

SUPPLEMENTARY MATERIAL

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I. Reassortment analysis of the replication complex from pre-1995 viruses

Pre-1995 data selection. Few older viruses have been sequenced, and rarely to full length. For these older viruses, we reduced the required length of sequence information to ~ 1000 nt per segment.

Reference tree for pre-1995 analysis (T1 = 1978–1985). As reassortment of the Eurasian lineage with the North American lineage is infrequent, ideally reference trees would contain at least two viruses from each lineage to allow intra-lineage reassortment detection. We could not achieve this goal for early viruses and sufficed with one virus from the Eurasian lineage and two from the North American lineage. Although analysis of reassortment within the Eurasian lineage is not possible at fine resolution with this reference tree, nevertheless a test virus can attach to a single virus or basally to multiple viruses, allowing identification of reassortment when bootstrap values are high. For these three taxa plus the outgroup, we inferred segment-specific reference trees and bootstrap values from 50 replicates by using PAUP* (Swofford, 1993) to maximize the likelihood of the data under the general reversible model of evolution with site-specific rates of variation. All four segments had the same topology, and all nodes had 99–100 % bootstrap support (Supplementary Fig. S1). The consistency of the segment-specific reference trees is not a strong test of reassortment because each tree contains only four sequences. However, the consistency does fit with the observation that reassortment between North American and Eurasian lineages is not common.

Test set for pre-1995 analysis (T2 = 1986–1994). Ten viruses (three from Eurasian and seven from North American lineages) from 1986 to 1994 had sufficient data to be testable. The ten viruses clustered into six clades (four North American and two Eurasian) with high bootstrap support; one virus from each clade was tested (Supplementary Table S2). In spite of the sparse reference trees, placement of the six test viruses on segment-specific trees had high confidence in most cases. Three of the six viruses were reassortants; no conclusion could be drawn about the other two viruses. There were no signs of relative coevolving segments.

Almost all bootstrap values involved in assessing the test viruses had values >80 %. The outgroup was independent of reassortment in all trees, indicating that the outgroup achieved its purpose of providing a reference point that was uninvolved with the reassortment events. The inability to draw conclusions about two of the viruses resulted from two trees losing topological certainty when the candidate reassortant was added, and five bootstrap values being <70 %.

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II. Derivation of the likelihood function for estimation of ρ

