ISSN: 0067-2904

Detection of Bacterial Contamination of Imported Chicken Meat in Iraq

Mustafa Basil Abdul Qader*, Marwa Hameed AlKhafaji
Department of Biology, College of Science, University of Baghdad, Baghdad, Iraq

Abstract

With the constant increase in poultry meat consumption worldwide and the large variety of poultry meat products and consumer demand, guaranteeing the microbial safety of poultry carcasses and cuts is crucial.

During 2018; one hundred-ten chicken meat samples were collected randomly from local markets in Baghdad. Selective and differential media were used to isolate and identify the contaminant bacteria from the collected samples, the predominant species was *Klebsiella pneumoniae*, 47 isolates (42%), followed by *Escherichia coli* 35 isolates (31%), 13 (11%) *Citrobacter freundii*, 9 (8%) *Salmonella*, and 6 (5%) *Shigella*. Vitek -2 system used to confirm the identification of *Citrobacter spp*, and *Klebsiella spp.* while 16s rRNA gene amplification using PCR technique was applied to confirm the identification of *C. freundii*.

Keywords: *Citrobacter*, Isolation, Chicken, Bacterial contamination, *Klebsiella*.

التحري عن التلوث البكتيري للحوم الدجاج المستوردة في العراق

مصطفى باسل عبد القادر* ، مروى حميد الخفاجي
قسم علوم الحياه، كليه العلوم، جامعة بغداد، بغداد، العراق

الخلاصة

مع الزيادة المستمرة في استهلاك لحوم الدواجن في جميع أنحاء العالم ، والتنوع الكبير في منتجات لحوم الدواجن و زيادة الطلب من قبل المستهلك ، فإن ضمان سلامة منتجات الدواجن أمر بالغ الأهمية. خلال 2018 ؛ تم جمع 110 عينة من لحوم الدجاج بشكل عشوائي من أسواق بغداد. تم استخدام الاوساط الزرعية الانتقائية والتفريقية لعزل وتحديد البكتيريا الملوثة من العينات التي تم جمعها ، وكانت الأنواع السائدة هي *Klebsiella pneumoniae* ، 47 عزلة (42 %) ، تليها 35 *Escherichia coli* (31 %) ، 13 (11 %) *Citrobacter freundii* و 9 (8%) *Salmonella* و 6 (5%) *Shigella*. تم استخدام نظام Vitek – 2 لتأكيد تشخيص *Citrobacter spp* ، و *Klebsiella spp*. . في حين تم تطبيق سلسلة البلمرة لجين 16S rRNA لتأكيد تشخيص *C. freundii*

Introduction

Poultry meat consumption is steadily increasing worldwide and the large variety of poultry meat products and consumer demand, ensuring the microbial safety of poultry carcasses and cuts is essential [1], in fact, during and after slaughtering, the bacteria from animal microbiota, the slaughterhouse environment, and the equipment used contaminate carcasses, their subsequent cuts, and processed meat products. Some of these bacterial contaminants can grow or survive during food processing and storage [2]. Bacterial contamination by equipment surfaces can take place early in the process. For example, the rubber fingers used for feather removal or conveyor belts can be sources of bacterial contamination [3, 4, 5], Even new rubber fingers can host bacteria and be a source of contamination

*Email: mustafabasil1993@yahoo.com

for carcasses, cross contamination between carcasses or cuts may occur by direct contact or through contact with contaminated surfaces [5].

During the subsequent processing steps (deboning, cutting, mincing, and mixing) for meat-based foodstuff production, manipulators, air and equipment surfaces are the main sources of contamination, in fact, transformation operations increase the surface area of meat in contact with working surfaces and air, consequently, the level of bacteria is higher in transformed products than on primary cuts [6]

Methods

I-Samples Collection

One hundred-ten chicken meat samples were collected randomly from local markets in Baghdad city according to the instruction of the Iraqi Standard Criterion No.2/2270 in sampling, (2006) [7]; from September 2018 to December 2018.

II-Bacterial Isolation

One gram of each chicken meat sample was suspended in 9 ml D.W., left for 30 minutes, then 1ml from each broth/sample was placed in the center of sterile Petri dish using a sterile pipette, Molten cooled agar (approx. 15ml) is then poured into the Petri dish containing the inoculum and mixed well [8].

