

Gut bacteria that strongly influence obesity are different in men and women, study finds

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New research being presented at the [European Congress on Obesity](#) (ECO) in Venice, Italy (12–15 May) identifies changes in the composition of gut bacteria that may play a key role in the onset and development of obesity, with differences in men and women, which might affect the metabolism of different nutrients and therefore the presence of bioactive molecules in the gut that influence the development of metabolic disease.

The gut microbiota consists of a complex community of microorganisms (bacteria, viruses, fungi and protozoa) that inhabit the gastrointestinal tract. Disruption in this community (dysbiosis) significantly affects metabolic health and influences the risk of certain diseases, including obesity. However, it is still unclear which species represent a greater or lesser likelihood of developing obesity, as well as the impact of these species on our metabolic health.

To find out more, researchers analyzed metagenomic and metabolomic data from a Spanish population to understand the mechanisms by which these microorganisms are involved in the development of obesity.

They examined the fecal metabolome—the diverse collection of metabolites ([small molecules](#)) found in the gut and shed in feces that are produced by gut bacteria as a byproduct of metabolizing food and make their way into the bloodstream impacting health.

Overall, 361 adult volunteers (251 women/110 men, average (median age 44 years old) were included from the Spanish Obekit study—a [randomized trial](#) examining the relationship between genetic variants and the response to a hypocaloric diet.

All participants (65 normal-weight, 110 overweight, and 186 with

obesity) were classified according to an obesity (OB) index—LOW (BMI ≤ 30 kg/m²; [fat mass](#) percentage $\leq 25\%$ [women] or $\leq 32\%$ [men]; [waist circumference](#) ≤ 88 cm [women] or ≤ 102 cm [men]) or HIGH (BMI > 30 kg/m²; fat mass $>25\%$ [women] or $>32\%$ [men]; waist circumference >88 cm [women] or >102 cm [men]) level of obesity.

Researchers made sure that participants in the LOW and HIGH groups were matched for sex and age.

Genetic microbiota profiling was done to identify the different types, composition, diversity, and relative abundance of bacteria present in stool samples of the participants.

The analysis revealed that individuals with a HIGH OB index were characterized by significantly lower levels of *Christensenella minuta*—a bacterium that has consistently been linked to leanness and health.

In men, greater abundance of *Parabacteroides helcogenes* and *Campylobacter canadensis* species—were strongly associated with higher BMI, fat mass, and waist circumference.

Whereas in women, greater abundance of three species—*Prevotella micans*, *Prevotella brevis* and *Prevotella sacharolitica*—were highly predictive of higher BMI, fat mass and waist circumference, but not in men.

In further untargeted metabolomics analyses, that looked at a broader range of metabolic compounds in the blood, researchers found variation in the abundance of certain metabolites—especially higher levels of bioactive lipids—phospholipids (implicated in the development of metabolic disease and critical modulators of insulin sensitivity) and sphingolipids (that play a role in the development of diabetes and the emergence of vascular complications)—in participants with a HIGH OB

index.

"Our findings reveal how an imbalance in distinct bacterial groups are likely to play an important role in the onset and development of obesity, with considerable differences between the sexes, which might affect the metabolism of different bioactive molecules present in the metabolome that influence the development of metabolic disease," says lead author Dr. Paula Aranaz from the Center for Nutrition Research at the University of Navarra in Spain.

She adds, "Gut microbiome composition, specifically higher levels of the *Christensenella minuta* bacterium, appeared to protect against obesity. Whereas the species that influence the risk of developing obesity appear to be different between the sexes and interventions to help prevent an obesity-favorable microbiome may need to be different in men and women.

"Further research is needed to better understand when the switch to an obesity favorable [gut microbiota](#) may take place, and therefore the right timing for possible interventions."

She concludes, "We hope that this study demonstrates that using metagenomics in combination with metabolomics enables researchers to study the mechanisms involved in the development of metabolic diseases such as [obesity](#) with a high degree of confidence. This novel, broader approach could help to develop nutritional precision strategies for weight loss that modify the presence of specific bacteria strains, or the levels of bioactive molecules."

Despite the important findings, the authors note some limitations, including the small sample size (especially for men) and that the study was conducted in one area in Spain, and because climate, geography, diet, and culture are known to influence the gut microbiome, the

findings might be not generalizable to other populations.

Provided by European Association for the Study of Obesity

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