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Microbial profiling and safety assessment of fish marketed in UAE: a quantitative, biochemical, and molecular study

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ABSTRACT

This study evaluated the microbial quality of two commonly consumed fish species, *Carangoides chrysophrys* (Jesh sal) and *Pomadasys argenteus* (Silver grunt), sold in a fish market in the Emirate of Sharjah, UAE. Bacterial loads, diversity, and presence of opportunistic pathogens were assessed using total viable counts (TVC), biochemical identification (VITEK), and molecular detection (PCR). Statistical analysis revealed that overnight/older fish samples had significantly higher bacterial loads compared to fresh/morning samples ($p < 0.05$). Despite this increase, all bacterial loads remained within acceptable limits set by ICMSF and GCC food safety standards. VITEK identified diverse bacterial genera, including *Pseudomonas*, *Aeromonas*, *Sphingomonas*, *Pasteurella*, and *Acinetobacter*, with *Proteus mirabilis* and *Citrobacter braakii* recognized as opportunistic pathogens. PCR analysis confirmed the presence of these pathogens using species-specific primers, validating their detection through successful gene amplification. The findings highlight the importance of proper handling, cold storage ($\leq 4^{\circ}\text{C}$), and routine monitoring to minimize bacterial growth and ensure seafood safety. This study also suggests environmental sampling (water, ice, handling surfaces) in future research to trace contamination sources. The integration of molecular techniques such as PCR can enhance pathogen detection, ensuring improved food safety practices in fish markets.

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1. Introduction

Fish and fishery products play a crucial role in global food security and nutrition, serving as a vital source of high-quality protein, essential vitamins, minerals, and healthy omega-3 fatty acids for millions of people worldwide (FAO, 2020). In 2018, global fish consumption reached an average of 20.5 kg per capita, with fish accounting for about 17% of the global population's intake of animal proteins (FAO, 2020). The United Arab Emirates (UAE) has a strong cultural and economic connection to the fishing industry, with an annual fish consumption per capita of 28.6 kg in 2017 (FAO, 2022). The country has also been actively promoting the development of its aquaculture sector to enhance food security and meet the growing demand for seafood products (Fischbach, 2018).

Despite the numerous health benefits associated with fish consumption, the perishable nature of fish and seafood makes them susceptible to rapid

microbial contamination and spoilage (Tahiluddin et al., 2022). The microbial quality of fish is influenced by a wide range of factors, including the aquatic environment, fish species, harvest season, handling practices, and storage conditions (Stratev et al., 2015; Alnofaie et al., 2024). Improper handling of fish by consumers creates a high risk of spread of bacterial diseases that may reach epidemic status; therefore, personal hygiene practices are important to save fish from microbial contamination and spoilage (Alnofaie et al., 2024).

Bacterial pathogens such as *Vibrio*, *Salmonella*, *Listeria*, *Clostridium*, and *Staphylococcus* are frequently implicated in seafood-related foodborne illness outbreaks (Iwamoto et al., 2010). Therefore, maintaining the microbial quality of fish and seafood products is of utmost importance to ensure food safety and protect public health.

In the UAE, *Carangoides chrysophrys* (Jesh sal) and *Pomadasys argenteus* (Silver grunt) are two commercially important fish species. Jesh sal, a member of

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the jack family (*Carangidae*), is characterized by its silvery body with dark brown to blackish markings (Belen, 2014). *Pomadasys argenteus* (Silver grunt) is a commercially important fish species in UAE, known as Nagroor, belongs to the grunt family (*Haemulidae*) and is widely distributed in the Indo-West Pacific (from Red Sea to Fiji) (Al-Harbi & Gabr, 2024). Assessing the microbial quality of these fish species is essential to ensure their safety for human consumption and to maintain consumer confidence in the local seafood market as well as the responsibility of the authorities and those who produce and market the processing product (Nguyen et al., 2023).

Traditional methods for assessing the microbial quality of fish, such as total viable counts (TVC) and biochemical tests, are widely used in the seafood industry for quality control purposes (Odeyemi et al., 2018). However, these methods can be time-consuming and may not always provide accurate identification at the species level. In recent years, rapid and reliable molecular techniques, such as polymerase chain reaction (PCR), have emerged as powerful tools for detecting specific bacterial pathogens in fish and seafood products (Mangal et al., 2016). Polymerase chain reaction (PCR) is one of the most common molecular techniques, and it is widely used to detect fish pathogenic bacteria (Mitiku et al., 2023) rapidly. These molecular methods offer high sensitivity, specificity, and the ability to detect even low levels of target pathogens, making them valuable tools for ensuring the safety and quality of seafood.

