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LETTER TO THE EDITOR

Scientific and Practical Solutions to Deal with the Possible Pandemic of Re-Emerging Langya Virus Disease Based on the Lessons Learned from the COVID-19 Pandemic

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Dear Editor,

A virus called "Langya" has recently been discovered and spread in the Henan and Shandong provinces, located in the East of China. The virus has spread among the peasants who have been in close contact with animals [1]. Belonging to the Henipavirus family, it was identified for the first time in 2018 as a 53-year-old peasant referred to a hospital in Shandong province in the northeast of China to seek treatment for a febrile infection [2, 3]. The genome of the Langva virus closely resembles that of the Mujiang virus, isolated for the first time in 2012 in mice found within an abandoned mine in Yunnan Province, located to the south of China. People may be infected by numerous respiratory viruses [4]. A number of other types of viruses have been identified in rats, lice, and bats from China to South Korea and Australia. However, only Nipah, LavV, and Hendra are currently responsible for viral infections in humans [5]. Among the abovementioned animals, bats serve as the natural reservoirs for the Nipah and Hendra viruses. The mentioned virus is transferable from bats to booster hosts, such as pigs and horses, and then to humans. Also, it may be transmitted to humans directly [6, 7]. Given the high pathogenicity of Henipa viruses and the absence of particular medical practices for controlling infections in humans, they are regarded as pathogens characterized by the significant potential to cause

epidemic infections [8]. One of the phylogenetically distinct henipaviruses, known as Langya henipavirus (LayV), was detected by inspecting febrile individuals that had a recent background of being in close contact with animals in the East of China. As a virologist working at the Duke-National University of Singapore School of Medicine, Linfa Wang suggested that the name of the mentioned virus is adopted from Langya, a town located in Shandong [5, 9]. A swab sample taken from a patient's throat that was subjected to metagenomic analysis followed by virus isolation showed that the genome of the Langya virus was composed of a number of 18402 nucleotides featuring a genomic organization that resembled that of other henipaviruses [5, 10]. According to the follow-ups carried out during the 2018-2021 period, 34 more individuals were infected with Langya in Shandong as well as the neighboring Henan province. Before that, the initial discoveries of the spread of the virus COVID-19 were reported at the end of 2019 in Wuhan, China. Given its rapid spread, a strain of coronavirus caused the World Health Organization (WHO) to announce a global state of emergency, so a great number of nations imposed quarantines and mandatory restrictions [11, 12].

The symptoms caused by the Langya virus in humans include fatigue, fever, loss of appetite, muscle pains, and cough [5, 13]. Roosters have been reported as a virus



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reservoir and pass Langya henipavirus among themselves, and as Gourley suggests, "and kind of randomly infecting people here and there" [5]. Given that the farmers constitute the majority of the individuals infected by the Langya virus, scholars have suggested that animals transfer the Langya virus to humans [5, 14]. In addition, the researchers have suggested that the potential virus origin is related to animals, and according to the evidence collected by research teams, the animal members of the mouse family are regarded as the natural carriers of the virus; however, such a claim still requires further investigations to be confirmed [14].

In conclusion, the COVID-19 pandemic demonstrated the devastating impact that a rapidly spreading, unknown virus can have on the world. A global surveillance system would enable the early detection and tracking of emerging virus strains, such as the Langya virus, allowing for a more proactive and coordinated response. This would help prevent the rapid transmission and potential escalation into a full-blown pandemic, as experienced with COVID-19. By identifying virus strains early, public health authorities can implement targeted measures to contain the spread and mitigate the risk of a widespread outbreak. Engaging and educating the global population about the risks of emerging viruses and the need for collective action can foster a sense of shared responsibility. By being informed and proactive, individuals can contribute to the early detection and reporting of potential virus outbreaks, further strengthening the effectiveness of the global surveillance system. Drawing from the lessons learned during the COVID-19 pandemic, it is evident that the world's readiness to address the potential re-emergence of the Langya virus as a pandemic is a critical concern. The global response to COVID-19 highlighted the importance of preparedness, early detection, and swift action in containing and mitigating the spread of infectious diseases. As such, proactive measures must be taken to enhance global readiness and response capabilities to effectively deal with the resurgence of the Langya virus.

The experiences of the COVID-19 pandemic underscore the need for improved coordination and collaboration among nations, international organizations, and public health agencies to address the threat of a potential Langva virus pandemic. Enhancing communication channels, sharing data and resources, and establishing early warning systems are essential components of a comprehensive strategy to prevent the re-emergence of the Langya virus from escalating into a global health crisis. By building on the lessons learned from COVID-19, the world can strengthen its collective capacity to respond swiftly and effectively to future pandemics. Furthermore, investing in research and development of vaccines, antiviral treatments, and diagnostic tools specific to the Langva virus is crucial in bolstering global readiness. So, to combat the spread of LavV, a comprehensive and coordinated approach is crucial at both the national and international levels. At the national level, strengthening disease surveillance and early detection systems is paramount to enable timely response. Vulnerable

populations, such as farmers and manufacturing workers, should be prioritized for monitoring and preventive measures. While there are no established treatments for LayV, antiviral drugs may be explored as potential remedies based on their effectiveness against similar viruses like Hendra and Nipah. Developing a specific vaccine for LayV should also be a top priority. Nationally, health authorities must work closely with various stakeholders, including the agricultural sector, to implement holistic prevention strategies and mitigate the impact of this emerging zoonotic threat.

