



Molecular Identification of 16S rRNA and Some Virulence Genes From *Aeromonas* spp. in Nasser Lake Fish Species, Aswan, Egypt

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FRESHWATER fish consider a major cheap source of animal protein in different parts of the world. In upper Egypt, Lake Nasser is the main source of fish production for human consumption. Fish can also be a cause of foodborne pathogens, such as the *Aeromonas* species, that pose a significant risk to public health. A total of 180 freshwater fish samples were represented, Nile tilapia, Nile perch, Pike perch, African sharp tooth catfish, Elephant-snout, and Fillet tilapia (30 of each) were randomly selected from Lake Nasser in Aswan province. Bacteriological examination reveals 117 (65%) occurrence of *Aeromonas* species. In isolated 60 *Aeromonas* species samples 10 from each fish species, 16S rRNA genes were found with a percentage of 96.67% by using PCR. In Egypt and around the globe, the *Aeromonas* species has been linked to several foodborne outbreaks brought on by the consumption of raw fermented fish which having many sever virulence gene. Additionally, two genes; Aerolysin (aer) and cytotoxic enterotoxin (act) genes were selected to be screened by PCR. Results were 51.7% and 27.6%, respectively. So hygienic precautions must be taken to eradicate Nasser Lake Fish species contaminated with *Aeromonas* species. Molecular investigating of some virulence genes of *Aeromonas* spp. in Lake Nasser from different fish species was the aim of the present study.

Keywords: *Aeromonas* species, 16S rRNA, Aerolysin (aer) gene, Cytotoxic enterotoxin (act) gene, PCR.

Introduction

Aeromonas spp. are Gram-negative, facultative anaerobes, non-spore-forming rods, positive for oxidase and catalase, resistant to the vibrio static O/129, capable to reduce nitrates to nitrites and motile spp. have a single polar flagellum that usually lives water environment [1]. *Aeromonas* is divided into two clusters; the first one is non-motile species like *A. salmonicida* that cause

disease in fish, another group includes motile species such as *A. hydrophila* which are implicated in human infections including gastroenteritis, peritonitis septicemia, urinary tract infection in neonates, osteomyelitis and wound infections [2]. *Aeromonas* species may spread through raw seafood [3]. *Aeromonads* have been associated with skin and soft-tissue infections, these pathogenic organisms have been recognized as a cause of foodborne and waterborne outbreaks

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[4]. Fish, however, can be a source of foodborne bacteria, such as the *Aeromonas* species, which have been identified as developing foodborne poisoning that pose a significant risk to community health [5]. *Aeromonas* members are related to foodstuff poisoning as well as certain human illnesses like abdominal and extra-intestinal disorders like skin and traumatic wound diseases, lower respiratory tract/urinary tract infections and soft-tissue illnesses [6]. *Aeromonas* is environmental microbe and their spread is global. Mesophilic motile aeromonads are common and indigenous aquatic microbes that can be found in both chlorinated and unchlorinated drinking water as well as sewage and brackish water [7]. The capability of *A. hydrophila* to produce diseases relates to a diversity of pathogenic factors which are compound and multifactorial [8]. *A. hydrophila* can produce a variety of virulence factors, especially toxins responsible for gastrointestinal infections including hemolysin, aerolysin, cytotoxin, enterotoxin, lipopolysaccharide and lipases, proteases gelatinase, DNases, and elastase enzymes [9,10]. Molecular identification is the most accurate identification tool of fish pathogens even in early infection phases. The rapid, confirmatory and accurate microbial identification in recent years is the molecular diagnosis, as well as the 16S rRNA gene, which is considered a stable molecular marker for identifying bacterial species since its distribution is universal and allows the comparison of microorganisms [11]. Some virulence genes were found in the isolated *A. hydrophila*, such as cytotoxic enterotoxins heat-stable (ast) and cytotoxic enterotoxin (act), while cytotoxic enterotoxin (alt) and hemolysin (hly) genes were absent. In contrast, the hly gene was present in *A. hydrophila* strains, and by amplification, the PCR products of 1500 bp were given [12,13]. Aerolysin and cytotoxic enterotoxin are an important and reliable molecular indicator for finding potentially pathogenicity of *Aeromonas* species. Aerolysin toxin lyses RBCs causing hemorrhagic lesions. Aerolysin toxin was found *A. hydrophila*, *A. caviae*, *A. sobria*, and *A. veronii*. Aer gene is absent in non-hemolytic *A. hydrophila*, but it can be absent in hemolytic *A. caviae* and *A. sobria* too [14]. The act gene encodes a type II secreted cytotoxic enterotoxin (Act) that is fatal to mice by having hemolytic, cytotoxic, and enterotoxic effects [15]. The current research focused on determining the occurrence of *Aeromonas*

species isolated from various species of fish from Lake Nasser in Aswan governorate. A vital role in the pathogenesis of *Aeromonas* sp. infection in fish is played by virulence genes. They are connected to various human illnesses and food poisoning. Two genes; Aerolysin (aer) and cytotoxic enterotoxin (act) genes were selected to be screened in this study.

