Egypt. J. Chem. **Vol.68** , No .8 pp 601- 611 (2025)

Egyptian Journal of Chemistry

http://ejchem.journals.ekb.eg/

Morphological Detection and Molecular diagnosis of some food-borne pathogens from Camel meat

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Abstract

A well-balanced diet requires essential vitamins, minerals, high protein, and essential amino acids, such as those found in camel meat. A total of 50 camel carcasses, weighing 25 kg, were obtained, with 500g samples collected from various retail markets in Jeddah city. Bacterial isolations, including *Escherichia coli, Staphylococcus aureus, Salmonella sp, Klebsiella pneumoniae, Pseudomonas aeruginosa, and Hafnia alvei*, were carried out using bacteriological plating, microscopic inspection, and serological testing. The camel samples' bacterial profiles revealed the presence of *Staphylococcus* spp. in approximately 70% and 40% of the analyzed samples, respectively. Positive aerobic bacteria constituted 50% of the entire camel samples. Only 2 out of 50 camel samples (5%) tested positive for *Pseudomonas spp.* All camel meat samples met the microbiological criteria for food (GSO 1016/2015) and were deemed safe for human consumption. This research offers promising solutions to combat *E. coli, Staphylococcus aureus, Staphylococcus saprophyticus, Pseudomonas aeruginosa, Klebsiella pneumoniae, and Hafnia alvei* contamination in meat products.

Keywords: *Staphylococcus aureus, Staphylococcus saprophyticus, Pseudomonas aeruginosa, Klebsiella pneumoniae, Hafnia alvei,* PCR detection.

1. Introduction

Meat is one of the most favorable food items for people around the world due to it delicious taste and aroma with variety of dishes and products which prepared by meat, in addition to its richness of essential proteins, minerals and vitamins [1]. Generally speaking, beef, poultry, chevon, and camel meat are some of the many varieties of meat that are frequently consumed in Islamic countries. Due to its high-quality protein and less fat, lower calories, and lower cholesterol levels than other animal meats, camel meat is one of the healthiest meat kinds from the standpoint of health and nutritional value [2].

Camel flesh contains between 20 and 23% protein, which considered as one of the excellent sources of protein in diet[3]. On the other side fat content in Camel meat about (1.51%) with lower cholesterol level (57.56 mg/100 g) which scored significantly lower results when comparing withbeef (6.83%) and mutton (4.56%) fat and (74.5 mg/100 g) beef cholesterol[4-6]**.**

As a result, camel meat can become a popular type of meat all over the world despite the fact that eating meat has a detrimental impact on human health due to the large level of saturated fat content. Furthermore, camel meat consumption has additional benefits due to the high amount of polyunsaturated fatty acids and low cholesterol [7].

According to **Ulmer *et al.*** [8] camel shoulder muscles contain the following amounts of minerals and vitamins per 100 g: calcium 6.5 g, magnesium 23.6 g, potassium 293 g, sodium 58.2 g, zinc 3.4 g, iron 2.1 g, copper 0.2 g, thiamine 0.12 g, riboflavin 0.18 g, pyridoxine 0.25 g, and alpha-tocopherol 0.61 g. The researchers discovered that camel meat has a high iron level (45.5 mg/100 g), compared to beef (1.8 mg/100 g), mutton (4.05 mg/100 g), and chicken (0.4 mg/100 g). Vitamin C, B3, B6, B12, D, and E are far more abundant in camel meat than in beef, mutton, and fowl [6].

There are many different types of foodborne diseases, and they continue to seriously harm people's health everywhere in the world. Many different microorganisms that are transmitted through food are the cause of human diseases. Microbes are present. (*Escherichia coli*(*E. coli*), *Staphylococcus aureus* and *Staphylococcus saprophyticus*) in food poses food poisoning problem [9].Foodborne infections caused by consuming

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Received Date: 16 October 2024, Revised Date: 13 December 2024, Accepted Date: 17 December 2024

DOI: 10.21608/EJCHEM.2024.328752.10637

contaminated food are becoming more common around the world. *E. coli*, *Staphylococcusaureus*, *Staphylococcussaprophyticus*, *Klebsiellapneumoniae*, *Pseudomonas aeruginosa,* and *Hafnia alvei* are examples of foodborne illnesses [10]. Food poisoning is a general word that refers to a number of unpleasant conditions. It is also sometimes referred to as foodborne illness or illness brought on by eating contaminated food. The majority of physical signs of food poisoning include nausea, vomiting, watery diarrhea (sometimes bloody), stomach cramps, fever, and other symptoms.These illnesses often last a few hours to several days and might manifest as mild to severe instances [11-13].

Additionally, microbial growth can develop inside of a person's body (food infection), generate toxins (food intoxication), or grow inside of a person's body (food poisoning) and release toxins (food toxico-infection) [14].
The purpose of meat hygiene practices is to avoid the spread of disease to humans and to provide them with safe whole-animal meat for eating, especially now that meat is regarded as a necessary food and a type of high-quality animal protein [15].
Although Arabian Consuming Camel meat more than other nations but there is shortage in studies which concern with microbial evaluation of Camel meat therefore this study aimed to Microbial evaluation and molecular identification of microorganisms isolated from camel meat sold in Jeddah markets.

2. Experimental

2.1. Collection and Preparation of Samples (Figure 1)

Fifty camel carcasses totaling 25 kg of camel samples were obtained; 500g of each sample was acquired from a different retail market in Jeddah city. Sterile technique was carefully observed during sample collection. Samples were gathered and sent right away to the microbiology postgraduate lab at the University of Jeddah's College of Science in pre-chilled, insulated containers with frozen packs. As demonstrated in the table below, all samples were made in accordance with the method advised by **APHA** [16]. Each sample was combined with 9 ml of sterile buffered peptone water 0.1% under aseptic conditions, and the mixture was then homogenized to create a dilution (1/10).

