Novel Reassortant Influenza A(H1N2) Virus Derived from A(H1N1)pdm09 Virus Isolated from Swine, Japan, 2012

Miho Kobayashi, Ikuyo Takayama, Tsutomu Kageyama, Hiroyuki Tsukagoshi, Mika Saitoh, Taisei Ishioka, Yoko Yokota, Hirokazu Kimura, Masato Tashiro, and Kunihisa Kozawa

We isolated a novel influenza virus A(H1N2) strain from a pig on January 13, 2012, in Gunma Prefecture, Japan. Phylogenetic analysis showed that the strain was a novel type of double-reassortant virus derived from the swine influenza virus strains H1N1pdm09 and H1N2, which were prevalent in Gunma at that time.

Influenza A viruses can be transmitted between humans, swine, and birds; virus subtypes have the potential to reassort and generate new viruses by cross-breeding in the various hosts (*1*). For example, influenza A subtype H1N1 viruses reassorted in swine, and the resulting swine influenza viruses (SIVs) were transmitted to humans. The reassorted combinations have resulted in pandemic viruses as well as low-pathogenicity viruses with low transmissibility among humans. Similarly, seasonal human subtypes of influenza are transmissible to swine (*2*). In 2009, a novel strain of the H1N1 SIV subtype emerged and was associated with a pandemic (*3*,*4*). The virus, later termed influenza A(H1N1)pdm09, hereafter referred to as pH1N1, was confirmed as a reassortant virus resulting from cross-breeding of a European avian subtype H1N1 virus and a North American triple reassortant virus (*5*). Subsequently, other strains reassorted from the pH1N1 virus (*6*–*8*). We report on an isolated new reassortant H1N2 SIV derived from the pH1N1 virus and SIVs originating in Japan.

Author affiliations: Gunma Prefectural Institute of Public Health and Environmental Sciences, Maebashi-shi, Gunma, Japan (M. Kobayashi, H. Tsukagoshi, M. Saitoh, T. Ishioka, Y. Yokota, K. Kozawa); and National Institute of Infectious Diseases, Musashimurayama-shi, Tokyo, Japan (I.Takayama, T. Kageyama, H. Kimura, M. Tashiro)

DOI: http://dx.doi.org/10.3201/eid1912.120944

The Study

We collected 109 nasal swab samples from pigs for swine influenza surveillance during November 2011–February 2012. Nasal swab samples were collected from healthy pigs, 6 months of age, at an abattoir in Gunma Prefecture, Japan. All samples were inoculated onto MDCK cells (*9*). All cell culture supernatants were tested by using a hemagglutination assay of a 0.7% solution of guinea pig erythrocytes (*9*). To determine the subtype of the isolate, a hemagglutination inhibition assay was performed by using ferret antiserum for A/California/07/2009 [A(H1N1)pdm09], A/Victoria/210/2009 [A(H3N2)], B/Bangladesh/3333/2007 [B/Yamagata-lineage], and B/Brisbane/60/2008 [B/Victoria-lineage] (*9*). One strain of influenza A virus, designated A/swine/Gunma/1/2012, was isolated from the samples.

For full genome sequencing of the influenza A/swine/Gunma/1/2012 strain, we conducted reverse transcription PCR (*10*). Segment-specific primers used for amplification and sequencing are shown in online Technical Appendix Figure, panel A (wwwnc.cdc.gov/EID/article/19/12/12-0944-Techapp1.pdf). Phylogenetic analysis of the nucleotide sequences was conducted by using MEGA version 5 software (www.megasoftware.net) and Tree Explorer version 2.12 (http://en.bio-soft.net/tree/TreeExplorer.html) (*11*). Evolutionary distances were estimated according to the Kimura 2-parameter method (*12*). The phylogenetic trees of hemagglutinin (HA) and neuraminidase (NA) genes were constructed by using the neighbor-joining method (*13*). In addition, phylogenetic trees based on the matrix protein, nucleoprotein genes, nonstructural protein, polymerase acid, polymerase basic 1, and polymerase basic 2 were constructed by using the neighbor-joining method. The reliability of the trees was estimated with 1,000 bootstrap replications. GenBank accession numbers assigned to the gene sequences of the analyzed strain are the following: polymerase basic 2 (AB731582), polymerase basic 1 (AB731583), polymerase acid (AB731584), HA (AB731585), nucleoprotein (AB731586), NA (AB731587), matrix protein (AB731588), and nonstructural protein (AB731589).

Phylogenetic trees based on HA and NA gene sequences are shown in the Figure, panels A and B. The identities of the nucleotide sequences of each gene are shown in the Table. The A/swine/Gunma/1/2012 strain was confirmed as a strain of pH1N1 virus Figure, panel A). NA gene sequences showed that the virus was located within clusters of swine-type viruses documented in Japan as the representative strains, such as A/swine/Ehime/1/1980 (Figure, panel B). The sequence identity of the NA gene between the A/swine/Gunma/1/2012 strain and other Japanese H1N2 SIV strains ranged from 85.0 to 97.5%. The identities of other genes between the A/swine/Gunma/1/2012 strain and pH1N1 virus vaccine strain (A/California/07/2009) were highly

