Poster number: P118

HIV DRUG THERAPY GLASGOW 2024

High prevalence of HIV drug resistance among people living with HIV on Dolutegravir based antiretroviral therapy with viral loads>200 Copies/mL in Francistown, Botswana

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Background

- Challenges like limited access to adherence support, viral load and resistance testing, drug recycling, and a shortage of HIV care specialists contribute to the emergence of drug-resistant HIV-1 variants in the context of widespread use of DTG-based ART. Additionally, drug stock-outs and the lack of supportive healthcare services exacerbate the risk of resistance development.
- To date, no study has characterized HIV-1 DRMs in PLWH on DTG-based ART in the Botswana National ART program.
- This study characterized HIV DRMs among PLWH with detectable VL>200 copies/mL who were predominantly on DTG-based ART in the central HIV VL testing laboratory in Francistown, Botswana.

Methods

- This was a cross-sectional study using residual HIV VL plasma samples of PLWH enrolled in the Botswana National ART program receiving care in Francistown and surrounding healthcare facilities.
- Among 434 participants with detectable VL, and on ART for at least 6 months in this period and have sufficient volume for testing were utilised in this study (Figure 1).
- Both HIV *protease*, *reverse transcriptase* and *integrase* regions were amplified using in-house genotyping assay and sequenced using oxford nanopore technology (Figure 2).

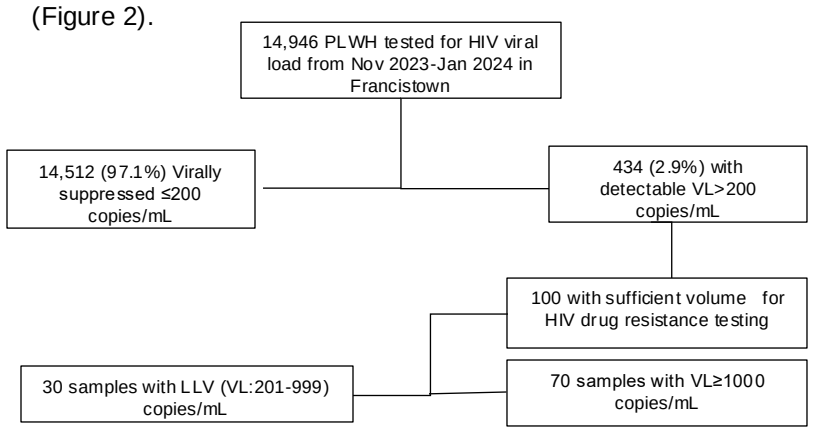

Figure 1. Schema used to select study participants.

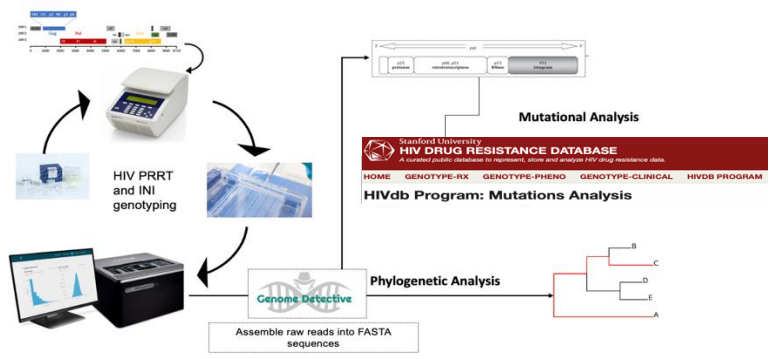

Figure 2. Flow chart for HIV pol genotyping and drug resistance analysis.

Results

- 58/100 sequences were successfully generated and 32.8% had at-least one drug resistance mutation. E138A, K103N and M184V were most predominant mutations (Figure 4).
- PLWH with LLV (33.3%) had the same prevalence of HIV DRMs as those with VL≥1000 copies/mL (32.6%) (p-value=0.99) (Figure 3).
- Amongst 58 PLWH with HIV-1 sequences, 53 had current ART regimen data; of these, 86.8% (46) were on DTG-based ART.
- Out of 46 individuals on DTG-based ART, 34.0% (16) had at least one DRM; 40.0% (4/10) at LLV and 33.3% (12/36) at VF had at least one DRM. Mutations were stratified by ARV classes in Figure 5.