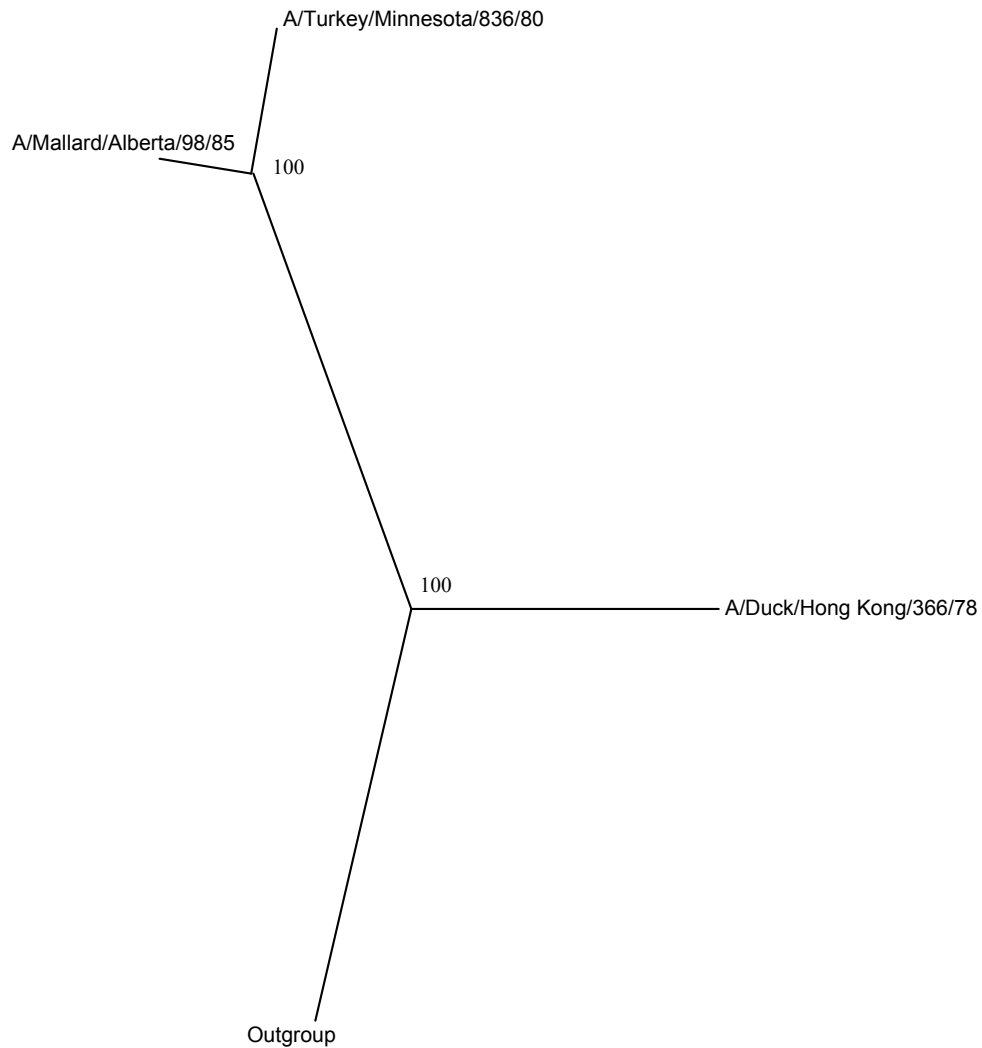
Because the longevity of a genotype, and not the number of isolates of a genotype, is most important in estimating the rate of reassortment, the dataset that we used to estimate ρ was that of Fig. 4. Based on section (i) of Methods and Results in the paper, we assumed that each segment of this complex reassorts independently of all other segments with annual probability $(1 - \rho)$. Under this model, when a novel genotype is created in year C , the probability that n out of its four segments have reassorted by time $C + R$ is Binomial($4, \rho^R$) and is proportional to $\rho^{(4-n)R} (1 - \rho^R)^n$ ($4 - n$ segments belong to the ancestral lineage for R years, while n have reassorted within the R years). To obtain a likelihood function for ρ , we assumed that that all reassortant viruses were generated independently of each other, clearly a simplification but one that led to conservative estimates of ρ ; accounting for ancestral relationships among viruses means that the same number of events must occur in a shorter total branch length of the phylogeny.

The likelihood function based on the viruses in Fig. 4 is

$$\begin{aligned} & \rho^{4(1996-R_{0G})} * \rho^{4(1997-R_{0G})} * \rho^{4(2000-R_{0G})} * \rho^{4(2001-R_{0G})} * \binom{4}{1} \rho^{3(2001-R_{0G})} (1 - \rho^{(2001-R_{0G})}) * \binom{4}{2} \rho^{2(2002-R_{0G})} [(1 - \rho^{(2002-R_{0G})})]^2 * \\ & \binom{4}{2} \rho^{2(2001-R_{0G})} [(1 - \rho^{(2001-R_{0G})})]^2 * \binom{4}{2} \rho^{2(2002-R_{0G})} [(1 - \rho^{(2002-R_{0G})})]^2 * \binom{4}{2} \rho^{2(2003-R_{0G})} [(1 - \rho^{(2003-R_{0G})})]^2 * \\ & \binom{4}{2} \rho^{2(2004-R_{0G})} [(1 - \rho^{(2004-R_{0G})})]^2 * \binom{4}{3} \rho^{(2001-R_{0G})} [(1 - \rho^{(2001-R_{0G})})]^3 * \binom{4}{3} \rho^{(2001-R_{0G})} [(1 - \rho^{(2001-R_{0G})})]^3 * \\ & \binom{4}{3} \rho^{(2002-R_{0G})} [(1 - \rho^{(2002-R_{0G})})]^3 * \binom{4}{3} \rho^{(2003-R_{0G})} [(1 - \rho^{(2003-R_{0G})})]^3 * \binom{4}{3} \rho^{(2004-R_{0G})} [(1 - \rho^{(2004-R_{0G})})]^3 * \\ & \binom{4}{3} \rho^{(2003-R_{0G})} [(1 - \rho^{(2003-R_{0G})})]^3 * \rho^{4(1995-R_{0O})} * \binom{4}{2} \rho^{2(2001-R_{0O})} [(1 - \rho^{(2001-R_{0O})})]^2 * \binom{4}{2} \rho^{2(2002-R_{0O})} [(1 - \rho^{(2002-R_{0O})})]^2 * \\ & \binom{4}{2} \rho^{2(2001-R_{0O})} [(1 - \rho^{(2001-R_{0O})})]^2 * \binom{4}{2} \rho^{2(2004-R_{0O})} [(1 - \rho^{(2004-R_{0O})})]^2 \end{aligned}$$