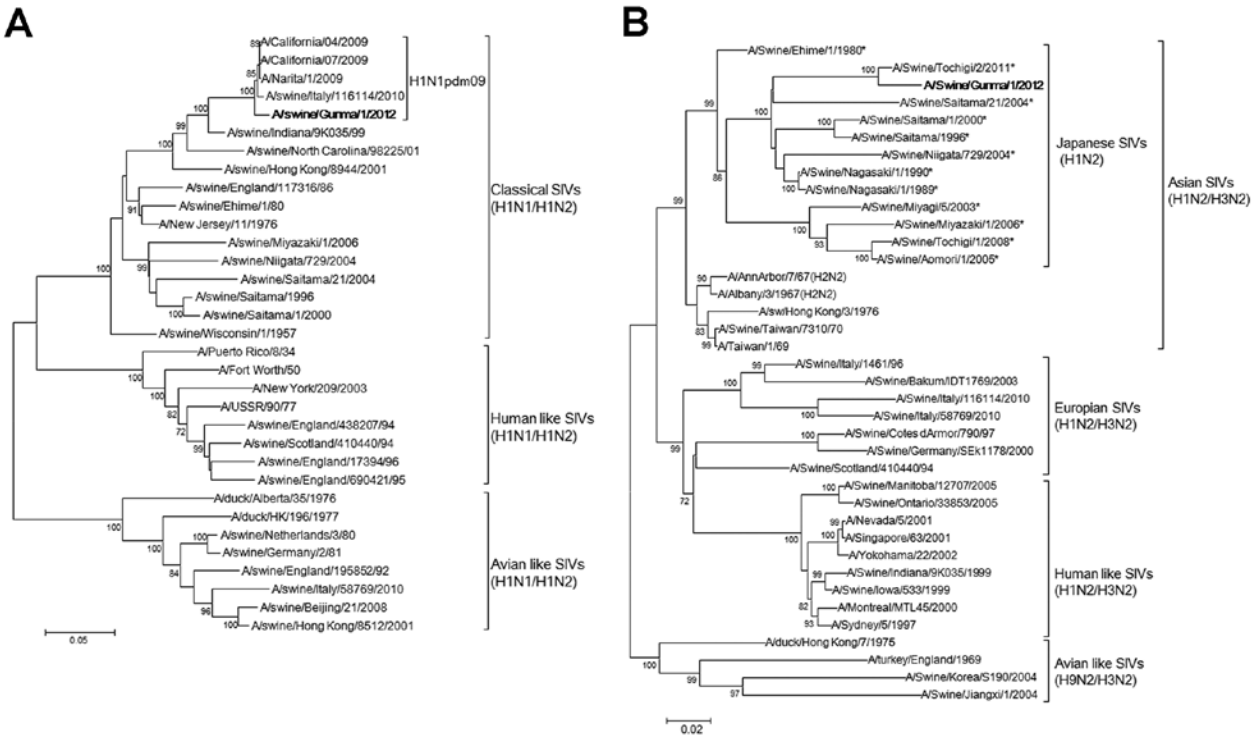


Figure. Phylogenetic tree based on the nucleotide sequences of hemagglutinin (A) and neuraminidase (B) genes of A/swine/Gunma/1/2012, a novel H1N2 swine influenza virus (SIV) strain. Distance was calculated according to the Kimura 2-parameter method; the trees were constructed by using the neighbor-joining method with labeling of the branches showing at least 70% bootstrap support. Boldface text indicates the novel strain reassorted from strains of the SIV H1N2 subtype. Asterisks indicate reference strains compared with A/Swine/Gunma/1/2012 used to calculate the identity of neuraminidase gene. Scale bars indicate nucleotide substitutions per site.

homologous (>90%; Table). These results suggest that the A/swine/Gunma/1/2012 strain was a new reassortant of the H1N2 SIV subtype derived from the pH1N1 virus.

We isolated 1 strain in this study. The samples (109 nasal swabs) were collected from different pig farms ≈60 km apart. The epidemiologic association may be low among the samples, because the quarantine inspection system is well established in Japan. All samples were collected from pigs 6 months of age; therefore, the potential for infection with the virus could have been low. Additional and larger studies investigating the emergence of the parent virus of the strain may be needed.

Table. Sequence identity of each gene of influenza strain A/swine/Gunma/1/2012, reassorted from influenza A(H1N1)pdm09 and A/California/07/2009*

Gene	Identity (%)
PB2	98.9
PB1	98.7
rPA	98.7
HA	98.4
NP	98.7
MP	99.3
NS	99.3

*PB, polymerase basic; PA, polymerase acid; HA, hemagglutinin; NP, nucleoprotein; MP, matrix protein; NS, nonstructural protein.

Conclusions

Vijaykrisna et al. found a new reassortant virus among avian-type, swine-type, and pH1N1 viruses (*6*). In addition, Monero et al. reported a new reassortant virus between SIV, identified in Italy, and pH1N1 viruses (*7*). Thus, pH1N1 virus and other types of influenza viruses can be reassorted. However, to our knowledge, reassortant H1N2 SIV strains derived from pH1N1 virus in Japan have not been identified before this report. Although the transmission of SIVs to humans has been reported sporadically, the infectious nature of this reassortant H1N2 strain among humans is unknown. The emergence of a novel H1N2 SIV strain raises further concerns about whether the virus will generate further genetic reassortments and gain virulence. Systematic influenza virus surveillance in pigs and humans should be considered.

This study was supported by National Epidemiological Surveillance of Vaccine-Preventable Diseases by the Ministry of Health, Labor and Welfare, Japan.

Ms Kobayashi is a research worker in the Gunma Prefectural Institute of Public Health and Environmental Sciences, Gunma, Japan. Her research interests are the epidemiology and molecular biology of respiratory viruses.

