

Replacement and predominance by clade 2.3.2.1 H5N1 influenza viruses in southern China

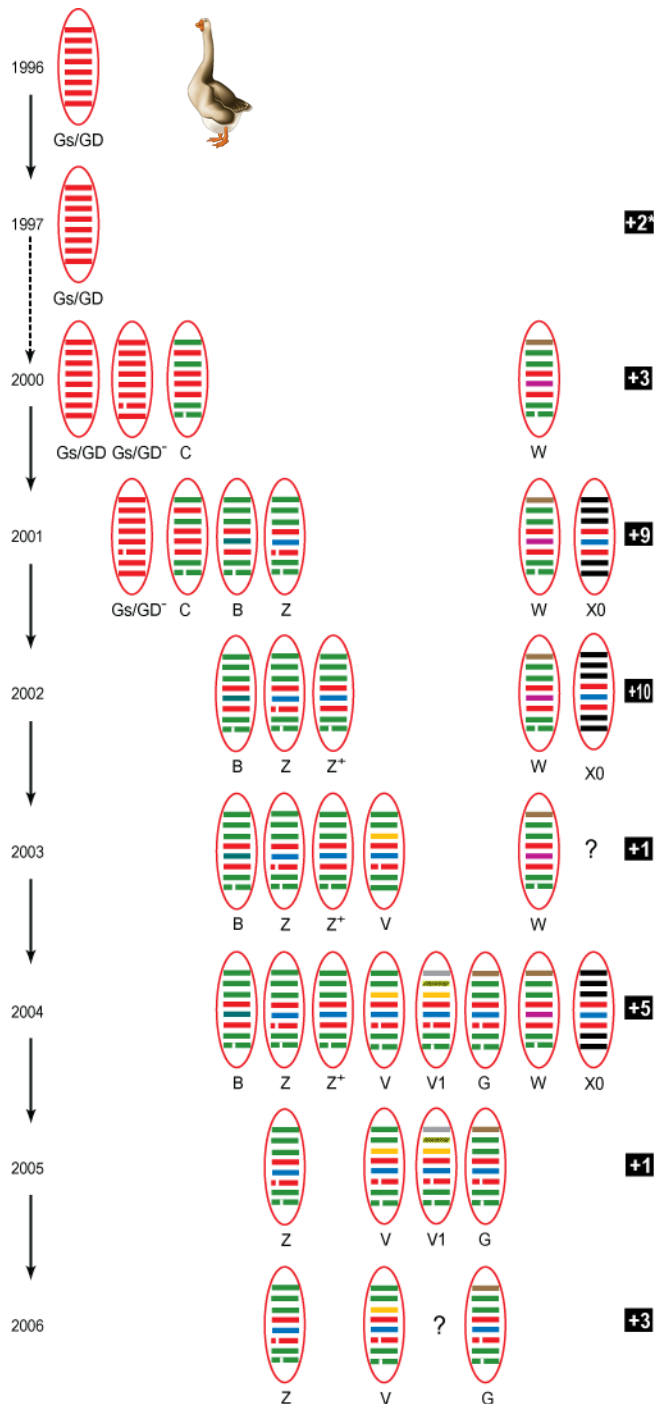
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Surveillance Network in Southern China





Emerged from aquatic waterfowl (Duan et al. 2007 JV)

Interspecies transmission and reassortment (Guan et al. 2002 Virol)

Emergence of multiple genotypes (Guan et al. 2002 PNAS)

Dominance of genotype Z (Li et al. 2004 Nature)

Wave 1 (Li et al. 2004 Nature)

Multiple sublineages (Chen et al. 2006 PNAS)

Wave 2 (Chen et al. 2005 Nature)
Wave 3 (Smith et al. 2006 PNAS)

