



Assessment of the Bacteriological Quality of Some Fish Products

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FISH products are considered a nutritionally significant component of the human diet because they contain macronutrients (proteins, fats, and ash) and micronutrients (vitamins and minerals). Accordingly, 200 different commercial fish product samples (25 each of canned solid tuna, canned chunks tuna, canned crumbled tuna, canned anchovy, canned mackerel, canned sardine, herring, and tilapia fillets) of different brands were collected from various local and high supermarkets in Aswan City during 2020-2021. The samples were subjected to microbial quality assessment, and PCR was carried out to detect some virulence genes of fish-borne pathogens to evaluate the control measures for food safety. The results presented that the highest bacterial loads (cfu/g) in the examined fish products were proven in fillets tilapia ($1.3 \times 10^4 \pm 0.32$) and herring ($1.0 \times 10^4 \pm 1.2$) while anchovy, mackerel, and crumbled tuna were the highest anaerobic count with means of $7.3 \times 10^3 \pm 1.2$, $7 \times 10^3 \pm 1.6$ and $6.7 \times 10^3 \pm 1.4$, respectively. The prevalence of *P. aeruginosa* occurs with an incidence of 29%. The *lasB* gene (50%) has been the most detected virulence gene, followed by *exoS* (40%). *V. parahaemolyticus* was present in 7.5%, and the regulator toxin genes (*toxR* and *L.tdh*) were found in 33.3% and 22.2%. Additionally, 20% of the samples had *A. hydrophila*, and the *aerA* and *act* genes were found in 60% of the isolates. In addition, *C. perfringens* was detected in 33% of examined products, and the virulence genes *cpa* and *etx* were present and discovered to be a proportion of 20% and 50%, respectively. The current study concluded that the examined fish products possess one or more food poisoning virulence genes indicating unsanitary handling, transport, processing, storage practices, and inappropriate environmental conditions.

Keywords: Fish products, Virulence genes, Quality, Food poisoning.

Introduction

The significance of wholesome meals is becoming more widely recognized, and fish consumption is rising due to its distinctive nutritional advantages. Fish is considered a nutritionally beneficial component of the human diet because they include macronutrients (proteins, fats, and ash) and micronutrients (vitamins and minerals). These nutrients are essential for human nutrition and

have been shown to play a role in many metabolic processes. But along with the benefits, bacterial contamination, and other biological, chemical, and physical contamination come with risks. Microbiological contamination is the leading risk associated with fish food [1]. Therefore, Fish food is a frequent source of food poisoning, resulting in illnesses of varying severity, from minor indisposition to persistent or fatal infections

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[2]. Due to their prevalence, related mortality, and detrimental economic effects, foodborne illnesses are regarded as a serious public health concern worldwide. Food's environment and microbiota include a wide variety of germs that can be transferred to people while handling and eating food. Fish and its products are extremely delicate foods that require cautious handling and storage [3]. Pathogens such as *Vibrio spp.*, *Aeromonas spp.*, *pseudomonas spp.*, *Clostridia spp.*, and *Salmonella spp.*, naturally found in any aquatic environment, can lead to contamination [4]. Therefore, monitoring the bacterial load to get information on the risk profile of fish products for the public's health was crucial. This study aimed to assess the bacteriological quality of several fish products available for sale in Aswan.

Material and Methods

Samples: 200 different commercial fish product samples of other brands (25 each of canned solid tuna, canned chunks tuna, canned crumbled tuna, canned anchovy, canned mackerel, canned sardine, herring, and tilapia fillet) were collected from various local and high supermarkets in Aswan City during 2020-2021. All the identified samples were then transported in an icebox container to the Meat Hygiene Lab; Department of Food Hygiene; Faculty of Veterinary Medicine; Aswan University for analysis.

Preparation of samples [5]: fish products were aseptically opened, and 10g of each sample was transferred to 90 ml of sterile peptone water (0.1%) and homogenized at 14000 r.p.m. for 2.5 min to provide a homogenate of 1/10 dilution. A 10 ml of this homogenate to another test tube containing 9 ml of sterile peptone water (0.1%) to give 10^{-2} , from which tenfold serial dilutions were prepared up to 10^{-3} . One ml from each previously prepared serial dilution was inoculated separately into two appropriately marked duplicated Petri dishes for the following analysis:

Total aerobic count [6]

Standard plate count agar was added after melting and cooling at 45°C to each inoculated petri dish, left to solidify before being incubated at 35 °C for 48 h.

Total anaerobic count [7]

Using reinforced clostridial agar was added after melting and cooling at 45°C to each inoculated petri dish, left to solidify, and put in an anaerobic jar before being incubated at 35 °C for 48 h.

