

The most important animal pest is the possibility of transmitting or reservoirs the Corona virus

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Abstract

Although the bat has unique characteristics compared to other mammals, but it currently enjoys a poor reputation, especially after being linked to being the source of the Corona virus, as international researchers recently published a large-scale research, which is the largest of its kind, about corona viruses in the bat. If this hypothesis is correct, then the Corona virus will be added to other dangerous viruses carried by the bat bird. The bird had caused, years ago, the spread of viruses such as "SARS" and "MERS", because the bat can carry different viruses without getting sick. The bat is a "reservoir for viruses" that have caused a number of diseases and epidemics in Africa, Malaysia, Bangladesh and Australia. It is not limited to the mentioned viruses, as the bat carries an "Ebola" infection, and the "rabies" virus also carries. Other mammals. It is possible that other animal pests such as rodents may be related to reservoiror transmitting the Corona virus.

Keywords: bat; corona viruses; SARS; MERS; Ebola; rabies; reservoir for viruses

Introduction

Bats have been recognized as the natural reservoirs of a large variety of viruses. Special attention has been paid to bat coronaviruses as the two emerging coronaviruses which have caused unexpected human disease outbreaks in the 21st century, Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and Middle East Respiratory Syndrome Coronavirus (MERS-CoV), are suggested to be originated from bats. Various species of horseshoe bats in China have been found to harbor genetically diverse SARS-like coronaviruses. Some strains are highly similar to SARS-CoV even in the spike protein and are able to use the same receptor as SARS-CoV for cell entry. On the other hand, diverse coronaviruses phylogenetically related to MERS-CoV have been discovered worldwide in a wide range of bat species, some of which can be classified to the same coronavirus species as MERS-CoV. Coronaviruses genetically related to human coronavirus 229E and NL63 have been detected in bats as well. Moreover, intermediate hosts are believed to play an important role in the transmission and emergence of these coronaviruses from bats to humans. Understanding the bat origin of human coronaviruses is helpful for the prediction and prevention of another pandemic emergence in the future Ben Hu et al (2015).

Rodents are the most diverse mammals on the planet and are important reservoirs of many pathogens example Coronaviruses infect various animals, but to date, relatively few coronaviruses have been identified in rodents worldwide. Rat coronaviruses are very contagious, with transfer to susceptible rats by direct contact with infected rats, and indirectly by

aerosol and fomites. The evolution and ecology of coronaviruses in rodent have not been fully investigated to human. Desoky (2020).

Background

Banerjee et al., (2019) They found, bats are speculated to be reservoirs of several emerging viruses including coronaviruses (CoVs) that cause serious disease in humans and agricultural animals. These include CoVs that cause severe acute respiratory syndrome (SARS), Middle East respiratory syndrome (MERS), porcine epidemic diarrhea (PED) and severe acute diarrhea syndrome (SADS). Bats that are naturally infected or experimentally infected do not demonstrate clinical signs of disease. These observations have allowed researchers to speculate that bats are the likely reservoirs or ancestral hosts for several CoVs. In this review, we follow the CoV outbreaks that are speculated to have originated in bats. We review studies that have allowed researchers to identify unique adaptation in bats that may allow them to harbor CoVs without severe disease. We speculate about future studies that are critical to identify how bats can harbor multiple strains of CoVs and factors that enable these viruses to "jump" from bats to other mammals. We hope that this review will enable readers to identify gaps in knowledge that currently exist and initiate a dialogue amongst bat researchers to share resources to overcome present limitations.

Latinne, et al. (2020). Bats are presumed reservoirs of diverse coronaviruses (CoVs) including progenitors of Severe Acute Respiratory Syndrome (SARS)-CoV and SARS-CoV-2, the causative agent of COVID-19. However, the evolution and diversification of these

coronaviruses remains poorly understood. Here we use a Bayesian statistical framework and a large sequence data set from bat-CoVs (including 630 novel CoV sequences) in China to study their macroevolution, cross-species transmission and dispersal. We find that host-switching occurs more frequently and across more distantly related host taxa in alpha- than beta-CoVs, and is more highly constrained by phylogenetic distance for beta-CoVs. We show that inter-family and -genus switching is most common in Rhinolophidae and the genus *Rhinolophus*. Our analyses identify the host taxa and geographic regions that define hotspots of CoV evolutionary diversity in China that could help target bat-CoV discovery for proactive zoonotic disease surveillance. Finally, we present a phylogenetic analysis suggesting a likely origin for SARS-CoV-2 in *Rhinolophus* spp. bats.

A novel coronavirus reported to cause pneumonia in 41 people during December 2019 in Wuhan, the capital of Hubei province, China, was identified and designated as the 2019 novel coronavirus (2019-nCoV) (Zhu et al., 2020; Li et al., 2020). Infection with 2019-nCoV results in clusters of severe respiratory illness similar to that caused by severe acute respiratory syndrome coronavirus (SARS-CoV) and is associated with high mortality (Chen et al., 2020; Huang et al., 2020).

After epidemiological investigation, it was revealed that a local seafood market, where wild animals and live poultry were for sale, was linked to this undiagnosed pneumonia (Wu et al., 2020). Wu et al. collected bronchoalveolar lavage fluid from a patient who worked in the seafood market and performed full genome sequencing of 2019-nCoV. It was shown that 2019-nCoV had a high nucleotide sequence similarity to a bat SARS-related CoV (bat-SL-CoVZC45, accession No. MG772933) and only 79.5% genome sequence similarity to SARS-CoV. Phylogenetic analysis showed that the virus was clustered with SARS-CoV and bat SARS-CoVs in subgenus Sarbecovirus (Wu et al., 2020; Wei et al., 2020; Yu et al., 2019; Xu et al., 2020). Genomic analysis of 2019-nCoV and four typical coronaviruses (bat SARSr-CoV-Rp3, CoV-ZC45, CoV-ZXC21, and SARS-CoV-Tor2) showed a likelihood of recombination between 2019-nCoV and other coronaviruses among the subgenus (Wu et al., 2020). So how did this novel coronavirus emerge? To investigate the origin of 2019-nCoV, Zhou et al. sequenced samples from seven patients and bats, and found that this new coronavirus shared 96.2% overall genome sequence identity with a bat coronavirus RaTG13 from horseshoe bats (*Rhinolophus*). This discovery provided further evidence that 2019-nCoV most likely originated from bats (Zhou et al., 2020). Previously, horseshoe bats were identified as natural hosts for SARS-related coronaviruses which were the direct progenitors for the origin of SARS-CoV (Hu et al., 2017).

Desoky, (2020) Rodents are important reservoirs of many pathogens example Coronaviruses. The previously infected mice have a lower degree of infection in future periods. The evolution and ecology of coronaviruses in rodent have not been fully investigated to human. A study of the immune system of infected rodents can be used to control the effect of coronaviruses on humans, especially the Coronavirus (COVID-19), it spreads all over the world and causes many deaths in the current period. From this, can also possible to study the immune system of people who have recovered from the disease in search of a new Therapy that useful all of humanity.

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