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Identifying areas of Australia at risk of H5N1 avian influenza infection from exposure to migratory birds: a spatial analysis

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Abstract. Since 2003, highly pathogenic avian influenza (HPAI) due to H5N1 virus has been reported from both domestic poultry and wild birds in 60 countries resulting in the direct death or slaughter of over 250,000,000 birds. The potential exists for HPAI to spread to Australia via migratory shorebirds returning from Asia with the most likely pathway of introduction into commercial poultry flocks involving the transfer of HPAI from migrating shorebirds to native waterfowl species that subsequently interact with poultry on low security poultry farms. 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. This study compared the distributions of migratory shorebirds and native waterfowl to identify six regions where the likelihood of exotic HPAI incursion and establishment in native waterfowl is highest. Analysis of bird banding records showed that native waterfowl did not move further than 10 km during the spring breeding season when migratory shorebirds arrived in Australia. Therefore, poultry farms within 10 km of significant shorebird habitat in these six regions of highest comparative risk were identified. The final analysis showed that the estimated risk to Australia is low with only two poultry farms, one at Broome and one at Carnarvon, located in the regions of highest risk.

Keywords: spatial analysis, H5N1 virus avian influenza, migratory birds 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 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 250,000,000 birds (FAO, 2007). Migratory birds, predominantly of the family Anatidae, have been implicated in the spread of HPAI from the eastern part of Asia to Russia, Europe and Africa although debate still continues over the relative importance of migratory birds and movement of poultry. In Australia, the importation of live poultry is not permitted without comprehensive quarantine precautions and thus the entry of H5N1 HPAI into Australia through the movement of poultry or poultry products is unlikely.

Gilbert et al. (2006) examined the spread of H5N1 HPAI from Russia and Kazakhstan to the Black Sea basin and concluded that the spread is consistent with the hypothesis that birds of the Anatidae family having seeded the virus along their autumn migration routes. In Australia, birds belonging to this family are not migratory (Tracey et al., 2004) and therefore unable to introduce HPAI from Asia. Various strains of avian influenza have

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also been isolated from several species of migratory shorebirds (family: Charidriidae), including some that migrate annually from Asia to Australia (Tracey et al., 2004). These migratory birds return to Australia each year during the August-October period (Beaumont et al., 2006) and, during their time in Australia, share habitat with species of native waterfowl from which avian influenza has been isolated (Gosper, 1989; Kingsford and Auld, 2005). This sharing of environmental niches provides the opportunity for the transfer of avian influenza (AI) from migratory birds (Charidriidae) to native waterfowl (Anatidae).

The transfer of AI from Charidriidae to Anatidae increases the potential risk to the poultry industry. McClintock et al. (1997) observed 32 species of birds in the vicinity of the poultry sheds on the University of Queensland Veterinary Science Farm. None of the Charidriidae species, from which AI has been isolated, were observed. However, five species of Anatidae, namely (i) plumed whistling-duck, (ii) Pacific black duck, (iii) grey teal, (iv) chestnut teal, and (v) the Australian wood duck, were observed. Subsequent testing of birds caught in the vicinity of two poultry farms revealed that 37% of the ducks tested (75 in total) returned either positive or suspect results possibly indicating antibodies to AI. These observations support the hypothesis that HPAI could be introduced to Australian commercial poultry through native Anatidae species acting as an intermediate link in the pathway of HPAI spread between migratory shorebirds and commercial poultry.

Early detection of an incursion of exotic HPAI will rely upon an effective and efficient surveillance programme. To be efficient, the surveillance system should be risk-based so as to target resources to those areas and sectors of the industry at highest risk of exposure. This paper describes the construction of a spatial model to determine a risk ranking for the introduction of exotic HPAI into the poultry farming regions of Australia based on the probability of introduction through migratory Charidriidae species.

