

Identifying areas of Australia at risk for H5N1 avian influenza infection from exposure to nomadic waterfowl moving throughout the Australo-Papuan region

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Abstract. Since 2003, highly pathogenic avian influenza (HPAI) due to the H5N1 virus has been reported from both domestic poultry and wild birds in over 60 countries and this has resulted in the direct death or slaughter of over 250 million birds. The potential for HPAI to be introduced to Australian commercial poultry via migratory shorebirds returning from Asia has previously been assessed as a low risk. However, introduction of HPAI from areas to the immediate north of Australia via nomadic waterfowl that range throughout the Australo-Papuan region provides a second potential pathway of entry. Surveillance programmes provide an important early warning for Australia's estimated 2,000 commercial poultry farms but to be efficient they should be risk-based and target resources at those areas and sectors of the industry at higher risk of exposure. In order to address this need, this study compared the distribution and movement patterns of native waterfowl to identify regions where the likelihood of HPAI incursion and establishment was highest. Analysis of bird banding records provided information on the maximum distances moved and dispersal patterns of the species of waterfowl of interest. Introduction via Cape York was found to be most likely and all poultry farms in Queensland were found to be within range of waterfowl that can shed H5N1 virus for up to 17 days. The final analysis showed that the area at greatest risk of HPAI introduction is the Atherton tableland near Cairns.

Keywords: H5N1 avian influenza, nomadic waterfowl, spatial analysis, Australia.

Introduction

The current pandemic of highly pathogenic avian influenza (HPAI) due to H5N1 virus is believed to have originated in China (Fauci, 2006). Since 2005 it has spread beyond China and South-east Asia to over 60 different countries (OIE, 2007) and the Food and Agriculture Organization (FAO) of the United Nations has estimated that efforts to control the disease have resulted in the direct death or slaughter of over 250 million birds (FAO, 2007).

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Migratory birds, predominantly of the family Anatidae, have been implicated in the spread of HPAI from east Asia to Russia, Europe and Africa although debate continues over the relative importance of migratory birds and movement of poultry (Kilpatrick et al., 2006). In Australia the importation of live poultry and fresh poultry products is not permitted without comprehensive quarantine precautions and consequently the entry of H5N1 HPAI into Australia through the movement of poultry or poultry products is unlikely. A previous study (East et al., 2008) determined that the risk of introduction of HPAI into Australia via migratory shorebirds returning from Asia was low.

Australian bird species within the family Anatidae are not migratory. However, they are nomadic throughout the Australo-Papuan region that includes the southern areas of the island of New

Guinea (Dingle, 2004). The term nomadic is used to differentiate the unpredictable movement of Australian waterbirds, usually in response to drought or flooding events from the predictable annual movement of truly migratory birds (Tracey et al., 2004; Roshier et al., 2006). Currently, HPAI has not become established in this region, however, isolated outbreaks have occurred in the Indonesian part of New Guinea at Manokwari in Irian Jaya Barat province and at Jayapura and Timika in Papua province (Pro-Med, 2007) (Fig. 1). Future establishment of HPAI in this region would open a second potential pathway of HPAI introduction into Australia through the movements of nomadic waterfowl.

Tracey et al. (2004) listed 107 species of birds that move between Australia and Asia and/or have ranges that include parts of New Guinea and South-east Asia. Avian influenza has been isolated from 25 of these species. This list includes several species of Anatidae that have nomadic movements throughout the Australo-Papuan region as far north as the Central Highlands of the island of New Guinea (Dingle, 2004). Timika is close to the south coast of New Guinea and falls within the Australo-Papuan region whereas Manokwari and Jayapura do not.

Of the 25 species of nomadic birds from which avian influenza (AI) has been isolated, 13 species have been reported from various freshwater bodies in eastern Australia including farm dams (East et al., 2008). Over a period of 35 years of observation, the four predominant species reported have been the grey teal duck (*Anas gibberifrons*), the Pacific black duck (*Anas superciliosa*), the plumed whistling-duck (*Dendrocygna eytoni*) and the Eurasian coot (*Fulica atra*). Prevalence of AI in these species has been found at levels up to 6% (East et al., 2008). Furthermore, aerial surveys of wetland birds in eastern Australia confirmed that these four species (particularly the grey teal and the Eurasian coot) are the most regularly observed among waterfowl from which AI has been isolated (Porter et al., 2006). This is consistent with Wallensten et al. (2007) who has reported that the dabbling ducks (genus *Anas*)

are the main natural reservoirs for low pathogenicity influenza A virus. The grey teal in particular is highly nomadic and individuals have been reported moving from south-eastern Australia to western Australia and New Zealand (Frith, 1982). The range of all three ducks extends to the south coast of New Guinea although the plumed whistling duck has only rarely been recorded there and all four species are dispersive in nature. Since infection with AI in Anatidae species is usually asymptomatic (Perkins and Swayne, 2002; Ellis et al., 2004), none these infections will limit the waterfowls' ability to disperse throughout their range after infection with HPAI.

