

# Global emergence of Langya virus: A serious public health concern

Zahra Z Piracha<sup>1\*</sup> , Umar Saeed<sup>2\*</sup> , Rawal AI Ahmed<sup>3†</sup> , Fatima NA Khan<sup>4†</sup> , Muhammad I Nasir<sup>5†</sup> 

<sup>1</sup>International Center of Medical Sciences Research (ICMSR), Islamabad, Pakistan

<sup>2</sup>Clinical and Biomedical Research Center, Foundation University School of Health Sciences (FUSH), Foundation University Islamabad, Pakistan

<sup>3</sup>Regional Disease Surveillance and Response Unit Sukkur, Sindh, Pakistan

<sup>4</sup>Baqai Medical University Karachi, Karachi, Pakistan

<sup>5</sup>Fazaia Ruth Pfau Medical College – FRPMC PAF Base Faisal Karachi

\*Joint first authorship.

†Equal contribution.

## EMERGENCE OF LANGYA VIRUS DURING COVID-19 PANDEMIC IS A THREAT TO GLOBAL COMMUNITIES

The newly-emerged Langya virus (LayV), classified as a henipavirus in the *Paramyxoviridae* family and closely related to the Mojianghenipavirus, has raised concerns among public health authorities worldwide. The coronavirus 2019 (COVID-19) pandemic, which started in China in 2019, is still ongoing, despite joint global efforts [1]. The ensuing global crisis has severely impacted the world's economy, affecting supply chains for medicines, food, and materials across low-, middle-, and high-income countries, most of which still have to recover. The simultaneous re-emergence of a life-threatening LayV from China raises serious questions and necessitates in-depth clinical investigations to prevent future pandemics. Timely diagnosis of LayV infections and the use of established prevention methods can significantly reduce the global burden of diseases [2].

## HUMAN-TO-HUMAN TRANSMISSION OF LANGYA VIRUS NEEDS EXTENSIVE RESEARCH

Most disease outbreaks during the past two decades have been of zoonotic origin [3]. Although as many as 10 000 different species of viruses could potentially affect human beings, most commonly circulate in wild animals [4]. Rapid climate changes and increased human activity has increased the risk of viral exchange across different species of animals, which occasionally results in the transmission of zoonotic diseases to human beings [5].

Langya viral human-to-human transmission collocation has been poorly understood and urgently needs global attention and extensive investigation.

LayV has emerged as a threat following the Hendra and Nipah viruses, taking its name after a town called Langya in China. From its emergence in 2018, 35 cases of LayV infection have been reported, all in eastern China. To date, no deaths have been reported. Despite its low global prevalence, this novel virus could lead to a global public health crisis, especially due to the potential high mortality from earlier species of the henipavirus genus, which is why it cannot



be underestimated [7,8]. Currently, the LayV spreads from animals to human beings. Although contact tracing and investigation discovered no person-to-person transmission cases, this cannot be excluded due to the small sample size. LayV symptoms include fever, cough, tiredness, gastrointestinal disturbance, loss of appetite, muscle pain, nausea, and vomiting. Most cases had leukopenia, pointing to their compromised immunity against infections. The second most common sign was a decreased number of platelets. Some of the infected individuals also exhibited hepatic symptoms, hinting at the LayVs possible effect on the liver [9]. The virus has recently been linked to the transfer of infections from animals to people in Eastern China. It was also discovered during COVID-19 and Monkeypox investigation and procedures [10]. However, human-to-human transmission of LayV has not yet been recognised.

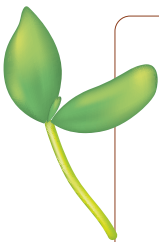
**Artificial intelligence-mediated rapid diagnostic advances for disease management setups will aid in lowering the langya viral global burden of disease.**

Langya virus is an enveloped virus containing single-stranded ribonucleic acid (RNA) with 18 402 RNA nucleotides. Its genomic structure consists of six structural proteins – nucleocapsid, phosphoprotein, matrix protein, surface glycoprotein, fusion protein, and large viral RNA-dependent RNA polymerase. These six structural proteins determine its closest genetic linkage with other henipaviruses like Mojiang henipavirus [8]. The detailed genomic sequences of LayV can be found in the GenBank (accession numbers OM101125- OM101130 and OM069567-OM069646).

As previously mentioned, the virus primarily transmits between animals, most likely among shrews. The LayV RNA was isolated from more than 25% of almost 260 shrews studied, leading researchers to conclude that the species may possibly serve as a direct or indirect vector for human transmission. The LayV RNA has also been isolated from other animals, including dogs and goats [7]. Among 35 identified human infections so far, none seems to be the result of human-to-human transmission. However, the high prevalence of LayV among shrews is alarming, necessitating large-scale studies to determine possible transmission routes of LayV.

