

Cat Que Virus (CQV): A potential threat of the tropics? “One Health Approach” to avert catastrophe: a narrative review

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Abstract

The world is now experiencing the catastrophe of global pandemic ‘COVID-19’, most serious public health crises in this century. Recently, another virus named “Cat Que Virus” (CQV) seems to be causing its terrible repercussions in the worlds’ largest populous country ‘China’, the origin of SARS-CoV during 2002-2003, and the current pandemic SARS-CoV-2 since December 2019. Recently, the presence of IgG antibody among two persons in the state of Karnataka for CQV was reported in India, the worlds’ second-largest populous country. This means the virus is in circulation in the sub-continent. The presence of the vector mosquitoes (*Aedes* species, *Culex* species) and the ambient climatic conditions suitable for vector breeding in the country needs to be taken into account while planning to implement holistic strategies appropriate for control and preventive measures. “One Health approach” is the topmost option covering humans, animals/vectors and the environment to curb the spread/transmission of infectious diseases in general. It is also necessary to study the transmission dynamics and pattern of this emerging virus, its life cycle, the natural reservoir of the virus, the intermediate host and the accidental host with respect South-East Asia, so that necessary remedial action can be planned well before an epidemic. At present, the outbreak of CQV is certainly a warning to the general population around the world. Considering the global imminent health threats posed by CQV, there is an urgent need for active surveillance, monitoring, effective vaccination, and a standard treatment modality of this disease. Given the epidemiological aspect of CQV, control and prevention measures are essential to stop the spread of the virus. At present, there is no information available on CQV; however, this current review article has covered the required data, which will be helpful to control the spread of the CQV.

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Cat Que Virus (CQV): A potential threat of the tropics? “One Health Approach” to avert catastrophe: a narrative review

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Abstract: (293 words)

The world is now experiencing the catastrophe of global pandemic 'COVID-19', most serious public health crises in this century. Recently, another virus named "Cat Que Virus" (CQV) seems to be causing its terrible repercussions in the world's largest populous country 'China', the origin of SARS-CoV during 2002-2003, and the current pandemic SARS-CoV-2 since December 2019. Recently, the presence of IgG antibody among two persons in the state of Karnataka for CQV was reported in India, the world's second-largest populous country. This means the virus is in circulation in the sub-continent. The presence of the vector mosquitoes (*Aedes* species, *Culex* species) and the ambient climatic conditions suitable for vector breeding in the country needs to be taken into account while planning to implement holistic strategies appropriate for control and preventive measures. "One Health approach" is the topmost option covering humans, animals/vectors and the environment to curb the spread/transmission of infectious diseases in general. It is also necessary to study the transmission dynamics and pattern of this emerging virus, its life cycle, the natural reservoir of the virus, the intermediate host and the accidental host with respect South-East Asia, so that necessary remedial action can be planned well before an epidemic. At present, the outbreak of CQV is certainly a warning to the general population around the world. Considering the global imminent health threats posed by CQV, there is an urgent need for active surveillance, monitoring, effective vaccination, and a standard treatment modality of this disease. Given the epidemiological aspect of CQV, control and prevention measures are essential to stop the spread of the virus. At present, there is no information available on CQV; however, this current review article has covered the required data, which will be helpful to control the spread of the CQV.

Keywords: Cat Que Virus; *Orthobunyaviruses* ; Vector-borne infection; Tropical nations; Public health; Global threat;

