

Swine Influenza A(H3N2) Virus Infection in Immurocompromised Man, Italy, 2014

Technical Appendix



Technical Appendix Figure 1. Phylogenetic tree based on the polymerase base (PB) 1, PB2, polymerase (PA), nucleoprotein (NP), matrix (M), and nonstructural (NS) gene gene sequences.

B

Strain: A/Pavia/07/2014 (H3N2)

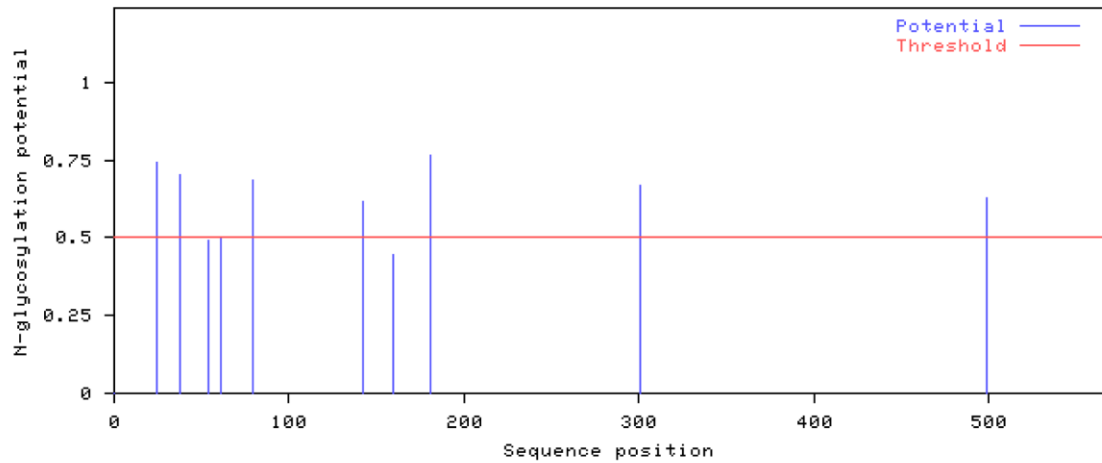
MKTVIALSYVFCLVFGQDFPGKGNNTATLCLGHHAVPNGTLVKTITDDQIEVTNATELVQNFMSGKICKNPHRILDGANCTLIDSLLGDPHCDGDFQNEKWDLFIERSRAFSNCYPYDVPEYTSLSRLIASSTLEFTNENFNWTGVTQNGGSSACKRGNNSFFSRLNLWLYKSGNTYPLMLNVTMPNSDDDFDKLYIWGVHHPSTDREQTNLYIQASGKIIVSTKRSQQTIIIPNIGSRPWVRLSSRSIYWTIVKPGDILINSNGNLIAPRGYFKIQTKGSSVMKSDAPIGTCNSECITPNGSIPNDKPFQNVNRITYGACPHYIKQSTLKLATGMRNIPERQTRGIFGAIAGFIENGWEGMVNGWYGFRHQNSEGIGQAADLKSTQAAINQINGKLNRYIEKTNEKFHQIEKEFSEVEGRIQDLERYVEDTKIDLWSYNAELLLVALENQHTIDLTDSEMNLFEKTRKQLRENAEDMNGCFCFIYHKCDNSCMESIRNGTYDHNEYRDEAVNNRFQIKSVELKSGYKDWILWISFAISCFLLCTIWMGFIIWACQKGNIRCNICI

.....N.....N.....N.....N.....
N.....
N.....
N.....

N.....

(Threshold=0.5)

SeqName	Position	Potential	Jury agreement	N-Glyc result
A/Pavia/07/2014 (H3N2)	24 NNTA	0.7412	(9/9)	++
A/Pavia/07/2014 (H3N2)	38 NGTL	0.7046	(9/9)	++
A/Pavia/07/2014 (H3N2)	54 NATE	0.4940	(3/9)	-
A/Pavia/07/2014 (H3N2)	61 NFSM	0.5011	(5/9)	+
A/Pavia/07/2014 (H3N2)	79 NCTL	0.6842	(9/9)	++
A/Pavia/07/2014 (H3N2)	142 NWTG	0.6148	(8/9)	+
A/Pavia/07/2014 (H3N2)	160 NNSF	0.4433	(7/9)	-
A/Pavia/07/2014 (H3N2)	181 NVTM	0.7646	(9/9)	+++
A/Pavia/07/2014 (H3N2)	301 NGSI	0.6674	(9/9)	++
A/Pavia/07/2014 (H3N2)	499 NGTY	0.6270	(9/9)	++

