



Phenotypic and molecular detection of *Aeromonas* and *pseudomonas* species isolated from fish with special reference to their virulence factors

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Abstract: The present study was conducted on 250 diseased Nile tilapia (*Oreochromis niloticus*) fish of various sizes were collected from different fish markets at Kaliobia Governorate, Egypt, during the period from May (2017) to January (2019) for inspection of *Aeromonas* and *Pseudomonas* strains. Samples were collected from apparently pathognomic lesions in muscle, liver, kidney, intestine and spleen for bacteriological examination. The results revealed that, 161 *Aeromonas* and *Pseudomonas* species; 118 *Aeromonas* (73.3%) and 43 *Pseudomonas* species (26.7%) were isolated mostly from 50 muscle lesion samples followed by 41 liver samples then 35 kidney samples; 32 intestine samples and 3 spleen lesion samples. Most isolated *Aeromonas* and *Pseudomonas* strains were enterotoxigenic ones, as they had haemolytic; amylase activity; proteolytic; lipolytic; Lecithinase activities and had the ability for biofilm production. PCR results showed that, specific gene of *A. hydrophila* (**16SrRNA**) and polar flagella gene (*fla*) genes were detected in all 8 studied strains; aerolysin (*aero*); *A. hydrophila* cytolytic enterotoxin (**AHcytoen**); cytotoxic enterotoxins- heat-stable (*ast*) virulence genes were detected in 5; 3 and 5 out of 8 *A. hydrophila* studied strains. In addition, specific gene of *Ps. aeruginosa* (**16SrDNA**); outer membrane lipoprotein L (*oprL*) and flagellin C (*fliC*) genes were detected in all 8 studied *Ps. aeruginosa* strains; exotoxin A (*toxA*) and exotoxin S (*exoS*) virulence genes were detected in 5 and 6 out of 8 studied ones.

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Key words: Fish, *Aeromonas*, *Pseudomonas*, Lecithinase, virulence genes

1. Introduction

Among the etiological agents of bacterial fish diseases, *Aeromonas* and *Pseudomonas* are considered as the most important fish pathogens which are responsible for ulcer type diseases including ulcerative syndrome leading to high mortalities and high economic losses (Zilberberg and Shorr, 2009; Shayo *et al.*, 2012 and Hanna *et al.*, 2014). The disease is characterized by petechial hemorrhage, darkness of the skin, detached scales, abdominal ascites and exophthalmia (Eissa *et al.*, 2010 and Hanna *et al.*, 2014). Members of the *Aeromonas* and *Pseudomonas*, are Gram-negative rods, either straight or curved facultative anaerobes, catalase-positive and most are motile by polar flagella. Their nutritional requirements are very simple and most will grow on common laboratory media. They are widespread in freshwater, sewage, soil and their numbers rise with the amount of organic matter present (Markey *et al.*, 2013). *Aeromonads* produce extracellular enzymes (haemolysins, lipases, proteases, β -lactamases,

amylases, chitinases and nucleases) involved in their ecology, survival and pathogenicity (Stratev *et al.*, 2015). In addition, the pathogenicity of *A. hydrophila* strains have been linked to some virulence factors produced by them including structural features associated with adhesion, cell invasion, resistance to phagocytosis as well as extracellular factors such as aerolysin, a pore-forming toxin, which is cytolytic and enterotoxin gene (Chopra and Houston 1999 and Rabaan *et al.*, 2001). Exotoxins are major virulence factors of *Aeromonads* that include a cytotoxic heat-labile enterotoxin (*act*), also known as aerolysin/hemolysin; a cytotoxic heat-labile enterotoxin (*alt*), known as lipase, extracellular lipase, or phospholipase and (*ast*) a cytotoxic heat-stable enterotoxin (Bin Kingombe *et al.*, 2010). Moreover, *Ps. aeruginosa* and *Ps. fluorescens* are considered problematic pathogens as they possess cell-associated virulence factors such as (pili, flagella, lipopolysaccharide, and alginate/biofilm), they also produce a number of extracellular products such as

protein exotoxin A, proteases, type III secretion system exoenzymes, rhamnolipid, haemolysin with lecithinase activity; elastase (*las B* and *las A*), siderophores (pyochelin, pyocyanin, and pyoverdine by *Ps. aeruginosa* and thioquinolobactin by *Ps. fluorescens*) and phospholipase C. (Mavrodi *et al.*, 2001 and Markey *et al.*, 2013). These virulence factors all play a role in disease pathogenesis. As *Aeromonas* and *Pseudomonas* are considered one of the most important fish pathogens and can be a

problem for human consumers too and fish had attained a great economic importance in Egypt, so, the present study was conducted to throw light over their infection in fresh water fish, Nile tilapia fish (*O. Niloticus*), beside phenotypic; genotypic characterization and detection of some virulence factors in some isolated *A. hydrophila* and *Ps. aeruginosa* strains by using P C R.

2. Material and Methods

Table (1): Primers sequences, target genes, amplicons sizes and cycling conditions

