



# Research describes genetic changes caused by Covid-19 and identifies medications that can combat the virus

Geovana Benites / 9 de novembro de 2023 / In English

## Bioinformatics | Study also compares genetic signatures of Covid-19 in cases ranging from mild to severe

\*By Geovana Benites

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\*Photo: Flávio Dutra/ Arquivo JUI June 03rd, 2020 --, Throughout a critical scenario of the pandemic, a professional works on testing to identify SARS-CoV-2 contamination, together with a task force from the Institute of Health Sciences (UFRGS)

Since 2020, the world has been fighting a common enemy called Covid-19. It has affected more than 760 million people and has killed more than 6.8 million worldwide, according to the World Health Organization (WHO). An article published in *Virus Research* has described the genetic alterations caused by the disease in order to better understand its patterns, especially in the case of severe illness. Such descriptive data have made the comparison of those alterations within a Protein Data Bank (PDB) possible and also identified 52 new therapeutic methods that can help counter Covid-19.

It was called "A comparative study of COVID-19 transcriptional signatures between clinical samples and preclinical cell models in the search for disease master regulators and drug repositioning candidates", written by the researcher Henrique Chapola of the Graduate Research Program in Biological Sciences – Biochemistry at UFRGS.

### The need to be still discussing about Covid-19

Even though vaccines have been developed faster than usual, there are still new variants, occurrences which indicate that the disease will continue to circulate at least for the next years. Investigating the mechanisms involved in the Covid-19 progress is a promising strategy for discovering new therapeutic candidates. The research was born of Master's thesis Chapola was writing about the regulatory mechanism of Cofilin gene expression. Cofilin is a protein often investigated by the research group. However, the wake of the pandemic made Henrique and his supervisor, Fábio Klamt, decide to analyze the genetic signature of Covid-19, i.e. the virus' patterns.

"I realized it would be awesome if we could help to combat the disease," says Professor Klamt, who happened to be the 37<sup>th</sup> patient hospitalized in Rio Grande do Sul because of Covid, in March 2020. "We adopt this very same Lab procedure Henrique embraced for his project kick-start (using the other protein), which is looking up for public database. Then we thought about directing our efforts to another subject, and Henrique agreed. He actually concluded his Master's research in record time," says the Professor.

In this study, we used gene expression database sets available in public repositories and derived from pulmonary autopsies of patients who underwent severe virus infection (the lung is one of the main targets of SARS-CoV-2). The aim was to find the key regulators, also named as signatures, which change the gene expression pattern as an effect of the disease.

As of this database, a meta-analysis (method that integrates results from independent studies) was carried out to understand the effect caused by the virus infection, i.e. how those cells extracted from the pulmonary autopsies were responding to it.

### New paths for the treatment

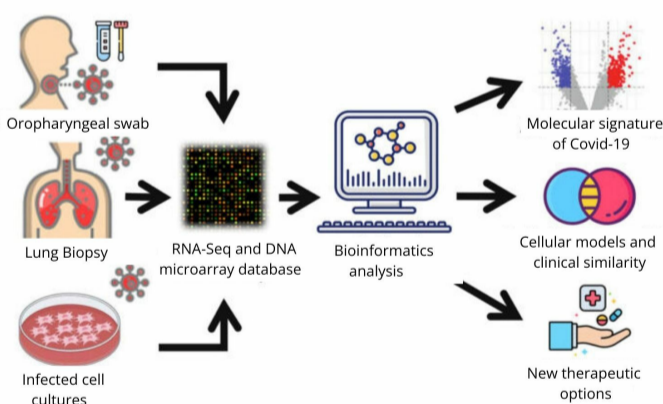
Hydroxychloroquine was the most "famous" drug during the first few months of the Covid-19 pandemic in Brazil, even though there were many scientific indications about its inefficacy. Chapola explains that the first studies regarding this drug, surrounded by a big fuss about its use, made use of inadequate experimental models, because Vero cells were used, along with questionable procedures.

