Human Infection with Avian Influenza A(H9N2) Virus, Cambodia, February 2021

Appendix 1

Additional References

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A

G9/BJ94 h9.3

G1, h9.4

Y439, h9.2

H9.1

MK553072|A/Duck/Guangdong/G2472/2018
MK553075|A/chicken/Guangdong/G2476/2018
MK553079|A/chicken/Guangdong/G2480/2018
MK553067|A/chicken/Guangdong/G2467/2018
MK553064|A/Pigeon/Guangdong/G2454/2018
MK553008|A/chicken/Guangdong/G2255/2018
A/Chicken/Cambodia/f0318251/2021
A/Cambodia/21020301/2021
EPI1765934|A/chicken/China/GD-40/2018
EPI1822782|A/chicken/Yunnan/12.22_DQXBL001-O/2018
EPI1826889|A/chicken/Guangdong/7.1B_SZBJ021-O/2018
EPI1826897|A/chicken/Guangdong/7.1B_SZBJ022-O/2018
MK553333|A/chicken/Guizhou/Q2045/2018
MK553108|A/chicken/Guangdxi/GX2267/2018
EPI1384083|A/Guangxi-Xianshan/11522/2018
EPI1815428|A/Guizhou/13392/2020
EPI1694146|A/Hong_Kong/623/2020
MK552429|A/chicken/Guangdong/G1425/2018
EPI1551841|A/chicken/Shaoguan/zd201603/2017
MK553651|A/chicken/Jiangxi/X2404/2018
EPI1841240|A/Guangdong/20SF15010/2020
MK553633|A/chicken/Jiangxi/X2368/2018
EPI1352836|A/Guangdong/18SF003/2018
EPI1384075|A/Guangdong/18SF064/2018
MK552427|A/chicken/Guangdong/G1319/2018
MK552786|A/chicken/Shanghai/S1175/2018
EPI1815744|A/_Szuzhou_GIRD01_2019/2019
MK552796|A/chicken/Shanghai/S1248/2018
MN103714|A/chicken/China/F4129/2015
EPI1315828|A/Anhui-Lujiang/39/2018
EPI1830092|A/chicken/Hubei/S340/2017
MK544428|A/chicken/Anhui/A166/2017
MK554390|A/chicken/Jiangxi/X2326/2017
EPI838241|A/Hunan/44557/2015
EPI680525|A/Hunan/44557/2015
MK544386|A/chicken/Guangdong/G2262/2015
EPI1103518|A/Beijing/1/2016
EPI1103526|A/Beijing/1/2017
MN103644|A/Duck/China/E552/2014
EPI498036|A/Hong_Kong/308/2014
EPI470861|A/chicken/Hong_Kong/G9/1997 *
EPI5929|A/chicken/Beijing/1/1994 *
EPI12030|A/Hong_Kong/1073/99
EPI241742|A/Hong_Kong/33982/2009
EPI5925|A/Quail/Hong_Kong/G1/97 *
EPI445995|A/Bangladesh/0994/2011
EPI1431479|A/Oman/2747/2019
EPI5923|A/Duck/Hong_Kong/Y439/97 *
EPI5935|A/Turkey/California/189/66

Candidate vaccine virus
Human infection
2021 Cambodian H9N2
* Clade defining strain

0.03

B

G9/BJ94 h9.3

G1 h9.4

Y439 h9.2

H9.1

EPI1678410|A/chicken/Vietnam/Raho6-DI3V3S5/2018
EPI1678433|A/chicken/Vietnam/Raho6-DI2V3S1/2018
EPI1677891|A/chicken/Vietnam/Raho6-17S2698/2017
EPI1678103|A/chicken/Vietnam/Raho6-17S3890/2017
EPI1851208|A/chicken/Laos/1147/2019
EPI1851176|A/chicken/Laos/1118/2019
A/Cambodia/21020301/2021
A/Chicken/Cambodia/f0318251/2021
EPI1678087|A/chicken/Vietnam/Raho6-17S3950/2017
EPI1678284|A/chicken/Vietnam/Raho6-18S-0804/2018
EPI1678473|A/chicken/Vietnam/Raho6-Tg1-V2-S1/2018
EPI1678300|A/chicken/Vietnam/Raho6-18S-0802/2018
EPI1678386|A/chicken/Vietnam/Raho6-Tg5-V2-S6/2018
EPI1275270|A/chicken/Cambodia/Z648W39M1/2015
EPI1275374|A/chicken/Cambodia/Z909W52M1/2015
EPI1275350|A/chicken/Cambodia/Z860W49M3/2015
EPI469706|A/chicken/Hong_Kong/NT270/2008
EPI470960|A/Hong_Kong/69955/2008
EPI241757|A/Hong_Kong/3239/2008
EPI469725|A/chicken/Hong_Kong/YU119/2009
EPI162341|A/chicken/Zibo/B1/2008
EPI487183|A/chicken/Henan/321/2008
EPI1275422|A/duck/Cambodia/a34W9M1/2016
EPI1576939|A/duck/Viet_Nam/TN-2897/2016
EPI1275118|A/chicken/Cambodia/Z308W22M1/2015
EPI241748|A/Hong_Kong/35820/2009
EPI469748|A/chicken/Hong_Kong/NT180W/2011
EPI241740|A/Hong_Kong/33982/2009
EPI469692|A/chicken/Hong_Kong/NT449/2007
EPI67037|A/pheasant/Shantou/841/2004
EPI470859|A/chicken/Hong_Kong/G9/1997 *
EPI451|A/Hong_Kong/1073/99
EPI5889|A/Quail/Hong_Kong/G1/97 *
EPI445996|A/Bangladesh/0994/2011
EPI1431480|A/Oman/2747/2019
EPI498037|A/Hong_Kong/308/2014
EPI1315830|A/Anhui-Lujiang/39/2018
EPI470965|Achicken/Beijing/1/1994 *
EPI470943|A/Duck/Hong_Kong/Y439/97 *
EPI5913|A/Turkey/California/189/66