Target M.O.	Target gene	Primer sequence (5'-3')	Amplified segment (bp)	Primary denaturation	Amplification (35 cycles)			Final extension	References
					Secondary	Annealing	Extension		
<i>A. hydrophila</i>	<i>16S rRNA</i>	F GAAAGGTTGATGCCTAATACGTA	625 bp.	94°C 5 min	94°C 30 sec.	50°C 40 sec.	72°C 45 sec.	72°C 10 min.	Gordon <i>et al.</i> (2007)
		R CGTGTGGCAACAAGGACAG							
	<i>Aero</i>	F CACAGCCAATATGTCGGTGAAG	326 bp.	94°C 5 min.	94°C 30 sec.	52°C 40 sec.	72°C 40 sec.	72°C 10 min.	Singh <i>et al.</i> (2008)
		R GTCACCTTCTCGCTCAGGC							
	<i>AHCToon</i>	F GAGAAGGTGACCACCAAGAACAA	232 bp.	94°C 5 min.	94°C 30 sec.	56°C 30 sec.	72°C 30 sec.	72°C 7 min.	Cagatay and Sen (2014)
		R AACTGACATGGCCTTGAAGTC							
<i>ast</i>	F TCTCCATGCTCCCTTCCACT	331 bp.	94°C 5 min.	94°C 30 sec.	55°C 30 sec.	72°C 30 sec.	72°C 7min.	Newaz <i>et al.</i> (2010)	
	R GTGTAGGGATTGAAGAAGCCG								
<i>fla</i>	F TCCAACCGTYTGACCTC	603 bp.	94°C 5 min.	94°C 30 sec.	55°C 40 sec.	72°C 45 sec.	72°C 10 min.	Nawaz <i>et al.</i> (2010)	
	R GMYTGGTTCGCRATGGT								
<i>Ps. aeruginosa</i>	<i>16S rDNA</i>	F GGGGGATCTTCGGACCTCA	956 bp.	94°C 5 min.	94°C 30 sec.	52°C 45 sec.	72°C 1 min.	72°C 10 min.	Spilker <i>et al.</i> (2004)
		R TCCTTAGAGTGCCACCCTCG							
<i>oprL</i>	F ATG GAA ATG CTG AAA TTC GGC	504 bp.	94°C 5 min.	94°C 30 sec.	55°C 45 sec.	72°C 45 sec.	72°C 10 min	Xu <i>et al.</i> (2004)	
	R CTT CIT CAG CTC GAC GCG ACG								
<i>tox A</i>	F GACAACGCCCTCAGCATCACCAGC	396 bp.	94°C 5 min.	94°C 30 sec.	55°C 45 sec.	72°C 45 sec.	72°C 10 min	Matar <i>et al.</i> (2002)	
	R CGCTGGCCCAITCGCTCCAGCGCT								
<i>exoS</i>	F GCGAGGTCAGCAGAGTATCG	118 bp.	94°C 5 min.	94°C 30 sec.	55°C 30 sec.	72°C 30 sec.	72°C 7 min	Winstanley <i>et al.</i> (2005)	
	R TTCGGCGTCACTGTGGATGC								
<i>flhC</i>	F TGAACGTGGCTACCAAGAACG	180 bp.	94°C 5 min.	94°C 30 sec.	56.2°C 30 sec.	72°C 30 sec.	72°C 7 min	Ghadaksaz <i>et al.</i> (2015)	
	R TCTGCAGTTGCTTCACTTCGC								

The present study was conducted on 250 diseased Nile tilapia (*O. niloticus*) fish of various sizes were collected from different fish markets at Kaliobia Governorate, Egypt, during the period from May (2017) to January (2019) for inspection of *Aeromonas* and *Pseudomonas* strains. After clinical and postmortem examination 445 samples were collected from apparently pathognomic lesions in muscle, liver, kidney, intestine and spleen by a number of 139, 118, 99, 70 and 19 respectively.

The surface of lesions were seared by hot spatula, then a sterilized loopful was introduced through seared portion and inoculated onto Tryptone soya broth then incubated aerobically at 37°C for 24 hours. A loopful from incubated Tryptone soya broth was streaked onto Tryptone soya agar and MacConkey's agar plates and incubated for 24 hours at 37°C. The pale colonies on MacConkey's agar and

white or greenish colonies on Tryptone soya agar were picked up and the following tests (Oxidase test and Catalase test) were performed. The suspected colonies that gave (Oxidase +ve and Catalase +ve) were taken and cultivated on the following media: *Aeromonas* base agar; Rimler- Shotts agar (R.S.) and Eosin methylene blue agar (EMB); *Pseudomonas* agar and *Pseudomonas* Cetrimide agar then incubated for another 24-48 hours at 25°C and 37°C, suspected colonies were picked up and purified by further sub culturing on nutrient agar and kept in Semi-solid nutrient agar. The purified colonies were morphologically identified by Gram stain and biochemical tests (Quinn *et al.*, 2002; Austin and Austin, 2007 and Markey *et al.*, 2013).

The In-Vitro sensitivity test was done on each isolated *Aeromonas* and *Pseudomonas* species strain to study its anti-microbial sensitivity according to

(Koneman *et al.*, 1997).

The phenotypic detection of virulence factors for isolated *Aeromonas* and *Pseudomonas* species was done through studying the haemolytic activities following Quinn *et al.* (2002); amylase activity (Palumbo *et al.* 1985); proteolytic activities (Marcy and Pruett, 2001); lipolytic activities (Haas, 2001); lecithinase activities (Anguita *et al.*, 1993) and the biofilm formation of them using tube method. In addition to, genotyping detection for specific gene of *A. hydrophila* (16SrRNA); aerolysin (*aero*); *A. hydrophila* cytotoxic enterotoxin (AHcytoen); cytotoxic enterotoxins- heat-stable (*ast*) and polar flagella gene (*fla*) in 8 random *A. hydrophila* strains, beside, specific gene of *Ps. aeruginosa* (16SrDNA); outer membrane lipoprotein L (*oprL*); exotoxin S gene

(*exoS*); exotoxin A gene (*toxA*) and flagellin C gene (*fliC*) in 8 random isolated *Ps. aeruginosa* strains using conventional PCR, following QIAamp® DNA Mini Kit instructions (Qiagen, Germany, GmbH), Emerald Amp GT PCR mastermix (Takara) with Code No. RR310A and 1, 5% agarose gel electrophoreses (Sambrook *et al.*, 1989) using the Primers sequences, target genes, amplicons sizes and cycling conditions showed in (Table 1).

3. Results

The results of bacteriological examination of examined fish; in- vitro sensitivity tests; phenotypic detection of virulence factors for the isolated strains and polymerase chain reaction (PCR) were tabulated in Tables (2 & 3) and Figures (1-10).