Vero cells are often used in the Virology area, but they are not the target cells of the disease. They were used only to study the infection mechanism and to make a selection of medications that could prevent the infection or spread of the virus. "In our research, we believe research models serve different roles. We must always be careful when we want to skip from something done in cells to something directed to human beings," says the researcher. "We must choose carefully which preclinical cell model to use for the data to be relevant. It is not that it does not work; it works with a Vero cell, but this is not the case for the SARS-CoV-2," he explains.

That is the reason why knowing the pathophysiology of the disease, i.e. its mechanisms, is key for the selection of new therapeutic options. Thus, after the full description of the virus, Chapola compared the genetic signature within a database to identify medications that could be helpful to the treatment of severe illnesses of Covid-19. As a result, 52 drugs that could revert the signature of the disease were found, identification which turned them into prospective candidates for further studies about new clinical treatments. Many medications are in the list, such as humor regulators, antifungals, and corticosteroids.

"Can you imagine? We are talking about bioinformatics. They are databases and Chapola did it all blindfold: he would enter the information and find the result. It is very interesting for us that (maybe) the corticosteroids category is the most representative one, as it was the first to be shown clinically effective. Then we celebrated!," says the Professor happily.

The work also compared the genetic signatures of Covid-19 in cases of severe illnesses (patients facing severe acute respiratory syndrome) and mild illnesses (data obtained through nasopharyngeal swab via PCR testing in positive cases but with no need of hospitalization). The contrastive analysis showed huge similarities between the two severity levels, even if it also showed some limitations in the overlap of clinical (severe illness) and preclinical (mild illness) data. This way, it stressed even more the necessity of a rigorous selection of the best model for each phase of the disease.



Chapola says that it was worth the hard work. He says that it is a small but important step on the fight against the virus. "We are working to somehow make our contribution. We haven't found an ultimate cure yet, and that is okay. However, we have 52 potential cures, and many of them have demonstrated to be effective for the treatment," Chapola. He also reinforces the importance of continuing to study Covid-19. "Even in a scenario of early vaccination and number of casualties dropping, we cannot take for granted that there will not exist new occurrences of severe cases of the disease. Unfortunately, the virus will remain with us for a long time," he completes.

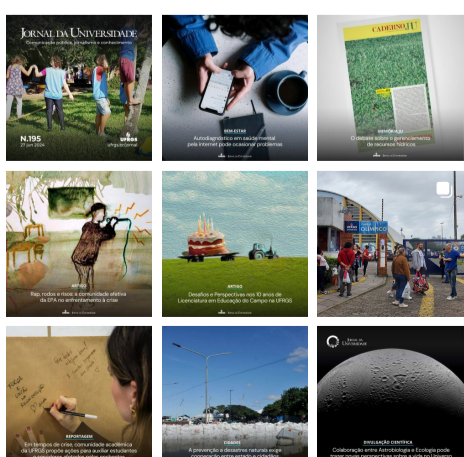
Translated into English by **Vitória Ribeiro Leal**, undergraduate student enrolled in the course "Supervised Translation Training I (English)" of the Undergraduate Program in Language and Literature, under the supervision and translation revision of Professor Elizamari R. Becker (P.h.D.) – IL/UFRGS.

### :: Read in portuguese:

[Pesquisa descreve as alterações genéticas causadas pela covid-19 e identifica medicamentos que podem ajudar no combate ao vírus](#)

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Jornal da Universidade  
Secretaria de Comunicação Social/UFRGS

Av. Paulo Gama, 110 | Reitoria – 8.andar | Câmpus Centro | Bairro Farrroupilha | Porto Alegre | Rio Grande do Sul | CEP: 90040-060

[\(51\) 3308.3368](tel:5133083368)

[jornal@ufrgs.br](mailto:jornal@ufrgs.br)