1890) first isolated *Aeromonas* and named as *Bacillus punctatus*. Later, Sanarelli (1891) isolated *Aeromonas* species from frogs and named as *Bacillus hydrophilus fuscus.* However, the present genus *Aeromonas* was mentioned in the book ‘Natural system of classification’ written by Kluyver and Van Niel (1936). Later, the genus *Aeromonas* has undergone a number of taxonomic and nomenclature revisions over the past 15 years. According to Veron (1965), *Aeromonas* was included in the family Vibrionaceae, which also included other genera like *Vibrio, Photobacterium* and *Plesiomonas*. Further investigations revealed that the genus *Aeromonas* is not in relation with family Vibrionaceae but exhibits similar characteristics with the sub group of class Proteobacteria (Martinez-Murcia *et al.,* 1992; Ruimy *et al.,* 1994). Following extensive DNA-DNA hybridization studies and 16S-rDNA sequence analysis (Popoff *et al*., 1981; Hickman-Brenner *et al.,* 1987; 1988; Kuijper *et al.*, 1989), removed the *Aeromonas* genus from the family Vibrionaceae and transferred to a new family, Aeromonadaceae (Colwell *et al*., 1986), order Aeromonadales of the class Gamma Proteobacteria (Garitty *et al*., 2001).

 Fernandez-Bravo and Figueras, (2020) reported that 41 species of *Aeromonas* have been described since 1943. The *Aeromonas* species identified so far include *A. hydrophila* (Stanier, 1943), *A. salmonicida* (Griffin *et al*., 1953), *A. media* (Allen *et al*., 1983), *A. veronii* (Hickman-Brenner *et al*., 1987), *A. caviae* (Schubert and Hegazi, 1988), *A. eucrenophila* (Schubert and Hegazi, 1988), *A. jandaei* (Carnahan *et al*., 1991), *A. trota* (Carnahan *et al*., 1991), *A. allosaccharophila* (Martínez-Murcia *et al*., 1992), *A. veronii bv veronii* (Abbott *et al*., 1994), *A. encheleia* (Esteve *et al*., 1995), *A. bestiarum* (Ali *et al*., 1996), *A. popoffii* (Huys *et al*., 1997), *A. veronii bv sobria (Joerg, 1999),* *A. sobria* (Harf-Monteil *et al*., 2004), *A. simiae* (Harf *et al*., 2004), *A. molluscorum* (Miñana-Galbis *et al*., 2004), *A. bivalvium* (Miñana-Galbis *et al*., 2007), *A. aquariorum* (Martinez-Murcia *et al*., 2008), *A. tecta* (Demarta *et al*., 2008), *A. piscicola* (Beaz-Hidalgo *et al*., 2009), *A. fluvialis*, *A. taiwanensis* and *A. sanarellii* (Alperi *et al*., 2010), *A. diversa* (Miñana-Galbis *et al*., 2010), *A. schubertii* (Alperi *et al*., 2010), *A. rivuli* (Figueras *et al*., 2011), *A. cavernicola* (Martínez-Murcia *et al*., 2013), *A. australiensis* (Aravena-Román *et al*., 2013), *A. dhakensis* (Beaz-Hidalgo and Figueras, 2013), *A. finlandiensis*, *A. lacus* and *A. aquatica* (Beaz-Hidalgo *et al*., 2015), *A. rivipollensis* (Marti and Balcazar, 2015) and *A. lusitana* (Martínez-Murcia *et al*., 2016), *A. lusitana* (Martínez-Murcia *et al*., 2016), *A. intestinalis*, *A. enterica, A. crassostreae and A. aquatilis*(Figueras *et al*., 2017).

 This genus has close relationships with several kinds of phyto and zooplankton, mainly inhabitants of aquatic environments (Simidu *et al.,* 1971; Chowdhury *et al.,* 1990 and Dumontet *et al.,* 1996). Denis (1971) reported the presence of motile aeromonads in sea water and plankton. According to Hazen *et al.* (1978) and Araujo *et al.* (1989), *Aeromonas* are mostly found in habitats of fresh, saline and brackish waters. This bacteria is also habitat of chlorinated and unchlorinated drinking waters (Burke *et al*., 1984; Kersters and Verstraete, 1996 and Emekdas *et al*., 2006); treated and untreated sewage water (Schubert, 1991), activated sludge (Neilson, 1978), irrigation water (Miranda and Castillo, 1998), clean river water (Pathak *et al*., 1988 and Sharma *et al.,* 2005), domestic and industrial waste water (Slade *et al*., 1986), abattoir waste water (Rossi *et al*., 2000), shell fish growing water (Rasmuseen, 1997), fish farm hatchery tanks (Rhodes *et al*., 2000), and even bottled mineral water (Tsai and Yu, 1997). Motile *Aeromonas*are also considered as normal inhabitants of the intestinal tract of fresh water fish (Chung and Kou, 1973; Horsley, 1977; Trust and Sparrow, 1974) and certain other poikilotherms (McCoy and Seidler, 1973; Shotts *et al.,*1972).