2.2. Isolation of Aerobic and Anaerobic Colony Count

Spread the inoculum over the surface of the agar using a glass spreader using the spread plate method to determine the aerobic colony count, the plates should be incubated for 48 h at 37°C in an anaerobic jar (Gaspak + anaerobic system) after solidification for anaerobic counts. count the colonies on dishes containing 30–300 colonies and record the results every dilution counted. The 10-fold reduced inoculation volume should be taken into consideration by multiplying final values by 10 (ten). CFU/g is used to express results.Isolation of total *E. coli* usingEosin methylene blue agarafter 30 - 35 °C for 24 h.incubation the colonies appeared as a green metallic luster which counted. While the intestinal air colonies are pink/orange in color with darker centers. Isolated typical colonies or colonies most likely to be *E. coli* were subjected to further identification by microscopic examination and biochemical tests including Indole (+), methyl red (+), Voges-Proskauer (-) and Citrate (-) [17].

K. pneumoniae colonies on Eosin-methylene blue (EMB) agar medium(Techno Pharmchem, Vardhman City Center, New Delhi, India)varies from pink to purple, grew, when incubated at 37°C/24 h, then isolate colony was found using Gram's staining, colony characteristics, and biochemical assays. Indole negative (-ve), Methyl red negative (-ve), Voges Proskauer test positive (+ve), citrate utilization tests positive (+ve), fermentation test (+ve), catalase (+ve), and oxidase test were the biochemical test features that were detected (-ve)[18]**.**
P. aeruginosa colonies are colorless indicating lack of fermentation on EMB and incubated at 35 °C within 48 h. Identification by biochemical tests as following; oxidase (+ve) however, some strain particularly the mucoid ones display a slow oxidase reaction and Catalase (+ve),indole (-ve), citrate (+ve), urease (-ve), nitrate Reduction (+ve)Methyl red negative (-ve) and Voges Proskauer test (-ve) [19]. While, ***Hafnia alvei*** incubated at 35 °C within 48 h on EMB appeared as colorless colonies with the following characters biochemically; Citrate positive (+ve), Flagella flagellated, Catalase positive (+ve), Indole Negative (-ve), Motility Motile, MR (Methyl Red) Variable, Gram Staining Negative (-ve), Positive (+ve) Nitrate Reduction, Oxidative Fermentative Fermentation Shap Rod, Spore Non-Sporing, Oxidase Negative (-ve), Pigment Negative (-ve), and Urease Negative (-ve).

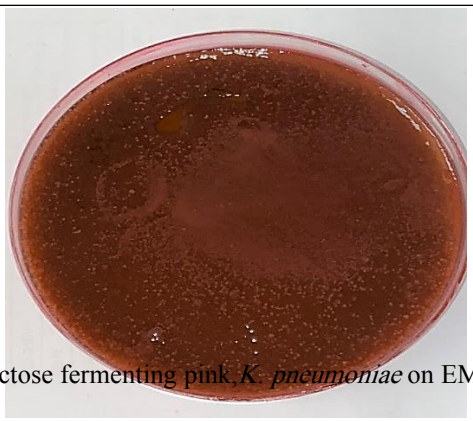
2.3. Isolation and identification of *S. aureus* and*S. saprophyticus* according to ISO [20]

Using mannitol salt agar(MSA Medium)(Techno Pharmchem, Vardhman City Center, New Delhi, India)and incubate the plates at 30°C in an inverted position for 24 to 48 h, the orange colonies represent *S. saprophyticus*, five typical colonies were selected on nutrient agar slant for additional confirmation. Suspected yellow colonies with yellow zones were counted to achieve the total *S. aureus* count. Biochemical assays were used to further identify isolated typical colonies or colonies*S. aureus* (coagulase +ve) or other bacterial species (coagulase -ve) like, *S.saprophyticus.*

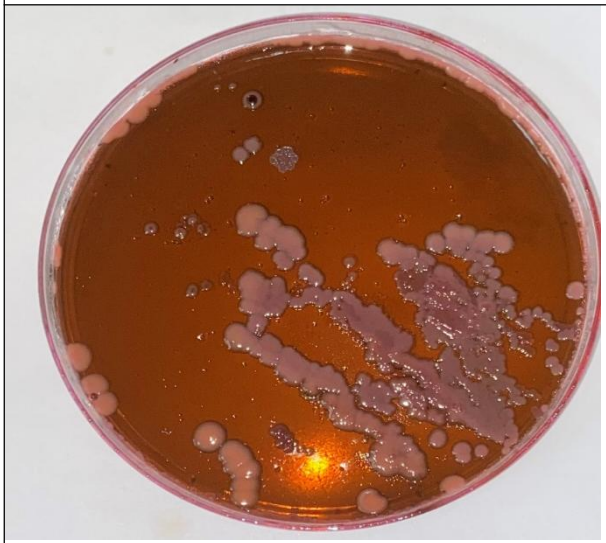
E. coli metallic green sheen on EMBagar

Yellow colonies of *S. aureus,* ferments MSA agar

Staphylococcus saprophyticus non mannitol fermenter on MSA agar



Lactose fermenting pink, *K. pneumoniae* on EMB agar



Pseudomonas aeruginosa, non-lactose fermenter

Hafnia alvei on EMB agar

Figure 1. Appearance of different isolated microorganisms

2.4. Serological Identification: Nucleic Acid Isolation

According to the manufacturing process, the samples were isolated using the "Quick-DNATM Fungal/Bacterial Miniprep" kit from Zymo research (cat. no. D6005) [21]**.**

Polymerase chain reaction: the primer sequences used for the PCR were 27 Forward (5'-AGAGTTTGATCMTGGCTCAG-3')and 1492 Reverse (5'-TACGGYTACCTTGTTACGACTT -3') and were made with DreamTaq Green PCR Master Mix (2X) (cat# K1081). With a total volume of 25 µl, the procedure is carried out as following; denaturation at 95°C/30 Sec.,followed by annealing at 58°C/ 30Sec and extension performed at 72°C/90 min. then final extension performed at 72°C/7 min and holding at 4°C until using **[**22]**.**

Primer design (Table 1): Using the MegAlign tool, relevant 16S rDNA sequences from the GenBank database were aligned (DNASTAR Inc., Madison, Wis.). Putative genus- and species-specific primers were created based on this alignment [22]**.**

Gel Electrophoresis: Verification of the PCR amplification product's quality and size is done using agarose gel electrophoresis. Utilizing Ultrapure Agarose from Cleaver Scientific and 1X TBE buffer, a 2% gel is created and stained with Safe DNA Stain (Invitrogen, California USA). Each gel well was filled with 4 µl of PCR product. Alongside the samples, a DNA ladder (100-1000) from molecule one was run for 30 minat 100 mV. Using a UV trans-illuminator called the Gel Doc system imager, DNA fragments were seen.