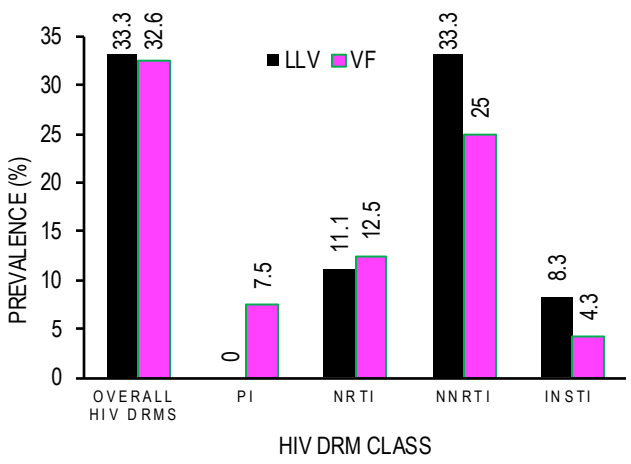

Figure 3. HIV DRMs by VL groups.

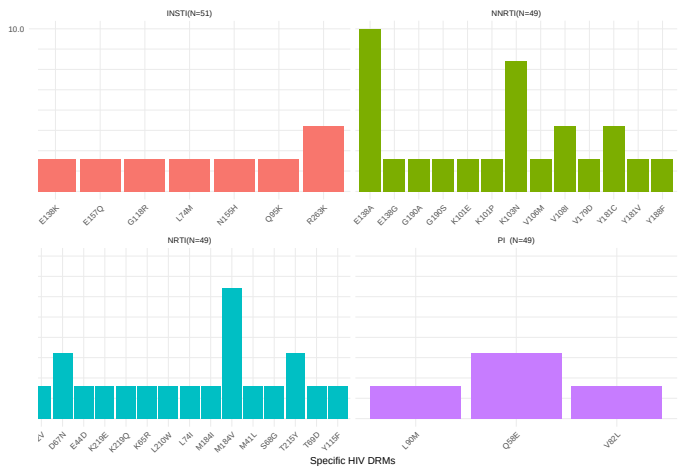

Figure 4. HIV DRMs by drug classes among all generated sequences.

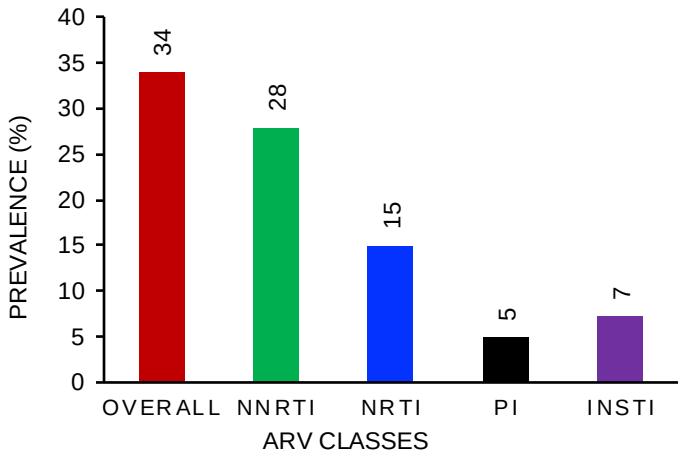

Figure 5. HIV DRMs among PLWH on DTG.

- Only 3 individuals had INSTI-associated mutations on DTG-based ART. Mutation N155H and Q95K was reported on participant 1, which lead to low-level resistance to DTG. Participant 2 had R263K and E157Q conferring intermediate resistance to DTG while participant 3 had G118R, E138K, R263K, L94M conferring high-level resistance to DTG. All these individuals were on DTG at the time of sampling.

Conclusion

- The prevalence of HIV DRMs in PLWH who are primarily on DTG-based ART with detectable VL>200 copies/mL in Francistown is high.
- However, a low prevalence of DTG-resistance-associated mutations was reported in this cohort supporting the continual use of DTG-based ART with HIV drug resistance monitoring.

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