Functional profiling of the gut microbiome in HIV infection

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Abstract #

INTRODUCTION

The gut microbiome is composed by ~14-14 microorganisms that carry ~x100 fold more human genes. It plays an essential role in human physiology, including the development of the immune system, the homeostasis maintenance and the production of essential metabolites. The gastrointestinal (GI) tract interacts with the largest immune compartment in the body, the gut-associated lymphoid tissue (GALT), which is the first point of contact with the HIV-1. The GALT of HIV-infected patients undergoes a severe and rapid deterioration, and one of its consequences is a harsh microbial imbalance, also called dysbiosis. Compositional shifts in the gut microbiome can predict the progression of HIV infection, which can be a useful biomarker for diagnosis and management. Dysbiosis can lead to unbalanced production of neurotransmitters and cytokines, which can affect immune function and tissue integrity. Dysbiosis is associated with inflammation, immune activation, and tissue damage, which can lead to disease progression. Dysbiosis can also be associated with metabolic abnormalities, such as dyslipidemia and diabetes, which can affect the progression of HIV infection.

MATERIALS AND METHODS

Total DNA was isolated from fecal samples of 80 individuals. Bacterial 16S rRNA genes were amplified by PCR with primers encompassing V3, V4 and V5 regions. The 16S rRNA amplicons obtained were sequenced using Illumina MiSeq.

RESULTS AND DISCUSSION

Most differences among HIV+ men involved the discordant (ID) and the early treated (ET) groups. The microbiome of ID patients was enriched for genes related to biotin metabolism; Ala, Asp and Glu metabolism; beta-lactam resistance and RNA degradation. The microbiome of ET patients contained more genes involved in D-Ala metabolism and fatty acid biosynthesis, among others. The gut microbiome of HIV negative subjects contained more genes associated to synthesis and degradation of ketone bodies, oxononanoate, 7,8-Diaminopimelate thioester through the activity of 5 enzimes. It has been reported that biotin regulates TNF-a production, which plays important roles in the pathogenesis of inflammatory diseases.

CONCLUSIONS

HIV infection is associated with bidirectional unbalances in intestinal metabolic activity, affecting mucosal barrier integrity and function, local and systemic inflammatory processes and energy storage and consumption.