Predicting the Risk of Other Species Susceptibility to SARS-COV-2 by Analyzing ACE2 Protein Sequences

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Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the cause of the global pandemic known as coronavirus disease-2019 or COVID-19 for short. SARS-CoV-2 is a zoonotonic disease, but there is very little research done on interspecies transmission or susceptibility. This means that there are unknown risks to pets, wildlife, and livestock that are yet to be identified. Furthermore, most animal species, including those that have frequent exposures to humans, have unknown susceptibilities. Therefore, methods to predict infection risk of animal species are in dire need. SARS-CoV-2 spike protein binding to angiotensin-converting enzyme 2 (ACE2) is critical for viral entry and infection. Due to ACE2's integral factor for the virus, the utilization of ACE2 is key for predicting the unknown SARS-CoV-2 animal species infection. In this project, I used big data and compared human ACE2 protein sequences against various animal species including house pet, wild animals, birds and fish. In this study, I compared ACE2 protein sequences across a plethora of animal species to determine the susceptibility of SARS-CoV-2 and predict which animals contained elevated risks of infection. The similarity of ACE2 protein sequences among the different species was observed by building a phylogenic tree. Also I calculated the potential susceptibility scores with biostatistics. The calculated susceptibility scores revealed that the naturally or experimentally infected species have high susceptibility while experimentally not-infected species have lowest susceptibility scores. Using the lowest susceptible score and highest non-susceptible score, animal species with SARS-CoV-2 susceptibility can be determined.

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