



Crossing the Species Barrier Bird Flu Spillover to Mammals and Humans in India

Emerging Risks and Preparedness

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AVIAN influenza, commonly known as “bird flu”, is a viral disease primarily infecting domestic poultry and other migratory birds. However, it has recently grabbed global headlines due to the surge in new mammalian species being infected. Though human cases of bird flu have been reported for more than a decade, the last few years have seen incidences of bird flu cases being detected in other species, for example, in marine mammals in South America from 2023, dairy cattle from the USA in 2024, sheep from the UK in 2025, and cats in India and other European countries since 2024. Additionally, in a few species of wild carnivores, both in captivity and in the wild, from different countries.

The bird flu spillover incidents in new mammalian species have raised alarm bells globally, requiring an understanding of the potential shift in the virus’s behaviour to jump species, transmission dynamics, risk factors posed to humans, and the possible threat of a new pandemic. The risk of spillover in densely populated countries like India is far greater because of close human-animal contact. Understanding the nature of this virus, its transmission routes, and preventive strategies is crucial at this juncture.

The Virus Behind Bird Flu: Influenza A Virus

The virus responsible for bird flu is a type of Influenza A virus, which belongs to the family Orthomyxoviridae. Influenza A

viruses are enveloped, negative-sense, and the viral genome consists of single-stranded segmented RNA. They are well-known for causing pandemics and major outbreaks, not just in humans, but also in a wide range of animals.

Influenza A viruses are subtyped based on two key surface proteins, Haemagglutinin (HA) and Neuraminidase (NA). Haemagglutinin protein is responsible for the virus’s ability to bind to the host cell receptor, while Neuraminidase helps the virus to release from the infected cell. There are currently 18 known HA subtypes (H1–H18), while there are 11 known NA subtypes (N1–N11).

The avian influenza has been classified into Highly Pathogenic Avian Influenza (HPAI) and Low Pathogenic Avian Influenza (LPAI) based on the cleavage pattern of the HA protein and the pathogenic potential in infected birds. HPAI is of greater concern, as its strains include H5N1, H7N9, and H9N2 combinations, which have been associated with major outbreaks in poultry and other mammals.

As the genome of the Influenza A virus is composed of RNA, it is prone to mutations within the genome, resulting in genetic diversity. The virus either undergoes small changes over time, leading to antigenic drift or major genetic changes. This results in antigenic shift, thereby enabling the virus to cross the species barriers. The segmented nature of the RNA genome (each segment codes for a viral protein) can also