 Aeromonads comprises of straight, cocco- bacillary to bacillary gram negative
bacteria with rounded ends (Martin-Carnahan and Joseph, 2005). They occur singly,
in pairs, and rarely as short chains. Motile strains produce a polar flagellum, though
peritrichous or lateral flagella may be formed on solid media by some species. They
grow optimally within a temperature range of 22-35 °C, however some species can
grow at temperature range of 0-45 °C (Mateos *et al*., 1993). They tolerate a pH range
from 4.5 to 9.0, but optimum concentration range between 5.5 and 9.0. According to
Isonhood and Drake (2002), the growth of *Aeromonas* spp. can occur at sodium
chloride concentrations of 0 to 4%. Popoff and Veron (1976) described in the
classical taxonomic scheme that the first psychrotrophic group strains are able to
grow at 22-28 °C (*A. salmonicida*) and the second group includes mesophilic strains
which grow at 35-37 °C.

**2.2. Isolation of *Aeromonas* spp.**

 *Aeromonas* can be isolated from food, environmental and clinical sources on
numerous types of media with varying success. It is generally not a difficult organism to culture, but separation from other organisms in mixed populations and eventual identification is more complex and difficult. Several factors should be considered in choosing a suitable culture medium. Sensitivity and selectivity are, of course, important.Rimler-Shotts (RS) medium, which is a modification from several media used for enterobacteria (Moller,1955; Taylor and Harris, 1965) was developed by Shotts- Emmett B and Richard Rimler (1973) for *Aeromoas* sp. Trypticase soy broth with ampicillin (TSBA) and alkaline peptone water (APW) were recommended as enrichment broths for isolation of *Aeromonas* spp. and inositol brilliant green bile salts agar (IBB), dextrin fuchsin sulphite agar (DFS), xylose sodium deoxycholate citrate agar (XDC) and pril xylose ampicillin agar (PXA) are best differential plating media (Von Graevenitz and Bucher, 1983). Gobat and Jemmi (1995) compared five selective agar media and two enrichment broths for isolation of mesophilic *Aeromonas* spp in fish, meat and shellfish samples. The selective agars evaluated were modified cefsulodin-irgasan-novobiocin agar, bile salts-irgasanbrilliant green agar, Starch-ampicillin-DNA agar, *Aeromonas* medium and Ampicillin sheep blood agar. Two enrichment broths evaluated were trypticase soy broth and alkaline peptone water.

 *Aeromonas* spp. produces greyish white, stippled, translucent, moist colonies,
when grown on agar plate and a heavy turbidity with thick pedicle developed in broth
(Merchant and Parker, 1977). Colonies on plain agar plate after 24 hours incubation
are 1-3 mm in diameter, circular, smooth, convex, whitish and translucent. It also
grows on enriched media such as trypticase soy agar, blood agar and also on
MacConkey’s agar (Sugita et al., 1994). Altwegg (1994) reported that *Aeromonas*
species are known to routinely grow on non-selective and selective media used for
cultivation of gram-negative organisms (MacConkey, Salmonella-shigella, Hektoen
enteric agar). The pH required for growth varies from 4.0 to 9.0, at NaCl
concentrations between 0 ppt and 0.04 ppt. *A. caviae* colonies on blood agar may be
hemolytic or non-hemolytic, and hemolytic strains are known to produce a wide zone
of β-hemolysis (Altwegg, 1994). Yogananth *et al*. (2009) isolated *A. hydrophila* from frozen fish. Aspectically weighed fish flesh was homogenized for 2 minutes in stomacher bags containing alkaline peptone water. Then incubated at 37°C for 18 hours and inoculated in Starch Ampicillin Agar. Isolated cultures were then purified by repeated streaking in nutrient agar. Modified Rimler shots agar was used as selective medium to isolate colonies. Brain heart infusion broth was also used for inoculation of *Aeromonas* spp isolated from different clinically diseased fishes. Bacteria were incubated on media for 28 °C for 24 hours (Matter *et al*., 2018). Wassif (2018) isolated *Aeromonas* spp. from 150 infected *Oreochromis niloticus* and *Ictalurus punctatus* samples. Trypticase soya broth was used for inoculation of bacteria initially, from which a loopfull colony was streaked onto Trypticase soya agar, *Aeromonas* selective agar with Ampicillin supplement media and Rimler’s Shotts medium which was incubated for 24-48 hrs at 24-25 °C. Recently Li *et al*. (2020) isolated *Aeromonas* sp. from septicemia infected *Myxocyprinus asiaticus* (chinese sucker fish) using brain heart infusion (BHI) agar medium and the agar plates were incubated at 28 °C for 48 hr.