Several opportunistic pathogens, including *Proteus mirabilis*, *Proteus vulgaris*, *Citrobacter freundii*, *Citrobacter braakii*, *Acinetobacter lwoffii*, and *Sphingomonas paucimobilis*, have been reported in fish and aquatic environments (Austin, 2006). These bacteria can cause infections in immunocompromised individuals and have been associated with various fish diseases (Kumaran et al., 2010). Developing species-specific PCR assays for the detection of these pathogens can facilitate their rapid identification and help in implementing effective control measures to prevent their spread in the seafood supply chain.

The present study aimed to evaluate the microbial quality of Jesh sal and Silver grunt sold in fish market, UAE, using a combination of microbiological and molecular methods. The specific objectives of the study were to (i) determine the total viable bacterial counts in fresh and overnight/older fish samples, (ii) identify the predominant bacterial genera using VITEK biochemical tests, and (iii) detect the presence of opportunistic pathogens using species-specific PCR assays. The findings of this study will contribute to a better understanding of the microbial ecology of these commercially important fish species and

highlight the importance of proper handling and storage practices to ensure the safety and quality of seafood products.

Moreover, the results of this study will provide valuable insights into the prevalence of opportunistic pathogens in Jesh sal and Silver grunt, which can help in developing targeted interventions to control their presence in the seafood supply chain. The application of molecular techniques, such as species-specific PCR, will demonstrate the potential of these methods for rapid and accurate detection of bacterial pathogens in fish and seafood products. This study will also emphasize the need for regular monitoring of the microbial quality of commercially important fish species to ensure compliance with food safety regulations and to protect consumer health.

In conclusion, assessing the microbial quality of Jesh sal and Silver grunt using a combination of microbiological and molecular methods will provide a comprehensive understanding of the microbial ecology of these fish species and the presence of opportunistic pathogens. The findings of this study will contribute to the development of effective strategies for ensuring the safety and quality of seafood products in the UAE and will highlight the importance of adopting advanced molecular techniques for the rapid detection of bacterial pathogens in the seafood industry.

2. Materials and methods

2.1. Sample collection and preparation

A total of 13 fish samples, consisting of 6 Jesh sal (*Carangoides chrysophrys*) samples (3 fresh morning catch, 3 overnight left catch) and 7 Silver grunt (*Pomadasys argenteus*) samples (3 fresh morning catch, 4 overnight left catch) were randomly selected from different vendors to ensure unbiased representation of the microbial quality in the market. Selection criteria were based on availability at the market, fish freshness (morning vs. overnight samples), and handling conditions. Each fish sample (25 g) was aseptically dissected, homogenized with 225 mL of buffered peptone water (BPW) in a stomacher bag, and mixed for 30–60 s using a stomacher mixer (Interscience, France).

2.2. Enumeration of total viable aerobic bacteria (TVAB)

Serial dilutions of the homogenized samples were prepared up to 10^{-5} in peptone water (HIMEDIA, India). Appropriate dilutions were poured plated on plate count agar (PCA; Merck, Germany) and incubated at 30 °C for 24–48 h for Jesh sal samples and

at 37 °C for 48 h for Silver grunt samples. Plates with 30–300 colonies were counted using a colony counter to determine the total viable aerobic counts (TVAC).

2.3. Isolation and identification of bacteria

Homogenized samples were streaked on selective media, including thiosulfate citrate bile salt sucrose agar (TCBS; Merck, Germany) for Jesh sal samples and Salmonella Shigella agar (SS agar) for Silver grunt samples. Plates were incubated at 37 °C for 24 h. Isolated colonies from plate count agar (PCA), TCBS, and SS agar were purified on nutrient agar (HIMEDIA, India) and tryptic soy agar (Mastgroup, UK) for Jesh sal and Silver grunt samples, respectively. Gram staining was performed, and biochemical identification was carried out using the VITEK 2 Compact system (Biomerieux, France) with Gram-negative (GN) cards.

2.4. Molecular analysis

Three bacterial strains from each of Jesh sal overnight left catch samples (*Proteus mirabilis*, *Acinetobacter lwoffii*, and *Sphingomonas paucimobilis*) and Silver grunt samples (*Citrobacter freundii*, *Citrobacter braakii*, and *Proteus mirabilis*) were selected for molecular analysis based on their potential pathogenicity.

2.4.1. Genomic DNA extraction and quantification

Isolated colonies were grown overnight in nutrient broth (HIMEDIA, India) at 37 °C with agitation. Genomic DNA was extracted using the Isolate II Genomic DNA Kit (Bioline, UK) following the manufacturer's protocol with modifications for increased yield. DNA concentration and purity were assessed using a NanoDrop One spectrophotometer (ThermoFisher, USA), with acceptable A260/A280 and A260/A230 ratios of 1.8 and 1.8–2.2, respectively.

