

To use wild resources properly: a lesson from two species of human coronaviruses

Yimin Zhang¹, Shiqiang Wang²

1 West China School of Basic Medical Sciences & Forensic Medicine, Sichuan University
Chengdu 610041, China

2 Air and Missile Defence College, Air Force Engineering University, Xi'an 710051, China
(Corresponding author)

Abstract: The global pandemic of COVID-19, a disease caused by a severe acute respiratory syndrome-related coronavirus (SARSr-CoV), is responsible for over a hundred million confirmed cases and more than two hundred deaths worldwide. Accumulating evidence indicates correlations between the abuse of wild resources and the outbreaks. To reduce the risks of getting infected with human coronaviruses (HCoVs), brief introductions to HCoVs were made, the hosts of them are listed, the probable transmission routes of the SARSr-CoVs and MERS-CoVs are analyzed, and the recommendation that we use wild resources properly was put forward.

Key words: severe acute respiratory syndrome-related coronaviruses; Middle East respiratory syndrome coronavirus; hosts; transmission routes

1. Introductions to human coronaviruses

Cornaviruses (CoVs), previously known as picornaviruses, are named for the crown-like spikes on their surfaces^[1]. These viruses are enveloped positive-sense, single-stranded ribose nucleic acid viruses with their 5' ends capped and 3' ends polyadenylated^[2].

Human CoVs (HCoVs) are actually close to us, however, the cognition of them is relatively limited. In fact, it wasn't until 1965 that Tyrrell et al. found a novel virus when cultivating the pathogens responsible for common colds, and the virus is now known as HCoV-229E^[3]. Two years later, another HCoV, HCoV-OC43, was reported by McIntosh K et al.^[4]. HCoV-229E and HCoV-OC43 are really common etiological agents that are unlikely to be responsible for severe symptoms^[5], consequently, the discoveries of the two HCoVs didn't raise much attention.

However, in 2002 and 2003, the world was struck by an outbreak of an unknown infectious disease, and in February 2003, severe acute respiratory syndrome (SARS) was put forward by Carlo Urbani, an expert on communicable diseases^[6], and the pathogen, now known as the first SARS-related CoV (SARSr-CoV), SARS-CoV, was isolated in March 2003^[7].

In 2004, Lia et al. identified HCoV-NL63^[8], and in 2005, HCoV-HKU1 was characterized by Patrick et al.^[9]. HCoV-NL63 and HCoV-HKU1 are very common etiological agents as well, and at the same time, not really harmful^[5]. In 2012, another lethal HCoV was reported^[10], and named as Middle East respiratory syndrome CoV (MERS-CoV) later.

At the end of 2019, Zhang et al. reported several cases with pneumonia. It didn't take much time to confirm that the etiological is a novel SARSr-CoV^[11]. And the diseases caused by the virus, now named as COVID-19, threaten

global public health greatly, and is responsible for more than a hundred million confirmed cases and has caused two hundred deaths worldwide ^[12].

Until today, six species of HCoV have been discovered, several strains of SARS-CoVs and MERS-CoV are lethal, while the others are usually not life-threatening.

2. Bats, the natural reservoir hosts

Bats are ideal natural reservoir hosts of tens of lethal human viruses, as the viruses fail to kill the hosts, and at the same time, the incomplete immune systems of the hosts fail to erase the pathogens.

However, the natural reservoir hosts are almost certain. In 2017, Ben et al. discovered a rich gene pool of bats, and concluded that, horseshoe bats (*Rhinolophus* species) are likely to be responsible for the outbreak of SARS ^[13], and Zhou et al. announced that the natural reservoir hosts of SARS-CoV-2 might be horseshoe bats as well ^[11]. Besides, accumulating evidence indicates that, MERS-CoV originates from *Nycteris* species, *Pipistrellus* species, or Egyptian tomb bats (*Taphozous perforatus*).

However, bats do react to viral infections, at least viral infections would usually trigger humoral immune responses, and the immunoglobulins against CoVs, WNV, EBOVs and Nipah Virus had been isolated in the serum of bats.