Isolation and identification of Pseudomonas aeruginosa [8]

A loopful was streaked onto MacConkey agar and *Pseudomonas* agar base medium plates and incubated at 37 °C for 24 h to observe the non-lactose fermenting colonies and sub-cultured onto nutrient agar plate to keep the pigmentation (blue, green colonies) considered positive result. Suspected colonies of *P. aeruginosa* were picked up and subjected to further identifications and other biochemical tests according to MacFaddin [9].

Isolation and identification of Vibrio parahaemolyticus [10]

A loopful was streaked onto thiosulfate citrate bile and sucrose agar plates and incubated at 37 °C for 24 h. The presumptive *V. parahaemolyticus* colonies (smooth and green) were picked up, purified, and then biochemically identified according to ISO-TS [5].

Isolation and identification of Aeromonas hydrophila [11]

A loopful was streaked onto *Aeromonas* isolation medium base agar supplemented with ampicillin (5 mg/L) plates and incubated at 37 °C for 24 h. Suspected colonies of *A. hydrophila* (green colonies with dark centers) were picked up and subjected to further identifications based on colonial morphology and other biochemical tests according to Markey et al. [12].

Isolation and identification of Clostridium perfringens [13]

The homogenates of each sample were placed in a water bath for 10-15 minutes at 80°C (heat shocking) to kill non-spore forming aerobic bacteria, 10 g from each sample separately in 90 mL of fluid thioglycolate medium were incubated at 37°C for the initial 3–4 h and then for 18–24 h at 44–45°C. A loopful of thioglycolate inoculum was streaked onto reinforced clostridial agar plates. The inoculated agar plates were placed in an anaerobic jar and incubated at 37 °C for 24h. Suspected colonies of *C. perfringens* (black colonies) were picked up and subjected to further identifications according to Bergey et al. [14].

PCR detection of virulence genes of fish-borne pathogens

Ten isolates of confirmed phenotypically studied bacteria were chosen randomly to

be analyzed for the detection of virulence genes of detected fish-borne pathogens using conventional PCR. DNA was extracted using GeneJET Genomic DNA Purification Kit (Catalog No. #K0721, Thermo Scientific, USA). Using specific oligonucleotide primers synthesized by Willowfort Company (United Kingdom) for the detection of virulence genes were shown in Table (1), and the cycling conditions of oligonucleotide primers during DNA amplification were shown in Table (2). Amplified DNA fragments were analyzed by 2% agarose gel electrophoresis (Applichem, Germany, GmbH) in 1X TAE buffer at 100 V for 45 min with 10 µl PCR product. The gel was stained with ethidium bromide, captured, and visualized on a UV transilluminator. The positive control was obtained from Animal Health Research Institute (AHRI), Agriculture Research Center (ARC), Dokki, Giza, Egypt.

Statistical Analysis

One-way Analysis of Variance (ANOVA) was performed for significant differences across fish samples using Microsoft Office Excel 2007 and Graph Pad Instant 3 for Windows programs to calculate sample means and standard errors.

Results

The results shown in Fig. 1 of Aerobic plate count presented that the highest microbial loads (cfu/g) in the examined fish products were proven in fillets tilapia ($1.3 \times 10^4 \pm 0.32$) and herring ($1.0 \times 10^4 \pm 1.2$), followed by anchovy ($8.1 \times 10^3 \pm 1.9$), crumbled tuna ($6.22 \times 10^3 \pm 2.3$), solid tuna ($4.85 \times 10^3 \pm 2.7$), mackerel ($4.53 \times 10^3 \pm 2.1$). Since chunks tuna ($0.68 \times 10^3 \pm 0.33$) and sardine ($0.57 \times 10^3 \pm 0.28$) had the lower microbial count. The data of Total anaerobic count revealed that the samples of anchovy, mackerel, and crumbled tuna were the highest anaerobic count with means of $7.3 \times 10^3 \pm 1.2$, $7 \times 10^3 \pm 1.6$ and $6.7 \times 10^3 \pm 1.4$, respectively. Afterthought, herring, fillets tilapia, and solid tuna with means of $6.31 \times 10^3 \pm 0.8$, $6.2 \times 10^3 \pm 1.9$ and $5.16 \times 10^3 \pm 1.2$, respectively. Meanwhile, sardine and chunks tuna had a mean anaerobic count of $4.9 \times 10^3 \pm 1.1$ and $3.8 \times 10^3 \pm 1.7$. Likewise, the difference between the analyzed samples was statistically significant at ($p < 0.05$).

