



Drug resistance and virulence traits of *Acinetobacter baumannii* from Turkey and chicken raw meat



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ABSTRACT

Acinetobacter baumannii (*A. baumannii*) is a miscellaneous bacterium with ability of extensive antibiotic resistance. *A. baumannii* strains have also been isolated from animal origins. The objective of our study was characterization of *A. baumannii* antibiotic resistance and virulence traits from turkey and chicken raw meat. Of 576 turkey and 424 chicken specimens during 2017–2019, 200 (120 from turkey and 80 from chicken) isolates were identified as *A. baumannii*. Virulence factors and antibiotic resistance patterns of *A. baumannii* were determined using polymerase chain reaction (PCR) technique and Kirby-Bauer test. All the isolates were resistant to tetracycline and cefoxitin and 81 % and 56 % of them produced ESBLs and carbapenemases. Also 74 % of them (34 % from chicken and 40 % from turkey) were multidrug-resistant (MDR) *A. baumannii*. Colistin and fosfomycin non-susceptibility was detected among 12 % and 10 % of them, respectively. The existence of *tetA*, *dfrA*, *tetB*, *bla*_{oxa-51-like}, *bla*_{oxa-23-like}, *sulI*, *bla*_{oxa-24-like}, *bla*_{oxa-58-like}, *fosA3* and *mcr-1* genes accounted for 80 %, 71 %, 70.5 %, 66 %, 62 %, 43 %, 34 %, 22 %, 11 % and 13 % of them, respectively. Additionally, predominant virulence factors included the *fimH*, *afa/draBC*, *sfa/foc DE*, *cnfI* and *cnf2* genes. The rate of antibiotic resistance genes and virulence factors was not significantly different between turkey and chicken ($p > 0.05$). High rate of antibiotic non-susceptibility even against last-line resorts in poultry products is a concern and suggest that animals play a potential role as reservoirs of transmission of MDR *A. baumannii*.

1. Introduction

As a ubiquitous species, *Acinetobacter baumannii* (*A. baumannii*) is commonly found in the both clinical and environmental sources [1]. Spread of strains with vast antibiotic non-susceptibility in hospital settings have limited last-line choices for their eradication [2]. It is noteworthy that some *A. baumannii* isolates from veterinary sources have nosocomial origins [3]. Multidrug resistance in *A. baumannii* is due to various mechanisms such as overexpression of intrinsic β -lactamases, MDR efflux pumps and accumulation of various resistance genes [4]. Given extensive drug resistance among *A. baumannii* strains, treatment of animals should be performed following in vitro susceptibility testing [5]. However, for prevention of possible infection spread from veterinary sources, sequence typing of strains can be supportive. Some studies have revealed that sequence types of strains from veterinary sources are not the same and far from those of nosocomial

pathogens [6].

Noticeably, the virulence potential of this bacterium is low and its determinants include cell surface hydrophobicity, outer membrane proteins (OMPs), toxic slime polysaccharides and verotoxins [7].

A. baumannii has evolved resistance to most of antibiotics in hospital settings and it is very likely that strains develop vast non-susceptibility in veterinary sources as well [8]. Although being a natural microflora in livestock, resistant strains have been isolated from animal products such as raw meat, milk, traditional cheese and other veterinary origins. Indeed, successful clones have been isolated from human and animal origins; however, data from animal origins is still in paucity. More importantly, carbapenem-resistant *A. baumannii* is ranked as priority 1 by world health organization [6]. Our objective was characterization of virulence and antibiotic resistance profile of *A. baumannii* from chicken and turkey meat samples.

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Table 1
Primers used for detection of virulence genes in *A. baumannii* [10–12].