H5N1 virus

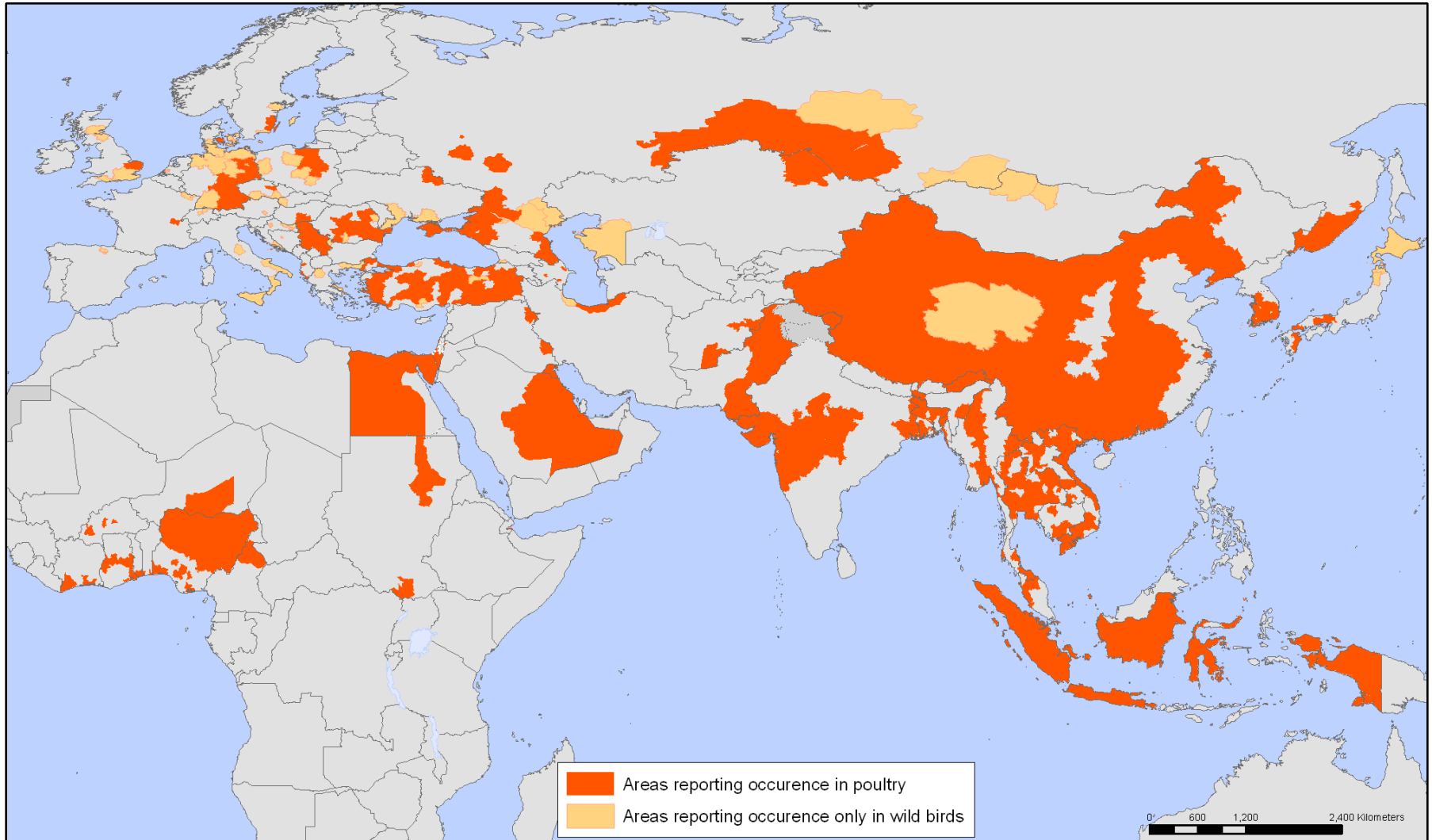
H5N1 influenza virus activity and genotype distribution in China, 1996–2006

Year	Province (Genotype)
1996	Guangdong (Gs/GD)
1997	Guangdong (Gs/GD, HK/97-like), Hubei (Hubei-like)
1999	Guangdong (Gs/GD)
2000	Fujian (F), Guangdong (Gs/GD, Gs/GD ⁻ , C, T1), Guangxi (ND*), Jiangsu (ND), Zhejiang (Gs/GD1, W)
2001	Fujian (B, W), Guangdong (Gs/GD ⁻ , A-E, X0, X10, W1, B2, T3), Guangxi (B, B1, Z), Hebei (Hubei-like), Henan (ND), Jiangsu (ND), Shanghai (Gs/GD ⁻ , C, X0), Zhejiang (ND).
2002	Fujian (X7), Guangdong (X0-X3, X9, B, B3, Z, Z+,W), Guangxi (X6), Hebei (X8), Henan (ND), Hubei (ND), Hunan (Z), Jiangsu (B), Jilin (ND), Shanghai (X4, X5, Z), Yunnan (Z), Zhejiang (ND).
2003	Beijing (V), Fujian (B, W), Guangdong (Z, V), Guangxi (ND), Henan (ND), Hubei (V), Hunan (Z), Jiangsu (ND), Jilin (T4, Z), Shandong (ND), Yunnan (Z)
2004	Anhui (ND), Fujian (Z+), Guangdong (Z, V, V1, Hubei-like), Guangxi (Z, W, G, W2, Hubei-like), Henan (Z, Hubei-like), Hubei (Z), Hunan (Z, V), Jiangsu (ND), Jilin (T5), Shandong (B, X0, Hubei-like), Shanghai (Z), Yunnan (Z)
2005	Anhui (ND), Fujian (Z, V), Guangdong (Z, V, V1), Guangxi (Z, V, G), Guizhou (Z, G, V), Hebei (V), Hubei (ND), Hunan (Z, V, G, T6), Jiangsu (ND), Jiangxi (Z, V), Qinghai (Z), Yunnan (Z, V, G), Zhejiang (ND).
2006	Fujian (V), Guangdong (Z, V, G, V2, V4), Guangxi (V, G), Guizhou (G, V, V3), Hunan (Z, V), Jiangsu (ND), Qinghai (Z), Shanxi (V), Yunnan (V), Zhejiang (V)

