







Potential for spread of HPAI H5N1 by wildfowl: dispersal range and rate determined from a large-scale satellite telemetry

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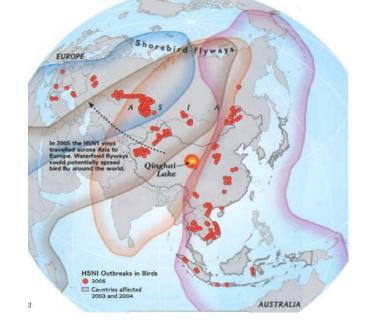




Context

- ✓ Rapid spread of HPAI H5N1 over Asia, Europe and Africa in 2005-2006
- ✓ Concurrent reports of mortality events in some migratory wildfowl
- ✓ Wildfowl are the primary reservoir of AI viruses

- → suspected role in long-distance spread of HPAI H5N1 virus
- → potential range and rate of long-distance dispersal of these viruses by wildfowl?







Potential for spread of HPAI H5N1 virus by wildfowl

Consistent findings from several experimental infection studies of wildfowl*:

- → asymptomatic HPAI H5N1 virus shedding in wildfowl for several days
- → potential for virus dispersion as they move?

Capacity for rapid long-distance movements within the time frame of virus shedding?

Probability for timing of infection to coincide with timing of longdistance movements?



^{*}Brown et al. 2006; Brown et al. 2007; Brown et al. 2008; Kalthoff et al. 2008; Keawcharoen et al. 2008; Kwon et al. 2010

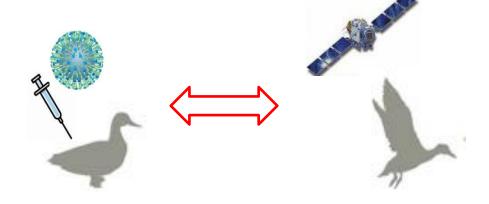
Evaluation of the dispersive potential of HPAI H5N1 by wildfowl

<u>Difficulty of a direct investigation:</u>

- ✓ tracking a known viremic free-living bird in the process of migration?
- ✓ releasing experimentally-infected birds?

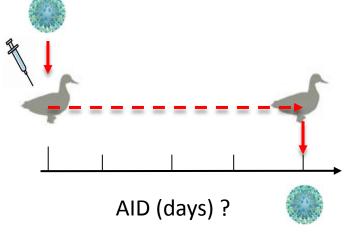
Indirect approach:

Combining experimental exposure and satellite telemetry based data

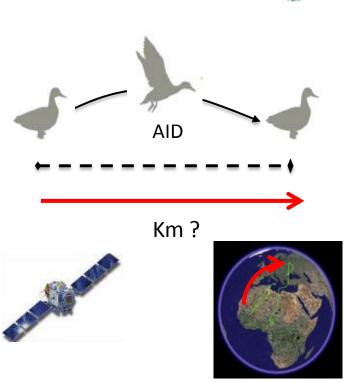


Methodology

Step 1: Experimentally-infected wildfowl→ Asymptomatic Infection Duration (AID)?



Step 2: Maximum distances covered by satellitetracked birds during timeframes of asymptomatic infection?

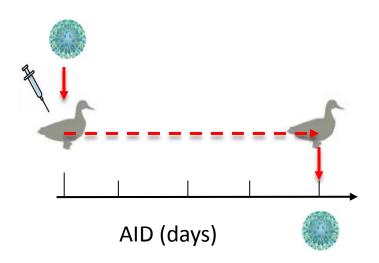


Step 1: Review of experimental infection studies of wildfowl with HPAI H5N1

Only wild species of duck, geese, swans:

→ 18 species, 135 birds*

Only Qinghai lineage viruses (clade 2.2)*



^{*}Brown et al. 2006; Brown et al. 2007; Brown et al. 2008; Kalthoff et al. 2008; Keawcharoen et al. 2008; Kwon et al. 2010