1. Introduction: (1875 words)

The world is now facing one of the most destructive pandemics ever recorded. Panic of death due to Corona Virus Disease-2019 (COVID-19) is all around the world and under the influence of this outbreak, another dangerous virus called Cat Que Virus (CQV) appears to have had its dreadful consequences in China. CQV was first identified from the mosquitoes of Cat Que Commune, Hoai Duc District of Ha Tay Province in Northern Vietnam during the improved surveillance activities for Japanese Encephalitis Virus (JEV), as well as surveys for arbovirus activity in regions where Acute Encephalitis Syndrome (AES) cases had occurred during the period of 2004 causing morbidity and mortality among children due to acute febrile illness and non-JEV AES. Several people in the world have been reported infected so far, and this outbreak is gradually beginning to spread in India as well. The findings of the recent study conducted by the ICMR-National Institute of Virology (NIV), Pune reported that 2 out of 883 human serum samples had anti-CQV IgG antibodies. This indicates that these two individuals have been infected by the virus at some point in time. In specific, CQV spreads through pigs and species of mosquitoes known as *Aedes* and *Culex* (*Ae. aegypti*, *Cx. quinquefasciatus*, and *Cx. tritaeniorhynchus*). Both of these life forms exist in India and are vulnerable to CQV. CQV can cause diseases such as meningitis, acute febrile illness, and pediatric encephalitis to humans (Shete et al., 2020).

2. Classification of CQV:

The order *Bunyvirales* is found to have more than 350 viruses with tripartite, negative-sense, single-stranded RNA (ssRNA) genomes, belonging to 9 viral families. The members of the *Feraviridae*, *Phenuiviridae*, *Fimoviridae*, *Nairoviridae*, *Peribunyaviridae*, *Tospoviridae*, *Jonviridae* and *Phasmaviridae* families are carried and transmitted through arthropods, while the viruses of the *Hantaviridae* family are carried by rodents and are transmitted through the communication of aerosolized excreta (Elliott, 2013; Whitmer et al., 2018). *Fimoviridae* and *Tospoviridae* family viruses infect plants, while the viruses of family *Nairoviridae*, *Peribunyaviridae*, and *Phenuiviridae* can transmit the disease to vertebrates. Genus *Orthobunyavirus* is the largest genus in the *Peribunyaviridae* family that contains more than 170 viruses. *Orthobunyaviruses* are categorized into 49 species and 19 serogroup complexes (Briese et al., 2013; Maes et al., 2018), consisting of extremely diverse arboviruses (Nguyen et al., 2013). Simbu serogroup has been the largest of these with 25 viruses isolated till date (Ladner et al., 2014) and with seven species complexes such as *Akabane*, *Simbu*, *Oropouche*, *Shuni*, *Sathuperi*, *Shamonda*, and *Manzanilla* (Zhang et al., 2015; Saeed et al., 2001). CQV is one of the members of the *Manzanilla* species complex belonging to the Simbu serogroup (Figure 1).

3. Symptoms and complications of CQV (Diseases in humans):

In present times, growing numbers of *bunyaviruses* have been recognized as the main human pathogens. Amongst the 170 *bunyaviruses*, 60 viruses can induce diseases to humans, containing pediatric encephalitis (*La Cross virus*), fever and joint pain (*Oropouche virus*), meningitis (*Cache valley virus*), Jamestown canyon encephalitis (*Jamestown canyon virus*), febrile illness (*Guaroa virus*), hemorrhagic fever (*Garissa virus*), influenza-like symptoms (*Tahyna virus*) and the recent research were reported that CQV has caused diseases like acute febrile illness (high fever), pediatric encephalitis (inflammation of the brain) and meningitis (inflammation of the meninges) in human beings (Nguyen et al., 2013; Bewick et al., 2016; Treangen et al., 2016; Pastula et al., 2015; Aguilar et al., 2010; Shete et al., 2020).

4. Epidemiology of CQV (Origin and Transmission):

CQV was first isolated in 2004 from mosquitoes and reported during the surveillance of arboviruses in acute pediatric encephalitis cases in Vietnam (Bryant et al., 2005) and late in Uganda (Mossel et al., 2017). Viruses of family *Peribunyaviridae* infect the vertebrates and reside in a zoonotic infection cycle that spreads across livestock and human beings through an arthropod intermediate (Saeed et al., 2001). Globally, arboviruses (arthropod-borne viruses) have turned into a major public health concern with the emergence and re-emergence of arboviral diseases. Most of the arboviruses act as a zoonotic spillover from an infected reservoir hosts (dogs, mosquitoes, birds, and ruminants) to humans (accidental host) (Go et al., 2014; Bodewes and Kuiken, 2018), i.e., the spread of a pathogen from an infected vertebrate to a human is

caused by mosquito bite (Figure-2) (Whitmer et al., 2018).