Occurrence of bacterial contamination in the examined fish products (Table 3):

Prevalence of P. aeruginosa: It is evident from the results that the *P. aeruginosa* occurs in an incidence of 29% out of 200 analyzed samples. The incidence of *P. aeruginosa* were 16% and 20% for solid tuna and chunks tuna, 28% for each crumbled tuna, anchovy, and mackerel, 32% for each sardine and herring, while fillet tilapia with an incidence of 48%. The molecular results (Fig. 2) based on detecting the *16S* rRNA gene showed that 100% of presumptive isolates belonged to *P. aeruginosa*. The *lasB* gene (50%) has been the most detected virulence gene, followed by *exoS* (40%).

Prevalence of V. parahaemolyticus: it is clear from the results that *V. parahaemolyticus* were present in 7.5% of the 200 inspected products. Only the sardine and herring samples include *V. parahaemolyticus*, present in those samples at a prevalence of 20% and 40%, respectively. The findings of the current investigation indicated the occurrence of *16S* rRNA in (9) 90% of the examined isolates, while the regulator toxin genes (*toxR* and *L.tdh*) were found in 33.3% and 22.2% of isolates based on *16S* rRNA (Fig. 3).

Prevalence of A. hydrophila: The data in the current study illustrate that 20% of the samples had *A. hydrophila* with an incidence of 12% for each solid tuna, sardine, and herring, 16% for each chunks tuna, crumbled tuna, and anchovy, 28% for mackerel, and 48% for fillet tilapia. According to the PCR results (Fig. 4), 50% of *A. hydrophila* had the *16S* rRNA gene. Based on identifying the *A. hydrophila 16S* rRNA gene, the *aerA* and *act* genes were found in 60% of the isolates.

Prevalence of C. perfringens: It is evident from the results that the *C. perfringens* was detected in 33% of examined products with an incidence of 12%, 28%, 40%, 32%, 52%, 20%, 20%, and 60%, respectively. According to the molecular findings (Fig. 5), the virulence genes *cpa* and *etx* were present and discovered to be a proportion of 20% and 50%, respectively.

Discussion

Canned fish are high in nutrients and minerals that must be included in the human diet [24]. Actual daily nutrient requirements for fish may vary depending on age, gender, physical activity level, and other factors [25]. Contamination with microbiological infections

is the most significant issue with fish product safety. Furthermore, fish products are extremely susceptible to spoiling due to their high water content, neutral pH, abundance of amino acids, and naturally occurring autolytic enzymes [26]. Direct contamination of the fish by polluted water or secondary contamination during processing, storage, distribution, or preparation contributes to bacterial contamination. Raw or lightly processed fish is especially susceptible to contamination [27].

Accordingly, the results in this study (Fig. 1) presented that the highest bacterial loads (cfu/g) in the inspected fish products were found in fillets tilapia and herring, followed by anchovy, crumbled tuna, solid tuna, mackerel, since chunks tuna and sardine had the lower microbial count. In addition, the differences in the count among examined products were considered significant at ($p < 0.05$). Aerobic plate count on fish is generally related to food safety risks and can sometimes be used to indicate quality, shelf life, and contamination after heat processing [28]. The findings of some authors [29, 30] are very similar.

Anaerobic bacteria are a significant group of microorganisms responsible for various health risks to canned food consumers. Consequently, the data achieved in Fig. (1) illustrate the difference between the samples that were analyzed was statistically significant at ($p < 0.05$). The regulations stipulated that clostridium or anaerobic spore-forming bacteria shouldn't be present in canned tuna, sardines, or mackerel [31, 32], therefore, all examined products were not accepted based on the anaerobic count. In contrast, higher results were obtained by some investigators [33]. These findings might be explained by the fact that mackerel contains a high proportion of fats and oils, both of which encourage the growth of bacteria [34].

P. aeruginosa is a bacterium capable of easily contaminating and spoiling fish meat [35]. The data in Table 3 showed that the prevalence of *P. aeruginosa* occurs in an incidence of 29% out of 200 examined samples. The investigated samples may have contained *P. aeruginosa* due to the importance of this species as a zoonotic agent, as it is found in humans, animals, and plants. Nearly similar results were reported by some scientists [36, 37].

The results were lower than those obtained by some authors [34, 38]. Molecular identification

of the *16S* rRNA gene quickly and accurately identified bacteria [39]. The results of this study confirm that a correct identification and characterization of *P. aeruginosa* can only be achieved by combining cultural, biochemical, and molecular tests. The molecular results (Fig. 2) of detecting the *16S* rRNA gene showed that 100% of presumptive isolates belonged to *P. aeruginosa*. Similarly, results were stated by some studies [40, 41]. According to the *lasB* gene (50%) has been the most detected virulence gene, followed by *exoS* (40%). The *exoS* is implicated in lung infection and may be crucial for bacterial dispersion. It caused tissue damage [42]. The most virulence genes discovered in *P. aeruginosa* were *lasB* and *exoS* achieved by many researchers [36, 41, 43]. Bacteriological evaluation of fish for the presence of *Pseudomonas* spp. has considerable significance since these bacteria can cause foodborne illness and are also indicators of meat quality. The high percentage of the existence of *P. aeruginosa* might be partially attributed to the suitability of the storage temperature for the survival and multiplication of these bacteria. The current results may be due to differences in cleanliness precautions used during fish collection, handling, freezing, storage, and processing methods [34].