2.4.2. Conventional PCR

PCR amplification was conducted using species specific primers targeting the following genes: ureR gene (*Proteus mirabilis*), cfa gene (*Citrobacter freundii*/*Citrobacter braakii*), rpoB gene (*Acinetobacter lwoffii*), and 16S-23S rRNA ITS gene (*Sphingomonas paucimobilis*); primer sequences are provided in Table 1. PCR reactions were prepared using a Biolab kit (Biolab, UK) and run in a Biorad T100 thermal cycler (Biorad, USA), with the following cycle conditions: Initial denaturation at 95 °C for 5 min, 35 cycles consisting of denaturation at 95 °C for 5 min, annealing optimized at 50–58 °C for 30 s (gradient PCR was used to determine optimal annealing temperature, and extension 72 °C for 1 min; and a final extension at 72 °C for 10 min. PCR products were visualized on a 2% agarose gel stained with ethidium bromide, run at 100 V for 50 min, and imaged using a Gel Doc EV Imager (BioRad, USA).

2.5. Statistical analysis

Student's t-test was performed using Microsoft excel. Statistical significance was set at $p < 0.05$, and results were reported as mean $\pm$ standard deviation (SD).

3. Results

3.1. Microbial load in fish samples

Total Viable Aerobic Counts (TVC) were assessed for both *Carangoides chrysophrys* (Jesh sal) and *Pomadasys argenteus* (Silver grunt) samples. Statistical analysis using a student's t-test confirmed that overnight or older fish samples exhibited significantly higher bacterial loads compared to fresh or morning samples ($p < 0.05$). In Jesh sal, overnight samples (SO) had TVC values ranging from 60×10^3 to 90×10^3 CFU/g, while fresh samples (SM) exhibited lower bacterial counts, ranging from 5×10^3 to 50×10^3 CFU/g (Figure 1). The difference in bacterial load between overnight and fresh samples was statistically significant for all samples: Sample 1 ($p = 0.018$), Sample 2 ($p = 0.027$), and Sample 3 ($p = 0.003$).

Table 1. Specific primer pairs used in the conventional PCR experiments for the detection of *Citrobacter freundii*/*Citrobacter braakii*, *Proteus mirabilis*, *Acinetobacter lwoffii*, and *Sphingomonas paucimobilis* (obtained from published literature) in Silver grunt and Jesh sal samples.

Gene	Primers	Length (bp)	Primer sequence (5' to 3')	Amplification products	Target organism	Reference
cfa	Crt4-F	19	TTGGCGTCCAGCGCATTCA	100 bp	<i>Citrobacter freundii</i> , <i>Citrobacter braakii</i>	Kacálková et al. (2005)
	Crt4-R	21	AATTCCAGCCTTCGGCAAACG			
ureR	UreR-F	19	GGTGAGATTGTATTAATGG	225 bp	<i>Proteus mirabilis</i>	Zhang et al. (2013)
	UreR-R	20	ATAATCTGGAAGATGACGAG			
rpoB	Alwo-F	20	CCGTGTCGGTCTGGTTCGTGTA	302 bp	<i>Acinetobacter lwoffii</i>	Li et al. (2016)
	Alwo-R	19	CCGGCGTTTCAATTGGACATAC			
16S-23S rRNA ITS	1492-F	18	AAGTCGTAACAAGGTAACC	729 bp	<i>Sphingomonas paucimobilis</i>	Tokajian et al. (2016)
	115-R	18	GGGTTTCCCATTCAG			

