The Effects of Antibiotics on the Gut Microbiome.

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Antibiotics have been a known source to treat bacterial infections, but the cost to the gut microbiota can be very detrimental. Mice in the presence of strong antibiotics like ampicillin or vancomycin can overall affect not just the luminal organism present in the gut microbiota, but also disrupt the entire metabolic process that is needed for a functioning gut. The impact of such a drug on the most important microbiomes of the body makes us wonder if taking antibiotics is truly safe for us.

Key Words:
Stem cell, transcription factors, mesenchymal, stem cell therapy

Introduction

Antibiotics have been the number one medication for treating bacterial infections since the early 1900s when the discovery of penicillin was produced. It is advancing technology and has been incorporated into the medical field, as well as the agriculture community. Antibiotics have been found in our everyday meals such as a lovely steak that can be found in the local grocery stores. Although this progressive medical treatment has been beneficial for the medical community as a whole, this medicine seems to have its downsides regarding the gut microbiota. Antibiotics are affecting the gut microbiota in both humans and animals. This can complicate things within our bodies and makes you wonder if the benefits of treating an infection are worth diminishing your entire gut microbiota. The alteration of the gut microbiota can lead to a variety of problems throughout the rest of the patient's life. A recent study on mice has found that antibiotics altered the metabolic homeostasis in mice, in which the lucimal Firmicutes and Bacteroidetes species are gravely affected, along with the alteration of glucose and insulin levels (Zarrinpar et al. 2018). With a depleted microbiota, the number of calories available within the gut will be decreased through absorption, which can lead to hypoglycemia or other insulin-affected conditions. Lucimal Firmicutes and Bacteroidetes are beneficial to the gut microbiota but can be reintroduced into the environment through the ingestion of probiotics. The real concern is if that is enough to help restore the destruction of the gut microbiota.

Recent Progress

A study was done by Zarrinpar et al. in 2018, where they tested the luminal bacteria within mice using different broad-spectrum antibiotics such as ampicillin, vancomycin, neomycin, metronidazole, and amphotericin B. It was found after administering these antibiotics to twelve-week-old mice that within their stool, there was a depletion of all luminal organisms. The mice were also found to have an increase in size and weight in the pouch of the large intestine, known as the cecal. The treated mice started with mostly Bacteroidetes and Firmicutes but after the introduction of antibiotics, the gut consisted of

over 85% of Proteobacteria. Proteobacteria weren't found to be within the gut of the pre-treated mice. The study by Zarrinpar et al. looked at glucose homeostasis within the mice that were treated with antibiotics and those that were not. The scientists were able to find that the mice treated with antibiotics had a lower fasting blood glucose level and the glucose clearance was much faster within the antibiotic mice. There was also a change in the tissue of the mice that the scientist couldn't describe as either lean or fat, but they believe the cause of that could be because of the change in the cecal content of the antibiotic-induced mice. The antibiotic mice had a complete absence of butyrate within the feces as well as a smaller amount of propionic acid. Many primary and secondary acids were very low within the stomach with the presence of antibiotics. The study then moved on to focusing on the metabolic signaling within the gut. Zarrinpar et al. measured different serum levels of glucagon-like peptide 1 and glucose-dependent insulinotropic peptide. Mice in the presence of antibiotics had a higher GLP-1 which most likely had a response after being fed again which initiated the insulin response. The gene that encodes GLP-1 (Gcg) was higher in response. The leptin levels within the antibiotic mice were lower and had nearly twice the amount of glucagon.

Discussion

Overall the antibiotic mice were largely affected by the presence of antibiotics. They were found to have a huge difference in the luminal organisms found within the gut. The decreased amounts of luminal organisms can lead to the presence of arthritis, colitis, or even gastritis. This also affects the signaling that can be found within the gut. Since there was a lack of butyrate within the gut microbiota, there is a lack of fuel for the gut which seemed to compensate by making higher amounts of glucose to replace the fuel that was lost. With the replacement of butyrate for glucose, the entire metabolic process was affected which further leads to the increase of GLP-1 and primary bile acid. The entire bile acid absorption was increased. Zarruboar et al. was able to confirm that glucose homeostasis was impacted, especially due to the lack of leptin that was found within the antibiotic mice which led them to be leptin-deficient. GLP-1 increases led to the reformation of the gut and initially slow the transit process. GLP-1 may inhibit leptin release, which the lack of leptin may be to try and regulate food/energy intake. Furthermore, with the presence of antibiotics causing a lack of biodiversity within the gut microbiota, the probability of becoming type II diabetic and/or obese is very likely. Overall, the presence of antibiotics can affect the gut microbiota and lead to many medical conditions, along with metabolic complications.

This is important because antibiotics are misused all the time. They get overprescribed as well as in most countries they are available over the counter and anyone can just go to the pharmacy and grab some like you would ibuprofen. Many other studies have found that antibiotics affect the gut microbiota with or without infection. A study done by Lange et al. (2016) found that there are potential consequences for health and disease from antibiotic-related changes. Overall the damage to mice in the Yang et al. study makes us ask what the consequences are on our gut microbiome with the presence of this wondrous drug.

References

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