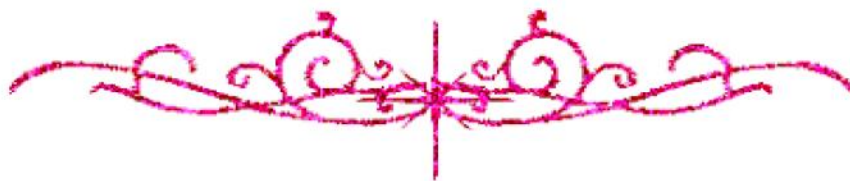


بسم الله الرحمن الرحيم





شبكة المعلومات الجامعية التوثيق الالكتروني والميكروفيلم



جامعة عين شمس

التوثيق الإلكتروني والميكروفيلم

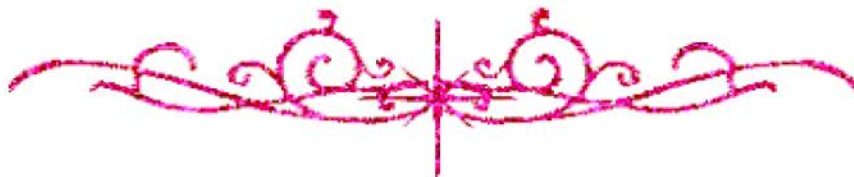
قسم

نقسم بالله العظيم أن المادة التي تم توثيقها وتسجيلها
علي هذه الأقراص المدمجة قد أعدت دون أية تغيرات



يجب أن

تحفظ هذه الأقراص المدمجة بعيدا عن الغبار



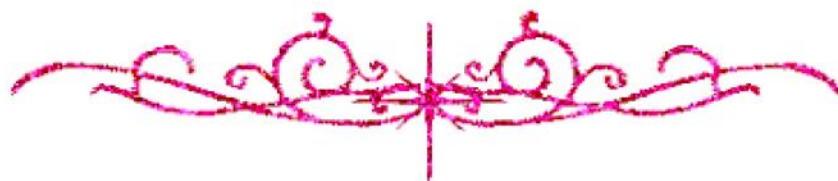


بعض الوثائق الأصلية تالفة





بالرسالة صفحات
لم ترد بالأصل





Cairo University



Cairo University
Faculty of Veterinary Medicine
Department of Medicine and Infectious Diseases

Advanced studies on infected calves with diarrheagenic *Escherichia coli*

Thesis presented by

Noha Mohamed Bakry Nady

(B.V.Sc., 2012; M.V.Sc., 2016)

Faculty of Veterinary Medicine, Cairo University

For the degree of Ph.D.

(Infectious Diseases)

Under the supervision of

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(2020)



APPROVAL SHEET

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Submitted to **Cairo University**
Entitled: **Advanced studies on infected calves with diarrheagenic *Escherichia coli***
For the degree of **Ph.D. (Infectious Diseases)**

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Cairo University
Faculty of Veterinary Medicine
Department of Medicine and Infectious Diseases

SUPERVISION SHEET

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Abstract

Escherichia coli is implicated as a major cause of diarrhea in young calves with significant economic losses worldwide. The emergence of antimicrobial resistance within *E. coli* is considered a major challenge to veterinary and public health. The phenotypic and genotypic characteristics of antibiotic multi-resistance within different *E. coli* pathotypes obtained from diarrheic calves have been performed. Furthermore, the role of *M. domestica* and milk has been identified in the transmission of pathogenic multi-resistant strains. A total of 213 *E. coli* strains were isolated from 157 diarrheic calves with molecular detection of ETEC, EPEC, STEC and AE-STEC at 13.6%, 14.1%, 15.5% and 13.1%, respectively. Hybrid pathotypes of ETEC/EPEC, ETEC/STEC and ETEC/AE-STEC were identified at 3.3%, 5.2% and 3.8%, respectively. Molecular detection of AE-STEC O157 strains was performed on 137 rectal swabs from 157 diarrheic calves and was presented at 8.02%. Virulence genes profile of AE-STEC O157 revealed the presence of *eae*, *stx*₁, *stx*₂ and *ehlyA* in percentages of 93.3%, 73.3%, 20% and 13.3%, respectively with the predominance of *eae*+*stx*₁ combination at 66.7%. The association of *M. domestica* and milk with the transmission of pathogenic multi-resistant strains was determined on 110, 80 and 26 *E. coli* strains isolated from 70 rectal swabs from 157 diarrheic calves, 60 milk samples and 20 *M. domestica*, respectively from dairy farms located on the Giza and Cairo-Alex desert road. Molecular pathotyping of these strains revealed the detection of pathogenic *E. coli* within diarrheic calves, *M. domestica* and milk at 81%, 76.9% and 33.7%, respectively. Phenotypic antimicrobial resistance revealed that 99.1% of fecal strains were antibiotic multi-resistant, while *M. domestica* and milk multi-resistant strains were found at 100% and 85%, respectively. The higher resistance for β -lactams was detected within different *E. coli* strains except for cefquinome that exhibited low resistance in *M. domestica* and milk strains at 30.8% and 30%, respectively. ESC resistant strains within fecal, *M. domestica* and milk strains were detected at 69.1%, 73.1% and 71.3%, respectively confirming the exact role of *M. domestica* and milk in the transmission of ESCs resistance. On the contrary, milk strains conferred lower resistance

for non β -lactams, particularly for nalidixic acid and ciprofloxacin, which were the most effective antibiotics for milk strains. Molecular detection of ESBLs and PABs encoding genes revealed the predominance of the *bla*_{TEM} gene in different *E. coli* strains, while none of these strains harbored the *bla*_{OXA} gene. The highest percentages for *bla*_{CTXM} and *bla*_{CMYII} genes were detected in *M. domestica* strains illustrating their role in the transmission of β -lactamases genes to diarrheic calves. Concerning colistin resistance, the *mcr-1* gene was not detected in *M. domestica* strains, while fecal and milk strains carried this gene at 35.5% and 15%, respectively. *E. coli* phylotyping revealed a higher frequency of phylogroup B2 within fecal and *M. domestica* strains, while milk strains were mainly assigned to B1 phylogroup. Pathogenic *E. coli* strains with the same phenotypic and genotypic antimicrobial resistance and phylogroups were identified for both diarrheic calves and *M. domestica*, which indicates that *M. domestica* serves as a multi-resistance reservoir and contributes to the dissemination of virulence and antimicrobial resistance in dairy farms.

Keywords: Diarrheic calves, *E. coli* pathotypes, Milk, *M. domestica*, Antimicrobial resistance, ESCs, ESBLs, *Mcr-1* and Phylogroups.