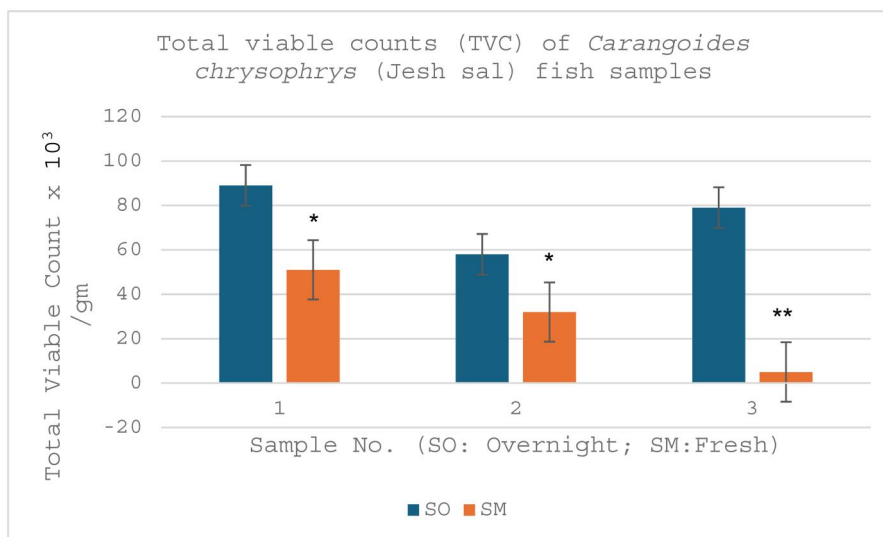


Figure 1. Total viable aerobic counts (TVAC) of *Carangoides chrysophrys* (Jesh sal) fish samples. The overnight (left catch) Jesh sal represented by SO1 to SO3 show higher bacterial counts compared to fresh morning catch ones (SM1 to SM3). Error bars represent mean $\pm$ standard deviation (SD). T-test assuming equal variance was used to compare fresh and overnight samples (* $p < 0.05$, ** $p < 0.005$).

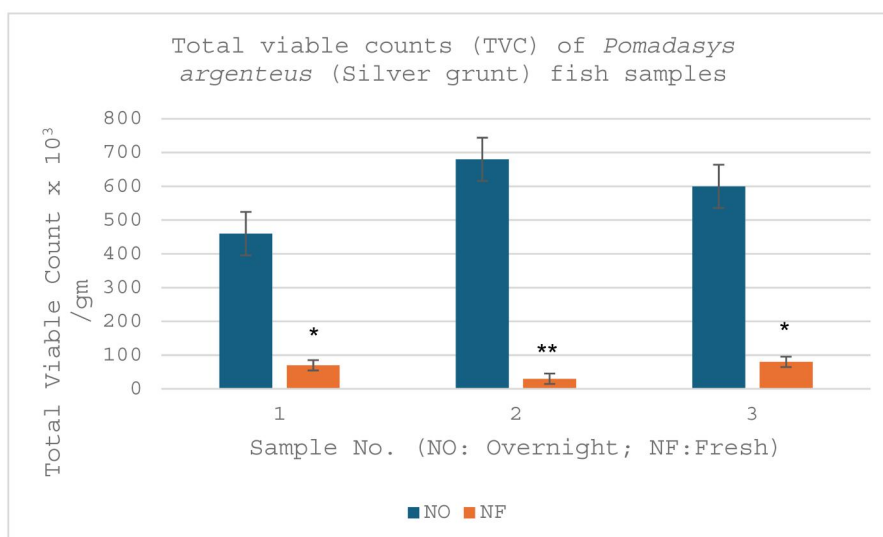


Figure 2. Total viable aerobic counts (TVAC) of *Pomadasys argenteus* (Silver grunt) fish samples. The figure shows that the overnight left catch fish (NO1 to NO3) samples have higher bacterial loads than morning catch (NF1-NF3) samples. Error bars represent mean $\pm$ standard deviation (SD). T-test assuming equal variance was used to compare fresh and overnight samples (* $p < 0.05$, ** $p < 0.005$).

Similarly, in Silver grunt, older fish samples (NO) processed 14 h after arrival had TVC values ranging from 450×10^3 to 680×10^3 CFU/g, whereas fresh samples (NF) processed within two hours of arrival had significantly lower bacterial counts, ranging from 20×10^3 to 90×10^3 CFU/g (Figure 2). The p-values for each sample comparison were as follows: Sample 1 ($p = 0.015$), Sample 2 ($p = 0.006$), and Sample 3 ($p = 0.019$), confirming significant differences between fresh and overnight samples.

3.2. Bacteria diversity and identification

Bacterial diversity in the fish samples was analyzed using the VITEK 2 Compact system for biochemical

identification. For Jesh sal fish samples, results indicated that in overnight left catch, genera of *Acinetobacter* and *Sphingomonas* are more dominant than other one as compared to morning catch fish which shows four different genera (*Pseudomonas*, *Enterobacter*, *Sphingomonas*, and *Stenotrophomonas*) with no dominance of one genus over the other. Moreover, seven distinct bacterial species were identified from the overnight catch (SO), compared to four species from the morning catch (SM) (Figure 3). These included *Proteus mirabilis*, *Aeromonas salmonicida*, *Sphingomonas paucimobilis*, *Acinetobacter lwoffii*, *Pseudomonas* spp., *Citrobacter braakii*, and *Pasteurella testudinis*.

