

Review

Marriage of Zoonotic Viruses with Human Life: Review

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Abstract

Zoonotic or zoonosis is a concept of animal infection transmitted in human beings. The zoonotic animal is a bat who is one of the primary reservoirs. Severe Acute Respiratory Syndrome Corona virus (SARS CoV) matches to genomic analysis and phylogenetically related to bats viruses. SARS CoV-2 is another virus related with bats. It is highly pathogenic, infectious, and affects or damages human respiratory system rapidly. In this review, we have provided short analysis of types of viruses responsible for zoonosis along with their clinically important manifestations and epidemiology.

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1. Introduction:

The term zoonotic animal has been appeared from the Greek word '*Zoonosis*' means zoo (animal) and nosis means disease, that is defined as an infection transmitted from animals which are wild, to humans as well as from human beings to animals through water borne infections, direct contact, food along with some vectors such as insects, flies and mosquitoes [1]. The maximum both re-emerging and emerging pathogenic diseases are zoonotic in nature and wild animals are sources of many of them.

The rate at which the diseases are emerging has been increased in the past decades as well as the many of pathogens along with infections that are emerging are viruses. More than 50% of the diseases that arise due to

microorganisms affect humans are related with zoonotic transfer from the animals which are wild that cause spread of diseases which are pathogenic in nature [2].

The zoonotic viruses are found in natural reservoirs and cause changes in environment in relation with disease causing agents from wild life to live stock, as well as activities in human in urbanization, intensification of agricultural sectors, and the trade of marketing are increasing the interface which is present between live stocks, people along with animals that provide non-interrupting chances for infections in population of humans and then, spreads across the world [3]. The infection by viruses between domestic animals and wild life or human beings probably takes place with higher

frequency than recognized, due to surveillance systems which is limited or poor [4].

Bats have their >1200 species in the globe that forms the order recognized as Chiroptera taking them at second level in case of number of species after rodents [4]. In this review, we have provided short analysis of types of viruses responsible for zoonosis along with their clinically important manifestations and epidemiology.

2. Epidemiology:

Bats are considered as special zoonotic animals as well as there is a combination of genetic, ecologic as well as immunologic factors [3]. There are many viruses that are present in bats viz. Marburg virus, Ebola virus, Nipah virus, Tick-borne emergence (TBE) virus, as well as corona viruses including Severe Acute Respiratory Syndrome (SARS), Middle East Respiratory Syndrome (MERS) along with Covid-19 which is novel [5]. Even if bats, generally, are not interested to contact people, their excreta connected with buildings, households, caves, mines can lead to infections of human by pathogens borne from bats [6]. Bats that are frugivorous prefer to consume the cultivated fruits such as rambutan, mangoes, guava along with food sources provided by humans that after contamination by excreta of bat, can serve as a way of infection to animals or people [7].

In maximum areas of the globe, bats are used for food, traditional medicine or sport [5]. The slaughtering as well as consumption of bats gives the chance to transmit the pathogens that originate from blood [5]. Nevertheless, discovery of viruses potentially increased understanding of the value of families of viruses viz. filo viruses, for instance Ebola virus, Corona viruses e.g SARS CoV, as well as Para-myxo viruses such as NiV that is needed for not only better understanding of the thing that makes viruses pathogenic in nature as well as in order to recognize the wild life reservoirs that contain viral pathogens after their more rapid emergence [8]. The viruses that are linked with human behaviors are responsible for causing significant mortality as well as morbidity among people; however, they have included other species in chain of transmission between bats as

well as people that make them related to not only human but also health of animals [9].

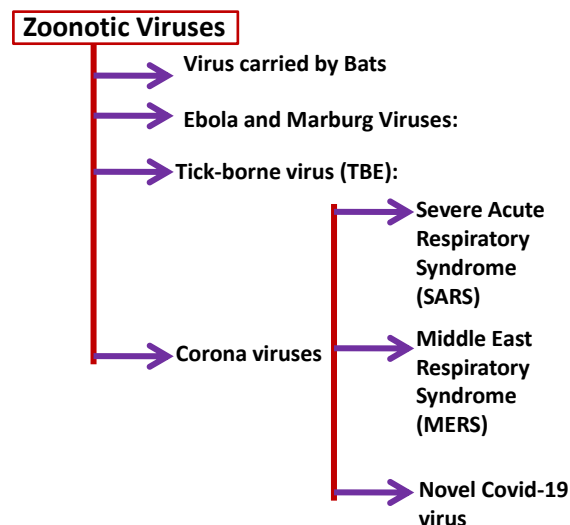


Figure 1: Different zoonotic viruses

2.1. Bats viruses:

The zoonoses which are emerging that are connected with bats (figure 1) are Nipah in addition to Hendra viruses, Henipa viruses, NiV that was first identified in Malaysia in 1998 that causes neurologic and respiratory disease among domestic pigs, consequently infected the workers in farm [7].