Gene	Primer name	Primer Sequence (5'–3')	Size of product (bp)
<i>afa/draBC</i>	afa1 afa2	GCTGGGCAGCAAACCTGATAACTCTCCATCAAGCTGTTTGTTCGTCCGCCG	750
<i>cnf1</i>	cnf1 cnf2	AAGATGGAGTTTCTATGCAGGAG CATTGAGAGTCTGCCCTCATTATT	498
<i>cnf2</i>	cnf2a cnf2b	AATCTAATTAAGAGAAC CATGCTTTGTATATCTA	543
<i>csgA</i>	M464 M465	ACTCTGACTTGACTATTACC AGATGCAGTCTGGTCAAC	200
<i>cvaC</i>	ColV-CF ColV-CR	CACACACAAACGGGAGCTGTT CTTCGGCAGCATAGTTCCAT	680
<i>fimH</i>	FimH F FimH R	TGCAGAACGGATAAGCCGTGG GCAGTACCTGCCCTCCGGTA	508
<i>fyuA</i>	FyuA f FyuA R	TGATTAACCCCGCAGCGGAA CGCAGTAGGCACGATGTTGTA	880
<i>ibeA</i>	ibe10 F ibe10 R	AGGCAGGTGTGCGCCGCTAC TGGTGTCCGGCAAACCATGC	170
<i>iutA</i>	AerJ F AerJ R	GGCTGGACATCATGGAACTGG CGTCGGGAACGGGTAGAATCG	300
<i>kpsMT II</i>	kpsII F kpsII R	GCGCATTGTGCTGATACTGTTG CATCCAGACGATAAGCATGAGCA	272
<i>PAI</i>	RPai F RPai R	GGACATCTGTTACAGCGCGCA TCGCCACCAATCACAGCCGAAC	930
<i>papC</i>	pap1 pap2	GACGGCTGTACTGCAGGGTGTGGCG ATATCCTTTCTGCAGGGATGCAATA	328
<i>PapG II, III</i>	pGf pGr	CTGTAATACGGAAGTATTCTG ACTATCCGGCTCCGGATAAACCAT	1070
<i>sfa/focDE</i>	sfa1 sfa2	CTCCGGAGAAGTGGGTGCATCTTAC CGGAGGAGTAATTACAAACCTGGCA	410
<i>traT</i>	TraT F TraT R	GGTGTGGTGCATGAGCACAG CACGGTTCAGCCATCCCTGAG	290
<i>A. baumannii</i> detection	16S-23S ribosomal DNA	(F) CATTATCACGGTAATTAGTG (R) AGAGCACTGTGCACCTAAG	208

Table 2
Primers used for detection of antibiotic resistance coding genes [13,14].

Gene	Primer Sequence (5'–3')	Size of product (bp)
<i>aadA1</i>	(F) TATCCAGCTAAGCGCAACT (R) ATTTGCCGACTACCTTGGTC	447
<i>aac(3)-IV</i>	(F) CTTCAGGATGGCAAGTTGGT (R) TCATCTCGTTCTCCGCTCAT	286
<i>sul1</i>	(F) TTCGGCATTCTGAATCTCAC (R) ATGATCTAACCCCTCGGTCTC	822
<i>blaSHV</i>	(F) TCGCCTGTGTATTATCTCCC (R) CGCAGATAAATCACCACAATG	768
<i>CITM</i>	(F) TGGCCAGAAGTACAGGGCAAA (R) TTTCTCCTGAACGTGGCTGGC	462
<i>cat1</i>	(F) AGTTGCTCAATGTACCTATAACC (R) TTGTAATTCATTAAGCATCTGCC	547
<i>cmlA</i>	(F) CCGCCACGGTGTGTTGTTATC (R) CACCTTGCCTGCCGATCATTAG	698
<i>tet(A)</i>	(F) GGTTCACTCGAACGACGTCA (R) CTGTCCGACAAGTTGCATGA	577
<i>tet(B)</i>	(F) CCTCAGCTTCTCAACGCGTG (R) GCACCTTGCTGATGACTCTT	634
<i>dfrA1</i>	(F) GGAGTGCCAAAGGTGAACAGC (R) GAGGCGAAGTCTTGGGTAATAAAC	367
<i>Qnr</i>	(F) GGGTATGGATATTATTGATAAAG (R) CTAATCCGGCAGCACTATTTA	670
<i>Imp</i>	(F) GAATAGAATGGTTAACTCTC (R) CCAAACCACTAGGTTATC	188
<i>Vim</i>	(F) GTTTGGTTCGCATATCGCAAC (R) AATGCGCAGCACCCAGGATAG	382
<i>Sim</i>	(F) GTACAAGGGATTCCGGCATCG (R) GTACAAGGGATTCCGGCATCG	569
<i>Oxa-51-like</i>	(F) TAATGCTTTGATCGGCCTTG (R) TGGATTGCACTTCATCTTGG	353
<i>Oxa-23-like</i>	(F) GATCGGATTGGAGAACCAGA (R) ATTTCTGACCCGATTTCCAT	501
<i>Oxa-24-like</i>	(F) GGTTAGTTGGCCCCCTTAAA (R) AGTTGAGCGAAAAGGGGATT	246
<i>Oxa-58-like</i>	(F) AAGTATTGGGCTTGTGCTG (R) CCCCTCTGCGCTCTACATAC	599
<i>Int1</i>	F: CAG TGG ACA TAA GCC TGT TC R: CCC GAC GCA TAG ACT GTA	160