After the solidification of the agar, the plate was incubated at 37°C for 24-48 hrs. Later the grown colonies were further investigated.

III-Identification

Bacterial isolates were identified to the genus level using both microscopic and macroscopic characteristic on selective and differential media, according to [9], While the identification of *C.freundii* and *Klebsiella* isolates to species level was accomplished by vitek-2 system and PCR technique.

III-Identification of Bacteria by PCR

DNA Extraction

Genomic DNA was isolated from Bacteria according to the protocol of Genomic DNA mini kit, Gene aid. A PCR reaction with a specific primer provided by Advanced Scientific Co alharthia , alkindi ST, Baghdad. (Table-1)

Table 1-Primers and their sequences

Primer Name	Sequences 5 ⟶ 3	Size (bp)
27F	AGAGTTTGATCCTGGCTCAG	1500 bp
1492R	TACGGTTACCTTGTTACGACTT	

(25µl) of PCR amplification mixture contained (12.5µl) Master mix, (1µl) forward primer, (1µl) reverse primer, (8.5µl) nuclease free water, and (2µl) DNA template. The protocol for PCR condition was initial denaturation 95°C for 5 min. denaturation 95°C for 30 sec., annealing 60 °C for 30 sec., extension 72 °C for 1 min. and final extension 72 °C for 7min, 32 cycles.

Results and Discussion

Isolation and Identification

The collected chicken meat samples were cultured on four selective and differential media; all isolates were purified by ABC streaking method on MacConkey agar.

MacConkey agar medium is a selective and differential culture medium for bacteria designed to selectively isolate gram negative and enteric bacilli and differentiate them based on lactose fermentation. After 18 hrs. incubation at 37^{o}C two types of colonies appeared, lactose fermenter pink colonies and non-lactose fermenter pale colonies.

The majority of the bacterial isolates were lactose fermenters with a percentage of 86 while the remaining were unable to ferment lactose (Figure-1)

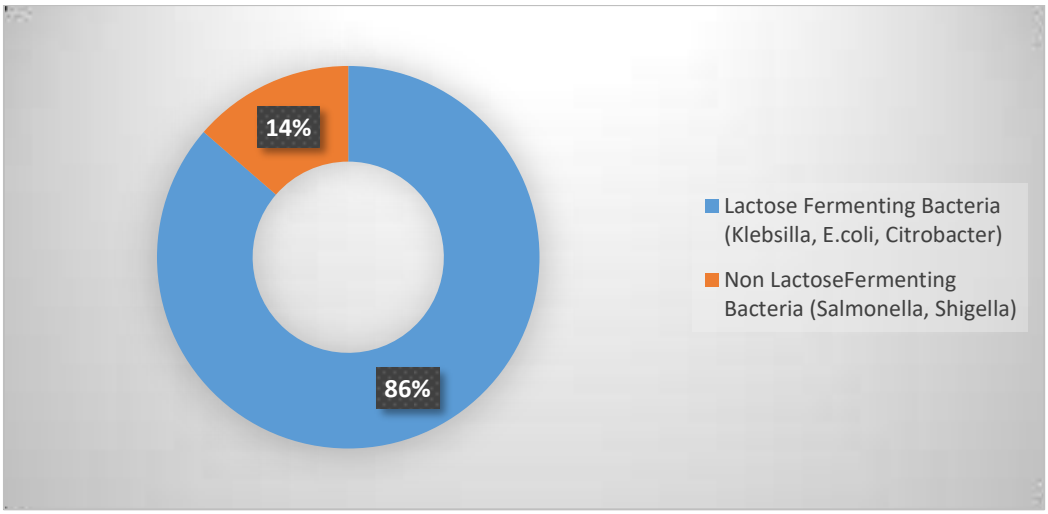

Figure 1-Percentages of lactose fermenting bacteria and lactose non-lactose fermenting bacteria isolated from chicken meat samples