Early detection of an incursion of HPAI in wild birds or poultry will rely upon an effective and efficient surveillance programme. To be efficient, the surveillance system should be risk-based so as to target resources towards those areas and sectors of the industry at higher risk of exposure. This paper describes a spatial analysis designed to determine a risk-ranking for the introduction of HPAI into the poultry farming regions of Australia based on the probability of introduction through nomadic waterfowl species returning from the island of New Guinea.

Materials and methods

Data sets

Spatial data sets for the distribution of wild bird species were obtained from "Birds Australia" (Carlton, Vic., Australia). Banding-recapture data for Anatidae species were obtained from the Australian Bat and Bird Banding Scheme (ABBBS) within the Commonwealth Department of Environment and Water Resources (<http://www.environment.gov.au/biodiversity/science/abbbs/>). Satellite images were sourced from Google Earth (<http://earth.google.com>).

Data for the density of poultry farms were obtained from a study commissioned by the Office of the Chief Veterinary Officer in 2005, the design

and conduct of which has been described previously (East et al., 2008). The location of farms was geocoded to the nearest suburb or town. For individual farms in areas of interest the precise location was identified by street address and confirmed by visualisation using Google Earth.

Identification of bird species of interest

Four native species of waterfowl, i.e. the grey teal duck (*A. gibberifrons*), the Pacific black duck (*A. superciliosa*), the plumed whistling-duck (*D. eytoni*) and the Eurasian coot (*F. atra*), have previously been identified as the species most likely to introduce AI into Australia (East et al., 2008).

Movement of waterfowl species

The distance travelled by native waterfowl species was calculated by examining banding-recapture data for the four species of interest. The maximum recorded distance travelled within the time frame of interest was used for the spatial analysis. The maximum single non-stop flight distance for grey teal was based on the findings of Roshier et al. (2006).

Spatial analysis

The bird abundance data for each individual species is presented as a fraction calculated by dividing the number of surveys conducted within each region in which the species of interest is observed by the total number of surveys conducted in that region. For this spatial analysis the overall waterfowl abundance used was the sum of the individual species abundance calculated for the four waterfowl species identified above.

Mapping studies were completed using MapInfo version 9.0 (MapInfo Corp., Troy, New York, USA) and Google Earth. The spatial analysis was based on a grid of 10' latitude by 10' longitude because the data from "Birds Australia" was supplied on that scale. The risk analysis was based on the method of Thomas et al. (2004). A 0.1 degree grid covering the

area between longitudes 110° and 155° E and latitudes 10° and 45° S was overlaid onto a map of Australia.

The abundance for each species of native waterfowl was adjusted to a linear scale from zero (no species of interest ever observed) to nine (highest observed abundance) in accordance with the method of Thomas et al. (2004). The abundance of the four native waterfowl species was added to provide a relative score for the overall abundance of native waterfowl in that grid square. A relative score for the abundance of poultry farms was calculated in the same way.

The time course of H5N1 HPAI shedding by ducks was sourced from the supplementary material submitted by Hulse-Post et al. (2005) and available from the journal's internet site at <http://www.pnas.org/cgi/data/0504662102/DC1/1>. Each grid square was assigned a risk score for virus excretion based on its distance from Cape York and the number of days a duck would take to travel that distance. Based on the longest recorded flight of an individual of the species of interest in the ABBBS database, the distance travelled by a duck in a day was set at 177.2 km. The values for virus shedding used in the analysis are shown in Table 1. A relative score for virus excretion was also calculated in accordance with the method of Thomas et al. (2004).

Table 1. Time course for the titre of H5N1 HPAI (EID₅₀/ml) excreted by native waterfowl used in the spatial analysis. Bold figures are sourced from Hulse-Post et al. (2005). Figures in italics were obtained by interpolating from a graph based on the figures published by Hulse-Post et al. (2005).

