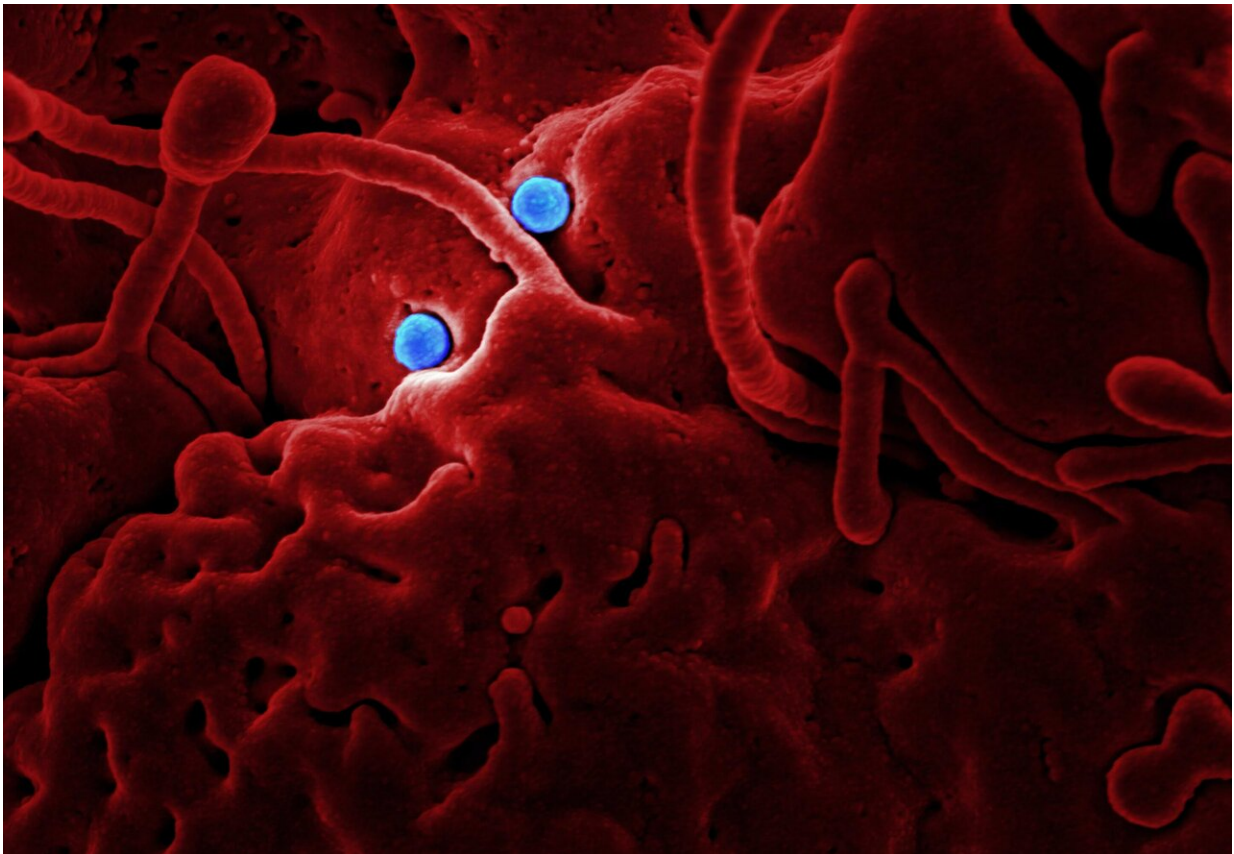# Gut microbiome data may be helpful in routine screening of cardiovascular disease

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Credit: Unsplash/CC0 Public Domain

Using artificial intelligence to analyze the bacteria in a person's gut microbiome shows promise as a new screening method for cardiovascular disease (CVD), according to preliminary research to be

presented Sept. 10-13, 2020, at the virtual American Heart Association's Hypertension 2020 Scientific Sessions. The full study published simultaneously today in *Hypertension*, an American Heart Association journal.

Recent studies have found a link between gut microbiota, the microorganisms in human digestive tracts, and CVD, which is the leading cause of mortality worldwide. Gut microbiota is highly variable between individuals, and differences in gut microbial compositions between people with and without CVD have been reported.

"Based on our previous research linking gut microbiota to CVD in animal models, we designed this study to test whether it is possible to screen for CVD in humans using artificial intelligence screening of stool samples," said Bina Joe, Ph.D., FAHA, the study director, Distinguished University Professor and Chairwoman of the department of physiology and pharmacology at the University of Toledo in Toledo, Ohio. "Gut microbiota has a profound effect on cardiovascular function, and this could be a potential new strategy for evaluation of cardiovascular health."

Researchers used data from the American Gut Project (an open platform for microbiome research based in the United States) to analyze microbial composition of stool samples with state-of-the-art machine learning modeling. Nearly 1,000 samples were analyzed, and approximately half of the samples were from people with CVD. The model was able to identify different clusters of gut bacteria that could potentially help identify individuals with existing CVD and without CVD.

Among the bacteria identified:

- Bacteroides, Subdoligranulum, Clostridium, Megasphaera, Eubacterium, Veillonella, Acidaminococcus and Listeria were

more abundant in the CVD group.

- Faecalibacterium, Ruminococcus, Proteus, Lachnospira, Brevundimonas, Alistipes and Neisseria were more abundant in the non-CVD group.

"Despite the fact that gut microbiomes are highly variable among individuals, we were surprised by the promising level of accuracy obtained from these preliminary results, which indicate fecal microbiota composition could potentially serve as a convenient diagnostic screening method for CVD," Joe said. "It is conceivable that one day, maybe without even assessing detailed cardiovascular function, clinicians could analyze the gut microbiome of patients' stool samples with an artificial machine learning method to screen patients for heart and vascular diseases."

More information: Sachin Aryal et al. Machine Learning Strategy for Gut Microbiome-Based Diagnostic Screening of Cardiovascular Disease, *Hypertension* (2020). DOI: 10.1161/HYPERTENSIONAHA.120.15885

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