Material and Methods

Collection of samples

One hundred eighty fish samples in different species were collected from Nasser Lake, Aswan, Egypt, in 2020-2021. 30 of each were represented Nile tilapia, Nile perch, Pike perch, African sharp tooth catfish, Elephant-snout, and Fillet tilapia weighing between 150 to 250g. The specimens were packed in sterilized flexible bags and transported, in an icebox without delay, to the lab of Microbiology and immunology Department, Faculty of Veterinary Medicine, Aswan University, where microbiological examination were performed.

Samples preparation

Under complete aseptic condition, 25 g of each fish muscle and viscera samples were aseptically transported into a sterilized homogenizer at 14000 rpm for 3 min then mixed with 225 ml sterile Tryptic soy broth (Oxoid:CM0129) incubated at 37 °C for 24 hrs. [16].

Isolation of Aeromonas species

From each enriched homogenate, a loopful was streaked on duplicate sterile Petri plates of *Aeromonas* Agar media supplemented with ampicillin (5 mg/L) (Biolife: CN0801), after incubation of plates for 24 hs at 28 °C the appearance of green colonies with dark centers were theoretically considered to be *Aeromonas* spp. [17].

Morphological and biochemical identification of Aeromonas species

Phenotypic recognition of positive samples was shown as stated by Austin & Austin [18] according to (Table 1 and Fig.1) based on morphological, biochemical, and metabolic properties. By optical microscopy using Gram's stain, Confirmed the isolates by biochemical characteristics, catalase, oxidase, growth at 4%, 10% NaCl, vibriostatic compound 0/129 (Thermo Scientific™, DD0015T), blood agar (Oxoid: CM0259) and Triple sugar iron (Oxoid: CM0277) esculin hydrolysis, indole, arginine hydrolysis, methyl red, Voges

Proskauer, hydrogen sulphide production, citrate utilisation, urease, nitrate reduction, gelatin liquefaction, ornithine decarboxylase, oxidation fermentation, L-lysine decarboxylase, arginine decarboxylase, -galactosidase, oxidation and sugar fermentation (Macfaddin, 2000). As shown in Table (2), suspected *Aeromonas* colonies were biochemically verified.

Molecular identification of selected isolates:

Amplification of 16S rRNA gene for the Aeromonas genus

According to the manufacturer's recommendations. The extraction of DNA was done by QIAamp DNA Gene JET Genomic DNA Purification Kit (Catalog No. #K0721, Thermo Scientific, USA). The reaction contained 25 µl of the following PCR master mix; 12.5 µl of COSMO PCR RED Master Mix (2x premix), 4.5 µl PCR grade water, 1 µl forward primer (20 pmol), 1 µl reverse primer (20 pmol), 6 µl template DNA. The amplification of the 16S rRNA gene for the *Aeromonas* genus was performed using primer pair F 5' AGAGTTTGATCATGGCTCA 3' and R 5'GGTTACCTTGTTACGACTT 3' amplifying 1502bp [19]. The amplification cycles (n=35) were carried out as follows: 5 min of primary denaturation at 94°C, 60 sec of secondary denaturation at 94°C, 56 sec of annealing at 60°C, 2 min of extension at 72°C, and 10 min of ultimate

extension at 72°C. Electrophoresis in 1.5% agarose gel was used to identify the amplified products (Applichem, Germany, GmbH). Gel recording system (Alpha Innotech, Biomedica) was used for photography, and computer software was used for analysis.