References

1. Brown IH. The epidemiology and evolution of influenza viruses in pigs. Vet Microbiol. 2000;74:29–46. http://dx.doi.org/10.1016/S0378-1135(00)00164-4
2. Katsuda K, Sato S, Shirahata T, Lindstrom S, Nerome R, Ishida M, et al. Antigenic and genetic characteristics of H1N1 human influenza virus isolated from pigs in Japan. J Gen Virol. 1995;76:1247–9. http://dx.doi.org/10.1099/0022-1317-76-5-1247
3. Peiris JS, Poon LL, Guan Y. Emergence of a novel swine-origin influenza A virus (S-OIV) H1N1 virus in humans. J Clin Virol. 2009;45:169–73. http://dx.doi.org/10.1016/j.jcv.2009.06.006
4. Novel Swine-Origin Influenza A. (H1N1) Virus Investigation Team, Dawood FS, Jain S, Finelli L, Shaw MW, Lindstrom S, et al. Emergence of a novel swine-origin influenza A (H1N1) virus in humans. N Engl J Med. 2009;360:2605–15. http://dx.doi.org/10.1056/NEJMoa0903810
5. Garten RJ, Davis CT, Russell CA, Shu B, Lindstrom S, Balish A, et al. Antigenic and genetic characteristics of swine-origin 2009 A(H1N1) influenza viruses circulating in humans. Science. 2009;325:197–201. http://dx.doi.org/10.1126/science.1176225
6. Vijaykrishna D, Poon LL, Zhu HC, Ma SK, Li OT, Cheung CL, et al. Reassortment of pandemic H1N1/2009 influenza A virus in swine. Science. 2010;328:1529. http://dx.doi.org/10.1126/science.1189132
7. Moreno A, Di Trani L, Faccini S, Vaccari G, Nigrelli D, Boniotti MB, et al. Novel H1N2 swine influenza reassortant strain in pigs derived from the pandemic H1N1/2009 virus. Vet Microbiol. 2011;149:472–7. http://dx.doi.org/10.1016/j.vetmic.2010.12.011
8. Howard WA, Essen SC, Strugnell BW, Russell C, Barass L, Reid SM, et al. Reassortant pandemic (H1N1) 2009 virus in pigs, United Kingdom. Emerg Infect Dis. 2011;17:1049–52.
9. WHO Global Influenza Surveillance Network. Manual for the laboratory diagnosis and virological surveillance of influenza. Geneva: World Health Organization; 2011. p. 35–77.
10. Hoffmann E, Stech J, Guan Y, Webster RG, Perez DR. Universal primer set for the full-length amplification of all influenza A viruses. Arch Virol. 2001;146:2275–89. http://dx.doi.org/10.1007/s007050170002
11. Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. Mol Biol Evol. 2011;28:2731–9. http://dx.doi.org/10.1093/molbev/msr121
12. Kimura M. A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. J Mol Evol. 1980;16:111–20. http://dx.doi.org/10.1007/BF01731581
13. Saitou N, Nei M. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol Biol Evol. 1987;4:406–25.

Address for correspondence: Kunihisa Kozawa, Gunma Prefectural Institute of Public Health and Environmental Sciences, 378 Kamiokimachi, Maebashi-shi, Gunma 371-0052, Japan; email: kozawa-ku@pref.gunma.lg.jp

etymologia

Sarcocystis nesbitti

[sahr″ko-sis′tis nez-bit′ē]

In 1843, Swiss scientist Friedrich Miescher found "milky white threads" in the muscles of a mouse, which for years were known as "Miescher's tubules." In 1882, Lankester named the parasite *Sarcocystis*, from the Greek *sarx* (flesh) and *kystis* (bladder). Scientists were unsure whether to classify the species as protozoa or as fungi because only the sarcocyst stage had been identified. In 1967, crescent-shaped structures typically found in protozoa were seen in sarcocyst cultures, and it was determined to be a protozoan, a close relative of *Toxoplasma* spp. In 1969, A. M. Mandour described a new species of Sarcocystis in rhesus macaques, which he named *Sarcocystis nesbitti*, after Mr. P. Nesbitt, who saw the trophozoites in stained smears. Snakes are now known to be the definitive hosts of *S. nesbitti*, and several primates, including humans, can be intermediate hosts.

Sources

1. Dubey JP, Speer CA, Fayer R. Sarcocystosis of animals and man. Boca Raton (FL): CRC Press, Inc; 1989.
2. Fayer R. Sarcocystis spp. in human infections. Clin Microbiol Rev. 2004;17:894–902. http://dx.doi.org/10.1128/CMR.17.4.894-902.2004
3. Lau YL, Chang PY, Subramaniam V, Ng YH, Mahmud R, Ahmad AF, et al. Genetic assemblage of Sarcocystis spp. in Malaysian snakes. Parasit Vectors. 2013;6:257. http://dx.doi.org/10.1186/1756-3305-6-257
4. Mandour AM. Sarcocystis nesbitti n. sp. from the rhesus monkey. J Protozool. 1969;16:353–4. http://dx.doi.org/10.1111/j.1550-7408.1969.tb02281.x

Address for correspondence: Ronnie Henry, Centers for Disease Control and Prevention, 1600 Clifton Rd NE, Mailstop E03, Atlanta, GA 30333, USA; email: boq3@cdc.gov

DOI: http://dx.doi.org/10.3201/eid1912.ET1912

Article DOI: http://dx.doi.org/10.3201/eid1912.120944

Novel Reassortant Influenza A(H1N2) Virus Derived from A(H1N1)pdm09 Virus Isolated from Swine, Japan, 2012