Table (2): Prevalence and distribution of *Aeromonas* and *Pseudomonas* species isolated from examined lesion samples

Isolates species	Lesion samples										Total	
	Muscle		Liver		Kidney		Intestine		Spleen			
	No.	%*	No.	%*	No.	%*	No.	%*	No.	%*	No.	%*
<i>Aeromonas</i> species	36	22.4	29	18.0	26	16.1	24	14.9	3	1.9	118	73.3
<i>A. hydrophila</i>	29	18.0	25	15.5	23	14.3	22	13.7	3	1.9	102	63.4
<i>A. caviae</i>	7	4.4	4	2.5	3	1.9	2	1.2	0	0.0	16	9.9
<i>Pseudomonas</i> species	14	8.7	12	7.5	9	5.6	8	5.0	0	0.0	43	26.7
<i>Ps. aeruginosa</i>	11	6.8	7	4.4	5	3.1	6	3.7	0	0.0	29	18.0
<i>Ps. fluorescens</i>	3	1.9	5	3.1	4	2.5	2	1.2	0	0.0	14	8.7
Total	50	31.0	41	25.5	35	21.7	32	19.9	3	1.9	161	100

%* percentage in relation to total number of isolated species (161)

Table (3): Phenotypic virulence factors of *Aeromonas* and *Pseudomonas* isolates

Phenotypic virulence activities	<i>Aeromonas</i> strains				<i>Pseudomonas</i> strains			
	<i>A. hydrophila</i> (102)		<i>A. caviae</i> (16)		<i>Ps. Aeruginosa</i> (29)		<i>Ps. Fluorescens</i> (14)	
	No.	%*	No.	%*	No.	%*	No.	%*
Haemolytic activity	93	91.2	13	81.3	26	89.7	9	64.3
Starchhydrolysis (amy lase activity)	98	96.1	14	87.5	27	93.1	11	78.6
Proteolytic (caseinase) activity	95	93.1	12	75.0	27	93.1	10	71.4
Lipolytic activity	90	88.2	10	62.5	25	86.2	10	71.4
Lecithinase activity	89	87.3	9	56.3	24	82.8	9	64.3
Biofilm production	91	89.2	11	68.8	27	93.1	11	78.6

*Percentage in relation to number of each *Aeromonas* and *Pseudomonas* species isolated

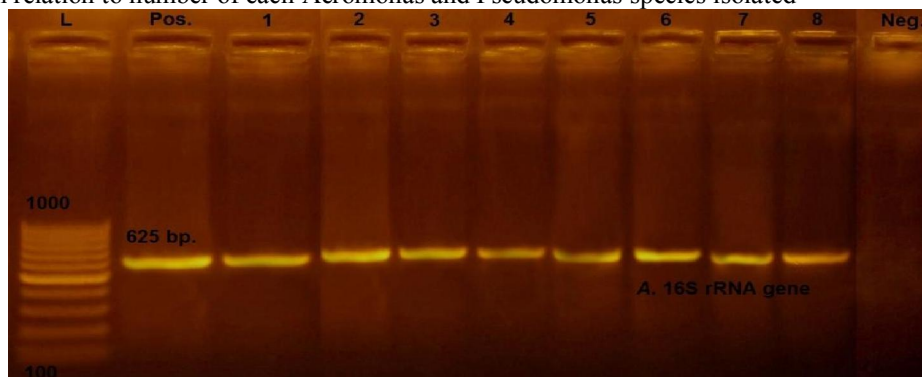


Fig. (1): Agarose Gel electrophoresis of specific gene of *A. hydrophila* (16SrRNA)

Lane L: 100-1000 bp. DNA Ladder. Neg.: Negative control. Pos.: Positive control (at 625 bp.)

Lane 1-8: *A. hydrophila* (Positive)

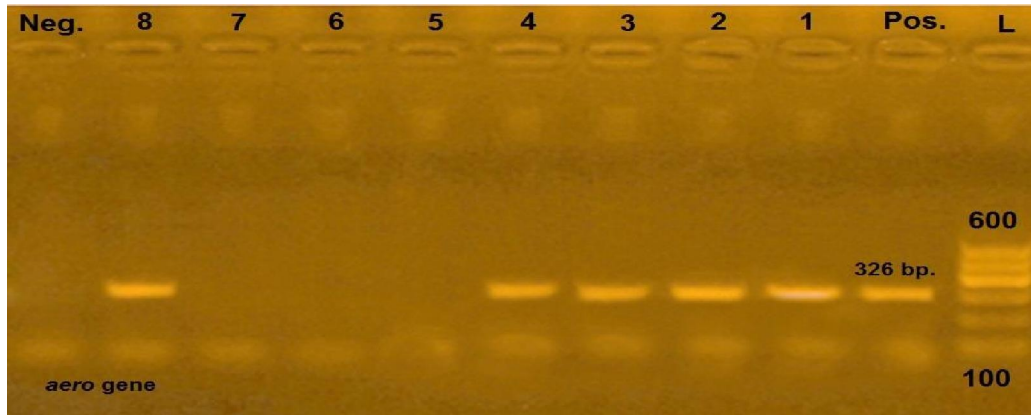


Fig. (2): PCR amplification of Aerolysin (*aero*) gene on agarose gel 1.5%.
 Lane L: 100-600 bp. DNA Ladder. Neg.: Negative control. Pos.: Positive control (at 326 bp.)
 Lane 1- 4 & 8: *A. hydrophila* (Positive) Lane 5, 6 & 7: *A. hydrophila* (Negative)