PCR Purification: ExoSAP-ITTM was used to purify the amplified DNA. Mix 5 l of PCR reaction product and 2 µl of ExoSAPITTM in accordance with the manufacturing protocol. The remaining primers and nucleotides should then be incubated for 15 min at 37°C before being incubated at 80°C for 15 min to inactivate the ExoSAP-ITTM reagent.

Cycle sequencing PCR: the PCR reaction for cycle sequencing was performed using the BigDye Terminator v3.1 Cycle Sequencing kit (Life Technologies, USA).

Cycle sequencing PCR: Using BigDye X Terminator, the cycle sequencing purification was carried out (Applied Biosystem, USA).

Sequencing Platform: SeqStudio(Life Technologies, USA) was used for sequencing, and it was run after a medium module.

Sequence Alignment: Sequence analysis by SNapGene version 6.0.2 and extract Fasta format and alignment through an online tool NCBI blast.

Table 1. Serological identification

Description	Sequencing primer
E. coli	>F5_S024-2-27F_2_20220403_124143 GGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTG GGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTA
Staphylococcus aureus	>E5_S024-2-27F_2_20220403_124195 TTTGTCACCTTCGACGGCTAGCTCCATAAATGGTTACTCCACCGGCTTCGGGTGTTACAAA CTCTCGTGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTCACCGTAGCATGCT GATCTACGATTACTAGCGATTCCAGCTTCATGTAGTCGA
Staphylococcus saprophyticus	>B2_S024-4-27F_2_20220403_124459 GTCACCGGCAGTCAACCTAGAGTGCCCAACTTAATGATGGCAACTAAGCTTAAGGGTTGC GCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCATGCACCAC CTGTCACT
Klebsiella pneumonia	>F6_S024-2-27F_2_20220403_124143 CTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAAT GGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTA CTTTCAG

	>G5_S024-3-27F_3_20220403_124144
Pseudomonas aeruginosa	CAGTCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATAT TGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGTGTGAAGAAGGTCTTCGGATT GTAAAGCA
	>F2_S024-2-27F_2_20220403_124143
Hafnia alvei	GTAATGTCTGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACC GCATGACGTCTTCGGACCAAAGTGGGGGACCTTCGGGCCTCACGCCATCAGATGTGCCCA GATGGGAT

2.5. Statistical analysis

Every value is displayed as a mean with standard error. The statistical analysis for this study was performed using **(SPSS16)**. Data were analyzed using the one-way analysis of variance approach (ANOVA test). The significant differences ($P<0.05$).

3. Results

3.1. Statistical Analysis of Different types of microorganisms in Camel Samples

Bacteriological profile of the camel samples revealed the positive aerobic bacteria were about 50/50 (100%) of the total camel sample same result detected in case of Anaerobic, while *Enterobacteriacea*spp.and *Staphylococcus* spp.count were about (70%), (40%) respectively while only about 2/50 (5%) of tested camel sample were have *Pseudomonas* spp.

Statistical analysis for different types of micro-organisms (CFU/g) in the minced camel samples discussed on Table (2) were; the total aerobic counts reported about; 9.0×10^2, 20.5×10^4, $4.2 \times 10^4 \pm 1.7 \times 10^4$as minimum, maximum, mean ±SE values respectively while, about; In the instance of the total anaerobic count, the minimum, maximum, mean, and standard error of the mean values were found to be 1.0×10^3, 1.9×10^5, 3.8×10^4, and 1.5×10^4, respectively.*Enterobacteriacea*spp. showed about; 1.06×10^4, 4.3×10^4, $2.9 \times 10^4 \pm 4.5 \times 10^3$as minimum, maximum, mean ±SE values respectively while, about;1.6×10^4, 3.3×10^4, $2.5 \times 10^4 \pm 2.4 \times 10^3$were detected as minimum, maximum, mean ±SE values respectively in case of *Staphylococcus* spp. counts.

Table 2. Statistical analysis for different types of microorganisms (CFU/g) in Camel samples

Micro-organisms	Minimum	Maximum	Mean	SE±
Aerobic count	9.00×10^2	20.5×10^4	4.2×10^4	1.7×10^4
Anaerobic count	1.00×10^3	1.90×10^5	3.8×10^4	1.5×10^4
*Enterobacteriacae*spp.	1.06×10^4	4.30×10^4	2.9×10^4	4.5×10^3
Staphylococcus spp.	1.60×10^4	3.30×10^4	2.5×10^4	2.4×10^3

3.2. Comparison with microbiological criteria for foodstuffs

The permitted level for various meat products falls between 5×10^5 and 5×10^6CFU/g, as per Saudi Arabia's microbiological requirements for foodstuffs. All samples should be free of any foodborne pathogens in the case of total aerobic count and anaerobic, 10^2 -10^3 CFU/g in the case of *Enterobacteriacae*, and 10^2 -10^3CFU/g in the case of *Staphylococcus*.

Comparison with the microbiological standards for food, as seen in Figure (2), revealed that all of the camel meat samples examined were acceptable for human consumption.

