بسم الله الرحمن الرحيم

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التوثيق الالكتروني والميكروفيلم

جامعة عين شمس

التوثيق الإلكتروني والميكروفيلم

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بالرسالة صفحات

لم ترد بالأصل

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

Prof. Walid Sayed Ahmed Abd Elkader Awad

Professor of Infectious Diseases
Dept. of Medicine and Infectious Diseases
Faculty of Veterinary Medicine
Cairo University

Prof. Samia Abd Elhamid Ahmed

Professor of Infectious Diseases
Dept. of Medicine and Infectious Diseases
Faculty of Veterinary Medicine
Cairo University

(2020)

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

APPROVAL SHEET

This is to approve that, the dissertation presented by **Mrs. Noha Mohamed Bakry Nady**

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Has been **Approved by the examining committee:**

Prof. Hussein Ibrahim Hussein Abd Elaal

Professor of Infectious Diseases and head of Animal Medicine Department

Department of Animal Medicine

Faculty of Veterinary Medicine, Beni Suef University

Prof. Diea Gamal Eldin Abo Elhassan Ellithy

Professor of Infectious Diseases

Department of Medicine and Infectious Diseases

Faculty of Veterinary Medicine, Cairo University

Prof. Walid Sayed Ahmed Abd Elkader Awad

Professor of Infectious Diseases

Department of Medicine and Infectious Diseases

Faculty of Veterinary Medicine, Cairo University

Prof. Samia Abd Elhamid Ahmed

Professor of Infectious Diseases

Department of Medicine and Infectious Diseases

Faculty of Veterinary Medicine, Cairo University

Date: 26-11-2020

Cairo University
Faculty of Veterinary Medicine
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SUPERVISION SHEET

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Prof. Walid Sayed Ahmed Abd Elkader Awad

Professor of Infectious Diseases
Dept. of Medicine and Infectious Diseases
Faculty of Veterinary Medicine
Cairo University

Prof. Samia Abd Elhamid Ahmed

Professor of Infectious Diseases
Dept. of Medicine and Infectious Diseases
Faculty of Veterinary Medicine
Cairo University

(2020)

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

Name: Noha Mohamed Bakry Nady
Birth date: 3/4/1990
Place of Birth: Arab Republic of Egypt
Nationality: Egyptian
Scientific degree: Ph.D. Degree, 2020
Specification: Infectious diseases
Thesis title: Advanced studies on infected calves with diarrheagenic *Escherichia coli*
Supervisors:

Prof. Walid Sayed Ahmed Abd Elkader Awad
Prof. Samia Abd Elhamid Ahmed

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 *ehylA* 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 PABLs 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.