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Effect of Prior Influenza A(H1N1)pdm09 Virus Infection on Pathogenesis of Human Influenza A(H5N1) Clade 2.3.4.4b Virus Isolate in Ferret Model

Appendix 2

Whole gene alignment NA

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1 60
Nebraska_14_2019 MNPNQKIITI GSICMTIGMA NLILQIGNII SIWVSHSIQI GNQSQIETCN KNVITYENNT
Texas_37_2024 .....T.. ....V..IV S.M..... .....T ...Y.P.P.. QSI.....
Srf res -----

61 82 120
Nebraska_14_2019 WVNQTYVNVIS NINSAAARQSV ASVKLAGNSS LCPVSGWAIY SKDNSVRIGS KGDVVFVIREP
Texas_37_2024 .....I... ..FL.E.A. T..T..... ..I..... ..GI..... .....
Srf res ----- -sss-s-sss sssss---ss s-s---s-s- s-s---sss-

121 180
Nebraska_14_2019 FISCSPLECR TFFLTQGALL NDKHNGTIK DRSPYRTLMS CPIGEVPSPY NSRFESVAWS
Texas_37_2024 .....H..... .....V..... .....V.A..... .....
Srf res ---ssssss s-----s----- ssss-sssss sssss---s- -ss-s----- s-sss---s-

181 240
Nebraska_14_2019 ASACHDGTNW LTIGISGPDG GAVAVLKYNG IITDTIKSWR NNILRTQESE CACVNGSCFT
Texas_37_2024 .....IS. ....N..... .....
Srf res -----s-sss -----s-ss --s-s--sss s-ssssssss sss-s--s-s -----s-s-

241 300
Nebraska_14_2019 IMTDGSPDGQ ASYKIFRIEK GKIIKSVEMK APNYHYECS CYPDSSEITC VCRDNWHGSN
Texas_37_2024 V.....N.. .....K... ..VV.....N .....AGD.M. ....
Srf res --s-sssss s--s-ss-ss -sssssssss -sss--ss-- -ssss-s- --s-sss-

301 360
Nebraska_14_2019 RPWVSNQNL EYQMGYICSG VFGDNPDPND KTGSCGPVSS NGANGVGFSS FKYNGVWIG
Texas_37_2024 .....I..... I..... G...S.M.P. ...Y.....
Srf res --s-s-sssss sssss----- --s--s--ss ssssssssss s-ss-s----- -ssss-----

361 420
Nebraska_14_2019 RTKSISRRKG FEMIWDPNGW IGTDNKFSKK QDIVGINEWS GYSGSFVQHP ELTGLDCMRP
Texas_37_2024 ...T...S. ....TE..SS..V. ....E.TD. ....N.I..
Srf res s-sssssss- ----s-ss-s ssssssssss s---sssss- -s-----s- sssssss-s-

421 469
Nebraska_14_2019 CFWVELIRGR PEENTIWTSG SSISFCGVDS DIVGWSWPDG AELPFTIDK
Texas_37_2024 .....K..... .....N. T.....
Srf res -----s-s ssssss-----s-ss ssssss---s ssssssssss

NA ectodomain (residues 82-469) = 388
Srf res = 223
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Tx37 vs Neb14 =
345/388 residues in the ectodomain were shared (89% similarity)
NA monomer 165 buried 5Å radius setting = 223 residues exposed
186/223 surface exposed residues were shared (83.4% similarity)

Appendix 2 Figure 1. Alignment of NA proteins of A(H1N1)pdm09 Nebraska/14/2009 and A(H5N1) Texas/37/2007 viruses. The surface exposed residues (Srf res) were marked with “s” in the alignments.