HPAI H5N1 affected regions

Areas reporting confirmed occurrence of H5N1 avian influenza in poultry and wild birds since 2003

Status as of 03 October 2008
Latest available update

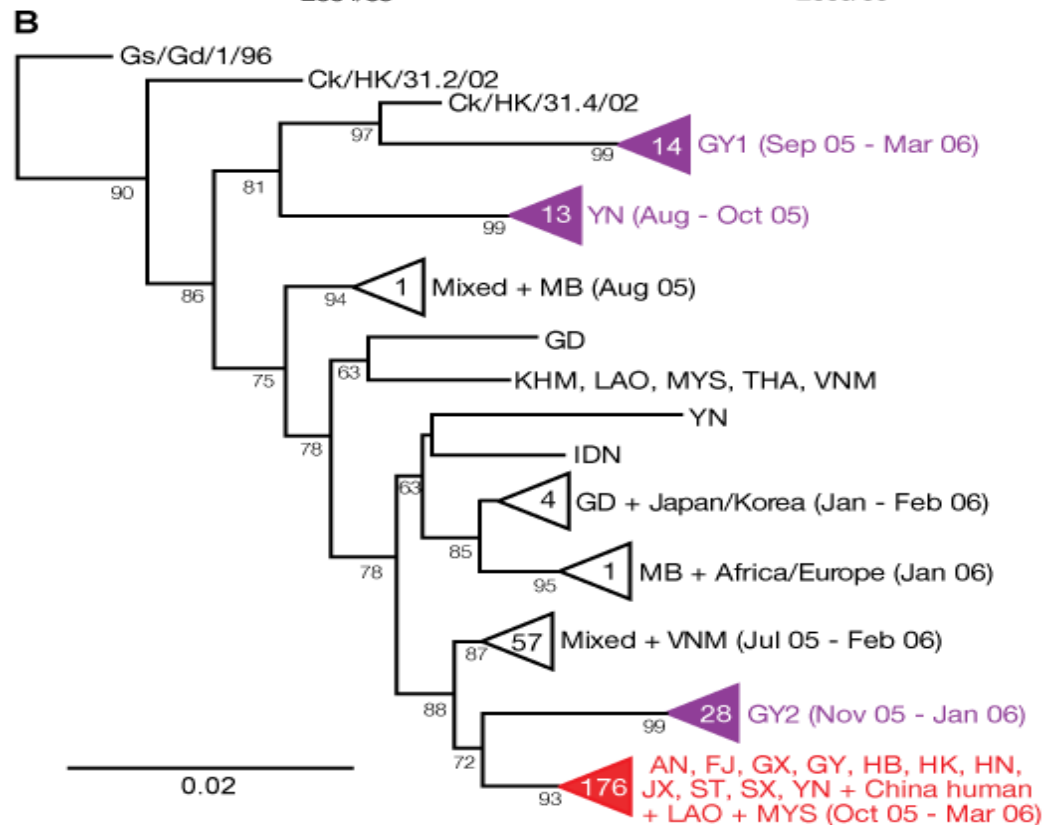
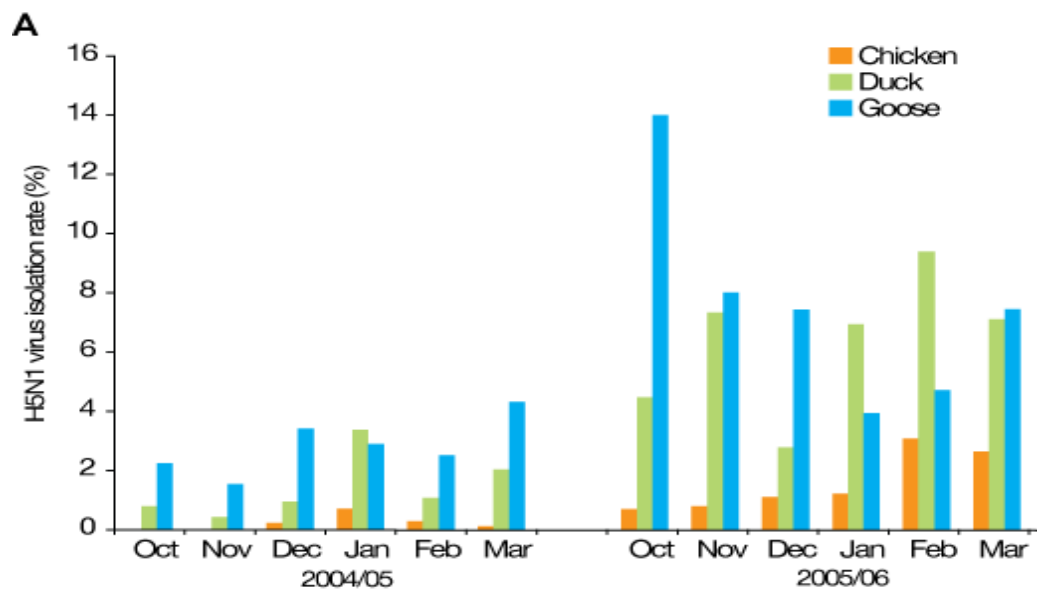