The farm size generated an environment which could assist a sustained outbreak of Para-myxo virus among the pigs over a year that resulted into the wide range epidemic [10]. The outbreak spread of infections in Malaysia was occurred because of movement of pigs that were infected resulted into reduction of population with shut down of farms in thousands of numbers as well as infection among 265 people in Singapore and Malaysia out of whom 105 persons lost their lives [7].

Hendra virus was tracked to bats that acted like the natural reservoir [11]. The study of genetic relations between Hendra viruses and Paramyxo viruses resulted into the exploration and authentication of two pteropid bat species that were endemic in Malaysia as NiV reservoirs [12]. Shockingly, NiV encephalitis outbreak was reported in Bangladesh in 2001 with 100% fatality rates [13,14]. The outbreaks that appeared in Bangladesh were not only seasonal but also spatially clustered in the

half side of western side of the country [13]. Taking the raw date palm in the diet was the source of infection and the sap of date palm harvesting timing was connected with outbreaks by human Paramyxoviruses (NiV) [13].

Pteropus bats excrete Paramyxoviruses such as Hendra virus in urine, saliva, feces, and as far as experimental infections were considered, it did not result into observable symptoms or potential pathology in spite of broad spread of virus infection in endothelial tissue [11]. The date palm sap can be contaminated if Pteropus medius (Indian flying fox) fed the flow of sap or collection of sap [15].

In India and Bangladesh, Pteropus medius was found to have antibodies against Hendra virus, Paramyxovirus (NiV), along with viral RNA [16]. Additionally, RNA sequences belonging to the closely connected Paramyxoviruses were found in the bat under study [17]. The domestic animals of Bangladesh such as goats, pigs in addition to cattle were found to contain non-neutralizing antibodies that were reactive to Hendra viruses, Paramyxoviruses which suggested that there was occurrence of Nipah like viruses, even though infections to humans by domestic animals was not reported in Bangladesh [18].

Among the horses of Queensland and adjacent state of New South Wales, Hendra virus was caused outbreaks since 1994, as well as proofs of infection were found in all four species of flying fox that were present in that range [17]. Even though specific transmission medium between horses and bats was uncertain, it was considered that the bats which were infected either feeding or roosting in trees within enclosures of horses can contaminate the beneath region and horses were out in the open by straight forward exposure to the excreta or through ingesting contaminated either water or feed [18].

The horses that are infected have capacity of spread of virus to other horses as well as to humans, ultimately [11]. In all over Asia and Australia, Hendra viruses are found in Pteropus medius that acts as their most important natural reservoir [8]. Recently, the antibodies used against Nipah-like viruses were identified in *Eidolon*

helvum (straw-colored fruit bat), pteropodid bat (migratory) in addition to others in Cameroon which suggested that the connected viruses might be spreading in the central part of Africa [19]. In China, antibodies that can act against Nipah-like viruses were detected in the bat species which were insectivorous in nature [17].

Infections of human were recognized in relatively a small number of nations as compared with distribution of Hendra viruses in bats (Bangladesh, India, Malaysia, Singapore, Philippines as well as Australia) [5]. Even if there was unavailability of vaccine or treatment for Paramyxovirus (NiV) existed, the commercial production as well as advent of a vaccine against Hendra virus for horses in year 2014 offered an efficient tool for restricting cases in Hendra viruses in Australia [19]. Nipah vaccines that are experimental use G proteins which are soluble in nature, such as Hendra vaccine, were efficient in primate models which were non-human [19].

