High prevalence of antiretroviral resistance among HIV-1-infected adults in Kinshasa, Democratic Republic of Congo (OKAPI Cohort)

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P-134

Background/Objective

- The lack of HIV-1 RNA viral load (VL) monitoring and resistance genotyping in sub-Saharan Africa leads to uncontrolled circulation of HIV strains with drug resistance mutations (DRM), compromising second-line antiretroviral therapy (ART) efficacy and favoring transmission of resistant viruses.
- In this context the use of Dried Blood Spots (DBS) has been recommended to perform molecular testing for HIV monitoring. This study describes the DRM rate among HIV(+) adults in Kinshasa (Democratic Republic of Congo, DRC).

Methods

- Ninety-six samples from patients 18-59 years old attending Voluntary Counseling and Testing at Monkole Hospital (Kinshasa, DRC) were collected during 2016 for HIV diagnosis/follow-up within Observational Kinshasa AIDS Prevention Initiative (OKAPI) Cohort.
- DBS samples were collected from positive patients and shipped to Pamplona (Spain) for confirmatory serology and molecular testing.
- Eleven patients were naïve, while 72 participants had received one (54%) or more ART combinations (32%).
- VL was performed with Roche and Xpert platforms. WHO protocols and ANRS procedures were followed for protease (PR), partial retrotranscriptase (RT) and integrase (IN) sequencing. Stanford HIV database was used for resistance interpretation.

Results

- Five out of 96 patients had received a false positive serology result.
- VL was above 3 log for 60% of patients and 44 samples could be genotyped. Considering association between VL and DRM, adult patients showed lower presence of wild-type strains as the viral load increases.
- Among 11 naïve adults, 18% showed transmitted DRM to NNRTI, being DRM to NRTI or PI absent. Regarding 33 adults under ART with available genotype, 63%, 43% and 10% carried DRM to NNRTI, NRTI and PI, respectively, with 40% of them resistant to two drug families. The most frequent mutations in RT were K103N (41%) and M184I/V (26%) followed by A98G, K101E/H, V108I, V179D/E, H221Y, D67N, K70R, V75M and Y181C.
- Three out of 41 patients (7%) showed DRM to IN inhibitors (INI) (T97A, S153F, E157Q). Additional IN mutations identified were: L74I (8/41, 19.5%), particularly linked to CRF09_cpx (2/4) and CRF45_cpx (2/3) variants; V165I (5/41, 12.1%), in 3/3 subtype F, and 2/3 subtype H; and E157K (2/41, 4.8%).

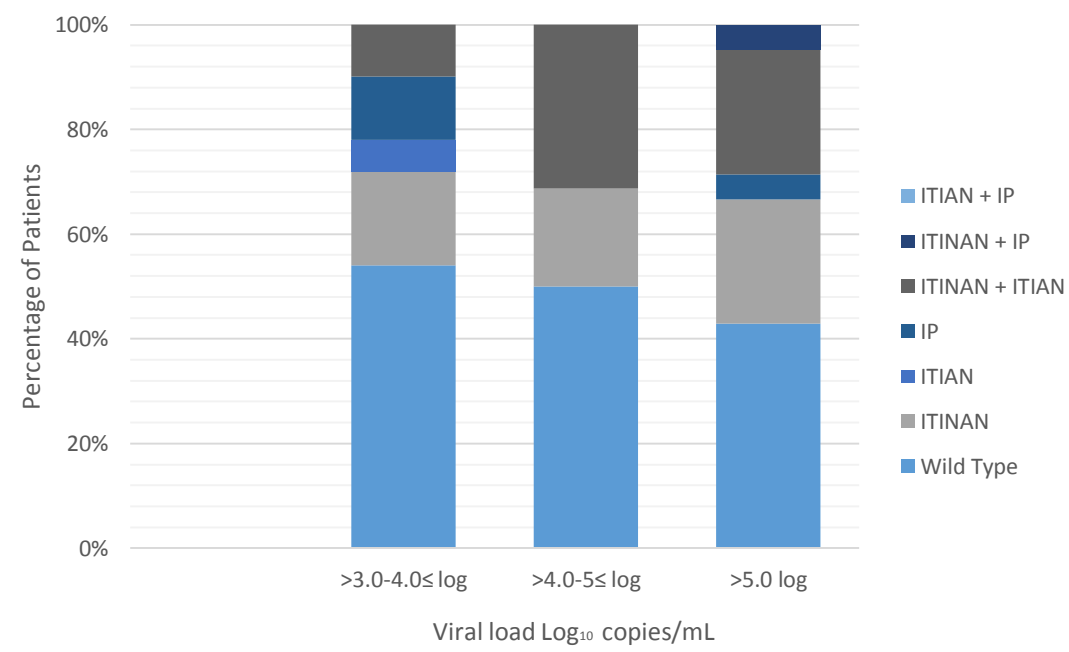

Figure 1. Distribution of patients with resistance mutations according to viral load level

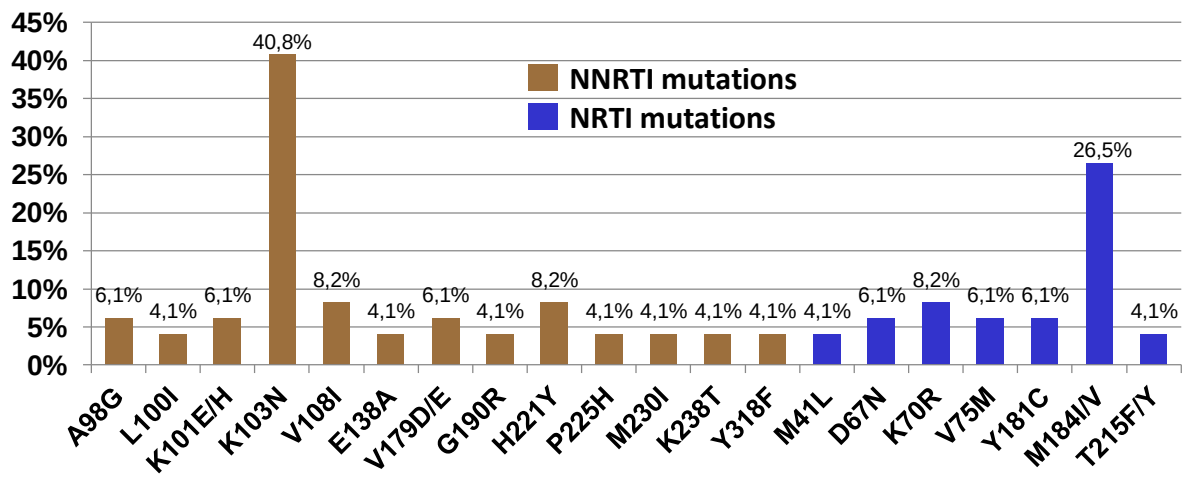

Figure 2. Most frequent RT resistance mutations detected in children and adults in Kinshasa receiving antiretroviral treatment. Other detected mutations were: V106A, Y188L, K65R, T69D, F77L, Y115F and K219Q.

Conclusions

Drug resistant viruses are highly prevalent among HIV infected adults in Kinshasa, compromising the 90-90-90 UNAIDS objectives in DRC. This situation may be promoted by late virological failure detection due the lack of routine VL testing and by the absence of resistance testing. Access to viral monitoring and new first-line regimens including PI or INI are recommended to reduce future resistance spreading.

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