

GUT MICROBIOTA: LITTLE THINGS MAKING A BIG DIFFERENCE

Eiman Kazi

When we deal with health issues such as obesity, diabetes, cardiovascular diseases and other metabolic disorders, we tend to look at the larger picture of what exactly are causing these problems. We all know that obesity is due to excessive food intake and diabetes is a result of high blood sugars. But sometimes we are oblivious of a very important ecological community that influences these disorders. This community contains a vast diversity of 100 trillion organisms. In this community there are about a 1000 different species with more than 3 million genes, and they colonize virtually every surface of their environment. They live in acidic conditions. They live in inflamed environments. And they all live in you!

The gut microbiota, or gut flora, is a community of bacteria and other microorganisms that live in the digestive tracts of humans and animals. These microorganisms in the gut benefit their host by regulating the development of the gut, aiding in digestion, producing essential vitamins and hormones, fermenting energy substrates, maintaining host energy homeostasis, and regulating our immune systems (Greiner, Papineni, Umar, 2014).

had the genes to encode molecules for hydrolysis of polysaccharides. The African children had two more bacterial species, the Prevotella and Xylanibacter, which are enzymes necessary for hydrolysis of cellulose. Fermentation of fiber produces SCFA, which is important for immunoregulation and the European children had less SCFA than the African children (Maslowski and Mackay, 2011).

They concluded that changes in the composition and function of microbiota could influence diseases and its progression. The gut of a healthy person is linked to the diversity of bacteria in the microbiome, since a more diverse array of bacteria can help break down different foods and molecules that develop the immune system.

Similar research shows that genetics, infant-feeding patterns, use of antibiotics, sanitary living conditions, and dietary habits all influence the development of human gut microbiome.

Researchers at the Colorado State University Department of Food science found evidence that failure of proper early bacterial colonization in a human's early life contribute to food sensitivities, allergies, and diabetes. These researchers found that breast fed infants had a more diverse gut flora community since breast milk contains more than

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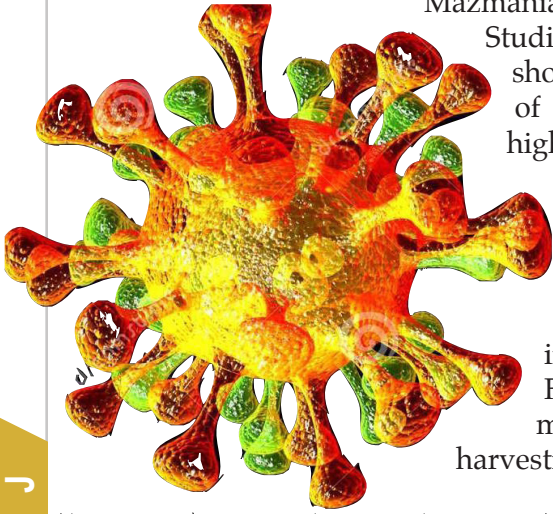
Although these bacteria are miniscule in size, research has shown that there is a relationship between human gut microbiomes and the development of obesity, cardiovascular disease, colorectal cancer, and diabetes. Researchers Kendle M Maslowski and Charles Mackay examined the relationship between the composition of the gut microbiome, diet, and immunoregulation. They explored differences in gut composition between children from rural Africa and urban Europe. Children from Africa had diet consisting of high fiber and their microbiotas were enriched with Bacteroidetes bacteria and other types of bacteria that

700 species of bacteria. The chemical composition of breast milk contributes to taxa diversity in an infant's gut microbiome. Once solid foods are introduced, a child's gut begins to look more like a stable adult microbiome (Voreades, Kozil, Weir, 2014).

An adult microbiome consists of six different bacterial phyla of which are mostly Bacteroidetes and Firmicutes. Diet and the consumption of macronutrients influence the composition of the gut microbiome and affect the abundance of dominant phyla and populations of different bacterial groups present. The term dysbiosis refers to a microbial or bacterial imbalance or unnatural

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shift in the composition of the microbiota (Round, Mazmanian, 2009).



