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RISK AND PREVALENCE OF RESIDUAL VIREMIA AFTER ART IN RESOURCE-LIMITED COUNTRIES

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BACKGROUND

- Tuberculosis, hepatitis B and C, sexually transmitted and tropical infections may contribute to higher residual viremia in virally suppressed people with HIV (PWH).
- There are limited data describing residual viremia from low- and middle-income countries (LMIC).
- We assessed the prevalence, and factors associated with residual viremia in PWH, who were virally-suppressed on antiretroviral therapy (ART). We also compared residual viremia prevalence between the US and LMIC.

METHODS

- This is a cross-sectional, retrospective study that utilized stored specimen samples from ACTG A5175 and A5208.
- The A5175 study included both male and female participants from US and LMIC sites, and prospectively evaluated the efficacy of protease inhibitor- and non-nucleoside reverse transcriptase-based regimens as initial treatment for PWH. The A5208 study compared efficacy of nevirapine versus lopinavir/ritonavir in women from International sites only.
- The last available sample among participants on ART who were virally suppressed with plasma HIV RNA <400 copies/mL for ≥3 years, were tested by the HMMCgag single copy assay (SCA).
- Detectable residual viremia was defined as having ≥1 copy/mL.
- Spearman's correlation and multivariable stepwise logistic regression were used to assess associations of various factors with residual viremia.

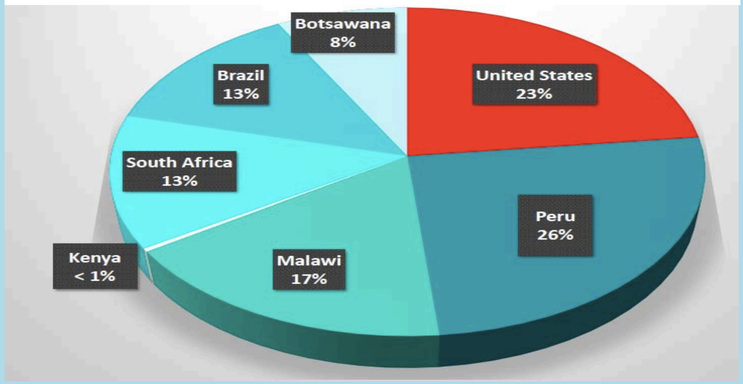


Figure 1: Country of Participants

- *The residual viremia between LMIC and US were not different and more than half of the participants had detectable viremia*
- *Higher baseline HIV RNA was independently associated with residual viremia*

RESULTS

- A total of 320 participants, 74 (23%) from US and 246 (77%) from LMIC, were analyzed (Figure1). Baseline Characteristic are shown in Table1 .
- Subtype data were available for 85 participants, 53% were subtype C, 42% subtype B and 5% other subtypes.
- Overall prevalence of residual viremia was 57% [95% CI, 52-63]; 51% [40-63] in US and 59% [53-65] in LMIC (p= 0.28) (Figure 2).
- The multivariable model conducted in LMIC participants showed higher baseline HIV RNA was associated with detectable residual RNA by SCA (OR 2.9, 95% CI 1.8, 4.6 for every $\log_{10}$ increase, p< 0.001). After including both US and LMIC in the final model, baseline HIV RNA remained significant.
- A sensitivity analysis restricted to A5175 participants yielded the same results.
- No difference in SCA detectability was found between US and LMIC sites (OR 1.1 [0.6, 2.0], p=0.72) after adjusting for baseline RNA and parent study.

