Available online at http://bjas.bajas.edu.iq
https://doi.org/10.37077/25200860.2025.38.2.07
College of Agriculture, University of Basrah

Basrah Journal of Agricultural Sciences

ISSN 1814 – 5868 Basrah J. Agric. Sci., 38(2), 103-112, 2025 E-ISSN: 2520-0860

Isolation and Molecular Identification of Bacterial Gills Pathogen Isolated from Cultured Common Carp *Cyprinus carpio* (L.) in Earthen Ponds in Basrah Governorate, Iraq

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Received 22nd May 2025; Accepted 25th December 2025; Available online 31st December 2025

Abstract: Fifteen common carp samples were collected from a three fish farms infected with bacterial gill disease in an epidemic manner in order to identify the causative bacterial pathogens. Bacterial gill disease was studied in farmed common carp in Basrah Governorate, Iraq. The pathological signs related to fish behaviour and gross damage in gill tissues were recorded. The pathogens of bacterial gill disease were diagnosed using VITEK 2 technique after isolation and purification of bacteria on suitable culture media and the diagnosis was confirmed genetically using 16s RNA technique. The results included recording two species of bacterial pathogens, namely *Aeromonas sobria* and *Sphingomonas paucimobilis* are isolated from all collected fish. *A. sobria* recorded in NCBI under ID: OR122346.1, while two isolated *S. paucimobilis* was under ID: OR121489.1 and OR128365.1 respectively. The obtained findings indicated that the causative bacterial pathogens were variable along with the variability of location and time the environment was the same, so this variation will cause the change in the species or strains causing the disease.

Keywords: Aeromonase sobria, Fish, Pond, Sphingomonas paucimobilis.

Introduction

Fish diseases are currently a major problem, as they alter the steady production of fishery resources globally and affect the economics of the fisheries sector (Bakhtiyar *et al*., 2022). Infections in fish leading to disease outbreaks are a major concern for the aquaculture sector because they can result in significant economic damage owing to morbidity and death (Irshath *et al*., 2023). Bacteria are very common in the aquatic environment, and most bacterial disease agents are part of the normal flora of water (AlShammari *et al*. 2019). The current development in aquaculture production comes with an increase in infectious diseases, which significantly impacts the production, profitability, and sustainability of the worldwide aquaculture business (Senthamarai *et al*., 2023).

The generic term “Gill disease” refers to a wide range of disorders that affect the gills and

severely impact salmonid aquaculture systems worldwide (Zamparo *et al*., 2024). Bacterial gills disease is one of the most important diseases in the field of fish health for several reasons, the most important of which is the great damage it causes, as the mortality rate is considered the highest among other bacterial diseases, and it is also the most widespread disease in fish farms. Jassim (2019) considered that the bacterial gill disease is the most virulent disease due to its high incidence in fish farms and that it was the most lethal in fish farms, as it caused the highest mortality rates in fish farms during the years 2014, 2015 and 2016. Another study by the same researcher also confirmed this meaning, as he recorded an infection rate of 51.47% for the same disease for the years 2018-2020 (Jassim, 2024). Abdulrahman *et al*. (2020) indicated that 60% of the most repeatable problems fish farms belong to bad management. Bacterial gill disease has become very common in fish farms in Basrah and has become a real problem facing farmers. Most of the health problems in fish farms in Iraq and in Basrah Governorate in particular are due to many reasons, the most important related lack experience and mismanagement, as the farmers themselves cause stress on the fish through a number of incorrect procedures and thus weaken the immunity. Farmers work unintentionally or causing an increase in the microbial load of the water and change water quality through feeding methods that are either unscientific or ill-considered, which increases the chances of infection.

The current study aims to isolate and identification the bacterial pathogens of bacterial gill disease in farmed carp fish in Basrah Governorate, Iraq, using VITEK 2 system and confirm the diagnosis genetically by 16s rRNA gene sequencing. The genetic technique to detect bacterial pathogen as species was based on the polymerase chain reaction (PCR) followed by DNA sequencing (Shendure *et al*., 2017).