Technical Appendix

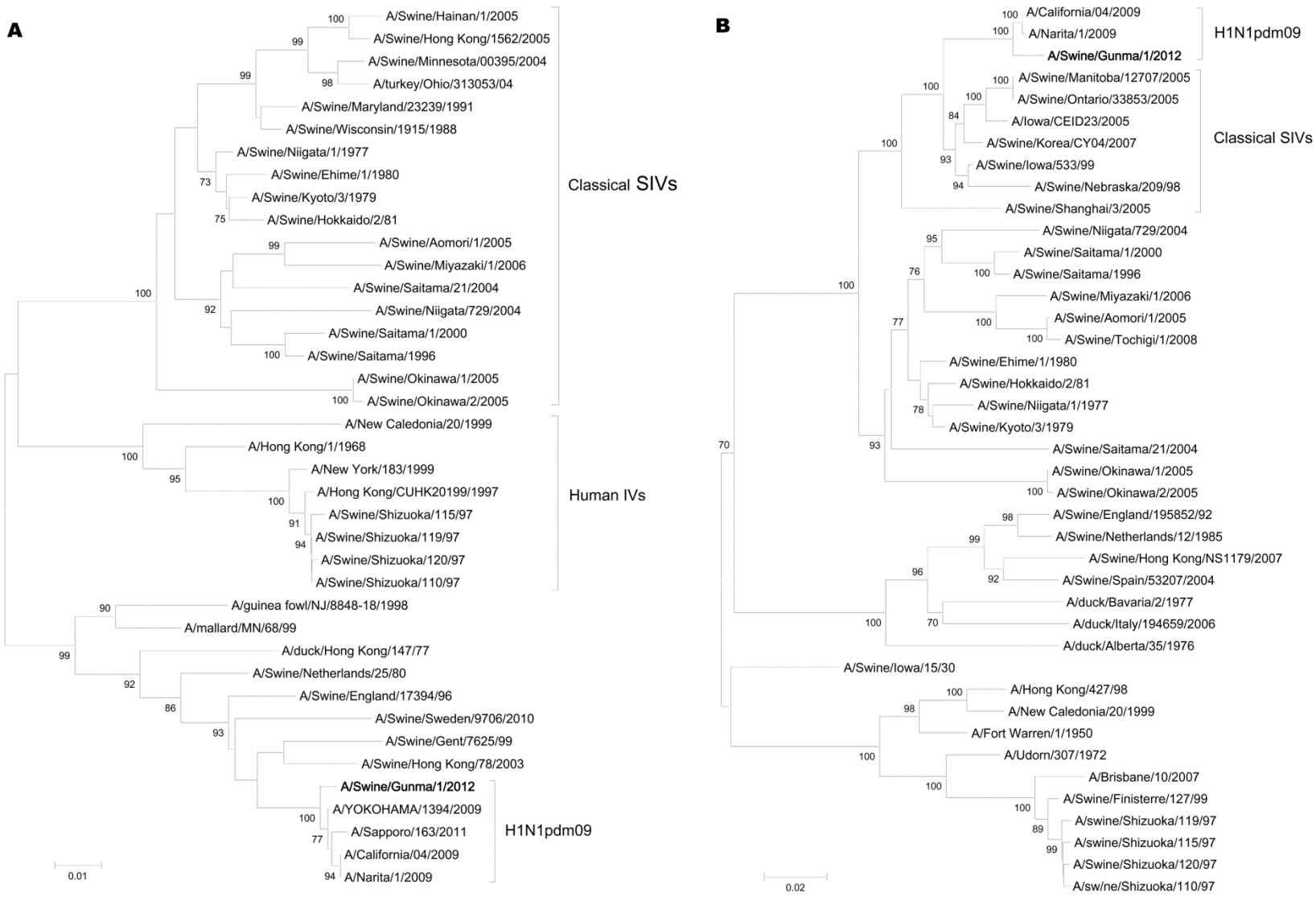
Genome Amplification, Sequencing, and Phylogeny of Novel Reassortant Influenza A(H1N2) Virus

