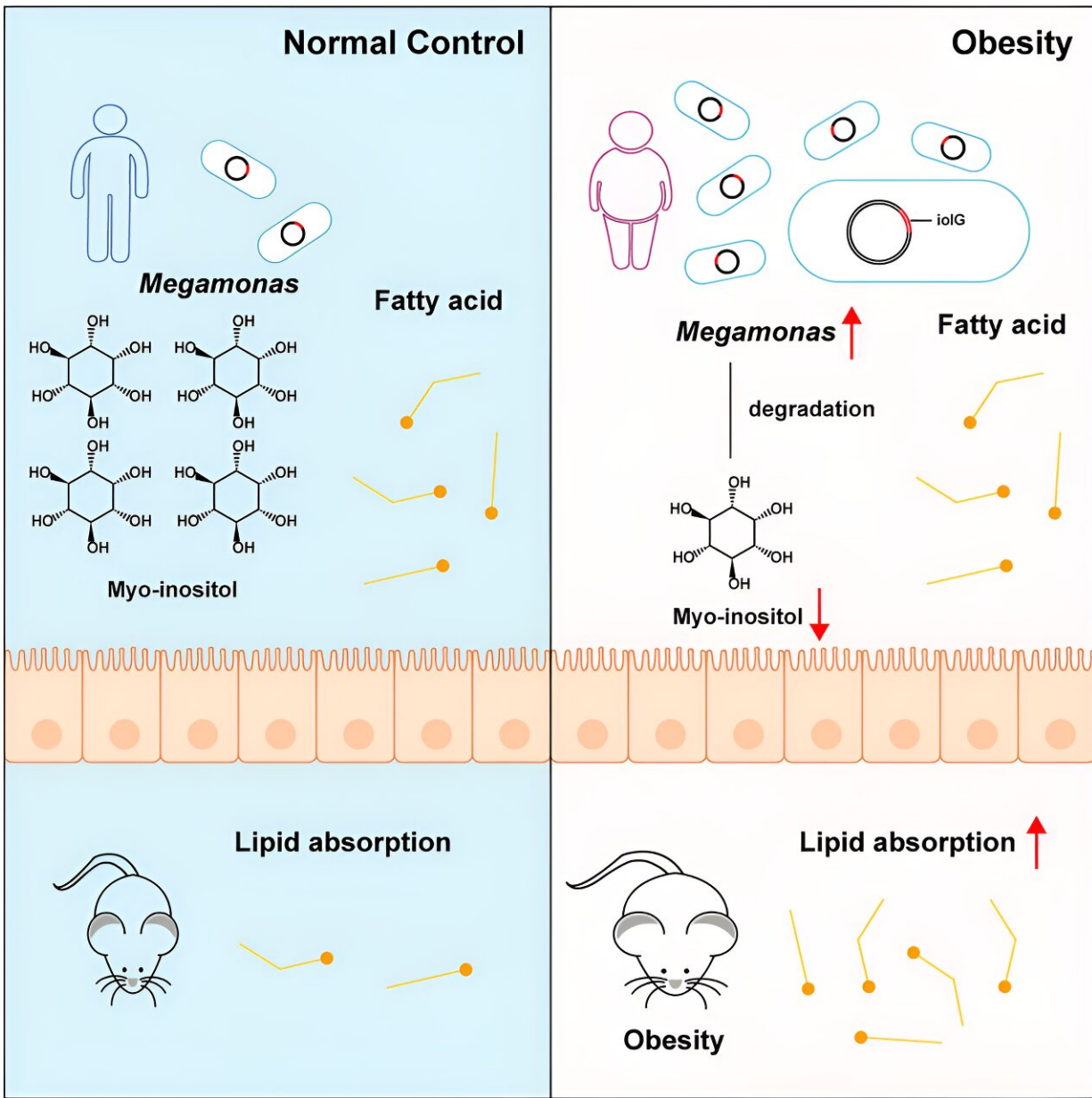


Research reveals gut bacterium *Megamonas* tied to obesity risk

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Graphical abstract. Credit: *Cell Host & Microbe* (2024). DOI: 10.1016/j.chom.2024.06.012

A study [published](#) in *Cell Host & Microbe* identifies a potential obesity-linked bacterium, *Megamonas*, from a large-scale cohort of obese individuals in China. The research suggests potential strategies for future obesity management by illustrating how the bacterium degrades intestinal myo-inositol, enhances lipid absorption, and contributes to obesity.

The study is jointly conducted by Ruijin Hospital affiliated with Shanghai Jiao Tong University School of Medicine, BGI Research, and BGI Genomics Institute of Intelligent Medical Research (IIMR).

"Through a large-scale study of intestinal metagenome and [host genome](#) in obese Chinese, this research reveals a strong link between gut *Megamonas* and [obesity](#)," said Dr. Yang Fangming, co-first author from BGI Genomics.

Dr. Yang adds, "The research uncovers the mechanism by which *Megamonas* induces obesity, providing a new target bacterium for the diagnosis and treatment of obesity."

The researchers performed metagenomic sequencing on [fecal samples](#) from 1,005 individuals, including 631 obese individuals and 374 normal-weight individuals, and conducted whole-genome sequencing (WGS) on 814 of these participants. They reveal a strong link between *Megamonas* and obesity—the combination of *Megamonas* and host genetic risk factors significantly increased the likelihood of obesity.

In the analysis, comprising both obese and normal-weight participants,

metagenomic sequencing showed a notable increase in *Megamonas* in the intestines of [obese individuals](#). All of the samples were further categorized into three enterotypes based on core genera: *Bacteroides*, *Prevotella*, and *Megamonas*. Individuals with the *Megamonas*-dominated enterotype had higher BMI and a greater incidence of obesity.

WGS was performed on 814 individuals to explore the influence of *Megamonas* across various genetic obesity risk backgrounds. The researchers discovered that gut microbial imbalance has a more significant impact on obesity in individuals with low genetic risk. They concluded that *Megamonas* has an additive effect with host genetics on obesity.

The findings were further supported by animal studies. *Megamonas rupellensis* significantly increased weight and fat accumulation in mice on a [high-fat diet](#). The bacterium degrades myo-inositol, a compound that effectively inhibits fatty acid transport. Its degradation enhances intestinal fat absorption, leading to obesity.

More information: Chao Wu et al, Obesity-enriched gut microbe degrades myo-inositol and promotes lipid absorption, *Cell Host & Microbe* (2024). [DOI: 10.1016/j.chom.2024.06.012](https://doi.org/10.1016/j.chom.2024.06.012)

Provided by BGI Shenzhen

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