Candidate vaccine virus
Human infection
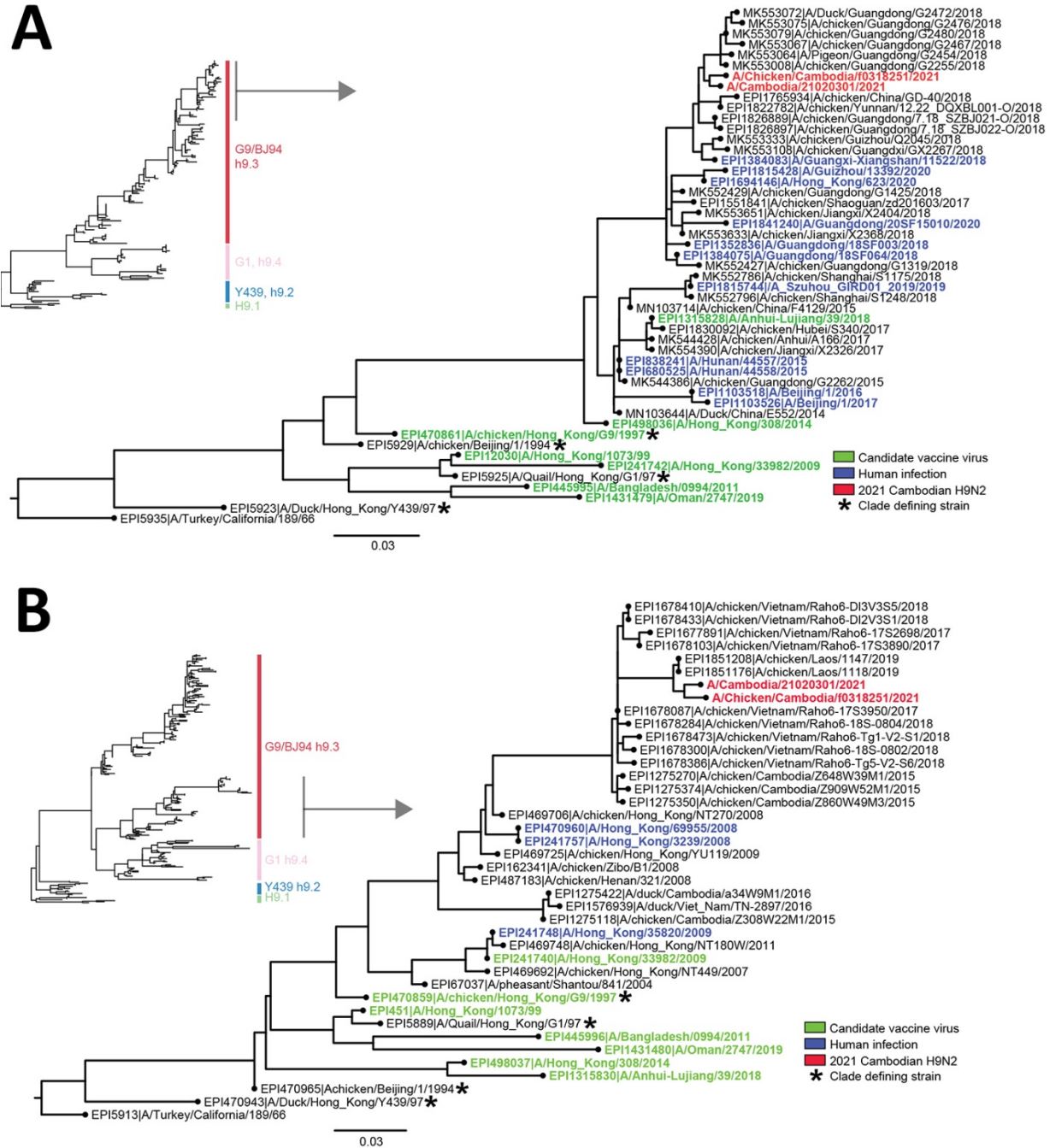2021 Cambodian H9N2
* Clade defining strain

0.03

Figure. Maximum likelihood phylogenetic tree of hemagglutinin (A) and neuraminidase (B) genes of avian influenza A(H9N2) viruses detected in human and chicken specimens, Cambodia, 2021. Sequences were aligned using MAFFT v7.450 in Geneious Prime 2021.0.1 against 47 and 38 A/H9N2 HA and NA sequences, respectively, downloaded from the GISAID and Genbank database (Appendix 2, https://wwwnc.cdc.gov/EID/article 27/10/21-1039-App2.xlxs). Maximum Likelihood (ML) phylogenetic trees were inferred with IQ-Tree (v2.0.3) using the best-fit nucleotide substitution model (FLU+I+G4) and visualized using FigTree (v1.4.4) and ggree (v2.4.1). Phylogenetic support was estimated using 1,000 ultrafast bootstrap replicates. Candidate vaccine viruses are indicated in bold green, human A(H9N2)

viruses in bold blue, and 2021 Cambodian H9N2 viruses in bold red. Clade defining strains are indicated with an asterisk. Scale bars indicate the number of nucleotide substitutions per site. Genbank accession and GISAID isolate ID numbers are provided in Appendix 2.