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Recent Studies on Multidrug Resistant (MDR) and Extensively Drug Resistant (XDR) Mycobacterium Tuberculosis Complex Isolates from Humans and cows

A thesis submitted by

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In the partial fulfillment of:
Ph.D degree in Veterinary Medical Sciences
Microbiology

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2019

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Specification: Microbiology

Thesis Title: Recent Studies on Multi-drug Resistant (MDR) and Extensively Drug Resistant (XDR) Mycobacterium Tuberculosis Complex Isolates from Humans and cows

Abstract

Tuberculosis (TB) is a serious infectious, contagious, airborne, chronic and zoonotic disease, in 2018; 136 years have passed since the discovery of *Mycobacterium tuberculosis* by Robert Koch as well as 25 years since the WHO declared TB as a global health emergency. The worldwide reemergence of DR-TB strains threaten TB control program; moreover the emergence of drug-resistant *M. bovis*. Monitoring and tracking TB and DR-TB is a critical component in the management of TB, because it allows the identification of trends, challenges and implemented treatment program successes, in areas that require additional attention.Our study is the first to shed light on genotyping of circulating MDR strains in Egyptian community using Whole Genome Sequencing (WGS). This study revealed that the highest mono-resistance was detected against rifampicin (RIF), there one MDR- *M. bovis* was detected, and the predominance of Euro-American lineage in Egypt among drug resistance strain.

Key words:.
Tuberculosis, *Mycobacterium Tuberculosis* complex, *M. bovis*, Multi-drug Resistant (MDR), spoligotyping, MIRU-VNTR, whole genome sequencing.

Acknowledgement

First of all, I would like to express my all-embracing gratitude and praise to ***ALLAH, glorified be He****, for his unmitigated support and graceful benevolence in carrying out this humble thesis.*

I would like to seize the opportunity to express my greatest indebtedness and sincere loyalty to ***Prof. Dr., Khaled Fraouk El-Amry,*** *Professor of Microbiology and Immunology, Microbiology Department, and Dean of Faculty of Veterinary Medicine Cairo University for his initiating power, effective scientific supervision, continuous encouragement and his generous help. It gives me the greatest honor to work under supervision.*

I am also greatly honored to express my gratitude and respect to ***Prof. Dr., Salah-El-Din Abd El K arim Selim,*** *Professor of Microbiology and Immunology, Microbiology Department, Faculty of Veterinary Medicine Cairo University.*

My thanks and appreciation to *Prof Stefan Niemann* ***, Head of*** *Molecular and Experimental Mycobacteriology, National Reference Center for Mycobacteria , Borstel ,Germany.*

I would also like to sincerely thank the MolyMyc Laboratory team, National Reference Center for Mycobacteria , Borstel ,Germany. ***Dr***

Mathias Merker, Tanja Ubban, Anja ludeemann, Fanja *for their great assistance during molecular typing and sequencing of my isolates.*

My sincere appreciation to ***the Science and Technology Development fund (STDF)*** *–Short Term Fellowship.*

Countless thanks and filial gratitude, which engulf my heart are kept for ***my father*** *who kindly insinuated in my heart the love of knowledge and the patience of a researcher.*

All thanks and love to my ***brother and sisters****; for their everlasting care genuine support, and sincere prayers; all of which were a source of undeniable assistance.*

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List of Abbreviations

***ahp*C**	Alkylhydroperoxide reductase
Am	Amikacin
BCG	Bacillus Calmette–Guérin
BTB	Bovine tuberculosis
Cm	Capreomycin
DNA	Deoxyribonucleic acid
DOTS	Directly observed thereby short-course
DST	Drug Susceptibility Test
GC	Guanine and cytosine
HIV	Human immunodeficiency virus
INH	Isoniazid
***Inh*A**	Enoyl acyl carrier protein reductase
INDELs	insertion deletions
***kat*G**	Catalase-peroxidase enzyme