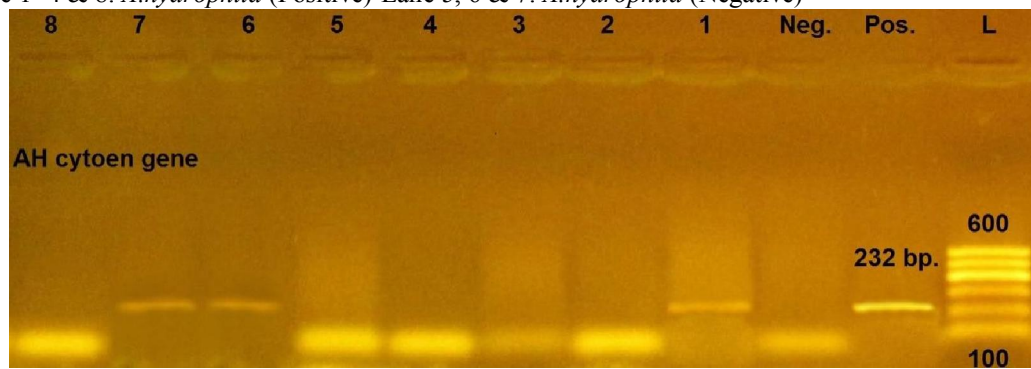


Fig. (3): PCR amplification of *A. hydrophila* cytolytic enterotoxin (*AHcytoen*) on agarose gel 1.5%.
 Lane L: 100-600 bp. DNA Ladder.
 Neg.: Negative control. Pos.: Positive control (at 232 bp.).
 Lane 1, 6, & 7: *A. hydrophila* (Positive). Lane 2,3,4, 5 & 8: *A. hydrophila* (Negative)

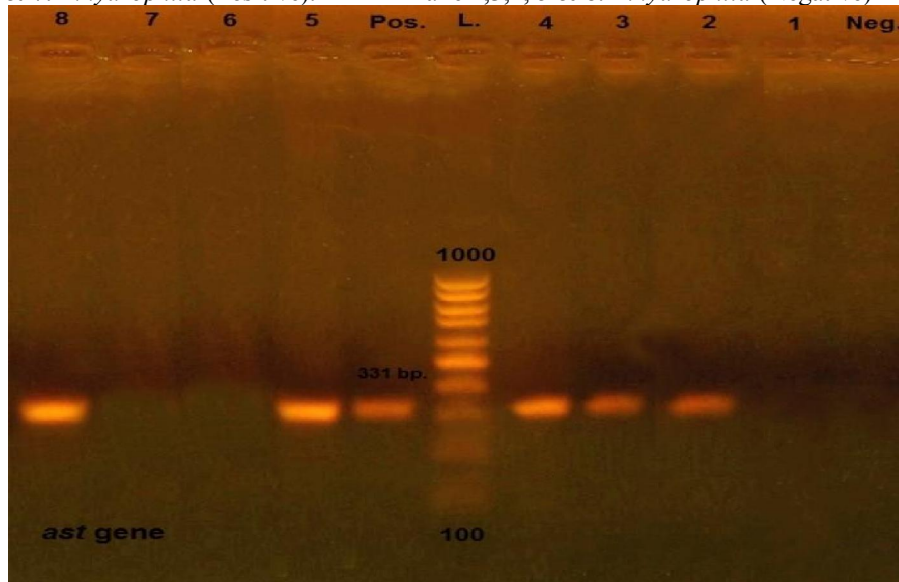


Fig. (4): PCR amplification of Cytotoxic enterotoxins- heat-stable (*ast*) gene on agarose gel 1.5%.
 Lane L: 100-1000 bp. DNA Ladder.
 Neg.: Negative control. Pos.: Positive control (at 331 bp.).
 Lane 2, 3, 4, 5 & 8: *A. hydrophila* (Positive). Lane 1, 6 & 7: *A. hydrophila* (Negative).

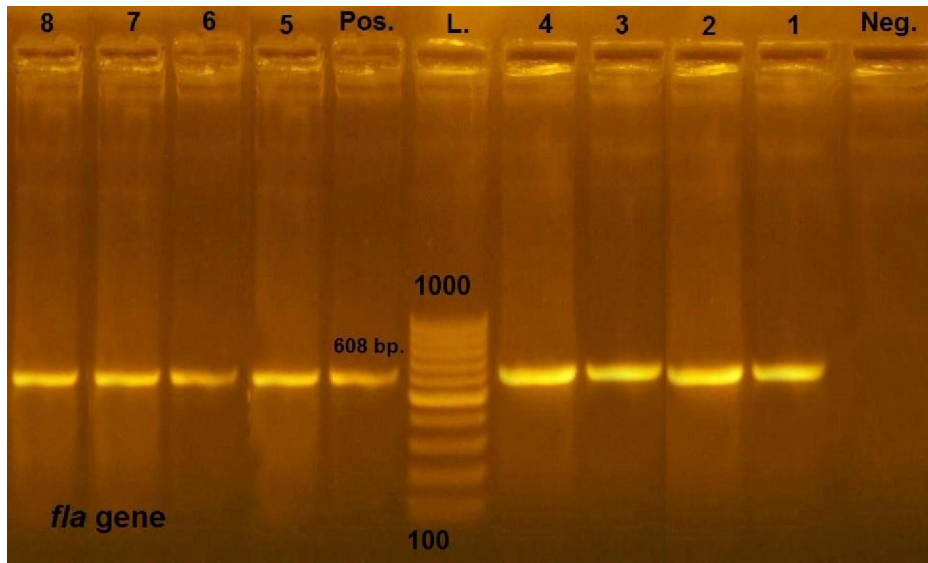


Fig. (5): Agarose Gel electrophoresis of polar flagella gene (*fla*) of *A. hydrophila* Lane L: 100-1000 bp DNA Ladder, Neg.: Negative control Pos.: Positive control (at 608 bp) Lane 1 – 8: *A. hydrophila* (Positive)