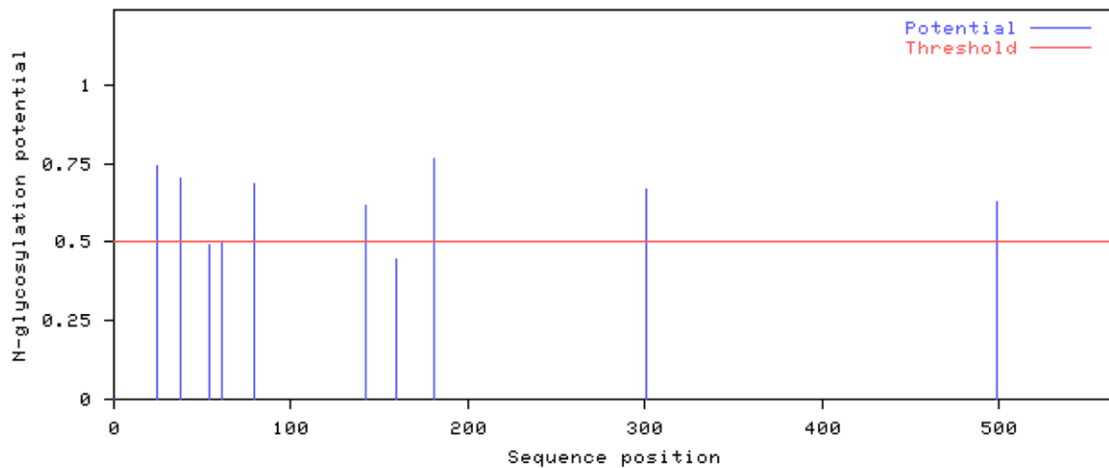


C

Strain: A/Swine/Italy/282811/2013 (H3N2)
 MKTVIALSYVFLVFGQDFPGKGNNTATLCLGHAVPNGTLVKITITDDQIEVTNATELVQNFMSGKICKNPHRILDGANC
 TLIDSLGDPHCDGFQNEKWDLFIERSRAFSNCPYDVPVEYTSLSRSLIASSGTLFTNENFNWTVGTQNGGSSACKRGPV
 NSFFSRLNWLKSGNTYPMNLVVTMPNSDDFDKLYIWGVVHPSTDREQTNLVIQASGKLIIVSTKRSQQTIIIPNIGSRPWVR
 GLSSRSISYWTIVKPGDILIIINSNGNLIAPRGYFKIQTKSSVMKSDAPIGTCNSECITPNGSIPNDKPFQVNRITYGA
 CPHYIKQNTLKLATGMRNIPERQTRGIFGAIAGFIENGWEGMVNGWYGFRHQNSEGIGQAADLKSTQAAINQINGKLNRV
 IEKTNEKFHQIEKEFSEVEGRIQDLERYVEDTKIDLWSYNAELLVALENQHTIDLTDSEMKNLFEKTRKQLRENAEDMGN
 GCFKIYHKCDNSCMESIRNGTYDHNEYRDEAVNRRFQIKSVELKSGYKDWLWISFAMSCFLLCATWGMGFIWACQKGN
 RCNICI
N.....N.....N.....N.
N.....
N.....
N.....
N.....
N.....

(Threshold=0.5)

SeqName	Position	Potential	Jury agreement	N-Glyc result
A/Swine/Italy/282811/2013 (H3N2)	24	NNTA	0.7412	(9/9) ++
A/Swine/Italy/282811/2013 (H3N2)	38	NGTL	0.7046	(9/9) ++
A/Swine/Italy/282811/2013 (H3N2)	54	NATE	0.4939	(3/9) -
A/Swine/Italy/282811/2013 (H3N2)	61	NFSM	0.5013	(5/9) +
A/Swine/Italy/282811/2013 (H3N2)	79	NCTL	0.6842	(9/9) ++
A/Swine/Italy/282811/2013 (H3N2)	142	NWTG	0.6148	(8/9) +
A/Swine/Italy/282811/2013 (H3N2)	160	NNSF	0.4433	(7/9) -
A/Swine/Italy/282811/2013 (H3N2)	181	NVTM	0.7647	(9/9) +++
A/Swine/Italy/282811/2013 (H3N2)	301	NGSI	0.6673	(9/9) ++
A/Swine/Italy/282811/2013 (H3N2)	499	NGTY	0.6271	(9/9) ++



Technical Appendix Figure 2. N-glycosylation predictions for the hemagglutinin proteins of the A/Brisbane/10/2007(H3N2) (A), A/Pavia/07/2014(H3N2) (B), and A/Swine/Italy/282811/2013(H3N2) (C) influenza strains. Predictions were made by using the NetNGlyc 1.0 server available online (<http://www.cbs.dtu.dk/services/NetNGlyc/>). Asn-Xaa-Ser/Thr sequons in the sequence output are highlighted in blue. Asparagines predicted to be N-glycosylated are highlighted in red.