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Investigation of spillover evidence of SARS-CoV-2 virus in dogs and cats in Egypt

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Abstract

SARS-CoV-2 zoonotic and reverse zoonotic transmission could be resulted from routine activities and interactions between humans and their companion animals. A combination of SARS-CoV-2 high mutation rate and homology of cellular ACE2 receptors enable SARS-CoV-2 to transcend species barriers and facilitate the viral transmission between humans and animals. The aim of this study to investigate spillover of SARS-CoV-2 between humans and companion animals with studying mutations of the detected SARS-CoV-2 spike glycoprotein and the effect of these mutations on the viral structure and function.

Oropharyngeal/Nasopharyngeal swabs, serum and blood samples were collected from 66 companion animals (33 cats and 33 dogs) which were close contact to SARS-CoV-2 positive owners from December 2020 to March 2021. Swabs were screened by rRT-PCR and some positive cases were confirmed by partial spike sequencing. Clinical pathology and pathological studies were also performed. Spillover of SARS-CoV-2 between humans and their companion animals were reported in Egypt with a rate of 30.3% of cats (10/33) and 24% of dogs (8/33) by using rRT-PCR. Partial spike gene sequencing of 6 positive samples collected in December 2020 were identical to SARS-CoV-2 that was detected in humans in Egypt in that time frame. Furthermore, the infected companion animals have suffered from lymphocytopenia, thrombocytopenia with elevation of ferritin, LDH, C-reactive protein and D-dimers levels. The latter infected animals have showed a wide range of clinical signs including

asymptomatic, mild and severe respiratory signs with some deaths in the infected cats. The dead cats exhibited multiple systematic pathological lesions in lung, heart, liver intestine and kidney. Thus, spillover of SARS-CoV-2 may be occurred between humans and pet animals.

Full spike sequencing for some detected SARS-CoV-2 in cats that were collected in December 2020, March 2021 and July 2021 has displayed 7 amino acid substitutions. Structural modelling has revealed that 4 of these mutations could affect the interaction with the neutralizing antibodies and others could influence S1/S2 cleavage, facilitate viral binding to the ACE2 host receptors and enhance viral infectivity. Bioinformatics analysis of ACE2 receptors in different animal hosts has provided in-depth investigation for RBD/ACE2 complex binding affinity and their relationship to SARS-CoV-2 infection susceptibility. Therefore, this thesis paves the way for studying SARS-CoV-2 host susceptibility in different animal species.

Keywords: SARS-CoV-2, companion animals, zoonoses, reverse zoonoses, spike, mutations, ACE2, structural modeling.



Dedication

*This thesis is dedicated to my parents;
for their limitless love, motivation, and support.*

To my lovely sisters and my brother.

To my supportive husband.

*To my little princess, who is the best thing
that ever happened to me.*

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