Days	Titre
1-4	<i>316.2</i>
5-7	316.2
8	<i>212.5</i>
9	100.0
10	<i>62.5</i>
11-13	17.8
14-17	<i>17.8</i>

A comparative score for the risk of establishment of HPAI was then calculated from the product of the abundance of the native waterfowl, the level of virus excretion and the number of poultry farms in each grid square. The calculated risk of establishment of HPAI for each grid square was assigned to one of five ranges (nil, rare, low, medium or high) using the method of Thomas et al. (2004). The score for the upper value of the nil risk range was arbitrarily set as 1.0.

Results

Longest single flight by nomadic waterfowl

The longest distances recorded between banding and recapture sites for individuals birds of the species of concern in this study over a period of 17 days or less were a grey teal travelling 2,304 km in 13 days (band 09014186), a Pacific black duck travelling 735 km in 11 days (band 11049801) and a Eurasian coot travelling 329 km in 5 days (band 10023841). No information was available in this

time range for plumed whistling ducks. These figures were used to estimate daily travel distances for this study. These distances are consistent with the distances of up to 343 km previously measured for single non-stop flight by grey teal (Roshier et al., 2006) and 215 km in a 24 hour period for a Pacific black duck (band 11049801).

Only four areas of Australia are within 350 km of New Guinea (Fig. 1) and three of these, i.e. the Cobourg Peninsula, Bathurst Island and Marchinbar Island in the Northern Territory, are all at the limit of the reported range of grey teal with each location being over 300 km from New Guinea. Cape York in Queensland, however, is only 153 km from New Guinea and the intervening islands reduce the longest over water distance to 52 km.

Dispersal of waterfowl from the Northern Territory

Mallard ducks (*Anas platyrhynchos*) have been recorded to shed H5N1 HPAI for up to 17 days after infection (Hulse-Post et al., 2005) and the

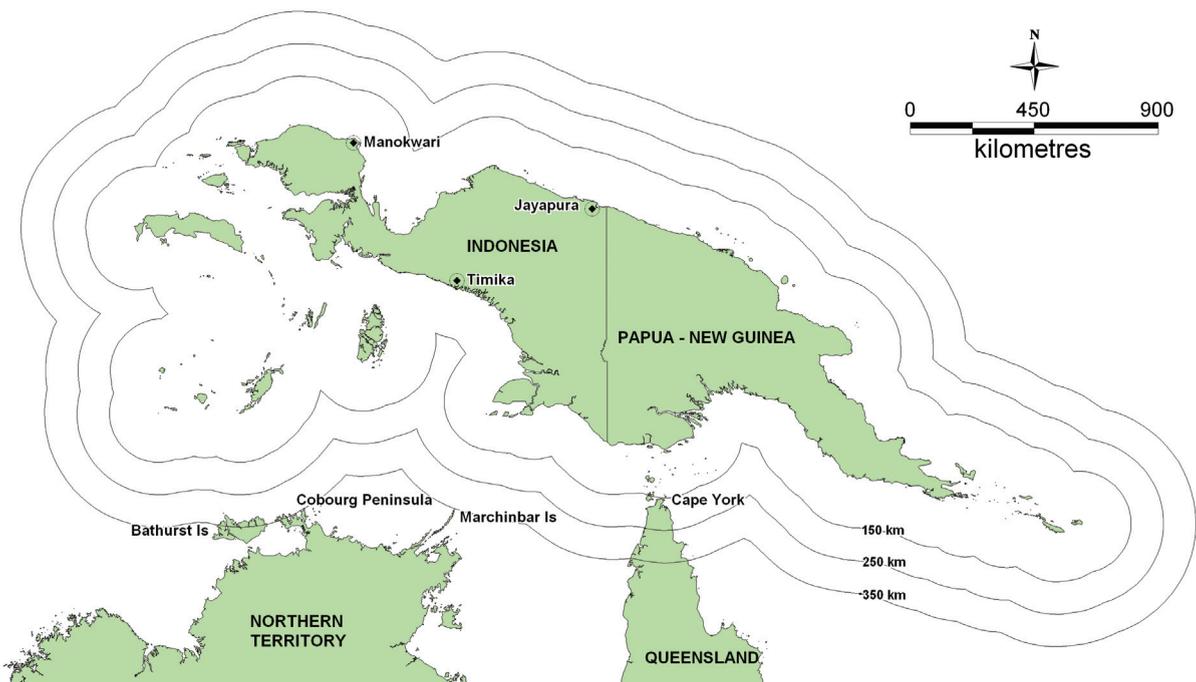


Fig. 1. Map of the island of New Guinea with distance contours (km).

longest recorded distance travelled by native waterfowl in this time frame is 2304 km (band 09014186). Travel over this distance would allow a bird to reach isolated poultry farms at Darwin, Broome, Carnarvon, Kalgoorlie and Ceduna together with three farms in the Port Pirie region of South Australia and most farms in Queensland other than those in the south eastern corner (Fig. 2).

