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"Prevalence of beta-lactam and fluoroquinolone resistance, and virulence factors in *Escherichia coli* isolated from different poultry species"

A Thesis Presented By

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(B. V. Sc., Suez Canal University, 2008)

(M. V. SC., Suez Canal University, 2014)

For

Ph.D. Degree in Veterinary Medical Science (Microbiology)

(Bacteriology, Immunology and Mycology)

Department of
(Bacteriology, Immunology and Mycology)
Submitted to
Faculty of Veterinary Medicine
Suez Canal University

(2020)

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Title	Prevalence of beta-lactam and fluoroquinolone resistance, and virulence
	factors in Escherichia coli isolated from different poultry species
Faculty	Veterinary Medicine, Suez Canal University
Department	Bacteriology, Immunology and Mycology
Degree	Doctor of Philosophy in Veterinary Medical Sciences
Language	English
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English abstract

A total of 252 samples were collected from different organs of diseased and freshly dead broiler chickens and ducks from different poultry farms at Ismailia Governorate. E.coli isolation rate was 80.6% (203/252). Thirty six of E.coli isolates were serogrouped into: O63, O111, O125, O143, O152, O157:H7, O164, O169, O55, O86a, O114, O115, O119 and O158, while 8 *E.coli* isolates found to be untyped. Forty *E.coli* isolates were examined for their antibiotic senstivity to 15 antibacterial agents (from 5 different antibiotic groups). All E.coli isolates (97.5%) were highly resistant to penicillin G and ceftriaxone, (92.5%) were resistant to cephalexin and (77.5%) were resistant to ampicillin, (62.5%) were resistant to amoxicillin/clavulanic acid and oxytetracycline, (45%) were resistant to nalidixic acid, (35%) were resistant to ciprofloxacin and neomycin, (32.5%) were resistant to norfloxacin, (22.5%) were resistant to cefotaxime and ceftazidime, while (65%) and (35%) were intermediate resistant to colistin sulphate and levofloxacin, respectively. All tested E.coli isolates were resistant to at least 3 antibiotic groups and multidrug resistance was seen. Conventional PCR (cPCR) results indicated that representative 18 E.coli isolates had virulence genes as iss, iutA and vat genes 100% (18/18), traT gene 88.8% (16/18), eaeA gene 27.7% (5/18), while only 11% (2/18) had papC gene. Also 18 E.coli isolates had betalactam and fluoroquinolone resistance genes as bla_{TEM}, bla_{SHV} and ampC genes100% (18/18), qnrS gene 83.3% (15/18), bla_{CTX-M} gene 27.7% (5/18), while only 16.6% (3/18) had qepA gene.

Keywords Poultry, *E.coli*, Serogroup, Antibiotic Resistance, cPCR, Virulence Genes, Resistance Genes

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