

The spread of H5N1 bird flu among animals and the growing possibility of a pandemic

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The panzootic—a pandemic in animal species—of the highly pathogenic strain of the H5N1 of avian influenza is cutting a swathe through wild and domestic bird populations internationally, and has now jumped into numerous mammalian species, including humans, several times.

The virus has spread to every continent except Australia, where scientists estimate it may arrive in the southern hemisphere by spring via migratory birds from Antarctica. Scientists have warned that bird flu poses an enormous danger of a human pandemic, which could easily dwarf the devastation wrought by the ongoing COVID-19 pandemic.

According to the World Health Organisation (WHO), 903 people have become infected with H5N1 since 2003. Of these, 463 died, a lethality rate of 51 percent. The ongoing COVID-19 pandemic, with a much lower infection fatality rate, has killed over 27 million people. If a bird flu pandemic does develop, it would likely have a catastrophic impact globally.

Most strains of avian influenza found in wild bird populations have a low pathogenicity (LPAI) with no ill effect on the infected animals. There are two highly pathogenic strains (HPAI), H5 and H7 that are extremely lethal. The virus that has reached panzootic levels and is of most concern is H5N1 clade 2.3.4.4b. A clade consists of viruses that have a common ancestor.

In a comment titled, “Chickens, ducks, seals and cows: a dangerous bird flu strain is knocking on Australia’s door,” senior research fellow at the Doherty Institute Dr. Michelle Wille maps the development of the panzootic from its first detection in a goose in China in 1996. The virus became established in wild bird populations and poultry, where it killed most of the birds it infected. It is spread through the migration of wild birds.

By 2003, the virus had become endemic in poultry in Southeast Asia. In an important communication by H. Chen et al., from the Joint Influenza Research Center at Shantou University in China and published in *Nature* in July 2005, “H5N1 virus outbreak in migratory waterfowl,” presciently warned that the virus “constitutes a major pandemic threat to humans.”

The communication described a mass-death event that occurred on 30 April 2005 of mostly bar-headed geese (*Anser indicus*) at Qinghai Lake in western China. By May 4, bird mortality was more than 100 per day. By May 20, approximately 1,500 birds were dead. The authors warned that the virus had the potential to migrate over the Himalayas.

Chen et al. stated, “There is a danger that it might be carried along the birds’ winter migration routes to densely populated areas in the south Asian subcontinent, a region that seems free of this virus, and spread along migratory flyways linked to Europe. This would vastly expand the geographical distribution of H5N1.”

In fact, this is what occurred, with the virus spreading to Europe and Africa in 2005. In 2014, the virus again entered Europe and then spread to North America, and in 2016 it re-entered Africa.

In 2020, a major shift occurred when outbreaks in wild birds and poultry

increased dramatically.

Dr. Wille stated, “In 2021, reports streamed in of mass mortality events in Europe and the virus rapidly travelled the world. The world was in the grip of a ‘panzootic’ – a global pandemic in animals.”

By October 2021, the virus crossed the Atlantic and reached North America. A year later the virus travelled the length of South America. In October 2023, the virus was detected in brown skuas, scavenging birds in sub-Antarctic islands. In February this year, it was detected in Antarctica.

The avian influenza virus is made up of a single strand of ribonucleic acid (RNA) with a genome consisting of eight gene segments. The virus can evolve very rapidly as it has a huge propensity to mutate. When one virus is in a host cell also occupied by another type of virus, it can acquire genes from the other virus in a process known as reassortment, giving the virus the potential to make great evolutionary leaps.

Although the avian influenza virus is mostly restricted to birds, the H5N1 clade 2.3.4.4b has infected numerous mammal species including humans. This has usually occurred in scavenger species when it eats a dead infected bird. When the virus crosses over into non-avian species, which is known as a spillover event, this increases its chances of evolving to enable infection within the species. The more times this occurs, the greater the probability.

The H5N1 clade 2.3.4.4b is known to be very lethal, with the panzootic killing a huge number of wild birds, poultry and mammals. Some bird species may have been driven to the edge of extinction.

An assessment by Ashley Banyard and his team at the Influenza and Newcastle disease work group, Animal and Plant Health Agency, Weybridge, United Kingdom, published in an OFFLU bulletin in December 2023, “Continued expansion of high pathogenicity avian influenza H5 in wildlife in South America and incursion into the Antarctic region,” outlined the devastating impact in South America.

Although the virus only arrived in South America in October 2022, within one year it had killed 597,832 birds of at least 82 species and 50,785 mammals of at least 10 species, with most of the deaths occurring in Peru and Chile. Most of the mammals killed were South American sea lions (*Otaria byronia*), with approximately 32,000 deaths, and southern elephant seals (*Mirounga leonina*), with approximately 17,000 deaths. This gives a glimpse of the horrific slaughter of wildlife internationally, most likely in the millions.