An analysis of the recovery locations of 663 native waterfowl banded in the greater Darwin/Kakadu area and subsequently recaptured shows that only seven were recaptured in Queensland and that only two of these (in the Townsville region) were recovered closer than 250 km from the nearest poultry farm (Fig. 3). Of these 663 banded birds, 448 were recovered within 17 days and 447 of these were recovered within 50 km of the banding location. Only the grey teal that travelled 2,304 km to the Gascoyne River in Western Australia in 13 days (see above) moved any substantial distance from the banding site.

Dispersal of waterfowl from Cape York

No banding-recovery data is available for native waterfowl originating in the Cape York area. Based on the short-term travel distances for the three bird species listed above and therefore projected daily movements of 135.5 km for grey teal, 111 km for Pacific black ducks and 65.8 km for Eurasian coots, 17 days travel commencing at Cape York places the farm in Darwin, all Queensland farms and several farms in northern NSW within the range of grey teal shedding virus whereas Pacific black ducks would only reach central Queensland and Eurasian coots, northern Queensland (Fig. 4). In the absence of data for the plumed whistling duck, the distances of the grey teal were substituted as a worst case analysis. A direct route to the farm in Darwin involves an over-water flight of more than 500 km, substantially longer than the longest non-stop flight recorded for a grey teal. Therefore, this farm can be considered as unlikely to be at risk from an entry via Cape York.

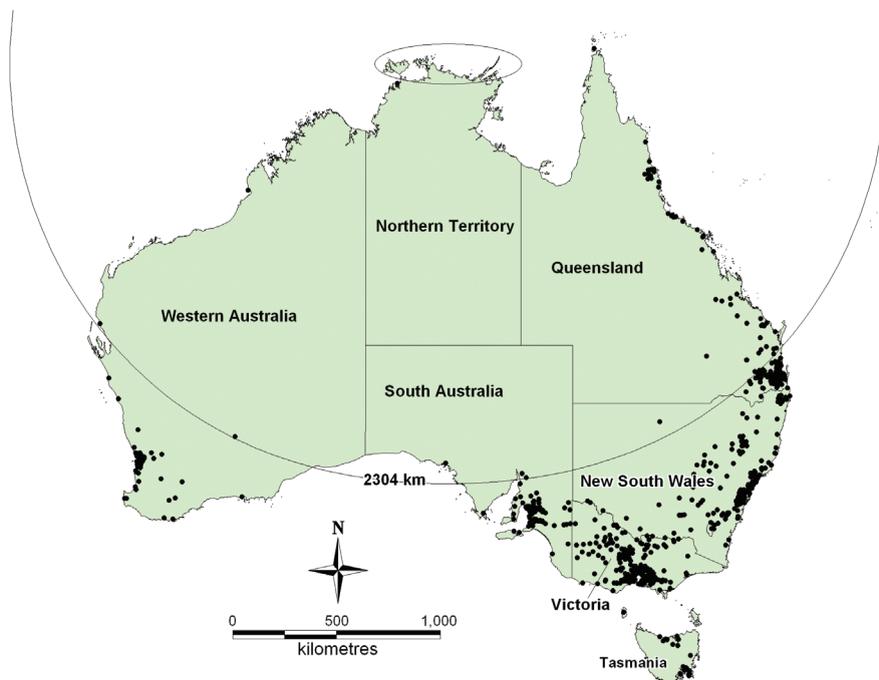


Fig. 2. Map showing Australian poultry farms within the maximum travel distance recorded for grey teal ducks in a 17 day period for flights commencing on the Northern Territory coastline.