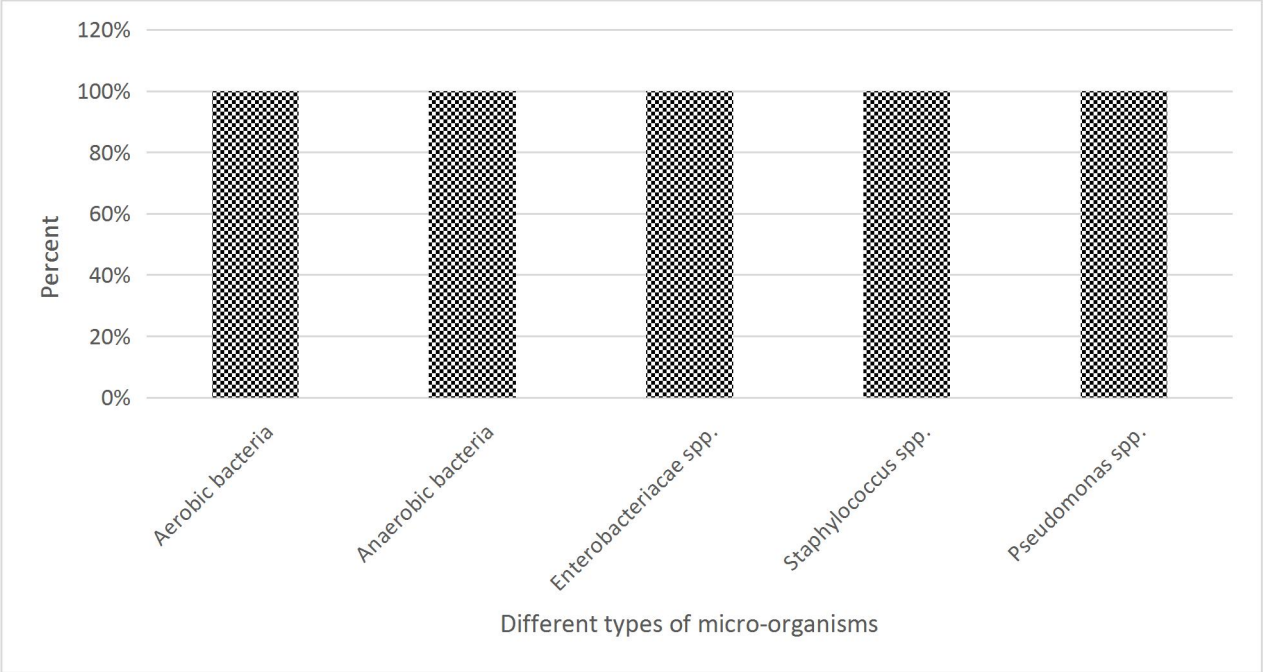
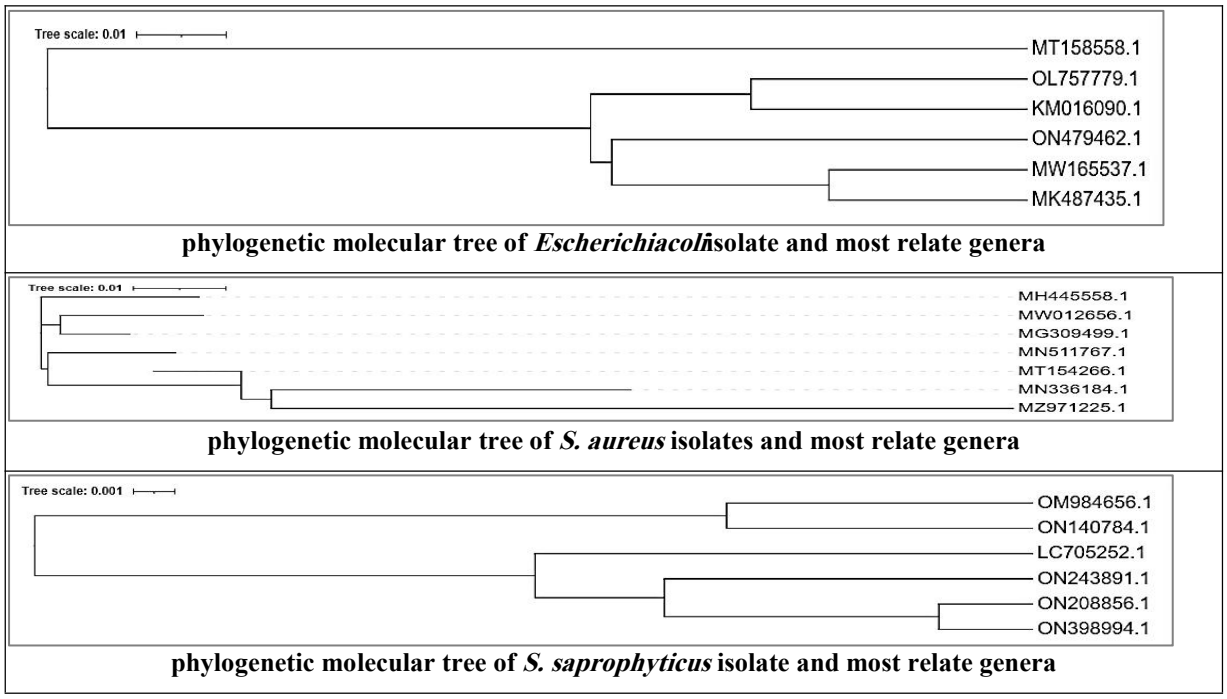


Figure 2. Comparison with microbiological criteria for foodstuffs

3.3. Molecular Identification of isolated microorganism:

Figure (3) show that thePCR identification was as following; *E. coli, Staphylococcussaprophyticus, Staphylococcus aureus, Klebsiella pneumoniae, Pseudomonas aeruginosa, Hafnia alvei*were 2/12 (16.6%) for all microorganisms.