Step 1: Review of experimental infection studies of wildfowl with HPAI H5N1

Species*	No.	Age (months)	Treatment group†	Strains‡	Dose§	Viral excretion			Clinical response**				AID††	
						Infect %‡‡	Onset dpi	Duration days	Onset dpi	Sick/ Total	Dead/ Total	MDT dpi	days	R
Asymptomatic														
North. pintail	3	2.5-4	In	WS/Mg/05	6_{a}	100	1	1-2		0/3	0/3		2.5 (2-3)	1
Comm. teal	3	2.5-4	In	WS/Mg/05	6_{a}	100	1	2		0/3	0/3		3 (3-3)	1
	8	8-11	In	Tk/Tk/05	$4_{\rm b}$	38	1	1-5		0/8	0/8		3.5 (2-6)	5
Eur. wigeon	8	8-11	In	Tk/Tk/05	4 _b	50	1	1-2		0/8	0/8		2.5 (2-3)	5
Mallard	8	8-11	In	Tk/Tk/05	4 _b	100	1	1-4		0/8	0/8		4 (2-5)	5
	3	3	In/Ct	Ck/Kr/06	6_{a}	100	1	2-3		0/3	0/3		3.5 (3-4)	6
Gadwall	8	8-11	In	Tk/Tk/05	4 _b	88	1	1-6		0/8	0/8		4 (2-7)	5
Redhead	3	2.5-4	In	WS/Mg/05	6_a	100	1	1–4		0/3	0/3		3.5 (2-5)	1
Symptomatic														
Wood duck	3	2.5-4	In	WS/Mg/05	6_{a}	100	1	4-6	5	2/3	2/3	7.5	5.5 (5-6)	1
	20	3-4	In	WS/Mg/05	$1.5-6_{a}$	95	2	2-4	NA	18/20	18/20	5.5	5 (4-6)	2
Mandarin duck	3	2	In/Ct	Ck/Kr/06	6_a	100	1	5–6	4	1/3	1/3	5	6 (4–7)	6
Eur. pochard	7	8-11	In	Tk/Tk/05	$4_{\rm b}$	100	1	2-5	3–6	4/7	1/7	4	3.5 (3-6)	5
Tufted duck	7	8-11	In	Tk/Tk/05	4 _b	86	1	2-4	3.5	7/7	3/7	4	3.5 (1-4)	5
Ruddy sheld.	3	3	In/Ct	Ck/Kr/06	6_a	100	4	6	5	3/3	3/3	7	5 (5-5)	6
Bar-hd. goose	5	3	In/Ct	WS/Mg/05	6_a	100	1-2	5-8	3-7	5/5	2/5	6.5	4.5 (3-7)	3
Cack. goose	4	3	In/Ct	WS/Mg/05	6_a	100	1-3	4-6	3–7	4/4	3/4	6	5 (3–7)	3
Greylag goose	3	1.75	In/Ct	Ck/Kr/06	6_a	67	1	5–6	5–6	3/3	0/3		5.5 (5-6)	6
Black swan	5	1-1.5	In/Ct	WS/Mg/05	6_a	100	1	2-3	1-2	5/5	5/5	2.5	1.5 (1-2)	3
Trump. swan	5	1-1.5	In/Ct	WS/Mg/05	6_a	100	1	4-6	2	5/5	5/5	4.5	2 (2-2)	3
Whooper swan	4	1-1.5	In/Ct	WS/Mg/05	6_a	100	1	4-6	2-4	4/4	4/4	4	3 (2-4)	3
Mute swan	5	1-1.5	In/Ct	WS/Mg/05	6_a	100	1	3–7	5–7	5/5	5/5	6.5	6 (5–7)	3
	14	12-48	In/Ct/Px	WS/Gm/06	$4-6_{a}$	100	1-3	6	4–8	12/14	11/14	9	5.5 (3-8)	4
	3	1.75	In/Ct	Ck/Kr/06	6_a	100	1	3-5	3-4	3/3	3/3	4.5	3.5 (3-4)	6
Total 18 sp.	135	1-48	3	4	1.5-6	90	1-4	1-8	1-8	0-100	0-100	2.5-9	4 (1-8)	

