In Australian Child after Travel to India Scientists Detect Rare H5N1 Avian Flu Strain

A team of Australian scientists has recently identified highly pathogenic avian influenza A (H5N1) virus clade 2.3.2.1a in a child who traveled back to Australia from India.

Study

The study involved a 2.5-year-old previously healthy girl who returned to Australia after visiting Kolkata, India, in February 2024. The child developed an illness in Kolkata and was hospitalized after returning to Australia.

She was subsequently admitted to the intensive care unit (ICU) with respiratory failure requiring mechanical ventilation. She was treated with a 5-day course of oseltamivir starting on day 3 after admission. She fully recovered and was discharged after 2.5 weeks.

Respiratory samples collected from the patient were tested using routine next-generation sequencing, which identified the H5N1 virus, designated as A/Victoria/149/2024 (H5N1).

Characterization of the Virus

The phylogenetic analysis of the identified virus revealed that it is a reassortant virus consisting of four segments similar to clade 2.3.2.1a viruses circulating in Bangladesh. The four segments were hemagglutinin, neuraminidase, nucleoprotein, and nonstructural segments.

Further analysis revealed that the matrix segment (regulation of viral replication) is similar to HPAI H5N1 clade 2.3.4.4b viruses, which predominantly circulate worldwide and have been detected in birds in Asia.

The polymerase basic 2, polymerase basic 1, and polymerase acidic segments showed similarity with the recent clade 2.3.4.4b low pathogenicity avian influenza viruses detected in wild birds and poultry in Asia since 2020. This reassortment suggests that clade 2.3.4.4b viruses, which have disseminated globally through wild birds, are transforming the genetic structure of other H5N1 clades endemic in poultry.

Mammalian Adaptation

The analysis of viral segments for mammalian adaptation, virulence, and antiviral susceptibility indicated retention of preferential binding to avian α2–3 but not to the mammalian α2–6 sialic acid receptors.

The viral segments did not show any markers for mammalian adaptation, virulence, or pathogenicity. However, the virus showed susceptibility to oseltamivir and baloxavir marboxil.

Conclusion

The study describes the identification and characterization of highly pathogenic avian influenza A(H5N1) virus clade 2.3.2.1a in an Australian child traveler returning from India. The virus is a previously unreported reassortant consisting of clades 2.3.2.1a, 2.3.4.4b, and wild bird low-pathogenicity avian influenza gene segments.

These findings call for robust monitoring of serious influenza A cases in travelers who have returned from regions with circulating avian influenza viruses. Subtyping these severe or even fatal viruses, especially H5N1 and H5N6 viruses currently circulating in South Asia, is vital for reducing nonseasonal influenza infections and initiating antiviral treatments promptly.

The case study reported here highlights the significant lack of H5N1 surveillance data in India, with only two H5 sequences reported from the country since 2020. In contrast, 314 sequences were recorded in Bangladesh during the same period, further underscoring the need for comprehensive surveillance efforts.

The viral genome characterized in this study is similar to that of a fatal case in New Delhi in 2021 and genetically similar to the H5N1 viruses present in Bangladesh. Although the New Delhi case was caused by contact with poultry, the current Australian case had no confirmed contact with poultry or raw poultry products. This lack of confirmed exposure highlights the challenge in determining the mode and route of infection, particularly in regions with limited data on circulating viruses.

The complex genetic recombination origins of the identified virus reveal that clade 2.3.4.4b viruses continue to play a major role in shaping the evolution of other H5N1 clades, emphasizing the importance of global surveillance.

Overall, the study highlights the need for increased surveillance of persistent HPAI H5Nx infections in Asia.

Source:

https://www.news-medical.net/news/20241218/Scientists-detect-rare-H5N1-avian-flu-strain-in-Australian-child-after-travel-to-India.aspx