


Skin exposure to sunlight: a factor modulating the human gut microbiome composition

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ABSTRACT

Background: The gut microbiome has been increasingly acknowledged as playing a pivotal role in human health. Therefore, a number of studies have focused on variables that impact its microbial structure and consequent functionality. A wide range of factors, such as diet, age, sex, life stage, behavior, ethnicity, and diseases have been considered, and strong links were set out. However, some aspects regarding the microbiome determinants are still under-explored. **Discussion:** Recently, Bosman et al. presented evidence that skin exposure to narrowband UVB light modulated the gut microbiome of a specific human cohort. This cohort presented an increase of biodiversity, Firmicutes and Proteobacteria, and a decrease of Bacteroidetes. Based on these findings, we revisited our data on a hunter-gatherer gut microbiome (Yanomami) and identified similarities in the gut microbiome of these two cohorts. Both presented a high abundance of Proteobacteria, which had been observed as a unique feature in the Yanomami gut microbiome, and based on Bosman et al study, could be associated with their natural sunlight exposure. **Conclusion:** In this commentary, we would like to point out that the human lifestyle concerning sunlight exposure should be considered as one force modulating the gut microbiome, highlighting, as proposed by Bosman et al, a novel skin-gut axis which is associated with health and disease.

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The influence of microbes on their hosts, and particularly the contribution of gut microbes for human health and physiology have been deeply explored with the advance of sequencing technologies and metagenomic analysis. In order to gain insights into the gut microbiome evolution and composition, intrinsic and extrinsic factors from the host should be considered, allowing the unraveling of differences among healthy and disease gut bacterial profiles. In the past decade, numerous studies on the gut microbiome of different populations have taken into account a wide range of factors, such as human diet, age, sex, life stage (pregnancy, lactating, menopausal stage), social behavior (use of alcohol, antibiotics, tobacco), geography, environment, ethnicity, and diseases.^{1–14} Most of these studies established a link of one or more of those factors and the gut microbiome composition. Therefore, the gut microbiome modulation is driven by a complex and dynamic network presenting a wide range of variables. However, some variables are still under-explored,

but their careful appraisal may bring insights into the understanding of this complex interaction scenario.

Here, we comment on the Ultraviolet B (UVB) light radiation, one variable that is not usually considered in most gut microbiome studies. Human exposition to UVB light is a direct consequence of the latitude, altitude, weather, time of day and season of the year and, indirectly, of human behavior and lifestyles.¹⁵ Bosman et al.¹⁶ recently reported that human exposure to UVB light could impact the human gut microbiome modulating diverse bacterial taxa. These changes in bacterial abundance/prevalence seem to bring health benefits to their hosts. In order to reach this conclusion, they analyzed a controlled cohort composed of healthy Caucasian females from Vancouver, Canada. The gut microbiome of this cohort was analyzed before and after repeated skin exposure to a Narrow Band UVB light using a phototherapy device. People living in this city located at 49°N latitude are often unexposed to

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natural UVB light for up to 6 months of the year. Under these circumstances, individuals are unable to produce significant vitamin D3 in their skin, resulting in its reduction in the serum level, with impact to their health.^{16,17}

Our research group has been exploring the diversity of the gut microbiome and its functionality among urban and traditional populations, especially the Yanomami ethnicity.¹⁴ These hunter-gatherers inhabit a vast area in the Amazon Region, located around the equator (0 – 4°N latitude) in distinct altitudes. Thus, they are exposed naturally to a high incidence of sunlight and ultraviolet radiation, and this region is devoid of air pollution, a factor that blocks the UVB light from sunlight.¹⁸ It is worth noting that this group mostly does not wear clothes and sunscreens of any type for protection from sun exposure.

The environmental and living conditions observed in Bosman et al. cohort and our studied groups would naturally lead to variations in their gut microbiomes. Nevertheless, similarities in the gut microbiome composition in the Bosman et al.'s group artificially exposed to UVB light and the Amazonian hunter-gatherer Yanomami were observed. Moreover, the UVB light exposure seems to modulate and explain some Yanomami gut microbiome features. In the Bosman et al.'s study, the gut microbiome of the

cohort presented a higher alpha diversity after the exposition to UVB light, as well as an increase in the relative abundance of Firmicutes and Proteobacteria and a decrease in the relative abundance of Bacteroidetes. Regarding the Firmicutes phylum, the abundance of *Lachnospiraceae*, *Ruminococcus* and *Clostridiaeeae* families was significantly enriched. Besides that, a Verrucomicrobia increase was observed in some individuals.¹⁶