Step 1: Review of experimental infection studies of wildfowl with HPAI H5N1

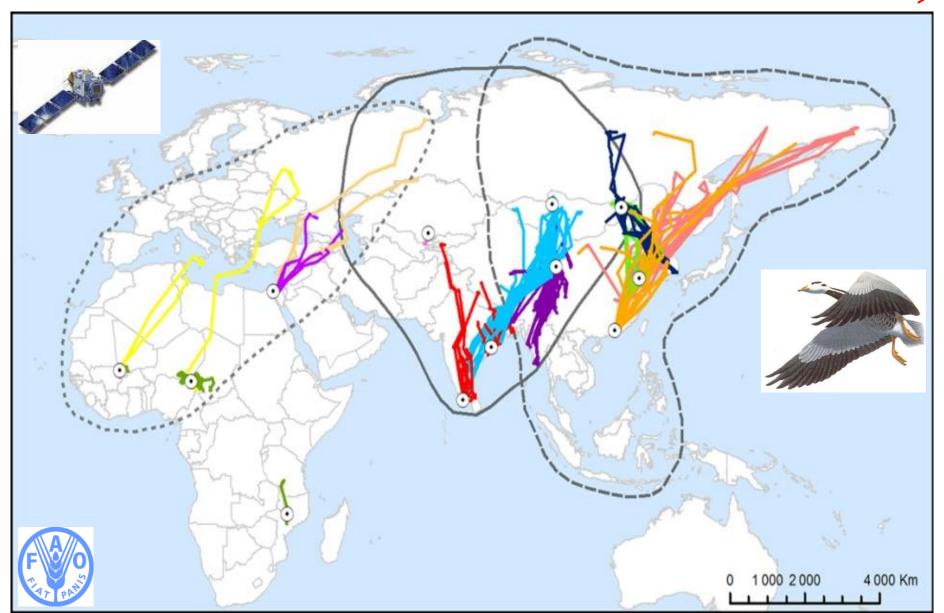
- ➤ All species were receptive to infection
- > Species heterogeneity in morbidity and mortality rates
- > A period of asymptomatic infection in all infected birds:
 - ✓ without any apparent clinical signs (6 species)
 - ✓ before the onset of detectable clinical signs (12 species)

→ Mean AID (min-max) = 4 days (1-8 days)

Species*	No.	Age (months)	Treatment group†	Strains‡	Dose§ log ₁₀	Viral excretion			Clinical response**				AID††	
						Infect %‡‡	Onset dpi	Duration days	Onset dpi	Sick/ Total	Dead/ Total	MDT dpi	days	R
Asymptomatic														_
North, pintail	3	2-5-4	In	WS/Mg/05	6.	100	1	1-2		0/3	0/3		2-5 (2-3)	1
Comm. teal	3	2-5-4	In	WS/Mg/05	6,	100	1	2		0/3	0/3		3 (3-3)	1
	8	8-11	In	Tk/Tk/05	45	38	1	1-5		0/8	0/8		3-5 (2-6)	5
Eur, wigeon	8	8-11	In	Tk/Tk/05	4,	50	1	1-2		0.78	0.78		2-5 (2-3)	5
Mallard	8	8-11	In	Tk/Tk/05	4.	100	1	1-4		0/8	0.78		4 (2-5)	5
	3	3	In/Ct	Ck/Kr/06	6,	100	1	2-3		0/3	0/3		3-5 (3-4)	6
Gadwall	8	8-11	In	Tk/Tk/05	40	88	1	1-6		0.78	0/8		4 (2-7)	5
Redhead	3	2-5-4	In	WS/Mg/05	6,	100	1	1-4		0/3	0/3		3-5 (2-5)	1
Symptomatic														
Wood duck	3	2-5-4	In	WS/Mg/05	6,	100	1	4-6	5	2/3	2/3	7-5	5-5 (5-6)	1
	20	3-4	In	WS/Mg/05	1.5-6,	95	2	2-4	NA	18/20	18/20	5.5	5 (4-6)	2
Mandarin duck	3	2	In/Ct	Ck/Kr/06	6.	100	1	5-6	4	1/3	1/3	5	6 (4-7)	6
Eur. pochard	7	8-11	In.	Tk/Tk/05	46	100	1	2-5	3-6	4/7	1/7	4	3-5 (3-6)	5
Tufted duck	7	8-11	In	Tk/Tk/05	4,	86	1	2-4	3-5	7/7	3/7	4	3-5 (1-4)	5
Ruddy sheld.	3	3	In/Ct	Ck/Kr/06	6.	100	4	6	5	3/3	3/3	7	5 (5-5)	6
Bar-hd. goose	5	3	In/Ct	WS/Mg/05	6,	100	1-2	5-8	3-7	5/5	2/5	6-5	45 (3-7)	3
Cack, goose	4	3	In/Ct	WS/Mg/05	6.	100	1-3	4-6	3-7	4/4	3/4	6	5 (3-7)	3
Greylag goose	3	1.75	In/Ct	Ck/Kr/06	6,	67	1	5-6	5-6	3/3	0/3		5-5 (5-6)	6
Black swan	5	1-1-5	In/Ct	WS/Mg/05	6,	100	1	2-3	1-2	5/5	5/5	2.5	1-5 (1-2)	3
Trump, swan	5	1-1-5	In/Ct	WS/Mg/05	6.	100	1	4.6	2	5/5	5/5	4.5	2 (2-2)	3
Whooper swan	4	1-1-5	In/Ct	WS/Mg/05	6,	100	1	4-6	2-4	4/4	4/4	4	3 (2-4)	3
Mute swan	5	1-1-5	In/Ct	WS/Mg/05	6.	100	1	3-7	5-7	5/5	5/5	6-5	6 (5-7)	3
	14	12-48	In/Ct/Px	WS/Gm/06	4-6,	100	1-3	6	4-8	12/14	11/14	9	5-5 (3-8)	4
	3	1.75	In/Ct	Ck/Kr/06	6,	100	1	3-5	3-4	3/3	3/3	4.5	3-5 (3-4)	6
Total 18 sp.	135	1-48	3	4	1-5-6	90	1-4	1-8	1-8	0-100	0-100	2-5-9	4 (1-8)	

