

شبكة المعلومات الجامعية التوثيق الإلكتروني والميكروفيلو

بسم الله الرحمن الرحيم





HANAA ALY



شبكة المعلومات الجامعية التوثيق الإلكتروني والميكرونيله



شبكة المعلومات الجامعية التوثيق الالكتروني والميكروفيلم



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جامعة عين شمس التوثيق الإلكتروني والميكروفيلم قسم

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Molecular Characterization of Emerging Viruses in Bats with Possibility of Spillover Between Species

A Thesis submitted by

Omar Sayed Ahmed Saeed

(BVSc., Cairo University, 2017)

For the Degree of Master in Veterinary Medical Science

(Virology)

Under supervision of

Prof. Dr. Hussein Ali Hussein Ahmed

Professor of Virology and Vice Dean for Graduate Studies and Research Faculty of Veterinary Medicine Cairo University

Dr. Ayman Hany Mahmoud EL-Deeb

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قسم القيروسات



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Abstract

Bats are now being highlighted as reservoir hosts for emerging viruses that are potentially deadly and zoonotic (Marburg virus, Ebola, Nipah, Hendra, and MERS corona viruses). Numerous studies were conducted on bats worldwide, little was known on viruses of Egyptian bats. The objective of this surveillance study was to screening bat associated viruses implicated in zoonotic events. Bat samples were collected using mist nets and hard traps and the species identification was morphologically determined into frugivorous and insectivorous species. We screened for RNA viruses; specifically, West Nile fever virus (WNV), Coronaviruses (CoVs; MERS-CoV, SARS-CoV and SARS-CoV-2), Henipaviruses (HeV and NiV), Rabies virus (RABV) and Influenza A viruses (IAVs) viruses using the one-step RT- qPCR technique. We used viral-specific primers and probes, as well as virus sequencing and phylogenetic analyses to further characterization of the virus. Except for Rift Valley Fever Virus, no evidence of all viruses genome in any studied samples. Rift valley virus RNAs were detected in two liver samples of insectivorous bats only. This study extends the current knowledge by obtaining additional sequences from bats that haven't been previously identified as hosts of these viruses. The finding of viruses highly correlated to human strains and hence of public health concern, claimed the significance of intensive surveillance. To our knowledge, this is the first bat-associated virus surveillance study in Egypt spanning from 2019-2021 that covering locations with moderate to high levels of interaction between bats and human and the first molecular detection of RVFV in *Pipistrellus* deserti bat in Egypt.

Keywords: Bats, Emerging viruses, Genome Sequencing, Molecular Screening, RT-qPCR.

Dedication

I dedicate my dissertation work to my family. A special feeling of gratitude to my Heroic Mom whose words of encouragement and push for tenacity ring in my ears. My beloved brother and sister have never left my side and are very special. I also dedicate this dissertation to my amorous friends (Tarek El Mehy, Amr Teama, Ahmed El gendy and Omar Khaled) who become family. I dedicate this work and give special thanks to my best students and Colleagues being there for me throughout the entire Master program.

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