Amplification of Aerolysin and cytotoxic enterotoxin genes

For detection of virulence genes, amplification of Aerolysin (aer) gene primer with nucleotide sequences of F 5'-AACCGAACTCTCCAT-3' and R 5'-CGCCTTGTCCTTGTA-3' (product size of 301 bp) and Cytotoxic enterotoxin (act) gene primer with nucleotide sequences of F 5'-GAGAAGGTGACCACCAAGAACA-3' and R 5'-AACTGACATCGGCCTTGAAGTC-3' (product size of 232 bp) were done according to Hu et al.[20] Table (4). All primers in this study were synthesized by Willow Fort Company (United Kingdom). Initial denaturation cycle was done at 94°C for 5 min, then 30 cycles at 94°C for 30 seconds, 54°C for 30 sec for aerolysin gene / 42°C for 30 seconds for Cytotoxic enterotoxin gene and then 72°C for 1 min followed by last extension at 72°C for 10 mins. Aliquots from PCR reactions were electrophoresed on 1.5% agarose gel and viewed under UV light.

Statistical Analysis

TABLE 1. Conventional identification of *Aeromonas* spp.

Fish sp.	No.	Cultural identification		Biochemical identification													
				Catalase		Oxidase		Blood agar		Growth on TSI		Growth with NaCl 4%		Growth with NaCl 10%		VSD	
				+Ve No.	-Ve No.	+Ve No.	-Ve No.	+Ve No.	-Ve No.	+Ve No.	-Ve No.	+Ve No.	-Ve No.	+Ve No.	-Ve No.	+Ve No.	-Ve No.
Nile Tilapia	30	21	9	20	10	19	11	18	12	16	14	20	10	19	11	19	11
Nile perch	30	19	11	15	15	13	17	13	17	12	18	17	13	13	17	13	17
Pike perch	30	17	13	14	16	15	15	13	17	13	17	16	14	15	15	15	15
African sharptooth catfish	30	21	9	18	12	17	13	16	14	17	13	18	12	17	13	17	13
Elephant-snout	30	12	18	10	20	12	18	11	19	11	19	12	18	10	20	10	20
Fillet Nile Tilapia	30	18	12	17	13	13	17	14	16	14	16	18	12	13	17	13	17
Total	180	108	72	94	86	89	91	85	95	83	97	101	79	87	93	87	93

