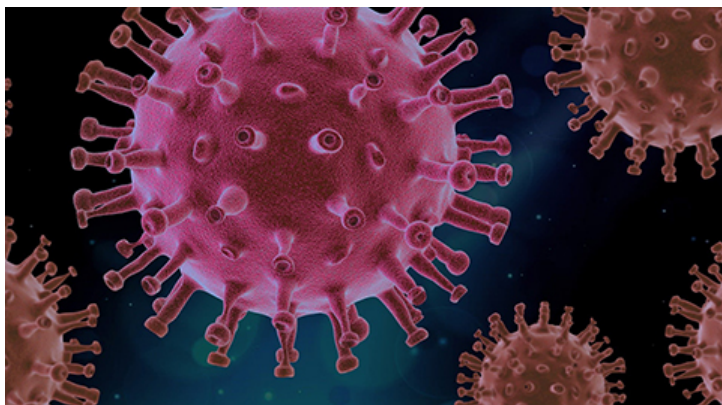


SibFU Researcher Explains Emergence of New Coronavirus Strains

Researchers have [discovered](#) a new genome of the coronavirus in Russia that has gained 18 mutations in four months of being in the body of a patient with suppressed immunity. This strain has already been called Russian by analogy with the British one. It has similar mutations to the British strain, which has already been shown to spread twice as fast as other strains on average (its reproduction number is 2, i.e., on average, one person infected with this strain infects other two, while for most other strains this value equals 1 on average).



According to the Russian experts, it is still premature to conclude about the new strain threat level, mainly because it is insufficiently studied. To date, only one such case with a patient has been described.

A research team from the Skolkovo Institute of Science and Technology (Skoltech), Kharkevich Institute for Information Transmission Problems (RAS), Pavlov First State Medical University, and Smorodintsev Research Institute of Influenza co-authored an article about a new strain of coronavirus.

The research describes a case of a woman with a stage 4 non-Hodgkin B-cell lymphoma (malignant neoplasm). She had contracted the coronavirus in the ward while undergoing chemotherapy in April. All PCR tests the patient underwent from April to September resulted positive up to September 9.



*"In the sensational British strain 20B/501Y.V1 or VOC 202012/01 (B.1.1.7 lineage), there have also been found many functional mutations, presumably caused by the fact that the virus was in a patient with a weakened or suppressed immune system for a long time. But only the Russian research team first described the exact case of SARS-CoV-2 virus acquiring numerous mutations from staying long in one organism. In such conditions, coronavirus gets the environment to mutate immensely and evolve towards adaptation to the human host organism. Most of these mutations are nonsynonymous, that is, they cause amino acid substitution in the proteins of the virus and can affect the function of the virus," explained **Konstantin Krutovsky**, professor at the Department of Genomics and Bioinformatics of Siberian Federal University, professor at the University of Göttingen (Germany).*

The professor reported that two of the 18 mutations are identical to those found in minks in Denmark. Due to the rapid spread of the virus among these animals, many minks were eliminated. The dangerous combination was designated as ΔF ; this combination gives the pathogen the ability to multiply rapidly and evade recognition by neutralizing antibodies. This raised concerns that such mutations could impact the vaccine effect.

"It is unlikely that the independent occurrence of similar combinations of mutations is accidental; most likely, this is a sign of directed natural selection favouring mutations that contribute to the adaptation of the virus to the host. Other mutations coincide with those previously observed during the evolution of the virus into SARS-CoV-2 in other immunosuppressed patients, and with those that arose in the rapidly spreading British variant (VOC-202012/01), which also, presumably, originated in a person with weakened immunity," concluded Prof Krutovsky.

20 february 2021

© Siberian federal university. Website editorial staff: +7 (391) 246-98-60, info@sfu-kras.ru.

Web page address: <https://news.sfu-kras.ru/node/24245>