

'Friendly' bacteria may impact COVID severity

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Contributors to the COVID-19 microbiome study include (front row, from left) Julie Bastarache, MD, Meghan Shilts, MS, MHS, (middle row, from left) Jodell Jackson, Ph.D., Suman Das, Ph.D., Angela Jones, MS, (back row, from left) Jonathan Schmitz, Ph.D., MD, Simon Mallal, MBBS, and Jordan Best, Ph.D. Credit: Donn Jones

The U.S. Centers for Disease Control and Prevention (CDC) has awarded Vanderbilt University Medical Center a two-year, \$3.7-million contract to determine genetic and bacterial factors that may increase the

risk for severe illness and death from COVID-19.

The "multi-omic" investigation will determine how the severity of COVID-19 disease may be affected by patients' genetic makeup and by the bacteria that live in their airways, their "respiratory microbiome."

In a paper published last month, VUMC researchers reported that the COVID-19 virus, SARS-CoV-2, interacts with respiratory bacteria in ways that potentially may worsen symptoms.

The CDC-funded project also will genotype, or determine the genetic sequence of, SARS-CoV-2 isolated from nasal swabs collected from 5,000 infected patients at VUMC to determine the presence of any COVID-19 variants.

The researchers hope that by understanding these interacting factors, they will be able to predict which patients are likely to become seriously ill or not respond to antiviral treatments including antibody therapy. The ultimate goal is to translate improved diagnosis into more effective treatments and better outcomes.

VUMC is uniquely positioned to do this kind of investigation because of the depth of its resources in genomics, virology and infectious disease, said Suman Das, Ph.D., associate professor of Medicine.

Das and Jonathan Schmitz, MD, Ph.D., medical director of the Molecular Infectious Diseases Laboratory, are the project's co-principal investigators. Simon Mallal, MBBS, scientific director of the VANTAGE (VUMC Technologies for Advanced Genomics) and IMGST (Immunogenomics, Microbial Genetics and Single Cell Technology) cores, is co-investigator.

Key resources include BioVU, VUMC's massive biobank of more than

400,000 individual samples of DNA and other biological materials.

BioVU is linked to a "synthetic derivative," electronic health records that have been stripped of identifying information and which enable researchers to study differences in the genetic make-up of patients with specific diseases—including COVID-19.

Another resource is MicroVU, which has bio-banked specimens containing more than 200 different species of bacteria linked to the VUMC research data warehouse. Co-directed by Schmitz and Maria Hadjifrangiskou, Ph.D., and managed by the Vanderbilt Institute for Clinical Research (VICTR), the resource includes respiratory specimens from COVID-19 patients.

The VANTAGE core will conduct high-throughput sequencing of the viral genome to determine the presence of variants, and the IMGSCCT core will do HLA and other immunogenomics typing, Mallal said.

Das and colleagues, including Christian Rosas-Salazar, MD, MPH, have studied interactions between respiratory viruses and the microbiome for several years.

In 2018, they [reported](#) that infants who have higher amounts of the "friendly" bacterium *Lactobacillus* present in their nose or upper part of the throat during an acute respiratory syncytial virus (RSV) infection are less likely to develop childhood wheezing later in life.

In the study published in the *Journal of Allergy and Clinical Immunology*, the researchers reported that SARS-CoV-2 infection and its viral load, how much virus is present, impacts the abundance of multiple bacteria in the airway.

"These bacteria may be important in modulating how you respond to the

virus itself," said Rosas-Salazar, assistant professor of Pediatrics and the paper's first author. "We know very little of the risk factors for outcomes in COVID-19, so understanding these viral-bacterial interactions may be key to predicting severity."

More information: Christian Rosas-Salazar et al. SARS-CoV-2 Infection and Viral Load are Associated with the Upper Respiratory Tract Microbiome, *Journal of Allergy and Clinical Immunology* (2021). [DOI: 10.1016/j.jaci.2021.02.001](https://doi.org/10.1016/j.jaci.2021.02.001)

Provided by Vanderbilt University

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