Table 1: Baseline characteristics of participants

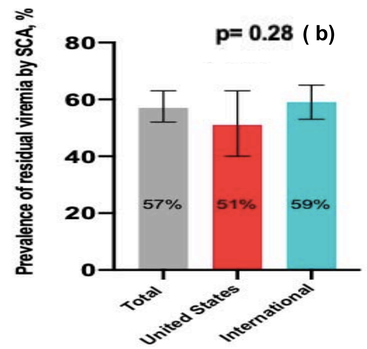
	Total (N=320)	Site location US (N=74)	Site location LMIC (N=246)	p-value
Age (years), Median (IQR)	33 (28, 40)	38.5 (30, 47)	32.5 (28, 38)	<.0001 (a)
Male (n,%)	152 (48%)	60 (81%)	92 (37%)	<.0001 (b)
Baseline CD4 (cells/mm^3), Median (IQR)	166 (88, 230)	179 (71, 255)	162 (90, 224)	0.43 (a)
Baseline HIV-1 RNA ($\log_{10}$ copies/mL), Median (IQR)	5.0 (4.5, 5.3)	5.0 (4.6, 5.4)	4.9 (4.5, 5.3)	0.58 (a)
Co-infection* disease at the time of SCA (n,%)	99 (31%)	21 (28%)	78 (32%)	0.67 (b)
Duration of viral suppression (years), Median (IQR)	3.4 (3.1, 4.0)	4.4 (3.6,4.7)	3.3 (3.0,3.8)	<.0001 (a)
ART regimens at study entry (n,%)				
NNRTI	215 (67%)	50 (68%)	165 (67%)	
PI	105 (33%)	24 (32%)	81 (33%)	

SCA: Single copy assay, ART: Antiretroviral therapy, NNRTI: Non-nucleoside reverse transcriptase inhibitors, PI: protease inhibitors (a) Wilcoxon Test, (b) Fisher's Exact Test. * Co-infection disease includes hepatitis B, hepatitis C, tropical infection, TB and sexually transmitted diseases

Table 2: Residual viremia by SCA among participants with detectable SCA

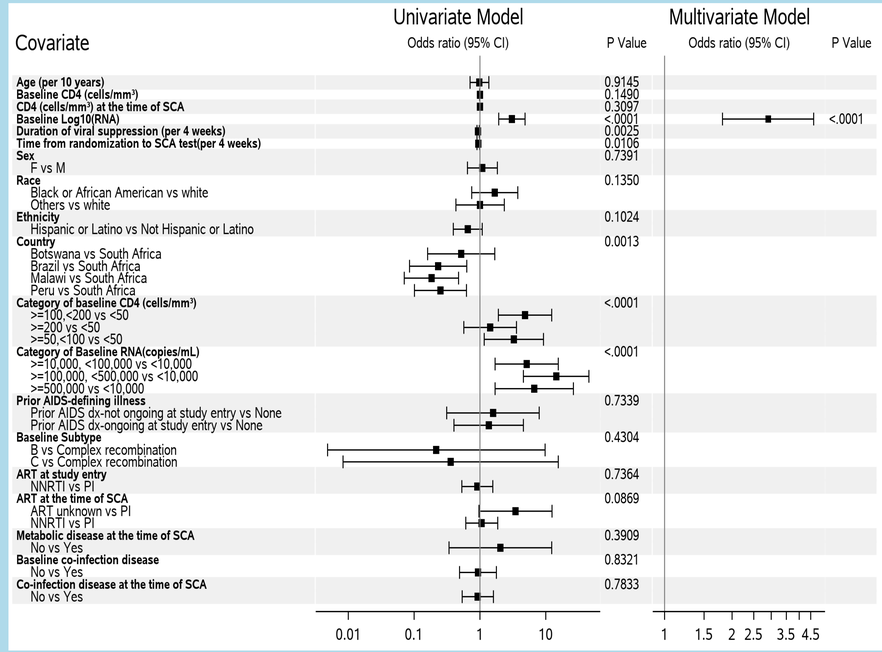
	Total (N=183)	Site location US (N=38)	Site location LMIC (N=145)	p-value
Level of residual viremia among participants with detectable SCA (copies/mL), Median (IQR)	3.8 (2.2, 8.1)	3.9 (2.2, 7.9)	3.8 (2.2, 8.2)	0.88 (a)

Figure 2: Prevalence of residual viremia among all participants



* Error bar are 95% CI.

Figure 3: Forest plot of univariate and multivariate analysis for risk factors associated with residual viremia



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