Gut microbiota changes – dysbiotic senescence pattern in the context of viral suppression

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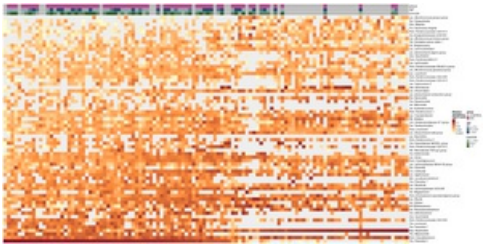
Purpose: A higher incidence of non-AIDS events in people living with HIV (PLWH) is linked to a senescence phenotype, likely influenced by gut microbial dysbiosis. Prior research identified similar dysbiotic patterns in PLWH and ageing HIV-negative population. Regional variations impact microbiota composition, necessitating testing of cohorts from diverse regions for reliable conclusions. This study aimed to compare bacterial genera diversity and representation between PLWH with sustained viral suppression and HIV-negative controls.
Method: Stool samples from a total of 67 male individuals living with HIV (mean age 45.2 years) and 47 HIV-negative controls (mean age 48.2 years) were analysed. For our study, a minimum of 10,000 reads per sample was necessary. PCR reactions targeting the V4 region of the bacterial 16S rRNA gene utilized isolated DNA as a template. Only bacterial taxa exhibiting a mean abundance of at least 0.5% in no fewer than 10 distinct samples were subjected to analysis.
Results: Based on diversity indices, no statistically significant difference in bacterial diversity was observed between PLWH and controls ($p>0.05$). Within the PLWH group, there was a noteworthy decrease in the abundance of genera associated with short-chain fatty acid (SCFA) production, namely *Akkermansia*, *Alistipes*, *Bacteroides*, *Barnesiella*, while *Prevotella*, *Alloprevotella* and *Catenibacterium* genera were significantly more abundant, compared with the control group. The distribution of bacterial genera remained consistent regardless of the duration of antiretroviral therapy (ART).



Conclusions: Despite viral suppression, HIV infection alters gut microbiota composition independently of ART duration. PLWH in our group were found to have reduced levels of SCFA-producing bacteria, which support immunoregulation and epithelial protection. Additionally, we observed higher levels of facultatively anaerobic species, compared with controls. This dysbiotic pattern probably mirrors changes seen in microbiota associated with ageing. Identifying connections between gut microbiota and premature senescence paves the way for new research directions and potential therapeutic interventions.

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