5. Genome structure of CQV:

Often, the total genome size of *bunyaviruses* ranges from 11 to 19 kb and around 80-120 nm in diameter (Schmaljohn, 1996). *Bunyaviruses* have tripartite genomes containing a large (L), medium (M), and small (S) RNA segments. Among this, the L segment encodes RNA-dependent RNA polymerase (RdRp), which is necessary for mRNA synthesis and replication of the viral RNA. The M segment encodes viral glycoproteins, which are on the viral surface and help the virus in attaching and entering into the host cell. The S segment encodes the nucleocapsid protein. Both ends of each gene segment are enclosed with 5'- and 3'-UTRs of various lengths (Ariza et al., 2013; Zhang et al., 2015). Most of the *bunyaviruses* have a negative-sense L and M segment. The S segment of the genus *Phlebovirus* (Elliott and Brennan, 2014) and both M and S segment of the genus *Tospovirus* (Lima et al., 2016) are ambisense. The ambisense M segment codes for glycoprotein (Gc and Gn) in the negative sense and a nonstructural protein (NSm) in the positive sense. The ambisense S segment codes for the viral nucleoprotein (N) in the negative sense and a nonstructural protein (NSs) in the positive sense (Figure 3) (Lima et al., 2016; Bouloy, 1991).

6. Pathobiology of CQV:

The ambisense genome of *bunyaviruses* including the CQV requires two rounds of transcription to be completed. Viral entry into its host cell occurs through the receptor-mediated endocytosis and the following steps take place in the cytoplasm. Cell receptors are not defined for several *bunyaviruses* (Lozach et al., 2010; Santos et al., 2008; Jin et al., 2002), but those that contribute to the binding of some *bunyaviruses* contain integrins and other cell receptor proteins, e.g., α 5 β 1/p32, which is expressed on dendritic cells, platelets, endothelial cells and lymphocytes (Albornoz et al., 2016). As the genome of single-stranded, negative-sense RNA viruses cannot be directly translated, the first step after permeation of the host cell and uncoating is the triggering of the virion RNA polymerase and its transcription of viral mRNAs from each of the three virion RNAs. Afterward primary viral mRNA transcription and translation, replication of the virion RNA takes place and the second round of transcription instigates, with favored amplification of the genes that encode structural proteins required for virion synthesis. (<https://www.sciencedirect.com/science/article/pii/B9780128009468000222>). Virions mature through budding using intracytoplasmic vesicles related to the Golgi complex and are released by the transport of vesicles through the cytoplasm and consequent exocytosis from the plasma membranes (Figure-4) (Weber et al., 2002; <https://en.wikipedia.org/wiki/Bunyavirales>).

7. Diagnosis:

Most of the diagnostic methods of this virus are carried by the identification of antigen in tissues (immunofluorescence) or serologically by IgG and IgM antibody (ELISA) (Bastos et al., 2012). The IgM capture ELISA method is carried out as a primary diagnostic tool, but reverse transcription-polymerase chain reaction (RT-PCR) tests are now accessible for identification of the CQV (Zhang et al., 2015; Ladner et al., 2014). Accurate confirmation of the presence of accurate virus can only be done through conventional RT-PCR that is followed by sequencing. However, an earlier study has been reported that the CQV has been isolated and then diagnosed by the next-generation sequencing (NGS) method. NGS of agents causing idiopathic human infections have been important in the detection of novel viruses (Whitmer et al., 2018; Yadav et al., 2016). Recently, a precise and a very sensitive multiplexed one-step RT-qPCR were assessed for CQV identification in the cell supernatants and mouse tissues (Naveca et al., 2017).

