LETTER TO THE EDITOR

COVID-19 and Zoonosis

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Dear Editor,

An exceptional outbreak of pneumonia emerged in Wuhan City, Hubei province in People's Republic of China in December 2019. A novel Coronavirus was recognized as the causative agent and termed by the World Health Organization (WHO) as Coronavirus disease 2019 (COVID-19). It was reflected as relative of Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory Syndrome (MERS), COVID-19, however is caused by a beta Coronavirus named SARS-CoV-2 that affects the lower respiratory tract and exhibits as pneumonia in human.[1] Considering origin of COVID-19, the zoonotic nature of Human Coronavirus (HCoV) is under discussion. Variety of zoonotic CoVs are mingling in world, bat CoVs with zoonotic prospective are so miscellaneous. Animal CoVs have also been known since late 1930s. In the past decade, seven HCoV have been identified namely as HCoV-NL63, HCoV-229E, SARS-CoV, MERS-CoV, SARS-CoV-2, HCoV-OC43 and HCoV-HKU1. To discuss the animal origin of HCoV, it will serve best to know the definitions and characters of evolutionary, natural, reservoir, intermediate and amplifying hosts of HCoVs. Animal serves as evolutionary host of HCoV if it harbors closely related ancestor sharinghigh homology at level of nucleotide sequence. Ancestral virus is well adapted and non-pathogenic usually in this host. Similarly, reservoir host harbors HCoV constantly and for long term. Hosts are naturally infected in both cases, so are natural host of HCoV or its parental virus. In contrast, if HCoV is newly introduced to an intermediate host just before or around its introduction to humans then it is not adapted well to new host and is pathogenic often. This intermediate host then can serve as zoonotic source to human infection and plays role of amplifying host. Thus, allows the virus to replicate transiently and transmits it to humans for amplifying the scale of human infection. HCoV undergoes dead-end infection if it cannot sustain its transmission within intermediate host. On the other hand, HCoVs if adapts to intermediate host then they can establish long-term endemicity. In this case, intermediate host becomes natural reservoir host (Fig.1).[2]

Before the isolation of first HCoV-229E strain B814 from nasal discharge of patients having slight common cold, there were different CoVs already isolated from various infected animals, including turkey, mouse, pig, cow, dog and cat.[3] These zoonotic CoVs may evolve and recombine, resulting in emergence of new CoVs that can be more transmissible and/or deadly for humans in future. SARS-CoV-2 is new public health crises threatening the world with the emergence that seems to come from a bat.[2] However, as for SARS-CoV and MERS CoV spillover effect linked to animal-human promiscuity, human activities including illegal bush trafficking and deforestation cannot be omitted.[4] Adaptationand mutation have driven the co-evolution of CoVs and their hosts, including human beings, for thousands of years.[2]

The emergence of SARS-CoV-2 in central China at the end of 2019 has propelled CoVs again into spotlight and shocked us with its high

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transmissibility but reduced pathogenicity compared to its sister SARS-CoV. Most HCoVs initiated from bats where they are non-pathogenic.[2] The probability of an intermediate host facilitating the emergence of virus in humans has already been shown with civet cats stand-in as intermediate hosts for SARS-CoVs and dromedary camels for MERS-CoV. HCoV infection is a zoonosis and understanding the zoonotic origins of HCoVs would assist us well. Exploring CoV-host interactions in animals will also stem important insight on CoV pathogenesis in humans.[5] Identifying the animal hosts will have direct implications in the prevention of human diseases.

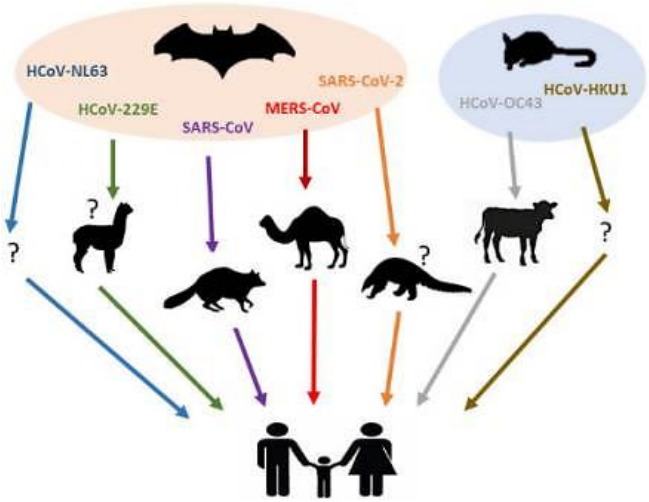

Fig.1: Animal hosts of HCoVs.
Blue, green, purple, red, orange, grey, brown arrows represent the transmission of HCoV-NL63, HCoV-229E, SARS-CoV, MERS-CoV, SARS-CoV-2, HCoV-OC43 and HCoV-HKU1 from their natural hosts (bats or rodents) to the intermediate hosts (camelids, civets, dromedary camels, pangolins or bovines), and eventually to the human population. No concrete evidence exists on the intermediated host(s) of HCoV-NL63 and HCoV-HKU1, which was shown as a question mark (?).[2]

CONFLICT OF INTEREST

None to declare.

FINANCIAL DISCLOSURE

None to disclose.

REFRENCES

1. Sohrabi C, Alsafi Z, O'Neill N, Khan M, Kerwan A, Al-Jabir A, et al. World Health Organization declares global emergency: a review of the 2019 novel Coronavirus (COVID-19). Int J Surg. 2020; 76 (1): 71–6.
2. Ye ZW, Yuan S, Yuen KS, Fung SY, Chan CP, Jin DY. Zoonotic origins of human Coronaviruses. Int J Biol Sci. 2020; 16 (10): 1686-97.
3. Singhal T. A review of Coronavirus Disease-2019 (COVID-19). Indian J Pediatr. 2020; 87 (4): 281-6.
4. Afelt A, Frutos R, Devaux C. Bats, Coronaviruses, and deforestation: toward the emergence of novel infectious diseases? Front Microbiol. 2018; 9 (702): 1-5.
5. Malik YA. Properties of Coronavirus and SARS-CoV-2. Malays J Pathol. 2020; 42 (1): 3-11.

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