

Impact of the Gut Microbiota

Abstract

A comprehension of the microbiota within health has everything to do with understanding the role it has within the human body. The microbiota is defined as a community of microbes that live in and on an individual which can vary between environmental sites and body location. The article focuses on what affects the microbiota composition within the microbiome over decades it has created an intricate relationship between the job of the microbiota and the gastrointestinal tract (GI) that may alter the composition completely. Within the always changing composition of the gut microbiota it varies from the exposure in diet, adequate water source, medications, and environmental toxins. Multiple factors contribute to the composition of the microbiota and how it impacts the host process through bioactive metabolites that can impact distal organs directly or indirectly (Thursby 2017).

Introduction

The impact of an impaired gut microbiota interferes with the altered microbial composition, known as dysbiosis. Impacts on the microbiota like personal hygiene that includes soap, deodorants, mouthwash, etc. that may alter the entire microbiome. The diet and access to improved water source also contribute towards the bacteria that are within the immune system. Medications depending on the type of antibiotics contribute to the intestinal microbiota. The antibiotic treatment kills off helpful as well as harmful bacteria, and can then allow for pathogens to take over (ex. *C. difficile*). Studies have shown the contribution the gut microbiota has impacted the interaction between cardiovascular disease (CVD). During research over the years, the gut microbiota has been found to have relations towards the contributing factors of other developmental diseases. The research is able to highlight the complicated complex between the microbiota, and the overall progression of cardiovascular diseases (Wilson et al., 2017). When all the testing subsided, the overall results suggested that the gut microbiota has produced numerous amounts of metabolites, which are absorbed within the systemic circulation and are biologically active (Wilson et al., 2017). This was completed through the changing environmental factors that ultimately impact the conditions of the gut microbiota. These studies are aimed towards revealing details that are associated with either the gut microbiota composition or their derived metabolites.

Discussion:

According to the study within the gut microbiota seven components are shown including choline, (TMA/TMAO), Uremic toxins, Bile acids, SCFAs, LPS, and bacterial wall products. The figure shown within the article explains the seven components as possible pathways that may be contributing to cardiovascular and cardiometabolic diseases. After many years of unraveling the mystery behind the role of the gut microbiota, contributes to the 'development of atherosclerosis or its adverse complications' (Tang et al 2017). Studies from both the known animal and human testings help support that the gut microbiota can influence the overall host and disease. The gut microbiota is a complex system and offers many benefits to the host 'through a range of physiological functions like

harvesting energy, protecting against pathogens, regulating host immunity, and even through shaping the intestinal epithelium.

The knowledge of the role of the human gut microbiota has expanded over the decades through the use of methods that includes 'intensive culture-based techniques' (Thursby et al, 2017). The improvement and importance of detecting the makeup of the gut microbiota have grown substantially through low-cost sequencing methods. The microbiota composition and diversity to this date implement techniques from combined data.

Within the article the MetaHit Project and the Human Microbiome Project; have continued to provide the most comprehensive view of the human gut-microbiota to this date in recent research. The compiled statistics from the research publication has identified 2172 species isolated from individuals, which have also been classified within 12 different identified phyla belonging to Proteobacteria, Firmicutes, Actinobacteria and Bacteroidetes (Thursby et al 2017). These findings have amplified further study towards identifying the diversity and complexity of the gut microbiota factors that show the overall impact. Researchers have discovered ground-breaking evidence in favor that supports the focus on host-microbe interactions. These findings pinpointed the specific 'divergence from the normal microbiota composition within the plethora' (Thursby et al 2017) of disease which shows the cause of the ranging conditions that function from chronic GI diseases to neurodevelopmental disorders.

Results:

Future components and perspective may contribute to the new results for what the gut microbiota targets. Steps are still needed for advancements in future research that has to do with the mechanistic understanding and components that emphasize the microbial growth. The researchers were able to show ample evidence from both current and past papers to help support their findings. The entire process through they emphasized the purpose of the study and why it was critical for understanding the connection between the gut microbiota, human health, and disease. Through the years of extensive research, scientists have finally unmasked the interactions of how the microbiota contributes to the progression of cardiovascular disease and other common risk factors.

The administration shows alterations within the gut microbiota and has been identified as a contributing factor in cardiovascular disease development (CVD). One of the findings looks at in particular TMAO. This is the hepatic oxidation product of the microbial metabolite TMA, has gained considerable attention as a potential promoter of other implemented diseases (Tang et al 2017). Altered composition of gut microbiota makes use of the pathogenic mechanism of our gut microbiota and metabolites in cardiometabolic diseases. The components discussed within the discussion of the five phyla included are (Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, and Cerrucomicrobia) showing diversity on the species level (Tang et al 2017). In conclusion, the findings made within this research have come a long way towards dissecting the complex and dynamic makeup of the human gut microbiota. Throughout the studies, they represent the influence they have on the bacterial communities along the GI tract that continue to alter and create other shown impacts on the microbiota. The current understanding that the human GI microbiota role is always changing. With research, scientists are able to focus more on the components that are underlying factors to the study entirely.

References:

Textbook: Murray, Patrick R., author. *Medical Microbiology* / Patrick R. Murray, Ken S. Rosenthal, Michael A. Pfaller; consultant, JMI Laboratories.—8th edition.

Tang, W.H. Wilson, et al. “Gut Microbiota in Cardiovascular Health and Disease.” *Arteriosclerosis, Thrombosis, and Vascular Biology*, 2 Mar. 2017, www.ahajournals.org/doi/abs/10.1161/circresaha.117.309715.

Thursby, Elizabeth, and Nathalie Juge. “Introduction to the Human Gut Microbiota.” *Biochemical Journal*, Portland Press Limited, 1 June 2017, www.biochemj.org/content/474/11/1823.