Studies in mice have shown that intake of foods with high fat or high polysaccharides results in a decrease of bacteroidetes and increase in firmicutes. Firmicutes are more efficient at harvesting energy from food, which results in

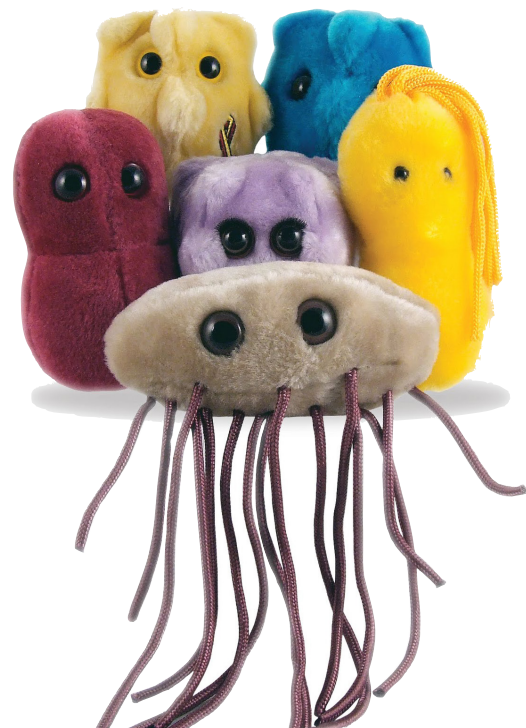
increased calorie intake and thus increases weight. Hence the disproportionality between bacteroidetes and firmicutes is potentially linked with obesity (Turnbaugh, Ley 2006). Furthermore, there was another study done by the American Diabetes Association on two mice groups where one group served as a control group and the other group of mice was fed high fat, high carbohydrate Western diet. The western diet doubled density of small intestinal villi capillaries that augmented monosaccharide uptake and promoted fat accumulation. An obese gut microbiome is enriched with glycoside hydrolases that can break down indigestible polysaccharides (Musso, Gambino, Cassader 2010).

Antibiotics and alcohol can also alter human intestinal bioreactor and overall metabolism of the gut microbiome. Martin Blaser and Isleung Cho did research demonstrating that antibiotic treatment in infants altered bacterial diversity, and contained bacteria that converts indigestible food to useable calories thereby increasing body fat and chances of obesity (Basler and Cho, 2012).

So if research suggests that these communities of extremely minute organisms can be causing large-scale problems such as obesity, then how can we use microbiomes to address these issues? Of course exercise and eating healthy are great solutions for reducing obesity and diabetes. But using current knowledge of microbiomes, researchers are looking into ways of manipulating the gut flora to reduce obesity. A study done by the American Diabetes Association found that mice given a high fat diet induced metabolic endotoxemia, adipose

tissue inflammation, and metabolic disorders. These mice had higher concentrations of bacterial lipopolysaccharide (LPS). Researchers designed an experiment where they changed the mice gut microbiota by using antibiotics to lower plasma LPS. The treatment reduced fat mass development and lowered inflammation. Regardless of diet, both the high fat treated mice and control group showed identical bacterial profiles, similar cecal bacterial composition and metabolic activity after the treatment (Cani, Bibiloni, Knauf 2014). Similarly, in another study, mice that were fed a high-fat diet were administered an engineered N-acetylphosphatidylethanolamines (NAPE) expressing *E.coli* bacteria in drinking water for 8 weeks. NAPE is produced in the intestine to reduce food intake and obesity. Mice that received this engineered bacteria had lower food intake, insulin resistance and adiposity (Chen, Guo 2014).

Whether you believe in traditional methods of reducing obesity through exercise and eating right, or have faith in future research in altering microbiomes to reduce obesity, there is no denying that these tiny organisms significantly impact the human body. We have to realize that our lifestyle and diet not only affect our own body but the composition of these microbiomes. With advanced technology and research we will come to realize that our overall well-being and health are in the hands of these miniscule organisms!



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IMAGE SOURCES

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