

Pandemic mutations in bird flu revealed

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Scientists have discovered how bird flu adapts in patients, offering a new way to monitor the disease and prevent a pandemic, according to research published in the August issue of the *Journal of General Virology*. Highly pathogenic H5N1 avian influenza virus has spread through at least 45 countries in 3 continents.

Despite its ability to spread, it cannot be transmitted efficiently from human to human. This indicates it is not fully adapted to its new host species, the human. However, this new research reveals mutations in the virus that may result in a pandemic.

"The mutations needed for the emergence of a potential pandemic virus are likely to originate and be selected within infected human tissues," said Professor Dr Prasert Auewarakul from Mahidol University, Thailand. "We analyzed specific molecules called haemagglutinin on viruses derived from fatal human cases. Our results suggest new candidate mutations that may allow bird flu to adapt to humans."

Viruses with a high mutation rate such as influenza virus usually exist as a swarm of variants, each slightly different from the others. These are called H5N1 bird flu quasispecies. Professor Dr Auewarakul and his colleagues found that some mutations in the quasispecies were more frequent than others, which indicates they may be adaptive changes that make the virus more efficient at infecting humans. Most of these mutations were found in the area required for the virus to bind to the host cell.

"This study shows that the H5N1 virus is adapting each time it infects a human," said Professor Dr Auewarakul. "Such adaptations may lead to the emergence of a virus that can cause a pandemic. Our research highlights the need to control infection and transmission to humans to prevent further adaptations."

The research has provided genetic markers to help scientists monitor bird flu viruses with pandemic potential. This means they will be able to detect potentially dangerous strains and prevent a pandemic. The research also gives new insights into the mechanism of the genesis of a pandemic strain.

"Our approach could be used to screen for mutations with significant functional impact," said Professor Dr Auewarakul. "It is a new method of searching for changes in H5N1 viruses that are required for the emergence of a pandemic virus. We hope it will help us to prevent a pandemic in the future."

Source: Society for General Microbiology

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