8. Prevention by “One Health approach”:

One Health (OH) approach has been described by the American Veterinary Medical Association as an integrative effort of multiple disciplines working locally, nationally and globally to gain optimal health for the humans, animals and the environment (American Veterinary Medical Association, 2008). The OH would be useful for a better understanding of the emerging and re-emerging diseases epidemiology, transmission dynamics and pathobiology. Hypothetically, different countries have approached implementing the principles

of OH in various infectious diseases with variable success and challenges (Okello et al., 2014). Previously, the Rift Valley Fever (RVF) in Eastern Africa Region during 2006-07 outbreak played a vital role in galvanizing collaboration in OH approaches among researchers, international organizations and government departments to alleviate effects of future outbreaks and catalyzed the essential for perfect understanding and implementation of OH approach with an attention on supporting continued animal health surveillance activities (Breiman et al., 2010). RVF caused by a virus, namely phlebovirus that causes the disease to animals and mosquitoes and can spread both by animal secretions and mosquito (*Aedes*) bites (Flick and Bouloy, 2005; Linthicum et al., 1998). China has been implementing OH approaches for the coronavirus outbreaks in the past and the present viz. SARS in 2002-03 and SARS-CoV-2 since 2019 and also for various other infectious diseases as well, which may have been prevented unnoticed (Menachery et al., 2015; Wu et al., 2016; Tan et al., 2017; Zheng et al., 2019; El Zowalaty and Järhult, 2020). Several studies reported that implementing OH approach against COVID-19 (Yoo and Yoo, 2020; Bonilla-Aldana et al., 2020). India also implemented OH surveillance system against COVID-19, which may be helpful to mitigate CQV infection on the whole (Yasobant et al., 2020; Manoj, 2020) to avoid huge loss.

9. Treatment:

As of now, there is no specific treatment method for the infection with CQV. In severe cases, intensive medical care is essential, with the constant monitoring of respiratory activity, control of fluid and electrolyte balance, and the prevention of secondary infections. Ways to prevent the CQV transmission and spread are similar to those routine preventive measures for the spread of other infectious viruses transmitted by mosquitoes (Carpenter et al., 2013; Sakkas et al., 2018). The use of insect repellent, anti-mosquito lotions, wearing a cloth that covers the arms and legs, and proper closing of window screens can reduce exposure to mosquito bites, thereby reducing the virus transmission. As an alternative, several natural compounds (picaridin, pyrethrins, and azadirachtin) and plant-derived essential oils (lemon eucalyptus, neem, geraniol, and eucalyptus) have been recommended as mosquito repellents (Carpenter et al., 2013; Hoch et al., 1986). Additionally, source reduction, i.e., removal of stagnant open water sources, including water in flower vases, potted plants, man-made containers, water-circulated air-coolers, refrigerators for stored water collection containers, etc., where mosquitoes tend to breed both indoor and outdoors around our house premises, and terrace. Most importantly, follow-general hygiene, limiting contact with vector saliva, urine, feces, or bedding might prevent the spread of the virus (González et al., 2016).

10. Conclusion and Future perspectives:

CQV is zoonotic and originates from pigs and/or mosquitoes. In Vietnam, CQV was first isolated in 2004 and was later discovered in China. Currently, the CQV is impacting and evolving in India and without the proper precautionary measures, it might spread throughout the world. And without proper awareness of this CQV outbreak, we may again be facing a public health crisis or even a pandemic like situation as caused by Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2). Therefore, to avoid a potential catastrophe in the near future, it is advisable to follow universal preventive measures and precautionary mechanisms. At present, without adequate medicine and vaccination, this is the only way to reduce the incidence of such diseases. In the future, to monitor a potential virus-related epidemic, we must have mandatory criteria for an effective vaccine, treatment modality and medicine. Regarding CQV in particular, there are several aspects that need an OH approach in order to better understand the outbreak and to mitigate further epidemics of a similar public health crisis in the future.

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Figure Legends:

Figure-1: Schematic representation of the Classification of Cat Que Virus (CQV).

Figure-2: Schematic representation of genome of Cat Que Virus (CQV). The genome comprises of Open Reading Frame (ORF) that encoding nucleocapsid proteins (N), external glycoproteins (Gn and Gc), large protein (L), medium protein (M), small protein (S), non-structural proteins (NSs and NSm) and both ends of each gene segment contained 5'-untranslated region (5'-UTR) and 3'-untranslated region (3'-UTR) of different lengths.