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The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted lines on maps represent approximate border lines for which there may not yet be full agreement.

Data Source: World Organisation for Animal Health (OIE) and national governments

Map Production: Public Health Information and Geographic Information Systems (GIS), World Health Organization



Summary of H5N1 isolates in poultry, wild birds and human from southern China during 2007 to 2012

Year	No. of positive isolates	No. of positive isolates belong to		Reference
		Clade 2.3.2.1	Clade 2.3.4	
2007	22	9	13	(X)
2008	20	6	14	(X)
2009	17	14	3	-
2010	3(1)	3(1)	0	-
2011	12(1)	11(1)	1	-
2012	22(1)	22(1)	0	-
Total ¹	68	51(3)	17	-

Note: Number of isolates from human are in parentheses

Abbreviation: ¹ Total number of positive isolates from June 2008 to June 2012

Polymerase genes of clade 2.3.2.1 of H5N1

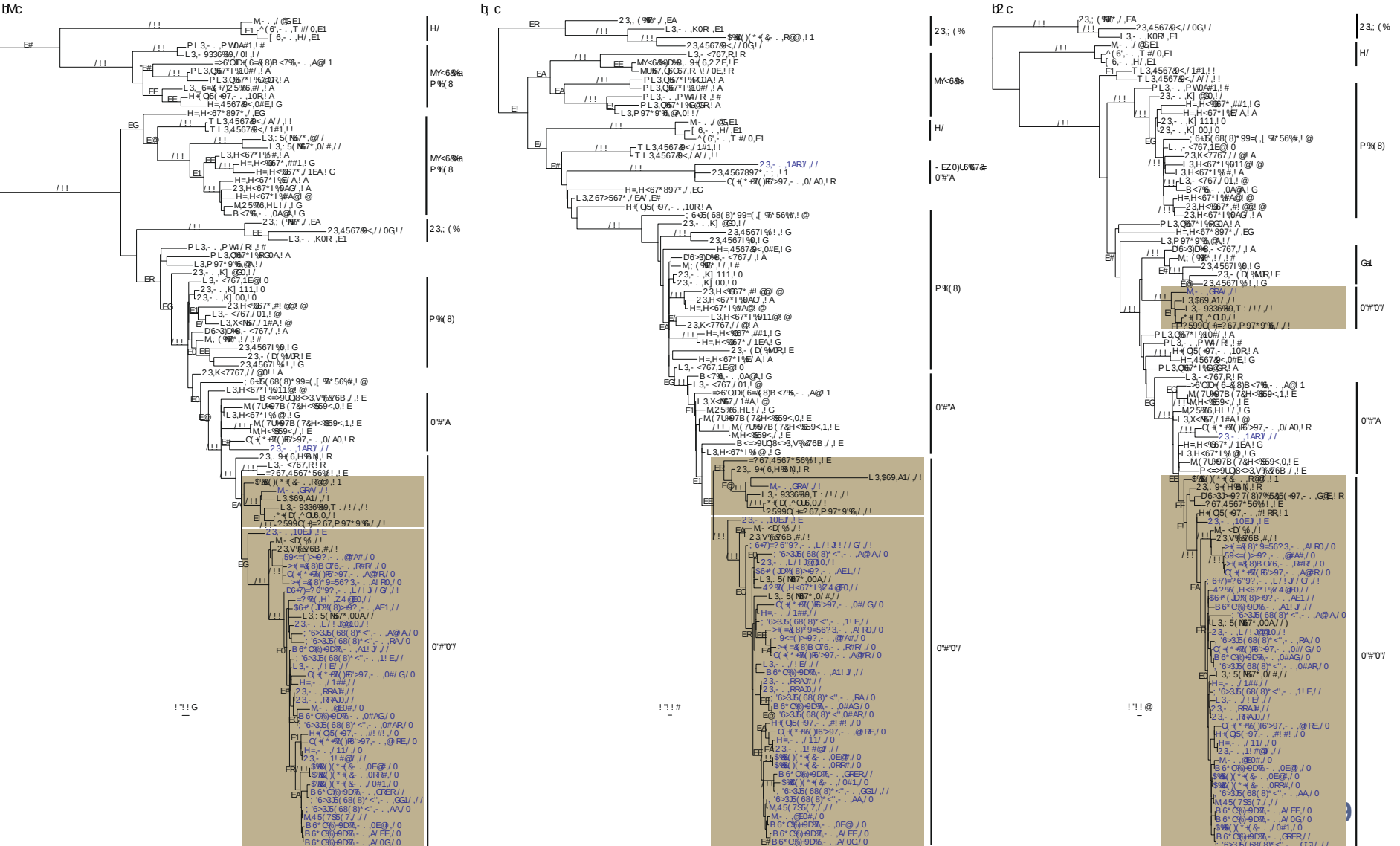
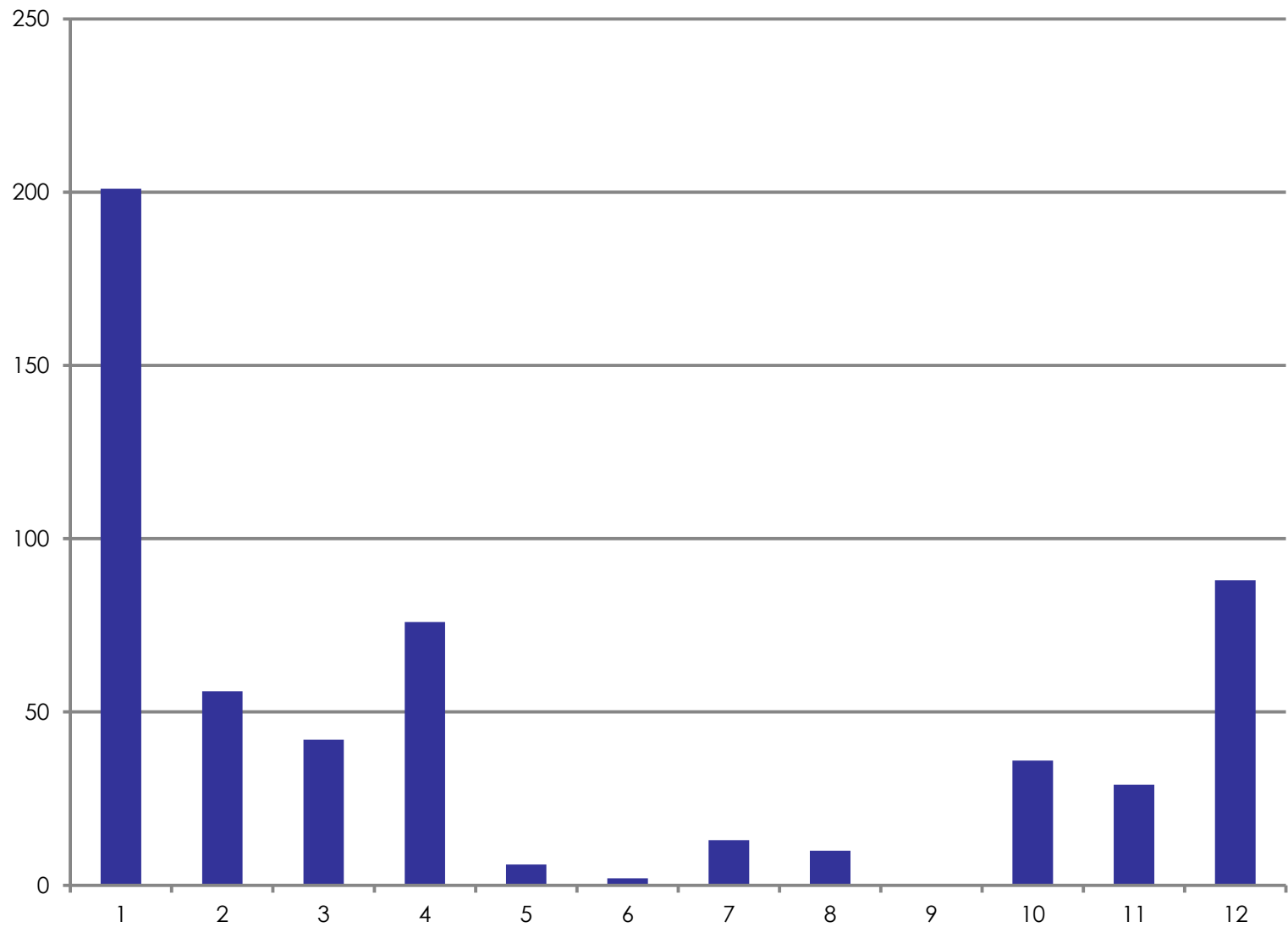


