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20 Things you Didn't Know About the Human gut Microbiome

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1. Unless you have avoided all mass media recently, you are likely hearing about the “human microbiome”, particularly the gut and how people are sampling their own feces for the purposes of science (more on that below in point #6), taking probiotics, eating loads of yogurt, kombucha or kimchi – to try to foster the “good” bacteria. The science is exploding and we are just in the early stages of making some sense of it all, so here are some things about the gut microbiome that you might find helpful to know. Cardiovascular nurses interested in prevention and diet counseling are encouraged to follow this line of work.
2. The microbiome is defined as all the bacteria, viruses, fungi, archaea, and eukaryotes that inhabit the human body. Collectively referred to as the “second human genome”¹, the gut microbiome in particular is now being considered a separate “organ” with distinct metabolic and immune activity. The two major areas of microbiota investigation include taxonomic diversity to identify “who” is there and functional metagenomics to figure out what they are doing.
3. There are 10x the number of microbial cells in the human gut than in the whole human body, totaling roughly 100 trillion microbes representing as many as 5,000 different species and weighing approximately 2 kilograms.² There are other human microbiome sites as well, including skin, oral, and vaginal, but the gut is the most popular and diverse neighborhood!
4. Until the entry of next generation sequencing in 2005 and the birth of metagenomics, the ability to measure the vast community of microbiota in the human GI tract was not possible since most of the bacteria which reside in the gut are anaerobic and unable to be grown via culture.
5. Our understanding of the “normal” microbiome patterns, including what constitutes a healthy versus diseased pattern is still in its infancy. Only a few associations have been established in human studies thus far.
6. The Human Microbiome Project, funded and directed by the NIH from 2007-2015 and the American Gut Project are the two major studies in the US aiming to characterize the composition and diversity of the human microbiome and establish a dataset library of human microbial communities. For a fee of \$99, anyone can

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participate in the American Gut Project to get their gut microbiome sequenced <http://humanfoodproject.com/americangut/>.

7. Though once thought that the fetal intrauterine environment and GI tract were sterile, the evidence of microbes in meconium suggests that the microbiome may develop sometime during fetal development.³ The neonatal microbiome is further influenced by delivery type (vaginal versus C-section) and feeding type (breast milk versus formula) and continues to develop until age 2-3 years when the gut microbiota stabilizes and resembles that of adults.
8. Antibiotic therapy alters the patterns of gut microbiota and when given early in life (infancy and childhood) may shift the bacterial profile towards one that promotes obesity, metabolic abnormalities and/or autoimmune diseases. This relationship is seen in livestock animals given low-dose antibiotics to enhance growth and weight gain, so this relationship in humans is also being explored.
9. “Normal” gut microbiota in healthy persons include such pathogenic strains as *E. coli* and Enterococci – but as of yet, there is no clear distinction of which are the good versus the bad bacteria,⁴ or if some have both roles.
10. Gut bacteria are involved in harvesting energy from food, balancing the good versus bad bacterial composition, manufacturing neurotransmitters such as serotonin, enzymes and vitamins like vitamin K and are involved with immune and metabolic functions.
11. The gut microbiome of Americans and most other Westernized, industrialized populations is less diverse and dominated by different bacterial species than that of people from rural, less developed populations. Diet plays a role, but a general shift away from natural environments with little exposure to soil, animals, and other environmental microbes seems to be impacting the gut microbiome in potentially detrimental ways. Children raised in homes with pets have less risk of allergic diseases and new evidence is demonstrating a link with gut microbiome patterns. Exposure to dogs seems to alter the gut microbiome to be protective against allergic airway issues and respiratory viruses.⁵ So, Lucy was wrong and a dog kiss a day may help keep bad things away!
12. Gut microbiota differ in obese individuals versus lean individuals, and those with atherosclerosis, diabetes, and metabolic syndrome but the significance of these differences is not yet understood.⁶
13. Fecal microbiota transplant, a treatment that dates back over 1000 years to Chinese practitioners and was first published as a modern therapeutic intervention in 1958,⁷ is the process by which a fecal sample from a “healthy” individual is transplanted into the gut via enema, nasogastric tube or colonoscopy of a diseased patient. It has been the most successful treatment for patients with antibiotic resistant *C. difficile* thus far.⁸ In fact, in 2012 a team of microbiologists, clinicians and public health professionals from M.I.T. established a nonprofit organization called OpenBiome (<http://www.openbiome.org/>) to collect and store fecal samples for fecal microbiota transplant for *C. difficile* patients. This is a new era of “organ” transplant!