The pink colonies were cultured on EMB, XLD and S.S agar for further investigation, *Citrobacter freundii* appeared as brown colonies on EMB, and small pale flattened colonies with black center on S.S agar due to their ability to produces H2S, as described by [10], this result agree with [11], who managed to isolate *C.freundii* from chicken meat using same selective and differential media. Figure-2 A, B, C, D

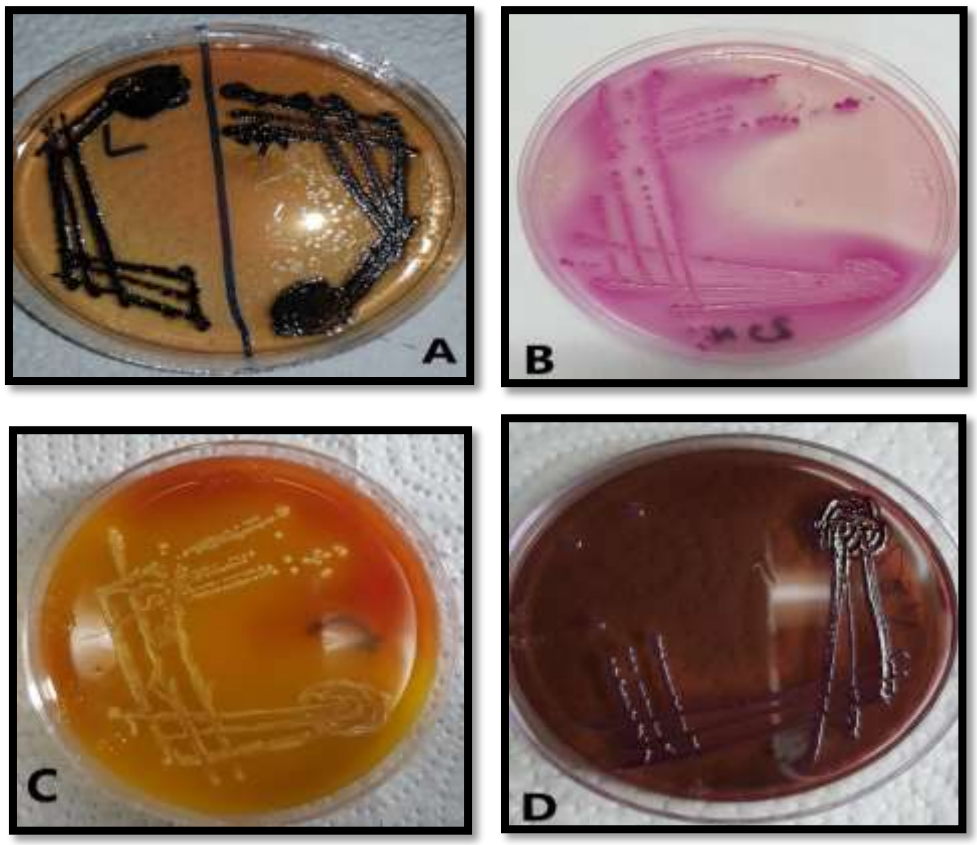

Figure 2-Different selective and differential media cultured with *Citrobacter spp*. after incubation at 37°C for 18 hr
A. Pale colonies with black center on S.S. agar
B. Small pink (Lactose fermenter) colonies on MacConkey agar
C. Yellow colonies on XLD agar
D. Brown colonies on EMB

Escherichia coli identified as pink colonies on MacConkey agar, and with a distinctive green-metallic color on EMB. Figures-(3A, B).

