

EDITORIAL

Stop H5N1 influenza in US cattle now

The relentless march of a highly pathogenic avian influenza virus (HPAIV) strain, known as H5N1, to become an unprecedented panzootic continues unchecked. The leap of H5N1 clade 2.3.4.4b from Eurasia and Africa to North America in 2021 and its further spread to South America and the Antarctic have exposed new avian and mammalian populations to the virus and led to outbreaks on an unrivaled scale. The virus has infected wild birds across vast geographic regions and caused wildlife deaths in some of the world's most biodiverse ecosystems. Hundreds of millions of poultry have died or been culled, affecting global food security in some of the world's poorest regions. Numerous mammalian species, including sea lions and fur animals, have been infected. Outbreaks in dairy cows in the United States have been occurring for months, seemingly unchecked in most affected states. Why is there not a greater sense of urgency to control these infections?

Although the H5 2.3.4.4b virus seems poorly optimized for infection or spread in humans, with fewer than 20 cases since 2016, influenza leaves no room for complacency. The sheer number of infected wild birds and poultry has caused spillover infections to occur in wild carnivores, marine mammals, and farmed animals, providing additional pathways for exposure and perhaps infection in humans. The H5 virus has evolved continuously since 1996 but has never infected so many bird species nor been able to transmit to, and replicate in, cows. The more than 140 dairy farms in 12 US states with the virus and the detection of viral RNA in milk products in grocery stores speak for themselves. Infection in cattle creates new possibilities for direct contact between the virus and humans, and also risks the virus evolving the ability to spread in cattle, a new livestock reservoir of around 1.5 billion animals worldwide.

Until now, human infections with H5 viruses were mainly associated with the keeping of infected poultry. But over the past 3 months, the United States has identified human H5 cases in farmworkers associated with one of the world's most industrialized dairy production systems. Even difficult viral adaptations can occur if there are enough opportunities for contact and replication in new host species. Adaptation of the virus to cattle must be prevented. The outbreak in

cattle in the United States must therefore be brought under control quickly. Key measures that should be initiated or intensified immediately include surveillance of all US dairy farms by testing, for example, bulk milk for influenza virus RNA, implementation of strict quarantine for infected cattle, and restriction of within-state transport to stop the circulation of the virus in cows. Only a couple of states are attempting this currently. Biosecurity and hygiene measures on US dairy facilities must be enhanced to avoid virus spread and spillover infections. This should include simple and practical steps such as keeping work clothing on the farm, thoroughly decontaminating stock vehicles and equipment, ensuring restricted access and movement of personnel among premises, and provid-

ing appropriate personal protective equipment. Human influenza surveillance should be bolstered during the summer and before the usual human seasonal influenza wave begins in the fall. The timely development of vaccine candidates for both livestock and humans should be undertaken along with associated policies on their distribution. This is the ultimate insurance against a worst-case scenario in which viral variants emerge that spread more easily in mammals.

Globally, surveillance of mammalian cases should be intensified and real-time genomic information on the virus should be made publicly available, especially in at-risk populations (such as pig and fur animal farms). There must be increased global awareness of data collection and data sharing on zoonotic influenza. Analyses for incursion risk and pandemic preparedness based on both genetic and phenotypic data (including identifying mammalian adaptive changes, antiviral therapeutic resistance, and diagnostic robustness) in all regions need to be substantially improved, and the detection of human infection clusters needs to be further optimized. National and international coordination in the spirit of a modern "One Health" approach is essential, and the quadripartite comprising the Food and Agricultural Organization of the United Nations, United Nations Environment Programme, World Health Organization, and World Organisation for Animal Health should step up to take a leading role.

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