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Detection of some virulence and antibiotics resistance genes in *Campylobacter* isolated from turkeys

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ABSTRACT

A total of 69 cloacal swabs were collected from turkey from different turkey farms in Giza and Sharkia governorates in Egypt for isolation of *Campylobacter* species. The results revealed that *Campylobacter* was isolated from 16 out of 69 (23.2%) cloacal samples. The samples were identified biochemically revealed that 4 out of 16 (25%) were identified as *Campylobacter jejuni* (*C. jejuni*) while 12 out of 16 (75%) were *Campylobacter coli* (*C. coli*). *Campylobacter* isolates were confirmed by multiplex PCR using *hipO* gene which responsible for Na hippurate hydrolysis for confirmation of *C. jejuni* and *ceuE* gene which designed for detection of *C. coli*. All isolates were examined for presence of tetracycline resistance gene *tetM* was detected in 8 out of 16 (50%) *Campylobacter* isolates. The *cdtB* virulence gene was detected in all isolates. From mentioned results we recommended the use of multiplex polymerase chain reaction (PCR) for identification of *Campylobacter* species. This study may indicate the extent of the existence of *campylobacter* species in some turkey farms in Giza & Sharkia governorates. In conclusion, biosecurity programs must be applied inside slaughter houses to avoid carcass contamination. Applying more efforts in surveillance programs in turkey farms for epidemiological mapping of *Campylobacter* existence and antimicrobial resistance distribution which obligate the stop of uncontrollable use of antibiotics in poultry farms.

INTRODUCTION

Poultry production considered an important source of protein in Egypt and all over the world. It represents about 20% of daily consumption of animal's protein in Egyptian society. Turkey production has a smaller scale of

production in comparison to poultry production due to the cost of breeding and the high price of turkey in Egypt. Moreover, turkey need a special condition in production due to its sensitivity to infection with many diseases, its expensive costs of feed, vaccines and treatment.

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(Moawad et al. 2017).

Poultry and poultry by-products causes about of 20-30 % of human *Campylobacter* infection (EFSA 2021) through consumption of under cooked food or contaminated food with *Campylobacter*, the carcass may be contaminated through the production chain of poultry inside slaughter houses (Hamed et al. 2014).

Thermophilic *Campylobacter* species are Gram negative motile bacilli by single polar flagella, S shape spirally curved bacilli. Mostly colonized normally in intestinal tract of poultry specially chicken and turkey without any pathogenic lesions, but sometimes it causes what is called vibronic hepatitis forming focal spots in the liver which related to infection with *Campylobacter jejuni*, and *Campylobacter coli*. Recently, a new species of *Campylobacter* with name *Campylobacter hepaticus* was found to be responsible of vibronic hepatitis, a disease which causes high morbidity, mortality, and drop in egg production in layer chickens. *Campylobacter jejuni* also may cause a gastrointestinal inflammation in chickens and turkeys (Zhage and Sahin 2020).

Campylobacter has four types of virulence genes which play an important role of its pathogenicity inside the host. Moreover, it carries invasion genes (*cadF*, *ciaB*, and *pldA*) genes, adherence genes (*cadF*), colonization genes (*caiB*, *pldA* and *dnaJ*) which play an important role in colonization in the intestinal tract of host, and the cytolethal toxin genes which are encoded in (*cdtA*, *cdtB*, and *cdtC*) genes responsible for appearance of the lethal symptoms of *Campylobacter* infection. (Reddy and Zshiri 2018).

Misuse of antibiotics as growth promoters or random use in treatment of any bacterial disease may affect the commensal bacteria in gastrointestinal tract like *Campylobacter* spp. and may lead to the production of generations carrying antibiotic resistance genes. (Peterson and Kaur 2018; Singh et al. 2019; Hamed et al. 2021). For many years, *Campylobacter* spp. were considered susceptible to various antimicrobial agents, while in the recent years, both animals and human isolates of

this bacterium have shown resistance to several antibiotics such as fluoroquinolones and tetracycline (Iovine 2013).

Due to limited information about presence of *Campylobacter* spp. in turkey farms, the present study was aimed to detect the incidence of their occurrence, using both conventional method and multiplex PCR, in addition to the presence of *cdtB* & *tetM* genes.