For bacterial diversity in *Pomadasys argenteus* (Silver grunt), results indicated that in overnight left

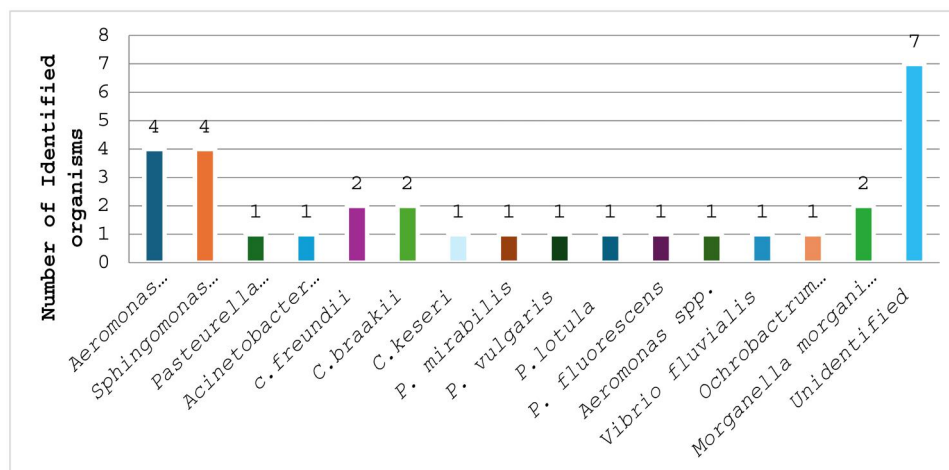


Figure 3. Bacterial diversity in *Carangoids Chrysophrys* (Jesh sal) and *Pomadasys argenteus* (Silver grunt). Bacterial species were identified from Jesh sal.

Table 2. Most prevalent bacterial species in both fresh and overnight samples.

Bacterial Species	Jesh sal (SM)	Jesh sal (SO)	Silver grunt (NF)	Silver grunt (NO)
<i>Proteus mirabilis</i>	–	+	–	+
<i>Aeromonas salmonicida</i>	+	+	+	+
<i>Sphingomonas paucimobilis</i>	–	+	–	+
<i>Acinetobacter lwoffii</i>	–	+	–	+
<i>Pseudomonas aeruginosa</i>	+	+	+	+
<i>Citrobacter freundii</i>	–	–	+	+

catch (old), genus *Citrobacter* is more dominant than other genera as compared to morning catch fish (fresh) which shows five different genera (*Pseudomonas*, *Citrobacter*, *Vibrio*, *Aeromonas*, and *Morganella*) with no dominance of one genus over the other. Moreover, the most encountered species were *Citrobacter* spp. (2 isolates *C. freundii*, 2 isolates *C. braakii* and 1 isolate *C. kesi*) which were found in old fish samples except for *C. kesi*, found in fresh fish. Followed by *Morganella morgani ssp sibonii* (2 isolates), which was found on both old and fresh samples, and *Proteus* spp. (1 isolate *P. mirabilis* and 1 isolate *P. vulgaris*), found in old fish and *Pseudomonas* spp. (1 isolate *P. lotula* and 1 isolate *P. fluorescens*) in fresh fish. After that comes *Aeromonas* spp. (either *hydrophilia/caviae*), *Vibrio fluvialis*, and *Ochrobactrum anthropi* (1 isolate each), which were found in fresh fish samples. However, three isolates were not identified.

Similarly, in Silver grunt samples, VITEK analysis identified 38 bacterial isolates, with the majority being Gram-negative opportunistic pathogens. The most common species isolated were *Citrobacter freundii*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii* (Table 2). Moreover, *Pseudomonas aeruginosa*, and *Aeromonas salmonicida* were more prevalent in both fish samples regardless of their conditions, fresh or overnight catch.

Results of VITEK microbiological identification of the various bacterial isolates from the fresh and

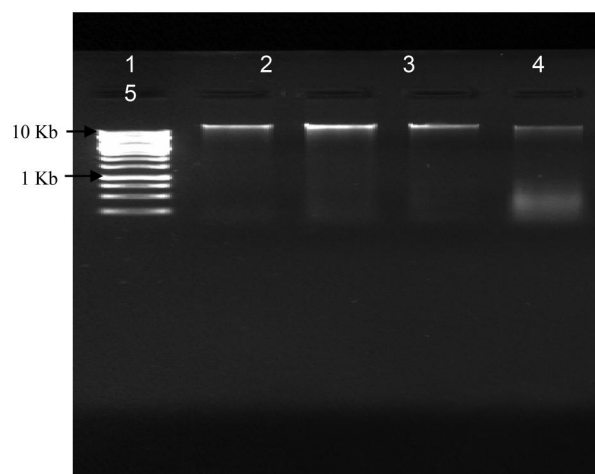


Figure 4. Gel electrophoresis of genomic DNA extracted from bacterial isolates. A 1% agarose gel electrophoresis confirms the extraction of genomic DNA from bacterial isolates collected from silver grunt samples. Lane 1: 1Kb ladder, lane 2: *Citrobacter braakii*, lane 3: *Proteus mirabilis*, lane 4: *Acinetobacter lwoffii*, and lane 5: *Sphingomonas paucimobilis*.

overnight left catch fish samples indicates an excellent confidence of identification with a probability of 90% and more (Data not shown).