**2.4. Distribution of *Aeromonas* species**

*Aeromonas* species are widely distributed in the microbial biosphere, which can be isolated from virtually every environmental niche where bacterial ecosystems exist. These include aquatic habitats, fish, shrimp, various foods, domesticated pets, invertebrate species, birds, ticks, insects and natural soils, although extensive investigations on the later subject are lacking (Janda and Abbott, 2010).

**2.4.1. *Aeromonas* species in aquatic environment**

The members of *Aeromonas* species are considered autochthonous microorganisms of aquatic environments, frequently isolated from fresh and estuarine water, surface waters, sewage and remains associated with varieties of phytoplankton and zooplankton (Simidu *et al*., 1971; Chowdhury *et al*., 1990; Dumontet *et al*., 1996; Janda 2001; Figueras, 2005; Janda and Abbott, 2010). The cosmopolitan nature of *Aeromonas* spp. in aquatic environment provides suitable opportunity for transmission to cold-blooded animals, particularly fishes and amphibians, which come into contact with and ingest these organisms (Hayes, 2000). This may lead to infection, which depends on the species, pathogenicity and the virulence of the strains encountered some times has life threatening consequences (Hayes, 2000).

The World Health Organization (WHO) considers the health significance of *Aeromonas* and lists *Aeromonas* spp*.* in the third edition of Guidelines for Drinking-Water Quality (USEPA, 2005). In USEPA (2005) it was mentioned that Environmental Protection Agency in 1998 listed *A. hydrophila* on its “Drinking Water Contaminant Candidate List”. Through the Consumer Confidence Report Rule, public water systems are required to report unregulated contaminants, such as *Aeromonas*, when detected (Edberg *et al*., 2007).

The motile aeromonads especially *Aeromonas hydrophila* are among the most common bacteria in freshwater habitats throughout the world (Cipriano *et al*., 1984; Inglis *et al*., 1993). *A. hydrophila* is widely distributed in the aquatic environment and is found in clean as well as organically polluted freshwater and in marine systems, except at the most extreme salinity and it also forms part of the intestinal flora of healthy fish (Newman, 1982; Holmes *et al*., 1996). Water contaminated with *Aeromonas* spp. may cause harm to both the environment and human health (Water, 2006). Presence of *Aeromonas* spp. in wastewater treatment plants (WWTPS), mainly in South Africa due to inefficiency in pathogen removal in WWTPs was reported (Olaniran *et al*., 2015).

Aeromonads have been isolated from chlorinated drinking water supplies
around the world (Hazen *et al*., 1978; Burke *et al*., 1984; Vander Kooij and Hijnen, 1988;
Fernandez *et al*., 2000; Figueras *et al*., 2005). Aeromonads have been found at a
frequency of 1 to 27% of examined drinking water supplies (Rusin *et al*., 1997).
*Aeromonas* spp. have been recovered from mineral water with isolation rates as high
as 35.5% and cell concentrations of greater than 3 log 10 cfu/ml (Quevedo-Sarmiento *et al*., 1986; Slade *et al*., 1986; Gonzales *et al*., 1987; Manaia*et al*., 1990;
Havelaar *et al*., 1990; Tsai and Yu, 1997; Warburton *et al*., 1998; Croci *et al*., 2001).
*Aeromonas* has also been reported to enter a viable but non-culturable state, similar
to other pathogens, including *Vibrio* (Mary *et al*., 2002). Aeromonads have been
recovered from different water sources of India like domestic waters of Chennai
(Alavandi *et al*., 2001), Narmada river water (Sharma *et al*., 2005), Sulphur spring in
Orissa (Patra *et al*., 2007), surface waters of Kolkata (Bhowmik *et al*., 2009), tap
water, well water and water from reservoirs of Manipal (Hande *et al*., 2009). Carnahan *et al*. (1991) reported that the density of *Aeromonas* varies with environmental conditions and suggested occurrence of *Aeromonas* species in sewerage sludge (>108 cfu/ml), lakes and reservoirs (102 cfu/ml), wastewater (102–107 cfu/ml), rivers (104 cfu/ml), drinking water (102 cfu/ml) and ground water (101 cfu/ml). These *Aeromonas* groups are found in all types of aquatic environments except thermal springs, hypersaline lakes and highly polluted waters (Janda and Abbott, 1999).

