

O1193 Gut microbiome and inflammation in elite controllers vs. progressor patients on antiretroviral therapy

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Background: HIV-1 infection is characterized by disruption of intestinal epithelial barrier, gut microbiota dysbiosis, microbial translocation and persistent immune activation and systemic inflammation. The elite controllers (EC), despite maintaining a sustained control of viremia, have a higher level of immunoactivation and inflammation than HIV patients undergoing antiretroviral therapy (ART). We investigated the impact of HIV infection and ART on the intestinal microbiome composition and its association with levels of microbial translocation, immune activation and inflammation.

Materials/methods: In this observational cross-sectional study we explored the gut microbiome composition of 33 ART-suppressed progressors, 18 ART-naïve controllers (15 elite and 3 viremic controllers), and 5 uninfected control subjects. Bacterial 16S rDNA sequencing (Illumina MiSeq) was performed on fecal samples and plasma markers of microbial translocation and inflammation were analyzed: LPS, I-FABP, sCD14, IL-6 and CD4/CD8. Epidemiological and clinical variables were evaluated.

Results: HIV-1 infected subjects showed increased abundances of Proteobacteria ($p=0.016$) and Actinobacteria ($p=0.002$), and a disruption of the Bacteroidetes bacterial community structure, with a significant increase in Prevotella ($p=0.009$) and a decrease in Bacteroides ($p=0.005$). Family Clostridiaceae ($p=0.020$) and genera Klebsiella ($p=0.037$) were more abundant in EC whereas Desulfovibrionaceae ($p=0.021$) was depleted, but the bacterial community composition of the EC was very similar to that of the ART-suppressed patients. HIV risk factor showed an important impact on microbiome composition and significant differences were detected between MSM and non-MSM (Proteobacteria ($p=0.003$), Bacteroides ($p=0.007$), Prevotella ($p=0.016$), Veionella ($p=0.008$) and Succinivibrio ($p<0.001$)). Plasma IL-6 level was significantly higher in EC than ART-progressors (median 3.6 vs. 1.7 pg/mL; $p=0.029$), whereas LPS and I-FABP were increased in progressors (0.68 vs. 0.97 ($p=0.005$) and 272 vs. 527 ($p=0.001$), respectively).

Conclusions: HIV-1 infection and sexual behavior are interrelated factors contributing to gut microbiota dysbiosis. Gut microbiome in HIV infected EC didn't showed great differences to that of ART-suppressed progressors although differences in microbial translocation and inflammation markers level were detected.