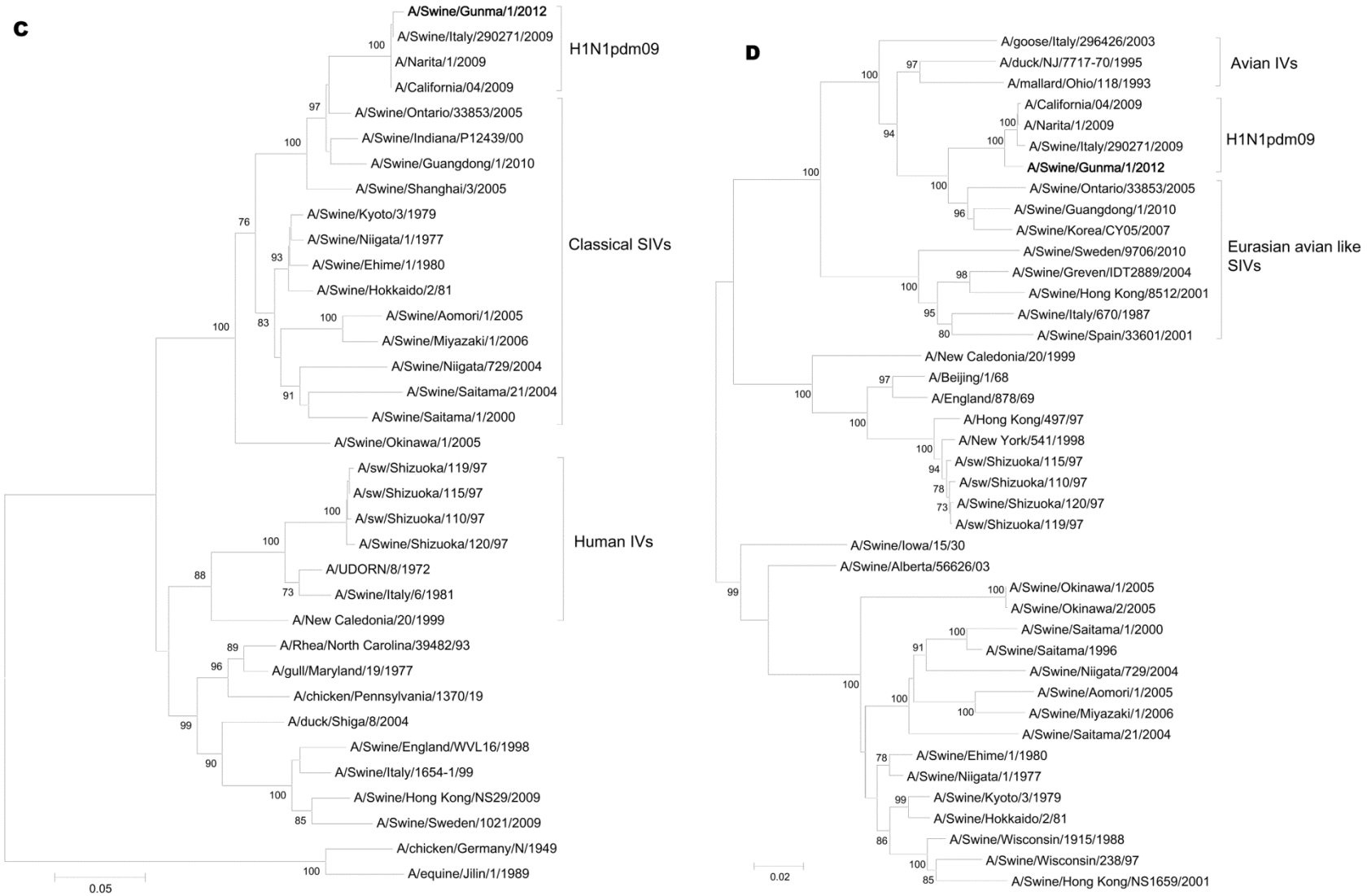
Technical Appendix Table. Primers for amplification and sequencing of the full genome of A/swine/Gunma/1/2012, a novel swine influenza A(H1N2) virus strain, Japan, 2012