14. Fecal microbiota transplant from lean healthy donors has also found to be successful in improving insulin sensitivity in men with metabolic syndrome.⁹
15. Diet seems to be the most powerful influence of the gut microbiome. Processed foods containing emulsifiers and detergent-like compounds may damage the intestinal lining, potentially leading to “leaky gut” and systemic inflammation (contributing to inflammatory-based diseases such as diabetes and CVD). Fibers – including food-based resistant starch, soluble fiber and insoluble fiber are some of the key nutrients for promoting fermentation and ensuring a diverse microbiome. Such non-digestible dietary components are known as prebiotics, which stimulate the growth or activity of the gut microbiota.
16. But what about the ever-popular probiotic supplements? Some studies have reported beneficial effects. However, most probiotic products that are commercially available to consumers have not been investigated for effectiveness. Furthermore, there are no standard formulas or dosages and some probiotic formulas include bacteria that may be beneficial for some problems, but not others. It’s interesting to note that when NY Times journalist and best-selling author, Michael Pollan asked the top experts in the field of microbiome research about their use of probiotics, most do not take them, but rather focus more on a whole-foods diet rich in prebiotic items and fermented foods.¹⁰
17. A wide diversity of gut microbiota is currently thought to be the healthier composition than having only a select few bugs. This diversity is affected by a varied diet rich in plants, vegetables and fruit, so those who have a limited diet also have a low diversity of microbiota. Aging is associated with decreasing microbial diversity and the reduced diversity correlates with nutritional status, increased inflammation and frailty.¹¹
18. In one study, individuals with type 2 diabetes (T2D) had a gut microbiome composition that was distinctive enough to be more predictive of the disease state than BMI compared to control subjects.¹² The individuals with T2D had fewer bacteria with anti-inflammatory properties. The shift in gut microbiota following gastric bypass may be the reason why T2D is improved or resolved even before weight reduction begins.¹³
19. Atherosclerosis is associated with specific gut microbiota and may be fueled by the intake of specific dietary components (phosphatidylcholine, choline, and L-carnitine – a component found in red meat). From these dietary components, the gut microbiota synthesize trimethylamine-N-oxide (TMAO) which is associated with increased risk of major cardiovascular events.¹⁴
20. So, to conclude - what we don’t know about the gut microbiome and its contribution to health and disease is a lot more than what we do know. But one thing is for sure - this is a tremendous area of research with new discoveries and relevant cardiovascular implications, published even faster than we could outline this list. There seems to be great potential for the role of this second human (or

non-human, rather) genome and the role it may have in future therapeutic targets.
Who knew the power of feces or the smooch of a pup!

References

1. Grice EA, Segre JA. The human microbiome: our second genome. *Annu Rev Genomics Hum Genet.* 2012; 13:151–170. [PubMed: 22703178]
2. Flint HJ. The impact of nutrition on the human microbiome. *Nutr Rev.* 2012; 70(Suppl 1):S10–13. [PubMed: 22861801]
3. Goldenberg RL, Hauth JC, Andrews WW. Intrauterine infection and preterm delivery. *N Engl J Med.* 2000; 342(20):1500–1507. [PubMed: 10816189]
4. Swidsinski, A.; Loening-Baucke, V. Functional Structure of Intestinal Microbiota in Health and Disease. In: Fredricks, DN., editor. *The Human Microbiota: How Microbial Communities Affect Health and Disease.* Hoboken, NJ: Wiley Blackwell; 2013. p. 211-253.
5. Brunst KJ, Wright RO, Digioia K, et al. Racial/ethnic and sociodemographic factors associated with micronutrient intakes and inadequacies among pregnant women in an urban US population. *Public Health Nutr.* 2013; 13:1–11.
6. Clarke SF, Murphy EF, Nilaweera K, et al. The gut microbiota and its relationship to diet and obesity: new insights. *Gut Microbes.* 2012; 3(3):186–202. [PubMed: 22572830]
7. Medici V, Shibata NM, Kharbanda KK, et al. Maternal choline modifies fetal liver copper, gene expression, DNA methylation, and neonatal growth in the tx-j mouse model of Wilson disease. *Epigenetics.* 2013; 9(2)
8. van Nood E, Vrieze A, Nieuwdorp M, et al. Duodenal infusion of donor feces for recurrent *Clostridium difficile*. *N Engl J Med.* 2013; 368(5):407–415. [PubMed: 23323867]
9. Vrieze A, Van Nood E, Holleman F, et al. Transfer of intestinal microbiota from lean donors increases insulin sensitivity in individuals with metabolic syndrome. *Gastroenterology.* 2012; 143(4):913–916. [PubMed: 22728514]
10. Pollan M. Some of My Best Friends Are Germs. *The New York Times.* May 19, 2013
11. Claesson MJ, Jeffery IB, Conde S, et al. Gut microbiota composition correlates with diet and health in the elderly. *Nature.* 2012; 488(7410):178–184. [PubMed: 22797518]
12. Karlsson FH, Tremaroli V, Nookaew I, et al. Gut metagenome in European women with normal, impaired and diabetic glucose control. *Nature.* 2013; 498(7452):99–103. [PubMed: 23719380]
13. Furet JP, Kong LC, Tap J, et al. Differential adaptation of human gut microbiota to bariatric surgery-induced weight loss: links with metabolic and low-grade inflammation markers. *Diabetes.* 2010; 59(12):3049–3057. [PubMed: 20876719]
14. Brown JM, Hazen SL. Metaorganismal nutrient metabolism as a basis of cardiovascular disease. *Curr Opin Lipidol.* 2014; 25(1):48–53. [PubMed: 24362355]