

# GENETIC CHANGES POWER H5N1 VIRUS SPREAD, SEVERITY IN ANIMALS

Relevant for: Science & Technology | Topic: Science and Technology- developments and their applications and effects in everyday life

To enjoy additional benefits

CONNECT WITH US

June 03, 2023 09:00 pm | Updated 10:12 pm IST

COMMENTS

SHARE

READ LATER

File photo of a Zoo staff member spraying chemicals near a rosy Pelican enclosure to prevent the Bird Flu (H5N1 avian influenza virus) at Delhi Zoo | Photo Credit: PTI

A study published recently has found that [the H5N1 virus \(clade 2.3.4.4b\)](#), which spread among wild birds across 30 countries or territories across continents by February 2022 collected different combinations of genes through reassortment with viruses circulating in wild birds in North America.

The reassortant A(H5N1) viruses are genotypically and phenotypically diverse, with many causing severe disease with dramatic neurologic involvement in mammals. The viruses have distinct in vitro characteristics including increased virus replication rates and ability to cause severe disease outcomes with dramatic neurologic involvement in mammalian animal models. The virus has a proclivity to target the central nervous system, says a study published in the journal Nature Communications.

**Also read | [Climate change increasing risk of new emerging viruses, infectious diseases in India](#)**

In December 2021, A(H5N1) viruses were detected in poultry and a gull in Eastern Canada. It was closely related to 2.3.4.4b viruses identified in Europe in spring of 2021. The virus quickly spread wild birds in several States in the U.S. soon thereafter.

As per the WHO update (September 2021-February 2022) the 2.3.4.4b virus clade had caused 26 infections in humans — 25 cases of A(H5N6) infection in China and one case of A(H5N1) in the U.K. This demonstrates the zoonotic transmission potential of these viruses. So far human-to-human transmission has not been reported. There is a grave risk of sustained transmission in humans once the virus collects a few mutations while spreading among mammals.

The A(H5Nx) clade 2.3.4.4 viruses was originally identified in North America in 2014-2015 among avian species and disappeared. This clade, like the current one (2.3.4.4b) was reassorted soon after detection in North America. However, the reassortment was not associated with changes in mammalian pathogenicity. In contrast, the clade now in circulation has enhanced virulence with neurological involvement in mammalian models, including ferrets.

The virus initially spread among aquatic mammals in the Americas before infecting a variety of land mammals.

**Also read | [Mammalian spread of H5N1 and its pandemic potential](#)**

The newer strains of the virus have a greater propensity to cause disease in mammals but currently it is of low-risk to humans. The reason being that the virus appears better adapted to spread among birds rather than between mammals. "Our data highlight how quickly things can change in a natural system, and the potential for further A(H5Nx) reassortment and phenotypic diversification will only increase as the unprecedented global distribution of these viruses broadens," the researchers write.

COMMENTS

SHARE

[genetics](#) / [science \(general\)](#)

BACK TO TOP

Comments have to be in English, and in full sentences. They cannot be abusive or personal. Please abide by our [community guidelines](#) for posting your comments.

We have migrated to a new commenting platform. If you are already a registered user of The Hindu and logged in, you may continue to engage with our articles. If you do not have an account please register and login to post comments. Users can access their older comments by logging into their accounts on Vuukle.

**END**

Downloaded from **crackIAS.com**

© **Zuccess App** by crackIAS.com

Crack