Vibrio spp. are microbiological water-borne diseases that are mostly found in various types of seafood and make people more vulnerable to dangers to their health [44]. The current investigation shows that *V. parahaemolyticus* was present in 7.5% of the 200 inspected products. Only the sardine and herring samples include *V. parahaemolyticus*, present in those samples at prevalences of 20% and 40%, respectively. Increasing salinity is one of the most commonly employed factors for food conservation and aquatic product processing. The literature regarding the impact of NaCl on *Vibrio* spp., growth is bifurcated. A study conducted on *V. parahaemolyticus* showed that the bacteria reached a viable state when the concentration of NaCl was elevated up to a level of 30% [45]. The results matched with some authors [46]. In contrast, [47] reported lower results. Variations in storage temperatures, incorrect handling, a lack of hygiene, and cross-contamination may be to blame for the fluctuation in *V. parahaemolyticus* incidences [48]. The PCR-based assay targeting the *16S* rRNA, *toxR*, and *L.tdh* genes, which are highly conserved between *V. parahaemolyticus*, has become a popular molecular technique for

detecting and identifying *V. parahaemolyticus* in marine specimens [49, 50]. The findings of the present investigation (Fig. 3) indicated the presence of 16S rRNA in (9) 90% of the examined isolates, while the regulator toxin genes (*toxR* and *L.tdh*) were found in 33.3% and 22.2% of isolates. All *V. parahaemolyticus* isolates had the *toxR* genes reported by some researchers [47, 49]. However, a lower percentage was reported by some reports [51, 52]. Meanwhile, [53] said higher results.

A. hydrophila is not only a fish pathogen but also a zoonotic pathogen that can cause gastroenteritis, septicemia, and traumatic and aquatic wound infections in humans [54]. The data achieved in Table 3 clarify that 20% of examined samples were contaminated with *A. hydrophila*. The results matched with [55]'s finding. Research has shown lower results, as reported by Morshdy et al. [56]. Likewise, higher results were reported by some literature [57, 58]. The results of the PCR test shown in Fig. 4 indicated that 5 (50%) out of 10 examined biochemically identified isolates, selected randomly, were contaminated with *A. hydrophila* based on the occurrence of the 16S rRNA gene. Nearly similar results were reported by [58] and [59]. As well as lower results revealed by Fauzi et al. [60]. These results were higher than the study conducted by Praveen et al. [57]. In this study discovery of two virulence genes to *A. hydrophila* by PCR (*aer A* and *act* genes) was done to assess the pathogenicity of the isolates. *aer A* and *act* genes were found in 3 (60%) of 5 isolates. The results were matched with Ninh et al. [58] while disagreed with the results of some authors [55, 57].

The *Clostridia* spp. produces the highest number of toxins of any type of food poisoning bacteria. Among *Clostridium* sp., *C. perfringens* is the largest toxin producer and also the most widespread, being found as part of the microbiota of animals and humans and in the soil. In most cases, *C. perfringens* food poisoning results by eating improperly cooked and stored foods [34]. On the other hand, it is evident from the results that *C. perfringens* was detected in 33% of examined products. These results disagreed with the finding of some researchers [33, 61]. The results cleared that the *cpa* gene was identified with a percentage of 20%, while the *etx* gene was detected with a rate of 50% (Fig. 5). The finding matched with

Hailegebreal [61] meanwhile lower than the finding by Ezzeldeen et al. [62]. *C. perfringens* in canned fish products indicate improper processing or contamination during handling and storage. Additionally, the quality of the raw fish used plays a significant role in the presence of *Clostridia* in examined canned fish. On the other hand, properly handling fish after landing can reduce the likelihood of any *C. perfringens*-related threat to public health [33].

Food safety is a global health goal, and foodborne diseases significantly impact global health. As a result, detecting microbial pathogens in food is the solution to preventing and recognizing health and safety issues. Conventional bacterial detection techniques, like colony counting, culture, and immunology-based techniques, might take many hours or even days to give a result. Compared to culture-based methods, rapid analysis using DNA hybridization and amplification techniques provides greater sensitivity and specificity to produce results and a sharply shorter processing time. Many factors influence fish product safety, including the origin of the fish, product characteristics, processing technique, and cooking. Contaminated fish could be hazardous, particularly for vulnerable populations such as children, older people, and those with compromised immune systems [63].

