HIV-1 infection recency and pre-treatment drug resistance in recently diagnosed individuals in Greater Gaborone, Botswana: A cross-sectional insight to the "Treat All" strategy

HIV DRUG THERAPY GLASGOW 2024

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BACKGROUND

- Botswana has a robust HIV treatment programme which has been at the forefront of reducing new HIV diagnosis, as well as achieving 98% viral suppression among its population of people living with HIV (PLWH)
- Despite this commendable success, the number of incident HIV cases in Botswana is still high, with estimated 4300 new HIV infections occurring annually (UNAIDS Data, 2022)
- We aimed to identify HIV-1 recent infection and pre-treatment HIV-1 drug resistance (PDR) using a two-step recent infection testing algorithm (RITA) and population-based sequencing in recently diagnosed, ART naive individuals within the Greater Gaborone area (Botswana).

METHODOLOGY

- Plasma samples were included from an ongoing prospective - longitudinal cohort study collecting samples from individuals who are recently HIV diagnosed from government clinics within the Greater Gaborone area (2023 – 2024), the ***Tekodiso*** study.
- All samples were collected using a consecutive census approach; where all participants diagnosed with HIV by double rapid HIV testing are included in the study on the same day of diagnosis before ART initiation (Figure 1A).
- Recent infection classification was determined using Limiting Antigen Avidity (LAg-Avidity), as well as HIV viral load (VL) >1000copies/mL: in a two step recent infection testing algorithm (RITA).
- LAg-normalized optical density (ODn) ⩽1·5 represented recency window of within 130 days post infection (Figure 1B).
- HIV VL in plasma was quantified by Abbott m2000sp/Abbott m2000rt (Figure 1B).
- Sanger sequencing of HIV *pol* was performed using the TaqPath Seq HIV-1 Genotyping Kit. HIV drug resistance associated DRMs were identified using the Stanford HIV Drug Resistance Database (Figure 1B).

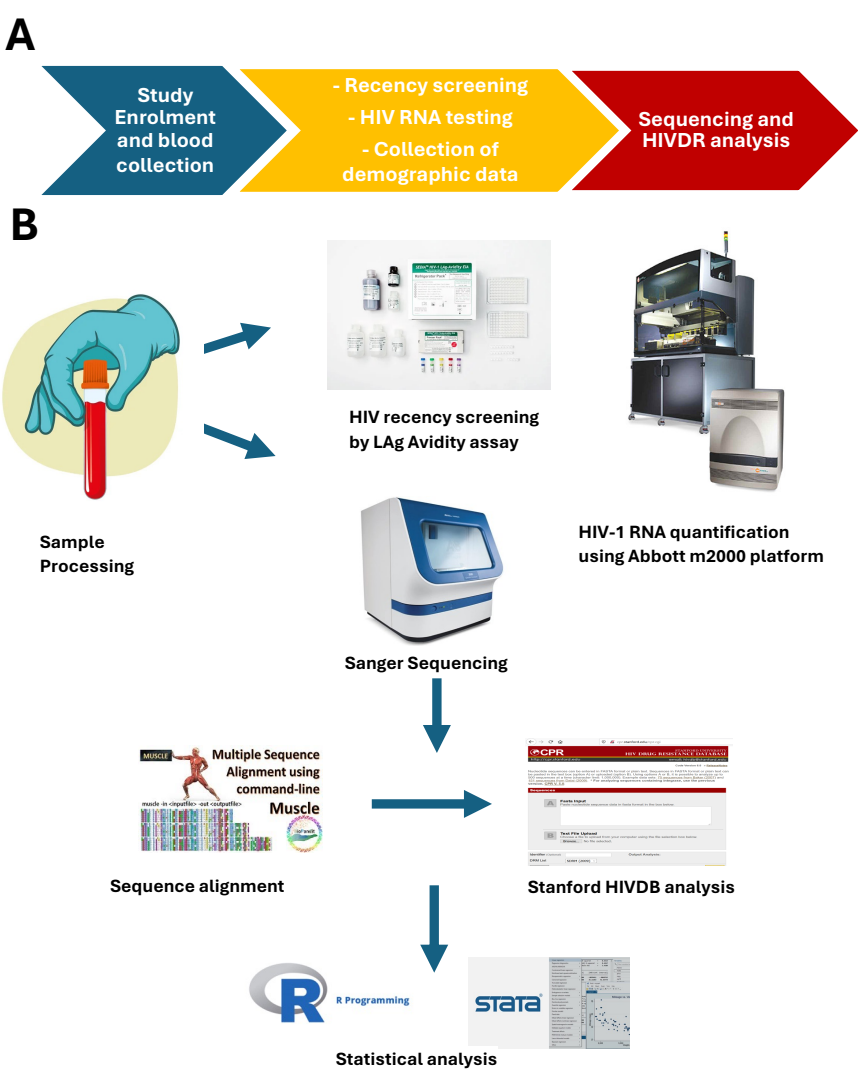

Figure 1: Study design (A) and analysis schema (B)