3.3. Molecular identification of bacterial pathogens

Genomic DNA was successfully isolated from *Citrobacter braakii*, *Proteus mirabilis*, *Acinetobacter lwoffii*, and *Sphingomonas paucimobilis* (Figure 4).

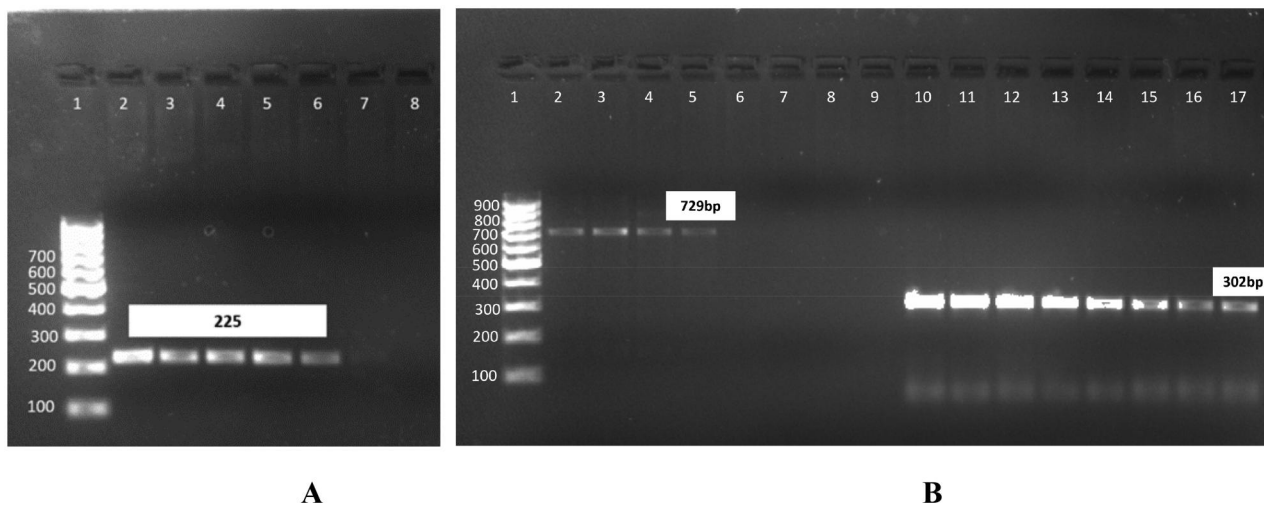


Figure 5. PCR detection of bacterial pathogens in *carangoides chrysophrys* (Jesh sal) fish samples. (A): Two specific primers targeting *ureR* gene were used for PCR amplification to detect *P. mirabilis*. Lane 1 shows 100 bp DNA ladder, lanes 2 through 7 (225 bp), and lane 8 is a negative control. (B): Two pairs of specific primers targeting *rpoB* gene were used for PCR amplification to detect *Acinetobacter lwoffii*. Lane 1 shows 100 bp DNA ladder, lanes 10 through 17 (302 bp), and 16S-23S rRNA ITS gene were used to detect *Sphingomonas paucimobilis*, lanes 2 through 5 (729 bp), and lanes 6 through 9 are negative controls. The PCR products were visualized on a 2% agarose gel.

