ABSTRACT: Highly pathogenic H5N1 influenza A viruses (HPAI H5N1) are widely distributed among poultry in Asia, but until recently only a limited number of wild birds were affected. During late April–June 2005, an outbreak of HPAI H5N1 infection occurred among wild birds at Qinghai Lake in China. First identified in bar-headed geese (Anser indicus), the disease soon spread to other avian species populating the lake. Sequence analysis of 15 viruses from 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. Importantly, H5N1 viruses isolated in Mongolia, Russia, and Inner Mongolia were genetically closely related to one of the genotypes isolated during the Qinghai outbreak. This genotype virus also spread to some countries in Europe and Africa, suggesting its dominant nature and underscoring the need for worldwide intensive surveillance to minimize its devastating consequences.

Key words: Avian influenza virus, highly pathogenic H5N1, wild birds.

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