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Covid-19 in Kazakhstan. Incidence statistics and new variations of the Sars-Cov-2 virus.

Coronaviruses are a group of diverse, enveloped, non-segmented, single-stranded, positive-sense RNA viruses. Since the onset of coronavirus infection at the end of 2019, the simultaneous circulation of different variants of the SARS-CoV-2 virus has been established. Currently, there are many different variants of SARS-CoV-2 that can be grouped into larger groups, including lineages, but the three main nomenclatures in use for SARS-CoV-2 are the GISAID (<https://gisaid.org/>), Nextstrain (<https://nextstrain.org/>) and Pango lines (<https://cov-lineages.org/>).

According to the GISAID nomenclature system for sharing all influenza data, most SARS-CoV-2 sequenced genomes have currently been grouped into one of twelve major clades as: L, S, O, V, G, GH, GR, GV, GK, GRY, GKA and GRY.

On March 13, 2020, the first cases of the previously unknown coronavirus SARS-CoV-2, which causes SARS, were officially recorded in Kazakhstan. On September 23, 2021, according to WHO data, a total of 944,733 cases were registered in Kazakhstan, with 15,503 deaths. Clyde GRY is the most common in our country, where its share is 43.5%. Other clades including GR, G, O, S and GK accounted for 18.6%, 17.6%, 8.06%, 8.06%, 4.7% and 5%, respectively. Lower prevalence was noted among the GH, GV, and L clades and identified 1.5%, 0.25, and 0.5% of the total genomes represented, respectively.

Among the males, the most common clades are GH and O, their proportion was 83.3% and 75%, respectively. Clydes GRY and S are often identified among females, which were 55.5% and 52.6%, respectively.

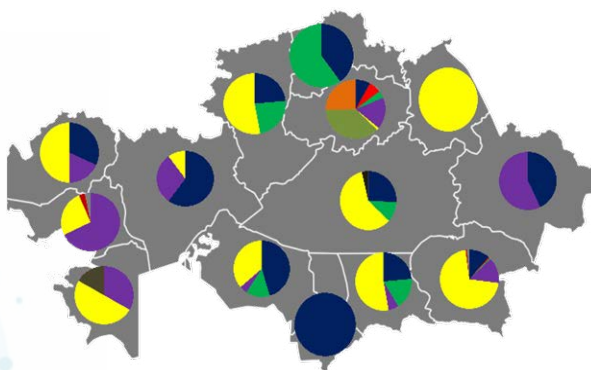


Figure 1 - Analysis of the distribution of various SARS-CoV-2 clades across the Republic of Kazakhstan.