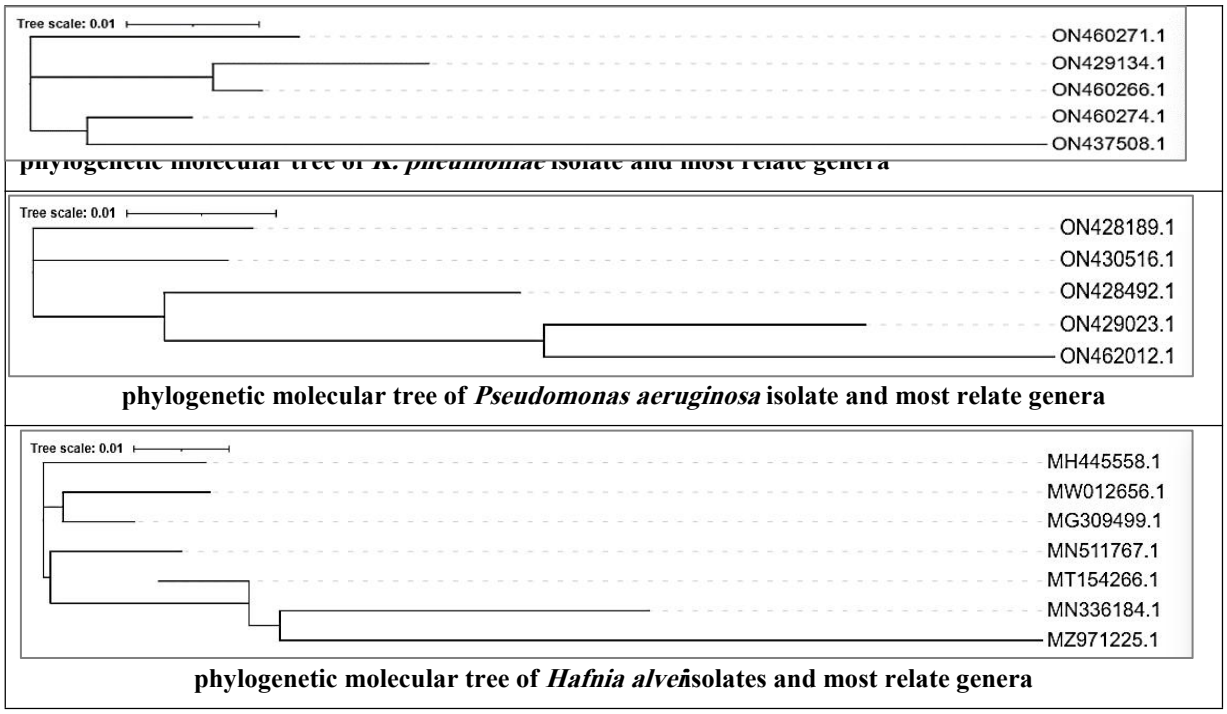


Figure 3. Molecular Identification of isolated microorganism

4. Discussion

Camel meat has been the most neglected animal as the meat source over the years whether its richness in nutrient elements specially protein [23-24]. This neglection not including the study of the nutritious compounds only but including the microbiological profile also [25-26].

Bacteriological analysis of the camel samples showed that the positive aerobic bacteria made up around 50%(100%) of the whole camel sample, while only about70%,40%, and 2/50(5%), respectively, of the tested camel samples contained *Staphylococcus* spp. and *Pseudomonas* spp., respectively. of the camel samples revealed; the positive aerobic bacteria were about 50/50 (100%) of the total camel sample same result detected in case of Anaerobic, *Enterobacteriacea*spp. count while, only about (70%), (40%) of tested camel sample have *Staphylococcus* spp. while only about 2/50 (5%) of tested camel sample were have *Pseudomonas* spp. Statistical analysis for Different Types of Micro-organisms (CFU/g) in the minced camel samples were; the total aerobic counts reported about; 9.0×10^2, 20.5×10^4, $4.2 \times 10^4 \pm 1.7 \times 10^4$ as minimum, maximum, mean ±SE values respectively while, about; 1.0×10^3, 1.9×10^5, $3.8 \times 10^4 \pm 1.5 \times 10^4$were detected as minimum, maximum, mean ±SE values respectively in case of total anaerobic count. *Enterobacteriacea*spp. showed about; 1.06×10^4, 4.3×10^4, $2.9 \times 10^4 \pm 4.5 \times 10^3$as minimum, maximum, mean ±SE values respectively while, about;1.6×10^4, 3.3×10^4, $2.5 \times 10^4 \pm 2.4 \times 10^3$ were detected as minimum, maximum, mean ±SE values respectively in case of *Staphylococcus* spp. counts. Comparison with microbiological criteria for foodstuffs [27]declared that; all tested camel meat samples were within permissible limit and fit for human consumption. PCR identification mentioned in table and figure (4.1.4) were as following; *E. coli, Staphylococcussaprophyticus, Staphylococcus aureus, Klebsiella pneumoniae, Pseudomonas aeruginosa, Hafnia alvei*were 2/12 (16.6%) for all microorganisms.

The abattoir and butcheries' internal sanitary conditions have always been gauged by the overall viable count. **Hassen *et al.*** [1] found a higher result when they examined Ethiopian camel meat samples and discovered 4.67.017 log10CFU/g aerobic plate counts. Poor handling and hygiene methods that caused cross contamination and recontamination of meat were blamed for the increased Activated Protein C (APC)APCs found in this study [28]. The APC values from the meat samples in the neighborhood butcheries, however, were higher than those from abattoirs but lower than the recommended amount of fewer than 6.00 log10CFU /g/cm2 recommended by the International Commission on Microbiological Specifications for Foods (ICMSF, the Commission). A high microbe count that is greater than 7.00 Log CFU/g of Total Plate Count (TPC) is a signof meat deterioration and significant health risks. Meat hygiene must be rapidly improved because the total plate count for raw meat surpassing 5 log10 CFU/g was unacceptable [29]**.**

The 60% of the samples in this investigation showed APC levels greater than 5 log10CFU/g, which is a sign of severely infected meat. The butcheries house's significantly higher mean APCs than the abattoirs indicate that meat is handled in an excessively unhygienic manner, that storage and transportation conditions are of lower quality, and that the butcheries house provides an environment that is conducive to the growth of aerobic bacteria. The current study's findings are significantly more polluted than those from **Al-Dughaymand Yassein**[30]. Our research found that the surface camel carcasses had mean aerobic plate counts of $4x10^3$, $5x10^3$ and $6.2x10^3$ CFU/cm^2, respectively, before skinning, after skinning, and after preparation and stamping. The increased amount of aerobic plate count seen in this study is consistent with other studies [31].

