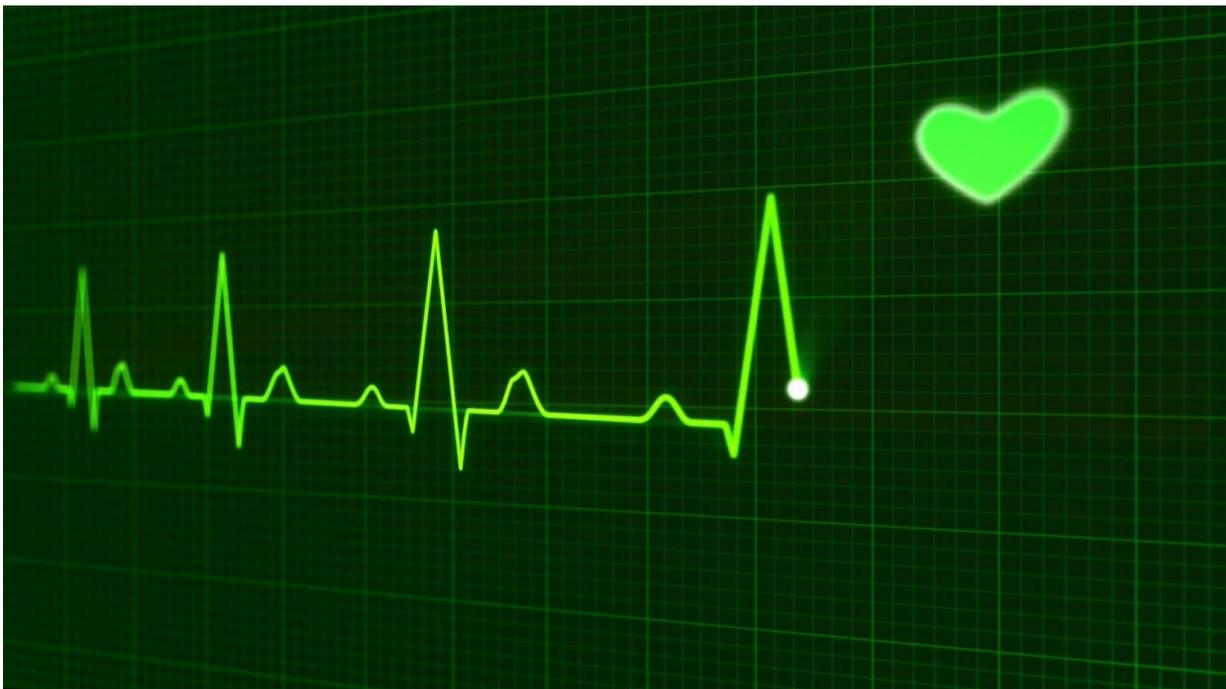


Heart failure is associated with loss of important gut bacteria

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In the gut of patients with heart failure, important groups of bacteria are found less frequently and the gut flora is not as diverse as in healthy individuals. Data obtained by scientists of the German Centre for Cardiovascular Research (DZHK) provide valuable points of departure for understanding how gut colonisation is associated with the development and progress of heart failure.

It has long been known that [heart failure](#) and gut health are linked. Thus, the gut has reduced blood supply in instances of heart failure; the intestinal wall is thicker and more permeable, whereby bacteria and bacterial components may find their way into the blood. Moreover, scientists know that the composition of the [gut bacteria](#) is altered in other widespread diseases such as type 2 diabetes. Against this backdrop, researchers at the DZHK site Hamburg/Kiel/Lübeck investigated whether and how the [gut flora](#) in patients with heart failure changes.

In order to do this, they analysed the gut bacteria in stool samples of healthy individuals and patients with heart failure. The project headed by Professor Norbert Frey of the University Hospital Schleswig-Holstein, Campus Kiel, was conducted in close cooperation with Professor Andre Franke's team at the Christian-Albrechts-Universität zu Kiel, which found that the sections of the bacterial genome deciphered the distinction of the microorganism. The results showed that a significantly lower proportion of different bacteria are found in the gut in patients with heart failure than in healthy controls. Individual important families of bacteria are significantly reduced. It is still unclear whether the gut flora is altered as a result of heart failure or whether it may be a trigger for this disease.

Influential factors: diet, medication, smoking

"Of course, other factors also affect the composition of our gut bacteria. We know that the gut flora of a vegan who starts eating meat changes within three days", explains associate professor Dr. Mark Lüdde of the University Hospital Schleswig-Holstein, Campus Kiel. For this reason, we asked the Kiel-based researchers of dietary habits beforehand. Individuals with an extreme diet, such as a vegan diet, were not allowed to participate in their study. Instead, they chose individuals with a standard diet comprising both meat and vegetables for both groups.

In addition to diet, medication also affect the gut flora. It was, therefore, important that the control group also took medicinal products that patients with heart failure must take routinely. Antibiotics could not have been administered for at least three months prior. Smokers were also included in both groups. All participants were from the same region and were the same age; gender distribution and BMI were equal in both groups.

Consequence or cause of the disease?

The observed pattern of the reduced genera and families of bacteria seems very characteristic of heart failure, which is why these results may be new points of departure for therapies. The differences between healthy individuals and those with heart failure, thus, came about mainly through the loss of bacteria of the genera *Blautia* and *Collinsella*, as well as two previously unknown genera that belong to the families *Erysipelotrichaceae* and *Ruminococcaceae*.

Other research projects have shown that the occurrence of *Blautia* curbs inflammations. Similarly, the genus *Faecalibacterium* is associated with anti-inflammatory mechanisms. It is, however, not only reduced in patients with heart failure. Since heart failure is accompanied by a chronic inflammation, one theory is that the gut flora fosters the systemic inflammation. Yet generally scientists currently believe that the gut flora changes as a consequence of heart failure. Lüdde and his colleagues believe it is plausible that an altered bacterial profile could also be a risk factor or an early disease marker for heart failure. This is supported by the recent characterisation of trimethylamine N-oxide (TMAO), a metabolic product of gut [bacteria](#), as an independent risk factor for the mortality rate in patients with heart failure. Further investigations are scheduled to clarify the cause and effect of altered gut [flora](#) in [patients](#) with heart failure. The scientists anticipate obtaining new knowledge on how [heart failure](#) occurs and progresses.

More information: Mark Luedde et al. Heart failure is associated with depletion of core intestinal microbiota, *ESC Heart Failure* (2017). [DOI: 10.1002/ehf2.12155](https://doi.org/10.1002/ehf2.12155)

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