Conclusion

The achieved results in the current study concluded that the examined fish products were contaminated with various microorganisms, including *P. aeruginosa*, *V. parahaemolyticus*, *A. hydrophila*, and *C. perfringens* possess one or more food poisoning virulence genes indicating unsanitary handling, transport, processing, and storage practices as well as inappropriate environmental conditions.

Conflicts of interest

The authors confirm that no interest's conflict regarding the research data and resources used for this work.

Ethical approve

Because the survey work was done with commercial products, no approval from research ethics committees was required to complete the objective of this study.

Funding statements

Not applicable.

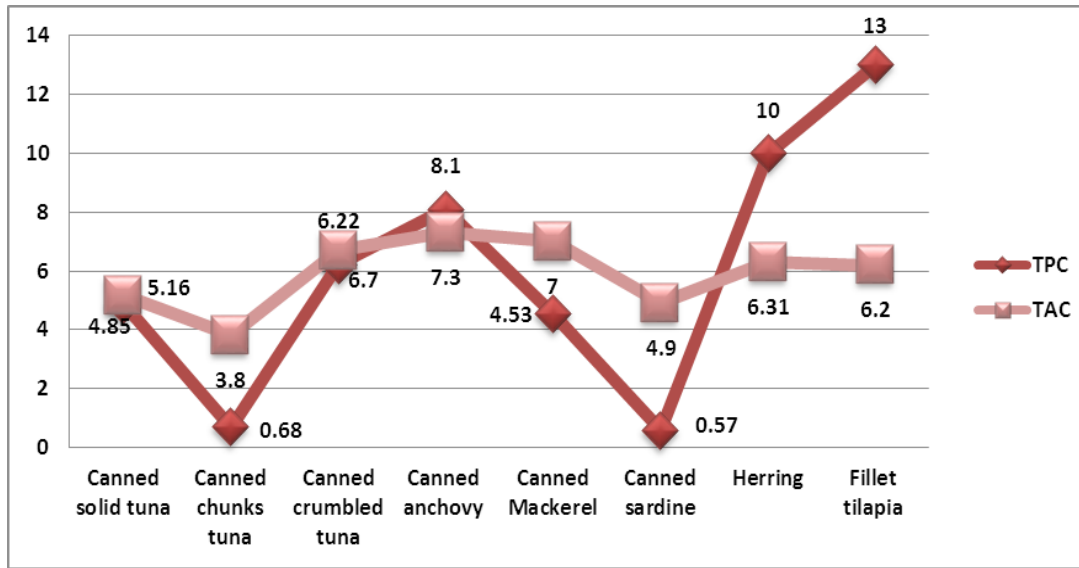


Fig. 1. Total plate and total anaerobic count (cfu/g 10³) in the examined products

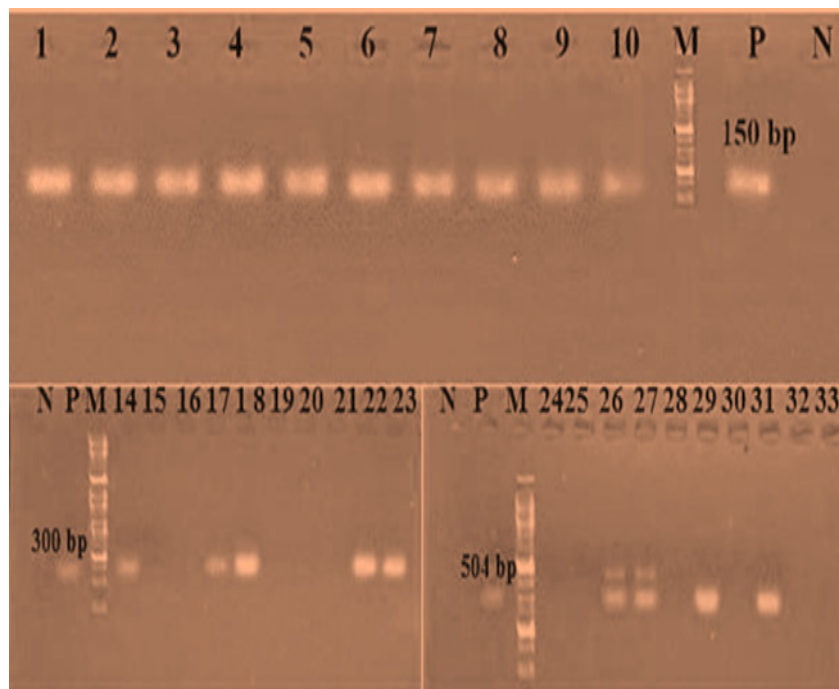


Fig. 2. Electrophoretic profile of amplification products of *P. aeruginosa* virulence genes. P: Positive control, N: Negative control, M: Marker (50bp). Lanes 1-10: Presence of *P. aeruginosa* 16S rRNA gene in analyzed products at 150 bp. Lane 14, 17, 18, 21 and 22: positive for *LasB* in researched products at 300 bp. Lane 26, 27, 29, and 31: positive for *ExoS* in analyzed products at 504 bp.