This study's outcome was less favorable than *E. coli* was found in fresh meat from the abattoir and (22.2%) butchers in Mekele, Ethiopia, according to **Haileselassie *et al.*** [32] research. *E. coli* contamination rates from raw meat were high at the butchers (38.2%) and the abattoir (55.9%)[33]. These results complement **Mohammed, *et al.*** [6] conclusion that *E. coli* was isolated from staff members' hands at the butcher shop and the abattoir in Ethiopia, respectively, in percentages of 46.2% and 52.6%. Higher results were reported by **Sternišа*et al.*** [34]. who examined 80 camel meat carcasses from Egyptian abattoirs and found that the mean *Enterobacteriaceae* counts were around ($9.77x10^7$;$3.44 x10^7$), higher rates of *Klebsiella pnumoniae* (35%), and approximately 5% of *E. coli* isolates. Almost same outcomes were reported by **Wie,** [35]**.** From 68 samples of camel meat, **Hassen *et al.***[1] evaluated the hygienic practices used in Ethiopia for handling raw camel meat. *S. aureus, E. coli*, and *Salmonella* spp. were found in 12 (35.3%), 16 (47%) and 8 (23.5%) of the raw camel meat samples, and in 19 (55.9%), 22 (64.7%) and 10 (29.4%) of the butcheries, respectively. On the other hand**, Babiker *et al.*** [36]. established that camel carcasses in a slaughterhouse in Sudan were contaminated with microorganisms. *Pseudomonas* spp. (18.69%) had the highest TBC and *Salmonella* spp. (1.62%) had the lowest. The TBC varied from 12 x 10^3cfu/ml to 1, 2 x10^3CFU/ml.

Alebie*et al.*[37]found about *Staphylococcus aureus* (8.7%), *Escherichia coli* (6.52%), *Kebsiellapnumoniae*(4.35%) from camel corpses in Ethiopia. This finding is less than that made public by **Regassa *et al.***[38]. and **Suheir *et al.*** [39] who discovered a prevalence of 36.87% and 39.4% in camel herds in Ethiopia and Sudan, respectively.This result agrees with the findings of **Mengistu *et al.*** [40]. which is 9.6% and 2.1%, for *E. coli*, *Klebsiella pnumoniae* respectively. Another study performed by **Osman *et al.*** [41]. Using PCR to identify *Pseudomonas* species, it was discovered that 10/100 samples of Egyptian camel flesh contained *Pseudomonas* species, with *Pseudomonas aeruginosa* accounting for 8/10 and *Pseudomonasfluorescens* for 2%. In addition to being resistant to four to eight different classes—four to six different antibiotics—the isolates were also multidrug resistant.

Gram-negative bacillus *Hafnia alvei* is a member of the *Enterobacter* ales order's newly proposed Hafniaceaefamily [42-43]. *H. alvei* can be found in a variety of natural settings, including fish farms, rivers, and streams that have been contaminated [44]. This bacterium is also common in the digestive tract of many animals[26]. Several animal species, including mammals, fish, birds, and insects, have been thought to be susceptible to some *H. alvei* strains, which are considered opportunistic pathogens [45]**,** and are also suspected to cause a variety of disorders in humans [46]. According to taxonomic identification, several *H. alvei* strains were related species' strains of *Escherichia*, Citrobacter, *Salmonella*, and *Serratia* [47-48].All systems were used to identify strains of *H. alvei* isolated from food with satisfactory results [49-50]**.** It's significant because some *H. alvei* strains found in various foods contain genes for toxins like the verodoxin and the heat-stable *E. coli* toxin. *H. alvei*include verodoxins, as demonstrated by in vitro studies against a tissue culture cell line made from monkey kidney epithelial cells[51]**.** *H. alvei* was also listed among the microorganisms that contribute favorably to food fermentations, and in some circumstances, it appears to play a significant role in food spoiling[52].

5. Conclusion

The presence of bacterial pathogens in camel meat poses a significant risk to consumers, as these pathogens can thrive and reproduce under favorable conditions. The growth of bacteria on meat surfaces can lead to a decline in product quality and potential health hazards. In addition to being a rich source of protein and essential amino acids, camel meat should also contain vitamins and minerals such as vitamin B, vitamin A, zinc, and iron to provide a complete diet. The isolation and identification of bacterial pathogens, including *E. coli, Staphylococcus aureus, Salmonella sp, Klebsiella pneumoniae, Pseudomonas aeruginosa, and Hafnia alvei*, were carried out using bacteriological plating, microscopic inspection, and serological testing. The camel meat samples analyzed showed the presence of *Staphylococcus spp.* in approximately 70% and 40% of the samples, respectively. Positive aerobic bacteria accounted for around 50% of the entire sample, while only 5% of the samples tested positive for *Pseudomonas spp.* The microbiological criteria for food were met by all camel meat samples, indicating their suitability for human consumption. To combat the presence of bacterial pathogens such as *E. coli,*

Staphylococcus aureus, Staphylococcus saprophyticus, Pseudomonas aeruginosa, Klebsiella pneumoniae, and *Hafnia alvei*, the use of Arabic gum extracts was investigated as a potential solution.

Supplementary Materials: None

Author Contributions:

All authors have made substantial, direct, and intellectual contribution to the work andapprove it for publication.

Funding: None

Data Availability Statement:

All datasets generated or analyzed duringthis study are included in this manuscript

Acknowledgments: None

Conflicts of Interest:

The authors declare that there is no conflict of interest.

