Introduce of *Pseudomonas psychrophila*, as a new Pathogen Causing Disease in Cultured Rainbow trout (Oncorhynchus mykiss)

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Abstract

This is the first report on the world that *Pseudomonas psychrophila* is a new etiological agent of disease in fish. A disease case occurred during the fall of 2017 in a rainbow trout farm in the north of Iran (Guilan province). Anorexia, lethargy and mortalities of 10% fish per week were observed in rainbow trout *Oncorhynchus mykiss* weighting 45-107g in three fresh water ponds of a farm on the north of Iran. The fish showed external signs of dark pigmentation, exophthalmia, and hemorrhage at the base of the fins and tissues damage. Internal signs were enlarged spleen, pale Liver and intestine filled with yellowish fluid. Kidney and liver of diseased fish were aseptically streaked on MacConkey and sheep blood agar. The cultured bacterial 16S rRNA gene was sequenced. Causative bacteria were identified as *pseudomonas psychrophila* using morphological and biochemical characteristics and genotypic method based on the 16S rRNA gene.

Keywords: Pseudomonas psychrophila, Oncorhynchus mykiss, New fish disease, Iran

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Introduction

Bacterial pathogens are naturally present in the fish environment and under some specific stress conditions. They are the etiological agents of the most important disease problems in aquaculture that induces mortalities and severe economic losses to fish farm (Shawna and Brian, 2020). Pseudomonas psychrophila is a psychrophilic, Gram-negative bacterium that is responsible for dairy spoilage (Samaržija et al., 2012). However, it has not yet been reported as a pathogen in aquaculture. Pseudomonas psycrophila does not produce siderophores, unlike other members of many the Pseudomonas genus (Carrion, et al., 2010). The optimal temperature for growth is 30°C, however it can grow between 0°C and 35°C (Hebraud et al., 1994). Pseudomonas psychrophila is recognized as pathogenic in rainbow trout fish farm in the north of Iran. Based on 16S rRNA analysis, Pseudomonas psychrophila has been placed in the P. chlororaphis group (Anzai et al., 2000). Austin and Austin (2007) suggested the reason for the widespread incidence of Pseudomonas sp. in the aquatic environment may be due to its spread through the water, which acts as the major reservoir of infection. The genus Pseudomonas was identified in different species of fish as etiological agents of Pseudomonas septicemia (Altinok et al., 2007; Sakar and Azza, 2008; Eissa et al., 2010; El-Nagar, 2010). The external changes related to infection bv Pseudomonas sp. bacteria in different fish were fin rot, detached scales,

hemorrhage and darkness of the skin, abdominal ascetic and exophthalmia (Eissa et al., 2010). Various studies have shown that the phenotypic identification methods are solely not enough for the classification of Pseudomonas sp. so the genotypic identification systems are required to confirm the traditional identification of particularly potential dangerous Pseudomonas (Alatossava Alatossava. 2008). and Molecular techniques using PCR-based methods allow fast. sensitive and exact identification of the bacteria that have been described for the detection of fish diseases. 16S rRNA gene is one of these important methods, especially when used alongside phenotypic characteristics microbial for identification diagnostic in the laboratory (Buller, 2004).

The present study aimed to isolate the causative agent of disease during the sporadic case in rainbow trout and identify the phenotypic and genotypic characterizations identified based on the 16S rRNA gene.

Materials and methods

Isolation of bacteria and characterization of bacterial isolates A disease case occurred during the fall of 2017 in a rainbow trout farm in the north of Iran (Guilan Province). Affected fish weights were ranged between 45g and 107g. Microbial examination revealed the presence of bacteria in affected fish at the farm. Fifty fish samples, five fish from each pond, were collected during disease outbreak and were translated to the Viromed laboratory in Guilan Province. Samples from kidneys and livers of collected fishes were streaked onto McConkey and sheep blood agar plates and incubated at 20°C for 48 h. Some growing colonies were picked up in pure where the identification of form selective colonies was done by morphological and biochemical characters for Gram-negative fish pathogens and they identified to the genus Preudomonas. The identification was confirmed by sequencing the 16S rDNA. Antimicrobial test was applied on Muller Hinton agar.