Material and methods

Data sets

Spatial data sets for the location of RAMSAR wetlands, significant shorebird areas and the Register of Important Wetland Areas were provided by the ERIN unit of the Commonwealth Department of Environment and Water Resources. 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 within the Commonwealth Department of Environment and Water Resources. Aerial photographs were sourced from Google Earth (http://earth.google.com/).

Data for the density of poultry farms was obtained from an unpublished study commissioned by the Office of the Chief Veterinary Officer in 2005 (Scott P, personal communication). 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

A review of the literature identified 25 species of Australian birds from which AI has been isolated (Table 1). Seven of these species regularly migrate between Asia and Australia: ruddy turnstone (*Arenaria interpres*), red knot (*Calidris canutus),* red-necked stint (*Calidris ruficollis*), common tern (*Sterna hirundo*), sooty tern (*Sterna fuscata*), bar-tailed godwit (*Limosa lapponica*) and sharp-tailed sandpiper (*Calidris acuminata*) (Tracey et al., 2004). The spring distribution of these species was used in our quantitative model because the migratory shorebirds return from Asia in the spring and are most likely to be shedding AI virus in the period immediately after contracting the virus in Asia. The spring distribution is also the species' widest distribution within Australia (Barrett et al., 2003).

Table 1. List of Australian bird species from which AI have been isolated (positive/examined).

Species	References					
	Downie et al., 1977	MacKenzie et al., 1984	Peroulis and O'Riley, 2004	Tracey et al., 2004	Warner et al., 2006	eWHIS, 2006
Plumed whistling-duck (*Dendrocygna eytoni*)				Present		
Gray teal duck (*Anas gibberifrons*)		3/115	Present	Present	7/154	
Chestnut teal duck (*Anas castanea*)					19/204	
Spotbill duck (*Anas poecilorhyncha*)		12/233				
Pacific black duck (*Anas superciliosa*)		12/211	Present	Present	1/70	
Australasian shoveler (*Anas rhynchotis*)					3/14	
Northern shoveler (*Anas clypeata*)				Present		
Northern pintail (*Anas acuta*)				Present		
Garganey (*Anas querquedula*)				Present		
Wood duck (*Chenonetta jubata*)			Present		2/96	
Australian shelduck (*Tadorna tadorna*)		3/74				
Pink ear duck (*Malacorhynchus membranaceus*)					5/144	
Eurasian coot (*Fulica atra*)		1/14				
Sooty tern (*Sterna fuscata*)		1/294		Present		
Common tern (*Sterna hirundo*)				Present		
Lesser noddy tern (*Anous stolidus*)		1/254				
Red knot (*Calidris canutus*)				Present		
Red-necked stint (*Calidris ruficollis*)				Present	2/667	5/14
Bar-tailed godwit (*Limosa lapponica*)					1/248	
Black swan (*Cygnus atratus*)					3/18	
Sharp-tailed sandpiper (*Calidris acuminata*)						5/97
Wedge-tailed shearwater (*Puffinus pacificus*)	2/289	3/561		Present		
Great cormorant (*Phalacrocorax carbo*)				Present		
Glossy ibis (*Plegadis falcinellus*)				Present		
Ruddy turnstone (*Arenaria interpres*)				Present		

Of the 25 species of Australian birds from which AI has been isolated, 13 species have been reported as resident on, or visiting, various freshwater bodies in eastern Australia, including farm dams (Table 2). 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*). Aerial surveys of wetland birds in eastern Australia confirmed that, of waterfowl species from which AI has been isolated, these four species particularly the grey teal and the Eurasian coot are the most regularly observed (Porter et al., 2006).

Movement of waterfowl species

The distance travelled by native waterfowl species during the spring season was calculated by examining banding-recapture data for the four species of interest. Analysis was restricted to those samples where the bird was recaptured within 30 days of banding. A maximum limit of 10 km travelled was

Table 2. List of Australian bird species from which AI has been isolated that have also been recorded on bodies of freshwater in Australia.