3. Evidence for the association between the outbreaks and the exposures to wholesale markets

Wholesale markets are the places where direct contact with infected animals. Shortly after the outbreak of SARS-CoV infection, Guan et al. isolated a SARS-CoV from the masked palm civets (*Paguma larvata*) and a raccoon dog in a live animal market in Guangdong, even though the sequences of these isolates differs from most of the human isolates ^[14].

Coincidentally, studied the early cases, and most of us have heard of Huanan seafood market, a wholesale market in Wuhan. This market mightn't be the origin of the outbreak of SARS-CoV-2 infection in Wuhan, most of the exposed to and the samples collected there were tested positive. Epidemiology studies indicated the correlation between another outbreak of SARS-CoV-2 infection and the exposure Xinfadi wholesale market, and the samples collected there tested positive, too.

However, Li reviewed the clinical uses of bats, he listed a fetal case of severe acute diarrhea in the Tang Dynasty, then he mentioned the clinical observations, and concluded that, bats are toxic, and would usually lead to diarrhea ^[15]. Actually, diarrhea is one of the typical symptoms of coronaviral infections ^{[5][16]}. Even though a variety of etiological agents are responsible for diarrhea, and we couldn't conclude whether HCoVs contributed to that death, the fact that hunting or slaughtering bats greatly increase the risks of bat-to-person transmissions of lethal etiological agents is self evident.

4. Wild meat trades increase zoonotic infection risks

We've mentioned that the live animal market in Guangdong is really likely to be responsible for the outbreak of SARS-CoV infection, and the first case isn't alone. Shortly after the outbreak of SARS-CoV-2 infection, the clinicians found that, at the beginning of the outbreak, most patients were exposed to Huanan Seafood Market ^[17].

Even though there isn't enough evidence to conclude that, pangolins are responsible for the SARS-CoV-2 pandemic, the fact that pangolins could be infected with SARS-CoVs that greatly resemble SARS-CoV-2 is evident ^[18].

It's well known that masked palm civets prefer eating fruits, however, growing evidence has shown that, the civets are capable for hunting, and enjoy eating meat as cats and dogs, their relatives, Zhou et al. found that, the food categories that masked palm civets consume could vary from seasons to seasons, while fruits, mammals and birds are

favorable^[19], indicating that the civets might hunt bats for food, and might somehow bite we human beings. The civets might bite we human beings, while some people hunt the civets for food, both would be risky. In other words, the bat-to-civet transmission is possible to be accomplished via the grazing food chain, and the exposure is usually increased greatly when slaughtering.

As for pangolins, their skins are typically covered by scales, which would reduce the exposure and prevent them from being bitten by other animals. More importantly, they're toothless.

As mentioned, bats are used in tradition Chinese medical practices. Actually, pangolins are even much more popular. The patients mightn't get infected when consuming, but hunting, slaughtering and preparing the drugs are really risky.

Even though Liu et al. suspected that reptiles could be the sources of SARS-CoV-2 infection^[20], up to now, any non-mammalian animal-to-person transmissions of SARS-CoVs or MERS-CoV haven't been reported, hunting other wild animals isn't always safe. Wild birds would be responsible for the transmission of H5N1 avian influenza virus^[21], and wild non-mammalian animals would make great contributions to the transmission of bacteria and parasites as well^[22].

In summary, reducing consuming wild animals, particularly wild mammals, would usually limit the unnecessary exposure, and protect us from getting infected.

5. Conclusion

This paper analyzed the probable transmission routes of the SARS-CoVs and MERS-CoVs, and the conclusion that wild resources properly should be used properly was drawn. First of all, the HCoV were introduced. Secondly, the natural reservoir hosts and candidate sources of infections of emerging infectious diseases, particularly SARS-CoVs were analyzed. Thirdly, based on the analyses, we drew a conclusion that making uses of wild resources properly would help limit the risks and provide us with more solutions to the diseases.