Figure-3: Schematic representation of life cycle and transmission of Cat Que Virus (CQV). Birds and/or swine are the primary reservoir hosts of CQV. The virus is transmitted to humans by the infected mosquitoes that have fed from reservoir hosts.

Figure-4: Schematic representation of replication of Cat Que Virus (CQV).

References:

1. Aguilar PV, Morrison AC, Rocha C, Watts DM, Beingolea L, Suarez V, Vargas J, Cruz C, Guevara C, Montgomery JM, Tesh RB, Kochel TJ. Guaroa virus infection among humans in Bolivia and Peru. *Am J Trop Med Hyg.* 2010;83:714-21.
2. Albornoz A, Hoffmann AB, Lozach PY, Tischler ND. Early Bunyavirus-Host Cell Interactions. *Viruses.* 2016;8:143.
3. American Veterinary Medical Association. One Health: a new professional imperative, one health initiative task force: final report July 15, 2008. Schaumburg: American Veterinary Medical Association; https://www.avma.org/KB/Resources/Reports/Documents/onehealth_final.pdf.
4. Ariza A, Tanner SJ, Walter CT, Dent KC, Shepherd DA, Wu W, Matthews SV, Hiscox JA, Green TJ, Luo M, Elliott RM. Nucleocapsid protein structures from orthobunyaviruses reveal insight into ribonucleoprotein architecture and RNA polymerization. *Nucleic acids res.* 2013;41:5912-26.
5. Bastos Mde S, Figueiredo LT, Naveca FG, Monte RL, Lessa N, Pinto de Figueiredo RM, Gimaque JB, Pivoto João G, Ramasawmy R, Mourão MP. Identification of Oropouche Orthobunyavirus in the cerebrospinal fluid of three patients in the Amazonas, Brazil. *Am J Trop Med Hyg.* 2012;86:732-5.
6. Bewick S, Agosto F, Calabrese JM, Muturi EJ, Fagan WF. Epidemiology of La Crosse Virus Emergence, Appalachia Region, United States. *Emerg Infect Dis.* 2016;22:1921-9.
7. Bodewes R, Kuiken T. Changing Role of Wild Birds in the Epidemiology of Avian Influenza A Viruses. *Adv Virus Res.* 2018;100:279-307.
8. Bonilla-Aldana DK, Holguin-Rivera Y, Perez-Vargas S, Trejos-Mendoza AE, Balbin-Ramon GJ, Dhama K, Barato P, Lujan-Vega C, Rodriguez-Morales AJ. Importance of the One Health approach to study the SARS-CoV-2 in Latin America. *One Health.* 2020 Jun 25;10:100147.
9. Bouloy M. Bunyaviridae: genome organization and replication strategies. *Adv Virus Res.* 1991;40:235-75.
10. Breiman RF, Minjauw B, Sharif SK, Ithondeka P, Njenga MK. Rift Valley Fever: scientific pathways toward public health prevention and response. *Am J Trop Med Hyg.* 2010;83:1-4.