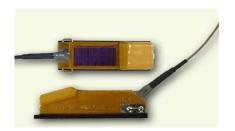
Step 2: Movements of satellite-tracked birds during AID timeframes





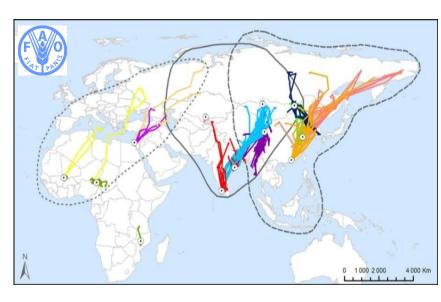
A large-scale satellite telemetry data set

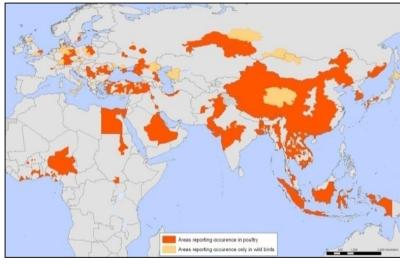
- ✓ International collaboration programme FAO
- √ 228 birds 19 species (ducks, geese, swans)
- ✓ over the main H5N1-affected regions
- ✓ some of the main candidate-vector species (mallard, bar-headed goose, whooper swan)







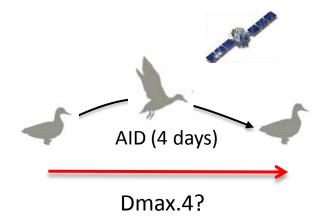




Method: estimation of the maximum potential dispersal range

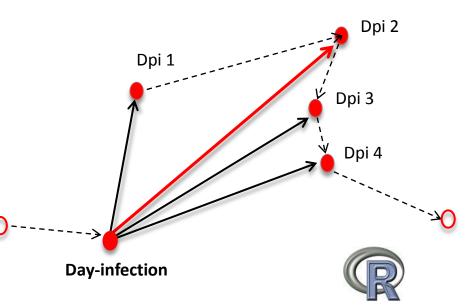
Maximum distance covered by a bird during every 4 day-timeframes (Dmax.4) ?