MATERIALS AND METHODS

Sampling

A total of 69 cloacal swabs were collected from apparent healthy turkey in turkey farms in Sharkia and Giza governorates. All samples were kept on Cary-Blair Medium (Oxoid) as transport media and submitted to Reference lab for veterinary quality control on poultry production for isolation of *Campylobacter* spp.

Isolation and identification of *Campylobacter*

Campylobacter spp. isolation and identification was done by standard methods according to (ISO 10272-1:2017). Samples were added to Bolton broth (1:9 v/v) as 1g to 9 ml of Bolton broth, incubated at 37 °C for 4 hrs then at 44 °C for 44 hrs then inoculated in selective agar plates mCCDA incubated at 41.5 °C for 48 hrs. The select the suspected colonies (metallic gray colonies) were subjected to Gram staining and examined under Microscope to see the specific shape of *Campylobacter* (curved gram negative bacilli).

Biochemical identification

For differentiations of thermophilic *Campylobacter* spp. biochemical tests of Na hippurate hydrolysis test, oxidase test and catalase test were used according to (ISO 10272-1:2017).

Molecular Assessment

DNA was extracted from culture broth using a QIAamp DNA Mini Kit (Qiagen, Germany, GmbH Catalogue No. 51304). The extracted DNA was used in subsequent (PCR) assays for species confirmation and to detect genes responsible for virulence and antimicrobial agent resistance. PCR was performed in a final

volume of 25 μ L that contained 12.5 μ L of EmeraldAmp MAX PCR Master Mix [EmeraldAmp GT (2 \times premix), Japan], 1 μ L of each primer at concentrations of 20 pmol, 4.5 μ L of diethyl pyrocarbonate water, and 6 μ L of the DNA template. The reaction was performed in a Biometra thermal cycler, T3000 (Germany). The oligonucleotide primers (Table 1) were supplied by Metabion, Germany.

The PCR products were separated by electro-phoresis according to (Sambrook et al. 1989) on a 1% agarose gel (AppliChem, Germany, GmbH) in 1 \times TBE buffer at room temperature using a gradient of 5 V/cm. Each well was loaded with 15 μ L of the PCR product. A GelPilot 100 bp (Qiagen) ladder was used to determine the fragment sizes. The gel was photographed by a gel documentation system (Biometra BDA digital, Germany), and the data were analyzed using a gel documentation system (Alpha Innotech, Biometra, Germany) and a piece of computer software (auto-matic image capture software, Protein Simple, formerly Cell Bioscience, USA). The temperature and time conditions of the primers during PCR are shown in Table (1).

The amplification efficiency was verified for positive field samples that might have the tested genes, which were previously examined in a veterinary quality control reference laboratory for poultry production, Animal Health research institute.

PCRAmplification:

The extracted DNA was further tested by Thermo two step PCR kit (Thermo scientific) for the presence of (*cdtB*, *hipO*, *ceuE*, and *tetM*) genes. The polymerase chain reactions were done according to the manual instruction of the PCR kit as following: 12.5ul PCR master mix, 1 ul of each primer with concentration 20 pmol, 5ul of DNA then complete the total volume to 20 ul with PCR grade water. The amplification condition ran as initial denaturation at 95 $^{\circ}$ C for 5 min for one cycle, 40 cycles for 3 following steps: denaturation at 95 $^{\circ}$ C for 45 sec., annealing for 40 seconds at 54 $^{\circ}$ C for *cdtB*, 59 $^{\circ}$ C for *hipO*, 47 $^{\circ}$ C for *ceuE*, 55 $^{\circ}$ C for *tet(M)*, extension at 72 $^{\circ}$ C for 1 minute, and final extension at 72 $^{\circ}$ C for 5 minutes.

The products of PCR were separated by electrophoresis on 1.5% agarose gel (Appllichem, Germany, GmbH) in 1x TBE buffer at room temperature. A generuler 100 bp ladder (Fermentas, Thermofisher) was used to determine the fragment sizes. The gel was photographed by a gel documentation system (Alpha Innotech, Biometra) and the data was analyzed through computer software.