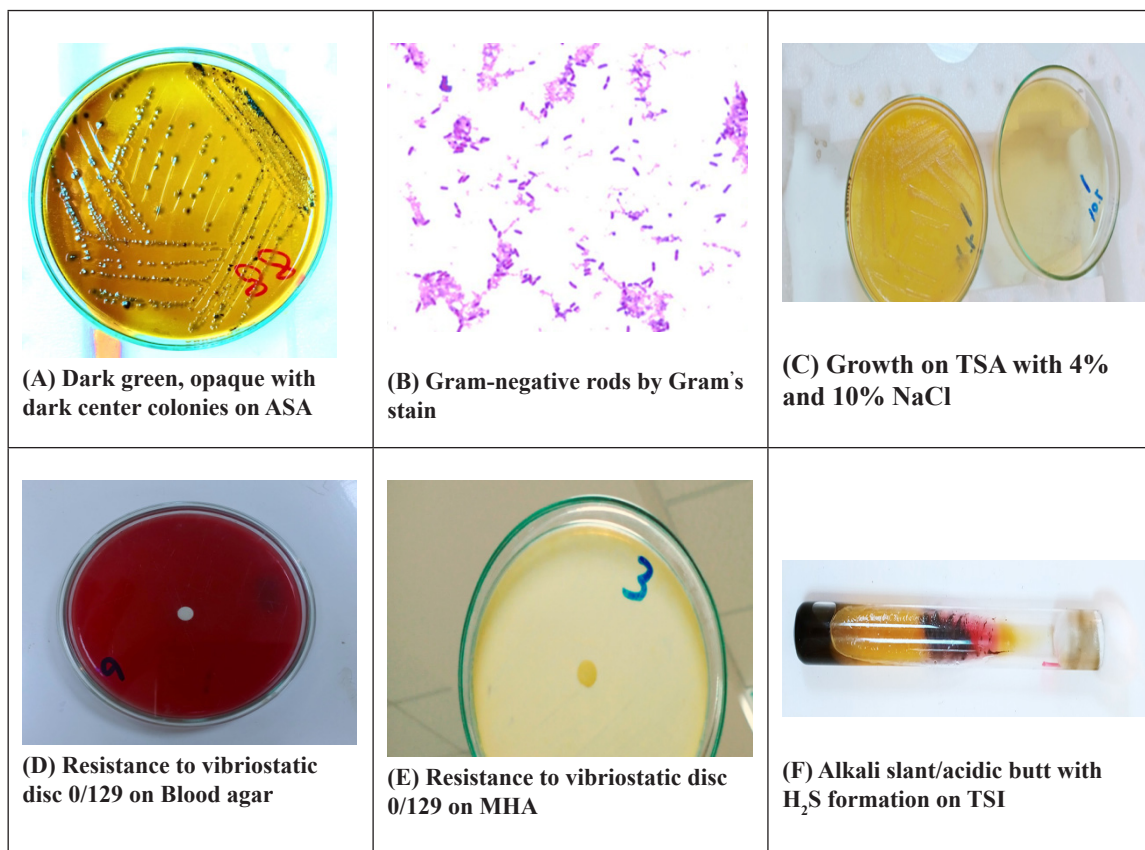


Fig. 1. Conventional identification of the suspected isolates

According to Feldman *et al.* [21] Statistical Analysis of Variance (ANOVA) was done for significant differences between samples.

Results

Conventional identification of isolates biochemically : according to the data in Table (3) in the current study positive *Aeromonas* spp. 117 (65%) isolates out of 180 fish samples were distributed as 24 (80%) Nile tilapia, 21 (70%) Catfish, 20 (66.7%) Pike perch, 19 (63%) Nile perch, 18 (60%) Fillet tilapia and 15 (50%) Elephant-snout respectively. According to the data there are 4 species of *Aeromonas* were represented by 117 (65%) isolates: *A. hydrophila* 78 (43.3%), *A. caviae* 26 (14.4%), *A. sobria* 7 (3.8%) and *A. veronii* 6 (3.3%), On the other hand, 10 samples biochemically identified *Aeromonas* spp. are taken from each fish species introduced in PCR findings showed that 16S rRNA was present in 58 (96.67%) out of a total of 60 isolates, distributed into 10 Nile tilapia, 10 Nile perch, 10 Pike perch, 10 Fillet tilapia, 9 Catfish and 9 Elephant-snout, respectively (Table 5 and Fig.2). Detection of other virulence genes, *aerA*

gene was detected in 30 (51.7%) out of 58 isolates previously detect of *Aeromonas* spp. 16S rRNA gene distributed into 7 Nile tilapia, 3 Nile perch, 5 Pike perch, 4 Catfish, 5 Elephant-snout, and 6 Fillet tilapia, respectively (Fig.3). Furthermore, the *act* gene was detected in 16 (27.6%) out of 58 isolates contingent on the detection of *A. Aeromonas* spp. 16S rRNA gene distributed into 4 Nile tilapia, 2 Nile perch, 2 Pike perch, 2 Catfish, 3 Elephant-snout, and 3 Fillet tilapia respectively (Table 6 and Fig.4).

Discussion

Nowadays microbiological examination of fish is very important for maintaining public health. In current study *Aeromonas* spp. was isolated from examined fish samples with a percentage of 65%, according to bacteriological analysis. Nile tilapia had the greatest isolation percentage (80%), followed by Cat fish (70%), pike perch (66.7%), Nile perch (63.3%), Fillet tilapia (60%), and Elephant snout (50%). The prevalence as, *A. hydrophila* (43.3%), *A. caviae* (14.4%), *A. sobria* (3.8%) and *A. veronii* (3.3%) (Table 3). In recent fish study in Egypt, the nearly similar result

TABLE 3. Prevalence of *Aeromonas* species in the examined fresh fish samples (n=30 each)

Fish species (number 30)	<i>Aeromonas</i> <i>sp.</i> (+)	<i>A.</i> <i>hydrophila</i>	<i>A.</i> <i>Caviae</i>	<i>A.</i> <i>veronii</i>	<i>A.</i> <i>sobria</i>
1-Nile Tilapia (<i>Oreochromis niloticus</i>)	24/30 (80%)	13/30 (43.3%)	7/30 (23.3%)	3/30 (10%)	1/30 (3.33%)
2- African sharptooth catfish (<i>Clarias gariepinus</i>)	21/30 (70%)	17/30 (56.7%)	3/30 (10%)	1/30 (3.33%)	-
3- Pike perch (<i>Sander lucioperca</i>)	20/30 (66.7%)	15/30 (50%)	3/30 (10%)	1/30 (3.33%)	1/30 (3.33%)
4- Nile perch (<i>Lates niloticus</i>)	19/30 (63.3%)	13/30 (43.3%)	4/30 (13.33%)	-	2/30 (6.7%)
5- Fillet Nile Tilapia	18/30 (60%)	10/30 (33.3%)	5/30 (16%)	1/30 (3.33%)	2/30 (6.7%)
6- Elephant-snout (<i>Mormyrus kannume</i>)	15/30 (50%)	10/30 (33.3%)	4/30 (13.3%)	-	1/30 (3.33%)
Total (180)	117/180 (65%)	78/180 43.3%	26/180 14.4%	6/180 3.3%	7/180 3.8%

