

SARS-OMICs: Multi-Omics atlas of the Brazilian COVID-19

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COVID-19 is a respiratory syndrome which was declared world pandemic in March 2020. The worst pandemic in the last 100 years. The disease is caused by severe acute respiratory syndrome coronavirus 2, also known as SARS-CoV-2. While most people have mild symptoms, some people develop acute and severe reactions, which may lead to ICU admission and death. Until now, factors that lead to different symptoms are not totally known, possibly being a mixture of host and viral genetic factors. This project aims to identify co-infections by pathogens that may influence the clinical outcome of COVID-19. The study is based on sequencing Generation (NGS) from naso/oropharyngeal swab samples from people infected by SARS-CoV-2 for the characterization of viruses, bacteria and fungi present in these patients. In this context, sequencing of the profile is being carried out microbiological study focused on bacteria and fungi (16S/ITS microbiome and metagenomics) and on the viral profile (virome). At the same time, target sequencing is being carried out aiming to obtain complete genomes of SARS-CoV-2 and provide data inth variants and evolution of the virus. About 600 patients were enrolled in this study. As main results we have: 1. Collection, receipt and application of TCLE in 508 samples. 2. Processing and carrying out the virome experiment on 398 samples. 3. Processing and carrying out the 16S/ITS microbiome experiment on 430 samples. 4. Genotyping of 315 samples of SARS-CoV-2, 215 with full genome recovery. 5. Development of a public dashboard to monitor performance metrics for the sequencing of the SARS-CoV-2 virus and monitoring the evolutionary dynamics and epidemiological data of the virus (<https://sarsomics.com/dashboard/>). 6. Validation of a approach to shotgun total DNA metagenomics sequencing of tract samples respiratory. 7. Development of an online platform for analysis and availability of the multi-omic data generated by the project, name Varsmetagen (<https://varsomics.com/varsmetagen>). Results are being integrated for network analyses and machine learning patterns finding, which we expect to address gaps of knowledge regarding microbial factors and clinical outcome of the COVID-19.