Compound derived from hops reduces abundance of gut microbe associated with metabolic syndrome

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Hops, like those growing on this trellis in Corvallis, Ore., can be a source of xanthohumol, which researchers believe may have value in addressing obesity and metabolic syndrome. Credit: USDA

Researchers have shown in a mouse model and lab cultures that a compound derived from hops reduces the abundance of a gut bacterium associated with metabolic syndrome.

The findings, published today in the journal *Microbiome*, are important because an estimated 35% of the U.S. adult population suffers from the syndrome, a common and serious condition linked with cognitive dysfunction and dementia as well as being a major risk factor for cardiovascular disease and type 2 diabetes.

A diet high in saturated fat results in chronic low-grade inflammation in the body that in turn leads to the development of metabolic syndrome.

Patients are considered to have metabolic syndrome if they have at least two of the following: abdominal obesity, high blood pressure, high blood sugar, low levels of "good" cholesterol, and high levels of triglycerides.

OSU researchers for years have been studying the potential health benefits of xanthohumol, a chemical found in hops, and its derivatives including tetrahydroxanthohumol. The latter is commonly abbreviated to TXN, the former to XN.

XN is a polyphenol, a type of abundant organic compound existing in plants and used for millennia by practitioners of traditional medicine. XN is one of the flavonoids—natural products found in fruits,

vegetables, grains, bark, roots, stems, flowers, tea and wine—that are well known for their positive effects on health.

In the most recent study, Andrey Morgun of the OSU College of Pharmacy, Natalia Shulzhenko of the Carlson College of Veterinary Medicine, and Adrian Gombart of the Linus Pauling Institute and College of Science demonstrated that TXN can combat metabolic syndrome by reducing the population of Oscillibacter species within the gut microbiome.

More than 10 trillion microbial cells from about 1,000 different bacterial species comprise the human gut microbiome, the community of microorganisms in the digestive tract.

The researchers employed a novel computational method developed earlier by Morgun and Shulzhenko, transkingdom network analysis, to uncover TXN's mechanism for ameliorating metabolic syndrome. The analysis predicts which types of bacteria control the expression of mammalian genes connected to specific medical conditions.

"We found TXN mainly works by reducing the abundance of gut microbes that promote inflammation in the adipose tissue's macrophage cells, and improving glucose metabolism," Morgun said.

Macrophage cells are large cells that are part of the immune system. Glucose metabolism, the body's ability to convert the sugar into fuel, generally suffers impairment as someone becomes obese, which in turn can lead to the person becoming more overweight.

Faulty glucose metabolism also negatively affects brain physiology and is at the root of multiple medical conditions including diabetes and heart disease.

"When exposed to a high-fat diet common to metabolic syndrome, Oscillibacter bacteria help prompt the inflammation of fatty tissue that drives the syndrome," Morgun said. "TXN serves to limit Oscillibacter species' numbers."

The research is a part of a larger collaborative effort spearheaded by Gombart, Fred Stevens of the OSU College of Pharmacy and Claudia Maier of the College of Science, who are exploring ways to improve human health, particularly as it pertains to diet and obesity, through hops compounds.

A little over a year ago, Morgun and Shulzhenko published research showing Oscillibacter and adipose tissue's link to type 2 diabetes, a finding that now suggests TXN may be able to help treat that condition too.

More information: N. K. Newman et al, Reducing gut microbiome-driven adipose tissue inflammation alleviates metabolic syndrome, *Microbiome* (2023). DOI: 10.1186/s40168-023-01637-4

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