DNA isolation

In order to isolate DNA, the pure isolates were incubated in tryptic soy broth (TSB) at 37°C for 24h. Bacterial genomic DNA was extracted using the GeneJET Genomic DNA purification kit based on the manufacturer's instruction. 2×10^9 bacterial cells translated in a 2 mL microcentrifuge tube and centrifuged for 10 minutes at 5,000x g. The supernatant was discarded and the pellet was resuspended in 180 µL of digestion solution. 20 µL of Proteinase K solution added and mixed thoroughly by uniform vortexing to obtain а suspension. Then, the sample was incubated at 56°C while vortexing occasionally until the cells were completely lysed (~30 minutes). 20 µL of RNase A solution added and mixed by vortexing and incubate the mixture for 10 minutes at room temperature. After, 200 µL of lysis solution added to the

sample and mixed thoroughly by vortexing for about 15 seconds until a homogeneous mixture was obtained. 400 µL of 50 % ethanol added and mixed by vortexing. The prepared lysate transferred to a GeneJET Genomic DNA Purification Column inserted in a collection tube and centrifuged column for 1 min at 6,000 x g. The collection tube containing the flow-through solution was discarded. The GeneJET Genomic DNA Purification Column (Žilinskien, 2011) placed into a new 2 mL collection tube. 500 uL of wash buffer I added and centrifuged for 1 minute at 8,000 x g. The flow-through discarded and placed the purification column back into the collection tube. 500 µL of wash buffer II added to the GeneJET Genomic DNA Purification Column and centrifuged for 3 minutes at maximum speed. The collection tube containing the flow-through solution discarded and transferred the GeneJET Genomic DNA Purification Column to a sterile 2 mL microcentrifuge tube. The eluted DNA was used as a template for PCR detection of the 16S rRNA gene. A 1500 base pair DNA fragment was amplified from the bacterial DNA from extracted а pure culture Pseudomonas. Thus, bacteria isolated from the diseased rainbow trout were confirmed as P. psychrophila. (Haghighi et al., 2018).

PCR and 16S rRNA gene sequencing

Universal bacterial primers specific for detection of 16S rRNA gene of bacteria was used 27F (5'-

AGAGTTTGATCMTGGCTCAG-3') and 1429R (5'-TACGGYTACCTTGTTACGACTT-

3'). The location of primers was 1500 bp. These primers were then used to yield a 1500 bp 16S rRNA gene product by PCR. The amplification was done in a thermal cycler with the following parameters: initial denaturation at 95°C for 10 min, followed by 30 cycles of amplification (denaturation) at 95°C for 20sec, annealing at 50°C for 20sec, extension at 72°C for 3 min and a final extension step of 72°C for 10 min (Table 1). After amplification, 10 µL of the PCR sample was loaded on a 1% agarose gel stained with ethidium bromide. PCR product was purified by QIAquick PCR purification kit and directly sequenced with a 3500/3500xl Genetic Analyzer (QIAquick® Spin Handbook, 2020).

Table 1: PCR	program.
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Initial denaturation	95°C	10 min
30 cycles	95°C 505°C 72°C	20 sec 20 sec 3 min
Final extension	72°C	10 min

Biochemical characteristics

Pure colonies of Gram-negative bacteria were isolated on MacConkey agar from the liver and kidney of affected fish. To isolated identify the bacteria, biochemical tests were done. The characteristic of the bacteria was oxidase catalase-positive, and lysine decarboxylase positive, Simmons citrate positive, Urea negative and nonfermentation glucose, β-hemolysis negative, weak motility. It grew well on MacConkey agar as it formed yellowpigmented colonies, which indicates lactose non-fermented status.

Antibiotic susceptibility test

Swab samples were collected from livers and kidneys of infected trout and cultured on 5% Sheep blood agar and MacConkey agar. All the plates were incubated at 20°C for 48 hours. For the determination of susceptibility to antibacterial agents, the disc diffusion method on Muller-Hinton agar according to the procedure of Bauer et al. (1966) was used. Some colonies of isolated bacteria from blood agar plate were transferred to a glass tube containing 3 ml saline and the suspension was vortexed and visually matched with 0.5 MacFarland standards for turbidity. The sterile cotton-tipped swab was dipped into the prepared bacterial suspension and then rolled on the upper part of the tube to remove the excess fluid and subcultured onto Muller-Hinton agar (Hudzicki, 2009).

Paper discs with predetermined amounts of antibiotics were used. The following antimicrobial agents based on the OIE List of Antimicrobial Agents of Veterinary Importance 2014, were tested. All antibacterial discs were provided from Padtan Teb Company (Tehran, Iran). The plates were incubated at 20°C for 48 hours. The diameters of the zones of inhibition were (millimetres) measured and were compared to internationally accepted measurements determine to the susceptibility or resistance of the isolates. Results were interpreted to the Clinical Laboratory Standard Institute (CLSI, 2013) guidelines. Drug resistance patterns of the organisms were determined at three levels: Susceptible (S), Intermediate (I) and Resistant (R).