At the international level, global health organizations must coordinate efforts to share information, resources, and best practices for managing LayV. Collaborative research is needed to better understand the transmission routes of viruses, their pathological changes, and potential reservoirs. Rapid diagnostic tools and artificial intelligence-based surveillance systems should be developed to enhance early detection capabilities. Ultimately, a proactive and multilateral approach, drawing lessons from the COVID-19 pandemic, is crucial to effectively contain the spread of LayV and prevent future zoonotic disease outbreaks. By prioritizing scientific innovation and preparedness efforts, the world can better equip itself to combat the potential threat posed by the Langya virus.

CONCLUSION

Additionally, promoting public awareness, education, and adherence to preventive measures can empower individuals to play an active role in disease prevention and control. Through a combination of strategic planning, international cooperation, and community engagement, the world can enhance its readiness to confront the reemergence of the Langya virus and safeguard global health security.

AUTHORS' CONTRIBUTIONS

It is hereby acknowledged that all authors have accepted responsibility for the manuscript's content and consented to its submission. They have meticulously reviewed all results and unanimously approved the final version of the manuscript.

LIST OF ABBREVIATIONS

WHO	=	World	Health	Organization	
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COVID-19 = COronavirus Disease of 2019

CONSENT FOR PUBLICATION

Not applicable.

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CONFLICT OF INTEREST

The authors declare no conflict of interest, financial or otherwise.

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REFERENCES

- Thien DH, Tran HB, Uyen NNP, et al. A comprehensive review of Langya virus and framework for future zoonotic disease control. Rev Med Virol 2024; 34(1): e2520. http://dx.doi.org/10.1002/rmv.2520 PMID: 38282399
- [2] Soman Pillai V, Krishna G, Valiya Veettil M. Nipah virus: Past outbreaks and future containment. Viruses 2020; 12(4): 465. http://dx.doi.org/10.3390/v12040465 PMID: 32325930
- [3] Sah R, Mohanty A, Chakraborty S, Dhama K. Langya virus: A newly identified zoonotic henipavirus. J Med Virol 2022; 94(12): 5621-2.
 - http://dx.doi.org/10.1002/jmv.28095 PMID: 36016482
- [4] Rissanen I, Ahmed AA, Azarm K, et al. Idiosyncratic Mòjiāng virus attachment glycoprotein directs a host-cell entry pathway distinct from genetically related henipaviruses. Nat Commun 2017; 8(1): 16060.

http://dx.doi.org/10.1038/ncomms16060 PMID: 28699636

- [5] Mallapaty S. New 'Langya' virus identified in China: What scientists know so far. Nature 2022; 608(7924): 656-7. http://dx.doi.org/10.1038/d41586-022-02175-z PMID: 35953571
- [6] Weatherman S, Feldmann H, de Wit E. Transmission of henipaviruses. Curr Opin Virol 2018; 28: 7-11. http://dx.doi.org/10.1016/j.coviro.2017.09.004 PMID: 29035743
- [7] Adesola RO, Miranda AV, Tran YSJ, et al. Langya virus outbreak: current challenges and lesson learned from previous henipavirus outbreaks in China, Australia, and Southeast Asia. Bull Natl Res

Cent 2023; 47(1): 87.

http://dx.doi.org/10.1186/s42269-023-01064-3 PMID: 37334163

- [8] Román RG, Tornieporth N, Cherian NG, Shurtleff AC, Jackson MLA, Yeskey D. Medical countermeasures against henipaviruses: A review and public health perspective. Lancet Infect Dis 2021. PMID: 34735799
- [9] Qiu X, Wang F, Sha A. Infection and transmission of henipavirus in animals. Comp Immunol Microbiol Infect Dis 2024; 109: 102183. http://dx.doi.org/10.1016/j.cimid.2024.102183 PMID: 38640700
- [10] Dehghanbanadaki H, Aazami H, Shabani M, Amighi D, Seif F, Dehnavi AZ. A systematic review and meta-analysis on the
- Definition AZ: A systematic review and meta-analysis on the association between lymphocyte subsets and the severity of COVID-19. Immunopathologia Persa 2021; 8(2): e29303.
 [11] Playford EG, Munro T, Mahler SM, et al. Safety, tolerability, physical discussion of a hyperpendicular provided and the several discussion.
- pharmacokinetics, and immunogenicity of a human monoclonal antibody targeting the G glycoprotein of henipaviruses in healthy adults: A first-in-human, randomised, controlled, phase 1 study. Lancet Infect Dis 2020; 20(4): 445-54. http://dx.doi.org/10.1016/S1473-3099(19)30634-6 PMID:
- 32027842
 [12] Soleimani P, Jahantigh HR, Yadollahifarsani S. Gender difference in COVID-19 vaccination; recent concepts. J Parathyr Dis 2022; 10(1): e11167.
- [13] Zhang XA, Li H, Jiang FC, et al. A zoonotic henipavirus in febrile patients in China. N Engl J Med 2022; 387(5): 470-2. http://dx.doi.org/10.1056/NEJMc2202705 PMID: 35921459
- [14] Hauser N, Gushiken AC, Narayanan S, Kottilil S, Chua JV. Evolution of Nipah virus infection: Past, present, and future considerations. Trop Med Infect Dis 2021; 6(1): 24. http://dx.doi.org/10.3390/tropicalmed6010024 PMID: 33672796