

Spread of bird flu strains slowed at some borders

Several strains of the bird flu virus that raged across southern China were blocked from entering Thailand and Vietnam, UC Irvine researchers have discovered.

This first-ever statistical analysis of influenza A H5N1's genetic diversity helps scientists better understand how the virus migrates and could, in the future, help health officials determine whether efforts to thwart its spread were successful.

"Some countries appear more exposed to bird flu invasion than others. Learning that is a good step in discovering which social and ecological factors promote, or, on the other hand, hamper the virus' spread," said Robert G. Wallace, a postdoctoral researcher and lead author of the study.

The results appear online Feb. 27 in the journal *PLoS ONE*.

Since its emergence in 1996, H5N1 has only sporadically been passed from birds to humans. Although only about 350 human cases of this influenza have been recorded worldwide, its high mortality rate raises concerns that if the virus mutates in such a way that humans can pass it on, a deadly flu pandemic may result. More than 60 percent of humans who contract the virus die from it.

In this study, Wallace and Walter M. Fitch, professor of ecology and evolutionary biology at UCI, analyzed nearly 500 publicly available genetic sequences of proteins found on the surface of the influenza virus. These sequences originally were collected from 28 Eurasian and African localities through 2006.

The study also showed that H5N1 strains circulating in Indonesia, Japan, Thailand and Vietnam shared the most evolutionary history with H5N1 circulating in several provinces in southern China. The provinces, Guangdong, Fujian and Hong Kong, are engaged in intensive international trade, including poultry. Previous research has concluded the poultry trade is a key mechanism for the spread of the H5N1 virus.

The researchers suggest that health officials trying to block new strains of the virus from spreading could use the methods employed in this study to determine whether interventions are working.

"You can think of it as a type of evolutionary forensics," Wallace said. "When a bomb explodes, investigators can determine how many charges went off and the strength and direction of the blast, all from the resulting damage alone. Here we can determine the way H5N1 has spread and evolved by the resulting viral diversity."

Source: University of California - Irvine

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