

Groundbreaking study reveals oral microbiome's role in immune response and COVID-19 severity

Newly developed AI model shows that saliva is a better predictor of COVID-19 severity than existing blood tests

LA JOLLA, CA, USA, April 18, 2024 /EINPresswire.com/ -- The human mouth is teeming with organisms collectively referred to as "the oral microbiome." A growing body of evidence shows

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*Marcelo Freire, DDS, PhD,
DMedSc*

that in healthy individuals, the oral microbiome acts as a critical first line of defense against unwanted bacteria, viruses, and other pathogens that enter our mouths, including the virus that causes COVID-19. The human microbiome has a direct relationship with the immune system.

In a newly published study, a team of researchers from [J. Craig Venter Institute \(JCVI\)](#) and other organizations sought to understand the specific relationship between the oral microbiome, oral immune response, and COVID-19 infections. They discovered that the variety of organisms

found in the mouth may be used to detect disease and, if present, its likely severity. People with a more diverse oral microbiome tend to have milder symptoms, while those with less diversity experience more severe symptoms and a dysregulated immune response in the mouth and blood.

By analyzing saliva with the aid of artificial intelligence, researchers can predict not only if someone has COVID-19 but also how severe their case might be. This discovery could lead to new ways of monitoring and understanding the disease using saliva, rather than an invasive blood sample.

“We confirmed our suspicions that an unhealthy oral microbiome leads to an overall more severe immune response, impacting the clinical symptoms of COVID-19. By contrast, a healthy microbiome is remarkably diverse. The variety of organisms and the balance between the blood and saliva microbiome keep the body's health in balance and offer the mouth a way to guard against the constant threat of infection,” said Marcelo Freire, DDS, PhD, DMedSc, an associate

professor at JCVI and senior author on the study.

The study also looked at certain immune proteins in saliva and blood, called cytokines, which are part of the body's immune response. Interestingly, the response in saliva was different from that in the blood, suggesting that our mouth reacts uniquely to SARS-CoV-2, the virus that causes COVID-19. While the blood showed high cytokine levels, mucosal tissues in the mouth did not, evidence of local immunosuppression caused by the virus.

The team was able to confirm their hypothesis that mucosal tissues, like those in the mouth, are used for viral replication and shedding, which in turn leads to a loss in diversity in the oral microbiome and consequently immunosuppression in the mouth. This finding reinforces the importance of caring for the oral microbiome in the overall health of an individual and the relevance of studying how these interactions work at the molecular level.



Senior author, Marcelo Freire, DDS, PhD, DMedSc

Because of the complex nature of the data, the team developed a new machine learning approach, based on previous work by some of the study authors, to further dissect the oral interactome, identifying patterns and relationships between the oral microbiome, immune response markers, and COVID-19.

They learned that the number of distinct organisms found in the mouth are inversely related to COVID-19 severity. That is, as the number of species in the oral microbiome dropped fewer were available to drive the immune response, thus the more serious the cases of COVID-19 became.

Cytokine response was also predictive of COVID-19 severity, but not as strongly as microbiome diversity. In combination, cytokine and microbiome data showed strong predictive features using the machine learning model and was more accurate than existing blood tests.

The team is planning to use similar techniques for Long COVID as viral persistence and dysbiotic host-microbial interactions need to be further investigated. Ultimately, their goal is to help develop less invasive diagnostic testing and to advance personalized medicine.

This work was a collaborative effort between J. Craig Venter Institute (JCVI), the Ministry of Health in Kuwait, Harvard School of Dental Medicine (HSDM), Tufts School of Dental Medicine (TSDM) and the University of Alberta. The full study, [“Host-microbiome associations in saliva predict COVID-19 severity.”](#) may be found in the journal PNSA Nexus.

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[About J. Craig Venter Institute](#)

The J. Craig Venter Institute (JCVI) is a not-for-profit research institute in Rockville, Maryland and La Jolla, California dedicated to the advancement of the science of genomics; the understanding of its implications for society; and communication of those results to the scientific community, the public, and policymakers. Founded by J. Craig Venter, Ph.D., JCVI is home to approximately 120 scientists and staff with expertise in human and evolutionary biology, genetics, bioinformatics/informatics, information technology, high-throughput DNA sequencing, genomic and environmental policy research, and public education in science and science policy. JCVI is a 501(c)(3) organization. For additional information, please visit www.jcvi.org.

Media Contact

Matthew LaPointe, mlapointe@jcvi.org, 301-795-7918

Matthew LaPointe
J. Craig Venter Institute
+1 301-795-7918
[email us here](#)

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