Materials & Methods

Sampling of fish

Infected 15 common carp (500-1000g weight) with BGD were collected from different location of fish farms in Basrah province, Iraq. Samples transported by ice box to laboratory in Marine Science centre to identification type of bacteria caused disease. The samples were investigated morphologically at first then gills cut and investigated under dissecting microscope (Optika SZM-1) to detect external signs of disease.

Clinical identification

Infected gills washed by normal saline to avoid the bacteria in mucus and squashed. One millilitre of the homogenate solutions was serially diluted (10-1 to 10-7). 0.1 ml of the serial dilutions were inoculated onto Nutrient agar (Hi media- India). The plates were incubated at 37°C for 24 h. One growth of colonies was selected and transported to new media (same above) at the same temperature and time above. *Sphingomonas paucimobilis* on culture media were deep yellow pigmented, smooth, round flat shaped colonies while *Aeromonas sobria* smooth, round, semi-translucent, greyish-white colour colonies. Isolated bacteria were identified morphologically and distinguished to positive and negative gram by Gram stain. Growths were purified by cultured on Nutrient agar at 37ºC for 24h, after that picked to bacterial identification using VITEK 2 system (Biomerieux- USA).

DNA extraction from Bacteria

G- spin DNA extraction kit, intron biotechnology, cat.No.17045 was used to extraction DNA of bacteria. In the table (1) below are the details and origins of the materials used in the process of extracting DNA from bacteria.

Table (1): The materials DNA extraction kit used in extracting DNA from bacteria.

No.	Material	Cat #	Company
1	Agarose	8100.11	Conda / USA
2	Red safe staining souluion	21141	Intron / Korea
3	6X Loading dye	21161	Intron / Korea
4	Ladder 100 bp	24073	Intron / Korea
5	Pre mix pcr	25025	Intron / Korea
6	TBE buffer 10 X	IBS.BT004	Conda / USA
7	Primer	---	Integrated DNA technologies /USA
8	G- spin DNA extraction kit	17045	intron biotechnology/Korea

Diagnosis of Gene

PCR amplification was carried out using the universal primer 16Sr RNA of gene as table (2) and mixture in table (3). Cycling condition as in table (4) preformed using a thermal cycler (GTC-96). The products of PCR were detected by gel electrophoresis and purity is measured under the 260/280 column of Nanodrop (Nanodrop (Nabi/ Korea).

PCR products were purified and sequenced in both directions using the BigDye Terminator v3.1 Cycle Sequencing kit on an ABI 3130 Genetic Analyzer (Applied Biosystems, Foster City, CA). Sequencing of gene was performed by macrogen Korea, Homology search was conducted using Basic Local Alignment Search Tool (BLAST) program which is available at the National Center Biotechnology Information (NCBI) online at (http://www.ncbi.nlm.nih.gov) and BioEdit program. The sequence was analysed in the nucleotide databases using the NCBI's Basic Local Alignment Search Tool Bio ID program to identify the sample and submitted to GenBank (ID).

Related sequences of sample or were obtained from the NCBI's nucleotide database (www.ncbi.nlm.gov/nucleotide) and included in the multiple alignment using the Bio ID program (Tamura *et al.*, 2011).

Table (2): The specific primer 16Sr RNA of gene.

Primer	Sequence	T (°C)	GC (%)	Product size
Forward	5'- AGAG TTTGA TCCTG GCTCAG- 3'	54.3	50.0	1250 base pair
Reverse	5'GGTT ACCTTGT TACGA CTT- 3'	49.4	42.1	

Table (3): Mixture of the specific interaction for diagnosis gene.

Components	Concentration
Taq PCR PreMix	5µl
Forward primer	10 picomols/µl (1 µl)
Reverse primer	10 picomols/µl (1 µl)
DNA	1.5µl
Distilled water	16.5 µl
Final volume	25µl

Results & Discussion

Through bacterial examination and diagnosis, whether using VITEK 2 system or using 16sr RNA genetic diagnosis technique, it was found that the cause of bacterial gill disease is two types of bacteria and in all samples of infected common carp. The disease causes great losses to fish farmers due to the high mortality rate.

Signs of diseases

Fish samples were collected from infected farms with this disease. It was observed that the fish is dispersed and not in groups, and they swim at an angle with their heads facing upward and make bubbles near the surface.