Table 1. Oligonucleotide sequences and thermal profiles used in PCR Test target Tested gene Primer

Test target	Gene	Sequence	Am- plicon size	Reference
Tetracycline resistance	<i>tet(M)</i>	F: ACAGAAAGCTTATTATATAAC R: TGGCGTGTCTATGATGTTTAC	171bp	(Aminov et al., 2004)
Virulence gene of <i>Campylobacter</i>	<i>cdtB</i>	F: CAC GGT TAA AAT CCC CTG CT R:GCA CTT GGA ATT TGC AAG GC	495bp	(González-Hein et al., 2013)
<i>Campylobacter jejuni</i>	(<i>hipO</i>)	F:GACTTCGTGCAGATATGGATGCTT R : GCTATAACTATCCGAAGAA- GCCATCA	344bp	(Persson and Olsen, 2005)
<i>Campylobacter coli</i>	<i>ceuE</i>	F: ATG AAA AAA TAT TTA GTT TTT GCA R: ATT TTA TTA TTT GTA GCA GCG	894bp	(Nayak et al., 2005)

RESULTS:***Campylobacter* spp. Isolation and Identification**

Campylobacter isolates were isolated from 16 out of 69 (23.2%) examined cloacal swabs which were collected from turkey farms in Giza and Sharkia governorates during the period

from 2021 to 2022. All samples were biochemically identified and confirmed by PCR, the highest prevalence was *C. coli* which constituted 12 out of 16 *Campylobacter* isolates (75%), while *C. jejuni* represented 4 out of 16 (25%) *Campylobacter* isolates as shown in Table (2).

Table 2. prevalence of *C. jejuni* and *C. coli* in turkey cloacal swabs in Giza and Sharkia governorates .

Governorates	No. of the examined samples	No. of positive samples		Positive samples by using Conventional cultural methods			
		No.	%*	<i>C. jejuni</i>		<i>C. coli</i>	
				No.	%**	No.	%**
Sharkia	55	4	7.2	2	50	2	50
Giza	14	12	85.7	2	16.7	10	83.3
Total	69	16	23.2	4	25	12	75

* % according to the total number of examined samples

** % according to the total number of positive *Campylobacter* isolates .

2-Molecular confirmation, typing and detection of *cdtB* and *tetM* of *Campylobacter* isolates.

All *Campylobacter* isolates were confirmed and typed by using multiplex PCR technique. The amplification of the DNA for *hipO* gene which used for detection *C. jejuni* and was found in 4 out of 16 *Campylobacter* isolates (25%) . On the other hand, *ceuE* gene which used for detection of *C. coli* was found in 12

out of 16 (75%) of *Campylobacter* isolates, as shown in Table (2)

All *Campylobacter* strains showed positive amplification of *cdtB* virulent gene, while only 8 out of 16 (50%) of total *Campylobacter* isolates harboured *tetM* gene . The *tetM* gene was detected in 1 out of 4 (25%) of *C. jejuni* isolates and 7 out of 12(58.3%) of *C. coli* isolates as shown in Table (3).

Table 3. Distribution of tetracycline resistance gene (*TetM*) and *cdtB* gene in isolated *Campylobacter* strains.

No. of Strain	Type	<i>tetM</i> gene	<i>cdtB</i> gene
1	<i>C. coli</i>	Positive	Positive
2	<i>C. jejuni</i>	Positive	Positive
3	<i>C. coli</i>	Negative	Positive
4	<i>C. coli</i>	Negative	Positive
5	<i>C. coli</i>	Negative	Positive
6	<i>C. coli</i>	Positive	Positive
7	<i>C. coli</i>	Positive	Positive
8	<i>C. coli</i>	Positive	Positive
9	<i>C. jejuni</i>	Negative	Positive
10	<i>C. coli</i>	Negative	Positive
11	<i>C. jejuni</i>	Negative	Positive
12	<i>C. coli</i>	Positive	Positive
13	<i>C. coli</i>	Negative	Positive
14	<i>C. coli</i>	Positive	Positive
15	<i>C. jejuni</i>	Negative	Positive
16	<i>C. coli</i>	Positive	Positive

DISCUSSION

Turkey meat is one of the consumed poultry meat in Egypt especially in occasion, which encourage us to identify potential microorganisms as *Campylobacter*. It is one of the most important food poisoning microorganism related to public health hazards in the last 20 years, as it has different ways to produce diseases through animals, contaminated food and one to one communication (Hakeem and Lu 2021).

