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Research Article

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Incidence of *Aeromonas* species isolated from fresh fish, canned fish and shrimp in Sohag Governorate, Egypt

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Abstract

A total of 180 samples of fish meat and canned fish were randomly collected from different markets and retail shops in Sohag city as the following; fresh water fish (Nile tilapia and catfish), marine water fish (mullet), shrimps, and canned fish (tuna and salmon) with 30 samples of each, to study the incidence of Aeromonas species (Aeromonas spp.) with special reference to Aeromonas hydrophila (A.hydrophila) and its virulence genes. The results of this study showed that the mean of Aeromonas counts were 0.122×10^2 , 0.504×10^2 , 0.124×10^2 , 0.037×10^2 cfu/g for Nile tilapia, catfish, mullet and shrimps, respectively. While in canned fish it was uncountable. Aeromonas spp. were isolated from 60 of 180 examined samples with a percentage of 33.3%, 7 species were identified: A. caviae, A. hydrophila, A. media, A. shubertii, A. sobria, A. veronii biovar sobria and A. veronii biovar veronii were detected at a percentage of 5%, 7.8%, 2.8%, 7.2%, 5%, 2.8% and 2.8%, respectively. The results of PCR showed that, 12 isolates out of 14 were positive for 16S rRNA gene of A. hydrophila with a percentage of 85.7 %. Virulence gene like, Aerolysin AHA was found in 41.6 % of the examined samples while, the heat stable *enterotoxin AST* gene was not detected. This study spots the lights on *Aeromonas* spp. especially A. hydrophila as potential biological hazard in fish meat and canned fish, as a foodborne pathogen.

Keywords:

Aeromonas spp., A. hydrophila, Canned fish, Fish meat, Virulence genes.

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Fish is healthy and low-calorie food provides essential that macro and micronutrients as protein, vitamins and minerals (Abisoye et al., 2011). On the other side, fish may act as a vehicle for pathogenic bacteria leading to human gastroenteritis. Mesophilic aeromonads are one of the most common bacteria in water habitats throughout the world, and frequently cause disease in fish and causative agents of acute diarrheal disease in man. Aeromonas spp. are emergent food-borne pathogens, belong to the family Aeromonadaceae. They are Gram-negative bacteria ubiquitous in soil, aquatic environments, and food products. Aeromonas can survive and multiply at low temperatures (2-10°C) that is applied for cold storage of food products (Igbinosa et al. 2012; NCBI, 2020). The genus Aeromonas currently comprises 21 validated species, 11 of which are related to human clinical samples (Carnahan and Joseph, 2015). Aeromonas spp., as emerging pathogens to humans, cause a broad spectrum of infections. gastroenteritis, such as peritonitis, and hepatobiliary infections, myositis, bacteremia, septicemia, meningitis, soft-tissue and wound infections (Janda and Abbott, 2010; Bravo and Figueras, 2020).

A. hydrophila has been isolated from retail foods including fish, seafood, raw milk, poultry and red meat (Tahoun et al., 2016; Sreeremya, 2017; Wamala et al., 2018). A. hydrophila has been isolated previously from various fish in Egypt (Abd-El-Malek 2017; Ramadan et al., 2018). Fish can be contaminated with pathogenic bacteria either by polluted water or by processing handling, and unhygienic storage conditions (Sarkar et al., 2013). A. hydrophila were responsible for small outbreaks of food poisoning caused by ingestion of raw fermented fish (Igbinosa et То isolates of al., 2012). identify Aeromonas biochemical, spp., morphological and molecular techniques

are required (Figueras and Hidalgo et al., 2015). The 16S rRNA gene is considered a stable molecular marker for identifying bacterial species, since its distribution is universal and allows comparison of microorganisms (Sánchez, 2015).

Pathogenicity of Aeromonas depends on several virulence factors which allow them to adhere, invade, and destroy the host cells, overcoming the immune host response, such as cytotoxins, adhesins, hemolysins, proteases and lipases, as well as their ability to form biofilms (Hidalgo and Figueras, 2013). A. hydrophila strains contain aerocytotoxin enterotoxin (AST) gene that releases a toxin (aerolysin) to cause tissue damage. Aerolysin AHA is a cytolytic and a hemolytic exotoxin, binds to specific glycoreceptors on the surface of eukaryotic cells before inserting into the lipid bilayer and forms holes, this plays a key role in the pathogenesis of A. hydrophila infection. Severe disease and waterv diarrhea caused bv strains with AST gene which produces a heat stable enterotoxin. Cytotoxin cytotonic and hemolysin activity increases when temperatures increase to 37°C (Bravo and Figueras, 2020).