where R_{0G} (R_{0O}) is the most recent common ancestor of the lineage represented by A/goose/Guangdong/3/97 (A/ostrich/South Africa/9508103/95) (estimated to be 1991 and 1987, respectively). One term appears in this function for every genotype in Fig. 4, with the exception of A/SCK/HK/YU100/2002 and A/duck/Shanghai/35/2002. Both of these viruses had two 'Uncharacterized' segments, and their phylogenetic association could therefore not be determined with confidence. The probabilities of each genotype are multiplied together to obtain the likelihood of the observed genotype evolution.

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Supplementary Fig. S1. Reference tree from 1978–1985 viruses. Numbers at nodes are bootstrap measures of support for the subtree descending from the node.

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Supplementary Table S1. List of all viruses included in this study.

Strain	Serotype	Dataset*
A/Turkey/California/189/66	H9N2	1
A/Duck/Hong Kong/86/76	H9N2	1
A/Gull/Maryland/704/77	H13N6	1
A/Duck/Hong Kong/366/78	H9N2	2
A/Turkey/Minnesota/833/80	H4N2	2
A/Mallard/Alberta/98/85	H6N2	2
A/Mallard/Alberta/321/88	H9N2	3
A/Mallard/Alberta/17/91	H9N2	3
A/Quail/Hong Kong/AF157/92	H9N2	3, 4
A/Quail/Arkansas/29209-1/93	H9N2	3, 4
A/Chicken/Mexico/26654-1374/94	H5N2	3, 4M
A/Chicken/Hidalgo/26654-1368/94	H5N2	3R, 4R
A/Chicken/Beijing/1/94	H9N2	3R, 4
A/Chicken/Puebla/14585-622/94	H5N2	3R, 4R
A/Chicken/Hong Kong/739/94	H9N2	3, 4R
A/Chicken/Puebla/8623-607/94	H5N2	3R, 4
A/Duck/Germany/113/95	H9N2	4
A/Chicken/Queretaro/14588-19/95	H5N2	4R
A/Ostrich/South Africa/9508103/95	H9N2	4
A/Shorebird/Delaware/9/96	H9N2	4
A/Goose/Guangdong/1/96	H5N1	4R
A/Chicken/Korea/25232-96006/96	H9N2	4M
A/Quail/Shanghai/8/96	H9N2	4R
A/Chicken/Korea/38349- p96323/96	H9N2	4R
A/Chicken/Sichuan/5/97	H9N2	4
A/Pigeon/Hong Kong/Y233/97	H9N2	4
A/Parakeet/Chiba/1/97	H9N2	4R
A/Duck/Hong Kong/Y439/97	H9N2	4M
A/Chicken/Hong Kong/915/97	H5N1	4R
A/Goose/Guangdong/3/97	H5N1	4
A/Chicken/Guangdong/11/97	H9N2	4M
A/Chicken/Hong Kong/G23/97	H9N2	4R
A/Chicken/Shenzhen/9/97	H9N2	4R
A/Teal/Hong Kong/W312/97	H6N1	4R