Fish in acute stages do not react to any stimuli and swim so calmly and solitarily that they can be caught by hand. Prevalence of infection in most locations was very high (more than 80%). In the gills of infected fish, the signs of inflammation were very clear through colour or changes as damage that can be seen with the naked eye, as in the fig. (1).

Clinical identification

Three isolates belong to two bacterial species of bacterial pathogen were identified. The identified bacterial species of BGD were Gram-negative include *Sphingomonas paucimobilis* and *Aeromonas sobria* were isolated from all collected fish. These species identified by VITEK 2 system and the Probability was high (Tables 4, 5, 6 and 7).

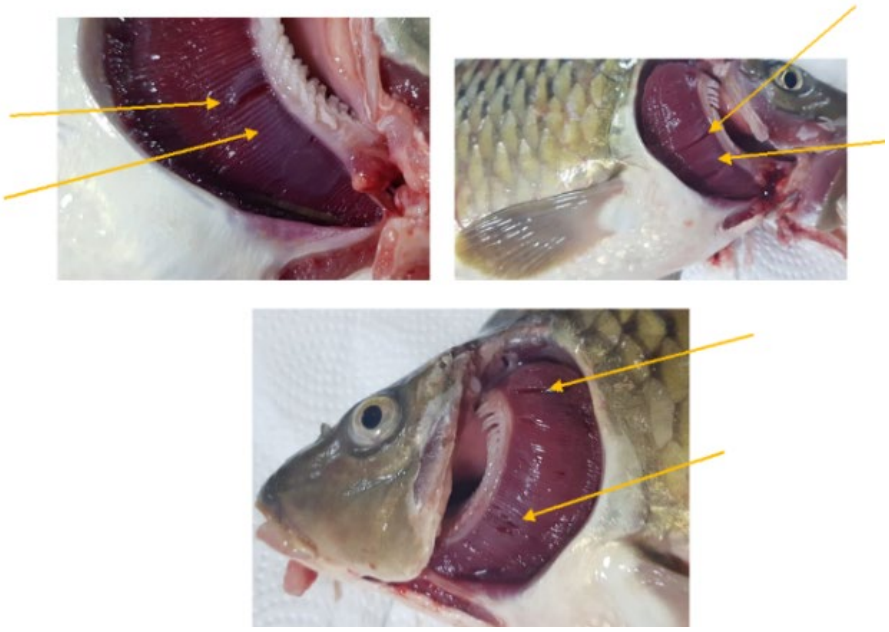

Fig. (1): Signs of infection (see arrows) with bacterial gill disease in *C. carpio*.

Table (4): The optimum condition of detection.

No.	Phase	Tm (°C)	Time	No. of cycle
1-	Initial Denaturation	94°C	5 min.	1 cycle
2-	Denaturation -2	94°C	45sec	35 cycles
3-	Annealing	56°C	1 min	
4-	Extension-1	72°C	1 min	
5-	Extension -2	72°C	7 min.	1 cycle

Table (4): The bacterial isolates diagnosed and the Probability of the diagnosis in using VITEK 2 system.

bacterial identification	Probability%	Time/h
Aeromonase soberia	96	5
Sphingomonas paucimobilis	95	4.82 7.50

Table (5): Identified species of *Sphingomonas paucimobilis* by Vitek 2 system.

Identification Information			**Analysis Time:**	7.50 hours		**Status:**	Final	
Selected Organism			95% Probability **Bionumber:**	**Sphingomonas paucimobilis** 1001201100100000				
ID Analysis Messages								

Biochemical Details																
2	APPA	+	3	ADO	-	4	PyrA	-	5	lARL	-	7	dCEL	-	9	BGAL	-
10	H2S	-	11	BNAG	-	12	AGLTp	-	13	dGLU	+	14	GGT	-	15	OFF	-
17	BGLU	-	18	dMAL	+	19	dMAN	-	20	dMNE	-	21	BXYL	-	22	BAlap	-
23	ProA	+	26	LIP	-	27	PLE	-	29	TyrA	+	31	URE	-	32	dSOR	-
33	SAC	-	34	dTAG	-	35	dTRE	-	36	CIT	-	37	MNT	-	39	5KG	-
40	lLATk	+	41	AGLU	-	42	SUCT	-	43	NAGA	-	44	AGAL	-	45	PHOS	-
46	GlyA	-	47	ODC	-	48	LDC	-	53	lHISa	-	56	CMT	-	57	BGUR	-
58	O129R	-	59	GGAA	-	61	lMLTa	-	62	ELLM	-	64	lLATa	-			