Seventeen antimicrobial drugs were evaluated for efficiency against tested. Some antibiotics include cell wall synthesis (colistin 10 μ g; lincospectin 15/200 μ g; enrofloxacin 5 μ g; difloxacin 5 μ g), protein synthesis inhibitors (erythromycin 15 μ g; gentamycin, 10 μ g; neomycin 30 μ g; danofloxacin 5 μ g; streptomycin 10 μ g; kanamycin 30 μ g; florfenicol 30µg; flumequine, 30µg; fosfomycin 200µg; tetracycline 30µg; oxytetracycline 30µg; chlortetracycline 30µg; doxycycline 30µg; and nucleic acid synthesis inhibitors (as listed in Table 1. *Pseudomonas* strain was characterized as sensitive (S), or resistant (R) according to the size of the inhibition zones around the discs (CLSI, 2010).

Results

Mass mortalities occurred in a rainbow trout farm in the north of Iran (Guilan Province) and cumulative mortality reached 20%. There was dark pigmentation, exophthalmia, hemorrhage at the base of the pectoral, pelvic, and anal fins and surrounding the anus externally (Fig. 1).



Figure 1: A= Dark pigmentation, B= Hemorrhage at the base of the pectoral, pelvic, and anal fins, C= Hemorrhage surrounding the anus.

Internal signs were enlarged spleen, pale liver and empty stomach and intestine filled with yellowish fluid. Pure colonies of Gram-negative bacteria were isolated on MacConkey agar (Fig. 2) and sheep blood agar (Fig. 3) from the liver and kidney of affected fish. It grew well on MacConkey agar as it formed yellowpigmented colonies, which indicates lactose non-fermented status. Some growing colonies were picked up in pure form where the identification of selective colonies was done by biochemical morphological and

characters for Gram-negative fish pathogens and they identified to the genus *Preudomonas* (Fig. 4).



Figure 2: Pure colonies on MacCankey Agar.



Figure 3: Pure colonies on Sheep Blood Agar.



Figure 4: Gram-negative bacteria (genus *Pseudomonas*).

Antibiotic sensitivity

Based on antibiotic susceptibility study showed that isolate (*P. psycrophila*) had intrinsically high sensitivity to colistin, <u>fluoroquinolones</u> (enrofloxacin, difloxacin, danofloxacin, flumequine), aminoglycosides (kanamycin, streptomycin, neomycin, gentamycin), while it had resistance to tetracyclines (tetracycline, oxytetracycline, chlortetracycline,

doxycycline, erythromycin), fosfomycin which is broad-spectrum antibiotics, and florfenicol (Table 2).

Table 2: Antibacterial activity of different

antibiotics against <i>Psedomonas psycrophila</i>				
Antibiotic	Concentration	Results		
Name	(µg)			
Tetracycline	30	R		
Oxytetracyclin	30	R		
e				
Chlortetracycli	30	R		
ne				
Doxycyclin	30	R		
Difloxacin	5	S		
Danofloxacin	5	S		
Enrofloxacin	5	S		
Flumequin	30	S		
Erythromycin	15	R		
Fosfomycin	200	R		
Gentamycin	10	S		
Kanamycin	30	S		
Streptomycin	10	S		
Neomycin	30	S		
Colistin	10	S		

Lincospectin 15/200 S= Susceptible; R= Resistant

Florfenicol

Phenotypic characterization and hemolytic activity

30

R

S

Some growing colonies were picked up in pure form where the identification of selective colonies was done by morphological and biochemical Gram-negative fish characters for They were identified pathogens. morphologically as Gram-negative rod motile bacteria. Biochemically, bacteria was oxidase and catalase-positive, lysine decarboxylase positive, Simmons citrate positive, Urea negative and nonfermentation glucose on MacConkey

agar, β -Hemolysis negative on sheep blood agar, weak motility in SIM medium Thus, it characterized as *Pseudomunas* genus. The characteristic of the bacteria has been shown in Table 3.

Identification by 16 S rRNA and sequencing 27F and 1429R primers were used to amplify 16S rRNA of bacterial isolate, with amplicon size 370 bp. The isolates collected and identified by 16S rRNA. The results of the 16S rRNA sequence correlated with the phenotypic The *Pseudomonas* of classification strain. A 1500 base pair DNA fragment was amplified from the bacterial DNA extracted from a pure culture Pseudomonas (Fig. 5). Thus, bacteria isolated from the diseased rainbow trout were confirmed as P. psycrophila (Fig. 6).