Strain	Serotype	Dataset*
A/Chicken/Hong Kong/G9/97	H9N2	4R
A/Duck/Nanjing/1/97	H9N2	4R
A/Chicken/Hong Kong/786/97	H5N1	4R
A/Pheasant/Ireland/PV18/97	H9N2	4M
A/Quail/Hong Kong/G1/97	H9N2	4
A/Chicken/Heilongjiang/10/97	H9N2	4R
A/Duck/Hong Kong/y283/97	H5N1	4R
A/Duck/Hong Kong/p46/97	H5N1	4R
A/Chicken/Hong Kong/258/97	H5N1	4R
A/Duck/Hong Kong/Y280/97	H9N2	4M
A/Goose/Hong Kong/W355/97	H5N1	4R
A/Chicken/Hong Kong/728/97	H5N1	4R
A/Chicken/Shanghai/F/98	H9N2	4M
A/Chicken/Beijing/8/98	H9N2	4R
A/Parakeet/Narita/92A/98	H9N2	4R
A/Chicken/Hebei/4/98	H9N2	4R
A/Chicken/Germany/R45/98	H9N2	4M
A/Chicken/Ningxia/5/99	H9N2	4R
A/Chicken/Saudi Arabia/532/99	H9N2	4M
A/Duck/Guangxi/07/1999	H5N1	4R
A/Pheasant/Hong Kong/SH39/99	H6N1	4R
A/Chicken/Korea/99029/99	H9N2	4
A/Quail/Hong Kong/1721-20/99	H6N1	4R
A/Quail/Hong Kong/1721-30/99	H6N1	4R
A/Chicken/Shijiazhuang/2/99	H9N2	4R
A/Chicken/Pakistan/2/99	H9N2	4R
A/Chicken/Iran/11T/99	H9N2	4M
A/Chicken/Taiwan/7-5/99	H6N1	4M
A/Duck/Hong Kong/2986.1/2000	H5N1	4M
A/Duck/Zhejiang/11/2000	H5N1	4M
A/Chukka/Hong Kong/FY295/00	H6N1	4R
A/Duck/Fujian/19/2000	H5N1	4M
A/Goose/Hong Kong/ww26/2000	H5N1	4R
A/Chicken/Guangdong/10/00	H9N2	4R
A/Duck/Guangdong/12/2000	H5N1	4R

Strain	Serotype	Dataset*
A/Goose/Hong Kong/3014.8/2000	H5N1	4R
A/Duck/Guangdong/40/2000	H5N1	4M
A/Goose/Hong Kong/ww28/2000	H5N1	4R
A/Pheasant/Hong Kong/FY294/00	H6N1	4R
A/Quail/Hong Kong/SF550/00	H6N1	4R
A/Duck/Guangdong/07/2000	H5N1	4R
A/Duck/Zhejiang/52/2000	H5N1	4M
A/Quail/Hong Kong/SF595/00	H6N1	4R
A/Chicken/California/431/00	H6N2	4M
A/Chicken/California/465/00	H6N2	4R
A/Chicken/Hong Kong/YU562/01	H5N1	5R
A/Chicken/California/6643/01	H6N2	5R
A/Chicken/Hong Kong/NT873.3/01	H5N1	5
A/Duck/Shanghai/38/2001	H5N1	5
A/Chicken/Hong Kong/YU822.2/01	H5N1	5
A/Duck/Guangxi/35/2001	H5N1	5
A/Chicken/California/905/01	H6N2	5R
A/Duck/Guangxi/50/2001	H5N1	5R
A/Duck/Guangxi/22/2001	H5N1	5
A/Chicken/Hong Kong/FY150/01	H5N1	5
A/Duck/Guangdong/01/2001	H5N1	5R
A/Chicken/California/139/01	H6N2	5
A/Duck/Fujian/17/2001	H5N1	5R
A/Duck/Shanghai/08/2001	H5N1	5
A/Duck/Anyang/AVL-1/2001	H5N1	5
A/Pheasant/Hong Kong/FY155/01	H5N1	5
A/Duck/Shanghai/13/2001	H5N1	5R
A/Duck/NC/91347/01	H1N2	5
A/Duck/Guangxi/53/2002	H5N1	5
A/Duck/Fujian/01/2002	H5N1	5R
A/Duck/Shanghai/37/2002	H5N1	5
A/Duck/Guangdong/22/2002	H5N1	5
A/Chicken/Chile/176822/02	H7N3	5
A/Chicken/Hong Kong/YU777/02	H5N1	5
A/Gf/Hk/38/2002	H5N1	5R
A/Duck/Fujian/13/2002	H5N1	5
A/Duck/Shanghai/35/2002	H5N1	5