TABLE 4. Primers used in the present study

Target gene	Primers sequences	Amplified segment	References
16S-rRNA	F 5' AGAGTTTGATCATGGCTCA 3' R 5' GGTTACCTTGTACGACTT 3'	1502 bp	[19]
<i>aerA</i>	F 5' AACCGAACTCTCCAT 3' R 5' TTGTCCGGGTTGTACTCGTC 3'	301 bp	
<i>act</i>	F 5' GAGAAGGTGACCACCAAGAAC 3' R 5' AACTGACATCGGCCTTGAAGTC 3'	232 bp	[20]

TABLE 5. Genotypic identification of 16S rRNA gene in the isolated *Aeromonas* species

Fish spp.	No. of examined samples	Identified 16S rRNA gene	
		No.	%
Nile tilapia	10	10	100
Nile perch	10	10	100
Pike perch	10	10	100
Catfish	10	9	90
Elephant-snout	10	9	90
Fillet tilapia	10	10	100
Total samples	60	58	96.67

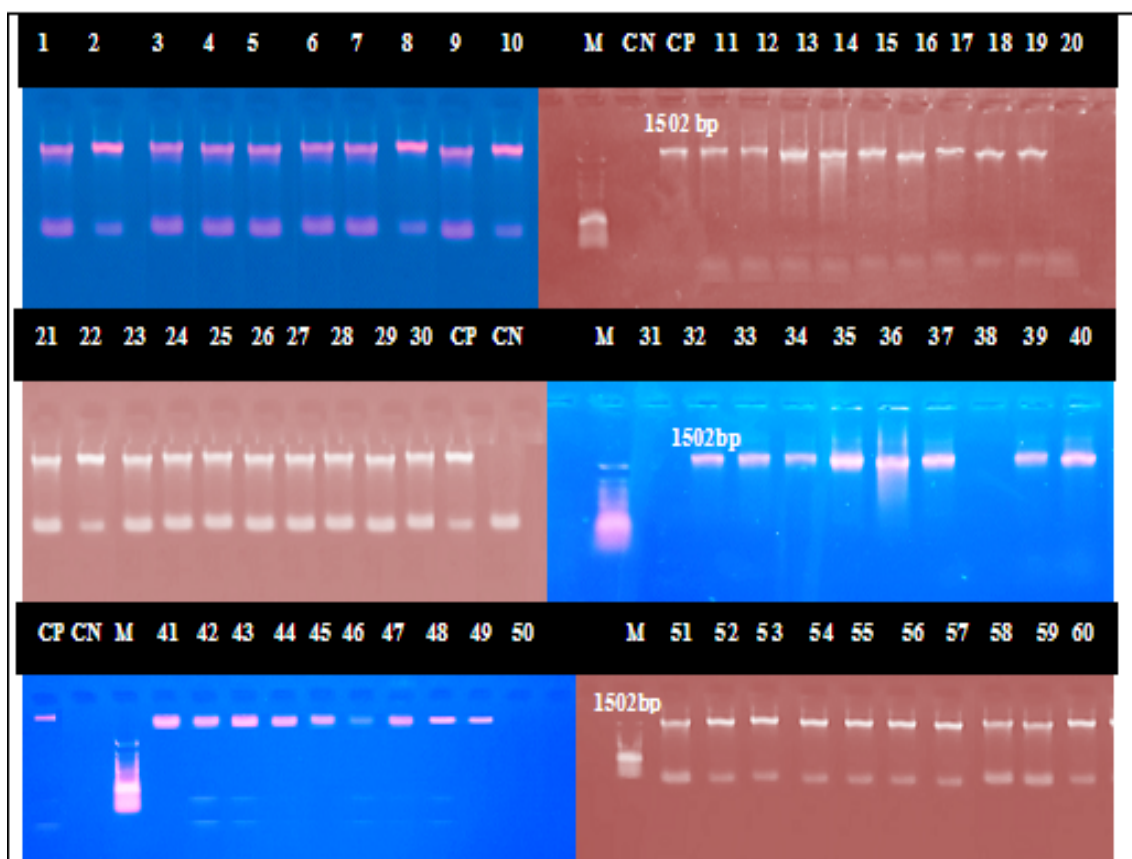


Fig. 2. Electrophoretic gel Fig.for detection of 16S rRNA gene in *A. hydrophila* detected by conventional PCR where CN= control negative, CP= control positive at 1500bp, M= Marker, Lane 1 to Lane 10: Nile tilapia, Lane 11 to Lane 20: Nile perch, Lane 21 to Lane 30: Pike perch, Lane 31 to Lane 40: Elephant-snout, Lane 41 to Lane 50: Catfish and Lane 51 to Lane 60 Fillet tilapia samples.

