

Metformin alters gut microbiota composition in diabetes (Update)

19 November 2016



Akkermansia muciniphila, known for mucin degradation, and several gut microbiota known for production of short-chain fatty acids (SCFAs), compared to participants without diabetes. Participants with diabetes not taking metformin had higher relative abundance of Clostridiaceae 02d06 and a distinct operational taxonomic unit of *Prevotella*, as well as lower abundance of *Enterococcus casseliflavus*, compared to those without [diabetes](#).

"Our results support the hypothesis that metformin shifts gut microbiota composition through the enrichment of mucin-degrading *A. muciniphila* as well as several SCFA-producing microbiota," the authors write. "Future studies are needed to determine if these shifts mediate metformin's glycemic and anti-inflammatory properties."

Several authors disclosed financial ties to the nutrition industry.

More information: [Full Text \(subscription or payment may be required\)](#)

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(HealthDay)—Metformin seems to alter gut microbiota composition, according to a study published online Nov. 14 in *Diabetes Care*.

Jacobo de la Cuesta-Zuluaga, from the Vidarium-Nutrition Health and Wellness Research Center in Medellin, Colombia, and colleagues examined the correlation between type 2 diabetes, [metformin](#), and [gut microbiota](#) among Colombian adults. Analyses focused on 28 [participants](#) diagnosed with diabetes (14 taking metformin) and 84 sex-, age-, and body mass index-matched participants without diabetes. Demographic information, anthropometry, and blood biochemical parameters were measured, and fecal samples were collected. The composition and structure of the gut microbiota was analyzed using 16S rRNA gene sequencing.

The researchers observed a correlation between diabetes and gut microbiota, which was modified by use of metformin. Participants with diabetes taking metformin had higher relative abundance of

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