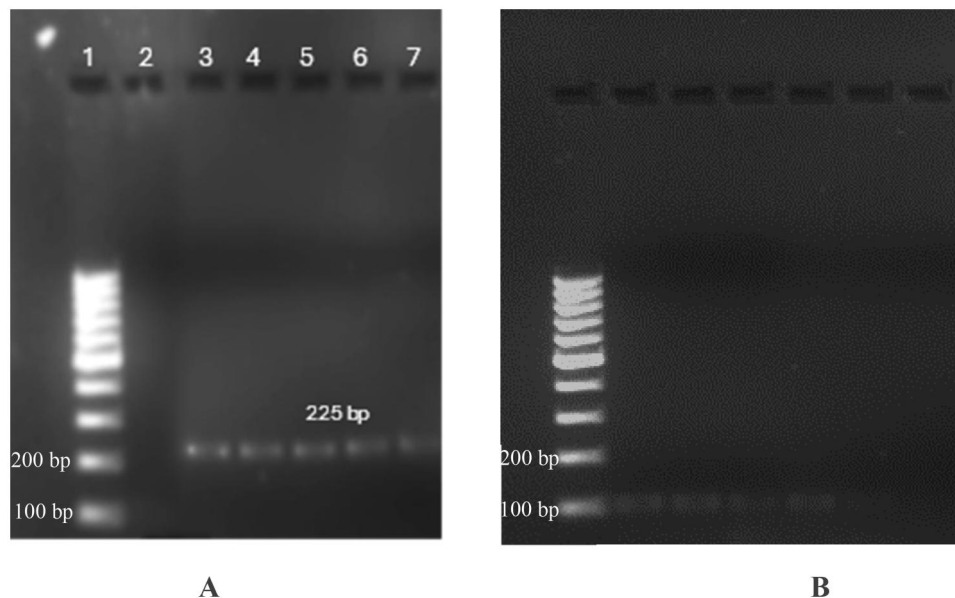


Figure 6. PCR detection of bacterial pathogens in *Pomadasys argenteus* (Silver grant) fish samples. (A): Two specific primers targeting *ureR* gene were used for PCR amplification to detect *P. mirabilis* lanes 3 through 7 (225 bp), and lane 2 is a negative control. (B): Two pairs of specific primers targeting *cfa* gene were used for PCR amplification to detect *Citrobacter braakii* and *Citrobacter freundii*. Lane 1 shows 100 bp DNA ladder, lanes 2 through 6 (100 bp), and lane 2 is a negative control. The PCR products were visualized on a 2% agarose gel.

PCR analysis confirmed the presence of key opportunistic pathogens in both Jesh sal and Silver grunt samples. In Jesh sal samples, *Proteus mirabilis* was identified through the amplification of the *ureR* gene (225 bp fragment) (Figure 5A), while *Acinetobacter lwoffii* was identified through the amplification of the *rpoB* gene (302 bp fragment) (Figure 5B), and *Sphingomonas paucimobilis* was identified via the amplification of the 16S-23S rRNA ITS gene (729 bp fragment) (Figure 5B).

In Silver grunt samples, *Proteus mirabilis* was also confirmed by amplification of the *ureR* gene (225 bp)

(Figure 6A). While *Citrobacter braakii* and *Citrobacter freundii* were identified through the amplification of the *cfa* gene (100 bp) (Figure 6B). Detection of these specific pathogens were also proved using gene-based PCR methods.

4. Discussion

Fish is a significant component of the global food supply, accounting for about 16% of animal protein consumption worldwide and up to 50% in some coastal and island countries(1). In the United Arab

Emirates (UAE), fishing is not only economically important but also deeply rooted in the country's cultural heritage. The UAE's fish and fishery product trade was valued at \$624 million in imports and \$100 million in exports in 2015 (Abdelbaset-Donya et al., 2020). Ensuring the microbial quality and safety of fish sold in local markets is crucial for protecting consumer health and maintaining the country's thriving fish trade.

4.1. Microbial load in fish samples

This study investigated the microbial quality of two commercially important fish species, *Carangoides chrysophrys* (Jesh sal) and *Pomadasys argenteus* (Silver grunt), sold in the fish market, Sharjah, UAE. The total viable aerobic counts (TVAC) for both species were within the acceptable limits set by the International Commission of FAO/WHO and the GCC standards. However, the significantly higher bacterial counts observed in the overnight catch samples of Jesh sal and the older samples of Silver grunt highlight the impact of storage time and environmental factors on microbial growth (Sanjee and Karim, 2016). The variance in the initial bacterial load of the examined fish samples can be attributed to the microbial load of the water in which they reside and the proliferation of bacteria that thrive under storing conditions (Nguyen et al., 2023). Despite the observed increase in bacterial load in overnight samples, all microbial counts remained below FAO/WHO's upper safety limit of 5×10^5 CFU/g, indicating that while storage time influences microbial growth, the tested fish samples were microbiologically acceptable for consumption.

Several studies have demonstrated that fish can act as reservoirs for opportunistic and foodborne pathogens, posing potential health risks to consumers. In this study, bacterial genera such as *Proteus mirabilis*, *Citrobacter freundii*, and *Acinetobacter lwoffii* were identified in fish samples, particularly in overnight-stored specimens, highlighting the importance of proper handling and storage conditions (Huang et al., 2021; Ma et al., 2022). Previous research has shown that microbial contamination in fish species, including *Mormyrus kannume*, can lead to foodborne illnesses due to the presence of pathogenic bacteria (Alikunhi et al., 2017; Elbarbary et al., 2024). These bacteria have been associated with gastrointestinal infections, urinary tract infections, and other opportunistic diseases, particularly in immunocompromised individuals (Huang et al., 2021). The presence of *Acinetobacter lwoffii* and *Sphingomonas paucimobilis* in overnight fish samples is noteworthy, as these bacteria are known to cause opportunistic infections, particularly in hospital environments (Huang et al.,

2021). Although these species are generally not considered primary foodborne pathogens, their presence in seafood highlights the potential for cross-contamination and underscores the need for enhanced microbial monitoring.