Species	References						
	Frith, 1959	Briggs, 1977	Whyte, 1981	Broome and Jarman, 1983	Woodall, 1985	Ambrose and Fazio, 1989	Leach, 1994
Location	Southwest NSW	New England (birds/dam)	Dangars Lagoon (birds/dam)	Namoi Valley (birds/ha)	Brisbane Region (birds/ observer)	New England (maximum population)	South-east Queensland (birds/dam)
Plumed whistling-duck (*Dendrocygna eytoni*)		-	-	1.22-32.20	3.7	-	0.17
Gray teal duck (*Anas gibberifrons*)	Regular	0-470	38-114	1.88-11.48	9.8	700	3.52
Pacific black duck (*Anas superciliosa*)	Regular	30-420	32-73	0.08-3.39	22.1	790	5.03
Australasian shoveler (*Anas rhynchotis*)	Regular	2-4	1-15	0.00-0.23	0.002	97	0.04
Pink ear duck (*Malacorhynchus membranaceus*)	Regular	-	<1	0.01-0.15	0.4	-	0.15
Chestnut teal duck (*Anas castanea*)	Regular	-	<1	-	1.7	-	-
Wood duck (*Chenonetta jubata*)	Regular	-	-	-	-	-	-
Australian shelduck (*Tadorna tadorna*)	-	-	-	-	0.001	-	-
Black swan (*Cygnus atratus*)	Regular	0-190	2-24	0.06-0.90	6.5	23	0.02
Eurasian coot (*Fulica atra*)	-	0-220	412-813	0.49-14.10	20.0	-	3.47
Sharp-tailed sandpiper (*Calidris acuminata*)	-	-	-	0.01-0.02	-	-	-
Great cormorant (*Phalacrocorax carbo*)			3-7	0.02-0.03	2.9		
Glossy ibis (*Plegadis falcinellus*)				0.00-0.13	0.6		0.005

consistent with the data examined and was confirmed by expert opinion (Kingsford R, personal communication).

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 migratory shorebird abundance used was the sum of the individual species abundance calculated for the seven shorebird species of interest. Estimates of waterfowl density were calculated in the same way using the four waterfowl species of interest listed above.

Mapping studies were completed using MapInfo version 8.5 (MapInfo Corp., Troy, New York) and Google Earth. The spatial analysis was dependent on the resolution of the available data. A grid of 1° latitude by 1° longitude was used because the data from Birds Australia data were supplied on that scale. The risk analysis was based on the method of Thomas et al. (2004) as follows. A 1° grid covering the area between longitudes 110 and 155 E and latitudes 10 and 45 S was overlaid over a map of Australia. The comparative risk of introduction of HPAI into each grid cell was calculated as the overall migratory shorebird abundance adjusted to a linear scale from 0 (no species of interest ever observed) to 9 (highest observed abundance). The combined abundance of the four native waterfowl species was similarly scaled and the comparative risk of establishment of HPAI within each grid cell was calculated as the product of the abundance of the migratory shorebirds and the abundance of the native waterfowl. The calculated risk of establishment of HPAI for each grid square was assigned to one of five ranges (nil, rare, low, medium or high). The score for the upper value of the nil risk range was arbitrarily set as 0.1. Grid cells with the highest calculated risk were then examined individually. Recorded shorebird areas were mapped and a 10 km buffer around the areas created to represent the areas over which local populations of waterfowl would be expected to range. Poultry farms falling within the 10 km buffer were considered to be at risk of exposure to HPAI.

Results

Risk of introduction of HPAI through migratory shorebirds

The 1° grid used in our analysis contained 1,575 individual grid squares and bird survey data was available for 789 of those squares. Of the remaining squares, 744 contained only ocean and 42 were in remote regions of central Australia at least 120 km from the nearest poultry farm. The combined abundance of the seven species of shorebirds is shown in Figure 1. The areas of highest abundance, and thus of highest comparative risk, tended to be around the coastline, particularly in the north and north-west.