TABLE 6. Occurrence of virulence genes in the *Aeromonas* species isolated from the examined samples

	16S rRNA gene Identified <i>A. hydrophila</i>	Virulence genes			
		AerA		Act	
	No.	%	No.	%	
Nile tilapia	10	7	70	4	40
Nile perch	10	3	30	2	20
Pike perch	10	5	50	2	20
Catfish	9	4	44.4	2	22.2
Elephant-snout	9	5	55.5	3	33.3
Fillet tilapia	10	6	60	3	30
Total samples	58	30	51.7	16	27.6

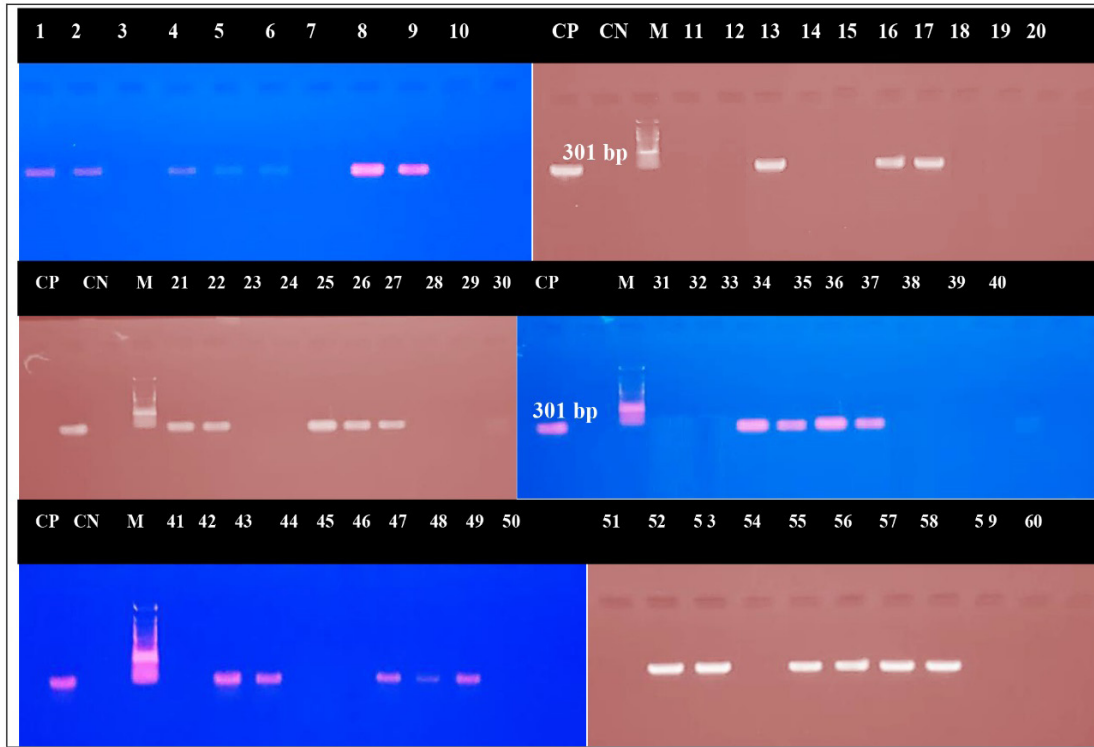


Fig. 3. Electrophoretic gel Fig.for detection of aerolysin (*aerA*) gene in *A. hydrophila* detected by conventional PCR where CN= control negative, CP= control positive at 303bp, M= Marker (100bp), Lane 1 to Lane 10: Nile tilapia, Lane 11 to Lane 20: Nile perch, Lane 21 to Lane 30: Pike perch, Lane 31 to Lane 40: Elephant-snout, Lane 41 to Lane 50: Catfish and Lane 51 to Lane 60 Fillet tilapia samples.