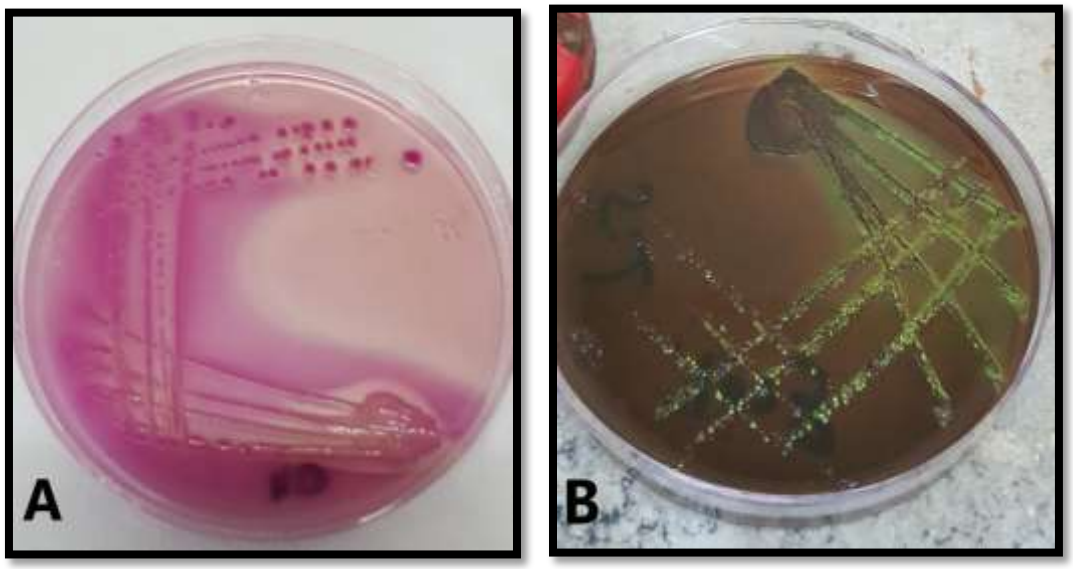

Figure 3-Selective and differential media cultured with food origin *E. coli isolate* after incubation at 37°C for 18 hr.: (A) pink (Lactose fermenter) colonies on MacConkey agar, (B) green metallic sheen colonies on EMB

Other researchers [12], also isolated food origin *E. coli* using these selective and differential media in order to characterize it from other lactose fermenting bacteria.
Klebsiella pneumoniae have two distinguishing characteristics are lactose fermentation on the medium and the viscosity of the colonies. Encapsulated strains of *Klebsiella* spp. are also mucoid in appearance, which is a characteristic of the strains of this genus other studies which used MacConkey as a selective media for *K. pneumoniae* identification [13] (Figure-4).

Figure 4-pink mucoid colonies of *K. pneumoniae* on MacConkey agar after incubation at 37°C for 18 hr.

SS Agar is a highly selective agar used for the isolation of *Salmonella* and *Shigella* species from contaminated samples, *Salmonella* appeared as colorless colonies, with a black center, *Shigella* appeared as colorless colonies on S.S agar. Figures-(5)A, B

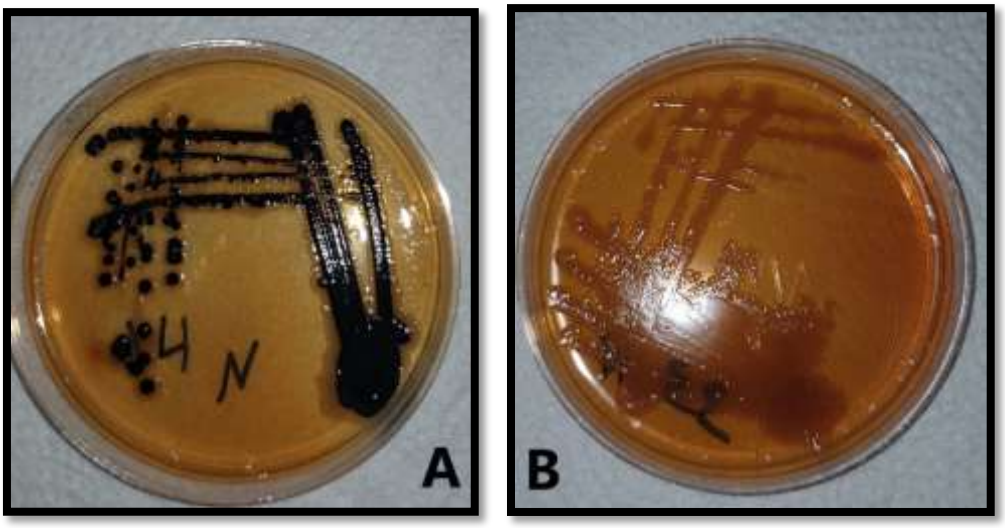

Figure 5-selective and differential S.S media cultured with *Salmonella and Shigella.* after incubation at 37°C for 18 hr.
A- *Salmonella* colorless colonies, with black center
B- *Shigella* colorless colonies, no H_2S
Other studies isolated *Salmonella* and *Shigella* using S.S agar [14, 15]