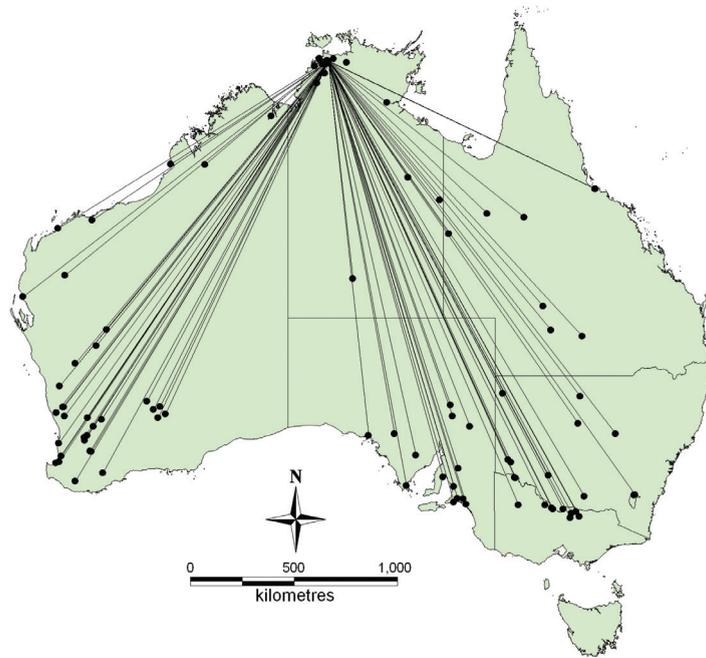


Fig. 3. Map showing the recovery locations of grey teal ducks after banding in the Darwin area.

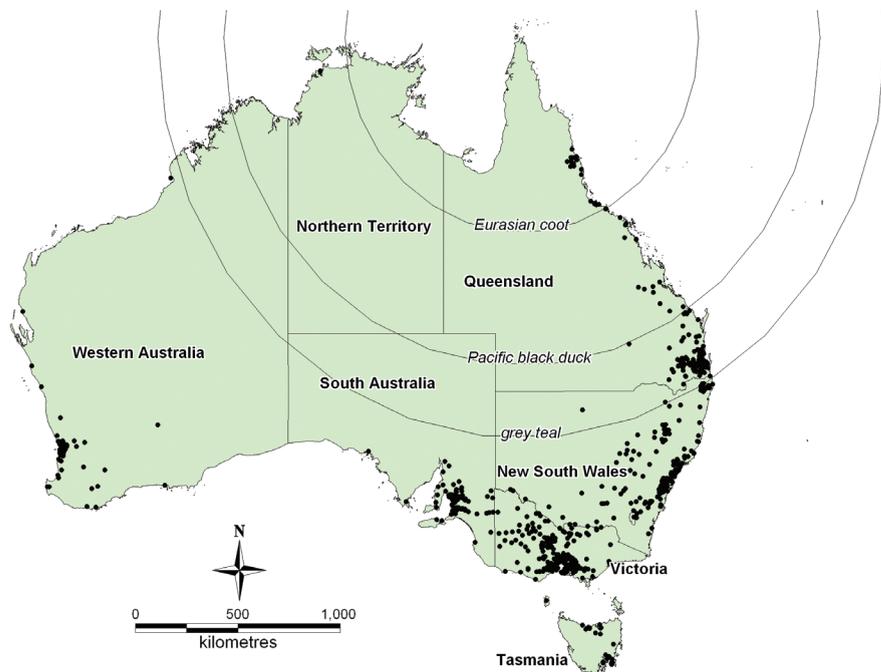


Fig. 4. Map showing Australian poultry farms within the flight range recorded for grey teal, Pacific black ducks and Eurasian coot in a 17-day flight commencing at Cape York.

The titres of AI virus shed by ducks decrease over the course of the infection. The daily titre was estimated from data previously published for mallard ducks by Hulse-Post et al. (2005) (Table 1).

The results of the final risk models for each species incorporating the three risk factors of waterfowl abundance, virus shedding rate and poultry

farm density are shown in Fig. 5. The areas of highest comparative risk for introduction of AI into the commercial poultry industry are clustered along the coast in the areas where the majority of the commercial poultry farms are located, the climate is wetter and there is more wetland suitable for waterfowl habitation. Whilst areas in the south of Queensland