The next step was the sub-Antarctic islands where the virus was detected in October 2023 in the South Georgia part of the Scotia Arc among several bird species. The first bird found with the virus was the brown skua (*Stercorarius antarcticus*) although numerous other infected species have been found since.

A groundbreaking paper published in *Nature* in April 2022, “Climate change increases cross-species viral transmission risk,” shows that climate change increases the probability of spillover events in which dangerous viruses come into contact with human populations, thereby increasing the risk of pandemics. This occurs when animals that naturally harbour

viruses are driven from their natural habitats due to the ravages of climate change.

Importantly, scientists have determined that the genetic changes in the bird flu's genome, that have accelerated the development of the panzootic, have been driven by climate change. A comment by wildlife ecologist Diann Prosser at the Eastern Ecological Science Center located in Maryland Laurel US and her team, published in *Nature Microbiology* in November 2023, titled, "Climate change impacts on bird migration and highly pathogenic avian influenza," stated that "Climate change patterns appear to parallel an unprecedented global spread of highly pathogenic avian influenza (HPAI)."

They note that "Three HPAI expansion events demarcating spread from a source region to a new, previously uninfected continent have coincided with EWEs (extreme weather events) and an increased amount of virus in the source region."

In 2005, the avian influenza spread out of Asia and was followed by increased outbreaks in Asia that were associated with extremely low temperatures in Europe and earlier frosts that altered the migration of wild birds. In December 2014, the H5N8 virus spread from Asia to North America, with a large expansion of outbreaks preceding Super Typhoon Nuri that moved up the coast of Asia and across the Bering Strait to the North American Pacific Flyway. The expansion of H5N1 to the Americas, following the 2021–2022 winter transatlantic introduction of H5N1 from Europe to North America, was associated with cyclone storms in this period.

Prosser et al. continued, writing:

Phylogenetic analyses have shown high virus sequence identity between source and introduction regions, supporting the hypothesis of wild bird dispersal of HPAI, whether from natural migration patterns where species from cross-continent wintering grounds share breeding locations (for example, Iceland or Bering Strait region), or from rapid EWE-induced vagrant bird movements.

The current outbreak in US dairy cows poses an enormous threat to human populations. This threat is being expanded by the US ruling elites' program of trashing basic public health measures in the interests of big business with the continuing SARS-CoV-2 pandemic. "Forever COVID" is being expanded to avian influenza, but with even more lethal consequences if it becomes a pandemic.

The US dairy cattle outbreak was first detected in March and has now extended to 15 states across 650 dairy cattle herds. The inexorable spread of the virus is shown in California, the largest dairy producer in the US, where 248 cattle herds have been affected just in the last month.

The recent detection in Oregon of the H5N1 strain among pigs this October raises very serious concerns, as pigs are known to harbour numerous viruses and, as well, present the virus with a rich environment for reassortment.

Over 40 humans have been infected so far in the US, mostly people who were in close contact with cows. In Canada, a previously healthy teenager has now been hospitalized for over a week with H5N1, requiring a ventilator in order to breathe.

Principled scientists are raising the alarm. The editorial of the *npj viruses* journal published in May stated:

Further adaptation of HPAIV H5N1 to cattle must be prevented. Stringent measures such as testing regimes (e.g. via bulk milk diagnostics), strict transport controls, quarantine measures and

optimized milking hygiene must be implemented. In addition, much more basic epidemiological data is needed It should also be considered that the most efficient virus shedding cows should be isolated or even euthanized.

A *Science* journal editorial published in July, titled, "Stop H5N1 influenza in US cattle now," raised the alarm and warned, "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."

However, these appeals are falling on deaf ears. Official "complacency" is a vast understatement. Indifference and even a eugenicist-style welcoming of the consequences of a devastating pandemic are more apt descriptions of the sentiments dominating in ruling circles. Even such basic requirements of testing and sequencing of viruses infecting affected animals is not being done in anywhere near a timely or rigorous manner, meaning scientists are flying blind to the scope of the virus.

The developing avian influenza panzootic and the growing possibility of a pandemic bring to the fore the existential questions for humanity of climate change and the destruction of public health, both of which must be stopped in order to control the growing threats.

President elect Donald Trump's recent selection of anti-vaccine zealot Robert F. Kennedy Jr. to head the Department of Health and Human Services (HHS), as well as his appointment of Great Barrington Declaration co-author Jay Bhattacharya to head the National Institutes of Health (NIH) and television doctor Mehmet Oz to head the Centers for Medicare & Medicaid Services (CMS), alongside other vicious opponents of public health to fill out the health agencies, clearly demonstrates that public health will be further eviscerated for the interests of big business, neutering the potential of science to solve these crucial questions for the future of humanity.

Although principled scientists are raising the alarm, they are powerless to effect any change by themselves. In order to meet these challenges, the working class must unite with these principled scientists to fight for a socialist program to defend the health, safety and future of humanity.



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