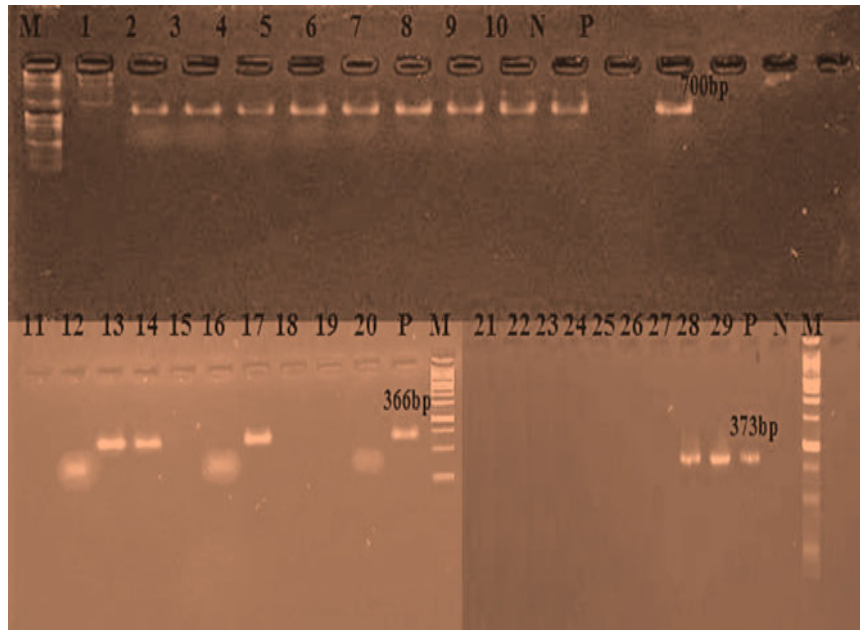


Fig. 3. Electrophoretic profile of amplification products of *V. parahaemolyticus* virulence genes. P: Positive control; N: Negative control; M: Marker (50bp). Lanes 2-10: Presence of *V. parahaemolyticus* 16S rRNA gene in analyzed products at 700 bp; Lanes 13, 14, and 17: positive for *ToxR* gene in researched products at 366 bp. Lane 23: Lane 28 and 29: positive for *L.tdh* gene in analyzed products at 373 bp.

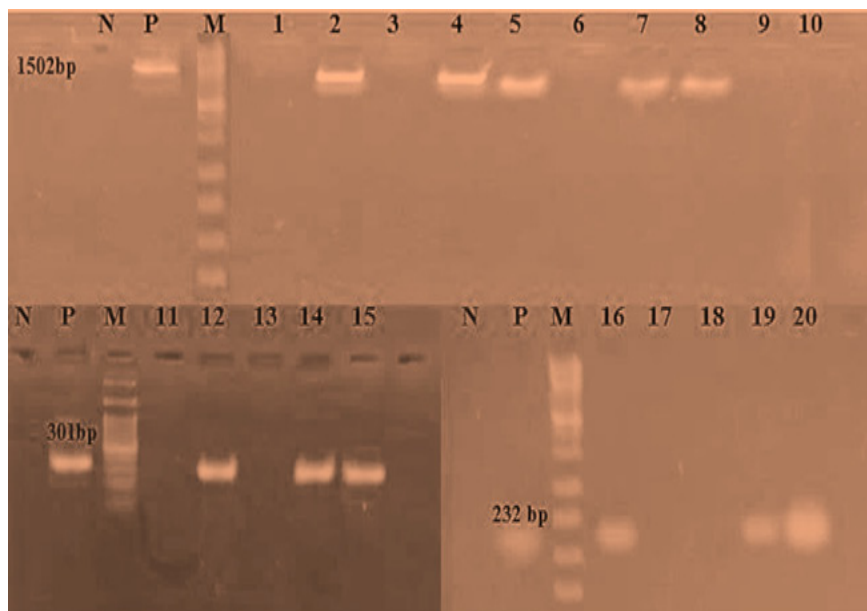


Fig. 4. Electrophoretic profile of amplification products of *A. hydrophila* virulence genes. P: Positive control; N: Negative control; M: Marker (50bp). Lanes 2, 4, 5, 7, and 8: Presence of *A. hydrophila* 16S rRNA gene in analyzed products at 1502 bp; Lanes 12, 14, and 15: positive for *aerA* in analyzed products at 301 bp. Lane 16, 19, and 20: positive for the *act* in analyzed products at 301 bp.