Table (6): Identified species of *Sphingomonas paucimobilis* by Vitek 2 system

Identification Information	**Analysis Time:**	4.82 hours	**Status:**	Final	
Selected Organism	95% Probability	**Sphingomonas paucimobilis**			
	Bionumber:	5401211150300000			
ID Analysis Messages					

Biochemical Details																
2	APPA	+	3	ADO	-	4	PyrA	+	5	lARL	-	7	dCEL	-	9	BGAL	+
10	H2S	-	11	BNAG	-	12	AGLTp	-	13	dGLU	+	14	GGT	-	15	OFF	-
17	BGLU	-	18	dMAL	+	19	dMAN	-	20	dMNE	+	21	BXYL	-	22	BAlap	-
23	ProA	+	26	LIP	-	27	PLE	-	29	TyrA	+	31	URE	-	32	dSOR	-
33	SAC	+	34	dTAG	-	35	dTRE	+	36	CIT	-	37	MNT	-	39	5KG	-
40	lLATk	+	41	AGLU	+	42	SUCT	-	43	NAGA	-	44	AGAL	-	45	PHOS	-
46	GlyA	-	47	ODC	-	48	LDC	-	53	lHISa	-	56	CMT	-	57	BGUR	-
58	O129R	-	59	GGAA	-	61	lMLTa	-	62	ELLM	-	64	lLATa	-			

Table (7): Identified species of *Aeromonas sorbia* by Vitek 2 system.

Identification Information	**Analysis Time:**	6.53 hours	**Status:**	Final	
Selected Organism	96% Probability	**Aeromonas sobria**			
	Bionumber:	1465613151510261			
ID Analysis Messages					

Biochemical Details																
2	APPA	+	3	ADO	-	4	PyrA	-	5	lARL	-	7	dCEL	-	9	BGAL	+
10	H2S	-	11	BNAG	+	12	AGLTp	+	13	dGLU	+	14	GGT	-	15	OFF	+
17	BGLU	-	18	dMAL	+	19	dMAN	+	20	dMNE	+	21	BXYL	-	22	BAlap	-
23	ProA	+	26	LIP	+	27	PLE	-	29	TyrA	+	31	URE	-	32	dSOR	-
33	SAC	+	34	dTAG	-	35	dTRE	+	36	CIT	+	37	MNT	-	39	5KG	-
40	lLATk	+	41	AGLU	-	42	SUCT	+	43	NAGA	+	44	AGAL	-	45	PHOS	-
46	GlyA	-	47	ODC	-	48	LDC	-	53	lHISa	-	56	CMT	+	57	BGUR	-
58	O129R	-	59	GGAA	+	61	lMLTa	+	62	ELLM	+	64	lLATa	-			

Genetic identification

DNA extracted of identified bacteria were analysed by PCR to detect 16Sr RNA of gene. All samples were showed positive PCR reaction. The results revealed distinct amplicon size (1250 bp) from all DNA isolates (Fig. 2). *A. soebia* recorded in NCBI under **ID: OR122346.1**, while two strains *Sphingomonas paucimobilis* was under **ID: OR121489.1**and **OR128365.1** respectively as following:

OR122346 *Aeromonas sobria* strain L10 16S ribosomal RNA gene, partial sequence:

```
   1 acacatgcaa gtcgagcggc agcgggaaag tagcttgcta cttttgccgg cgagcggcgg
  61 acgggtgagt aatgcctggg gatctgccca gtcgaggggg ataactactg gaaacggtag
 121 ctaataccgc atacgcccta cgggggaaag caggggacct tcgggccttg cgcgattgga
 181 tgaacccagg tgggattagc tagttggtga ggtaatggct caccaaggcg acgatcccta
 241 gctggtctga gaggatgatc agccacactg gaactgagac acggtccaga ctcctacggg
 301 aggcagcagt ggggaatatt gcacaatggg ggaaaccctg atgcagccat gccgcgtgtg
 361 tgaagaaggc cttcgggttg taaagcactt tcagcgagga ggaaaggttg gtagctaata
 421 actgccagct gtgacgttac tcgcagaaga agcaccggct aactccgtgc cagcagccgc
 481 ggtaatacgg agggtgcaag cgttaatcgg aattactggg cgtaaagcgc acgcaggcgg
 541 ttggataagt tagatgtgaa agccccgggc tcaacctggg aattgcattt aaaactgtcc
 601 agctagagtc ttgtagaggg gggtagaatt ccaggtgtag cggtgaaatg cgtagagatc
 661 tggaggaata ccggtggcga aggcggcccc ctggacaaag actgacgctc aggtgcgaaa
 721 gcgtggggag caaacaggat tagataccct ggtagtccac gccgtaaacg atgtcgattt
 781 ggaggctgtg tccttgagac gtggcttccg gagctaacgc gttaaatcga ccgcctgggg
 841 agtacggccg caaggttaaa actcaaatga attgacgggg gcccgcacaa gcggtggagc
 901 atgtggttta attcgatgca acgc
```

OR128365.1 *Sphingomonas paucimobilis* strain E6-5 16S ribosomal RNA gene, partial sequence

```
  1 gtgcgtagca gcagctacca tgcagtcgag cggatgatgg agcttgctcc ttgattcaac
 61 ggcggacggg tgagtaatgc ctatgaatct gcctggtagt gggggacaac gtttcgaagg
121 gaacgctaat accgcatacg tcctaccgga gaaagtgggg gatcttccga cctcccgcta
181 tctaatgaac ctacgtcgga ttaactagtt ggtgaggtaa aggctcaccc ggcgaccatc
241 cataactggt ctgacaggat gatcaatcac actggaactg agacacggtc cagactccta
301 cgggaggcaa cagtggggaa tattggacaa tgggcgaaag cctgatccag ccatgccgcg
361 tgtgtgaaga aggtcttcgg attgtaaagc actttaagtt gggaggaagg gcagaagtta
421 ataccttgct gttttgacgt taccaacaga ataacaccgg ctaacttcgt gccagccgcc
481 gcggtaattc atacaa
```

OR121489 *Sphingomonas paucimobilis* strain K3 16S ribosomal RNA gene, partial sequence

Sequences of 16S rRNA of A. soebia strain L10, *Sphingomonas paucimobilis* strain K3 and *Sphingomonas paucimobilis* strain E6 - 5 isolates were compared with GenBank sequences through BLAST program. The results confirmed identification of the studied bacteria with 100% as A. sobria, 87% as S. paucimobilis strain K3 and 81% as S. paucimobilis strain E6-5 identified with partial sequence ID MK828155.1, JN540025.1 and KY938114.1 respectively.

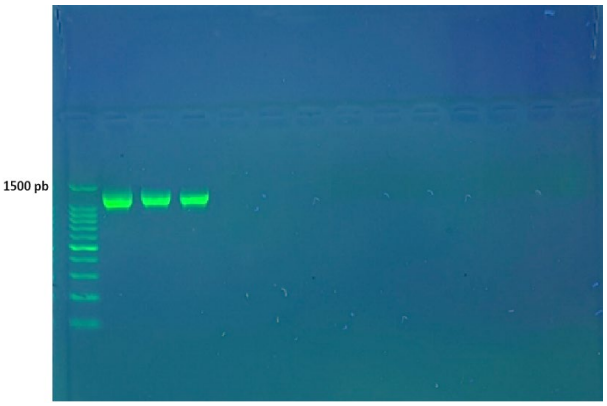

Fig. (2): PCR product the band size 1250 bp. The product was electrophoresis on 2% agarose at 5 volt/cm^2. 1x TBE buffer for 1hr. L: DNA ladder (100), 1, 2 and 3: samples.

