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Genetic characterization of influenza A/H3N2 viruses circulating in Georgia during 2016/2017 influenza season

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Introduction

Influenza virus remains one of the main causes of acute respiratory illness in humans worldwide. Genetic study of influenza viruses plays essential role to determine evolution of influenza viruses and select candidate strains for next season vaccine composition. The objective of this study was molecular characterization of influenza A/H3N2 viruses detected in Georgia during 2016/2017 influenza season and comparison to ones circulating globally.

Methods

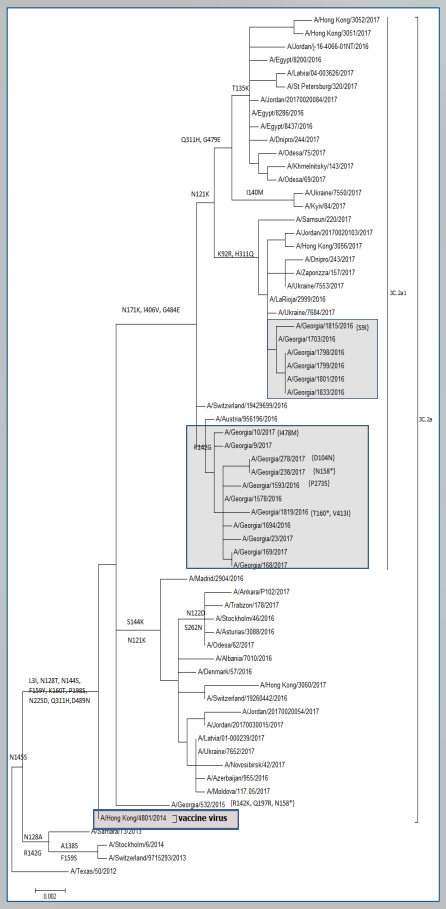
Sanger sequencing was used for genetic characterization of HA and NA genes of four influenza A/H3N2 viruses at National Influenza Center, Tbilisi, Georgia. DNA sequencing raw data were analyzed and assembled into HA and NA full length sequences using Sequencher 5.0 software. In addition, sequences of 13 Georgian strains were downloaded from GISAID. Mega 6 software was used for constriction phylogeny trees.

Results

Totally 17 Georgian A/H3N2 viruses were analyzed and compared to A/Hong Kong/4801/2014 representing Northern hemisphere 2016/2017 vaccine virus. Georgian HA gens fall into genetic group 3C that further divides into subdivisions 3C.1, 3C.2 and 3C.3. Georgian strains belonged to 3C.2a1 subclade characterized with HA amino acid substitutions N171K in HA1 and I77V and G155E in HA2 compared to vaccine virus (Pic 1). Two strains showed polymorphism encoding the glycosylation motif at residues 158-160 in HA1. Georgian viruses clustered in two subgroups: first caring R142G substitution in HA1(11 strains) and second with amino acid changes K92R, N121K, H311Q in HA1 (6 strains). Some viruses in addition had substitutions on various positions S9I, D104N, P273S in HA1 and V84I, I149M in HA2 (Table 1).

NA gens of Georgian strains revealed same pattern of clustering as observed for HA gene (Pic. 2). All NA gens of our viruses differed from A/Hong Kong/4801/2014 by 7 amino acid substitutions: S245N (mutation resulted in the gaining of new glycosylation site), S247T (mutation maintained glycosylation motif), I231V, T267K, I380V, T392I and P468H. 11 viruses carried also amino acid changes L140I, V143M, S315R and D339N. Five viruses had additional single amino acid substitutions I20L, D113N, S331N (forming new potential glycosylation site) and L372F (Table 1).

Picture 1. Phylogenetic tree of HA gene of Georgian H3N2 viruses, 2016/2017 season



Picture 2. Phylogenetic tree of NA gene of Georgian H3N2 viruses, 2016/2017 season

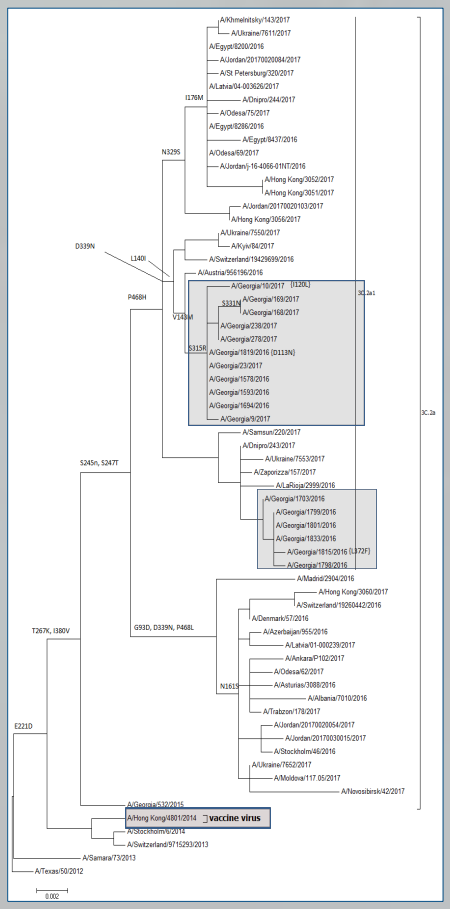


Table 1. Amino acid changes of HA and NA gene of Georgian H3N2 viruses of 2016/2017 season compared to A/Hong Kong/4801/2014

HA gene		NA gene
HA1	HA2	I20L (1)
S9I (1)	I77V (17)	D113N (1)
K92R (6)	V84I (1)	L140I (11)
D104N (1)	I149M(1)	V143M (11)
N121K (6)	G155E (17)	I231V (17)
R142G (11)		S245N (17)
158N or K (1)		S247T (17)
160T or K (1)		T267K (17)
N171K (17)		S315R (11)
P273S (1)		S331N (2)
H311Q (6)		D339N (1)
		L372F (1)
		I380V (17)
		T392I (17)
		P468H (17)

Conclusion

Influenza A/H3N2 viruses circulating in Georgia during 2016/2017 influenza season belonged to most commonly observed subgroups 3C2a1 worldwide. The data obtained from this study confirms the continuous genetic variability of A/H3N2 influenza viruses and therefore the need for routine molecular surveillance.

Acknowledgements

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