2. Material and methods

2.1. Sample preparation

Of 576 turkey and 424 chicken specimens during 2017–2019, 200 (120 from turkey and 80 from chicken) isolates were identified as *A. baumannii* from healthy poultry.

2.2. Isolation and identification of *A. baumannii*

Following sampling from meat, 25gr of each was added to 225 ml of Dijkshoorn enrichment medium and incubated at 30 °C for 24 h. Next, one loopful of enrichment broth was cultured onto blood (Merck, Germany) and Macconky agar media (Merck, Germany). Then, non-hemolytic, opaque, creamy and nonlactose fermenting colonies were isolated and identified based on colonial and microscopic characteristics and various biochemical tests, streaking on CHROMagar™ Acinetobacter (CHROMagar, Paris, France) and 16S–23S ribosomal DNA amplification. Stock cultures were cultured in trypticase soy broth containing 30 % sterile glycerol and kept at –70 °C.

2.3. DNA extraction

Total bacterial DNA was extracted using DNA Extraction Kit (CinnaGen, Iran) considering the manufacturer's protocol.

in a total volume of 50 µL PCR was performed. Each reaction contained 2 mM of MgCl₂, 5 µL of 10X PCR buffer, one unit of Taq DNA polymerase (Fermentas-Lithuania), 150 µM of dNTPs mix, 1 µM of reverse and forward primers, and 3 µL of template DNA. The PCR program contained denaturing at 94 °C for 60 s, followed by 30 cycle amplification where each cycle involved three separate stages (denaturing at 94 °C, annealing at 58 °C for 30 s, extension at 72 °C (40 s) and final extension at 72 °C for 5 min. a thermocycler (Eppendorf Mastercycler 5330; Eppendorf-Nethel-Hinz GmbH, Hamburg, Germany) was employed for amplification purposes. PCR products were visualized following electrophoresis using 1.5 % agarose gel. a 208 bp fragment confirmed the existence of *A. baumannii*.

2.4. Antimicrobial susceptibility patterns

Antimicrobial susceptibility profile of isolates was assessed using the Kirby–Bauer disk diffusion method onto the Mueller–Hinton agar (HiMedia Laboratories, Mumbai, India, MV1084), following the Clinical and Laboratory Standards Institute guidelines (CLSI, 2017). Antimicrobial disks included trimethoprim (5 µg), cephalothin (30 µg), cefoxitin (30 µg), tetracycline (30 µg), ceftazidime (30 µg), tobramycin (10 µg), streptomycin (10 µg), amikacin (30 µg), gentamicin (10 µg), cotrimoxazole (23.75/1.25 µg), erythromycin (15 µg), rifampicin (5 µg), azithromycin (15 µg), colistin (10 µg), nitrofurantoin (300 µg), chloramphenicol (30 µg), fosfomicin trometamol (200 µg/ml),

Table 3
PCR conditions for virulence and antibiotic genes detection in *A. baumannii*.