2.2. Ebola and Marburg Viruses:

In 1976, Ebola virus (figure 1) was discovered the first time of 26 outbreaks by the Ebola virus disease [20]. Even if some outbreaks were because of animal contact, very fewer cases were observed owing to direct contact with bat [5]. Animals like gorilla, duiker or chimpanzee caused human infections in Central Africa [21]. The Marburg virus was firstly found in fruit bat *Rousettus aegyptiacus* that was commonly observed in African continent as well as in Middle East [22]. The infection by Marburg virus takes place in *Rousettus aegyptiacus* seasonally, having infection rates at highest level happening during the season which is birthing [23].

Like Hendra viruses, infections based on experiments with help of Marburg virus in bat *Rousettus aegyptiacus* reveal minimum pathology along with absence of observable symptoms of disease were recorded in the bats under study when infected by virus that required time of 19 days after inoculation [21]. In the Central Africa, Ebola virus Zaire was found in many bat species including both little collared fruit bat as well as the fruit bat [21]. In China, such filoviruses, were identified in

cave nectar bat *Eonycteris spelea* as well as *Rousettus leishenaulti* [24].

2.3. Tick-borne virus (TBE):

The tick-borne virus is non-segmented, endemic having single stranded RNA which belongs to *Flavivirus* genus that belongs to the family *Flaviviridae* [25]. The cases of tick-borne virus were reported in less developed nations such as Lithuania, Bulgaria, as well as Kazakhstan and well developed nations Denmark, Austria, Germany along with Switzerland, where cleanliness and hygiene standards are enormously high [26]. The tick-borne viruses are having three principle subtypes viz. Siberian, Far-Eastern and Siberian [27]. The consumption of both unpasteurized milk as well as cheese that is made up from such type of milk resulted into spread of infection by the tick-borne viruses [24]. The research showed that the consumption of milk of goat that contain tick bites resulted into Tick-borne virus (TBE) [28]. Shockingly, it was reported that the non-pasteurized milk consumption received from cows and sheep transmitted the TBE virus [29].

2.4. Corona viruses:

2.4.1. Severe Acute Respiratory Syndrome (SARS):

SARS corona virus appeared from bats as well as transmitted among live stocks in Southern China in 2003 [30]. In 2012, after approximately 10 years of primary finding of SARS like CoVs, the Corona virus (CoV) which was very close to SARS was identified or it has ability of direct infection to humans among Chinese horseshoe bats, in Yunnan of China [5].

2.4.2. Middle East Respiratory Syndrome (MERS):

Middle East Respiratory Syndrome virus (figure 1) was another new corona virus which was detected the first time among citizens of Saudi Arabia [31]. Additionally, the corona virus (CoV) which was related with MERS virus was reported in bat species in both Africa and Asia [32]. The MERS corona virus has camels as a zoonotic source and belongs to beta-corona virus [33]. Camels are the animals that mostly spread the infections among humans and these are related with the respiratory disease which is mild [32].

Even though Porcine Epidemic Diarrhea virus (PEDV) was not directly related to bats, it does gather phylogenetically with additional alpha corona viruses which was found in bats [32]. Severe Acute Respiratory Infection (SARI) observation in biodiversity among populations among human interfaces e.g guano mining can consider novel Corona virus viewing as a section of treatments of diarrheal or respiratory diseases in animals [32].

2.4.3. Novel Covid-19 virus:

The Chinese government informed World Health Organization (WHO) about many patients of pneumonia along with unknown etiology as well as the outbreak was started from a market in sea food in Wuhan and transmitted and infected the people with speed in December 2019 [34]. The researchers of China named the novel virus as Wuhan Corona virus (2019-nCoV) while SARS-CoV-2 was the name given by the International Committee on Taxonomy of Viruses (ICTV) to the virus as well as the disease received the name as Covid-19 [35]. Even if no vaccines or specific drugs against the disease under study are available currently, attempts of vaccine development are under process with a speed but doctors tested not only Ebola but also HIV drugs to treat patients of Covid 19, but the treatment failed and death of patients occurred [36].

2.4.4. Importance:

The diseases originated from zoonotic viruses presented potential challenge to humans. However, awareness about it has not reached up to the mark across globe, and as result, many countries have not strict regulations regarding consumption of wild lives. This gives a platform to zoonotic viruses to enter in human life leading to health risk. This review will help to make the worldwide people aware about the zoonotic viruses and take necessary steps to lower the probability of their entry in their lives.