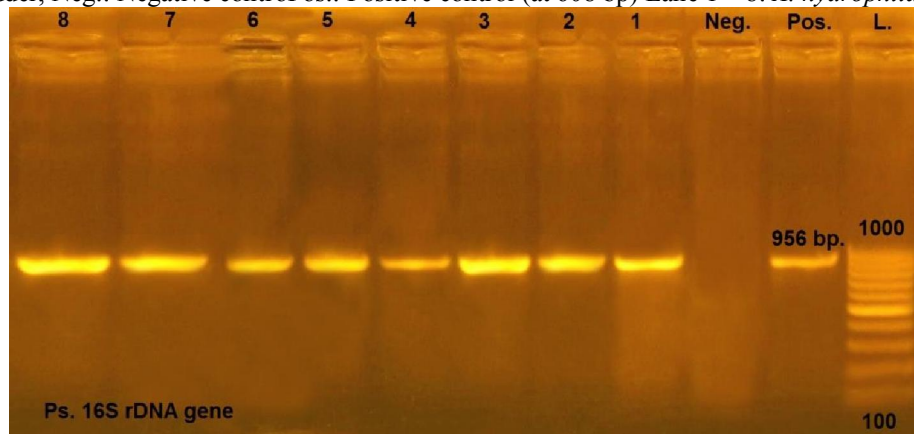


Fig. (6): Agarose Gel electrophoresis of specific gene of *Ps. aeruginosa* (16SrDNA) Lane L: 100-1000 bp DNA Ladder. Neg.: Negative control. Pos.: Positive control (at 956bp.) Lane 1- 8: *Ps. aeruginosa* (Positive)

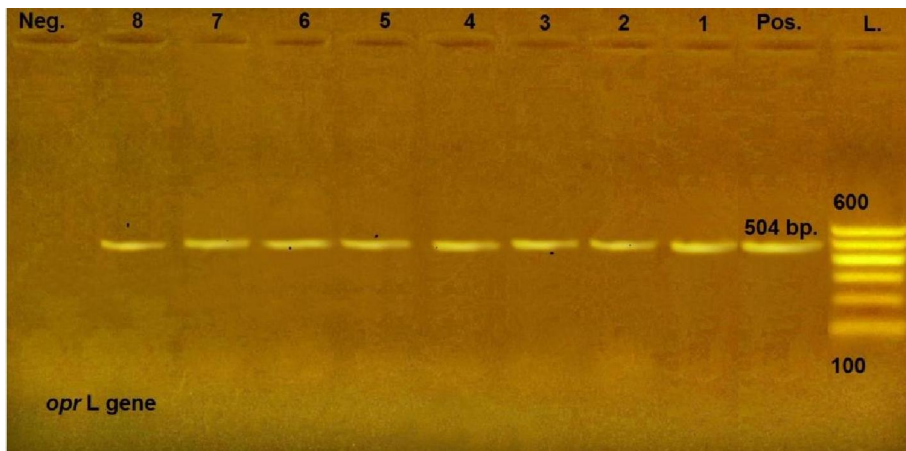


Fig. (7): Agarose Gel electrophoresis of outer membrane lipoprotein L gene (*oprL*) of *Ps. aeruginosa* Lane L: 100-600 bp DNA Ladder. Neg.: Negative control. Pos.: Positive control (at 504 bp) Lane 1- 8: *Ps. aeruginosa* (Positive)

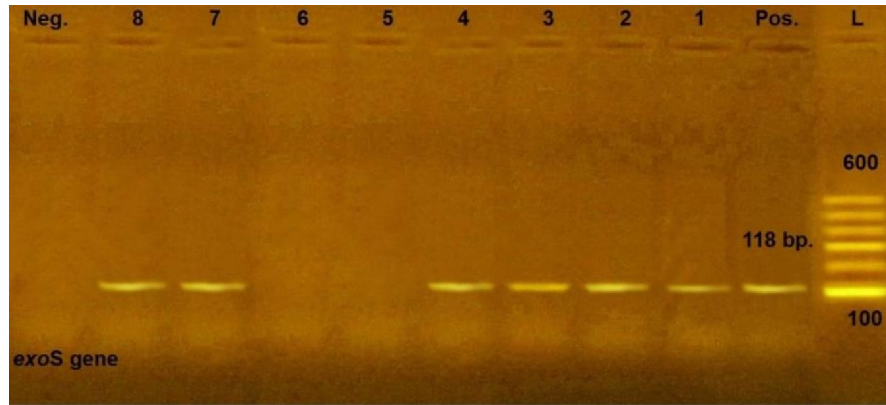


Fig. (8): Agarose Gel electrophoresis of exotoxin S (*exoS*) gene of *Ps. aeruginosa*
 Lane L: 100-600 bp DNA Ladder. Neg.: Negative control Pos.: Positive control (at 118 bp)
 Lane 1-4,7 & 8: *Ps. aeruginosa* (Positive) Lane 5 & 6: *Ps. aeruginosa* (Negative)

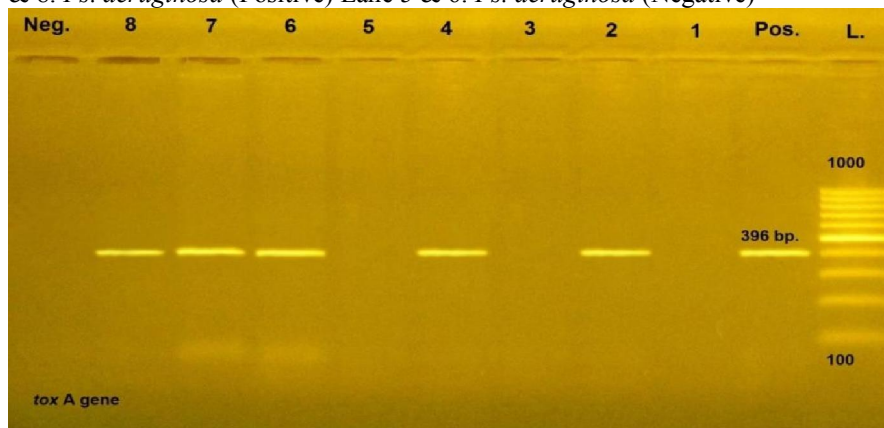


Fig. (9): Agarose Gel electrophoresis of exotoxin S (*tox A*) gene of *Ps. aeruginosa*
 Lane L: 100-1000 bp. DNA Ladder. Neg.: Negative control Pos.: Positive control (at 396 bp.)
 Lane 2, 4, 6, 7 & 8: *Ps. aeruginosa* (Positive) Lane 1, 3 & 5: *Ps. aeruginosa* (Negative)