<i>draBC, cnf1, csgA, cvaC, iutA, fyuA</i>	1 cycle: 95 OC _____ 4 min. 30 cycle: 95 OC _____ 50 s 58 OC _____ 60 s 72 OC _____ 45 s 1 cycle: 72 OC _____ 8 min	5 μ L PCR buffer 10X 1.5 mM Mgcl2 200 μ M dNTP (Fermentas) 0.5 μ M of each primers F & R 1.25 U Taq DNA polymerase (Fermentas) 2.5 μ L DNA template
<i>cnf2, kpsMT II, PAI, papC</i>	1 cycle: 94 OC _____ 6 min. 34 cycle: 95 OC _____ 50 s 58 OC _____ 70 s 72 OC _____ 55 s 1 cycle: 72 OC _____ 10 min	5 μ L PCR buffer 10X 2 mM Mgcl2 150 μ M dNTP (Fermentas) 0.75 μ M of each primers F & R 1.5 U Taq DNA polymerase (Fermentas) 3 μ L DNA template
<i>fimH, ibeA, PapG II-III, sfa/focDE, traT</i>	1 cycle: 95 OC _____ 4 min. 34 cycle: 94 OC _____ 60 s 56 OC _____ 45 s 72 OC _____ 60 s 1 cycle: 72 OC _____ 10 min	5 μ L PCR buffer 10X 2 mM Mgcl2 200 μ M dNTP (Fermentas) 0.5 μ M of each primers F & R 1.5 U Taq DNA polymerase (Fermentas) 5 μ L DNA template
16S-23S ribosomal DNA	1 cycle: 94 OC _____ 6 min. 30 cycle: 95 OC _____ 60 s 58 OC _____ 60 s 72 OC _____ 40 s 1 cycle: 72 OC _____ 5 min	5 μ L PCR buffer 10X 2 mM Mgcl2 150 μ M dNTP (Fermentas) 1 μ M of each primers F & R 1 U Taq DNA polymerase (Fermentas) 3 μ L DNA template
Antibiotic resistance genes <i>aadA1, aac(3)-IV, sul1, blaSHV, CITM, cat1, cmlA, tet(a), tet(B), dfrA1, and qnr.</i>	1 cycle: 94 OC _____ 6 min. 33 cycle: 95 OC _____ 70 s 55 OC _____ 65 s 72 OC _____ 90 s 1 cycle: 72 OC _____ 8 min	5 μ L PCR buffer 10X 2 mM Mgcl2 150 μ M dNTP (Fermentas) 0.5 μ M of each primers F & R 1.5 U Taq DNA polymerase (Fermentas) 2 μ L DNA template
<i>imp, vim, and sim</i>	1 cycle: 95 OC _____ 4 min. 30 cycle: 95 OC _____ 45 s 58 OC _____ 60 s 72 OC _____ 40 s 1 cycle: 72 OC _____ 5min	5 μ L PCR buffer 10X 1.5 mM Mgcl2 100 μ M dNTP (Fermentas) 1 μ M of each primers F & R 1 U Taq DNA polymerase (Fermentas) 2.5 μ L DNA template
<i>Oxa-23-like, Oxa-24-like, Oxa-51-like, Oxa-58-like</i>	1 cycle: 94 OC _____ 5 min. 32 cycle: 95 OC _____ 50 s 60 OC _____ 60 s 72 OC _____ 70 s 1 cycle: 72 OC _____ 10 min	5 μ L PCR buffer 10X 2.5 mM Mgcl2 200 μ M dNTP (Fermentas) 0.5 μ M of each primers F & R 1.5 U Taq DNA polymerase (Fermentas) 2 μ L DNA template

imipenem (10 μ g), ciprofloxacin (5 μ g) and levofloxacin (5 μ g) and *A. baumannii* ATCC 19606 was used as a quality control organism in antimicrobial susceptibility determination test. Colistin resistance was also evaluated using broth micro-dilution method [9].

2.5. virulence factors and antibiotic resistance genes

PCR primers sequences and amplification conditions have been depicted in Tables 1–3. Using 1.5 % agarose gel (Fermentas, Germany), DNA Safe Stain (CinnaGen, Iran), 1X TBE buffer (Fermentas, Germany)

and 80 V for 30 min the PCR products were visualized.

2.6. Statistical analysis

Data analysis was conducted by SPSS (Statistical Package for the Social Sciences) software version 21. The Chi-square and Fisher's exact tests were employed to verify relationships between antibiotic resistance and the distribution of virulence genes, and characterization of the *A. baumannii* isolates from chicken and turkey meat samples. A P value < 0.05 was considered statistically significant.

Table 4
Antimicrobial resistance pattern *A. baumannii* strains.