3. Conclusion:

There is urgent need to control spread of zoonotic viruses to avoid potential damage to human beings and future pandemic.

Authors' contributions:

SK: Developed an idea. BS: Wrote manuscript RK: verified the data.

Competing interest:

Authors declare that no competing interest exists among them.

Ethical Statement:

Since it is review article, no ethical permission required.

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References:

- Hubálek Z. (2003). Emerging human infectious diseases: anthroponoses, zoonoses, and sapronoses. *Emerging infectious diseases*, 9(3), 403-404. <https://doi.org/10.3201/eid0903.020208>
- Taylor, L. H., Latham, S. M., & Woolhouse, M. E. (2001). Risk factors for human disease emergence. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 356(1411), 983–989. <https://doi.org/10.1098/rstb.2001.0888>
- Olival, K. J., Hosseini, P. R., Zambrana-Torrel, C., Ross, N., Bogich, T. L., & Daszak, P. (2017). Host and viral traits predict zoonotic spillover from mammals. *Nature*, 546(7660), 646–650. <https://doi.org/10.1038/nature22975>
- Teeling, E. C., Springer, M. S., Madsen, O., Bates, P., O'Brien, S. J., & Murphy, W. J. (2005). A molecular phylogeny for bats illuminates biogeography and the fossil record. *Science (New York, N.Y.)*, 307 (5709), 580–584. <https://doi.org/10.1126/science.1105113>
- Epstein, J.H., & Field, H.E., (2015). *Anthropogenic epidemics*. Bats Viruses. 249-79. [doi: 10.1002/9781118818824.ch10](https://doi.org/10.1002/9781118818824.ch10)
- Olival, K. J., & Hayman, D. T. (2014). Filoviruses in bats: current knowledge and future directions. *Viruses*, 6(4), 1759–1788. <https://doi.org/10.3390/v6041759>
- Chua, K. B., Bellini, W. J., Rota, P. A., Harcourt, B. H., Tamin, A., Lam, S. K., Ksiazek, T. G., Rollin, P. E., Zaki, S. R., Shieh, W., Goldsmith, C. S., Gubler, D. J., Roehrig, J. T., Eaton, B., Gould, A. R., Olson, J., Field, H., Daniels, P., Ling, A. E., Peters, C. J., ... Mahy, B. W. (2000). Nipah virus: a recently emergent deadly paramyxovirus. *Science (New York, N.Y.)*, 288(5470), 1432–1435. <https://doi.org/10.1126/science.288.5470.1432>
- Epstein, J. H., & Anthony, S. J. (2017). Viral discovery as a tool for pandemic preparedness. *Revue scientifique et technique (International Office of Epizootics)*, 36(2), 499–512. <https://doi.org/10.20506/rst.36.2.2669>
- Wolfe, N. D., Dunavan, C. P., & Diamond, J. (2007). Origins of major human infectious diseases. *Nature*, 447(7142), 279–283. <https://doi.org/10.1038/nature05775>