REFERENCES

1. Hassen KA, Omer SA, Hassen NA. Assessment of hygienic practice on camel meat handlers, and identification of bacterial contamination in Abattoir and Butcheries of Nagelle Town, Southern Oromia, Ethiopia. International Research Journal of Science and Technology. 2021;2(2):384-97.
2. Maqsood S, Al Haddad NA, Mudgil P. Vacuum packaging as an effective strategy to retard off-odour development, microbial spoilage, protein degradation and retain sensory quality of camel meat. LWT-Food Science and Technology. 2016 Oct 1; 72:55-62.
3. Al-Owaimer AN, Suliman GM, Sami AS, Picard B, Hocquette JF. Chemical composition and structural characteristics of Arabian camel (*Camelus dromedarius*) m. longissimus thoracis. Meat science. 2014 Mar 1;96(3):1233-41.
4. Elsharawy NT, Ahmad AM, Abdelrahman HA. Quality assessment of nutritional value and safety of different meat. Journal of Food: Microbiology, Safety & Hygiene. 2018;3(1):1-5.
5. Mohammed SA. A study of cholesterol concentrations of camel meat and beef. International Journal of Agricultural Research, Innovation and Technology 2019;7(4):397-401.
6. Mohammed HH, Jin G, Ma M, Khalifa I, Shukat R, Elkhedir AE, Zeng Q, Noman AE. Comparative characterization of proximate nutritional compositions, microbial quality and safety of camel meat in relation to mutton, beef, and chicken. LWT. 2020 Jan 1; 118:108714.
7. Bekhit AE, Farouk MM. 13 Nutritive and Health Value of Camel Meat. Camel meat and meat products. 2013:205.
8. Ulmer K, Herrmann K, Fischer A. Meat products from camel meat. Milk and meat from the camel. 2004:137-228.
9. Umesha S, Manukumar HM. Advanced molecular diagnostic techniques for detection of food-borne pathogens: Current applications and future challenges. Critical Reviews in Food Science and Nutrition. 2018 Jan 2;58(1):84-104.
10. Bhardwaj N, Bhardwaj SK, Nayak MK, Mehta J, Kim KH, Deep A. Fluorescent Nano biosensors for the targeted detection of foodborne bacteria. Trends in Analytical Chemistry. 2017 Dec 1; 97:120-35.
11. Hennekinne JA, Herbin S, Firmesse O, Auvray F. European food poisoning outbreaks involving meat and meat-based products. Procedia Food Science. 2015 Jan 1; 5:93-6.
12. Al-Agroudi MA, Morsy AT, Ismail MA, Morsy TA. Protozoa causing food poisoning. Journal of the Egyptian Society of Parasitology. 2016 Dec 1;46(3):497-508.
13. Sadilek A, Kautz H, DiPrete L, Labus B, Portman E, Teitel J, Silenzio V. Deploying nEmesis: Preventing foodborne illness by data mining social media. Ai Magazine. 2017 Mar 31;38(1):37-48.
14. Pal M, Ayele Y, Patel AS, Dulo F. Microbiological and hygienic quality of Meat and Meat Products. Beverage Food World. 2018;45(5):21-7.
15. Mousa MM, Rizk MM, Makled EA. Microbial profile of fresh beef meat. Alexandria Journal of Veterinary Sciences, 2015; 46(1), 146-154.
16. American Public Health Association: Standard Methods for the Examination of Water and Wastewater (20th ed.). APHA. (2002).
17. Divya PS, Paul S, Fathima PA, Abdulla MH. Comparative evaluation of EMB agar and hicrome E. coli agar for differentiation of green metallic sheen producing non-E. *Coli* and typical *E. Coli* colonies from food and environmental samples. Journal of Pure and Applied Microbiology. 2016 Dec;10(4):2863-70.
18. Patel SS, Chauhan HC, Patel AC, Shrimali MD, Patel KB, Prajapati BI, Kala JK, Patel MG, Rajgor M, Patel M. Isolation and identification of *Klebsiella pneumoniae* from sheep-case report. International Journal of Current Microbiology and Applied Sciences. 2017;6(5):331-4.
19. Aprameya IV. Non-fermenters other than *Pseudomonas* species. Journal of The Academy of Clinical Microbiologists. 2013 Jul 1;15(2):62-5.
20. ISO 6888-2 (1999): Microbiology of food and animal feeding stuffs – Horizontal method for the enumeration of coagulase-positive *Staphylococci* (*Staphylococcus aureus* and other species) – Part 2: Technique using rabbit plasma fibrinogen agar medium.
21. Al-Azawi IH, Al-Hamadani AH, Hasson SO. Association between biofilm formation and susceptibility to antibiotics in *Staphylococcus lentus* isolated from urinary catheterized patients. Nano Biomedicine and Engineering, 2018 Jun 1;10(2):97-103.