In the present study, the investigation of the prevalence of *Campylobacter* in turkeys from turkey farms was done during the period from 2021 to 2022 in Giza and Sharkia governorates. On examination of a total of 69 cloacal swabs, 16 (23.2%) were positive for *Campylobacter* isolation, our results were in accordance with previous findings which recorded 22.5% *Campylobacter* from Delta governorates, Egypt (Khalil et al. 2020), and higher than that detected by Eid et al. (2018) who isolated *Campylobacter* in percentage of 16% of examined turkey farms in Sharkia, Egypt.

In this study the percentage of detection of *C. coli* was higher than the percentage of *C. jejuni* in examined turkey farms, this finding is contrary to that reported by Eid et al. (2018) and Khalil et al. (2020) who reported that *C. jejuni* in high percentage than *C.coli* in examined Turkey farms in Sharkia and Delta governorates in Egypt .

Campylobacter can be differentiated by multiplex PCR through using *hipO* gene which is responsible for hippurate hydrolysis activity of *C. jejuni* (Linton et al. 1997), and *ceuE* which designed encoding a 34.5 to 36.2 KDa lipoprotein compound of binding-protein dependent transport system for siderophore enterochelin characterized for *C. coli* (984bp) (Park and Richardson 1995; Richardson and Park 1995). Also *ceuE* gene has two primer (COL1 and COL2) were designed for identified *C.coli* only. (Gonzalez et al. 1997). Multiplex PCR is a rapid and accurate technique in *Campylobacter* detection and identification (El-Adawy et al. 2012). In this study we use *hipO* gene for confirmation of *C. jejuni*. Also, Khalil et al., (2020) and Karmi (2019) used the same gene in their studies for detection *C. jejuni* while Eid et al. (2018) and Gahamany et al. (2021)

were used *CJ* gene for detection of *C. jejuni* in their studies. In the present investigation *ceuE* gene designed for detection of *C. coli* at 984bp was used. That was similar to the results of He et al. (2010); Rajagunalan et al. (2014); and Eid al al. (2018). On the other hand, Karmi (2019); and El Baaboua et al. (2022) used *glyA* and, *cadF* genes for detection of *C. coli* respectively.

Our study detected the *cdtB* gene which is one of virulence genes of *Campylobacter* spp. which responsible for production of *Campylobacter* cytolethal distending toxin. This gene was detected in 100% of *Campylobacter* isolates that nearly accord the result of Bang et al. (2004) who detected *cdtB* gene in 87.1% in *Campylobacter* species that isolated from turkeys while Kavan et al. (2015) detected the presence of *cdtB* gene in 6% of *Campylobacter* spp. isolated from turkeys in Iran.

The ribosomal protection genes (*tetM*, *tetO*, *tetQ*) are encoded on conjugative elements and many are encoded on transposons, but the vast majority is present on transferable plasmids. They have the widest host range and are found in a number of Gram-positive and Gram-negative bacteria (Chopra and Roberts, 2001; Roberts, 1996). Tetracycline resistance in *Campylobacter* spp. is primarily mediated by ribosomal production protein (*tetO*), which is transferred as plasmid-encoded gene (Gibreel et al. 2004). In the present study, the identification of a new class of tetracycline-resistant determinants in *Campylobacter* spp. like *tet(M)* gene was done. This gene might be transferred to *Campylobacter* spp. by means of a plasmid, by conjugative transposons (Hormeño et al. 2020). Our results are supportive of this finding and indicate a need for closer investigation of these interactions.

In conclusion

The prevalence of *Campylobacter* spp. in turkey farms exists in a proportion which can't be underestimated.

In addition to the dissemination of antimicrobial resistance such as *tetM* gene, which directs us to apply more efforts in surveillance programs in turkey farms for epidemiological mapping of *Campylobacter* spp. existence and

antimicrobial resistance distribution, it emphasizes the need for cautious use of tetracycline in turkey production to decrease the extension of tetracycline-resistant *Campylobacter* spp.

Presence of *tetM* gene, which is responsible for tetracycline resistance in the family *Enterobacteriaceae* and gram positive bacteria, not for *Campylobacter* spp. That leads us to give more focus on the possibility of transmission of antibiotic resistance genes from bacteria to others, so it is recommended to stop uncontrollable use of antibiotics in poultry farms.

CONCLUSION

Multiplex PCR is a more reliable rapid technique than conventional methods in *Campylobacter* detection and identification.

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