11. Briese T, Calisher CH, Higgs S. Viruses of the family Bunyaviridae: are all available isolates reassortants? *Virology*. 2013;446:207-16.
12. Bryant JE, Crabtree MB, Nam VS, Yen NT, Duc HM, Miller BR. Isolation of arboviruses from mosquitoes collected in northern Vietnam. *Am J Trop Med Hyg*. 2005;73:470-3.
13. Carpenter S, Groschup MH, Garros C, Felipe-Bauer ML, Purse BV. Culicoides biting midges, arboviruses and public health in Europe. *Antiviral Res*. 2013;100:102-13.
14. El Zowalaty ME, Järhult JD. From SARS to COVID-19: A previously unknown SARS- related coronavirus (SARS-CoV-2) of pandemic potential infecting humans - Call for a One Health approach. *One Health*. 2020;9:100124.
15. Elliott RM, Brennan B. Emerging phleboviruses. *Curr Opin Virol*. 2014;5:50-7.
16. Elliott RM. Bunyaviridae. In *Fields Virology*, 6thed.; Knipe, D.M., Howley, P.M., Eds.; Wolters Kluwer Health: Philadelphia, PA, USA, 2013; Volume 1.
17. Flick R, Bouloy M. Rift Valley fever virus. *Curr Mol Med*. 2005;5:827-34.
18. Go YY, Balasuriya UB, Lee CK. Zoonotic encephalitides caused by arboviruses: transmission and epidemiology of alphaviruses and flaviviruses. *Clin Exp Vaccine Res*. 2014;3:58-77.
19. González M, Alarcón-Elbal PM, Valle-Mora J, Goldarazena A. Comparison of different light sources for trapping Culicoides biting midges, mosquitoes and other dipterans. *Vet Parasitol*. 2016;226:44-9.
20. Hoch AL, Roberts DR, Pinheiro FD. Breeding sites of Culicoides paraensis and options for control by environmental management. *Bull Pan Am Health Organ*. 1986;20:284-93.
21. Jin M, Park J, Lee S, Park B, Shin J, Song KJ, Ahn TI, Hwang SY, Ahn BY, Ahn K. Hantaan virus enters cells by clathrin-dependent receptor-mediated endocytosis. *Virology*. 2002;294:60-9.
22. Ladner JT, Savji N, Lofts L, Travassos da Rosa A, Wiley MR, Gestole MC, Rosen GE, Guzman H, Vasconcelos PFC, Nunes MRT, J Kochel T, Lipkin WI, Tesh RB, Palacios G. Genomic and phylogenetic characterization of viruses included in the Manzanilla and Oropouche species complexes of the genus Orthobunyavirus, family Bunyaviridae. *J Gen Virol*. 2014;95:1055-66.
23. Lima RN, De Oliveira AS, Leastro MO, Blawid R, Nagata T, Resende RO, Melo FL. The complete genome of the tospovirus Zucchini lethal chlorosis virus. *Virol J*. 2016;13:123.
24. Linthicum KJ, Bailey CL, Davies FG, Kairo A, Logan TM. The horizontal distribution of Aedes pupae and their subsequent adults within a flooded dambo in Kenya: implications for Rift Valley fever virus control. *J Am Mosq Control Assoc*. 1988;4:551-4.
25. Lozach PY, Mancini R, Bitto D, Meier R, Oestereich L, Overby AK, Pettersson RF, Helenius A. Entry of bunyaviruses into mammalian cells. *Cell Host Microbe*. 2010;7:488-99.
26. Maes P, Alkhovsky SV, Bào Y, Beer M, Birkhead M, Briese T, et al. Taxonomy of the family Arenaviridae and the order Bunyavirales: update 2018. *Arch Virol*. 2018;163:2295-310.
27. Manoj K. Wastewater monitoring and public health surveillance of SARS-CoV-2. *Indian J Public Health*. 2020;64:S247-S248.
28. Menachery VD, Yount BL Jr, Debbink K, Agnihothram S, Gralinski LE, Plante JA, Graham RL, Scobey T, Ge XY, Donaldson EF, Randell SH, Lanzavecchia A, Marasco WA, Shi ZL, Baric RS. A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence. *Nat Med*. 2015;21:1508-13.
29. Mossel EC, Crabtree MB, Mutebi JP, Lutwama JJ, Borland EM, Powers AM, Miller BR. Arboviruses Isolated From Mosquitoes Collected in Uganda, 2008-2012. *J Med Entomol*. 2017;54:1403-9.
30. Naveca FG, Nascimento VAD, Souza VC, Nunes BT, Rodrigues DSG, Vasconcelos PFDC. Multiplexed reverse transcription real-time polymerase chain reaction for simultaneous detection of Mayaro, Oropouche, and Oropouche-like viruses. *Mem Inst Oswaldo Cruz*. 2017;112:510-3.
31. Nguyen NL, Zhao G, Hull R, Shelly MA, Wong SJ, Wu G, St George K, Wang D, Menegus MA. Cache valley virus in a patient diagnosed with aseptic meningitis. *J Clin Microbiol*. 2013;51:1966-9.
32. Okello AL, Bardosh K, Smith J, Welburn SC. One Health: past successes and future challenges in three African contexts. *PLoS Negl Trop Dis*. 2014;8:e2884.
33. Pastula DM, Hoang Johnson DK, White JL, Dupuis AP 2nd, Fischer M, Staples JE. Jamestown Canyon Virus Disease in the United States-2000-2013. *Am J Trop Med Hyg*. 2015;93:384-9.

