

## EDITORIAL

## THE H10N3 INFLUENZA STRAIN: A CANDIDATE FOR THE NEXT PANDEMIC?

Syed Abdullah Monawwer, Haris Taufiq, Muhammed Muneeb, Khubaib Muhammad Shamim Meah

Department of Internal Medicine, Ziauddin Medical University, Karachi-Pakistan

The COVID-19 pandemic has devastated the world's demographics. As of December 2021, the virus has claimed over 5.3 million lives and has caused high morbidity across the globe. As the recently developed vaccines provided some hope of relief, a recent development is a cause of further distress as the first human case of the rare avian influenza A (H10N3) virus was detected in a 41-year-old man from the Zhenjiang province, China. The man has since recovered and has been discharged. The avian influenza A(H10N3) virus belongs to the *Orthomyxoviridae* family which mainly causes respiratory symptoms with primary viral pneumonia being the main cause of mortality. Genetic analysis on the patient's bronchoalveolar lavage confirmed the presence of the H10N3 subtype and that the virus had gone under reassortment with multiple other avian strains. Although the virus is deemed incapable of human-to-human spread, further mutations in its genome may allow it to do so. This would lead to a large-scale outbreak and reap calamitous outcomes, causing high morbidity and mortality. Moreover, this would further disrupt daily activities, spiking mental health issues. As the global economy tries to recover from the destitution caused by Covid-19, another pandemic would cripple the already struggling businesses and cause a further loss of livelihood. This calls for increased surveillance in poultry and an upscale in research for vaccine development as well as a contingency plan in case a large-scale outbreak was to occur.

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The Covid –19 pandemic has its roots in the city of Wuhan, China where a sudden rise in the number of pneumonia cases was reported in December 2020. These were later diagnosed as severe acute respiratory syndrome coronavirus-2 (SARS-COV-2). By January 2020 it was declared a public health emergency of international concern (PHEIC) by the World health organization (WHO) and two months later, a Pandemic. The Virus is transmitted by airborne droplets through coughing or sneezing and causes respiratory symptoms ranging from asymptomatic patients to having fatal complications such as acute cerebrovascular disease, myocarditis, pulmonary embolism, ischemic stroke and deep venous thrombosis.<sup>1</sup> As of December 2021 the virus has claimed over 5.3 million lives across the globe with a total of over 274 million confirmed cases.<sup>2</sup> While the recent ongoing vaccination drives across the globe provide hope to contain and bring an end to this catastrophe, a recently made finding is a cause of great concern for healthcare professionals and the general public as the first human case of H10N3 was reported.<sup>3</sup>

On May 28, a 41-year-old man from the city of Zhenjiang was diagnosed as the first human case of H10N3 infection a month after he was

hospitalized. The man has since been stabilized and discharged. According to officials, contact tracing has not revealed any further cases however details are yet to be revealed as to how the man was infected. According to the country's National Health Commission (NHC) the virus has low pathogenicity in poultry making a large-scale outbreak unlikely.<sup>1</sup> Until 2018 only 160 virus isolates were reported in either waterfowls or wild birds mainly in Asia or North America for the past 40 years making H10N3 a rare strain.<sup>3</sup>

H10N3 is an avian influenza subtype belonging to the *Orthomyxovirus* family.<sup>4</sup> Although the Avian viruses are commonly restricted to wild as well as domesticated birds there have been certain strains which could be transferred to humans. The virus primarily causes pulmonary symptoms with primary viral pneumonia being the most common cause of mortality. Although close proximity, human to human spread is yet to be officially ruled out, to date, there has been no sustained human to human transmission. However, owing to its segmented genome, the virus through assortment with a mammalian strain can give birth to a chimeric strain that can transmit between humans. Such genetic shifts have reaped catastrophic results evoking 4

pandemics including the Spanish flu of 1918 which caused around 50 million deaths worldwide. An explanation for lack of human-to-human transmissibility of the virus is that the avian viruses primarily target the lower respiratory system. Although this increases the severity of the symptoms the lack of involvement of the upper respiratory system greatly diminishes the virus' transmissibility. However, a mutation in the hemagglutinin protein will cause an antigenic drift enabling the virus to bind to both upper and lower respiratory systems. This will allow it to spread through coughing and sneezing making it a serious threat to humans.<sup>4</sup>

A genomic analysis run on the patient's bronchoalveolar lavage fluid confirmed that he was indeed infected by an avian H10N3 virus. Although incapable of human-to-human spread, the virus, now designated A/Jiangsu/428/2021/H10N3 (JS428) was proven to be a chimeric strain realizing the fears of many amongst the healthcare community. The presence of 226Q and 228S HA protein receptor binding sites suggest the dual binding specificity of human-like receptor and avian-like receptor. Further, avian replication characteristics were indicated by the presence of Glu in the PB2 protein's residue 627. Further the respective positioning of Asp and Lys at the PB2 protein's 701 and 702 residues are highly suggestive of the virus' preference for avian replication. The virus' heightened level of replication in mammals can be explained by the presence of Val at residue 473 of PB1. Moreover, the presence of 31Ser in the M2 protein is suggestive that the virus is resistant to Amantadine treatment.<sup>5</sup>

Phylogenetic analysis revealed that the MP and PB1 genes found in JS428 identified closely with the genes of A/chicken/China/1102/2019/H9N2 (99.12%;99.06%). HA and NA genes of JS428 were very similar to those found in A/chicken/Jiangsu/0110/2019/H10N3 (99%) while the PB2 gene identified closely with A/chicken/China/1101/2019/H9N2 (98.63%). Further analysis of JS428 revealed that its NS gene was closest to that of A/chicken/Vietnam/HU9-506/2018/H9N2 (99.32). Finally, from further assessment it was revealed that the NP and PA genes of JS428 to their counterparts found in A/chicken/China/H1072/2017/H9N2 (98.59%; 98.52%).<sup>5</sup>

Although the virus is yet to demonstrate transmissibility amongst humans, it is important to

take precautionary measures given the fact that the world is still battling the destitution caused by the Covid-19. Any spread may be an unbearable challenge for the already overwhelmed health care system. Moreover, the disruption in daily activities alongside the uncertainty caused by the lockdown has led to severe psychological stress in the local public. Another pandemic may lead to a further surge in mental disorders which may in turn cause increased suicide rate, self-harm and other adverse outcomes. Lastly, the global economy is still recovering from the devastation caused by Covid-19 with the expected GDP for the year 2022 being 3.2% lower than the pre-pandemic predictions (world banks).<sup>6</sup> Any disruption caused by a second pandemic will cripple the already struggling economies.<sup>1</sup>

## CONCLUSION

In conclusion, all these factors call for proper measures to contain the virus. Increased surveillance of poultry and vaccine development will help stop any virus outbursts in the future. Further there is a need for a contingency plan in case the virus does become capable of human-to-human transmission in which case the mass media may also play its crucial role in teaching safety precautions to the general public. Perhaps the lessons learned from the Covid-19 will serve as an important guide in case of any future outbreaks.<sup>1</sup>

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## Address for Correspondence:

Syed Abdullah Monawwer, Department of Internal Medicine, Ziauddin Medical University, Karachi-Pakistan  
Email: [abdullah.munawwer@gmail.com](mailto:abdullah.munawwer@gmail.com)