Discussion

Pathogenic diseases are more common and broadly classified as bacterial diseases, and they are typically associated with high mortality and morbidity rates, as well as widespread negative (Mala & Abdullah, 2022). Major bacterial pathogens responsible for infectious diseases in *C. carpio* have a negative economic impact on aquaculture and decrease the quantity of fish production (Mahmood *et al*., 2023). The most common pathogen of gram-negative isolated from *C. carpio* were from fish farms in Sulaymaniyah City, Iraq was *A. sobria* (Mahmood *et al*., 2023).

Bacterial gill disease is one of the diseases that posed a real threat to fish farms in the study area, which necessitated studying the causes of this disease and identifying the bacterial species present in fish farms in Basrah Governorate. The health problems caused by this disease and the huge economic losses in the agricultural sector in Basrah province were very clear and led in addition to more use of antibiotics. The selection of this study was designed as a first step towards reducing the damage through accurate diagnosis of the pathogens and identification of the bacterial diversity causing this disease. Two techniques, namely VITEK 2 and genetic diagnosis technology (16S rRNA), were used to confirm the diagnosis of bacterial species (*A. sobria* and *S. paucimobilis*). The diagnosis using the VITEK method and the genetic method was very consistent, as *A. sobria* was diagnosed conclusively, and there was a difference in the analysis time of VITEK 2 system results for the *S. paucimobilis*, as it was revealed through genetic examination that there were two strains of this species. The study of the causes of this disease genetically and the recorded of the species *S. paucimobilis* is the first in fish farms of Basrah Governorate, as the bacterial strains were registered in GenBank sequences through BLAST program for the first time in the previous study, *A. sobria* was the

predominant species which caused with health problems in semi-closed and pond systems (Jassim *et al*., 2019). In Central Europe, infections caused by *Aeromonas* spp. are the most common among bacterial fish diseases, causing motile *Aeromonas septicaemia* (Olesen *et al*., 2015)

Sphingomonas paucimobilis is a gram-negative pathogen that causes urinary tract infections, diarrhea, septicemia, and wound infections in human (Ahmed *et al*., 2021). The first record of *S. paucimobilis* in Iraq by Al-Jubouri *et al.* (2022), which was discovered in common carp cultured in floating cages at the Al-Hilla River.

Gram-negative bacteria commonly known to be pathogenic to fish, like *Aeromonas* spp., *Flavobacterium* spp., *Pseudomonas* spp., and *S. putrefaciens* are replaced by other species, which until now have not been known to be virulent or even conditionally pathogenic to fishes (Pękala-Safińska, 2018). Several microbial pathogens are known to cause gill disease and, in many instances, multiple pathogens or factors can be involved in the disease, resulting in complex gill disease (CGD) (O'Halloran *et al*., 2022). Therefore, monitoring the change in the causes of bacterial gill disease is important not only to identify the pathogenic bacteria, but also to provide an important indication that there are environmental changes that may be complex and have led to this change, or that the matter is related to the management of fish farms and the physiological state of the fish.

Conclusions

Based on the results obtained and their comparison with previous studies, it can be concluded that the bacterial pathogens that cause bacterial gill disease vary from location to another and even from time to time. Even within the same environment, changes in the species causing this disease can occur. Therefore, several factors may play a role in stimulating certain species of bacteria to reach high microbial loads that may cause infection, and changes in these factors are what cause the change in the species or strains causing the disease.

Acknowledgments

The authors would like to express their sincere gratitude to the Marine Science Center, University of Basrah, for providing laboratory facilities and technical support.

Contributions of authors

A.A.R.J, conducted fish sample collection and was involved in the isolation and identification of bacterial pathogens. He also contributed significantly to data interpretation and manuscript writing.

E.A.A, performed laboratory isolation and identification using different microbiological and molecular techniques. She also contributed significantly to data interpretation and manuscript writing.

A.R.A., performed laboratory isolation and identification using different microbiological and molecular techniques.

A.Y.H.: performed laboratory isolation and identification using different microbiological and molecular techniques.