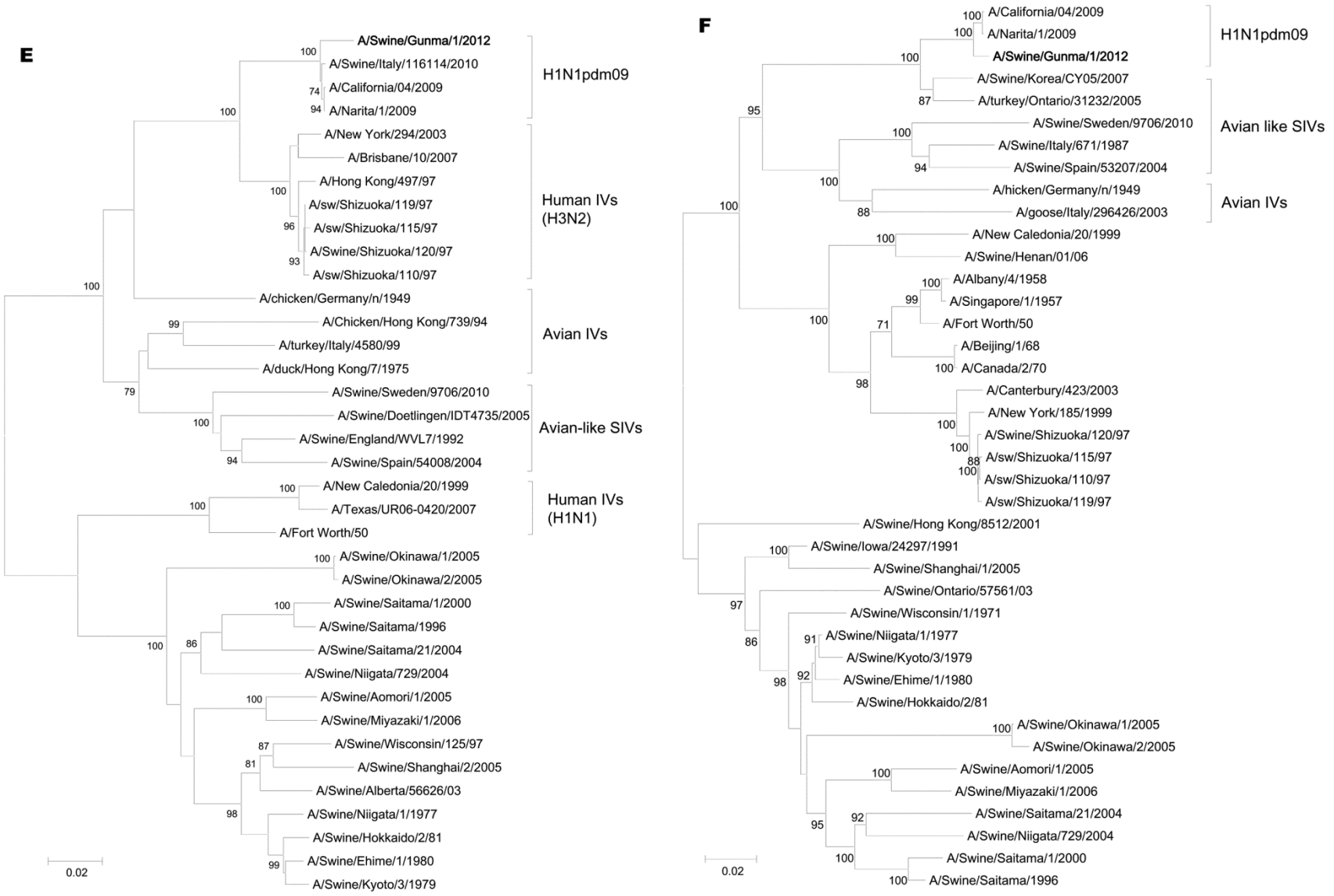
Gene	Primer	Sequence (5′→3′)
Amplification		
HA	5+HA-1	CAGGGAGCAAAAGCAGGGG
	11+NS-890R	CGTCTCGTATTAGTAGAAACAAGGGTGTTTT
NA	7+NA-1	CTCAGGGAGCAAAAGCAGGAGT
	12+NA-1413R	TGGTCTCGTATTAGTAGAAACAAGGAGTTTTTT
PB2	PB2-F	AGCAAAAGCAGGTCAAWTATTC
	PB2-R	AGTAGAAACAAGGTCGTTTTTAAA
PB1	PB1-1	AGCAAAAGCAGGCAAACCATT
	PB1-R	AGTAGAAACAAGGCATTTTTTCA
PA	PA-1-26F	AGCRAAAGCAGGTACTGATYCRAAAT
	PA-2228R	AGTAGAAACAAGGTACTTTTTTGGACAG
NP	NP-F	AGCAAAAGCAGGGTARATAATCACTC
	Bm-NP-1565R	AGTAGAAACAAGGGTATTTTT
MP	MP-F	AGCAAAAGCAGGTAGATRTTKAAAG
	MP-R	AGTAGAAACAAGGTAGTTTTTTACTC
NS	NS-F	AGCAAAAGCAGGGTGACAAA
	NS-890R	AGTAGAAACAAGGGTGTTTTTTATCA
Sequencing		
HA	5+HA-1	CAGGGAGCAAAAGCAGGGG
	swineH1-56-76F	CATTATGTATAGGTTATCATG
	swineH1-366-385F	GAGCTCAGTGTCATCATTTG
	swineH1-596-578R	GGATGGTGAATGCCCCATA
	swineH1-768-788F	AATAACATTCGAAGCAACTGG
	swineH1-1106-1087R	TGATAACCGTACCATCCATC
	H1N1pdmHA-1300-1320F	GACATTTGGACTTACAATGCC
NA	7+NA-1	CTCAGGGAGCAAAAGCAGGAGT
	N2-548R	TGACAACTTGAGCTGGACCA
	N2-1062R	AAGGCCCAGCCTTTCACYCC
	N2-902F	TGGAAGGGCTCYAATAGGCC
	12+NA-1413R	TGGTCTCGTATTAGTAGAAACAAGGAGTTTTTT
PB2	PB2-F	AGCAAAAGCAGGTCAAWTATTC
	PB2-599R	ATGTATGCCACCATYAAGGG
	H1N1pdmPB2-280-300R	TTCCACCATGTTACGGCCAGA
	H5PB2-1241R	TATCATGCAATCCTCCTGTG
	H5PB2-1071F	CCTCCAAACATTGAAAATAAGAG
	PB2-R	AGTAGAAACAAGGTCGTTTTTAAA
	H1N1pdmPB2-1650-1670F	CAATGGATAATCAGGAACTG
PB1	H1N1pdmPB1-290-310R	CAAATATTCCTGGGTGGGATT
	PB1-1	AGCAAAAGCAGGCAAACCATT
	PB1-1240R	AACATGCCCATCATCATTCC
	PB1-1334R	GATTGGAGTCGATCCCACCA
	PB1-1121F	CACAAATACCAGCAGAAATGC
	PB1-R	AGTAGAAACAAGGCATTTTTTCA

Gene	Primer	Sequence (5′→3′)
	PB1-1651F	ACAGCTCAGATGGCTCTTCA
PA	PA-230-249R	TTCAATTATCTCAAATCGGT
	H5PA-583R	TGACGAAAGGAATCCCATAG
	H5PA-686R	TTCAAGGCTGGAGAAGTTCG
	PA-940Rv2	TCTTCATGCATTTGATTGCATC
	PA-1-26F	AGCRAAAGCAGGTACTGATYCRAAAT
	H5PA-583F	CTATGGGATTCCTTTCGTCA
	H5PA-1818R	TCTCTTTGACAGAAGACTCG
	PA-940F	GATGCAATCAAATGCATGAAGA
	H5PA-1147F	GCACCAGAGAAAGTAGACTT
	PA-2228R	AGTAGAAACAAGGTACTTTTTTGGACAG
	H5PA-1619F	TGGAGCCACACAAGTGGGAA
	H5PA-F1792	GCCGAGTCTTCTGTCAAAGA
NP	H1N1pdmNP-500-520R	TGGGAAGTGTTGACCCTTGCA
	NP-F	AGCAAAAGCAGGGTARATAATCACTC
	H5NP-1075R	GTCCCTCTGATGAAACTTGA
	H5NP-451F	CTGATGATATGGCATTCCAA
	NP-1565R	AGTAGAAACAAGGGTATTTTTCTT
	H5NP-451F	CTGATGATATGGCATTCCAA
	H1N1pdmNP-1000-1020F	CACTCTGCTGCATTTGAAGAT
MP	MP-501r2	CGATGCTGTGAATCTGCAAT
	MP-R	AGTAGAAACAAGGTAGTTTTTTACTC
	MP-F	AGCAAAAGCAGGTAGATRTTKAAAG
	H5MP-501F	ATTGCAGATTCACAGCATCG
NS	NS-F	AGCAAAAGCAGGGTGACAAA
	H5NS-535R	GTGTTATCATTCCATTCAAGTCC
	NS-890R	AGTAGAAACAAGGGTGTTTTTTATCA
	H1N1pdmNS-450-470F	CACTGAGGAGGGAGCAATAGT