Strain	Serotype	Dataset*
A/Chicken/Chile/4957/02	H7N3	5R
A/Duck/Hong Kong/821/02	H5N1	5R
A/Chicken/Hong Kong/31.4/02	H5N1	5
A/SCK/HK/YU100/2002	H5N1	5
A/Ck/Indonesia/BL/2003	H5N1	5R
A/Avian/Netherlands/219/03	H7N7	5R
A/Chicken/Germany/R28/03	H7N7	5R
A/Chicken/Netherlands/1/03	H7N7	5
A/Duck/China/E319-2/03	H5N1	5R
A/Ck/Indonesia/PA/2003	H5N1	5R
A/Chicken/Korea/ES/03	H5N1	5R
A/Duck/Korea/ESD1/03	H5N1	5R
A/Egret/Hong Kong/757.2/03	H5N1	5R
A/Duck/Yokohama/aq10/2003	H5N1	5
A/Chicken/Guangdong/178/04	H5N1	5R
A/Ck/Viet Nam/C57/2004	H5N1	5R
A/Peregrine		
Falcon/HK/D0028/2004	H5N1	5R
A/Dk/Viet Nam/11/2004	H5N1	5R
A/Ck/Thailand/9.1/2004	H5N1	5R
A/Chicken/Guangdong/174/04	H5N1	5
A/Ck/Viet Nam/38/2004	H5N1	5R
A/Chicken/Ayutthaya/Thailand/CU-23/04	H5N1	5R
A/Bird/Thailand/3.1/2004	H5N1	5R
A/Dk/Indonesia/MS/2004	H5N1	5
A/Chicken/Guangdong/191/04	H5N1	5
A/Chicken/Oita/8/2004	H5N1	5R
A/Chicken/Yamaguchi/7/2004	H5N1	5R
A/Crow/Osaka/102/2004	H5N1	5R
A/Chicken/Kyoto/3/2004	H5N1	5R
A/Chicken/Vietnam/C58/04	H5N1	5R
A/Ck/Thailand/9.1/2004	H5N1	5R
A/Dk/Thailand/71.1/2004	H5N1	5R
A/duck/Guangdong/173/04	H5N1	5
A/Duck/Shandong/093/2004	H5N1	5
A/Ck/Viet Nam/35/2004	H5N1	5R

Strain	Serotype	Dataset*
A/Ck/Viet Nam/39/2004	H5N1	5R
A/Ck/Viet Nam/33/2004	H5N1	5R
A/Ck/Viet Nam/36/2004	H5N1	5R
A/Ck/Viet Nam/37/2004	H5N1	5R
A/Chicken/Hubei/489/2004	H5N1	5R

Strain	Serotype	Dataset*
A/Chicken/British Columbia/04	H7N3	5
A/Qa/Thailand/57/2004	H5N1	5R
A/Chicken/Hubei/327/2004	H5N1	5R
A/Chicken/Jilin/9/2004	H5N1	5

*Datasets:

- 1 Prior to 1978–1985 reference data
- 2 1978–1985 reference set
- 3 Candidate reassortants tested against 1978–1985 reference set
- 3R As 3, but not tested (not significantly diverged from a virus in 3)
- 4 1991–2000 reference set
- 4M Trimmed from 4 because attached at internal node with low bootstrap value
- 4R As 4, but not tested (not significantly diverged from a virus in 4)
- 5 Candidate reassortants from 2001–2004 tested against 1991–2000 reference set
- 5R As 5, but not tested (not significantly diverged from a virus in 5)

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Supplementary Table S2. Reassortment status of viruses from 1986–1994 tested against the 1978–1985 reference tree

Abbreviations: DkHK (A/Duck/Hong Kong/366/78); MallAlb (A/Mallard/Alberta/98/85); TkMN (A/Turkey/Minnesota/833/80); ND, not determined [either because it was not possible to infer a phylogeny or because the attachment of the candidate to the reference tree occurred with low (<70 %) bootstrap support].