Table 2-Distribution of samples according to different bacteria isolated from meat chicken

Isolated	No.	Percentage (%)
K.pneumoniae	47	42.73
E. Coli	35	31.82
C. freundii	13	11.82
Salmonella	9	8.18
Shigella	6	5.45
Total	110	100%
Chi-Square (χ^2)	---	9.027 **
** (P<0.01).		

K. pneumoniae is not only a major hospital-acquired pathogen but also an important food-borne pathogen that can cause septicaemia, liver abscesses, and diarrhea in humans. *K.pneumoniae* was the highest containment (42.73%) found in chicken meat samples, according to other researchers *K.pneumoniae* was found in high numbers in different food product including dairy product, meat and retail food These findings are in agreement with previous studies [16] which reported that A total of 78 samples of street foods in Malaysia were examined for the presence of *K. pneumonia* contamination was recorded in 32% of the samples examined.

Vitek -2 system was used to confirm the identification. Figures-(6 A, B).

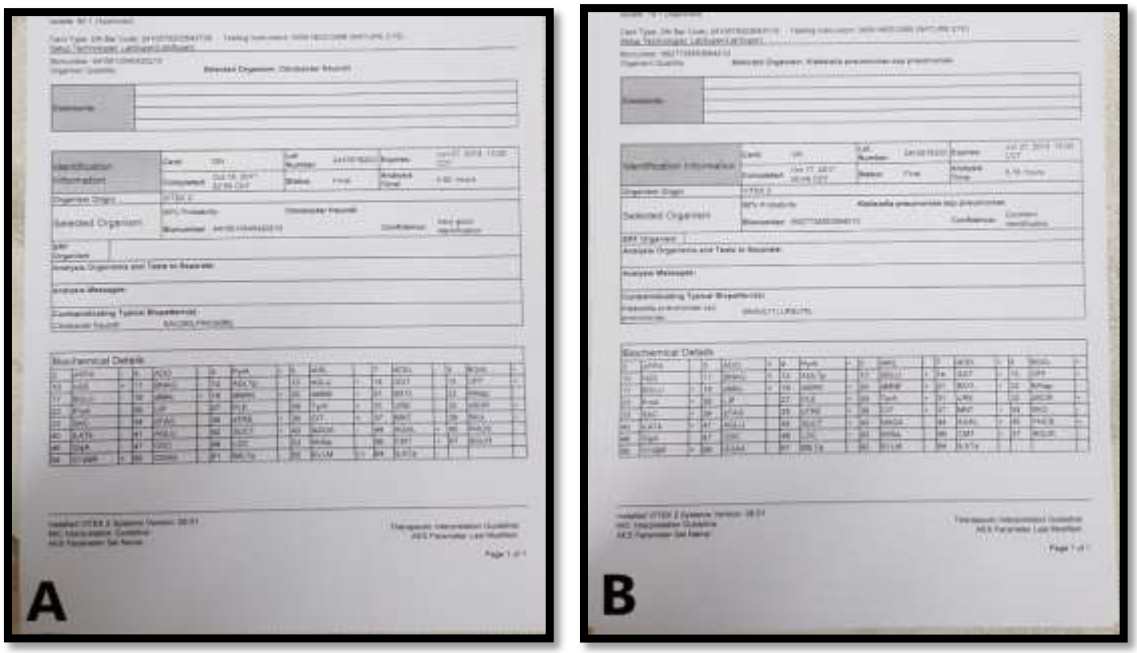

Figure 6-Identification of *C.freundii* (A) and K. *pneumonia* (B) by Vitek 2 compact system

Another study [17] on Retail Foods in China had also reported the presences of *K.pneumonia.* Followed by *E.coli* (31.82%) this result in agreement with previous studies [18] on poultry meat in Nigeria *E.coli* contamination was at 43.4%**,** and *C.freundii* (11.82%). Another study was able to isolate *C.freundii* from chicken meat samples in Iraq [11], *Salmonella* (8.18%), other studies [18] managed to isolate *Salmonella* from poultry meat and it was found in high numbers up to (33%).
Shigella were found in low numbers (5.45%) These findings are in agreement with previous studies [15], which reported low numbers of *shigella* in food samples in Tunisia only six *Shigella* spp. strains were isolated from 280 food samples.