Technical Appendix Figure (following pages). Phylogenetic analysis of the A/swine/Gunma/1/2012 strain of the influenza A(H1N1)pdm09 virus isolated from swine. Phylogenetic trees based on A) the matrix protein (MP), B) nucleoprotein (NP), C) nonstructural protein (NS), D) polymerase acid (PA), E) polymerase basic 1 (PB1), and F) polymerase basic 2 (PB2) genes were constructed by using the neighbor joining method. Bold text represents novel H1N2 swine influenza virus (SIV) isolated in Japan during January 2012. Numbers along branches represent estimates made with 1,000 bootstrap replications to demonstrate the reliability of the trees. Scale bars represent nucleotide substitutions by site.


A
A/Swine/Hainan/1/2005
A/Swine/Hong Kong/1562/2005
A/Swine/Minnesota/00395/2004
A/turkey/Ohio/313053/04
A/Swine/Maryland/23239/1991
A/Swine/Wisconsin/1915/1988
A/Swine/Niigata/1/1977
A/Swine/Ehime/1/1980
A/Swine/Kyoto/3/1979
A/Swine/Hokkaido/2/81
A/Swine/Aomori/1/2005
A/Swine/Miyazaki/1/2006
A/Swine/Saitama/21/2004
A/Swine/Niigata/729/2004
A/Swine/Saitama/1/2000
A/Swine/Saitama/1996
A/Swine/Okinawa/1/2005
A/Swine/Okinawa/2/2005
Classical SIVs
A/New Caledonia/20/1999
A/Hong Kong/1/1968
A/New York/183/1999
A/Hong Kong/CUHK20199/1997
A/Swine/Shizuoka/115/97
A/Swine/Shizuoka/119/97
A/Swine/Shizuoka/120/97
A/Swine/Shizuoka/110/97
Human IVs
A/guinea fowl/NJ/8848-18/1998
A/mallard/MN/68/99
A/duck/Hong Kong/147/77
A/Swine/Netherlands/25/80
A/Swine/England/17394/96
A/Swine/Sweden/9706/2010
A/Swine/Gent/7625/99
A/Swine/Hong Kong/78/2003
A/Swine/Gunma/1/2012
A/YOKOHAMA/1394/2009
A/Sapporo/163/2011
A/California/04/2009
A/Narita/1/2009
H1N1pdm09
0.01
B
A/California/04/2009
A/Narita/1/2009
A/Swine/Gunma/1/2012
H1N1pdm09
A/Swine/Manitoba/12707/2005
A/Swine/Ontario/33853/2005
A/Iowa/CEID23/2005
A/Swine/Korea/CY04/2007
A/Swine/Iowa/533/99
A/Swine/Nebraska/209/98
A/Swine/Shanghai/3/2005
Classical SIVs
A/Swine/Niigata/729/2004
A/Swine/Saitama/1/2000
A/Swine/Saitama/1996
A/Swine/Miyazaki/1/2006
A/Swine/Aomori/1/2005
A/Swine/Tochigi/1/2008
A/Swine/Ehime/1/1980
A/Swine/Hokkaido/2/81
A/Swine/Niigata/1/1977
A/Swine/Kyoto/3/1979
A/Swine/Saitama/21/2004
A/Swine/Okinawa/1/2005
A/Swine/Okinawa/2/2005
A/Swine/England/195852/92
A/Swine/Netherlands/12/1985
A/Swine/Hong Kong/NS1179/2007
A/Swine/Spain/53207/2004
A/duck/Bavaria/2/1977
A/duck/Italy/194659/2006
A/duck/Alberta/35/1976
A/Swine/Iowa/15/30
A/Hong Kong/427/98
A/New Caledonia/20/1999
A/Fort Warren/1/1950
A/Udorn/307/1972
A/Brisbane/10/2007
A/Swine/Finisterre/127/99
A/swine/Shizuoka/119/97
A/swine/Shizuoka/115/97
A/Swine/Shizuoka/120/97
A/sw/ne/Shizuoka/110/97
0.02


