Whole genome characterization of SARS-CoV-2 viruses from respiratory specimens using Oxford Nanopore's MinION Sequencing

Научный руководитель - Аракелян Арсен Арташесович

Cирунян $T.K.^1$, Xачатрян $\Gamma.B.^2$, Mурадян $H.\Gamma.^3$

1 - Российско-Армянский (Славянский) университет, Ереван, Армения, E-mail: $t_sirunyan@mb.sci.am;$ 2 - Российско-Армянский (Славянский) университет, Ереван, Армения, E-mail: $g_khachatryan@mb.sci.am;$ 3 - Российско-Армянский (Славянский) университет, Ереван, Армения, E-mail: nelli.muradyan@edu.isec.am

Sirunyan T.K.^{1,2}, Khachatryan G.V.^{1,2}, Muradyan N.G.^{1,3}, Avetyan D.G.¹ Student, senior laboratory assistant

- ¹ Laboratory of Human Genomics and Immunomics, Institute of Molecular Biology National Academy of Sciences RA, 0014, Yerevan, Armenia
- ² Department of Bioengineering, Bioinformatics and Molecular Biology, Institute of Biomedicine and Pharmacy, Russian-Armenian University, 0051, Yerevan, Armenia
- ³ Department of Molecular and Cellular Biology, International Scientific-Educational Center of National Academy of Sciences RA, 0019, Yerevan, Armenia

E-mail: t sirunyan@mb.sci.am

Severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) was first identified in China, Wuhan, in December 2019, which causes novel coronavirus pneumonia COVID-19. The SARS-CoV-2 outbreak quickly spread throughout the world and became a major healthcare concern worldwide. Previously, several new variants of concern of the virus have emerged in the UK, South Africa and Brazil, which were characterized by increased transmissibility.

This study was aimed at genetic characterization of SARS-CoV-2 in Armenia. We performed whole genome nanopore sequencing of 24 clinical samples isolated from COVID-19 positive patients using an ARTIC protocol [1]. Samples were collected during January 2021.

In this 24 obtained complete genomes of SARS-CoV-2, 26 variations were identified in at least two samples, with an average depth of coverage around 300. Analysis of PANGO lineages identified B.1.1.163 as a major lineage (in 87.5% samples) as well as B.1.1 (in 4.2% samples) and B.1.1.208 (in 8.3% samples). All variants were characterized by the presence of D614G mutation in Spike protein, indicative of the dominant form of the virus circulating globally. No variants of concerns (UK (B.1.1.7), Brazil (P.1), and South Africa (B.1.351)) were identified. Phylogenetic analysis placed Armenian samples in a cluster along with variants detected in Europe and Russia, suggesting the main transition routes of these variants. Furthermore, 3 previously undescribed mutations were identified in our samples. These results warrant the necessity of large population based screenings for epidemiologic surveillance, epidemics monitoring as well as understanding the impact of specific mutations on viral properties and the effectiveness of diagnostics, therapeutics and vaccines.

References

1) Josh Quick 2020. nCoV-2019 sequencing protocol v3 (LoCost). protocols.io https://protocols.io/view/ncov-2019-sequencing-protocol-v3-locost-bh42j8ye