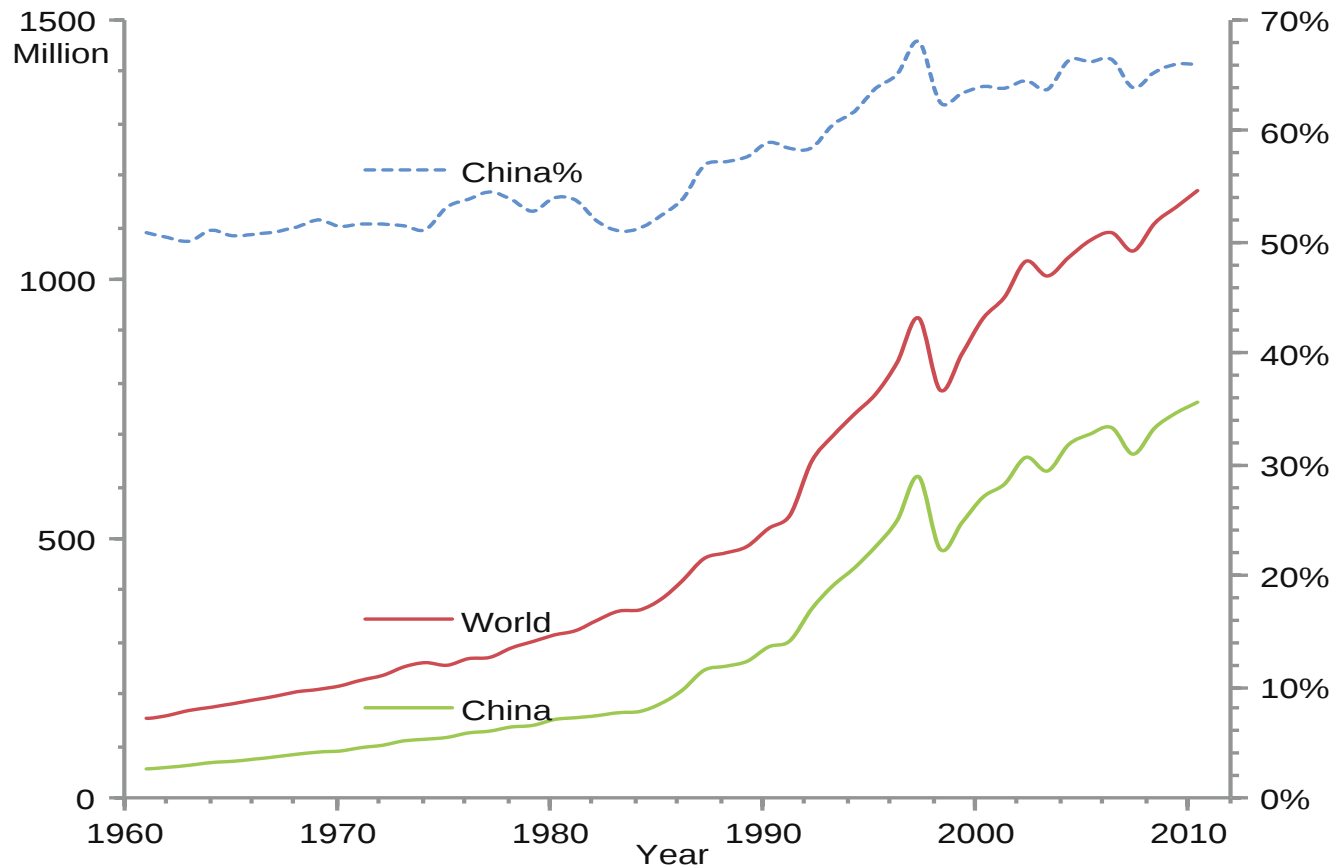
Table 3 Antigenic analysis of H5N1 influenza viruses by hemagglutinin inhibition test (HI) in southern China, during 2009-2012