Midilli (1998) isolated *Aeromonas* strains from 87.7% of environmental water samples and 40% of drinking water samples in Istanbul. Mete et al. (2002) isolated *Aeromonas* strains from 3.3% of 449 tap water samples around Denizli city. In Turkey, Emekdas *et al*. (2006) isolated *A. hydrophila* from 148 tap water samples. Yuceland Erdogan (2010) isolated 35 strains from environmental samples (water and soil) collected from Ankara. Among them 57.1% were identified as *A. hydrophila*, 37.1% of *A. veronii bv. sobria* and 5.8% of *A. caviae***.** Rather *et al*. (2019) isolated 116 isolates of *Aeromonas*, of which 48 (26.37%) were from water and 68 (34.62%) were from fish samples collected from retail markets and fish farms. The Aeromonads were recovered from all types of water sources viz. drinking water (13%), surface waters (26%) and fish ponds (69%). The most prevalent species recovered from drinking water was *A. hydrophila*. *A. hydrophila and A. caviae* were recovered more frequently from surface water sources. Estuaries are ideally suited for aeromonads, since salinity concentrations are substantially lower there than in the deeper (benthic) regions of the ocean. Fiorentini *et al*. (1998) reported that aeromonad numbers varying from 102 to 106 CFU per 100 ml throughout the year from Italian coast.

Anoxic ground water also may support growth of *Aeromonas*, and aeration has proven successful in reducing the organic nutrients that support its growth (Massa *et* *al*., 2001). Maalej *et al*. (2002) studied the seasonal occurrence of *Aeromonas* in urban effluents and the costal marine environment. In urban sewage effluents, presence of *Aeromonas* exhibited a seasonal cyclic distribution similar to faecal coliforms, with the highest numbers (29x106 cfu/100 mL) in winter months and the lowest levels in summer months. In coastal waters, *Aeromonas* reached highest levels (56 cfu/100 mL) in summer months. Lowest levels of *Aeromonas* occurred under conditions of maximal solar irradiation and minimum turbidity. Faecal coliforms and increased salinity was associated with higher *Aeromonas* counts (Bonadonna *et al*., 2002). Inactivation of *Aeromonas* in seawater is thought to result from lower water turbidity with increased solar penetration and lower levels of available organic nutrients compared to urban effluents.

**2.4.2. *Aeromonas* species in foods**

Members of the genus *Aeromonas* are widely prevalent in the aquatic environment and are frequently isolated from various foods, mainly seafood, meat, milk and vegetables (Grassi *et al*., 2003; Ottaviani *et al*., 2011). The number of motile mesophilic *Aeromonas* spp. in foods varies from <102 cfu/g to 105 cfu/g (Neyts *et al*., 2000). Palumbo *et al.* (1985) also reported that *Aeromonas* spp. counts in lamb, veal, pork and minced beef ranged from 102 to 105 cfu/g. Aeromonads have been recovered from fish and fishery products like catfish fillets (Wang and Silva, 1999), freshwater fishes (Yucel *et al*., 2005). Prawns were also contaminated with *Aeromonas* spp. (Vivekanandhan *et al*., 2002). Other than this, *Aeromonas* spp. are also isolated from mammalian meat such as lamb meat (Ibrahim and Macrae,1991), pork (Ibrahim and Macrae, 1991), buffalo meat (Osman *et al*., 2012), red meat stored in fridge (Schuman *et al*., 1997), beef and pork sausage (Ibrahim and MacRae, 1991), poultry eggs (Schuman *et al*., 1997), turkey (Koca and Sarimehemtoglu, 2009).

Park *et al*. (2021) isolated *A. hydrophila* from seafood and ready-to-eat sushi in South Korea. They isolated *A. hydrophila* in refrigerated oysters, sashimi, the unprocessed seafoods at 19.2% to 57.1% concentration and 3.3% in frozen tuna.

**2.4.3. *Aeromonas* species in humans**

 Generally, humans carry *Aeromonas* bacteria in their gastro-intestinal tract both symptomatically and asymptomatically. However, isolation of aeromonads rates for human faecal specimens vary widely as geographical areas, patient populations, food habits, level of sanitation and culture methods influence the recovery rates (Dumontet *et al*., 2003). The rates of faecal carriage in asymptomatic persons in developed countries range from 0% to 4% (Svenungsson *et al*., 2000), while the isolation rate from persons with diarrheal illness ranges from 0.8 to 7.4% (Albert *et al*., 2000). Recovery rates among children with diarrhea vary geographically *viz*., 2.3% in Taiwan (Juan *et al*., 2000).