Whole Gene alignment HA mature protein

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1                               60
Texas_37_2024    DQICIGYHAN NSTEQVDTIM EKNVTVTHAQ DILEKTHNGK LCDLNGVKPL ILKDCSVAGW
Nebraska_14_2019 .TL..... .DT...VL .....SV NL..DK.... .K.R..A.. H.GK.NI...
Srf res         ss-s--ss-s sssss-s--s sssss-ssss s-ssssssss --s-ssssss s-ss-s--s

61                               119
Texas_37_2024    LLGNPMCDEF IRVPEWSYIV ERANPANDLC YPGSLNDYEE LKHMLSRINH FEKIQIIPK-
Nebraska_14_2019 I....E.ESL STARS..... .TS.SD.GT. ...DFIN... .REQ..SVSS ..RFE.F..T
Srf res         --s-ssssss sssss-s--- sssssssss- sssssssssss -s-s--s-ss sssss-sss

120                              179
Texas_37_2024    SSWPNHETSL GVSAAQPYQG APSFFRNQVW LIKKNDAYPT IKISYNNTR EDLLILWGIH
Nebraska_14_2019 .....DSDK ..T...HA. .K..YK.LI. .V..GNS..K LNQT.I.DKG KEV.V.....
Srf res         ssssssssss ss-ss-ssss sssss-s-s -ssssssss -ssss-s-ss ss---s---

180                              239
Texas_37_2024    HSNNAEQTN LYKNPITYIS VGTSTLNQRL APKIATRSQV NGQRGRMDFE WTILKPDDAI
Nebraska_14_2019 .PPTIAA.ES ..Q.ADA.VF ...RYSKKF K.E...PK. RD.E...NY .LVE.G.K.
Srf res         s-ssss-s-ss s-ssss-s-- ---ssssss sss-s-s-ss ssss---s-s sss-ssss-

240                              299
Texas_37_2024    HFESNGNFIA PEYAYKIVVK GDSTIMKSGV EYGHCKTKCQ TPVGAINSSM PFHNIHPLTI
Nebraska_14_2019 T..AT..LVV .R..FTMERD AG.G.II.DT PVHD...T.. .E...T.L ..Q.V..I..
Srf res         s-s-s----- -ss--ssss ss--s-s-ss sssssss-- -ss-s-ssss ---ssss-

300                              359
Texas_37_2024    GECPKYVKS NKLVLATGLRN SPLREKRRR GLFGAXAGFI EGGWQGMVDG WYGYHHSNEQ
Nebraska_14_2019 .K.....T ..R..... V.SIQS---. ....I.... ...T..... ....Q...
Srf res         -ssss-s-ss s-s--s--ss ss-ssssss sssss--ss ss--ss-ss ss--ssss-

360                              419
Texas_37_2024    GSGYAADKES TQKAIDGVTN KVNSIIDKMN TQFEAVGREF NNLEERRIENL NKKMEDGFLLD
Nebraska_14_2019 .....LK. ..N...KI.. ....V.E... ..T...K.. .H..K..... ..VD.....
Srf res         ssssssssss sss-ss-ss s-ss-ssss sss-s-ssss sssssss-- sssssss-

420                              479
Texas_37_2024    VWTYNAELLV LMENERTLDF HDSNVKNLYD KVRLQLRDNA KELGNGCFEF YHKCDNECME
Nebraska_14_2019 I..... .L.....Y .....E ...N..KN.. ..I..... ....T...
Srf res         ---ss-s-ss sss-ss--ss sssss-s-ss s-sss-ss-s ssss---sss s-s-sss--s

480                              539
Texas_37_2024    SVRNGTYDYP QYSEEARLKR EEISGVKLES VGTQILSIY STAASSLALA IMMAGLSLWM
Nebraska_14_2019 ..K..... K.....K.N. .K.D..... TRI....A.. ..V....V.V VSLGAI.F..
Srf res         s-ssssssss sssss-ssss ss----- -----

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HA Tx37 vs Neb14 =
 HA1 (1 to 329); HA2 (330 to 499)
 107/238 HA1 surface residues were shared (45% similarity)
 111/138 HA2 surface residues were shared (80.4% similarity)

Appendix 2 Figure 2. Alignment of HA proteins of A(H1N1pdm09 Nebraska/14/2009 and A(H5N1) Texas/37/2007 viruses. The surface exposed residues (Srf res) were marked with “s” in the alignments.