Virus	Ferret antisera titers to†						
	Ck/HK/729.1/09 (clade 2.3.2.1)‡	Barn swallow/ HK/1161/10 (clade 2.3.2.1)	Ck/HK/5572/10 (clade 2.3.2.1)	A/HK/6841/10 (clade 2.3.2.1)	Black-headed gull/ HK/84/12 (clade 2.3.2.1)	Peregrine falcon/ HK/2142/08 (clade 2.3.4)	Muscovy duck/ Vietnam/1/09 (clade 2.3.4)
peregrine falcon/HK/2142/08	<40	<40	<40	40	<20	320*	40
Muscovy duck/Vietnam/1/09	<40	<40	<40	<40	<20	160	640
Ck/HK/729.1/09	1280	640	160	1280	40	320	80
Barn swallow/HK/1161/10	40	160	80	320	20	40	<40
Ck/HK/5572/10	<40	40	640	320	80	<40	<40
A/HK/6841/10	40	160	160	640	<20	40	<40
Black-headed gull/HK/84/12	<40	<40	160	80	40	<40	<40
Ck/Vietnam/3/10	640	160	80	640	20	160	<40
Large-billed crow/HK/497/11	40	80	320	320	40	80	<40
Dk/HK/1091/11	<40	80	160	320	40	<40	<40
Black-headed gull/HK/44/12	80	40	80	80	<20	<40	<40
Black-headed gull/HK/6671/11	160	40	80	160	<20	40	<40
A/Shenzhen/1/11	160	40	160	160	20	80	<40
Little egret/HK/1237/12	80	40	80	80	<20	40	<40
maggie robin/HK/6898/11	40	<40	80	40	<20	<40	<40
Ck/HK/7035.1/11	<40	40	160	160	40	<40	<40
Gs/HK/1771/12	<40	80	80	320	20	40	<40

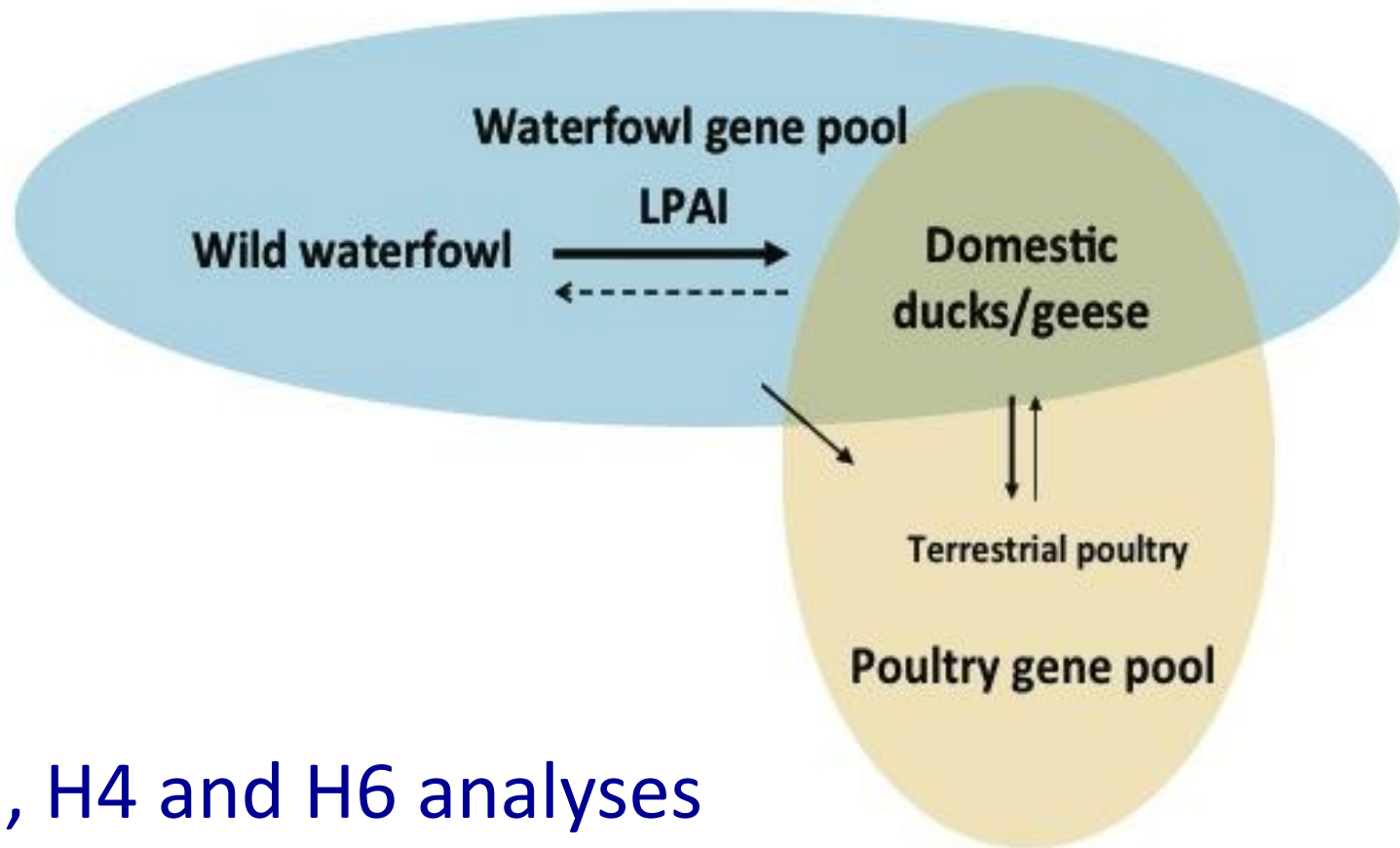
* Boldface underlined numbers indicate titers to prototype viruses; †Ferret antisera dilution started at 1:20; ‡clade designations according to WHO H5N1 nomenclature system



