

Gut Microbes Associated With HDL, Triglycerides, and BMI

Becky McCall | September 11, 2015

Decreased gut microbial diversity is strongly associated with high body mass index (BMI) and triglyceride levels, as well as a low level of high-density lipoproteins (HDL), according to results of the first study to determine how the gut microbiome relates to body weight and blood lipids.

Specifically, associations were established for 34 intestinal bacteria with BMI and lipids, and the composition of gut microbiota was found to explain up to 6% of the variation in lipid levels, independent of age, gender, and host genetics.

However, the gut microbiome had little effect on low-density lipoproteins (LDL) or total-cholesterol levels.

Jingyuan Fu, PhD, from University Medical Center Groningen, the Netherlands, was lead investigator of the study, published online September 10 in *Circulation Research*. "Lower gut microbial diversity can now be added as a new risk factor for heart disease," she asserted.

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Dr Fu and her colleagues aimed to determine whether there was a link between the gut microbiome, BMI, and lipid levels.

"For the first time, our study provides solid evidence for the link between gut microbes and blood lipids in a large human population," she confirmed. "This supports the potential of microbiota-modifying interventions to control BMI and blood lipids, thereby helping to prevent cardiovascular disease."

Largest Human Study Linking Microbiome With Lipids and BMI

Explaining the rationale behind the study, Dr Fu said, "It has been known that the bacterial community is associated with an individual's susceptibility to many diseases, including cardiovascular diseases.

"However, we still know very little about the extent to which the gut microbiome contributes to the risk associated with blood lipids and heart disease and which bacteria play an important role."

Because less than 30% of bacteria in the human gut can be cultured, very little has previously been known about them, she added.

But recently available state-of-the-art deep sequencing technology, as used in this study, has enabled the identification of such bacteria and allowed her and her team to determine their effects on blood lipid levels.

The researchers conducted a systematic analysis of the host genome, the gut microbiome, BMI, and blood lipids in 893 human subjects from the Dutch LifeLines-DEEP cohort, which is assessing the biomedical, sociodemographic, behavioral, physical, and psychological factors that contribute to the health and disease of the general population.

Using the new sequencing technology, they investigated which particular gut bacteria were associated with BMI and blood lipids and how much of the variation in blood lipids could be explained by the gut microbiome, relative to age, gender, BMI, and host genetics.

Dr Fu clarified that the participants had a wide range of BMIs (16.9–44.9) and lipid levels and that the incidence of obesity (BMI >30) or dyslipidemia was representative of the Dutch population.

Patients taking lipid-lowering or antibiotic medication were excluded.

Novel Microbes Associated With Lipids and BMI Identified

Healthy lipid levels were associated with increased microbial diversity, and 34 microbial taxonomies associated with BMI and blood lipids were identified.

"Most of these are novel," Dr Fu commented.

The researchers then looked at the degree of variance in lipid levels and found that by including age, gender, genetic factors, and gut microbiome in a novel risk model, up to 25.9% of HDL variance was explained, "significantly outperforming the risk model without microbiome," they write.

Strikingly, the microbiome was found to have little effect on LDL or total cholesterol, note the authors.

But microbiota explain 4.5% of the variance in BMI, 6% in triglycerides, and 4% in HDL, independent of age, gender, and genetic risk factors, they add.

Of the bacteria identified within the microbiome, associations with obesity were confirmed for several species previously implicated — for example, genus *Akkermansia*, phylum *Firmicutes*, and phylum *Tenericutes*, all of which are associated with low BMI, noted Dr Fu.

Lower abundances of families *Christensenellaceae* and *Rikenellaceae*, class *Mollicutes*, genus *Dehalobacterium*, and kingdom *Archaea* were associated with a high BMI.

"We found that these [low]-BMI-associated bacteria are also associated with lower levels of triglycerides and higher levels of HDL. This indicates the overall role of these bacteria in human metabolism," Dr Fu reported.

The researchers also observed several new associations, including genus *Eggerthella* with increased triglycerides and decreased HDL and family *Pasteurellaceae* with decreased triglycerides.

Implications of the Findings

Commenting on the implications, Dr Fu explained that the microbiome plays a part at the interface between human diet and drugs.

"Fecal transplantation [the process of transplantation of fecal bacteria from a healthy individual into a recipient] has become an attractive intervention for disease prevention and therapy," she noted.

Establishing the degree of influence the gut microbiota has on body weight and lipid levels is important, she said, "because it has implications for how we could control body weight and blood lipid levels through microbiome-targeted interventions."

Also, an individual's microbiome may modulate diet and drug pharmacokinetics and as such is considered a key element in designing personalized medicine and precision medicine.

Looking toward future work, she explained that their study had insufficient numbers of patients with cardiovascular disease, so further research would need to identify the causal axis of microbiome-lipids-CVD and to gain more mechanistic insight into the gut bacteria functions.