C
A/Swine/Gunma/1/2012
A/Swine/Italy/290271/2009
A/Narita/1/2009
A/California/04/2009
H1N1pdm09
A/Swine/Ontario/33853/2005
A/Swine/Indiana/P12439/00
A/Swine/Guangdong/1/2010
A/Swine/Shanghai/3/2005
A/Swine/Kyoto/3/1979
A/Swine/Niigata/1/1977
A/Swine/Ehime/1/1980
A/Swine/Hokkaido/2/81
A/Swine/Aomori/1/2005
A/Swine/Miyazaki/1/2006
A/Swine/Niigata/729/2004
A/Swine/Saitama/21/2004
A/Swine/Saitama/1/2000
Classical SIVs
A/Swine/Okinawa/1/2005
A/sw/Shizuoka/119/97
A/sw/Shizuoka/115/97
A/sw/Shizuoka/110/97
A/Swine/Shizuoka/120/97
A/UDORN/8/1972
A/Swine/Italy/6/1981
A/New Caledonia/20/1999
Human IVs
A/Rhea/North Carolina/39482/93
A/gull/Maryland/19/1977
A/chicken/Pennsylvania/1370/19
A/duck/Shiga/8/2004
A/Swine/England/WVL16/1998
A/Swine/Italy/1654-1/99
A/Swine/Hong Kong/NS29/2009
A/Swine/Sweden/1021/2009
A/chicken/Germany/N/1949
A/equine/Jilin/1/1989
0.05
D
A/goose/Italy/296426/2003
A/duck/NJ/7717-70/1995
A/mallard/Ohio/118/1993
Avian IVs
A/California/04/2009
A/Narita/1/2009
A/Swine/Italy/290271/2009
A/Swine/Gunma/1/2012
H1N1pdm09
A/Swine/Ontario/33853/2005
A/Swine/Guangdong/1/2010
A/Swine/Korea/CY05/2007
A/Swine/Sweden/9706/2010
A/Swine/Greven/IDT2889/2004
A/Swine/Hong Kong/8512/2001
A/Swine/Italy/670/1987
A/Swine/Spain/33601/2001
Eurasian avian like SIVs
A/New Caledonia/20/1999
A/Beijing/1/68
A/England/878/69
A/Hong Kong/497/97
A/New York/541/1998
A/sw/Shizuoka/115/97
A/sw/Shizuoka/110/97
A/Swine/Shizuoka/120/97
A/sw/Shizuoka/119/97
A/Swine/Iowa/15/30
A/Swine/Alberta/56626/03
A/Swine/Okinawa/1/2005
A/Swine/Okinawa/2/2005
A/Swine/Saitama/1/2000
A/Swine/Saitama/1996
A/Swine/Niigata/729/2004
A/Swine/Aomori/1/2005
A/Swine/Miyazaki/1/2006
A/Swine/Saitama/21/2004
A/Swine/Ehime/1/1980
A/Swine/Niigata/1/1977
A/Swine/Kyoto/3/1979
A/Swine/Hokkaido/2/81
A/Swine/Wisconsin/1915/1988
A/Swine/Wisconsin/238/97
A/Swine/Hong Kong/NS1659/2001
0.02


E
A/Swine/Gunma/1/2012
A/Swine/Italy/116114/2010
A/California/04/2009
A/Narita/1/2009
H1N1pdm09
A/New York/294/2003
A/Brisbane/10/2007
A/Hong Kong/497/97
A/sw/Shizuoka/119/97
A/sw/Shizuoka/115/97
A/Swine/Shizuoka/120/97
A/sw/Shizuoka/110/97
Human IVs (H3N2)
A/chicken/Germany/n/1949
A/Chicken/Hong Kong/739/94
A/turkey/Italy/4580/99
A/duck/Hong Kong/7/1975
Avian IVs
A/Swine/Sweden/9706/2010
A/Swine/Doetlingen/IDT4735/2005
A/Swine/England/WVL7/1992
A/Swine/Spain/54008/2004
Avian-like SIVs
A/New Caledonia/20/1999
A/Texas/UR06-0420/2007
A/Fort Worth/50
Human IVs (H1N1)
A/Swine/Okinawa/1/2005
A/Swine/Okinawa/2/2005
A/Swine/Saitama/1/2000
A/Swine/Saitama/1996
A/Swine/Saitama/21/2004
A/Swine/Niigata/729/2004
A/Swine/Aomori/1/2005
A/Swine/Miyazaki/1/2006
A/Swine/Wisconsin/125/97
A/Swine/Shanghai/2/2005
A/Swine/Alberta/56626/03
A/Swine/Niigata/1/1977
A/Swine/Hokkaido/2/81
A/Swine/Ehime/1/1980
A/Swine/Kyoto/3/1979
0.02
F
A/California/04/2009
A/Narita/1/2009
A/Swine/Gunma/1/2012
H1N1pdm09
A/Swine/Korea/CY05/2007
A/turkey/Ontario/31232/2005
A/Swine/Sweden/9706/2010
A/Swine/Italy/671/1987
A/Swine/Spain/53207/2004
Avian like SIVs
A/hicken/Germany/n/1949
A/goose/Italy/296426/2003
Avian IVs
A/New Caledonia/20/1999
A/Swine/Henan/01/06
A/Albany/4/1958
A/Singapore/1/1957
A/Fort Worth/50
A/Beijing/1/68
A/Canada/2/70
A/Canterbury/423/2003
A/New York/185/1999
A/Swine/Shizuoka/120/97
A/sw/Shizuoka/115/97
A/sw/Shizuoka/110/97
A/sw/Shizuoka/119/97
A/Swine/Hong Kong/8512/2001
A/Swine/Iowa/24297/1991
A/Swine/Shanghai/1/2005
A/Swine/Ontario/57561/03
A/Swine/Wisconsin/1/1971
A/Swine/Niigata/1/1977
A/Swine/Kyoto/3/1979
A/Swine/Ehime/1/1980
A/Swine/Hokkaido/2/81
A/Swine/Okinawa/1/2005
A/Swine/Okinawa/2/2005
A/Swine/Aomori/1/2005
A/Swine/Miyazaki/1/2006
A/Swine/Saitama/21/2004
A/Swine/Niigata/729/2004
A/Swine/Saitama/1/2000
A/Swine/Saitama/1996
0.02