Reference

1. Tyrrell D., Sparrow P, Beare A. Relation between Blood Groups and Resistance to Infection with Influenza and some Picornaviruses[J]. *Nature*, 1968; 220. 819-20.
2. Weiss S R, Navasmartin S. Coronavirus Pathogenesis and the Emerging Pathogen Severe Acute Respiratory Syndrome Coronavirus[J]. *Microbiology & Molecular Biology Reviews* Mmbr, 2005; 69(4):635.
3. Tyrrell D., Bynoe M.L. Cultivation of a novel type of common cold virus in organ culture[J]. *Br Med J*. 1965;1(5448):1467-70.
4. McIntosh K, Becker W B, Chanock R M. Growth in suckling-mouse brain of "IBV-like" viruses from patients with upper respiratory tract disease[J]. *Proceedings of the National Academy of Sciences*, 1967; 58(6):2268-2273.
5. Zumla Alimuddin, Chan Jasper, Azhar Esam, Hui, David, Yuen Kwok-Yung. Coronavirus-drug discovery and therapeutic options[J]. *Nature reviews Drug discovery*, 2016; 15.
6. Reilley B, Herp M V, Sermand D et al.. SARS and Carlo Urbani[J]. *New England Journal of Medicine*, 2003; 348(20):1951-1952.
7. Peiris Joseph S et al.. Coronavirus as a possible cause of severe acute respiratory syndrome[J]. *Lancet*, 2003; 361. 1319-25.
8. van der Hoek Lia et al.. Identification of a new coronavirus[J]. *Nature medicine*, 2004; 10. 368-73.
9. Woo Patrick et al.. Characterization and Complete Genome Sequence of a Novel Coronavirus, Coronavirus HKU1, from Patients with Pneumonia[J]. *Journal of virology*, 2005; 79. 884-95.
10. Zaki A M, Van Boheemen S, Bestebroer T M et al.. Isolation of a Novel Coronavirus from a Man with Pneumonia in Saudi Arabia[J]. *New England Journal of Medicine*, 2012; 367(19):1814-1820.

11. Zhou Peng et al.. A pneumonia outbreak associated with a new coronavirus of probable bat origin[J]. *Nature*, 2020.
12. Epidemiology Group of New Coronavirus Pneumonia Emergency Response Mechanism, Chinese Center for Disease Control and Prevention. Analysis of epidemiological characteristics of new coronavirus pneumonia [J]. *Chinese Journal of Epidemiology*, 2020.
13. Ben H, Lei-Ping Z, Xing-Lou Y, et al.. Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus[J]. *PLOS Pathogens*, 2017; 13(11):e1006698.
14. Guan Y et al.. Isolation and Characterization of Viruses Related to the SARS Coronavirus from Animals in Southern China[J]. *Science*, 2003; 302(5643):276-278.
15. Li S Z. Poultry Department Volume 48 [M]. *Compendium of Materia Medica*.
16. Wang D et al.. Clinical Characteristics of 138 Hospitalized Patients With 2019 Novel Coronavirus-Infected Pneumonia in Wuhan, China[J]. *JAMA*, 2020.
17. Huang C , Wang Y , Li X , et al. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China[J]. *The Lancet*, 2020, 395(10223).
18. David Cyranoski. Mystery deepens over animal source of coronavirus[J]. *Nature*, 2020.
19. Zhou Y, Zhang J, Slade E et al.. Dietary Shifts in Relation to Fruit Availability among Masked Palm Civets (*Paguma larvata*) in Central China[J]. *Journal of Mammalogy*, 2008; 89(2):435-447.
20. Liu Zhixin et al.. Composition and divergence of coronavirus spike proteins and host ACE2 receptors predict potential intermediate hosts of SARS-CoV-2[J]. *Journal of Medical Virology*, 2020.
21. Lewis, David B. Avian Flu to Human Influenza[J]. *Annual Review of Medicine*, 2006; 57(1):139-154.
22. Jones M K, Oliver J D. *Vibrio vulnificus*: Disease and Pathogenesis[J]. *Infection and Immunity*, 2009; 77(5):1723-1733.