## GLOBAL PERSPECTIVES ON LANGYA VIRAL PREVENTION AND MANAGEMENT

Farmers and manufacturing workers are the populations most vulnerable to LayV [7,11], as research has shown that proximity to animals and working in agricultural settings are linked to LayV virus infection. To stop LayV from spreading, monitoring must be strengthened to enable early discovery [12]. There is no particular therapy for LayV, akin to henipaviruses and other viruses with similar clinical presentation; few antiviral drugs have been tested by experts in animal experiments, and there is no specific vaccine. However, ribavirin could be an effective remedy. It is frequently prescribed by healthcare providers for treating viral infections and is beneficial against RNA viruses and those that cause respiratory symptoms. Research has shown that ribavirin is also effective against both Hendra and Nipah viruses. These two viruses can also be treated with chloroquine, which is a tested medication for malaria. Based on available data, these two treatments may aid in the management of the Langya virus [11,12]. Viral infections are mounting over time [13-23], so prevention at all levels against viruses – including the novel LayV – remains the optimal strategy. As with any other zoonotic agent, holistic knowledge and adequate preparedness will be our best defence. Future studies should provide evidence regarding possible transmission routes, pathological changes, vulnerable groups, potential reservoirs, susceptible hosts, and rapid viral diagnostic advances via artificial intelligence tools, to ensure the effective containment of this new virus. We call for international and national health strategic organisations to prevent zoonotic diseases spread and design timely prevention strategies against Langya viral transmission.



**Funding:** This study received no funding.

**Authorship contributions:** US conceived of the idea and was the principal investigator of the study. US, RAI, FNAK, MIN and ZZP wrote the manuscript. The US reviewed the manuscript. All the authors participated in data gathering and analysis. The final draft of the manuscript has been read and approved by all the authors.

**Disclosure of interest:** The authors completed the ICMJE Disclosure of Interest Form (available upon request from the corresponding author) and disclose no relevant interests.