In order to confirm the identification of *Citrobacter*to species level 16S rRNA gene amplification was performed using monoplex PCR technique, 1.5 % agarose gel electrophoresis was used to detect the positive result as shown in Figure-7.

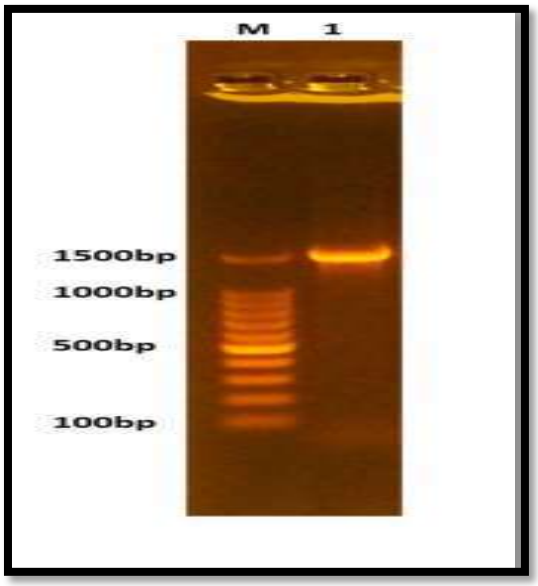

Figure 7-Amplified PCR products of 16SrRNA gene (1500 bp): Agarose gel electrophoresis, ethidium bromide stained, 1.5 % agarose, electrophoresed in 75 volts for 2 hrs. and photographed under ultraviolet trans-illuminator. M: The DNA molecular weight marker (100 bp ladder) and 1: the amplified PCR product of 16SrRNA of C4 isolate of *Citrobacter freundii.*

One of the most attractive potential uses of 16S rRNA gene sequence informatics is to provide genus and species or taxa identification for isolates [19]. Although 16S rRNA gene sequencing is highly useful in regards to bacterial classification [20]. PCR products were subjected to direct sequencing, both strands of PCR products were sequenced with an automatic sequencer. Sequences were analyzed with the Basic Local Alignment Search Tool (BLAST) in the National Center for Biotechnology Information (NCBI) website (http://www.ncbi.nlm.nih.gov) (Table-3).