22. Spilker T, Coenye T, Vandamme P, LiPuma JJ. PCR-based assay for differentiation of *Pseudomonas aeruginosa* from other *Pseudomonas* species recovered from cystic fibrosis patients. Journal of clinical microbiology. 2004 May;42(5):2074-9.
23. Wambui JM, Lamuka PO, Njage PM. Lactic acid bacteria isolate from fermented camel milk (Suusac) are potential protective cultures of raw camel meat. International Journal of Agriculture and Environmental Research. 2017 Jun 30;3(3):2960-75.
24. Kalalou I, Zerdani I, Faid M. The growth and survival of *P. aeruginosa* (ATCC 29733) and E. coli O157: H7 inoculated onto ground raw dromedary and beef meat stored at 10° C. World Journal of Dairy & Food Sciences. 2010, 5 (1): 30–38.
25. ALI S, Rehman R, Abbas A, Mahmud T, Anwar J, Salman M. Minerals and nutritional composition of camel (Camelus dromedarius) meat in Pakistan. Journal of the Chemical Society of Pakistan. 2011 Dec 11;33(6):835.
26. Kadim IT, Al-Amri IS, Alkindi AY, Haq QM. Nutritional values and health benefits of dromedary camel meat. Animal Frontiers. 2022 Aug 1;12(4):61-70.
27. Standardization Organization (GSO) GSO 1016/2015. (E) Microbiological Criteriafor Food. Technical Committee for Standards for Food and Agricultural Products" GSO updated Technical Regulation No. 1016 \ 1998 "Microbiological Criteriafor Food".1-26.
28. FAO/WHO, Food safety risk analysis a guide for national food safety authorities. FAO, Rome. FAO Food and Nutrition Paper No. 87. 2006.
29. FAO/WHO, Joint FAO/WHO Food Standards Programmed FAO/WHO coordinating committee for Africa, seventeenth session, Rabat, Morocco, 2007: 23-26.
30. Al-Dughaym, A. M., and N. A. Yassien. "Surface contamination of camel carcasses." Journal Faisal University (2001) 129-138.
31. Hassan Ali N, Farooqui A, Khan A, Khan AY, Kazmi SU. Microbial contamination of raw meat and its environment in retail shops in Karachi. PakistanJournal of Infection in Developing Countries2010;4(6):382-8.
32. Haileselassie M, Taddele H, Adhana K, Kalayou S. Food safety knowledge and practices of abattoir and butchery shops and the microbial profile of meat in Mekelle City, Ethiopia. Asian Pacific journal of tropical biomedicine. 2013 May 1;3(5):407-12.
33. Neufeld LM, Hendriks S, Hugas M. Healthy diet: a definition for the United Nations Food systems summit 2021. In Science and innovations for food systems transformation 2023 Jan 2 (pp. 21-30). Cham: Springer International Publishing.
34. Sterniša M, Klančnik A, Smole Možina S. Spoilage *Pseudomonas* biofilm with *Escherichia coli* protection in fish meat at 5 C. Journal of the Science of Food and Agriculture. 2019 Aug 15;99(10):4635-41.
35. Wie SH. Clinical significance of Providencia bacteremia or bacteriuria. The Korean journal of internal medicine. 2015 Mar;30(2): 167
36. Mohammed BM, Abdalla MA, Elfadil AA, Abdalla NA. Determination of the bacterial contamination of fresh camel meat (Camelus dromedarius) in Tambool town slaughter-house, Sudan, 2014. International Journal of Veterinary Science. 2019: 157-160.
37. Alebie A, Molla A, Adugna W, Tesfaye A, Ejo M. Prevalence, isolation, identification, and risk factors of major bacterial cause of camel subclinical mastitis. BioMed Research International. 2021 Jul 2;2021.
38. Regassa A, Golicha G, Tesfaye D, Abunna F, Megersa B. Prevalence, risk factors, and major bacterial causes of camel mastitis in Borana Zone, Oromia Regional State, Ethiopia. Tropical animal health and production. 2013 Oct; 45:1589-95.
39. Suheir IA, Salim MO, Yasin TE. Bacteria, mycoplasma, and fungi associated with subclinical mastitis in camel. Sudan Journal of Veterinary Research. 2005; 20:23-31.
40. La Chamelle MC. Camel mastitis, associated bacterial pathogens and its impact on milk quality in Gewane District, Afar Regional State, Northeastern Ethiopia. Animal Health and Production. 2010; 58:243.
41. Osman K, Orabi A, Elbehiry A, Hanafy MH, Ali AM. *Pseudomonas* species isolated from camel meat: quorum sensing-dependent virulence, biofilm formation and antibiotic resistance. Future Microbiology. 2019 May;14(7):609-22.
42. Adeolu M, Alnajar S, Naushad S, S. Gupta R. Genome-based phylogeny and taxonomy of the '*Enterobacteriales':* proposal for*Enterobacterales ord. nov.*divided into the families *Enterobacteriaceae, Erwiniaceae fam. nov., Pectobacteriaceae fam. nov., Yersiniaceae fam. nov., Hafniaceae fam. nov., Morganellaceae fam. nov.,* and *Budviciaceae fam.*nov. International journal of systematic and evolutionary microbiology. 2016 Dec;66(12):5575-99.
43. Padilla D, Remuzgo-Martínez S, Acosta F, Ramos-Vivas J. *Hafnia alvei and Hafnia paralvei.* Taxonomy defined but still far from virulence and pathogenicity. Veterinary Microbiology. 2012 Dec 8;163(1-2):200-1.
44. Awolope OK, O'Driscoll NH, Di Salvo A, Lamb AJ. The complete genome sequence of Hafnia alvei A23BA; a potential antibiotic-producing rhizobacterium. BMC Research Notes. 2021 Dec; 14:1-4.
45. Lang H, Duan H, Wang J, Zhang W, Guo J, Zhang X, Hu X, Zheng H. Specific strains of honeybee gut Lactobacillus stimulate host immune system to protect against pathogenic Hafnia alvei. Microbiology Spectrum. 2022 Feb 23;10(1): e01896-21.
46. Ionescu MI, Neagoe DŞ, Crăciun AM, Moldovan OT. The Gram-negative bacilli isolated from caves—*Sphingomonaspaucimobilis and Hafnia alvei* and a review of their involvement in human infections. International journal of environmental research and public health. 2022 Feb 17;19(4):2324.
47. Wright WF, Utz JL, Bruckhart C, Baghli S, Janda JM. Yokenellaregensburgei necrotizing fasciitis in an immunocompromised host. Journal of Infection and Chemotherapy. 2019 Oct 1;25(10):816-9.
48. Koivula TT, Juvonen R, Haikara A, Suihko ML. Characterization of the brewery spoilage bacterium *Obesumbacterium proteus* by automated ribotyping and development of PCR methods for its biotype 1. Journal of applied microbiology. 2006 Feb 1;100(2):398-406.5555

49. Vithanage NR, Yeager TR, Jadhav SR, Palombo EA, Datta N. Comparison of identification systems for psychrotrophic bacteria isolated from raw bovine milk. International journal of food microbiology. 2014 Oct 17; 189:26-38.
50. Höll L, Behr J, Vogel RF. Identification and growth dynamics of meat spoilage microorganisms in modified atmosphere packaged poultry meat by MALDI-TOF MS. Food Microbiology. 2016 Dec 1; 60:84-91.
51. Abbott SL, Moler S, Green N, Tran RK, Wainwright K, Janda JM. Clinical and laboratory diagnostic characteristics and cytotoxigenic potential of *Hafnia alvei* and *Hafnia paralvei* strains. Journal of Clinical Microbiology. 2011 Sep;49(9):3122-6.
52. Bourdichon F, Casaregola S, Farrokh C, Frisvad JC, Gerds ML, Hammes WP, Harnett J, Huys G, Laulund S, Ouwehand A, Powell IB. Food fermentations: microorganisms with technological beneficial use. International journal of Food Microbiology. 2012 Mar 15;154(3):87-97.