Risk of establishment of HPAI in native waterfowl

A map of the combined abundance data for the four species of native waterfowl is shown in Figure 2. The native waterfowl are more evenly distributed across Australia with only the surveys from the driest areas of central Australia not reporting the presence of waterfowl. After combination of the abundance data for the migratory shorebirds with that for the native waterfowl, a map showing the calculated risk of establishment of HPAI in native waterfowl populations was obtained (Fig. 3). There were no regions of high risk establishment of HPAI identified, one region of medium risk in the vicinity of Broome in the Kimberley region of Western Australia and five areas of low risk in the vicinities of:

(i) Port Macdonnell in South Australia;
(ii) the eastern end of the Great Australian Bight;
(iii) Carnarvon in Western Australia;
(iv) West of Karratha in Western Australia; and
(v) Julia Creek in Western Queensland.

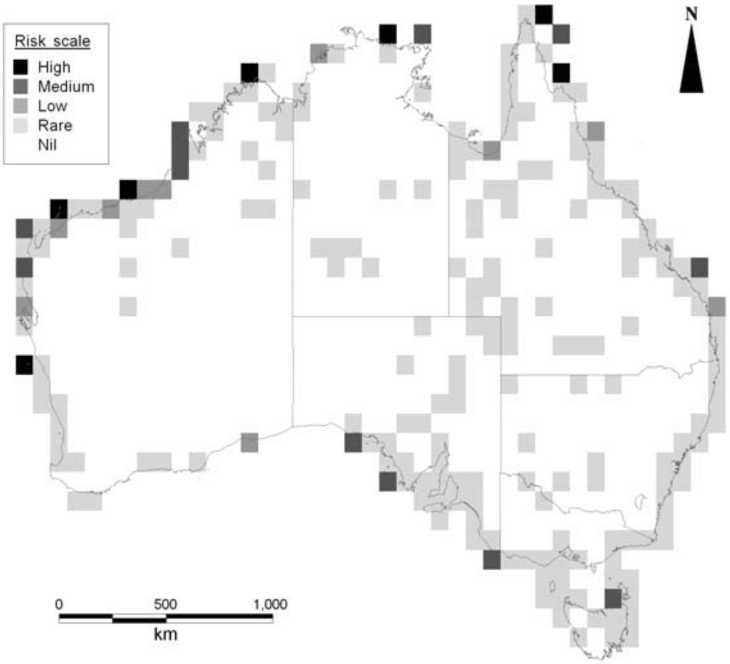

Fig. 1. Map showing the risk of entry of H5N1 HPAI into Australia (relative abundance of migratory shorebirds).

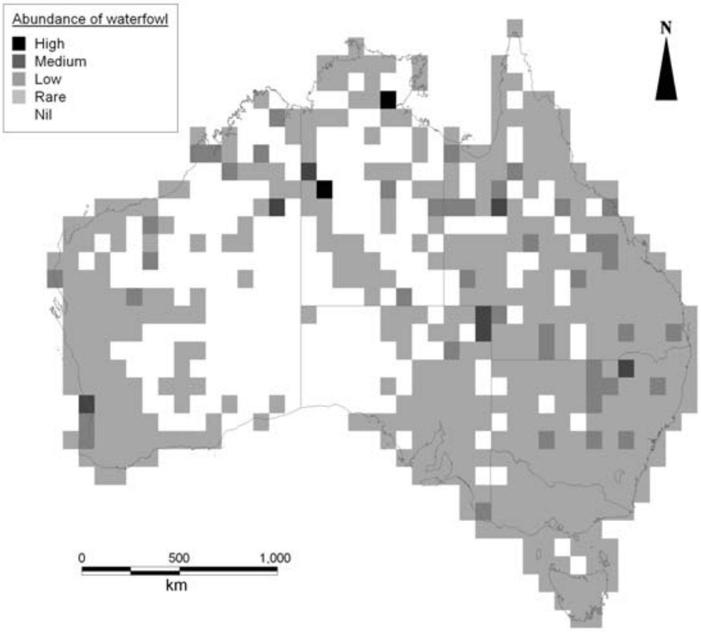

Fig. 2. Map showing the relative abundance in Australia of native waterfowl.