Table 3-16S rRNA gene of *C. freundii* isolate BLAST with reference sequences

Score	Expect	Identities	Gaps	Strand
2590 bits(1402)	0.0	1402/1402(100%)	0/1402(0%)	Plus/Plus

```
Query  1
GTCGAACGGTAGCACAGAGGAGCTTGCTCCTTGGGTGACGAGTGGCGGACGGGTGAGTAA  60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5
GTCGAACGGTAGCACAGAGGAGCTTGCTCCTTGGGTGACGAGTGGCGGACGGGTGAGTAA  64
Query  61
TGTCTGGGAAACTGCCCGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCAT  120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  65
TGTCTGGGAAACTGCCCGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCAT  124
Query  121
AACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCGGATGTGCCCAGATG  180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  125
AACGTCGCAAGACCAAAGAGGGGGACCTTCGGGCCTCTTGCCATCGGATGTGCCCAGATG  184
Query  181
GGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGA  240
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  185
GGATTAGCTAGTAGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGA  244
Query  241
GGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGG  300
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  245
GGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGG  304
Query  301
GGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCT  360
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  305
GGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCT  364
Query  361
TCGGGTTGTAAAGTACTTTCAGCGAGGAGGAAGGTGTTGTGGTTAATAACCGCAGCAATT  420
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  365
TCGGGTTGTAAAGTACTTTCAGCGAGGAGGAAGGTGTTGTGGTTAATAACCGCAGCAATT  424
Query  421
GACGTTACTCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAG  480
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  425
GACGTTACTCGCAGAAGAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAG  484
Query  481
GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTCG  540
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct  485
GGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGCGGTCTGTCAAGTCG  544
Query  541
GATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCCGAAACTGGCAGGCTAGAGTCTT  600
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  545
GATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCCGAAACTGGCAGGCTAGAGTCTT  604
Query  601
GTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACC  660
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  605
GTAGAGGGGGGTAGAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACC  664
Query  661
GGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCA  720
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  665
GGTGGCGAAGGCGGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGAGCA  724
Query  721
AACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGCC  780
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  725
AACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGCC  784
Query  781
CTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGCA  840
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  785
CTTGAGGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGCA  844
Query  841
AGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAAT  900
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  845
AGGTTAAAACTCAAATGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAAT  904
Query  901
TCGATGCAACGCGAAGAACCTTACCTACTCTTGACATCCAGAGAACTTAGCAGAGATGCT  960
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  905
TCGATGCAACGCGAAGAACCTTACCTACTCTTGACATCCAGAGAACTTAGCAGAGATGCT  964
Query  961
TTGGTGCCTTCGGGAACTCTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGA  1020
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  965
TTGGTGCCTTCGGGAACTCTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTTGTGA  1024
Query  1021
AATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTTAGGC  1080
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1025
AATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTTAGGC  1084
Query  1081
CGGGAACTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTC  1140
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1085
CGGGAACTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAAGTC  1144
Query  1141
ATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCATATACAAAGAGAAGCG  1200
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct  1145
ATCATGGCCCTTACGAGTAGGGCTACACACGTGCTACAATGGCATATACAAAGAGAAGCG  1204
Query  1201
ACCTCGCGAGAGCAAGCGGACCTCATAAAGTATGTCGTAGTCCGGATTGGAGTCTGCAAC  1260
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1205
ACCTCGCGAGAGCAAGCGGACCTCATAAAGTATGTCGTAGTCCGGATTGGAGTCTGCAAC  1264
Query  1261
TCGACTCCATGAAGTCGGAATCGCTAGTAATCGTGGATCAGAATGCCACGGTGAATACGT  1320
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1265
TCGACTCCATGAAGTCGGAATCGCTAGTAATCGTGGATCAGAATGCCACGGTGAATACGT  1324
Query  1321
TCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGT  1380
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1325
TCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAAGTAGGT  1384
Query  1381  AGCTTAACCTTCGGGAGGGCGC  1402
              ||||||||||||||||||||
Sbjct  1385  AGCTTAACCTTCGGGAGGGCGC  1406
```

Conclusions:

Although *Citrobacter freundii* is a food borne bacterium but it is so difficult to be differentiated from other closely related bacterial species, and its isolation from imported chicken meat samples was accompanied with so many difficulties one of which; competition with other bacteria e.g. *Klebsiella*, *E.coli*, *Salmonella* and *Shigella*, so the complete identification using vitek-2 system is very necessary to confirm its identification to the species level since it was further confirmed using 16SrRNA sequencing.

References

1. Rouger**,** A., Tresse, O. and Zagorec, M. **2017**. Bacterial Contaminants of Poultry Meat: Sources, Species, and Dynamics, *Microorganisms*. **5**(3): 50.
2. European Food Safety Authority and European Centre for Disease Prevention and Control (EFSA and ECDC). "The European Union summary report on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in **2017**." *European Food Safety Authority and European Centre for Disease Prevention Control* 16.12 (2018): e05500.
3. Arnold, J. **2007**. Bacterial contamination on rubber picker fingers before, during, and after processing, *Poultry science*. **86**(12): 2671-2675.
4. Arnold, J. and Yates, I. **2009**. Interventions for control of Salmonella: clearance of microbial growth from rubber picker fingers, *Poultry science*. **88**(6): 1292-1298.
5. Veluz, G., Pitchiah, S., and Alvarado, C. **2012**. Attachment of Salmonella serovars and Listeria monocytogenes to stainless steel and plastic conveyor belts, *Poultry science*. **91**(8): 2004-2010.
6. Álvarez, A., Maite, Capita, R., Alonso-Calleja, C., Moreno, B. and García-Fernández, C. **2002**. Microbiological quality of retail chicken by-products in Spain, *Meat Science*. **62**(1): 45-50.
7. . Iraqi Central Organization for Standardization and Quality Control (C.O.S.Q.C). **2006**. Iraqi Standard Criterion No.2/2270 in Sampling.
8. Hoben, H. J. and Somasegaran, P. **1982**. Comparison of the pour, spread, and drop plate methods for enumeration of Rhizobium spp. in inoculants made from presterilized peat. *Applied and Environmental Microbiology.*, **44**(5): 1246-1247.
9. MacFaddin, J. **2000**. Individual biochemical tests, Biochemical tests for identification of medical bacteria: p. 3-453.
10. Janda, J., Abbott, L., Cheung, W. and Hanson, D. **1994**. Biochemical identification of *Citrobacteria* in the clinical laboratory. *Journal of Clinical Microbiology*, **32**(8): 1850-1854