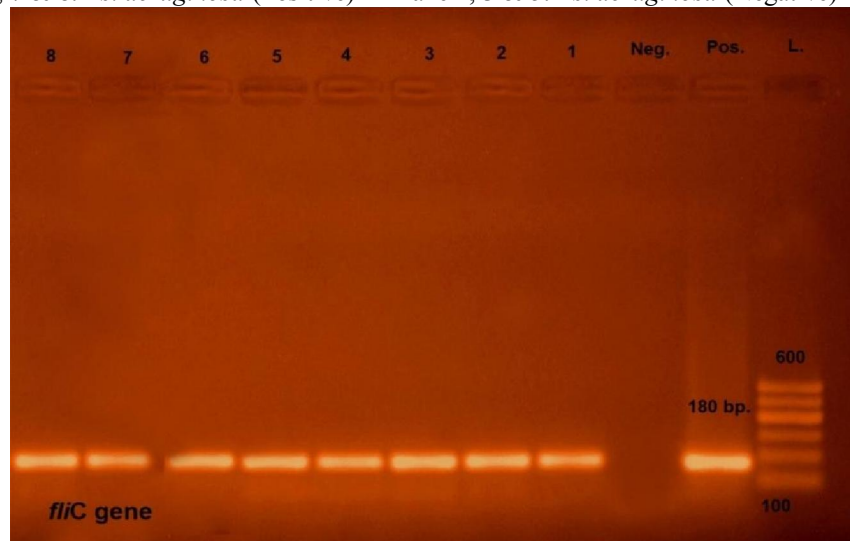


Fig. (10): Agarose Gel electrophoresis of flagellin C gene (*fliC*) gene of *Ps. aeruginosa*
 Lane L: 100-600 bp DNA Ladder. Neg.: Negative control.
 Pos.: Positive control (at 180 bp.) Lane 1- 8: *Ps. aeruginosa* (Positive)

4. Discussion

Aeromonas and Pseudomonas species are widely distributed microorganisms that responsible for wide range spectrum of ulcer type diseases among fish leading to high mortalities, high economic losses and decreases fish farm efficiencies (Roberts, 2001 and Shayo *et al.*, 2012), beside their role in gastrointestinal and extra intestinal infections in humans (Zilberberg and Shorr, 2009 and Parker and Shaw, 2011).

The results recorded in this study revealed that, 128 out of 250 examined fish (51.2%) were positive for Aeromonas and Pseudomonas species isolation, where 95(74.2%) were positive with pure single cultures; 85 Aeromonas spp. (66.4%) and 10 Pseudomonas spp. (7.8%) as well as 33(25.8%) mixed ones. These results came in accordance with that obtained by El- Dien *et al.* (2010); Shayo *et al.* (2012); Abd El Tawab *et al.* (2016) and Abd El Tawab *et al.* (2017). The results of bacteriological examination (Table, 2) revealed that, 161 Aeromonas and Pseudomonas species; 118 Aeromonas (73.3%) and 43 Pseudomonas species (26.7%) were isolated mostly from 50 muscle lesion samples (31.0%) followed by 41 liver samples (25.5%) then 35 kidney

(21.7%); 32 intestine samples (19.9%) and 3 spleen lesion samples (1.9%). Nearly similar results were recorded by El-Hady and Samy (2011); Hanna *et al.* (2014); Ibrahim- Lamis (2015) and Maarouf *et al.* (2017). Moreover, 36(22.4%) Aeromonas species were isolated from muscle lesion samples (29 *A. hydrophila*, 18.0% and 7 *A. caviae*, 4.4%); 29 (18.0%) from liver (25 *A. hydrophila*, 15.5% and 4 *A. caviae*, 2.5%); 26 (16.1%) from kidney (23 *A. hydrophila*, 14.3% and 3 *A. caviae*, 1.9%); 24 (14.9%) from intestine (22 *A. hydrophila*, 13.7% and 2 *A. caviae*, 1.2%) and 3 (1.9%) from spleen lesion samples that was *A. hydrophila* only. These results agree with those of Thayumanavan *et al.* (2003); Ibrahim- Lamis (2015); Abd El Tawab *et al.* (2017) and Maarouf *et al.* (2017). In addition, 14(8.7%) Pseudomonas species were isolated from muscle lesion samples (11 *Ps. aeruginosa*, 6.8% and 3 *Ps. fluorescens*, 1.9%); 12 (7.5%) from liver (7 *Ps. aeruginosa*, 4.4% and 5 *Ps. fluorescens*, 3.1%); 9 (5.6%) from kidney (5 *Ps. aeruginosa*, 3.1% and 4 *Ps. fluorescens*, 2.5%) and 8 (5.0%) from intestine (6 *Ps. aeruginosa*, 3.7% and 2 *Ps. fluorescens*, 1.2%) but both Pseudomonas species were failed to be isolated from spleen samples. Nearly similar results were recorded by Sakr and Abd El-Rhman (2008); Eissa *et al.*, (2010); El-Hady and Samy (2011); Hanna *et al.*, (2014) and Abd El Tawab *et al.* (2016).