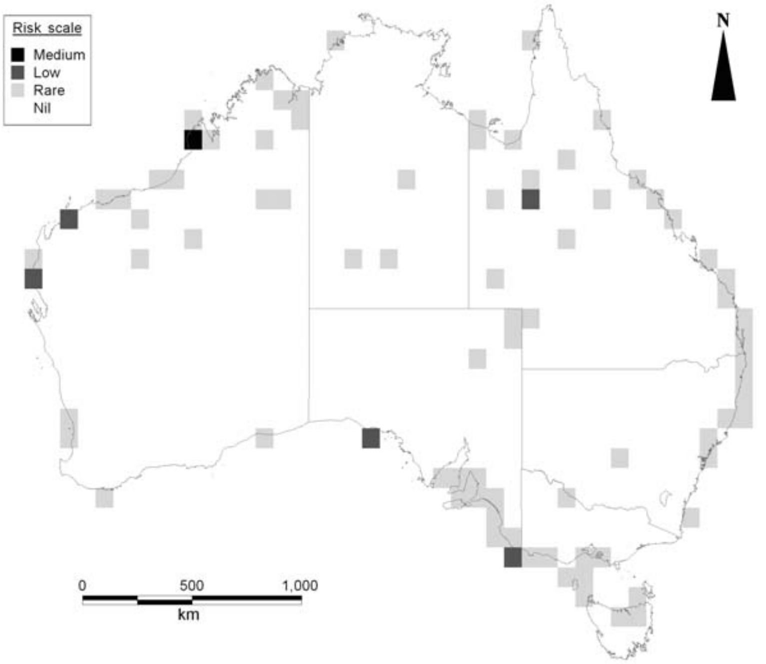

Fig. 3. Map showing the risk of establishment of H5N1 HPAI, for regions of Australia (transfer of HPAI from migratory shorebirds to native waterfowl).

Risk of spread of HPAI to the poultry industry

Initially, the risk of spread of HPAI to commercial poultry was calculated by including the density of poultry farms as a third risk factor (Fig. 4). This result indicates that there is little if any risk to Australian commercial poultry farms from HPAI. However, this method ignores the large size of the individual grid squares (over 14,000 km^2) and the clustering of both bird populations and poultry farms within each grid square. It also ignores the sedentary nature of the native waterfowl during spring. Therefore, the proximity of waterfowl habitat to poultry farms is a critical parameter.

Banding-recapture records from the Australian Bat and Bird Banding Scheme showed that over 95% of 351 Anatids recaptured within 30 days of initial banding in the September-December period were captured within 2 km of the original banding site (Fig. 5). Based on these findings, a buffer of 10 km was used to identify farms at risk from proximity to areas where migratory shorebirds and native waterfowl are known to interact.

Each of the six individual areas identified as medium or low comparative risk in the determination of the risk of establishment of HPAI in native waterfowl was examined separately. A 10 km buffer was established around known shorebird areas in these regions and poultry farms falling within this buffer were identified. Only two poultry farms, those at Broome and Carnarvon were located in these six regions of higher comparative risk and were also within 10 km of a significant shorebird area (Fig. 6).

Discussion

In the absence of data on infection prevalence, a predictive model using surrogate risk factors can be used to identify regions of higher ranked risk of infection. This study demonstrates that the risk of introduction of H5N1 HPAI through migratory shorebirds is low and that only a very few poultry