This study aimed to identify the incidence of Aeromonas species in fish meat and canned fish as well as the incidence of A. hydrophila and its virulence genes, which play important roles in human gastro-intestinal infections. bv using cultural and molecular methods.

Materials and methods **Collection and preparation of samples:**

A total of 180 samples of fish meat represented in freshwater fish (Nile tilapia and catfish), marine fish (mullet), shrimps as well as canned fish (tuna and salmon) with 30 samples of each, were collected randomly from different shops and supermarkets located in Sohag Governorate. Samples were prepared according to FDA, 2018.

Determination of *Aeromonas* **counts:**

Surface counting method was used according to (Austin, 2014). Inoculate 0.1 ml of the diluted samples and subsequent decimal dilutions onto plates of *Aeromonas* medium base (Himedia) supplemented with Ampicillin (Oxoid, SR0136), incubate plates at 30°C for 24hr.Examine the plates and count typical colonies "dark green, opaque colonies with a darker center" (Fig.1). Subculture five typical colonies (or all if fewer than five) to a nutrient agar slope, then incubate at 30°C for 18–24 h. Perform an oxidase test. Retain oxidasepositive strains and identify by biochemical tests.

Isolation and identification of *Aeromonas spp*.

Samples were homogenized into Alkaline peptone water (APW) with 2.5mg/L Ampicillin selective supplement, Oxoid and incubated at 30° C for 18-24hr. A loopful of the enriched culture was inoculated on *Aeromonas* medium base plates, Himedia, then incubated at 30°C for 24hr (Austin, 2014). Identification is made by morphological, and biochemical characteristics according to Carnahan and Joseph (2015)

Identification of *A. hydrophila* and its virulence genes by PCR

Suspected isolates examined for *16S rRNA* gene and then the positive isolates examined for virulence genes such as *AHA* and *AST*. Three pairs of primers were supplied from Metabion, Germany as shown in Table 1.

Table 1: Oligonucleotide primers sequences for A. hydrophila and its virulence genes

Gene	Primer sequence (5'-3')	Product size	Reference			
165 r DNA	CTACTTTTGCCGGCGAGCGG	053 hn	Gordon et al. 2007			
105 / KIVA	TGATTCCCGAAGGCACTCCC	955 op	Goldon et al., 2007			
Aerolysin	CACAGCCAATATGTCGGTGAAG	326 hn	Singh et al 2008			
AHA	GTCACCTTCTCGCTCAGGC	526 op	Shigh et ul., 2000			
AST	TCTCCATGCTTCCCTTCCACT	331 bp	Nawaz et al., 2010			
	GIGIAGGGAIIGAAGAAGCCG	1	,			



Fig. 1. *Aeromonas* spp. on *Aeromonas* medium base appears as green colony with dark green center

Molecular identification of *A. hydrophila* by PCR

DNA was extracted from the suspected isolates using QIAamp DNA

mini kit, Qiagen. PCR was done for the detection of *16S rRNA* gene using specific primer for *A. hydrophila* using an applied biosystem thermal cycler. PCR condition

was initial denaturation at 94°C for 5 minutes, 35 cycles at 94°C for 30 sec., then 50 °C for 40 sec., 72° C for 45 sec. and final extension for 10 minutes 72° C according to Gordon et al. (2007). The products of PCR examined were in agarose gel (1.5%)with electrophoresis ethidium and photographed by light promide transilluminator (Biometra).

Detection of virulence genes by PCR

A. hydrophila strains were examined for the presence of two virulence genes such as AHA and AST. The aerolysin AHA gene cycling condition was primary denaturation at 94°C for 5 minutes, then 30 cycles at 94°C for 30 sec., 52°C for 30 sec., 72° C for 30 sec. and final extension for 10 minutes 72° C according to Singh et al. (2008). The (AST) gene cycling condition was initial denaturation at 94°C for 2 minutes, then 35 cycles at 94°C for 30 sec., 50 sec at 1°C, and 72°C for 10 min. according to Nawaz et al. (2010).