The results of phenotypic Virulence factors of isolated Aeromonas and Pseudomonas strains (Table, 3) showed that, 93 *A. hydrophila* (91.2%); 13 *A.*

caviae (81.3%); 26 *Ps. aeruginosa* (89.7%) and 9 *Ps. fluorescens* (64.3%) isolated strains had haemolytic activity, as Aeromonas strains showed large grayish circular, smooth, glistening colonies and surround by beta haemolysis and newly isolated strain have a pungent foul odour on blood agar plus 10 ug /liter ampicillin. Similar results were recorded by Singh *et al.* (2008); Kozinska and Pekala (2010); Stratev *et al.* (2015) and Abd El Tawab *et al.* (2017). Meanwhile, Pseudomonas strains showed irregular colonies surround by a clear zone of β -haemolysis with green-blue pyocyanin pigment is most obvious in areas of heaviest growth, *Ps. aeruginosa* on blood agar and *Ps. fluorescens* showed narrow zone of β -haemolysis. These results were agreed with those of Jvo (2010); Kamel *et al.* (2011) and Panda *et al.* (2013). For starch hydrolysis (amylase activity), 98 *A. hydrophila* (96.1%); 14 *A. caviae* (87.5%); 27 *Ps. aeruginosa* (93.1%) and 11 *Ps. fluorescens* (78.6%) isolated strains hydrolyzed starch on starch agar and detected by logus iodine due to amylase enzyme. Similar results for Aeromonas strains were recorded by Pemberton *et al.* (1997); Sreedharan *et al.* (2012) and Abd El Tawab *et al.* (2017) for Aeromonas strains and for Pseudomonas strains with Tole *et al.* (2016); Alam and Imran (2018) and Mankar and Barate (2018). For Proteolytic (caseinase) activity, 95 *A. hydrophila* (93.1%); 12 *A. caviae* (75.0 %); 27 *Ps. aeruginosa* (93.1%) and 10 *Ps. fluorescens* (71.4%) isolated strains had protease enzyme that was shown by the formation of a clear zone on milk agar media due to proteolysis of milk casein. Similar results for Aeromonas strains were obtained by Castro-Escarpulli *et al.* (2003); Zhu-DaLing *et al.* (2006); Sreedharan *et al.* (2012) and Stratev *et al.* (2015) and for Pseudomonas strains with Pollack (2000); Jvo (2010) and Patil and Chaudhairy (2011). The lipolytic activity showed that, 90 *A. hydrophila* (88.2%); 10 *A. caviae* (62.5%); 25 *Ps. aeruginosa* (86.2%) and 10 *Ps. fluorescens* (71.4%) isolated strains presented lipolytic activity on agar supplemented with tributyrin and were detected by a transparent zone surrounding the colony on an opaque background. Similar results for Aeromonas strains were recorded by Gonzalez-Serrano *et al.* (2002); Castro-Escarpulli *et al.* (2003); Sreedharan *et al.* (2012) and Stratev *et al.* (2015) and with those recorded by Picot *et al.* (2001); Jvo (2010) and Stoyanova *et al.* (2012) for Pseudomonas strains. Also, 89 *A. hydrophila* (87.3%); 9 *A. caviae* (56.3%); 24 *Ps. aeruginosa* (82.8%) and 9 *Ps. fluorescens* (64.3%) isolated strains had lecithinase activity that was clearly marked by an opaque zone extending from the edge of the colony. These results were agreed with those of Gonzalez-Serrano *et al.* (2002); Sreedharan *et al.* (2012); Stratev *et al.* (2015) and Abd El

Tawab et al. (2017) for *Aeromonas* strains and with those of **Pollack (2000)** and **Jvo (2010)** for *Pseudomonas* strains. Moreover, most isolated *Aeromonas* and *Pseudomonas* strains were multi-drug resistant where 91 *A. hydrophila* (89.2%); 11 *A. caviae* (68.8%); 27 *Ps. aeruginosa* (93.1%) and 11 *Ps. fluorescens* (78.6%) strains had the ability for biofilm production that was clearly marked by a visible film lined the wall and the bottom of the tube. These results came in harmony with those of **Castro-Escarpulli et al. (2003)**; **Stratev et al. (2015)** and **Maarouf et al. (2017)** for *Aeromonas* strains and with those of **Pollack (2000)**; **Meliani and Bensoltane (2015)**; **Banu et al. (2017)**; **Omar et al. (2017)** and **Abdel-Haq- Fatma El- Zahraa (2018)** for *Pseudomonas* strains. So, most isolated *Aeromonas* and *Pseudomonas* strains were enterotoxigenic ones, as they had haemolytic; proteolytic; lipolytic; Lecithinase activities and had the ability for biofilm production.

The genotypic identification and detection of some virulence genes in isolated *A. hydrophila* and *Ps. aeruginosa* strains using PCR results showed that, specific gene of *A. hydrophila* (**16SrRNA**) and polar flagella gene (**fla**) genes were detected in all 8 studied strains; aerolysin (**aero**); *A. hydrophila* cytolytic enterotoxin (**AHCytoen**); cytotoxic enterotoxins- heat-stable (**ast**) virulence genes were detected in 5; 3 and 5 out of 8 *A. hydrophila* studied strains, respectively (Fig. 1-5). In addition, specific gene of *Ps. aeruginosa* (**16SrDNA**); outer membrane lipoprotein L (**oprL**) and flagellin C (**fliC**) genes were detected in all 8 studied *Ps. aeruginosa* strains; exotoxin A (**toxA**) and exotoxin S (**exoS**) virulence genes were detected in 5 and 6 out of 8 studied ones, respectively (Fig. 6- 10).

Regarding to *A. hydrophila* strains, they were identified genotypically through the detection specific gene of *A. hydrophila* (**16SrRNA**) and the PCR results showed that, it was amplified in all 8 studied *A. hydrophila* strains giving product of 625 bp. (Fig., 1) so, all of them were *A. hydrophila*. Similar detection was recorded by **Gordon et al. (2007)**; **Hussain et al. (2013)**; **Skwor (2014)** and **Stratev et al. (2016)**.