Among Western Peace Corp workers in Thailand, Aeromonads were
recovered from 8.5% of healthy persons and 30.8% of persons with diarrhea
(Echeverria *et al*., 1981). In South-east Asia, asymptomatic carriage rates reported as
high as 27.5% and recovery rates from patients with diarrhea are 34% (Pazzaglia *et
al*., 1990). Reports on isolation of Aeromonads from symptomatic patients range from
0.04% to 21% (Kuijper and Peeters, 1991; Dumontet *et al*., 2003; Maraki *et al*., 2003). The frequency of recovery of *Aeromonas* spp. from stools corresponded to the warm summer months when *Aeromonas* growth reached their maximum and postulated that fresh vegetables may be a source (Saad *et al*., 1995). Faecal carriage rates of 6.6% of symptomatic 10-year olds have been reported (Komathi *et al*., 1998). Kannan *et al*. (2001) isolated *Aeromonas* spp. from clinical specimens in India which included *A. hydrophila* (59.3%), *A. caviae* (18.7%), *A. veronii* (10.9%), *A. schubertii* (4.6%), *A. jandaei* (3.1%) and *A. trota* (3.1%). Aeromonads were reported in 6.9% of adult patients with acute diarrhea in Hong Kong. Prediger *et al*. (2019) isolated *A. veronii* biovar *sobria* strains from diarrheal stools and performed phenotypic tests. The relationship between presence of *Aeromonas* spp. in human faecal specimens and clinical manifestations of disease continues to challenge epidemiologists.

**2.4.4. *Aeromonas* species in animals**

The presence of Aeromonads in animal populations probably reflects in their
feed and water quality. Aeromonads have been isolated from faeces of wild and pet birds and also causes septicemia in poultry (Saif and Busch, 1974). The total faecal
carriage rate in animals is slightly higher than the faecal carriage rate of normal
humans, which is < 1 to 7% for most studies, although some studies report higher
rates (Pitaragnsi *et al*., 1982). In domestic livestock, *A. hydrophila* was isolated from
faeces of normal horses, pigs, sheep, and cows (Gray, 1984). *A. hydrophila* was
isolated more frequently than *A. caviae* in faeces of pigs. Stern *et al*. (1987) isolated Aeromonads from 1 of 32 cows and 3 of 21 turkeys. The use of medicinal leeches to treat vascular infiltration in surgical wounds has been
recognized as a risk factor for *A. hydrophila* infections since 1983, and there are
numerous reports of cellulitis and septicemia resulting from leech therapy (Snower *et al*. 1989). *A. hydrophila* and *A. caviae* were isolated in cow and pig faeces respectively and reports showed that diet and water sources influenced recovery of Aeromonads from faeces of domestic animals (Gray, 1984). *Aeromonas* spp. also infects warm blooded animals including terrestrial and arborheal animals such as cattle, swine, dogs, horses, donkeys, several avian species, wild zoo and laboratory animals (Carter *et al*., 1995). *Aeromonas* have been found in association with marine copepods and plankton, where they are present at cell densities from 4 to 1.3x103 CFU/ 100mL in seawater and from 1.5x101 CFU/ 100mL to 6x102 CFU/ 100mL in plankton (Dumontet *et al*., 1996 and 2003). *A. hydrophila* has been isolated from diseased turtles, alligators, snakes, frogs and concluded that *A. hydrophila* may be an opportunistic pathogen of stressed animals (Gosling, 1996). *Aeromonas* infection in poultry is characterized by egg infection, cystic ovaries, salphingitis, osteomyelitis, bladder infections and kidney problems (Calnek *et al*., 1997).

The distribution of *Aeromonas* spp. in marine ecosystem and retail seafood outlets is well documented and the organism is considered to be the normal flora of a variety of fishes, only to act as an opportunistic pathogen under conditions of stress (Yogananth *et al*., 2009). These stressors depress fish immunity and allow this pathogen to invade fish, causing haemorrhagic septicemia or motile aeromonas septicemia (MAS) characterized by high mortality rate leads to severe economic loss to fisheries (Maleky *et al*., 2011). *A. hydrophila* causes red-leg disease in frogs but due to the association of fish and frogs with water, they can also infect fish regardless of its species (Austin and Austin, 1985). The motile mesophilic *A. hydrophila*, *A. sobria* and *A. caviae* cause haemorrhagic septicemia and ulcerative disease in fish (Austin and Adams, 1996). Other diseases include trout ulcer disease, goldfish ulcer disease and carp erythro-dermatitis associated with *Aeromonas* spp. *A. hydrophila* has been associated with several diseased conditions in fish including tail rot, fin rot, skin ulcer and haemorrahagic septicemia which is characterized by the presence of surface lesions and may lead to sloughing of the scales, haemorraging in the gills and anus (Gavriel *et al*., 1998). There may also be ulcers, abscesses, exophthalmia, abdominal swelling, myonecrosis, cellulitis, ecthyma gangrenosum and necrosis of the scales and protrusion of the eye balls in fish (Hayes, 2005).