Table 3:	Biochemical	characteristics	isolated	bacteria,	Psedomonas	psycroph	hila.
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Characteristics	Results
Glucose	-
Sucrose	-
Lactose	-
Indole	-
H ₂ S production	-
Urease	-
Simmon citrate	+
Motility	+
MacConkey agar	+
Sheep Blood agar	+
B-Hemolysis	-
Oxidase	+
Catalase	+
Nagativa- Positiva-+	

Negative=- Positive=-



Figure 5: PCR product electrophoresis in 16S rRNA region on 1% agarose gel ethidium bromide staining (by Genfanavaran Co). M: molecular weight marker.



Figure 6: Identification of 16S rRNA gene sequencing (by Macrogen Co).

Discussion

A disease case occurred during the fall of 2017 in a rainbow trout farm in the north of Iran (Guilan province) for the first time with cumulative mortality of 20%. Clinical signs were ulceration and hemorrhage. The causative bacteria isolated from this fish farm were identified as Pseudomonas psychrophila phenotypical according to characteristics and sequence of 16S rRNA. Despite the fact P. fluorescencs and P. aeruginosa have been considered as opportunistic pathogenic species in aquaculture (Angelini and Seigneur, 1988; Altinok et al., 2006). However, it has been reported that other species of the *Pseudomunas* genus may induce serious infection in various fish for example, P. anguilliseptica in eel and Anguilla japonica (Wakabayashi and Egusa, 1972), P. chlororaphis in amago trout and Oncorhynchus rhodurus (Hatai et al., 1975), P. plecoglossicida in ayu (Wakabayashi 1996). et al., Plecoglossus altivelis (Kobayashi et al., 2000) and P. putida infection in rainbow trout (Altinok et al., 2006). The result of the present study showed that the isolate identified as Pseudomonas was characterized by Gram-negative motile rod with oxidase, catalase-positive and lysine decarboxylase and Simmons citrate positive, Urea negative and nonfermentation glucose, β-hemolysis However biochemical negative. identification gave incomplete result at the species level that was identified as *Pseudomonas* sp. PCR was reported to be a sensitive screening technique to detect bacterial communities (Teng et al., 2004). In the present study was used

PCR technique targeting 16S rRNA for detection of bacteria isolate from infected fish through universal primers (27F and 1429R), which was identified as Pseudomonas psycrophila. The isolate was well identified at the species level by 16S rRNA sequences that were identified Pseudomonas as The antibiotic psychrophila. susceptibility study recorded that P. psycrophila exhibited sensitivity to lincospectin, enrofloxacin, difloxacin, danofloxacin. colistin, flumequine, kanamycin, streptomycin, neomycin and gentamycin (Table 1). Eissa et al. (2010) reported that strains of P. putida, P. anguilliseptica and P. aureginosa were sensitive to fluoroquinolone antibiotics, erythromycin and gentamicin. Also, Darak and Barde (2015) reported that P. fluorescens was very sensitive to kanamycin, nalidixic acid, gentamicin, neomycin, less sensitive to amikacin and tetracycline, and chloramphenicol and the least sensitive to oxytetracycline, erythromycin and penicillin. Also, P. fluorescens exhibited susceptibility to oxytetracycline and amikacin more than kanamycin, neomycin and gentamicin (Markovic et al., 1996). Thus, these that *Pseudomonas* results showed psycrophila is sensitive to colistin, fluoroquinolones (enrofloxacin, difloxacin, danofloxacin, flumequin), aminoglycosides (kanamycin, streptomycin, neomycin, gentamycin). However, *Pseudomonas* psycrophila resistance had to tetracyclines (tetracycline, oxytetracycline, chlortetracycline,

doxycycline, erythromycin), fosfomycin which are broad-spectrum antibiotics, and florfenicol (Table 1). Altinok *et al.* (2006) reported that *P. putida* has high resistance to ampicillin, erythromycin, chloramphenicol, tetracycline, naladixic acid, rifampicin and streptomycin. Also, *P. fluorescens* exhibited complete resistance to penicillin and erythromycin (Markovic *et al.*, 1996).

Conclusion

In conclusion. phenotypic characteristics gave a good identification of *Pseudomonas* isolates. Using 16S rRNA gene sequencing proves that diagnosing fish's bacterial diseases is important for successful epidemiological studies and disease control. The results concluded that pathogenic Pseudomonas psychrophila is sensitive to colistin, fluoroquinolone antibiotics (enrofloxacin, difloxacin, danofloxacin). and aminoglycosides (kanamycin, streptomycin, neomycin, gentamycin).

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