	Pattern of antibiotic resistance (%)																	
	TMP	TE	CAZ	FOX	SXT	TOB	AN	GM	S	E	RA	AZM	F/M	C	MPR	IPM	LOM	CP
Chicken meat (80)	58 (72.5)	80 (100)	66 (82.5)	80 (100)	59 (73.7)	37 (46.2)	37 (46.2)	42 (52.5)	29 (36.2)	28 (35)	27 (33.7)	24 (30)	28 (35)	21 (26.2)	20 (25)	41 (51.2)	30 (37.5)	57 (71.2)
Turkey meat (120)	66 (55)	67 (59)	93 (77.5)	120 (100)	60 (50)	49 (40.8)	60 (50)	61 (50.8)	41 (34.1)	66 (55)	67 (59)	41 (34.1)	41 (34.1)	29 (24.1)	28 (23.4)	56 (46.7)	45 (37.5)	62 (51.6)

TMP = trimethoprim (5 µg/disk); TE = tetracycline (30 µg/disk); CAZ = ceftazidime (30 µg/disk); FOX = co-trimoxazole (23.75/1.25 µg/disk); SXT = ceftriaxone (30 µg/disk); TOB = tobramycin (10 µg/disk); AN = amikacin (30 u/disk); GM = gentamicin (10 µg/disk); S = streptomycin (10 µg/disk); CAZ = ceftazidime (30 µg/disk); E = erythromycin (15 µg/disk); RA = rifampicin (5 µg/disk); AZM = azithromycin (15 µg/disk); F/M = nitrofurantoin (300 µg/disk); C = chloramphenicol (30 µg/disk); MPR = mupirocin (30 µg/disk); IPM = imipenem (10 µg/disk); LOM = levofloxacin (5 µg/disk); CP = ciprofloxacin (5 µg/disk).

3. Results

Herein, we identified 200 *A. baumannii*, all of which were resistant to tetracycline and cefoxitin and 81 % and 56 % of them produced ESBLs and carbapenemases (data not shown). Also 74 % of them (34 % from chicken and 40 % from turkey) were multidrug-resistant (MDR) *A. baumannii*. Colistin and fosfomycin non-susceptibility was detected among 12 % and 10 % of them, respectively. There was significant difference between chicken and turkey isolates regarding resistance rate against erythromycin (p = 0.021) and rifampicin (p = 0.030) (Table 4). Notably, 23/120 (19.17 %) and 16/80 (20 %) of *A. baumannii* from turkey and chicken meat, respectively were pandrug-resistant (PDR) strains.

Noticeably, we also identified *A. pittii* (n = 17), and *A. bereziniae* (n = 12) among meat products.

3.1. Antibiotic resistance genes and virulence determinants

The existence of *tetA*, *dfrA*, *tetB*, *bla*_{oxa-51-like}, *bla*_{oxa-23-like}, *sul1*, *bla*_{oxa-24-like}, *bla*_{oxa-58-like}, *fosA3* and *mcr-1* genes accounted for 80 %, 71 %, 70.5 %, 66 %, 62 %, 43 %, 34 %, 22 %, 11 % and 13 % of them, respectively. The rate of antibiotic resistance genes and virulence factors was not significantly different between turkey and chicken (p > 0.05) (Table 5). Among 23 PDR *A. baumannii* from turkey meat, all carried the *dfrA1*, *tetB*, *tetA*, *bla*_{CITM}, *bla*_{SHV}, *sul1*, *aac(3)-I*, *oxa-58-like*, *oxa-24-like*, *oxa-23-like*, *oxa-51-like*, *cmlA*, *cat1*, *imp*, *sim*, *vim* genes and 19/23 (82.60 %) of them contained the *aadA1* gene. Additionally, of 16 PDR *A. baumannii* from chicken meat, all carried all of the genes. Interestingly, two colistin-susceptible *A. baumannii* carried the *mcr-1* gene and other two fosfomycin-susceptible *A. baumannii* carried the *fosA3* genes.

Predominant virulence factors among *A. baumannii* from chicken meat included the *fimH*, *afa/draBC*, *sfa/foc DE*, *cnfI* and *cnf2* genes. Moreover, those predominant determinants among *A. baumannii* from turkey meat included the *fimH*, *afa/draBC*, *cnf2*, *sfa/foc DE*, *cnfI* and *fyuA* genes. There was a significant difference regarding *fimH* (p = 0.001) and *traT* (p = 0.001) genes rates between turkey and chicken strains. It is notable that 8 strains from chicken and 17 from turkey meat contained all virulence genes. There was not significant association between existence of virulence genes and antibiotic resistance genes among these virulent strains.