Some strains of *Aeromonas* are reported to be invasive to epithelial cells and one of the major virulence factors in gastroenteritis is aerolysin (**Chu and Lu, 2005**), the results of PCR for amplification of **aero** gene in *A. hydrophila* strains (Fig., 2) showed that, the **aero** gene was amplified in 5 out of 8 *A. hydrophila* studied strains giving product of 326 bp. Similar results were decided by **Singh et al. (2008)**; **Aravena et al. (2014)**; **Furmanek (2014)**; **Stratev et al. (2016)** and **Abd El Tawab et al. (2017)**. In addition, the results of PCR for amplification of **AHCytoen** gene in *A. hydrophila* strains (Fig., 3) showed that, the **AHCytoen** gene was amplified in 3 out of 8 *A. hydrophila* studied strains giving product of

232 bp. Similar results were recorded by **Sarkar et al. (2013)**; **Cagatay and Şen (2014)** and **Abd El Tawab et al. (2017)** who reported that the detection of this cytolytic enterotoxin gene in such isolates and considered them a potential risk to human health. Also, the **ast** gene was amplified in 5 out of 8 *A. hydrophila* studied strains giving product of 331 bp. as shown in Fig. (4). Similar results were recorded by **Sha et al. (2002)**; **Ashok et al. (2009)**; **Bin Kingombe et al. (2010)**; **Nawaz et al. (2010)**; **Ye et al. (2013)** and **Abd El Tawab et al. (2017)**. Moreover, the polar flagella (**fla**) gene is important for invasive ability; enterocyte adhesions and could be related to persistent or dysenteric presentation seen during *Aeromonas* infections and needed to be fully functional for optimal biofilm formation (**Ashok et al., 2009**). The results of PCR amplification of **fla** gene in *A. hydrophila* isolates showed that, the **fla** gene was amplified in all 8 studied *A. hydrophila* strains giving product of 608 bp. (Fig., 5). Similar findings were recorded by **Nawaz et al. (2010)**; **Aravena et al. (2014)** and **Furmanek (2014)**. Meanwhile, for *Ps. aeruginosa* strains, they also identified genotypically through the detection specific gene of *Ps. aeruginosa* (**16SrDNA**) and the PCR results showed that, it was amplified in all 8 studied *Ps. Aeruginosa* strains giving product of 956 bp. (Fig.,6) so, all of them were *Ps. aeruginosa*. Similar detection was recorded by **Spilker et al. (2004)**; **Kumaran et al. (2010)**; **Uğur et al. (2012)**; **Abd El-Aziz (2015)** and **Abdel-Haq-Fatma El- Zahraa (2018)**. The high virulence of *Ps. aeruginosa* is mostly due to its ability to produce a large number of virulence factors that can contribute to different ways to their pathogenicity (**Markey et al., 2013**). The outer membrane lipoprotein L (**oprL**) is a potent pro-necrosis factor for cells (**Picot et al., 2001**). It play important roles in the interaction of the bacterium with the environment as well as the inherent resistance of *Ps. aeruginosa* to antibiotics where the consequence of the presence of these specific outer membrane proteins that have been implicated in efflux transport systems that affect cell permeability (**Markey et al.,2013**). The obtained PCR result for amplification of **oprL** gene in *Ps. aeruginosa* strains revealed that, it was amplified in all 8 studied strains giving product of 504 bp. as shown in Fig. (7), as these protein is found only in this organism, it could be a reliable factor for rapid identification of *Ps. aeruginosa* in clinical samples (**De Vos et al., 1997**) so, all of them were *Ps. aeruginosa*. These results came in accordance with those recorded by **Xu et al. (2004)**; **Lavenir et al. (2007)**; **Abdullahi et al. (2013)**; **Khattab- Mona et al. (2015)** and **Abd El Tawab et al. (2016)**. The exotoxin S gene (**exoS**) is toxic virulence factor causing death in the infected cell as it causes a decrease in DNA synthesis and viability

of host cells (Kaufman *et al.*, 2000). The results of PCR for amplification of exotoxin S (*exoS*) gene in *Ps. aeruginosa* isolates (Fig.,8) showed that, it was amplified in 6 out of 8 studied strains giving product of 118 bp. Similar findings were recorded by Winstanley *et al.* (2005); Todar, (2011); Nikbin *et al.* (2012); Khattab- Mona *et al.* (2015) and Abd El Tawab *et al.* (2016). In addition, exotoxin A (*toxA*) is the most toxic virulence factor of the pathogenic *Ps. aeruginosa* for animals, fish and human (Pollack, 2000 and Michalska and Wolf, 2015). The results of PCR amplification of exotoxin A (*toxA*) gene (Fig., 9) revealed that, it was amplified in 5 out of 8 *Ps. aeruginosa* studied strains giving product of 396 bp. These results were agreed with those obtained by Matar *et al.* (2002); Nafee (2012); Nikbin *et al.* (2012); Khattab- Mona *et al.* (2015) and Abd El Tawab *et al.* (2016). Moreover, the results of PCR amplification of flagellin C (*flhC*) gene (Fig., 10) cleared that, it was amplified in all 8 *Ps. aeruginosa* studied strains giving product of 180 bp. These results came in harmony with those recorded by Choi *et al.* (2002) and Ghadaksaz *et al.* (2015).

Finally, most isolated *A. hydrophila*; *A. caviae*; *Ps. aeruginosa* and *Ps. fluorescens* strains were enterotoxigenic ones, as they had haemolytic; proteolytic; lipolytic; Lecithinase activities and had the ability for biofilm production, beside the detection of virulence genes in them. In addition, virulence genes were detected in them indicates their pathogenicity for fish; a potential risk for causing fish - originated food poisoning and increasing prevalence of community-acquired infection is a dangers problem for public health.

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