Statistical analysis

67%

The mean value and the standard error of *Aeromonas* spp. counts of the tested

samples were analyzed by SPSS 18 software.

Results

Aeromonas spp. represented highly count in catfish with mean 0.504 ± 0.154 , followed by mullet 0.124±0.042, Nile tilapia 0.122 ± 0.032 , and shrimp 0.037 ± 0.008 , and cannot be counted in canned fish samples (Table 2). The incidence of Aeromonas spp. in mullet samples was 63.3% which reported the highest percent, followed by catfish 60%, Nile tilapia 53.3%, shrimp 13%, tuna 10%, and cannot be detected in salmon samples (Table 3 and Fig.1). A. hvdrophilla was identified in 14 (7.8 %) of the examined fish samples using biochemical tests (Figs. 2&3). PCR using specific 16S rRNA gene reported that 12 (85.7%) out of 14 samples were positive for A. hydrophilla (Fig. 4). Two virulence genes of A. hydrophilla of such as AHA and AST genes was examined by PCR and AHA was detected in 5 out of 12 samples, while AST gene cannot be detected (Fig. 5 and Fig. 6).

Sample	Min	Max	Mean±SE		
Nile tilapia	0.01 X 10 ²	$0.25 \text{ X} 10^2$	0.122 ± 0.032		
Catfish	0.05 X 10 ²	$2 \ge 10^2$	0.504 ± 0.154		
Mullet	$0.05 \text{ X} 10^2$	$0.5 \text{ X } 10^2$	0.124 ± 0.042		
Shrimps	$0.02 \text{ X} 10^2$	$0.06 \text{ X } 10^2$	0.037 ± 0.008		
Canned fish	0	0	0		

Table 2: Aeromonas counts (cfu/g) in the examined samples of fish, canned fish and shrimp



Fig. 2. Incidence of *Aeromonas* spp. in fish meat, canned fish and shrimp by using biochemical method

veronii biovar

veronii

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Table 3: Incidence of *Aeromonas* spp. isolated from fish meat, canned fish and shrimp by using biochemical method.

Species	r til: n:	Nile apia =30	Ca n:	tfish =30	Mu n:	ullet =30	Shi n:	rimp =30	Can Tu n=	ined ina :30	Car Salı n=	nned mon =30	To (n=	otal :180)
Sample	No	%	No	%	No	%	No	%	No	%	No	%	No	%
A. caviae	3	10.0	2	6.6	3	10.0	1	3.3	0	0.0	0	0.0	9	5.0
A.hydrophilla	3	10.0	4	13.3	5	16.6	1	3.3	1	3.3	0	0.0	14	7.8
A. media	2	6.6	3	10.0	0	0.0	0	0.0	0	0.0	0	0.0	5	2.8
A. shubertii	1	3.3	4	13.3	8	26.6	0	0.0	0	0.0	0	0.0	13	7.2
A. sobria	2	6.6	3	10.0	1	3.3	1	3.3	2	6.6	0	0.0	9	5.0
A.veronii	2	6.6	0	0.0	2	6.6	1	3.3	0	0.0	0	0.0	5	2.8
biovar sobria														
A.veronii biovar	3	10.0	2	6.6	0	0.0	0	0.0	0	0.0	0	0.0	5	2.8
veronii														
Total	16	53.3	18	60.0	19	63.3	4	13.3	3	10	0	0.0	60	33.3

Table 4: PCR results of A. hydrophilla and its virulence genes

Sample	16S rRNA	AHA gene	AST gene	
Bampie	n=14	n=12	n=12	
Nile tilapia	3	1	0	
Catfish	3	2	0	
Mullet	5	2	0	
Shrimp	1	0	0	
Canned fish	0	0	0	
Total	12 (85.7%)	5 (41.7%)	0 (0.0%)	



Fig. 3. Incidence of *A. hydrophila* in fish meat, canned fish and shrimp by using biochemical method



Fig. 4. PCR result for *16srRNA* gene of *A.hydrophila*, Lane L: 100 bp DNA marker. Lane P: Control positive (953 bp); Lane N: Control negative; Lanes 1-5: positive strains of *A. hydrophila* isolated from mullet. Lane 6: negative strains isolated from canned tuna. Lane 7: positive strains isolated from shrimp. Lanes 8: negative strains isolated from catfish. Lanes 9,10&11: positive strains isolated from catfish. Lanes 12, 13 & 14 positive strains isolated from Nile tilapia.