**2.5. Diseases caused by *Aeromonas* species in fish**

Aeromonadsare opportunistic pathogens under condition of stress such as increase in water temperature, poor water quality, excessive handling etc., are the major causes for disease outbreaks (Figueras *et al*., 2011; Beaz-Hidalgo and Figueras, 2012) or secondary invaders in fish already suffering from another disease (Camus *et al*., 1998). Aeromonads cause diverse pathologic conditions that include acute, chronic, and covert infections in fish. Severity of disease is influenced by a number of inter-related factors, including bacterial virulence, the kind and degree of stress exerted on a fish population, the physiologic condition of the host and the degree of genetic resistance inherent within specific populations of fishes (Singh and Sanyal, 1997). Motile aeromonads differ inter-specifically and intra-specifically in their relative pathogenicity or their ability to cause disease. Pathologic conditions attributed to members of the motile aeromonad complex may include dermal ulceration, tail or fin rot, ocular ulcerations, erythrodermatitis, hemorrhagic septicemia, red sore disease, red rot disease and scale protrusion disease. In the acute form of disease, a fatal septicemia may occur so rapidly that fish die before they have time to develop anything but for a few gross signs of disease**.**

**2.5.1. Motile aeromonad septicemia**

The motile aeromonads are responsible for high
economic losses in fish farms due to motile aeromonas septicemia or red sore
disease (Camus *et al*., 1998). Chronic motile aeromonad infections manifest
themselves primarily as ulcerous forms of disease, in which dermal lesions with focal
hemorrhage and inflammation are apparent. Both the dermis and epidermis are
eroded and the underlying musculature becomes severely necrotic (Huizinga *et al*.,
1979). Gross symptoms of the MAS such as hemorrhages on skin, scale erosion,
ulceration around mouth and distended abdomen were noticed in rohu of all sizes
irrespective of sex, where as liver and kidney are the target organs of these bacteria
during acute infections (Mohanty *et al*., 2008). The disease signs reported in common
carp were loss of scales, eye abnormalities and internal gross signs include pale liver,
occasionally with hemorrhagic spots and necrotic kidneys showing liquefaction. El-Bouhy *et al*. (2015), observed septicaemia with hemorrhages on mouth in Nile tilapia and mullet species.

Highest prevalence of motile aeromonads occurs in organically polluted waters
(Hazen *et al*., 1978). Motile group of aeromonads was formerly divided into three
species viz., *A. hydrophila, A. caviae and A. sobria* (Popoff, 1984). Two other similar
motile aeromonads, causing similar pathologies as that of *A. hydrophila* include *A.
bestiarum and A. dhakensis* (Orozova *et al*., 2009). *A. hydrophila, A. bestiarum, A. veronii biovar sobria, A. caviae, A. veronii and A. jandaei* have been reported as pathogens of various fish species (Pridgeon and Klesius, 2011; Sharma *et al*., 2017; Hassan et al., 2017; Wassif, 2018). The motile Aeromonads *viz*., *A. hydrophila* and *A. veronii biovar sobria* have been linked with human infections, were isolated from fish by Erdem *et al*. (2010). El-Bouhy *et al*. (2015) identified *A. sobria* by using Analytical profile index API20E system, which was responsible for septicaemia with clinical signs of redness and haemorrhages of mouth in cultured *O. niloticus* and mullet species obtained from a private fish farm of Egypt. Physiological conditions like spawning stress and environmental factors such as crowding, low-dissolved oxygen and higher organic content, industrial pollution, temperature fluctuation, physical injuries are the predisposing factors of *A. hydrophila* infection (Shotts *et al*., 1976). *A. hydrophila* and *A. sobria* are the etiological factors of MAS that cause dangerous bacterial diseases to freshwater fishes (Cipriano *et al*., 1984), especially in warm water environments (Stevenson, 1998). Motile aeromonads exhibit decreased erythrocyte counts, haemoglobin levels, as well as a decrease in blood glucose, albumin, globulin, total protein and cholesterol and elevated uric acid and bilirubin in carp species. A highly virulent strain of *A. hydrophila* from *Catla catla* has been isolated in Andaman during 1996 to 1998 (Shome, 1999). Hatha *et al*. (2005) reported motile aeromonads in farmed freshwater fishes viz., *C. catla, L. rohita and C. idella*. Furthermore, species-level characterization revealed that *A. hydrphila* as the dominant species (50-70%) in the intestine of these fish, followed by *A. caviae* and *A. sobria* (Hatha *et al*., 2005). Similarly, MAS was also reported in gouramy, *Trichogaster* spp. (Sreedharan *et al*., 2013), Nile tilapia (El-Bouhy *et al*., 2015), gold fish Harikrishnan *et al*., 2009), eel (Esteve *et al*., 1994).

 Hu *et al*. (2012) isolated10 *Aeromonas* species from 202 fish samples both healthy and diseased including *A. veronii* (69%), *A. hydrophila* (10%), *A. sobria* (11%), *A. media* (4%), *A. Caviae* (2%), *A. jandaei* (1%), *A. salmonicida* (1%), *A. allosaccharophila* (1%), *A. bivalvium* (0.5%). In another study, a total of 90 *Oreochromis niloticus* (Nile tilapia) and 60 fish of *Ictalurus punctatus* (Channel cat fish) fish were collected randomly during an outbreak of disease mass mortalities from different fish farms in El Sharkia and El Ismailia governorate. *Aeromonas veronii* were isolated and presumptively identified using API20E system with recovery rate of 36.66% from total number of fish (Wassif, 2018). Saharia *et al.* (2018) reported MAS in the freshwater fish ponds of Assam. Out of 293 ponds, 91 (31.05%) were found to be positive for *Aeromon*as species which includes *A. hydrophila, A. veronii* and *A. sobria* with 51.64%, 21.97% *and* 18.68% respectively.