4.2. Bacteria diversity and identification

The bacterial diversity found in the fish samples included several opportunistic pathogens, such as *Citrobacter spp.*, *Proteus spp.*, *Aeromonas spp.*, and *Pseudomonas spp.* Notably, opportunistic pathogens such as *Citrobacter spp.* and *Proteus spp.* were more prevalent in overnight samples, suggesting that prolonged storage may contribute to the growth of these bacteria. These findings are in line with previous studies that have reported the presence of these bacteria in fish and their potential to cause foodborne illnesses (Alhussaen et al., 2022; Alikunhi et al., 2017). The occurrence of opportunistic pathogens in fish can be influenced by various factors, including diet, age, size, harvest time, ecological traits, and geographical location (Alikunhi et al., 2017). Additionally, the aquatic environment serves as a reservoir for these pathogens, which can be transferred to fish through contaminated water, sediment, or feed (Amuneke et al., 2020).

4.3. Molecular identification of bacterial pathogens

The molecular identification of specific pathogens, such as *Sphingomonas paucimobilis*, *Acinetobacter lwoffii*, *Proteus mirabilis*, *Citrobacter braakii*, and *Citrobacter freundii* and using PCR-based methods underscores the importance of employing advanced techniques for accurate pathogen detection in fish (González et al., 2004). The successful amplification of the ureR gene in *P. mirabilis* and the cfa gene in *C. braakii* and *C. freundii* demonstrates the specificity and reliability of these molecular markers for pathogen identification (Zhang et al., 2013; Kacliková et al., 2005).

The successful application of molecular techniques, such as PCR, in this study demonstrates the value of incorporating these methods into routine surveillance programs for the accurate detection and identification of pathogens in fish. The use of molecular markers specific to opportunistic pathogens can improve the efficiency and sensitivity of pathogen detection, enabling early intervention and the implementation of appropriate control measures (González et al., 2004; Huang et al., 2021).

4.4. Microbial quality and proper practices in local seafood market

The presence of opportunistic pathogens in the fish samples emphasizes the need for stringent hygiene practices and proper storage conditions to minimize the risk of microbial contamination and ensure consumer safety. Previous studies have highlighted the importance of maintaining the cold chain and implementing strict hygiene protocols during fish handling, transportation, and storage (Sanjee & Karim 2016; Stratev et al., 2015). Temperature control is crucial in preventing bacterial growth and preserving fish quality (Tewari et al., 2014; Tavares et al., 2021). Therefore, it is recommended that fresh fish be stored at low temperatures (below 4 °C) and that the time between catch and consumption be minimized to reduce the risk of microbial spoilage and the growth of opportunistic pathogens (Fadel & El-Lamie, 2019).

In addition to proper storage and handling practices, regular monitoring and surveillance of fish sold in local markets are essential for ensuring food safety and protecting public health. The findings of this study contribute to the understanding of the microbial communities in Jesh sal and Silver grunt and highlight the importance of implementing effective control measures to minimize the risk of foodborne illnesses. Although the aquatic environmental conditions (e.g. water, ice, handling surfaces) will help to trace the contamination origin and thus affecting the microbial quality of fish, we did not study the surrounding environmental conditions. However, future research should focus on identifying the sources of contamination, such as the aquatic environment, fishing practices, and post-harvest handling, to develop targeted interventions for reducing microbial contamination in fish (Alikunhi et al., 2017; Carnevia et al., 2013).

5. Conclusion

In conclusion, while the microbial quality of Jesh sal and Silver grunt sold in the Kalba fish market was generally within acceptable limits, the presence of opportunistic pathogens underscores the need for continuous monitoring. The findings reinforce the necessity of proper refrigeration ($\leq 4^{\circ}\text{C}$), enhanced hygiene practices, and routine microbial monitoring to ensure seafood safety. The integration of biochemical and molecular techniques into routine surveillance programs can enhance the accuracy and speed of pathogen detection, facilitating timely interventions to mitigate the risk of foodborne illnesses. By implementing these measures and raising awareness among consumers and stakeholders, the

UAE can safeguard public health and maintain the sustainability of its thriving fish trade.

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Ethical approval

The authors announce that no experiments were performed on animals and no data were collected from patients in this research.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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