Fig. 5. PCR results for *AHA* gene, Lane L: 100 bp DNA marker; Lane P: Control positive; Lane N: Control negative; Lanes 1, 2& 3: negative results for AHA gene of *A. hydrophila* strains isolated from mullet. Lanes 4& 5: positive results from shrimp. Lanes 7& 8: positive results from catfish. Lane 9: negative results from catfish. Lane 10: positive result from Nile tilapia. Lanes 11&12: negative results from Nile tilapia.



Fig. 6. PCR results for *AST* gene, Lane L: 100 bp DNA marker; Lane P: Control

positive Lane N: Control negative; Lanes 1, 2, 3, 4, 5, 7, 9, 10, 11, 12, 13 &14: negative.

Discussion

Aeromonas counts

Aeromonas contamination was detected in Nile tilapia, catfish, mullet and shrimp samples with mean counts 0.122 \pm $0.032, 0.504 \pm 0.154, 0.124 \pm 0.042$ and 0.037 ± 0.008 , respectively. While cannot be detected by direct plating in canned fish samples (Table 2). These results were lower than mean counts that was reported by Manna et al. (2013) where all or most of the samples of Indian major carps, tilapia and shrimp were contaminated with mean count 1.1×10^3 , 2.1×10^3 and 1.6×10^4 cfu/g and Ramadan et al. (2018) who mentioned that Aeromonas sp. were found with 3.35 log10 cfu/g in mullet samples. Variable counts and incidences between studies may be attributed to the difference in the examined samples, the status of fish prior to sampling time and place and geographical range. Also, fish may be contaminated with several pollutants during the production chain, transporting and retailing through bad hygiene, as well as absence of monitoring programs at farms (Eltholth et al., 2015; Hafez et al., 2018)

Incidence of *Aeromonas* spp. in fish meat and canned fish samples

Results in Table 3 and Fig. 2 showed that *Aeromonas spp*. incidence in fish meat and canned fish was 60 of 180 (33.3%). This result agrees with Elgohary et al. (2020) who detected *Aeromonas spp*. in 33.3 % of fish samples and disagrees with Yucel et al. (2005) and Yucel and Erdogan (2010) who reported 80.3% and18.4%, respectively. While, in Egypt, Attia et al. (2018) found *Aeromonas* spp. in 44.3% of raw fish. Our results revealed that highest incidence of *Aeromonas* spp. was found in mullet 19(63.3%) followed by catfish 18

(60%), tilapia 16 (53.3%), shrimps 4 (13.3%) and canned tuna 3 (10%) while couldn't be detected in canned salmon.

The incidence of Aeromonas spp. in Nile tilapia was 53.3% (Table 3). This result agrees with Ebeed et al. (2017) and Elghareeb et al. (2019) who revealed that Aeromonas was isolated from Nile tilapia fish with a percentage of 51.4 % and 57.33%, respectively. However, our results were lower than that were reported by Kishk et al. (2020) who found Aeromonas spp. in farmed tilapia with a percentage of 68%, and higher than El-Gamal et al. (2018) and Salem et al. (2020) who found Aeromonas spp. in 25.9% and 29.84 % of Nile tilapia samples. The frequency distribution of isolated Aeromonas species of examined Nile tilapia samples was A. hydrophila, A. caviae and A. veronii biovar veronii 3 (10%) for each, followed by A. media, A. sobria and A. veronii biovar sobria 2 (6.6%) for each, and A. shubertii 1 (3.3%). These results disagree with El-Gamal et al. (2018) who detected A. hydrophila in (23.3%) and A. caviae in (2.6%), and Kishk et al. (2020) who found A. caviae 13 (40.6%), A. hydrophila 8 (25%), A. sobria 7 (21.9%), and A. fluvialis 1 (3.1%) while A. veronii 3 (9.4%) represented slightly similar results.