- Pulliam, J. R., Epstein, J. H., Dushoff, J., Rahman, S. A., Bunning, M., Jamaluddin, A. A., Hyatt, A. D., Field, H. E., Dobson, A. P., Daszak, P., & Henipavirus Ecology Research Group (HERG) (2012). Agricultural intensification, priming for persistence and the emergence of Nipah virus: a lethal bat-borne zoonosis. *Journal of the Royal Society, Interface*, 9(66), 89–101. <https://doi.org/10.1098/rsif.2011.0223>
- Field, H., Crameri, G., Kung, N. Y., & Wang, L. F. (2012). Ecological aspects of hendra virus. *Current topics in microbiology and immunology*, 359, 11–23. https://doi.org/10.1007/82_2012_214
- Rahman, S. A., Hassan, L., Epstein, J. H., Mamat, Z. C., Yatim, A. M., Hassan, S. S., Field, H. E., Hughes, T., Westrum, J., Naim, M. S., Suri, A. S., Jamaluddin, A. A., Daszak, P., & Henipavirus Ecology Research Group (2013). Risk Factors for Nipah virus infection among pteropid bats, Peninsular Malaysia. *Emerging infectious diseases*, 19(1), 51–60. <https://doi.org/10.3201/eid1901.120221>
- Luby, S. P., Hossain, M. J., Gurley, E. S., Ahmed, B. N., Banu, S., Khan, S. U., Homaira, N., Rota, P. A., Rollin, P. E., Comer, J. A., Kenah, E., Ksiazek, T. G., & Rahman, M. (2009). Recurrent zoonotic transmission of Nipah virus into humans, Bangladesh, 2001–2007. *Emerging infectious diseases*, 15(8), 1229–1235. <https://doi.org/10.3201/eid1508.081237>
- World Health Organization (2015). Nipahvirus outbreaks in the South East Asia: World Health Organization Southeast Asia Office.
- Khan, M. S., Hossain, J., Gurley, E. S., Nahar, N., Sultana, R., & Luby, S. P. (2010). Use of infrared camera to understand bats' access to date palm sap: implications for preventing Nipah virus transmission. *EcoHealth*, 7(4), 517–525. <https://doi.org/10.1007/s10393-010-0366-2>
- Khan, M. S., Hossain, J., Gurley, E. S., Nahar, N., Sultana, R., & Luby, S. P. (2010). Use of infrared camera to understand bats' access to date palm sap: implications for preventing Nipah virus transmission. *EcoHealth*, 7(4), 517–525. <https://doi.org/10.1007/s10393-010-0366-2>
- Bates, P.J.J., & Harrison, D.L., (1997). *Bats of The Indian Subcontinent*. Harrison Zoological Museum Publications, Sevenoaks, United Kingdom, 258pp+8pls.
- Anthony, S.J., Epstein, J.H., Murray, K.A., Navarrete-Macias, I., Zambrana-Torrel, C.M., Solovyov, A., et al. (2013). A strategy to estimate known viral diversity in mammals. *mBio*, 4(5):1–15. <https://doi.org/10.1128/mBio.00598-13>
- Chowdhury, S., Khan, S. U., Crameri, G., Epstein, J. H., Broder, C. C., Islam, A., Peel, A. J., Barr, J., Daszak, P., Wang, L. F., & Luby, S. P. (2014). Serological evidence of henipa virus exposure in cattle, goats and pigs in Bangladesh. *PLoS neglected tropical diseases*, 8(11), e3302. <https://doi.org/10.1371/journal.pntd.0003302>