- 1 World Health Organization. Coronavirus disease (COVID-19). Available: <https://www.who.int/news-room/questions-and-answers/item/coronavirus-disease-covid-19>. Accessed: 28 June 2023.
- 2 European Centre for Disease Prevention and Control. Langya henipavirus under ECDC monitoring. Available: <https://www.ecdc.europa.eu/en/news-events/langya-henipavirus-under-ecdc-monitoring>. Accessed: 28 June 2023.
- 3 Choudhary OP, Priyanka, Ali RK, Maulud SQ, Dhawan M, Mohammed TA. Will the next spillover pandemic be deadlier than the COVID-19?: A wake-up call. *Int J Surg.* 2022;97:106208. [Medline:34995807](#) [doi:10.1016/j.ijssu.2021.106208](#)
- 4 Carlson CJ, Albery GF, Merow C, Trisos CH, Zipfel CM, Eskew EA, et al. Climate change increases cross-species viral transmission risk. *Nature.* 2022;607:555-62. [Medline:35483403](#) [doi:10.1038/s41586-022-04788-w](#)
- 5 Olival KJ, Hosseini PR, Zambrana-Torrel C, Ross N, Bogich TL, Daszak P. Host and viral traits predict zoonotic spillover from mammals. *Nature.* 2017;546:646-50. [Medline:28636590](#) [doi:10.1038/nature22975](#)
- 6 Kreuder Johnson C, Hitchens PL, Smiley Evans T, Goldstein T, Thomas K, Clements A, et al. Spillover and pandemic properties of zoonotic viruses with high host plasticity. *Sci Rep.* 2015;5:14830. [Medline:26445169](#) [doi:10.1038/srep14830](#)
- 7 Choudhary OP, Priyanka, Fahrni ML, Asmaa A, Metwally AA, Saied AA. Spillover zoonotic 'Langya virus': is it a matter of concern? *Vet Q.* 2022;42:172-4. [Medline:36001038](#) [doi:10.1080/01652176.2022.2117874](#)
- 8 Zhang XA, Li H, Jiang FC, Zhu F, Zhang YF, Chen JJ, et al. A Zoonotic Henipavirus in Febrile Patients in China. *N Engl J Med.* 2022;387:470-2. [Medline:35921459](#) [doi:10.1056/NEJMc2202705](#)
- 9 Joi P. Five things you need to know about Langya virus. Available: <https://www.gavi.org/vaccineswork/five-things-you-need-know-about-langya-virus>. Accessed: 28 June 2023.
- 10 Thomas L. Does Langya virus pose a spillover threat? *News Medical life Sciences.* Available: <https://www.news-medical.net/news/20220830/Does-Langya-virus-pose-a-spillover-threat.aspx>. Accessed: 28 June 2023.
- 11 Mallapaty S. New 'Langya' virus identified in China: what scientists know so far. *Nature.* 2022;608:656-7. [Medline:35953571](#) [doi:10.1038/d41586-022-02175-z](#)
- 12 Sah R, Mohanty A, Reda A, Siddiq A, Mohapatra RK, Dhama K. Marburg virus re-emerged in 2022: recently detected in Ghana, another zoonotic pathogen coming up amid rising cases of Monkeypox and ongoing COVID-19 pandemic- global health concerns and counteracting measures. *Vet Q.* 2022;42:167-71. [Medline:35993230](#) [doi:10.1080/01652176.2022.2116501](#)
- 13 Saeed U, Piracha ZZ, Uppal SR, Waheed Y, Uppal R. SARS-CoV-2 induced hepatic injuries and liver complications. *Front Cell Infect Microbiol.* 2022;12:726263. [Medline:36189356](#) [doi:10.3389/fcimb.2022.726263](#)
- 14 Saeed U, Uppal SR, Piracha ZZ, Uppal R. SARS-CoV-2 Spike Antibody Levels Trend among Sinopharm Vaccinated People. *Iran J Public Health.* 2021;50:1486-7. [Medline:34568189](#) [doi:10.18502/ijph.v50i7.6640](#)
- 15 Saeed U, Piracha ZZ, Kwon H, Kim J, Kalsoom F, Chwae YJ, et al. The HBV Core Protein and Core Particle Both Bind to the PPIase Par14 and Par17 to Enhance Their Stabilities and HBV Replication. *Front Microbiol.* 2021;12:795047. [Medline:34970249](#) [doi:10.3389/fmicb.2021.795047](#)
- 16 Piracha ZZ, Saeed U, Kim J, Kwon H, Chwae YJ, Lee HW, et al. An Alternatively Spliced Sirtuin 2 Isoform 5 Inhibits Hepatitis B Virus Replication from cccDNA by Repressing Epigenetic Modifications Made by Histone Lysine Methyltransferases. *J Virol.* 2020;94:e00926-20. [Medline:32493816](#) [doi:10.1128/JVI.00926-20](#)
- 17 Saeed U, Kim J, Piracha ZZ, Kwon H, Jung J, Chwae YJ, et al. Parvulin 14 and Parvulin 17 Bind to HBx and cccDNA and Upregulate Hepatitis B Virus Replication from cccDNA to Virion in an HBx-Dependent Manner. *J Virol.* 2019;93:e01840-18. [Medline:30567987](#) [doi:10.1128/JVI.01840-18](#)
- 18 Piracha ZZ, Kwon H, Saeed U, Kim J, Jung J, Chwae YJ, et al. Sirtuin 2 Isoform 1 Enhances Hepatitis B Virus RNA Transcription and DNA Synthesis through the AKT/GSK-3 $\beta$ / $\beta$ -Catenin Signaling Pathway. *J Virol.* 2018;92:e00955-18. [Medline:30111572](#) [doi:10.1128/JVI.00955-18](#)
- 19 Saeed U, Piracha ZZ. PIN1 and PIN4 inhibition via parvulin impedes Juglone, PiB, ATRA, 6,7,4'-THIF, KPT6566, and EGCG thwarted hepatitis B virus replication. *Front Microbiol.* 2023;14:921653. [Medline:36760500](#) [doi:10.3389/fmicb.2023.921653](#)
- 20 Saeed U, Piracha ZZ. Viral outbreaks and communicable health hazards due to devastating floods in Pakistan. *World J Virol.* 2016;5:82-4. [Medline:27175353](#) [doi:10.5501/wjv.v5.i2.82](#)
- 21 Saeed U, Mazoor S, Jalal N, Zahid Piracha Z. Contemplating the Importance of Toll-like Receptors I and II Regarding Human Viral Pathogenesis. *Jundishapur J Microbiol.* 2014;8:e13348. [Medline:25763131](#) [doi:10.5812/jjm.13348](#)
- 22 Saeed U, Waheed Y, Manzoor S, Ashraf M. Identification of novel silent HIV propagation routes in Pakistan. *World J Virol.* 2013;2:136-8. [Medline:24255884](#) [doi:10.5501/wjv.v2.i3.136](#)
- 23 Saeed U, Uppal SR, Piracha ZZ, Rasheed A, Aftab Z, Zaheer H, et al. Evaluation of SARS-CoV-2 antigen-based rapid diagnostic kits in Pakistan: formulation of COVID-19 national testing strategy. *Virol J.* 2021;18:34. [Medline:33581714](#) [doi:10.1186/s12985-021-01505-3](#)

**Correspondence to:**

Prof. Dr. Umar Saeed  
 Clinical and Biomedical Research Center, Foundation  
 University School of Health Sciences (FUSH),  
 Foundation University Islamabad (44000)  
 Pakistan  
[umarsaeed15@yahoo.com](mailto:umarsaeed15@yahoo.com)