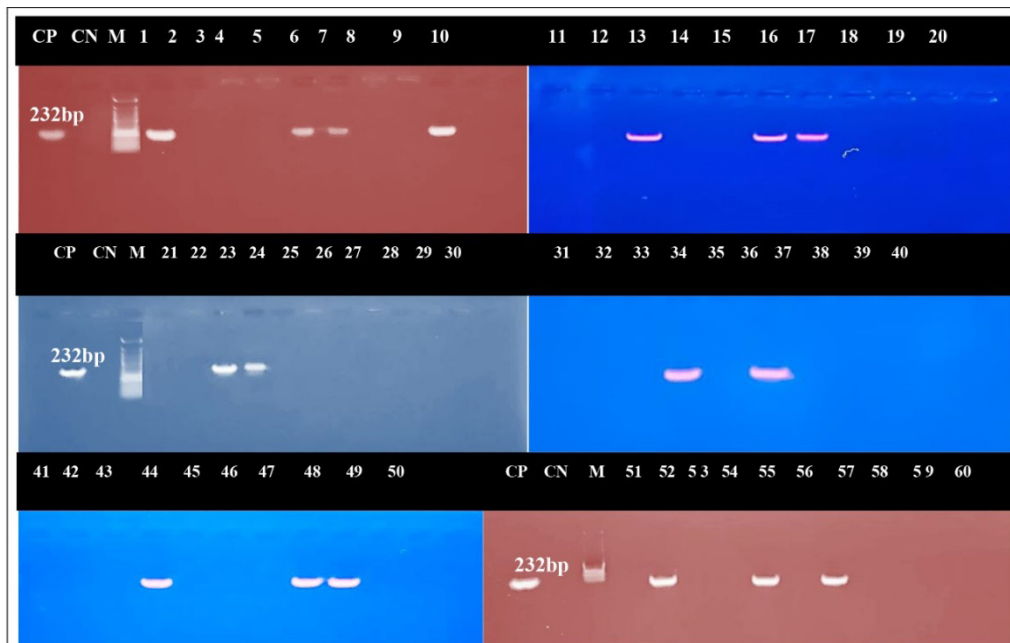


Fig. 4. Electrophoretic gel Fig.for detection of aerolysin enterotoxin (*act*) in *A. hydrophila* detected by conventional PCR where CN= control negative, CP= control positive at 232bp, M= Marker (100bp), Lane 1 to Lane 10: Nile tilapia, Lane 11 to Lane 20: Nile perch, Lane 21 to Lane 30: Pike perch, Lane 31 to Lane 40: Elephant-snout, Lane 41 to Lane 50: Catfish and Lane 51 to Lane 60 Fillet tilapia samples.

found by Morshdy et al.[22] *Aeromonas* spp. in 39.3% of the fish samples they investigated, Four *Aeromonas* species (*A. hydrophila*, *A. caviae*, *A. fluvialis* and *A. sobria*) were isolated from the tested fish samples (12%, 15.3%, 2.7% and 9.3%, respectively), with *A. hydrophila* is the most frequently found isolates from Nile tilapia. According to Kishk et al.[23], the incidence of *Aeromonas* species in Nile tilapia 32 (64%). The most prevalent *Aeromonas* species isolated from Nile tilapia was *Aeromonas caviae* 13 (40.6%), *Aeromonas hydrophila* 8 (25%), *Aeromonas sobria* 7 (21.9%), *Aeromonas veronii* 3 (9.4%), and *Aeromonas fluvialis* 1 (3.1%). Ebeed et al.[24], revealed that the incidence of *Aeromonas* spp. in Nile tilapia was 34 (68%). The most frequently identified *Aeromonas* species isolate from Nile tilapia was *A. caviae* 18 (36%), *Aeromonas sobria* 14 (28%). But, Ismail et al.[25] revealed 20.3% *A. hydrophila* is the most frequently found isolates (20.3%) from *Clarias gariepinus* fish (Catfish). Additionally fish study in Dhanapala et al. [26] identify eight distinct *Aeromonas* spp. from freshwater fish as *A. veronii* (75.8%), *A. hydrophila* (9.3%), *A. caviae* (5%), *A. jandaei* (4.3%), *A. dhakensis* (3.7%), and 0.6% for each of *A. sobria*, *A. media* and *A. popoffii*. Our results of the PCR indicated that 58 (96.67%) out of a total of 60 isolates biochemically identified *Aeromonas* spp., the 16S rRNA distributed into 10 Nile tilapia, 10 Nile perch, 10 Pike perch, 9 Catfish, 8 Elephant-snout, and 10 Fillet tilapia, respectively. On the other hand, Aer gene detected in 30 out of 58 (51.7%) and Act gene detected in 16 out of 58 (27.6%) The isolation of 16S rRNA can be used to validate the isolation of *Aeromonas* spp. [27,28] 40.67% was confirmed as *A. hydrophila* by using PCR amplification based on 16S rRNA gene analysis. [29] 42% of the fish samples have *A. hydrophila* depending on the occurrence of the 16S rRNA. [30-32], reported that 11.47%, 75.4% and 50.65% of freshwater fish were recognized as *A. hydrophila* using the 16S rRNA. These variances may be because of the altered species, geographical location, and selection time. Moreover, The high prevalence rate achieved by Elsheshtawy et al. [33] reported that 100% of tested samples recognized as *Aeromonas* spp. depend on the 16S rRNA detection. Aer gene was detected in 53.57% of isolates that was confirmed by the hemolysis occurred on the blood agar [14, 34,31] were recorded aerA gene has