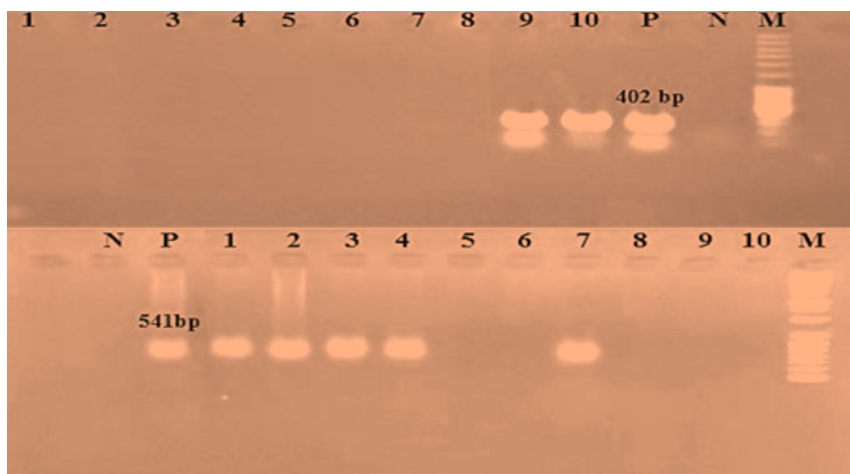


Fig. 5. Electrophoretic profile of amplification products of *Cl. perfringens* virulence genes. P: Positive control; N: Negative control; M: Marker (50bp). Lane 9 and 10: positive for *cpa* in analyzed products at 402 bp. Lane 1, 2, 3, 4, and 7: positive for *etx* in analyzed products at 541 bp.

TABLE 1. Oligonucleotide primers and amplified products used

Bacteria	Target gene	Oligonucleotide sequence (5'- 3')	size (bp)	References
	<i>16S rRNA</i>	CTACGGGAGGCAGCAGTGG TCGGTAACGTCAAAACAGCAAAGT	150	[15]
<i>P. aeruginosa</i>	<i>ExoS</i>	C TTGAAGGGACTCGACAAGG TTCAGGTCCGCGTAGTGAAT	504	[16]
		<i>LasB</i>	GGAATGAACGAGGCGTTCTC GGTCCAGTAGTAGCGGTTGG	
	<i>16S rRNA</i>	CAGGCCTAACACATGCAAGTC GCATCTGAGTGTCAGTATCTGTCC	700	[17]
<i>V. Parahaemolyticus</i>	<i>ToxR</i>	GTCTTCTGACGCAATCGTTG ATACGAGTGGTTGCTGTCATG	366	[18]
	<i>L.tdh</i>	CCATCTGTCCCTTTTCCTGC CCAAATACATTTTACTTGG	373	[19]
	<i>16S-rDNA</i>	AGAGTTTGATCATGGCTCA GGTTACCTTGTTACGACTT	1502	[20]
<i>A. hydrophila</i>	<i>aerA</i>	AACCGAACTCTCCAT TTGTCCGGGTTGTACTCGTC	301	[21]
		<i>act</i>	GAGAAGGTGACCACCAAGAAC AACTGACATCGGCCTTGAAGTC	
	<i>cpa</i>	AGATGGCATCATTCAAACGCTAATGTTACTGCCGTTGA CCTCTGATACATCGTGTGTA	400	[22]
<i>C. perfringens</i>	<i>etx</i>	GCGGTGATATCCATCTATTC CCACTTACTTGTCTACTAAC	655	[23]

TABLE 2. The cycling conditions of oligonucleotide primers during DNA amplification of PCR reaction

Bacteria	Target gene	Primary denaturation	Secondary denaturation	Annealing	Extension	No. of cycles	Final extension
	<i>16S rRNA</i>	95 °C / 5 min	95 °C / 30 sec	60 °C / 30 sec	72 °C / 45 sec	30	72 °C / 10 min
<i>P. aeruginosa</i>	<i>LasB</i>	94 °C / 5 min	94 °C / 35 sec	60 °C / 1 min	72 °C / 1 min	35	72 °C / 7min
	<i>ExoS</i>						
	<i>16S rRNA</i>	95 °C / 10 min	95 °C / 1 min	55 °C / 1 min	72 °C / 1.5 min	30	72 °C / 5 min
<i>V. Parahaemolyticus</i>	<i>ToxR</i>	94 °C / 10 min	94 °C / 1 min	63 °C / 1.5 min	72 °C / 1.5 min	20	72 °C / 10 min
	<i>L.tdh</i>	94 °C / 5 min	94 °C / 1 min	54 °C / 1 min	72 °C / 1 min	30	72 °C / 10 min
	<i>16S rDNA</i>	94 °C / 5 min	94 °C / 1 min	56 °C / 1 min	72 °C / 2 min	30	
<i>A. hydrophila</i>	<i>aerA</i>	94 °C / 5 min	94 °C / 30 sec	54 °C / 30 sec	72 °C / 1 min	35	72 °C / 10 min
	<i>act</i>	94 °C / 5 min	94 °C / 30 sec	42 °C / 30 sec	72 °C / 1 min		
<i>C. perfringens</i>	<i>cpa</i>	95 °C / 2 min	94 °C / 1 min	55 °C / 1 min	72 °C / 1 min	35	72 °C / 10 min
	<i>etx</i>						

