

MedLife research team sequenced the genome of SARS-CoV-2 virus

"At this time, it is very unlikely that patients who have gone through the disease could be re-infected"

- *The virus circulating in the country originates in Wuhan*
- *The SARS-CoV-2 virus was transmitted in Romania through European countries. It did not come directly from China, other countries in Asia, North or South America*
- *Most cases of SARS-CoV-2 virus infection in various parts of the country are most likely due to local spread and less to direct import from other countries*

Bucharest: June 26, 2020: MedLife research team announces the first results of a new study which obtained a series of information on the entire genome of SARS-CoV-2 virus circulating in Romania. The research was conducted entirely with local human and operational resources and involved the sequencing of virus genomes in different geographical regions of the country, from both asymptomatic and symptomatic patients; 53 samples from 7 cities were sequenced: Bucharest, Galați, Slatina, Suceava, Cluj, Focșani and Tulcea.

It is not a conspiracy theory, the SARS-CoV-2 virus circulating in Romania certainly comes from Wuhan

MedLife researchers found that the origin of the SARS-CoV-2 virus circulating in Romania is in Wuhan, the virus in Romania having a sequence identity of 99.97% with the original virus identified in China (on average 9 mutations were identified per genome, the maximum number being 13). In addition, according to the research team, the new coronavirus arrived in Romania following the spread of the virus from China through Europe. In fact, the analyzed data show that the mutations detected in the viruses sequenced by the Romanian research team are similar to those most frequently identified in Great Britain. However, it cannot be said with certainty that the virus was mainly brought from this area, as the mutations identified are also found in other European countries.

"Research teams are making huge efforts globally to sequence SARS-CoV-2 strains. This process is very important for identifying the origin of the virus, the sources of epidemics in different regions and the dynamics of intra- and inter-community transmission. Understanding how it spreads is essential to the fight we all have against this virus. Moreover, genome sequencing could go a long way in developing future treatments and vaccines. For this study, the sequencing method developed by CDC (Centers for Disease Control) in the United States was used, being a method that allows complete sequencing of the viral genome", said biologist Dumitru Jordan, doctor of medical sciences, scientific coordinator of the study.

According to MedLife representatives, in order to identify the viral profile specific to Romania, the study is based on the analysis of the genetic mutations of the virus.

Tracking the genetic diversity of the virus allows us to have certain epidemiological information such as - how the virus reached us. This is possible because as the virus spreads, it gathers mutations and by tracking these mutations that could be specific to certain areas, you can see where the virus came from a certain region and possibly intervene to stop its way of spreading. On the other hand, it is very important to analyze the mutations that occur in the virus. During the epidemic, certain mutations may occur that cause infected people to develop a more serious or perhaps more mild disease. Equally, new mutations may occur that could allow the virus to re-infect people who have already gone through the disease and are immune to the older "virus". Moreover, new mutations could make the virus immune to any treatments we develop and make vaccines ineffective. In conclusion, the virus is constantly adapting, so studying the evolution of the virus genome will always be in the foreground, if we want to stop this pandemic" said Dumitru Jardan, biologist, scientific coordinator of the study.

Most likely, the spread of the SARS-COV-2 virus in Romania was local, through intra-community transmission in the regions of the country

MedLife research team also evaluated the spread of the virus in the country, and the analyzed data show that the transmission of the new coronavirus was mostly local.

"On our study sample it was observed that in each outbreak the genetic diversity of viruses is relatively small, being detected rather noticeable differences between outbreaks, which means that in each outbreak there were few people who brought the virus from outside the country, virus transmission being largely intra-community. This is probably due to the traffic restrictions imposed during this period" said biologist Dumitru Jardan.

At this time, it is very unlikely that patients who have gone through the disease could be re-infected

The same study focused on mutations in the S gene, which are thought to allow the virus to infect people who have already gone through the disease. Thus, the mutations identified at Romanian patients show that the virus is unlikely to re-infect cured patients.