4. Discussion

A. baumannii has been isolated from a variety of wild and domestic animals [15–17]. Owing to ubiquitous nature of the microorganism, queries regarding development and spread of antibiotic non-susceptibility remains to be completely determined thanks for narrow investigations [18]. Noticeably, differences in identification methods or enrichment step and compliance with good manufacturing practices influence on bacterial recovery rate [19]. It is worth considering that we detected mixed species contamination per sample including *A. baumannii* + *A. pittii* + *A. bereziniae* in nine samples.

In this study, 74 % of isolates (34 % from chicken and 40 % from turkey) were MDR-*A. baumannii* among which ~45 %, 12 % and 10 % were carbapenem, colistin and fosfomycin non-susceptible, respectively which was higher than previous studies in Switzerland, Peru and Lebanon [20–22]. Notably, 23/120 (19.17 %) and 16/80 (20 %) of *A. baumannii* from turkey and chicken meat, respectively were PDR strains being high rate. Tetracyclines and penicilins are most often used antibiotics consumed for meat production, leading to spread of high resistance rate.

In Gurung' study, all *A. baumannii* isolates were resistant to ciprofloxacin, levofloxacin, cefepime, imipenem, meropenem and colistin [23]. Carbapenems and colistin resistance (as last-line resorts) among animals menace human health.

In a study in Iran, 8.0 % of meat samples and 7.7 % of animal

Table 5
Distribution of antimicrobial resistance genes.

Isolates	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)
Chicken meat (80)	<i>qnr</i> -	<i>dfrA1</i> 57 (71.2)	<i>tetB</i> 48 (60)	<i>tetA</i> 66 (82.5)	<i>blaCITM</i> 22 (27.5)	<i>blaSHV</i> 29 (36.2)	<i>vim</i> 34 (42.5)		
Turkey meat (120)	-	86 (71.7)	93 (77.5)	97 (80.8)	33 (27.5)	42 (35)	52 (43.4)		
Isolates	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)
Chicken meat (n = 80)	<i>afa/draBC</i> 43 (53.75)	<i>CnfI</i> 38 (47.5)	<i>CnfI</i> 47 (39.17)	<i>CnfI</i> 38 (47.5)	<i>Cnf2</i> 36 (45)	<i>csgA</i> 37 (46.2)	<i>cvaC</i> 25(31.2)		
Turkey meat (n = 120)	59 (49.17)	47 (39.17)	47 (39.17)	47 (39.17)	59 (49.17)	48 (40)	37 (30.8)		
Isolates	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)
Chicken meat (80)	<i>aac(3)-IV</i> 41 (51.5)	<i>aadA1</i> 27 (33.7)	<i>aacA1</i> 27 (33.7)	<i>Oxa-58-like</i> 17 (21.2)	<i>Oxa-23-like</i> 50 (62.5)	<i>Oxa-24-like</i> 27 (33.7)	<i>Oxa-51-like</i> 52 (65)		
Turkey meat (120)	59 (49.17)	41 (34.17)	41 (34.17)	28 (23.3)	75 (62.5)	42 (35)	81 (67.5)		
Isolates	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)
Chicken meat (n = 80)	<i>cvaC</i> 25(31.2)	<i>iuzA</i> 29 (36.2)	<i>fyuA</i> 20 (25)	<i>fimH</i> 65(81.2)	<i>KpsMT II</i> 21 (26.2)	<i>PAI</i> 24 (30)	<i>ibcA</i> 25 (31.2)		
Turkey meat (n = 120)	37 (30.8)	52 (43.4)	52 (43.4)	59 (49.17)	31 (25.8)	34 (28.4)	32 (26.7)		
Isolates	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)	Resistance genes, No. (%)
Chicken meat (80)	<i>Oxa-51-like</i> 52 (65)	<i>cmIA</i> 12 (15)	<i>catI</i> 17 (21.2)	<i>imp</i> 6 (7.5)	<i>sim</i> 7 (8.7)	<i>sim</i> 7 (8.7)	<i>vim</i> 8 (10)		
Turkey meat (120)	81 (67.5)	21 (17.5)	33 (27.5)	14 (11.67)	12 (10)	12 (10)	16 (13.34)		
Isolates	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)	Virulence factors No. (%)
Chicken meat (n = 80)	<i>papC</i> 24 (30)	<i>PapG II</i> 21 (26.2)	<i>PapG III</i> 12 (15)	<i>Sfa/facDE</i> 40 (50)	<i>traT</i> 20 (25)	<i>traT</i> 20 (25)	<i>traT</i> 20 (25)		
Turkey meat (n = 120)	31 (25.8)	32 (26.7)	22 (18.34)	54 (45)	48 (40)	48 (40)	48 (40)		