34. Saeed MF, Li L, Wang H, Weaver SC, Barrett ADT. Phylogeny of the Simbu serogroup of the genus Bunyavirus. *J Gen Virol.* 2001;82:2173-81.
35. Sakkas H, Bozidis P, Franks A, Papadopoulou C. Oropouche Fever: A Review. *Viruses.* 2018;10:175.
36. Santos RI, Rodrigues AH, Silva ML, Mortara RA, Rossi MA, Jamur MC, Oliver C, Arruda E. Oropouche virus entry into HeLa cells involves clathrin and requires endosomal acidification. *Virus Res.* 2008;138:139-43.
37. Schmaljohn CS, Fields BN, Knipe DM, Howley PM. Bunyaviridae: the viruses and their replication. *Fields virology, 3rded.* Lippincott Raven Publishers, Philadelphia, Pa. 1996:1447-71.
38. Shete A, Yadav PD, Gokhale M, Jain R, Pardeshi P, Majumdar T, Mourya DT. Proactive preparedness for Cat Que virus: An Orthobunyavirus existing in India. *Indian J Med Res.* 2020;151:571-7.
39. Tan J, Wang R, Ji S; Nanjing Agricultural University research group of The Challenge Cup Rabies Research Group, Su S, Zhou J. One Health strategies for rabies control in rural areas of China. *Lancet Infect Dis.* 2017;17:365-7.
40. Treangen TJ, Schoeler G, Phillippy AM, Bergman NH, Turell MJ. Identification and Genomic Analysis of a Novel Group C Orthobunyavirus Isolated from a Mosquito Captured near Iquitos, Peru. *PLoS Negl Trop Dis.* 2016;10:e0004440.
41. Weber F, Bridgen A, Fazakerley JK, Streitenfeld H, Kessler N, Randall RE, Elliott RM. Bunyamwera bunyavirus nonstructural protein NSs counteracts the induction of alpha/beta interferon. *J Virol.* 2002;76:7949-55.
42. Whitmer SLM, Yadav PD, Sarkale P, Chaubal GY, Francis A, Klena J, Nichol ST, Ströher U, Mourya DT. Characterization of Unknown Orthobunya-Like Viruses from India. *Viruses.* 2018;10:451.
43. Wu J, Liu L, Wang G, Lu J. One Health in China. *Infect Ecol Epidemiol.* 2016;6:33843.
44. Yadav P, Shete A, Bondre V, Patil D, Kokate P, Chaudhari S, Srivastava S, Jadhav S, Mourya D. Isolation and characterization of Oya virus a member of Simbu serogroup, family Bunyaviridae, isolated from Karnataka, India. *Infect Genet Evol.* 2016;44:122-6.
45. Yasobant S, Patel K, Saxena D, Falkenberg T. COVID-19 in India: Making a case for the one health surveillance system. *Indian J Public Health.* 2020;64:S135-S138.
46. Yoo HS, Yoo D. COVID-19 and veterinarians for one health, zoonotic- and reverse-zoonotic transmissions. *J Vet Sci.* 2020;21:e51.
47. Zhang J, Wang J, Wang L, Fu S, Li M, Zhao G, Zhu W, Wang D, Liang G. Molecular Characterization and Seroprevalence in Pigs of SC0806, a Cat Que Virus Isolated from Mosquitoes in Sichuan Province, China. *Vector Borne Zoonotic Dis.* 2015;15:423-31.
48. Zheng Z, Lu Y, Short KR, Lu J. One health insights to prevent the next HxNy viral outbreak: learning from the epidemiology of H7N9. *BMC Infect Dis.* 2019;19:138.