TABLE 3. Occurrence of bacterial contamination in the inspected fish products

Examined product	No.	<i>P. aeruginosa</i>		<i>V. parahemolyticus</i>		<i>A. hydrophila</i>		<i>Cl. peregrines</i>	
		No.	%	No.	%	No.	%	No.	%
Canned solid tuna	25	4	16	0	0	3	12	3	12
Canned chunks tuna	25	5	20	0	0	4	16	7	28
Canned crumbled tuna	25	7	28	0	0	4	16	10	40
Canned anchovy	25	7	28	0	0	4	16	8	32
Canned mackerel	25	7	28	0	0	7	28	13	52
Canned sardine	25	8	32	5	20	3	12	5	20
Herring	25	8	32	10	40	3	12	5	20
Fillet tilapia	25	12	48	0	0	12	48	15	60
Total samples	200	58	29	15	7.5	38	20	66	33

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تقييم الجودة البكتريولوجية لبعض المنتجات السمكية

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تعتبر المنتجات السمكية عنصراً هاماً من الناحية الصحية في النظام الغذائي البشري لأنها تحتوي على المغذيات الأساسية (البروتينات، الدهون، والرماد) وبناء على ذلك، جُمعت ٢٠٠ عينة مختلفة من منتجات الأسماك التجارية (٢٥ عينة من كل من التونة المعلبة قطعة واحدة، التونة المعلبة قطع، التونة المعلبة المفتتة، الأنشوجة المعلبة، الماكريل المعلبة، الساردين المعلب، الرنجة، وفيلية البلطي) من علامات تجارية مختلفة من مختلف المحلات التجارية المحلية في مدينة أسوان خلال الفترة ٢٠٢٠-٢٠٢١. وأخضعت العينات لتقييم نوعية الميكروبات، وأجريت عملية كشف عن بعض الجينات الضراوة لمسببات الأمراض المنقولة عن طريق الأسماك لتقييم تدابير الرقابة على سلامة الأغذية. وأظهرت النتائج أن أعلى الأحمال البكتيرية (cfu/g) في منتجات الأسماك التي تم فحصها قد ثبتت في فيلية البلطي ($10^4 \pm 0.32 \times 1.3$) والرنجة ($10^4 \pm 1.2 \times 1.0$) في حين أن الأنشوجة والماكريل والتونة المفتتة هي أعلى نسبة لاهوائية ($10^3 \pm 1.2 \times 7.3$, $10^3 \pm 1.6 \times 7$, and $6.7 \times 10^3 \pm 1.4$)، على التوالي. وكان معدل انتشار *Pseudomonas spp.* بين العينات التي تم فحصها هو ٨٢,٥٪، في حين أن *P. aeruginosa* يحدث بمعدل ٢٩٪. وكان الجين (50% *LasB*) هو أكثر الجينات اكتشافاً، يليه *exoS* (40%). وكان *V. parahaimolyticus* موجوداً في ٧,٥٪، وعثر على جينات التوكسين المنظم *ToxR* و *L.tdh* في ٣٣,٣٪ و ٢٢,٢٪. وعلاوة على ذلك، كانت نسبة ٣٦,٥٪ من العينات التي تم فحصها ملوثة بالأيرومونس. وبالإضافة إلى ذلك، كانت ٢٠٪ من العينات هي *A. hydrophila*، وعثر على جينات *AerA* وفعل في ٦٠٪ من العزلات. وبالإضافة إلى ذلك، اكتشفت مادة *C. perfringens* في ٣٣٪ من المنتجات المفحوصة، وكانت الجينتين الفروسييتين *cpa* and *etx* موجودتين واكتشف أنهما نسبة ٢٠٪ و ٥٠٪ على التوالي. وخلصت الدراسة الحالية إلى أن المنتجات السمكية التي تم فحصها تحتوي على جين أو أكثر من جينات التسمم الغذائي التي تشير إلى ضعف الحالة الصحية والظروف البيئية غير الملائمة أثناء النقل أو التخزين أو التجهيز.

الكلمات الدالة: المنتجات السمكية، جينات الضراوة، الجودة، التسمم الغذائي.