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Conflict of interest

The authors declare that there is no conflict of interest regarding the publication of this article

Ethical approval

All ethical guidelines concerning the care and handling of fish, as issued by national and international organizations, were strictly followed in this study. Fish sampling was conducted with the permission of the farm owners, and all efforts were made to minimize stress and suffering of the animals.

References

Abdulrahman, N.M.A., Hussein, A.J., & Sulaiman, S.S., & Rasul, B.A. (2020). Survey of fish diseases in Ranya (raparin administration)/ Sulaimaniya governorate; case study. *Basrah Journal of Veterinary Research, 19*(3), 32-47. https://doi.org/10.23975/bjvetr.2020.174095

Ahmed, A.M., Ali, F.A., Al-Sudani, S.F.K., Othman, P. A., Nuri, B.H., Ali, B.H.M., & Hameed, H.A. (2021). *Sphingomonas paucimobilis* bacteria isolation from different clinical samples of a nosocomial infection in Erbil City. *Al-Qadisiyah Journal of Pure Science*, *26*(4). Article 49. https://doi.org/10.29350/qjps.2021.26.4.1336

Al-Jubouri, M.O., Al-Haider, S.M., Judi, H.K., & Judi, R.K. (2022). A first record of *Sphingomonas paucimobilis* isolated from common carp (*Cyprinus carpio*) cultivated in floating cages at Al-Hilla River, Babylon Province, Iraq: Antibiotic Resistance. *Life Science Archives, 8*(6), 2529-2535. https://doi.org/10.22192/lsa.2022.8.6.2

AlShammari, N.A.H.; Al-Taee, A.M.R. & Khamees, N.R. (2019). Bacterial disease agents of *Cyprinus carpio* from some farms in Basrah. *Ecology, Environment and Conservation Paper, 25*(4), 1554-1558.472. https://www.envirobiotechjournals.com/issues/article_abstract.php?aid=10105&iid=287&jid=3

Bakhtiyar, Y., Yousuf, T., & Arafat, M.Y. (2022). Chapter 13 - *Bacterial gill disease and aquatic pollution: a serious concern for the aquaculture industry*. Pp, 269-278. In Dar, G.H., Bhat, R.A., Qadri, H., Al-Ghamdy, K.A., & Hakeem, K.R. (Editors). *Bacterial Fish Diseases*. Academic Press, 424pp. https://doi.org/10.1016/B978-0-323-85624-9.00012-9

Mala, H.H., & Abdullah, S.M.A. (2022). Isolation and identification of some Bacterial Species from Common carp (*Cyprinus carpio* Linnaeus, 1758) in Taqtaq District in Erbil Province, Kurdistan Region, Iraq. *Zanco Journal of Pure and Applied Sciences ZJPAS, 34*(5), 131–140. https://doi.org/10.21271/ZJPAS.34.5.12

Irshath, A.A., Rajan, A.P., Vimal, S., Prabhakaran, V.-S., & Ganesan, R. (2023). Bacterial pathogenesis in various fish diseases: Recent advances and specific challenges in vaccine development. *Vaccines*, *11*(2), 470. https://doi.org/10.3390/vaccines11020470

Jassim, A.A.R. (2019). Cultured fish diseases in Basrah province for the years 2014, 2015 and 2016. *Iraqi Journal of Aquaculture, 32*(Special Issue 2), 75-84. https://doi.org/10.58629/ijaq.v16i1.464

Jassim, A.A.R. (2024). Survey of fish diseases in Basrah province farms during 2018-2020. *Egyptian Journal of Aquatic Biology and Fisheries, 28*(5), 1793-1806. https://doi.org/10.21608/ejabf.2024.387022

Jassim, A.A.R., Abdulhameed, D.B., & Al Shammari, N.R. (2019). Bacterial Fish Diseases in some Semi-close Aquaculture Systems in Basrah Province, Iraq. *Basrah Journal of Agricultural Sciences*, *32*, 75–84. https://doi.org/10.37077/25200860.2019.258

O'Halloran, E., Mooney, R., Rodgers, K., & Henriquez, F.L. (2022). Microbial interactions that contribute to gill disease in Aquaculture. *Parasitologia, 2*(4), 266-291. https://doi.org/10.3390/parasitologia2040023

