H5N1 virus outbreak in migratory waterfowl in China

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H5N1 influenza A viruses are widely distributed among poultry in Asia, but until recently only a limited number of wild birds were affected. During late April through June 2005, an outbreak of H5N1 virus infection occurred among wild birds at Qinghai Lake in China.

Here, we describe the features of this outbreak. First identified in bar-headed geese, the disease soon spread to other avian species populating the lake. Sequence analysis of 15 viruses representing six avian species and collected at different times during the outbreak revealed four different H5N1 genotypes. Most of the isolates possessed lysine at position 627 in the PB2 protein, a residue known to be associated with virulence in mice and adaptation to humans. However, neither of the two index viruses possessed this residue.

All of the viruses tested were pathogenic in mice, with the exception of one index virus. Importantly, H5N1 viruses isolated in Mongolia, Russia, Inner Mongolia and Liaoning provinces of China, after August 2005 were genetically closely related to one of the genotypes isolated during the Qinghai outbreak, and this genotype virus was also spread to some countries in Europe and Africa, suggesting the dominant nature of this genotype and underscoring the need for intensive surveillance worldwide to minimize its devastating consequences.

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