- ✓ calculated for each bird
- ✓ for each day, considering each location as a site
 and time of potential infection



Day post-infection (Dpi)

- → iterative process: sliding 4-day timeframe over the entire monitoring period
- ✓ for AID of 1, 4, 8 days
 - → Dmax.1, Dmax.4, Dmax.8



Results: maximum potential dispersal range

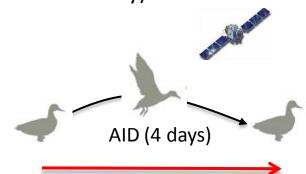
Mean maximum distances covered by migratory birds (satellite telemetry):

✓ Spring and fall migrations:

~300 to 1700 km* within the mean AID (4 days)

up to 2900 km in some individuals

~100 to 1000 km* within min. AID (1 day)



✓ Outside migration or in non-migratory birds:

Dmax4 <350 km*

→ Migratory wildfowl have the potential to disperse HPAI H5N1 virus over extensive distances

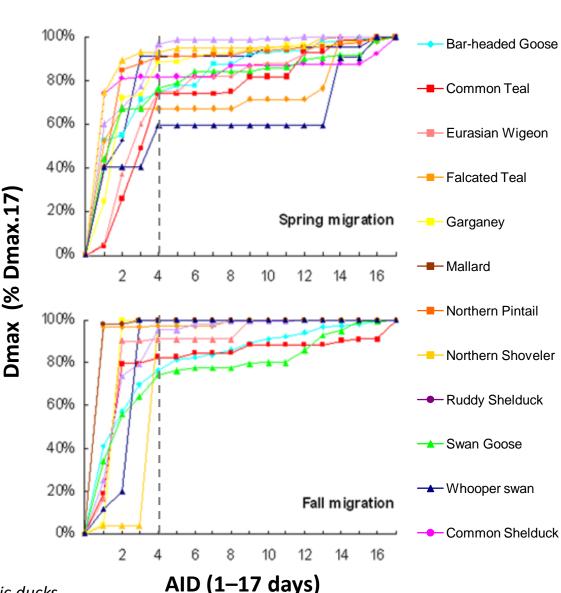


Results: maximum potential dispersal range

Dmax.4 ≈ Dmax.8

→ Plot Dmax ~ AID (1-17 days*)

- → A threshold in the maximum dispersal distance:
- ≥75 % of maximum distance in 17 days performed in1-4 days
- no consecutive long-distance movements





Results: maximum potential dispersal range

Migration is sequential rather than continuous:

- ✓ completed in a few rapid long-distance flights
- ✓ interrupted by staging period > period of infection and shedding.
- → Birds are unlikely to spread virus over several consecutive but interrupted long-distance movements
- → Potential for virus dispersal limited to a single long-distance movement (<2000 km)

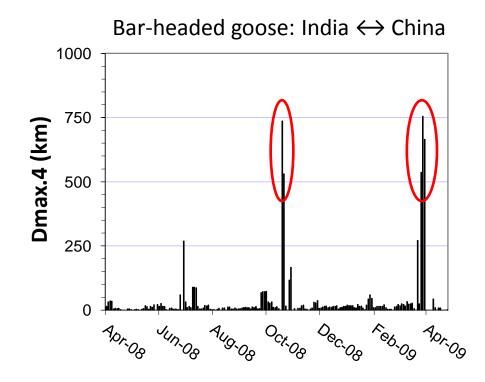
Estimation of the potential dispersal rate

Proportion of days/year when an infection could result in a long-distance dispersal of HPAI H5N1 virus in the following days?

 \rightarrow % of days/year with Dmax.4 \geq 500 km?



- → a low individual dispersal rate:
- ✓ potential for virus dispersal >500 km
 = 5 to 15 days per year*
- ✓ restricted to the migration periods



^{*}on average per species

Conclusion

1. A potential for dispersal of HPAI H5N1 viruses over extensive distances:

- ✓ All experimentally infected species showed a period of asymptomatic infection
- ✓ Long-distance movements were performed within timeframes compatible with the duration of asymptomatic infection
- ✓ Impact of infection on migration performance? migration-mediated immune changes?

Conclusion

2. A low individual likelihood for long-distance virus dispersal:

- ✓ Asymptomatic infection must coincide with timing of long-distance movements
 - → Few long-distance movements per individual per year
- √ Migration is interrupted by staging periods > period of infection
 - → Intercontinental virus dispersion likely require a relay transmission
 - → Role of stop-over/congregation sites

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Potential spread of highly pathogenic avian influenza H5N1 by wildfowl: dispersal ranges and rates determined from large-scale satellite telemetry

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