more commonly occurred between isolates with an incidence of 64.3% and 80.5% respectively. From another point, Lower results were reported in previous studies by Abdel-Latef [35] who indicated the aerA gene in examined fish with a lower value of 3.3%. Act gene was detected in 30.35% of isolates [15,36] documented that 80% of examined samples harbored act genes. As well Nhin et al.[31] identified the acting gene in 80.1% of the examined fish samples. Furthermore, Ahangarzadeh et al. [37] reported that (74.19%) of isolates possessed act genes. 40% of Nile tilapia and 30% tilapia fillet *Aeromonas* isolates are carrying both aer and act gene together that makes them a great threat for human health via consumption of their meat. Also Cat fish (70%) and pike perch (78%) consider of great health concern as most of isolates carrying virulence genes.

Conclusion

In addition to affecting fish quality, shelf life, and acceptability, *Aeromonas* species infection in fishes is a risk to the public's health. Therefore, hygienic measures must be taken to control microbial contamination either in the aquatic environment or during the transportation of seafood to consumers. Using 16s rRNA primer together with aer and act genes can be used as fast screening methods for determination of virulence of *Aeromonas* sp.

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Conflict of interest

No conflict of interest

Authors contribution

The research is extracted from a Master's thesis in the Department of Microbiology and Immunology for the fourth author

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التحديد الجزيئي لـ 16 S rRNA وبعض جينات الضراوه من *Aeromonas spp* في أنواع أسماك بحيرة ناصر ، أسوان ، مصر

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38.

تعتبر أسماك المياه العذبة مصدرًا رئيسيًا رخيصًا للبروتين الحيواني في أجزاء مختلفة من العالم. في صعيد مصر ، تعد بحيرة ناصر المصدر الرئيسي لإنتاج الأسماك للاستهلاك البشري. يمكن أن تكون الأسماك أيضًا عامل لمسببات الأمراض المنقولة بالغذاء ، مثل أنواع *Aeromonas* ، التي تشكل خطرًا كبيرًا على الصحة العامة. تم اختيار مجموعه ١٨٠ عينة من أسماك المياه العذبة مثل البلطي النيلي ، وسمك الفرخ النيلي ، وسمك البايك ، والقرموط الأفريقي ذو الأسنان الحادة ، وأنف الفيل ، وقلبه البلطي (٣٠ عينة لكل منها) تم اختيارها عشوائياً من بحيرة ناصر في محافظة أسوان. يكشف الفحص البكتريولوجي عن حدوث ١١٧ (٦٥٪) من أنواع الأيرومونات. في ٦٠ عينة معزولة 10 من كل نوع سمكي ، تم العثور على جينات 16S rRNA بنسبة ٩٦,٦٧٪ باستخدام تفاعل البوليميراز المتسلسل. في مصر وحول العالم ، تم ربط أنواع *Aeromonas* بالعديد من الامراض المتفشيه المنقولة عن طريق الأغذية التي نتجت عن استهلاك الأسماك المخمرة النيئة التي تحتوي على العديد من الجينات الشديدة الضراوة. بالإضافة إلى ذلك ، تم اختيار اثنان من الجينات المحدثة للسميه الجينات *(aer)Aerolysin* والسم المعوي السام للخلايا (*Act*) ليتم فحص تواجدها بواسطة PCR. كانت النتائج ٥١,٧٪ و ٢٧,٦٪ على التوالي ، لذلك يجب اتخاذ الاحتياطات الصحية للقضاء على أنواع أسماك بحيرة ناصر الملوثة بأنواع الأيرومونات. الفحص الجزيئي لبعض جينات الضراوه من *Aeromonas spp*. في بحيرة ناصر من أنواع مختلفة من الأسماك كان الهدف من هذه الدراسة.