Recently, Saharia *et al*. (2020) found the incidence of MAS in freshwater fishes *viz*., IMC, exotic carp and some minor carps with gross symptoms such as haemorrhagic skin, scale erosion, ulceration around mouth and distended abdomen, as well as fin rot and tail rot collected from three districts of Assam. A total of 293 samples were screened for bacteriological study. Out of 293 pools, 91 (31.05%) were *Aeromonas* genera like *A. hydrophila* (51.64%), *A. veronii* (21.97%) and A. *sobria* (18.68%) and other bacterial species. Li *et al.* (2020) also isolated 54% of *A. veronii* from several freshwater fish like *Carassius auratus*, *Cyprinus carpio*, *Ctenopharyngodon idella*, and *Silurus asotus*. U-taynapun *et al*. (2020) isolated 50 isolates of four *Aeromonas* spp. from tilapia. *A. veronii* or *A. veronii* biovar *veronii* was dominant species (39 isolates, 78%), followed by *A. hydrophila* (6 isolates, 12%), *A. veronii* biovar *sobria* (3 isolates, 6%) and *A. jandaei* (2 isolates, 4%).

**2.5.3. Abdominal Dropsy**

Freshwater fishes like Catla and mrigal collected from freshwater pond showing clinical signs *viz*., distended abdomen, loose scales and deep ulcers on the dorsal surface and extensive hemorrhages on the ventral part (Mathur *et al*., 2005). Sreedharan *et al*. (2011) observed the gross pathology of cichlid oscar fish infected with infectious dropsy such as abdominal distension, scale protrusion and petechial hemorrhages, yellow coloured ascitic fluid in abdominal cavity and hemorrhage in all the internal organs. The 20 pure cultures obtained from abdominal fluid were biochemically and genotypically identified as *A. veroni*. Aly and Ismail (2016) isolated *A. hydrophila* and *Pseudomonas fluorescens* from dropsy affected common carp farms at sharkiya province, Egypt. The gross signs of the clinical specimens showed hemorrhagic lesions in the skin, fin, tail and eye and scale loss. Histopathological changes observed were congestion and hemorrhages in the skin and internal organs with distended anus, exophthalmia and ascites. Further, experimental Intraperitoneal injection done on 100 common carps with 0.5 ml (108 cells/ml) of equal mixture of isolated *A. hydrophila* and *P. fluorescens* from infected fish revealed same clinical findings and gross lesions of the field study with 76% mortality. Sughra *et al*. (2020) isolated *A. hydrophila* from dropsy affected rohu collectd from Punjab and Pakistan. The observed pathological signs of diseased fish were abdominal dropsy, exophthalmia, skin discoloration, shedding of the scales, hemorrhages on body surface, distended vent, ulceration on skin assorted from deep of necrotizing skin ulcers, fin erosions, sero-hemorrhagic and discharge of fluid from vent.

**2.5.4. Tail rot and fin rot**

 The tail and fin rot is caused by *Pseudomonas* and *Aeromonas* which are mainly responsible for ulcerative syndrome, bacterial hemorrhagic septicaemia and ascites (Paniagua *et al.,* 1990). *A. hydrophila* is an opportunistic and most common pathogen, capable of causing disease in stressed fish or as secondary pathogen of suffered fish with other pre existing diseases (Cipriano *et al*., 2001). *A. hydrophila* was also the causative agent for tail and fin rot in fish (Rodriguez *et al*., 2008)*.* According to Theron and Cloete (2002), *A. hydrophila* is the significant pathogen causing tail and fin rot in association with hemorrhagic septicaemia in cultured fish, which were collected from worldwide fish farms. Mohanty *et al.* (2008) experimentally challenged the rohu fish with *A. hydrophila* by intraperitoneal injection at 107 CFU/ml, showed gross symptoms such as haemorrhagic skin, scale erosion, ulceration around mouth, distended abdomen and fin- and tail-rot in all sizes irrespective of sex. Whereas the symptoms of severe dermal necrosis, fin and tail rot were also noticed in other weed fishes like *Puntius* sp. in same pond.