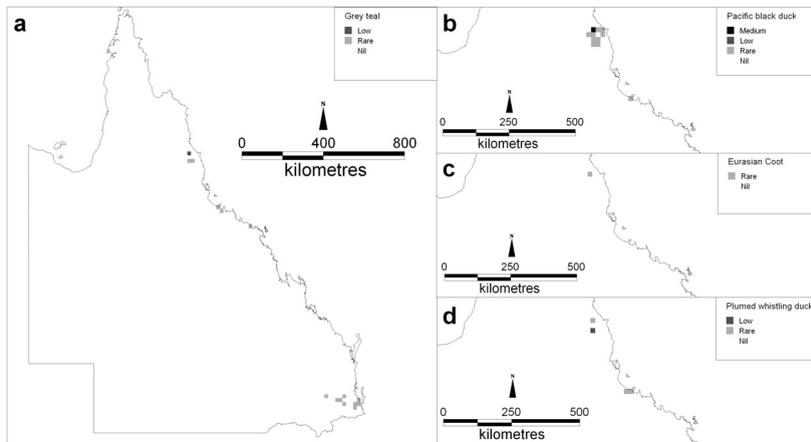


Fig. 5. Map of northern Australia showing the comparative risk of infection with H5N1 HPAI for poultry farms from waterfowl originating in New Guinea.

a = grey teal; b = Pacific black duck; c = Eurasian coot; d = plumed whistling duck.

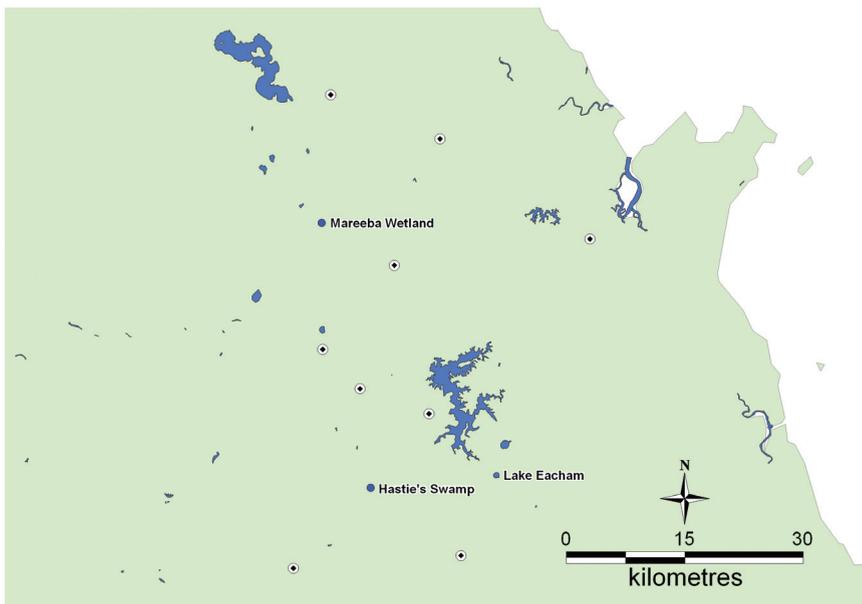


Fig. 6. Map of the Atherton Tablelands showing the proximity of poultry farms (⊙) to perennial water bodies.



Fig. 7. Aerial photo of a poultry farm in the highest risk area showing the proximity of the poultry housing to a water body.

are exposed to a rare threat level from the grey teal, the cluster of highest risk occurs around the Atherton tablelands (near Cairns) where a total of 17 poultry farms are found. This area includes a number of large lakes and waterbird habitats including lakes Tinaroo, Barrine, Eachem, Mitchell as well as the Mareeba wetland reserve, Hastie's swamp and the Mareeba-Dimbulah irrigation area (Fig. 6).

Of the 17 poultry farms in the Atherton tablelands, the location of 13 could be identified from aerial photos; one of these farms had water bodies within 100 m of the poultry sheds (Fig. 7) and the proximity of these water bodies may attract waterbirds and increase the risk of AI introduction for these particular farms.