Olesen, N.J., & Vendramin, N. (2016). Overview of the disease situation and surveillance in Europe in 2015. In: *20th Annual workshop of the National Reference Laboratories for fish diseases*, National Veterinary Institute, Technical University of Denmark, Copenhagen, Denmark, 2016, 13–15. https://www.eurl-fish-crustacean.eu/-/media/sites/eurl-fish-crustacean/fish/annual-workshop/20th-aw-2016/report-20th-aw-2016.pdf

Mahmood, R.M., Muhammed Ameen, S., & Abdullah, S.M.A. (2023). Record of aerobic bacterial species from the cyprinid fish *Cyprinus carpio* from fish farms in Sulaimani Province, Kurdistan Region, Iraq. *Applied Ecology and Environmental Research, 21*(6), 5607-5624.

http://dx.doi.org/10.15666/aeer/210656075624

Pękala-Safińska, A. (2018). Contemporary threats of bacterial infections in freshwater fish. *Journal of Veterinary Research,62*(3),261-267. https://doi.org/10.2478/jvetres-2018-0037

Shendure, J., Balasubramanian, S., Church, G.M., Gilbert, W., Rogers, J., Schloss, J.A., & Waterston, R.H. (2017). DNA sequencing at 40: past, present and future. *Nature*, *550*, 345-353. https://doi.org/10.1038/nature24286

Senthamarai, M.D., Rajan M.R., & Bharathi P.V. (2023). Current risks of microbial infections in fish and their prevention methods: A review. *Microbial Pathogenesis*, *185*, 106400, https://doi.org/10.1016/j.micpath.2023.106400

Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M., & Kumar, S. (2011). MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Molecular biology and evolution*, *28*(10), 2731–2739. https://doi.org/10.1093/molbev/msr121

Zamparo, S., Orioles, M., Brocca, G., Marroni, F., Castellano, C., Radovic, S., Mandrioli, L., Galeotti, M., & Verin, R. (2024). Novel insights on microbiome dynamics during a gill disease outbreak in farmed rainbow trout (*Oncorhynchus mykiss*). *Scientific Reports*, *14*, 17791. https://doi.org/10.1038/s41598-024-68287-w

العزل والتشخيص الجزيئي لمسببات مرض الغلاصم البكتيري المعزولة من أسماك الكارب الشائع (*Cyprinus carpio*) المستزرعة في الأحواض الترابية بمحافظة البصرة، العراق

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المستخلص: جمعت خمس عشرة عينة من أسماك الكارب الشائعة من ثلاث مزارع سمكية مصابة بمرض الخياشيم البكتيري بشكل وبائي، وذلك لتحديد البكتيريا المسببة للمرض. دُرِس مرض الخياشيم البكتيري في أسماك الكارب الشائعة المستزرعة في محافظة البصرة، العراق. سُجلت العلامات المرضية المتعلقة بسلوك الأسماك والتلف الجسيم في أنسجة الخياشيم. شُخصت مسببات مرض الخياشيم البكتيري باستخدام تقنية VITEK 2 بعد عزل البكتيريا وتنقيها على أوساط زرعية مناسبة، وتأكد التشخيص جينيًا باستخدام تقنية الحمض النووي الريبوزي 16 .Sشملت النتائج تسجيل نوعين من البكتيريا المسببة للمرض، وهما *Aeromonas sobria* و*Sphingomonas paucimobilis*، وقد عُزل كلا النوعين البكتيريين من جميع الأسماك التي جُمعت. سُجلت *A. sobria* في قاعدة بيانات NCBI تحت المعرفOR122346.1 :، بينما سُجلت عزلتان من *S. paucimobilis* تحت المعرفين : OR121489.1 و OR128365.1على التوالي. أشارت النتائج التي تم الحصول عليها إلى أن مسببات الأمراض البكتيرية كانت متغيرة مع اختلاف الموقع والوقت، حتى وان كانت في بيئة متشابهه، لذا فإن هذا الاختلاف سيؤدي إلى تغيير في الأنواع أو السلالات المسببة للمرض.

الكلمات المفتاحية: *Aeromonase sobria* الاحواض، الاسماك، *Sphingomonas paucimobilis*.