Domestic Duck Population

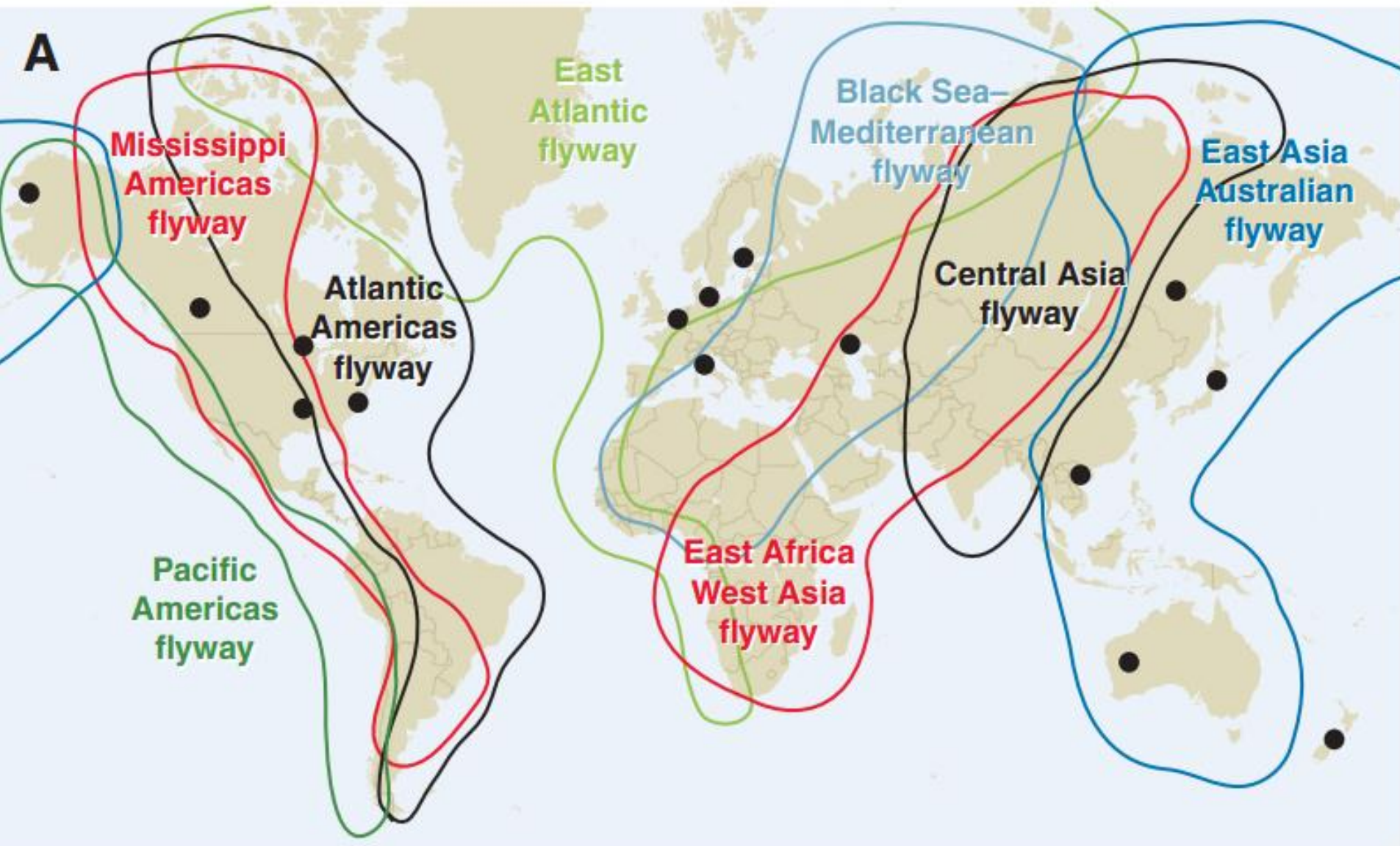


Interaction between domestic and migratory ducks



H3, H4 and H6 analyses

Migration flyway and Gene pool isolation



Summary

H5N1 HPAI viruses are still evolving and are endemic in southern China

Sporadic interspecies transmissions to humans continue to occur

Wild and migratory birds may be involved the spread of this virus lineage

Vaccination, domestic ducks and geese are key factors to facilitating its endemicity