Strain	Placement of candidate reassortant in segment-specific reference tree*			
	PB2	PB1	PA	NP
A/Mallard/Alberta/321/88	ND	ND	ND	ND
A/Mallard/Alberta/17/91	MallAlb	(MallAlb,TkMN)†	ND	MallAlb
A/Quail/Hong Kong/AF157/92	DkHK	DkHK	(MallAlb,TkMN)†	DkHK
A/Quail/Arkansas/29209-1/93	(MallAlb,TkMN)†	(MallAlb,TkMN)†	ND	MallAlb
A/Chicken/Mexico/26654-1374/94	MallAlb	(MallAlb,TkMN)†	(MallAlb,TkMN)†	ND
A/Chicken/Hong Kong/739/94	DkHK	DkHK	ND	DkHK

*When a single virus is named, then attachment occurs with high bootstrap support for being the nearest neighbour to that virus. When multiple viruses are named, then attachment occurs basal to those viruses.

†Candidate reassortant attaches to the reference tree basal to the viruses in parentheses, with bootstrap support >70% for this place of attachment ; details of topology of reference tree, including bootstrap values, are maintained.

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Supplementary Table S3. Reassortment status of viruses from the 1991–2000 reference set that were excluded from the 1991–2000 reference tree because of low bootstrap support at non-tip nodes for at least one segment

Abbreviations: GsGu (A/Goose/Guangdong/3/97); Ostr (A/Ostrich/South Africa/9508103/95); DkGer (A/Duck/Germany/1113/95); CkKor (A/Chicken/Korea/99029/99); Pg (A/Pigeon/Hong Kong/Y233/97); QuG1 (A/Quail/Hong Kong/G1/97); CkBeij (A/Chicken/Beijing/1/94); CkSich (A/Chicken/Sichuan/5/97); CkPueb (A/chicken/Puebla/8623-607/94); Shore (A/shorebird/Delaware/9/96); QuArk (A/quail/Arkansas/29209-1/93).

Strain	Placement of viruses in segment-specific reference tree*			
	PB2	PB1	PA	NP
A/Chicken/California/431/00	CkPueb	(CkPueb,Shore,QuArk)	CkPueb	(Shore,QuArk)
A/Chicken/Germany/R45/98	DkGer	Ostr	GsGu	Ostr
A/Chicken/Guangdong/11/97	CkBeij	CkBeij	CkBeij	Pg
A/Chicken/Iran/11T/99	DkGer	(DkGer,Ostr)	GsGu	Ostr
A/Chicken/Korea/25232-96006/96	CkKor	CkKor	CkKor	Pg
A/Chicken/Saudi Arabia/532/99	DkGer	(DkGer,Ostr)	(CkKor,GsGu,Ostr)	CkKor
A/Chicken/Shanghai/F/98	Ostr	GsGu	(QuG1,CkSich)	DkGer
A/Chicken/Taiwan/7-5/99	GsGu	Ostr	GsGu	CkKor
A/Duck/Fujian/19/2000	(Ostr,GsGu)	Ostr	(CkKor,GsGu,Ostr)	GsGu
A/Duck/Guangdong/40/2000	Ostr	GsGu	GsGu	(DkGer,Ostr,QuG1,CkKor,GsGu)
A/Duck/Hong Kong/2986.1/2000	Ostr	GsGu	(CkKor,GsGu,Ostr)	GsGu
A/Duck/Hong Kong/Y280/97	CkBeij	CkBeij	Pg	Pg
A/Duck/Hong Kong/Y439/97	GsGu	Basal to Eurasian	(CkKor,GsGu,Ostr)	Ostr
A/Duck/Zhejiang/11/2000	Ostr	GsGu	GsGu	GsGu
A/Duck/Zhejiang/52/2000	GsGu	GsGu	(CkKor,GsGu,Ostr)	Ostr
A/Pheasant/Ireland/PV18/97	DkGer	(DkGer,Ostr)	DkGer	Ostr

*When a single virus is named, attachment occurs with high bootstrap support for being the nearest neighbour to that virus. When multiple viruses are named, attachment occurs basal to those viruses.