Discussion

The risk of introduction of H5N1 HPAI to domestic poultry through nomadic waterfowl moving from New Guinea to Australia is rare or nil for all regions of Australia except North Queensland. In this area the comparative risk rises to low to medium with the greatest risk occurring on the Atherton Tableland where 17 poultry farms are located in the same general area as several large freshwater bodies and an irrigation area that provide habitat attractive to waterfowl. Most of the 17 farms are within 10 km of a perennial water body; within the daily for-

aging range recorded for these species (East et al., 2008) with one farm having poultry housing within 100 m of a water body. The absence of surface water bodies from the immediate vicinity of most of the farms suggests that the risk of AI infection may be reduced because of lack of suitable habitat for ducks in the immediate area of the poultry housing. In addition to the "Birds Australia" data used as a risk factor in this study, all four waterfowl species of interest have been independently recorded at the Mareeba wetland reserve, Hastie's swamp and lake Eacham (Fig. 6) (MWR, 2007; Birdwatching Australia, 2008). All five previous outbreaks of HPAI in Australia have had epidemiological connections with wild or range farmed ducks (Westbury, 1998; Animal Health Australia, 2007) and wild ducks sampled at Hastie's swamp in August 2007 have tested positive for antibodies to influenza A virus indicating exposure to AI (J. Wallner, Northern Australia Quarantine Strategy, personal communication).

Whilst little information is available on the movement of waterfowl through this region, Frith (1962) reported that Cape York contained little surface water that would provide attractive habitat to grey teal, possibly causing waterfowl returning from Papua New Guinea to eastern Australia to move quickly through Cape York and on to the lakes and swamps of the Atherton Tablelands. The timing of this movement will be critical because of the limited period during which the birds shed virus. Whilst the duration of H5N1 AI virus excretion in Australian species of ducks has not been determined, extended periods of shedding have been reported for several species including 17 days for Mallard ducks (*A. platyrhynchos*) (Hulse-Post et al., 2005), 12 days for the common teal (Keawcharoen et al., 2008) and at least nine days (but less than 19 days) in Muscovy ducks (*Carina moschata*) (Steensels et al., 2007). Based on historical bird movements determined from banding records, this would be more than sufficient time for the waterfowl to move the 800 km from Cape York to the Atherton Tableland.

There have been no reported cases of HPAI in wild birds or poultry on the Atherton Tableland and all

five previous Australian incidents of HPAI have involved Australasian strains of the virus rather than strains related to Asian isolates (Banks et al., 2000).

In addition to the duration of excretion of the virus, the level of excretion would also be of critical importance. Keawcharoen et al. (2008) demonstrated that common teal (*Anas crecca*) excrete significantly less virus than the mallard (*A. platyrhynchos*). Neither species exhibits clinical symptoms after experimental infection with H5N1 HPAI and thus the authors conclude that both species have the potential to be long distance vectors of the virus. Comparative excretion levels for the four species of duck included in this study are not available although the common teal and grey teal are closely related (Livezey, 1991).

Whilst the level of risk determined in our study is a regional measure of the relative infection pressure, the specific risk to any individual farm will be a combination of this infection pressure together with the protective effect of any biosecurity practices adopted by the individual farm. Actions such as providing a secure, uncontaminated water supply and bird proofing poultry housing will substantially reduce the risk for the introduction of HPAI (Alexander, 1995; Capua et al., 1999; Tracey et al., 2004).

This study suggests that there is a low to medium risk of introduction of H5N1 AI into Australian poultry via nomadic waterfowl introducing the virus when returning from New Guinea. Establishment of the H5N1 HPAI virus in the southern regions of the island of New Guinea would therefore substantially increase the threat of introduction into Australia compared with the threat of introduction via migratory birds returning from Asia (East et al., 2008). Currently there is little known about the status of H5N1 in Indonesia's Papua province apart from the three reported incidents at Manokwari, Timika and Jayapura (ProMED-mail, 2007). Our study highlights the value of offshore activities designed to enhance early detection of H5N1 in Australia's nearest neighbours, including surveillance in Indonesia and Papua New Guinea by the Northern Australia

Quarantine Strategy (<http://www.daff.gov.au/aqis/quarantine/naqs>) and of capacity building in the countries of the region through programmes such as AusAid's AI programme (<http://www.ausaid.gov.au/keyaid/avian.cfm>).

One other consideration is the possibility that HPAI may persist in the Australian environment through on-going infection of native waterfowl. If this happened, the potential exists for the virus to spread throughout Australia. However, given a narrow corridor of entry through Cape York, it is still likely that the waterfowl populations on the Atherton Tablelands would be one of the first groups infected.

The initial aim of this study was to identify the areas of highest risk in order to maximise the chance of early identification of H5N1 and rapid implementation of control measures to control the spread of the disease. Targeting surveillance can help make the best use of limited resources and maximise the chances of detecting the disease. Our study demonstrates that both wild waterfowl and poultry farms in North Queensland, particularly those on the Atherton Tableland, should be included in any surveillance programme for HPAI.

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