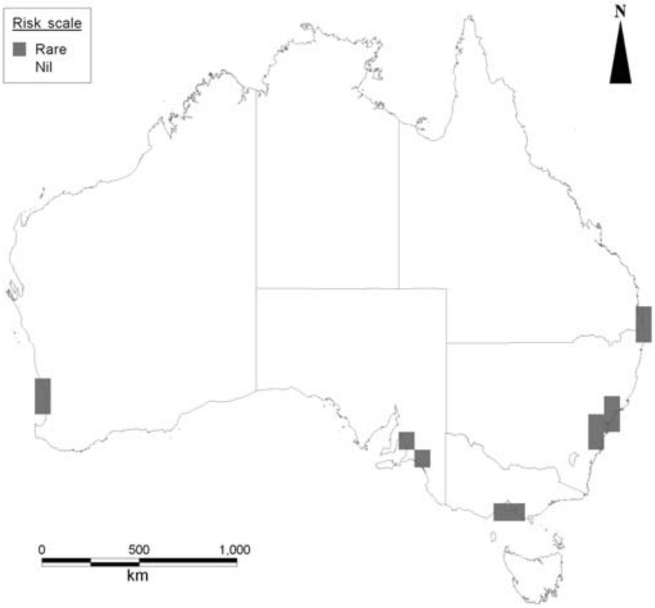

Fig. 4. Map showing the risk of spread of H5N1 HPAI into the Australian poultry industry.

farms are located in areas of the highest comparative risk. This finding is consistent with the fact that H5N1 HPAI has been circulating throughout Asia since 1996 and has not been detected in Australia despite the annual migration of hundreds of thousands of birds. The calculated risk of HPAI introduction may be further mitigated by a number of factors that this study has not included.

First, the bird species implicated in the westward spread of HPAI from Asia to Europe and Africa are primarily those of the family Anatidae. In contrast, the model presented here relies on introduction of HPAI into Australia through birds of the family Charadriidae. Studies have shown that Charadriidae appear to shed lower quantities of AI virus than Anatidae (Perkins and Swayne, 2001, 2002a,b) and therefore they may present a lower risk for introduction of HPAI.

Second, laughing gulls (*Larus atricilla*) artificially infected with H5N1 HPAI only shed virus for seven days after infection (Perkins and Swayne, 2002b). The shortest time recorded of the migratory journey from Australia to Asia is 7 days by a great knot and 11 days by a bar-tailed godwit (ABBBS data). This would suggest that any birds infected in Asia at the time of their migration would be unlikely to be shedding virus by the time they arrive in Australia. The journey of an infected bird may even be delayed in commencing and take longer than uninfected birds. Van Gils et al. (2007) found that Bewick's

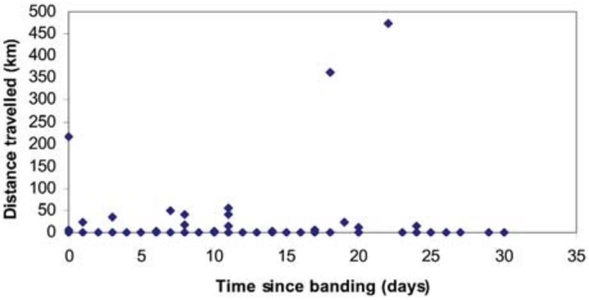

Fig. 5. Distance between banding and recapture sites for 351 individuals of Anatidae species banded between September and December.