samples were contaminated with *A. baumannii* and all of them were susceptible to most of the antibiotics such as carbapenems, except for one carrying the *bla*_{OXA-143} gene. Their study suspected the possibility of emerging carbapenemases from animals. In another study among 22 raw meat samples, the highest resistance rate was against tetracycline (90.90 %), trimethoprim (59.09 %), cotrimoxazole (54.54 %) and gentamicin (50.00 %) [24].

In our survey, the *dfrA*, *bla*_{OXA-51-like}, *bla*_{OXA-23-like}, *bla*_{OXA-24-like}, *bla*_{OXA-58-like}, *fosA3*, *mcr-1*, *sul1* genes accounted for 71 %, 66 %, 62 %, 34 %, 22 %, 11 %, 13 % and 43 %, respectively. Among 23 PDR *A. baumannii* from turkey meat, all carried the *dfrA1*, *tetB*, *tetA*, *bla*_{CITM}, *bla*_{SHV}, *sul1*, *aac(3)-I*, *oxa-58-like*, *oxa-24-like*, *oxa-23-like*, *oxa-51-like*, *cmlA*, *cat1*, *imp*, *sim* and *vim* genes and 19/23 (82.60 %) of them contained the *aadA1* gene. Additionally, all 16 PDR *A. baumannii* from chicken meat carried these genes.

Similar to our study, among 22 *A. baumannii* from meat samples, *tetA*, *tetB*, *dfrA1*, *aac(3)-IV* and *sul1* genes were predominant [24]. We observed that two colistin-susceptible *A. baumannii* carried the *mcr-1* gene and other two fosfomycin-susceptible *A. baumannii* carried the *fosA3* genes. This finding suggest the existence of non-functional genes.

Predominant virulence factors among *A. baumannii* from chicken meat included the *fimH*, *afa/draBC*, *sfa/foc DE*, *cnf1* and *cnf2* genes. Furthermore, those predominant determinants among *A. baumannii* from turkey meat included the *fimH*, *afa/draBC*, *cnf2*, *sfa/foc DE*, *cnf1*, *iutA* and *fyuA* genes. There was a significant difference regarding *fimH* ($p = 0.001$) and *traT* ($p = 0.001$) genes rates between turkey and chicken strains. It is notable that 8 strains from chicken and 17 from turkey meat contained all virulence genes. Similarly, in a previous study, the *fimH*, *afa/draBC*, *csgA*, *cnf1* and *cnf2* were most commonly found virulence genes [24].

As control measures, meat manipulation should be performed with care and extensive use of antimicrobials in livestock husbandary must be limited or controlled. Moreover, compliance with good production practices is necessary to lower the contamination rate [19]. *A. baumannii* isolates prevail in natural environments and colonize human, hence early detection combined with determination of resistance profile and rigorous control strategies are crucial to prevent spread of drug-resistant strains. It is notable that transmission routes patient-to-patient or from staff hands and hospital equipment/environment should be prevented. The limitations of this study included low number of samples, lack of source tracking and expression assessment of genes.

5. Conclusion

Of 1000 poultry meat samples, 25 % were contaminated with *A. baumannii*. We observed high rate of resistance against tetracycline, cephalosporins, trimethoprim-sulfamethoxazole, aminoglycosides and carbapenems among *A. baumannii* from poultry meat and resistance determinants such as *tetA*, *tetB*, *dfrA*, *bla*_{OXA-51-like}, *bla*_{OXA-23-like} and *bla*_{OXA-24-like} were detected. Furthermore, the *fimH*, *afa/draBC*, *sfa/foc DE*, *cnf1* and *cnf2* genes were predominant virulence determinants. Of total 200 isolates, MDR and PDR *A. baumannii* was detected among 74 % and ~half of them, respectively which mostly carried virulence determinants. However, virulent strains exhibited relatively lower rate of resistance determinants.

Declaration of Competing Interest

The authors certify that they have NO affiliations with or involvement in any organization or entity with any financial interest or non-financial in the subject matter or materials discussed in this manuscript.

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