High Prevalence of Transmitted Drug Resistance in HIV-1-infected Antiretroviral-naïve Patients from Conakry, Guinea-Conakry

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BACKGROUND

To assess the prevalence of transmitted drug resistance and to study viral tropism in HIV-1-infected antiretroviral naïve patients from Conakry (Guinea-Conakry).

METHODS

100 newly HIV-1 diagnosed patients, ARV-naïve and followed-up at the University Hospital of Donka in Conakry, Guinea-Conakry, were included.

Protease and reverse transcriptase genes were sequenced using the ARIS procedures.

Drug resistance mutations were identified according to the 2009 update surveillance drug resistance mutations list (Bennett et al., Plac Ome, 2009).

For wildtype SAR-CoV-2, 4,500 mutations

Viral RNA load was assessed by qPCR, using and interpretation of the Geno2Pheno software.

Plasma concentrations of all ARV drugs were determined by HPLC coupled with fluorometric detection.

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RESULTS

Resistance Associated Mutations

**Protease and reverse transcriptase sequencing was successful in 94 (94%) samples.**

**Most of the patients, 84 (89%), were infected with CRF02_AG recombinant virus.**

**HIV tropism could be assessed in 79 samples, among them 63 (80%) were R5 viruses, 11 were R5X4 (14%), and 5 were X4 viruses (6%).**

**Resistance analysis among the 94 samples showed that at least one drug resistance mutation was observed in 9 samples, leading to a prevalence of primary resistance of 9.6% (CI95, 3.63%-15.51%).**

**NRTI resistance mutations were identified in 3 samples (3.2%; CI95, 0.0%-6.7%). Among them, the M184V mutation was present in 2 cases. The remaining patient exhibited multiresistant virus harboring 8 NRTI mutations (M41L-D67N-T69D-K70R-L74V-T72I-K219Q-I222L).**

**NNRTI mutations were detected in 8 samples (8.5%; CI95, 2.91%-14.11).**

**The most prevalent NNRTI mutations were the Y181C and K103N mutation, each detected in 4 cases. The K101E, K103S, and K219Q mutations were detected in 2 cases each. Among these, the K103S mutation was present in 2 cases.**

**Overall, 3 patients of our series exhibited dual class resistant viruses (3%; CI95, 0.0%-6.7%).**

**ARD virus concentration measurements were performed in samples harboring drug resistance mutations (n = 9) and also in samples failing to be amplified for sequencing (n = 6), showing undetectable ARV plasma concentrations in all cases.**

CONCLUSIONS

A high prevalence of 9.6% of transmitted drug resistance was observed on this population of 100 ARV-naïve patients from Conakry, mostly infected with CRF02_AG viruses.

Further surveillance in Conakry and in other cities of the country is warranted to precise the level and evolution of HIV-1 transmitted drug resistance in Guinea-Conakry.