The impact of HIV and length of post-partum period on the gut microbiota in South African Women

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BACKGROUND

- The gut microbiota (GM) has been linked to cardiometabolic health outcomes, including type 2 diabetes (T2D)
- During pregnancy, GM changes are associated with increased inflammation and reduced insulin sensitivity.
- Emerging evidence suggests an impact of HIV on the GM.
- There is a lack of data on the postpartum GM composition, in women living with HIV (WLH) vs. those without HIV.

We hypothesized that the composition of the GM differed by HIV status and postpartum period length among South African women.

In the postpartum period, the composition of the **gut microbiota** was observed to differ by **HIV status** and by **time since delivery.**

METHODS

- A single early morning stool sample was collected from 65 postpartum women enrolled in the Cardiometabolic Health in Pregnancy study (2019-2022) in Gugulethu, South Africa.
- Participants were 6-18 months postpartum, and WLH were on either a dolutegravir (DTG) or Efavirenz (EFV)-based antiretroviral regimen.
- Body composition was measured using dual x-ray absorptiometry and IS measured using an oral glucose tolerance test to derive the Matsuda Index.
- GM composition was analysed using 16S rRNA amplicon sequencing.
- Diversity and differential proportion analysis was performed, using analysis of compositions of microbiomes with bias correction

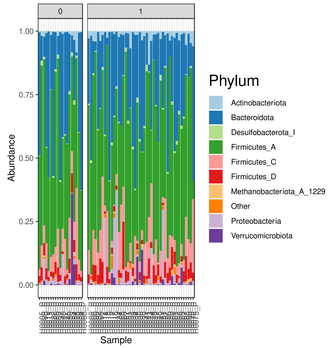

Figure 1: abundance of phyla in sample

RESULTS

- 65 participants were included: 46 WLH (70.7%) and 19 HIV- (29,2%), with no differences in the length of the postpartum period by HIV status.
- WLH had lower BMI, fat mass, and fat free mass, but similar fasted glucose, insulin, and Matsuda Index (Table 1).
- 1,569 amplicon sequence variants (ASVs) including 19 phyla and 370 genera were identified
- The most abundant phyla were *Firmicutes*, *Bacteroidetes*, *Firmicutes C* and *D* and *Proteobacteria*. (Figure 1)
- Differential abundance of 13 microbial taxa significantly differed by HIV status, with 11 being over-represented in WLH, including *Fusobacterium*, *Bilophila*, *Sneathia* and *Clostridium*. (Figure 2)
- Participants >12 months had a greater proportion of *Ellagibacter*, associated with anti-inflammatory activity, irrespective of HIV status

Table 1: Participant characteristics by HIV status *adjusted for age and postpartum period

	HIV negative (N=19)	WLH (N=46)	P-value
Age (years)	30 (26-35)	31 (26-34)	0.774
Days post-partum	369 (291-469)	277 (225-507)	0.519
Weight (kg)*	86.1(65.4-105.9)	72.2 (65.3-86.7)	0.052
BMI (kg/m^2)*	31.2 (27.8-40.2)	28.1 (24.1-33.8)	0.046
FM (kg)*	40.3 (27.1-54.5)	31.9 (25.1-43.3)	0.050
FFM (kg)*	42.6 (36.9-49.0)	37.7 (34.6-43.6)	0.044
Matsuda Index*	5.23 (3.27-6.32)	6.69 (1.01-1.47)	0.113

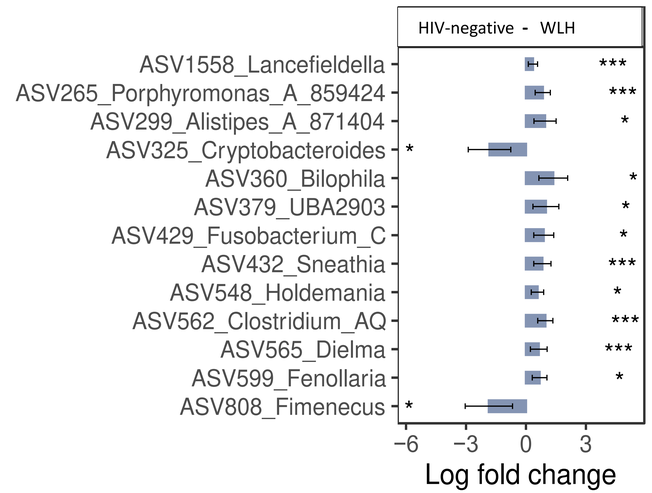

Figure 2: differential abundance in WLH and women without HIV, adjusted for age and obesity

CONCLUSIONS

- The postpartum GM differs by HIV status; over-represented genera have previously been associated with persistent immune dysfunction.
- Participants who were more than 12 months postpartum had a significantly different GM composition, regardless of HIV status.
- Future research should explore the persistent effects of the postpartum period and the long-term health consequences for WLH.
- This is of particular importance given the increasing burden of cardiometabolic conditions, such as T2D, in WLH in South Africa.

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