Supplementary Table S4. Status of all reassortant viruses identified in this study

Strain	Subtype	Pattern*
A/Mallard/Alberta/321/88	H9N2	11
A/Mallard/Alberta/17/91	H9N2	12
A/Quail/Hong Kong/AF157/92	H9N2	3
A/Quail/Arkansas/29209-1/93	H9N2	13
A/Chicken/Mexico/26654-1374/94	H5N2	14
A/Chicken/Hong Kong/739/94	H9N2	15
A/Chicken/Korea/25232-96006/96	H9N2	2
A/Chicken/Guangdong/11/97	H9N2	2
A/Duck/Hong Kong/Y280/97	H9N2	5
A/Duck/Hong Kong/Y439/97	H9N2	10
A/Pheasant/Ireland/PV18/97	H9N2	7
A/Chicken/Shanghai/F/98	H9N2	10
A/Chicken/Germany/R45/98	H9N2	8
A/Chicken/Iran/11T/99	H9N2	10
A/Chicken/Taiwan/7-5/99	H6N1	7
A/Chicken/Saudi Arabia/532/99	H9N2	10
A/Duck/Guangdong/40/2000	H5N1	9
A/Duck/Hong Kong/2986.1/2000	H5N1	8
A/Duck/Zhejiang/11/2000	H5N1	4
A/Duck/Zhejiang/52/2000	H5N1	6
A/Chicken/Henan/62/00	H9N2	10
A/Chicken/California/431/00	H6N2	7
A/Duck/Fujian/19/2000	H5N1	6
A/Duck/Guangxi/35/2001	H5N1	4
A/Chicken/Hong Kong/YU822.2/01	H5N1	4

Strain	Subtype	Pattern*
A/Duck/Anyang/AVL-1/2001	H5N1	6
A/Duck/Shanghai/38/2001	H5N1	6
A/Chicken/Hong Kong/NT873.3/01	H5N1	10
A/Chicken/California/139/01	H6N2	10
A/Duck/Guangxi/22/2001	H5N1	8
A/Pheasant/Hong Kong/FY155/01	H5N1	8
A/Chicken/Hong Kong/FY150/01	H5N1	10
A/Duck/Shanghai/08/2001	H5N1	1
A/Duck/NC/91347/01	H1N2	10
A/Duck/Shanghai/35/2002	H5N1	10
A/Chicken/Chile/176822/02	H7N3	10
A/Duck/Fujian/13/2002	H5N1	6
A/Chicken/Hong Kong/YU777/02	H5N1	10
A/Duck/Guangxi/53/2002	H5N1	8
A/Duck/Guangdong/22/2002	H5N1	8
A/Duck/Shanghai/37/2002	H5N1	6
A/Chicken/Hong Kong/31.4/02	H5N1	8
A/SCK/HK/YU100/2002	H5N1	10
A/Chicken/Netherlands/1/03	H7N7	10
A/Duck/Yokohama/aq10/2003	H5N1	10
A/Chicken/Guangdong/174/04	H5N1	9
A/Chicken/British Columbia/04	H7N3	10
A/Chicken/Jilin/9/2004	H5N1	10
A/Crow/Kyoto/53/2004	H5N1	9
A/Dk/Indonesia/MS/2004	H5N1	10

Strain	Subtype	Pattern*
A/Chicken/Guangdong/191/04	H5N1	10
A/Quail/Vietnam/36/04	H5N1	10

Strain	Subtype	Pattern*
A/Duck/Guangdong/173/04	H5N1	10
A/Duck/Shangdong/093/2004	H5N1	6

*An 'equal to' sign (=) means that the lineages of the segments are the same.

- 1 PB2=PB1=PA=NP
- 2 PB2=PB1=PA, PB1 distinct
- 3 PB2=PB1=NP, PA distinct
- 4 PB1=PA=NP, PB2 distinct
- 5 PB2=PB1, PA=NP
- 6 PB2=PB1, PA, NP distinct
- 7 PB2=PA, PB1, NP distinct
- 8 PB1=NP, PB2, PA distinct
- 9 PB1=PA, PB2, NP distinct
- 10 All distinct
- 11 Could not be determined
- 12 PB2=NP, PB1 distinct, PA could not be computed
- 13 PB2=PB1, NP distinct, PA could not be computed
- 14 PB1=PA, PB2 distinct, NP could not be computed
- 15 PB2=PB1=NP, PA could not be computed

Macken, C. A., Webby, R. J. & Bruno, W. J. (2006). Genotype turnover by reassortment of replication complex genes from avian *Influenza A virus*. doi:10.1099/vir.0.81454-0