 Sreedharan *et al*. (2013) characterized *A. veronii* isolates from the internal organs of tail and fin rot affected gold fish from ornamental fish farms of kerala state, India. Satish *et al.,* (2013) isolated *A. hydrophila* from the infected tails and fins of tail and fin rot affected *C. catla* and *L. rohita* from nursery ponds of Guntur district of Andhra Pradesh. Highly infected fingerlings almost lost their fins and swimming ability. Kumari *et al*. (2019) isolated *Aeromonas* sp. and *Pseudomonas* sp. from the farm reared Indian major carp in the Tarai Region, Udham Singh Nagar of Uttarakhand, India during October 2012 to March 2013 and the diseases were identified as tail and fin rot and *Aeromonasis*. Kubilay *et al*. (2020) reported *A. sobria* as a pathogenic agent of tail and fin rot disease in yellow tail cichlid (*Pseudotropheus acei*) fish with clinical signs includes lethargy, abdominal swelling, lack of appetite and erosion of the caudal fins and the internal findings included accumulation of acidic fluid in the abdominal cavity, enlarged and necrotic kidney, enlarged and anaemic liver, congestion and hyperemia.

**2.6. Diseases caused by *Aeromonas* species in human**

**2.6.1. Gastroenteritis**

*Aeromonas* associated diarrhea is a worldwide phenomenon and affecting all
age groups, and while principally observed in healthy persons, it can also be found in
those suffering from immune disorders (Figueras, 2005). There are a numerous unusual presentation and complications of *Aeromonas* gastroenteritis, *Aeromonas* colitis or dysentery (Dixon, 2008). In some cases, *Aeromonas* produced cholera-like disease (Janda and Duffey, 1988) with rice-watery-stools, refractory inflammatory bowel disease (Doman *et al*., 1989), *Aeromonas* segmental necrotizing gastroenteritis, intramural intestinal hemorrhage with small bowel obstruction (Block *et al*., 1994) and *Aeromonas* enteritis/colitis include ileal ulceration (Yamamoto *et al*., 2004). The gastroenteritis attributed to aeromonads includes various combinations of fever, vomiting, and increased faecal leucocytes or erythrocytes (Janda and Abbott, 1996), Nausea, abdominal cramps occur in some patients, while colitis occurs in a third of diarrhea cases caused by *Aeromonas* (Graevenitz, 2007).

**2.6.2. Bacteremia/Septicemia or *Aeromonas* septicemia**

The incidence of bacteremia can range from 0.12–3.3% and the mortality rate associated with *Aeromonas* bacteremia is about 30% (Janda and Abbott, 2010). Additionally, several studies demonstrated that the most prevalent species associated with blood infections were *A. caviae*, *A. veronii*, *A. dhakensis*, and *A. hydrophila* (Figueras and Beaz-Hidalgo, 2015)*.* The underlying diseases found in cases of bacteremia/septicemia were most commonly malignancy (Figueras and Beaz-Hidalgo, 2015) and diabetes (Shizuma *et al.,* 2011). Moreover, the most common symptoms associated with *Aeromonas* bacteremia according to Janda and Abbott (2010) included fever (74–89%), jaundice (57%), abdominal pain (16–45%), septic shock (40–45%), and dyspnea (12–24%). Wu *et al*. (2015) reported that *A. veronii, A. dhakensis, A. caviae* and *A. hydrophila* were the important causative agents for bacteremia.

**2.6.3. Other infections of *Aeromonas***

Abbott *et al*. (1994) reported the first case of *A. veronii* biovar *veronii* sepsis in an elderly man with advanced colorectal cancer who developed jaundice. Brann (2001) reported intra-abdominal infections of *Aeromonas* spp. spread throughout the hollow viscus into the peritoneal space and such infections include pancreatitis, acute cholangitis, and hepatic abscesses as well as peritonitis.

Skin and soft tissue infection caused by *Aeromonas* spp. resulting in cellulitis and bacteremia in deeper soft tissues underlying the epidermis by following traumatic injury. Swimming, diving, boating and fishing are all aquatic recreational activities placing persons are at risk of *Aeromonas* infection (Voss *et al*., 1992). Necrotizing
fasciitis (NF) is a rapidly advancing form of cellulitis characterized by muscle necrosis.
Trauma is most closely associated with *Aeromonas* wound infections, severe burns
may lead to osteomylitis, myonecrosis or gangrene (Larka *et al*., 2003). NF is commonly known as a flesh-eating disease that can cause hypotension, fever, necrosis, and gangrene and can be a life-threating infection**.**

**Conclusion:**

*Aeromonas* species are the important pathogenic bacteria of the aquatic environment system, distributed widely in natural habitates, food products and drinking water also. Once *Aeromonas* colonizes in the host, it can cause infections both in fishes and humans. *Aeromonas* infections are the major health concern in the future. Although we have extensive knowledge about the genus *Aeromonas*, but more questions are rising due to new species are origin, there by it is increasing the taxonomy complexicity. Based on this, it is important to continue studies about the *Aeromonas* species.

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