Several of these taxonomic features were also observed in the Yanomami and other hunter-gatherers. The microbiome of these traditional groups has been characterized by higher biodiversity and higher Firmicutes to Bacteroidetes ratio contrasting with urban groups (Figure 1).^{1,3–5,14} In Bosman et al.'s study, Firmicutes increased after UVB exposure with the enrichment of *Lachnospiraceae*, *Ruminococcus* and *Clostridiaeeae* families.¹⁶ These Firmicutes families were also abundant in the traditional groups, and abundance of other Firmicutes families/genera was also observed. In fact, genera from Firmicutes phylum are biomarkers of Amazonian traditional groups: *Roseburia* and *Enterococcus* (Yanomami/Brazil), *Streptococcus* and *Anaerostipes* (Yanomami/Venezuela), *Eubacterium* and *Lachnoclostridium* (Matses), *Intestinomonas*, *Flavonicater* and *Magasphaera* (Tunapuco).¹⁴ Therefore, we concluded that Firmicutes taxa could

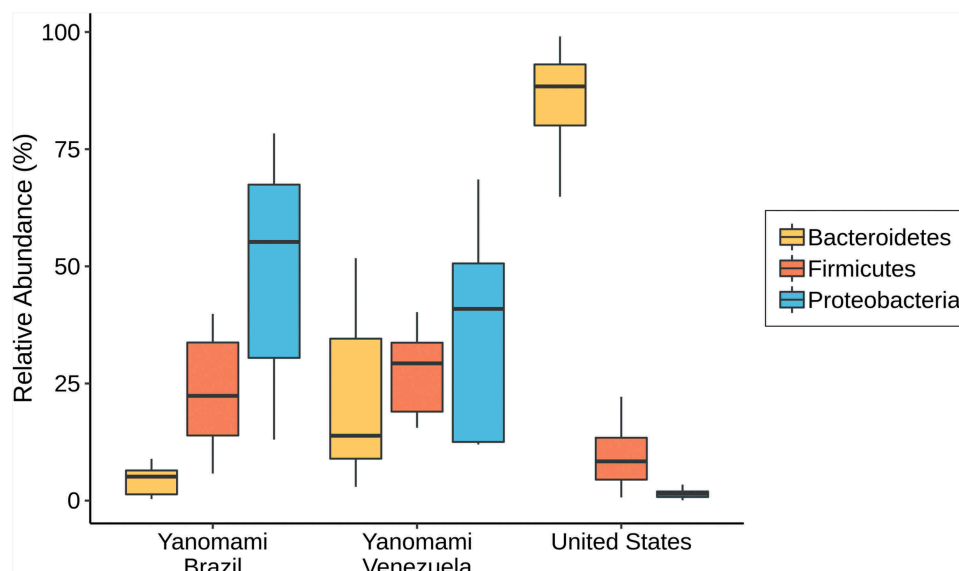


Figure 1. Boxplot showing the relative abundance of the main phyla identified in each group studied: Bacteroidetes, Firmicutes and Proteobacteria. The Yanomami present high Proteobacteria and higher Firmicutes to Bacteroidetes ratio as Bosman et al.'s group exposed to UVB light. This graph was generated based on the relative abundance of the main phyla identified by Kraken in the metagenomes of Yanomami and USA groups, as described in Conteville et al, 2019.¹⁴

be related to the lifestyle, diet, and environment among human groups. Another outstanding factor from Bosman et al.'s study is the fact that Proteobacteria was enriched after UVB light exposure.¹⁶ A high abundance of Proteobacteria was a unique feature within the Yanomami gut microbiome when compared to other traditional groups and urban groups (Figure 1).¹⁴ This aspect remained inexplicable and now it seems that the high exposure to UVB light by the Yanomami due to the environment and their particular lifestyle may be related to the enrichment of Proteobacteria. Additionally, the genus *Akkermansia* from Verrucomicrobia phylum is a Yanomami biomarker and this phylum also presented an increase in few individuals from Bosman et al. after artificial UVB exposure.^{14,16} Altogether, the association of UVB light with specific microbiome taxonomic profiles observed in distinct populations leads us to consider that UVB light/sunlight is a tangible factor that should be considered as a modulator of the gut microbiome.

Since the environment represents one of the main forces associated with the inter-person microbiome variability over the host genetics and other factors,¹² further studies on gut microbiome should consider the sunlight exposure and latitude in-depth, as the one originally addressed by Bosman et al. Therefore, a broad exploration of the relationship between human beings, the microbiome and the environment fills gaps in knowledge that can lead us to understand the relationship between the preservation of health and the development of diseases.

Author Contributions

Both authors actively contributed to the conceptual development of this commentary.

Disclosure of Potential Conflicts of Interest

The authors report no conflict of interest.

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