"S gene is the most important gene for virus infectivity because it encodes a protein that binds directly to the receptor on the surface of human cells, which is often the target of an antiviral immune response. The mutations identified by our team in the S gene do not support the theory that the virus is capable of reinfection. In the future, however, the situation could change. Researchers around the world are closely studying the changes that occur in this gene to identify in advance whether the virus has undergone a mutation, which could in turn lead to a reinfection" said biologist Dumitru Jardan.

Last but not least, genome sequencing for this virus allowed the verification of the SARS-CoV-2 virus detection method used in MedLife Medical System. The method used for the patients is based on the identification of sequences in the genome of viruses, and mutations that may occur in these sequences interfere with the effectiveness of the test. The research team showed that the mutations identified at patients in Romania do not interfere with the method used. Consequently, it was validated that the virus did not undergo mutations that would make it more difficult to be detected.

In the future, MedLife aims to constantly monitor by sequencing the cases of SARS-CoV-2 in Romania for a better understanding of viruses circulating in the country.

"MedLife will monitor the recognized antibody sequence to find out if patients who have had the disease can be re-infected or if they are protected by any vaccine. It is very important to monitor whether the virus circulating in Romania undergoes mutations that make it resistant to the vaccines and treatments that will appear" said Mihai Marcu, President & CEO of MedLife Group.

We consider that in the next period the curve of SARS-CoV-2 virus infections in Romania will continue to increase. The business community, especially large employers, and central and local public administrations must be very careful to further relax the restrictions that prevent the spread of the disease.

MedLife ran in April the first study on the natural immunization of the population following which it was found that less than 2% of Romanians were immunized to the SARS-CoV-2 virus. The company is currently conducting its fourth study in partnership with Matei Balș Institute of Infectious Diseases on the dynamics of naturally acquired antibodies to COVID-19 in the case of infected patients. According to the company's representatives, the first results will be communicated in the coming weeks, the sample used in this study being larger than the one used in the study of Chinese specialists.

"A different side is that of infections. At this time the number of community infections is on the rise. In fact, two weeks ago, although less than 200 cases were reported daily, MedLife contacted the Ministry of Health and the Directorate of Public Health to signal the imminent increase in cases, based on the distribution of positive cases, through isolated cases rather than focused ones, specific to community spread. We believe that the business community, especially large employers, and central and local public administrations must be very careful to further relax the restrictions that prevent the spread of the disease. Certainly a possible increase in the number of tests performed and a deepening of epidemiological investigations will lead to the identification of a larger number of cases and to the gradual extinction of the community spread. There is also an important responsibility of the citizens, of each individual, related to education and social maturity. We have a great chance as a country to come out on top in this fight against the pandemic" said Mihai Marcu, President and CEO of MedLife Group.

"We welcome the intention of the Ministry of Health to reduce the number of hospitalization days for asymptomatic patients. There are at least two important reasons: in this way the resistance of Romanians to test will decrease considerably as it represents a firm confirmation of the fact that they will not have to remain hospitalized for a long time, an extremely important detail especially for employers who have employees in production, and in addition, there will be a saving of the number of tests necessary for the monitoring of asymptomatic patients cured, thus increasing the number of tests allocated for epidemiological investigations", added Mihai Marcu.

Beyond the evolution of this pandemic, we are very proud that at a time when all countries have closed their borders to protect their resources and internal infrastructure, a Romanian company has managed to conduct studies of such magnitude exclusively with specialists and local resources, the entire research being done by MedLife research division, respectively by Romanian specialists" said Mihai Marcu, President & CEO of MedLife Group.

Pentru detalii suplimentare vă stăm la dispoziție:

Ina Bădărău
PR Manager
Mobil: 0756 56 56 37
E-mail: ibadarau@medlife.ro
<http://www.medlife.ro>

MedLife completed the first stage of the SARS-CoV-2 virus genome sequencing study. The company will monitor genetic mutations on a monthly basis in relevant outbreaks to identify if other mutations might occur and if a strain other than European strains which may behave epidemiologically different might be important. At this stage, MedLife has already completed the sequencing of a second group of 50 samples and will publish an analysis in July.