As shown in Table 3 and Fig. 3, *A. hydrophila* was detected in 16.6 % of the examined mullet, this result is lower than the results obtained in Kafr El-sheikh and Dakahliya Governorate by Ebeed et al. (2017) and Ramadan et al. (2018) who reported 62% and 37% contamination percentage in mullet samples, respectively. Frequency distribution of *Aeromonasspp*.in mullet samples were *A. shubertii* 8 (26.6%), *A. hydrophila* 5 (16.6%), *A. caviae* 3 (10%) and *A. veronii biovar sobria* 2 (6.6%) and *A. sobria* 1 (3.3%). These results disagree with Kishk et al. (2020) who found several species of *Aeromonas* as *A. sobria* 11 (44%), A. caviae 7 (28%), A. hydrophila 5 (20%), and A. veronii 2 (8%). Aeromonas spp. were detected in 6 shrimp samples at a percentage of 13.3%, of which A. hydrophila was 3.3%, this result disagreed with Khamesipour et al. (2014) in Iran who reported that incidence of A. hydrophila in shrimp was 13.89%. while, Kahraman et al. (2017) detected A. hydrophila in 15% of shrimp samples.

From previous results, it is denoted the ability of Aeromonas spp. to survive in freshwater and marine water environments with slight differences in incidence rates. The variations of Aeromonas species incidence could be attributed to various species, time and place of sampling, geographical area, post-capture and contamination, the type of water, fish species, handling, and manipulations during catching, storage, and transportation. and this agrees with Hafez et al. (2018). Aeromonas spp. were detected in 3(10%) canned tuna and not isolated in canned salmon. The identified species were 2 A. sobria(6.6%) and 1 A. hydrophila (3.3%), this may be attributed to treatments which applied to these products, as temperature, lack of Oxygen in vacuum packaging, salt or brine concentration and preservatives.

A. hydrophila has the highest incidence (14 out of 60) among the isolated Aeromonas spp. in the examined samples collectively; 5 mullet, 4 catfish,3 Nile tilapia, 1 shrimp and 1 canned tuna while it was not found in canned salmon (Fig. 3). These isolates were tested for 16S rRNA gene as well as AHA and AST genes.

PCR results of *A. hydrophila* and its virulence genes

Results in Table 4 and Figure 4 showed that *16S rRNA* gene of *A. hydrophila* was detected in 12 of 14 examined samples with

a percentage of (85.7%), distributed as 25% (3/12) in each of freshwater (Nile tilapia and catfish) samples, 5 mugil (41.6%) and 1shrimp (8.3%). While, it was not detected in canned fish. A higher incidence was reported by Abd-El-Malek (2017) who detected *16S rRNA* gene in 35% of *A. hydrophila* isolated from tilapia samples.

Our findings revealed that the AHA gene (Fig. 5) was encoded in 5 (41.7%) of A. hydrophila isolates, with the highest incidence in catfish 2/3 (66.7%), mugil 2/5 (40 %) and Nile tilapia1/3 (33.3%). While, it was not detected in shrimp isolates. Wang et al. (2003) reported A. hydrophila AHA gene at a percentage of (37.5%). However, Blaszk (2014) reported that 85% A. hydrophila were encoding aerolysin gene. Also, Abd-Elall et al. (2014), Attia et al. (2018); Mansour et al., (2019) and Salem et al. (2020) reported that Aerolysin AHA gene was found in 100%, 55%, 51% and 83.3%, respectively. While, lower 13.15% incidence was reported by Sharma et al. (2010).

AST gene give negative results in all A. hydrophila isolates (Fig. 6), similar results were reported by Ghenghesh et al. (2014) and Silva et al. (2017). Opposite to De Jagoda et al. (2014) and Mansour et al. (2019) who reported that AST gene was encoded in 38% and 34% of A. hydrophila isolates, respectively.

Conclusion

The present study highlights the incidence of *Aeromonas sp.* in different fish species inhabit fresh and marine water and focused on *A. hydrophila* with its virulence genes as *AHA* and *AST* which may pose possible public health threats, given the importance of aeromonads as emerging human pathogens. Good hygienic practices are needed to provide safe and wholesome foods.

Conflict of interest

The authors declare that there is no conflict of interest.

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