Deficiency in how gut microbiome-produced substances are detected in high blood pressure

August 2 2021, by Silvia Dropulich

Credit: CC0 Public Domain

A new study led by Monash University scientists has found that microbial genetic pathways are different in people suffering from hypertension.

The research also found that those with hypertension also have a deficiency in a newly identified target gene that senses gut microbiota -derived metabolites that lower blood pressure.

The study, led by Associate Professor Francine Marques from the Monash University School of Biological Sciences in collaboration with the Baker Heart and Diabetes Institute, is published today in *Hypertension*.

If left untreated, hypertension, also referred to as high blood pressure, can lead to stroke and, myocardial infarction, the main causes of death globally. Long-term, hypertension causes a stiffening of the arteries and the muscles of the heart, leading to heart failure. This is important as the research team also found in another recently published study that patients with heart failure, for which hypertension is a major risk factor, have a distinct gut microbiome composition.

"Hypertension is the most common risk factor for cardiovascular disease ," said Associate Professor Marques, a National Heart Foundation Future Leader Fellow, whose work on high blood pressure and cardiovascular disease has been recognized by the Australian Academy of Science.

The research team assessed human gut microbiota in the setting of high blood-pressure levels and heart failure to better understand the complex nature of these diseases. Changes in gut microbiome were particularly associated with bacteria that are known to produce short-chain fatty acids, substances their team has previously shown to ameliorate blood pressure and heart disease in mice.

Previous studies have found that gut microbiota can interact with the host's environment and genome.

"We performed the first gut microbiome study recruited in metropolitan

(Melbourne) and regional (Shepparton) areas of people with normal and high blood pressure, both men and women, whose blood pressure was measured using gold standard blood pressure monitoring," explains Associate Professor Marques.

"This work addresses many gaps in the current literature including a comparison across metropolitan and regional areas, men and women, all with 24-hour blood pressure measurements."

The researchers found that the gut microbiome was mostly similar between normotensive and essential hypertensive groups, but the gut microbial gene pathways were different, suggesting major differences in the function of the microbiota.

They also found that hypertensive subjects have a deficiency in a new target gene that senses gut microbiota derived metabolites that lower blood pressure.

In a separate but related development Associate Professor Marques is currently working on a clinical trial funded by the National Heart Foundation to determine if a modified fiber supplement, which produces high levels of beneficial gut substances as a result of microbial fermentation, could be used as a new strategy to lower blood pressure.

More information: Michael Nakai et al, Essential Hypertension Is Associated With Changes in Gut Microbial Metabolic Pathways, *Hypertension* (2021). DOI: 10.1161/HYPERTENSIONAHA.121.17288

Anna L. Beale et al, The Gut Microbiome of Heart Failure With Preserved Ejection Fraction, *Journal of the American Heart Association* (2021). DOI: 10.1161/JAHA.120.020654

Provided by Monash University