Abstract

Mongolia combines a near absence of domestic poultry, with an abundance of migratory waterbirds, to create an ideal location to study the epidemiology of highly pathogenic avian influenza virus (HPAIV) in a purely wild bird system. Here we present the findings of active and passive surveillance for HPAIV subtype H5N1 in Mongolia from 2005–2011, together with the results of five outbreak investigations. In total eight HPAIV outbreaks were confirmed in Mongolia during this period. Of these, one was detected during active surveillance employed by this project, three by active surveillance performed by Mongolian government agencies, and four through passive surveillance. A further three outbreaks were recorded in the neighbouring Tuva Republic of Russia on a lake that bisects the international border. No HPAIV was isolated (cultured) from 7,855 environmental fecal samples (primarily from ducks), or from 2,765 live, clinically healthy birds captured during active surveillance (primarily shelducks, geese and swans), while four HPAIVs were isolated from 141 clinically ill or dead birds located during active surveillance, while environmental feces and live healthy birds yielded 56 and 1 LPAIV respectively. All Mongolian outbreaks occurred in 2005 and 2006 (clade 2.2), or 2009 and 2010 (clade 2.3.2.1); all years in which spring HPAIV outbreaks were reported in Tibet and Qinghai provinces in China. The occurrence of outbreaks in areas deficient in domestic poultry is strong evidence that wild birds can carry HPAIV over at least moderate distances. However, failure to detect further outbreaks of clade 2.2 after June 2006, and clade 2.3.2.1 after June 2010 suggests that wild birds migrating to and from Mongolia may not be competent as indefinite reservoirs of HPAIV, or that HPAIV did not reach susceptible populations during our study.

Introduction

Since its emergence in 1997 and subsequent re-emergence in 2003, highly pathogenic avian influenza virus (HPAIV subtype H5N1) has caused the deaths of at least 357 people in 15 countries [1] and been responsible for losses of many millions of domestic poultry, negatively impacting economic growth and food security in affected countries. Prior to 2005, outbreaks in wild birds were sporadic, associated with high mortality, and thought to relate to spillers from infected domestic poultry [2–4]. This situation changed in April 2005, with an outbreak among wild migratory waterbirds at Qqghai Lake in northern China, where over 6,000 wild birds died over a period of two months [7–9].

Following events at Qqghai, there was a marked increase in outbreaks involving wild birds elsewhere in Asia, Europe and Africa. However, the extent to which wild birds contributed to the spatial expansion of HPAIV outbreaks, particularly in relation to that of the legal and illegal movement of wild and domestic fowl is difficult to resolve [10,11]. Many outbreaks involving wild birds occurred in close proximity to cases among domestic poultry [12], making it difficult to attribute the source of infection to a wild or domestic host. In such environments, it can be difficult to isolate the contribution that wild birds play in cycles of HPAIV transmission [13].

In response to the Qinghai outbreak, a wild bird surveillance system was implemented in Mongolia in 2005 to elucidate the role of wild birds in the transmission of HPAIV H5N1. Bird species show variable susceptibility to infection with HPAIV H5N1, with experimental exposures resulting in high mortality rates among swans, geese and gulls [14,15], and variable levels of mortality or subclinical infections in ducks [15–17]. Active surveillance approaches involved searching for the presence of HPAIV through screening diagnostic specimens from healthy, ill and dead birds and from the environment. In contrast, passive surveillance relied on reports of sick and dead birds received from the general public, who were requested to report waterbird mortality to provincial veterinary authorities.

Several features make Mongolia an ideal location for understanding the epidemiology of HPAIV in wild birds. Mongolia supports large populations of migratory waterfowl and shorebirds [18], including species breeding across Mongolia’s extensive wetlands during the boreal summer, then departing to spend the winter in milder climates in Australia, the Indian Subcontinent, Africa, Southeast Asia, China, Korea, and Japan [19–23]. HPAIV H5N1 is either endemic or has occurred in domestic and/or wild bird populations in all these areas except for Australia. Other species visit Mongolia for short periods to feed while migrating to and from northerly breeding areas. Mongolia also represents an important site for migrating Anseriformes (ducks, geese and swans) that congregate during the post-breeding period when early on from them to vacate their Siberian breeding sites.

Mongolia presents an opportunity to study viruses in wild populations in isolation from domestic poultry. It has a small domestic poultry industry with a population of fewer than 100,000 birds in 2005 [24], on overall density of 0.6 birds per km2 [25], with most birds raised for egg production in moderately biosecure facilities located in urban centers. In contrast, China produces approxi-