KEY FINDINGS

Table 1: Baseline characteristics Tekodiso study participants

Baseline Characteristics (N=148)	
Age (years), Median (IQR)	33 (23, 41)
Gender, n (%)	
Female	98 (66.2)
Male	50 (33.8)
HIV RNA load (log10 copies/mL), Median (IQR)	4.6 (3.9, 5.2)
Baseline CD4 (cells/mL) , Median (IQR)	358 (220,519)
Marital status, n (%)	
Married	15 (10.1)
Single	133 (89.9)
Highest education level, n (%)	
None	1 (0.7)
Primary/Non formal	8 (5.4)
Secondary	108 (73.0)
Tertiary	30 (20.3)
Recruitment Site, n (%)	
Bontleng Clinic	36 (24.3)
Lesirane Clinic	48 (32.4)
Mogoditshane Clinic	14 (9.5)
Nkoyaphiri Clinic	34 (23.0)
Tlokwenng Main Clinic	16 (10.8)
Non Motswana Nationality, n (%)	29 (22.6)
Employed, n (%)	
No	40 (27.0)
Yes	108 (73.0)

- A total of 131/141 plasma samples were included in this analysis.
- Median age at enrolment was 33 years and majority 85 (65%) were female.
- The median log10 HIV VL was 4.6 copies/mL. Median CD4 cell count was 358 cells/mL (Table 1).
- A total of 28 (36%) samples were successfully amplified and sequenced for HIV *protease* and *reverse transcriptase*.
- Two (7.1%) ART naïve individuals had E138A major non-nucleoside reverse transcriptase inhibitor mutation.
- We record no presence of integrase strand transfer inhibitor (INSTI) mutations of 30 (39%) successfully amplified and sequenced HIV integrase samples. (Data not shown).

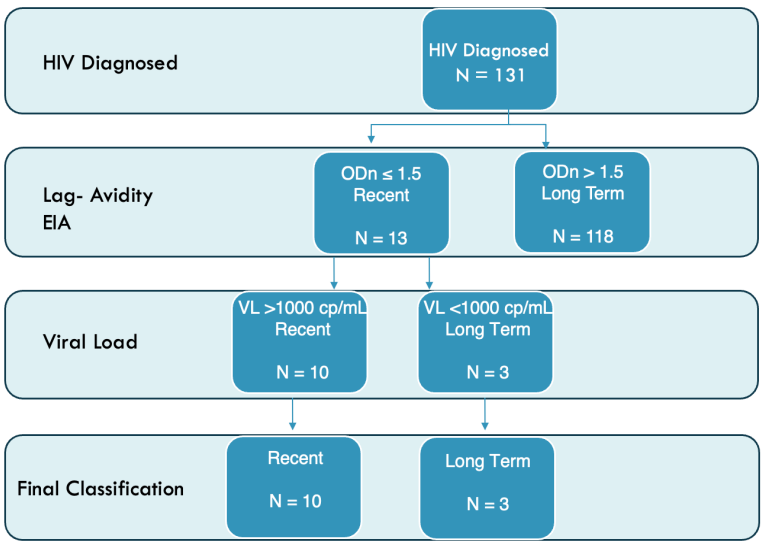

Figure 2: HIV RITA using LAg and HIV-1 viral load testing to determine recent infection

- A total of 131/148 participants were screened for HIV recency using the two step RITA.
- A total of 10 (7.6%) individuals were classified as recent HIV infections. (Figure 2).

CONCLUSIONS

- **We report low rates of PDR and HIV recent infection by LAg based RITA in recently diagnosed antiretroviral therapy naïve individuals in Botswana.**
- **Our results show no INSTI associated HIV DRMs, supporting the use of Dolutegravir based treatment as first line for recent diagnosis in Botswana.**

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Tekodiso Study Participants

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