20. Broder, C. C., Weir, D. L., & Reid, P. A. (2016). Hendra virus and Nipah virus animal vaccines. *Vaccine*, 34(30), 3525–3534. <https://doi.org/10.1016/j.vaccine.2016.03.075>
- Outbreaks Chronology, (2017): Ebola Virus Diseases: CDC.
21. Leroy, E. M., Rouquet, P., Formenty, P., Souquière, S., Kilbourne, A., Froment, J. M., Bermejo, M., Smit, S., Karesh, W., Swanepoel, R., Zaki, S. R., & Rollin, P. E. (2004). Multiple Ebola virus transmission events and rapid decline of central African wildlife. *Science (New York, N.Y.)*, 303(5656), 387–390. <https://doi.org/10.1126/science.1092528>
22. Towner, J. S., Amman, B. R., Sealy, T. K., Carroll, S. A., Comer, J. A., Kemp, A., Swanepoel, R., Paddock, C. D., Balinandi, S., Khristova, M. L., Formenty, P. B., Albarino, C. G., Miller, D. M., Reed, Z. D., Kayiwa, J. T., Mills, J. N., Cannon, D. L., Greer, P. W., Byaruhanga, E., Farnon, E. C., ... Rollin, P. E. (2009). Isolation of genetically diverse Marburg viruses from Egyptian fruit bats. *PLoS Pathogens*, 5(7), e1000536. <https://doi.org/10.1371/journal.ppat.1000536>
23. Amman, B.R., Carroll, S.A., Reed, Z.D., Sealy, T.K., Balinandi, S., Swanepoel, R., et al. (2012). Seasonal Pulses of Marburg Virus Circulation in Juvenile *Rousettus aegyptiacus* Bats Coincide with Periods of Increased Risk of Human Infection. *PLoS Pathog*, 8(10):e1002877. <https://doi.org/10.1371/journal.ppat.1002877>
24. Dumpis, U., Crook, D., & Oksi, J. (1999). Tick-borne encephalitis. *Clinical infectious diseases: an official publication of the Infectious Diseases Society of America*, 28(4), 882–890. <https://doi.org/10.1086/515195>
25. Mandl, C. W., Ecker, M., Holzmann, H., and Heinz, F. X. (1997). Infectious cDNA clones of tick-borne encephalitis virus European subtype prototypic strain Neudorfl and high virulence strain. *Hypr. J. Gen. Virol.*, 78:1049–1057.
26. Ormaasen, V., Brantsaeter, A. B., & Moen, E. W. (2001). Flåttbårenencefalitti Norge [Tick-borne encephalitis in Norway]. *Tidsskrift for den Norske laegeforening:tidsskrift for praktiskmedicin, nyraekke*, 121(7), 807–809.
27. Ecker, M., Allison, S. L., Meixner, T., & Heinz, F. X. (1999). Sequence analysis and genetic classification of tick-borne encephalitis viruses from Europe and Asia. *The Journal of general virology*, 80 (Pt1), 179–185. <https://doi.org/10.1099/0022-1317-80-1-179>
28. Korenberg, E.I., Pchelkina, A.A. (1975). Multiple viremia in goats following sequential inoculation with tick-borne encephalitis virus. *Med Parazitol Mosk*, 44,181-4.
29. Leonov, V. A., Kogan, V. M., Nekipelova, G. A., Vasenin, A. A., & Shikharbeev, B. V. (1976). K voprosu o tipizatsiiochagovkleshchevogoentsefalita v Predbaikal'e [Typifying foci of tick-borne encephalitis in the pre-Baikal]. *Zhurnalmikrobiologii, epidemiologiiimmunobiologii*, (5), 56–60.
30. Ksiazek, T. G., Erdman, D., Goldsmith, C. S., Zaki, S. R., Peret, T., Emery, S., Tong, S., Urbani, C., Comer, J. A., Lim, W., Rollin, P. E., Dowell, S. F., Ling, A. E., Humphrey, C. D., Shieh, W. J., Guarner, J., Paddock, C. D., Rota, P., Fields, B., DeRisi, J., ... SARS Working Group (2003). A novel coronavirus associated with severe acute respiratory syndrome. *The New England journal of medicine*, 348(20),1953–1966. <https://doi.org/10.1056/NEJMoa030781>
31. Zaki, A. M., van Boheemen, S., Bestebroer, T. M., Osterhaus, A. D., & Fouchier, R. A. (2012). Isolation of a novel coronavirus from a man with pneumonia in Saudi Arabia. *The New England journal of medicine*, 367(19), 1814–1820. <https://doi.org/10.1056/NEJMoa1211721>
32. Hemida, M. G., Elmoslemay, A., Al-Hizab, F., Alnaeem, A., Almathen, F., Faye, B., Chu, D. K., Perera, R. A., & Peiris, M. (2017). Dromedary Camels and the Transmission of Middle East Respiratory Syndrome Coronavirus (MERS-CoV). *Transboundary and emerging diseases*, 64(2), 344–353. <https://doi.org/10.1111/tbed.12401>
33. Paden, C. R., Yusof, M., Al Hammadi, Z. M., Queen, K., Tao, Y., Eltahir, Y. M., Elsayed, E. A., Marzoug, B. A., Bensalah, O., Khalafalla, A. I., Al Mulla, M., Khudhair, A., Elkheir, K. A., Issa, Z. B., Pradeep, K., Elsahel, F. N., Imambaccus, H., Sasse, J., Weber, S., Shi, M., ... Al Muhairi, S. (2018). Zoonotic origin and transmission of Middle East respiratory syndrome coronavirus in the UAE. *Zoonoses and public health*, 65(3), 322–333. <https://doi.org/10.1111/zph.12435>
34. Wang, C., Horby, P. W., Hayden, F. G., & Gao, G. F. (2020). A novel coronavirus outbreak of global health concern. *Lancet (London,England)*, 395(10223),470–473. [https://doi.org/10.1016/S0140-6736\(20\)30185-9](https://doi.org/10.1016/S0140-6736(20)30185-9).
35. Cui, J., Li, F., & Shi, Z. L. (2019). Origin and evolution of pathogenic coronaviruses. *Nature reviews. Microbiology*, 17(3), 181–192. <https://doi.org/10.1038/s41579-018-0118-9>
36. *World Health Organization* (2020). Summary of Novel Covid-19 infections cases illness from 1 December to 15 March, 2020.

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