11. Hashim, M. H. and AlKhafaji, M. H. **2018**. Isolation and identification of *Citrobacter freundii* from chicken meat samples using cultural and molecular techniques. *Iraqi Journal of Science*, **59**(3A): 1216-1224.
12. Leininger, D. J., Roberson, J. R. and Elvinger, F. **2001**. Use of eosin methylene blue agar to differentiate *Escherichia coli* from other gram-negative mastitis pathogens. *Journal of veterinary diagnostic investigation*, **13**(3): 273-275.
13. Bruce, S. K., Schick, D. G., Tanaka, L., Jimenez, E. M. and Montgomerie, J. Z. **1981**. Selective medium for isolation of *Klebsiella pneumoniae*. *Journal of clinical microbiology*, **13**(6): 1114-1116.
14. Gunasegaran, T., Rathinam, X., Kasi, M., Sathasivam, K., Sreenivasan, S. and Subramaniam, S. **2011**. Isolation and identification of *Salmonella* from curry samples and its sensitivity to commercial antibiotics and aqueous extracts of Camelia sinensis (L.) and Trachyspermum ammi (L.). *Asian Pacific journal of tropical biomedicine*, **1**(4): 266-269.
15. Mokhtari, W., Nsaibia, S., Majouri, D., Ben Hassen, A., Gharbi, A. and Aouni, M. **2012.** Detection and characterization of *Shigella* species isolated from food and human stool samples in Nabeul, Tunisia, by molecular methods and culture techniques. *Journal of applied microbiology*, **113**(1): 209-222.
16. Haryani, Y., Noorzaleha, A. S., Fatimah, A. B., Noorjahan, B. A., Patrick, G. B., Shamsinar, A. T. and Son, R. **2007**. Incidence of *Klebsiella pneumonia* in street foods sold in Malaysia and their characterization by antibiotic resistance, plasmid profiling, and RAPD–PCR analysis. *Food Control*, **18**(7): 847-853.
17. Zhang, S., Yang, G., Ye, Q., Wu, Q., Zhang, J. and Huang, Y. **2018**. Phenotypic and genotypic characterization of *Klebsiella pneumoniae* isolated from retail foods in China. *Frontiers in microbiology*, **9**: 289.
18. Adeyanju, G. T. and Ishola, O. **2014**. *Salmonella* and *Escherichia coli* contamination of poultry meat from a processing plant and retail markets in Ibadan, Oyo State, Nigeria. *Springerplus*, **3**(1): 139.
19. Janda, J. M. and Abbott, S. L. **2007**. 16S rRNA gene sequencing for bacterial identification in the diagnostic laboratory: pluses, perils, and pitfalls. *Journal of clinical microbiology*, **45**(9): 2761-2764.
20. Bosshard, P. P., Zbinden, R., Abels, S., Böddinghaus, B., Altwegg, M. and Böttger, E. C. **2006.** 16S rRNA gene sequencing versus the API 20 NE system and the VITEK 2 ID-GNB card for identification of nonfermenting Gram-negative bacteria in the clinical laboratory. *Journal of clinical microbiology*, **44**(4): 1359-1366