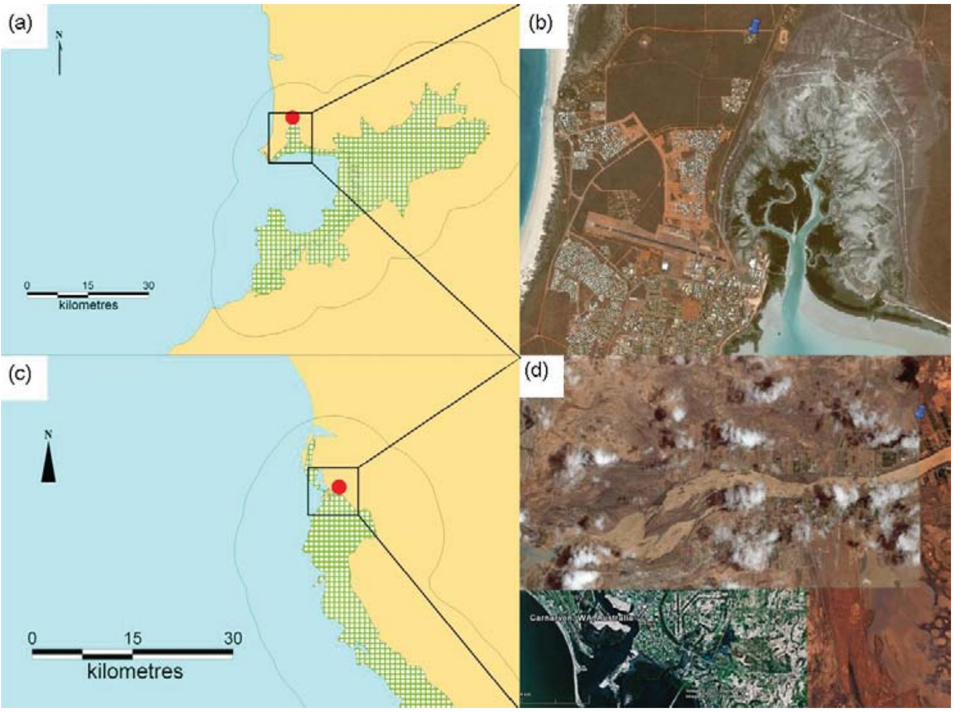

Fig. 6. Maps of Broome (a) and Carnarvon (c) showing the proximity of poultry farms (•) to bird habitat (hatching); (b) and (d) aerial photographs showing exact locations of each poultry farm (📌).

swans naturally infected with LPAI virus experienced delayed migration, travelled shorter distances and fed at reduced rates. This suggests that there is only a low probability that birds actively infected even with a low pathogenicity virus will transport the virus long distances.

Third, the overall risk to an individual farm is a combination of the infection pressure, as estimated in the current study, 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).

Fourth, one of the initial aims of this study was to identify areas of highest risk to maximise the efficacy of surveillance programmes. The study suggests that the two farms at Broome and Carnarvon should be included in any surveillance programme for HPAI. Beyond identification of these two farms, the data arising from the bird banding studies was also instructive in identifying the short range of travel for Anatidae during the breeding season. This sedentary nature actually works in favour of preventing spread by restricting any infected birds to one area during the time when there is a large population of naïve young birds susceptible to infection entering the population. This finding also suggests that farms within close proximity to water bodies that host Anatidae would be at a higher risk and this is consistent with previous outbreaks of HPAI in Australia where affected farms have had unprotected water supplies sourced from surface water and/or significant populations of wild Anatidae in the area (Westbury, 1998).

A consideration of the data used in this study reveals a potential for observer bias due to unequal levels of observer activity across the study area. With the Birds Australia data, the number of surveys conducted in each region of the grid varied from one to 2,611. The possibility exists that in areas where very few surveys have been completed, the bird species of interest may have been absent at the time of the survey but present at other times. However, within each grid square containing poultry farms (the grid squares of interest), a minimum of 13 surveys had been conducted during spring. This should be sufficient surveys to identify birds that are present on a regular basis. If the species is not present on a regular basis, then it is unlikely to present a significant risk. In addition, the patterns of distribution of bird species indicated by the Birds Australia data is broadly similar to the distribution patterns reported for the same species by the Australian Bat and Bird Banding Scheme.

Observer bias is also a potential problem with the bird banding and recapture data. If, for example, a bird bander is operating in a particular area, he/she is far more likely to make short term recoveries at that site than anywhere else. However, we attempted to address this issue by also seeking advice on the daily distance travelled by Anatidae from an expert in the field. The advice of this expert was consistent with the observed banding data.

This analysis suggests that there is a very low risk of introduction of H5N1 AI into Australian poultry via migratory shorebirds introducing the virus from Asia. This conclusion is consistent with the finding that all strains of AI isolated within Australia have been Australasian strains and that to date no Asian-type strains have ever been isolated within Australia. Notwithstanding these findings it is prudent that poultry producers continue to ensure that they maintain a high level of biosecurity, including preventing access to their shed by wild birds and treating drinking water derived from surface water sources.

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