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Virological and Molecular Profile of People Living with the Human Immunodeficiency Virus Starting Dolutegravir Based Antiretroviral Treatment in Kinshasa, Democratic Republic of Congo

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Abstract

Context: Despite the new recommendations "Test and Treat", the virological and molecular parameters remain important information for Antiretroviral Treatment and adequate for monitoring of patients infected with HIV/AIDS. **Objective:** the Objective of this study is to present the virological and molecular profile of People Living with HIV starting Antiretroviral Therapy in Kinshasa in the era of the Dolutegravir. **Methods:** This was a transversal study to determine virological and molecular profile of People Living with HIV (PLHIV) starting an ARV Treatment. The patient's inclusion period was from October 04, 2021 to February 15, 2022. A sample of 5 ml of blood was taken in a tube with EDTA anticoagulant for Molecular Biology analyzes (Viral Load and Sequencing) in all HIV patients, after reading and signing informed consent. The population was made up of adult patients over the age of 18, infected with HIV and starting ART. **Results:** 119 patients (56.3% of women) were included in this study, thus a sex-ratio of 1.29. The average age of patients included was 39.87 ± 12.36 years. The most represented age group is that of 36 to 45 with 37 patients (31.9%) followed by that from 26 to 35

years with 24 patients (20.7%). Out of 119 patients, 21 patients had an undetectable Viral Load (VL). The median value of VL was 4.16 $\log_{10}$ RNA copies/ml. 114 samples were successfully amplified. Subtype A was dominant with 23 cases (20.2%); followed by the subtype C and CRF02_AG each with 14.0%, and D (10.5 %). K65R (1.8%), T69P/N (4.4%), K70R (7.9%) and M184V (7.0%) mutations were listed as existing mutations for Nucleotide Transcriptase Inhibitors. **Conclusion:** 38 patients (31.93%) started the TARV with a positive virological prognosis. The subtype A remains dominant in Kinshasa with 23 cases (20.2%); followed by the subtype C and CRF02_AG each with 14.0%. For Inhibitors of Transcriptase Reverse Nucleotide; K65R, T69P/N, K70E/R and M184V mutations were found in patients' naive of ARV Treatment.

Keywords

Virological Profile, Molecular Profile, PLHIV, Start of ART, Kinshasa

1. Introduction

After more than four decades of fighting the infection of the Human Immunodeficiency Virus (HIV) and the Acquired Immuno Deficiency Syndrome (AIDS), these are still major public health problems around the world. According to the United Nations Organization of Nations to Combat HIV/AIDS (UNUSA), in 2020, 37 million were estimated [30.2 millions - 45.1 millions] the number of People Living with HIV/AIDS (PLHIV) and 1.5 millions [1.0 million - 2.0 million] people were newly infected with HIV/AIDS in the same year [1]. Similarly, the World Health Organization (WHO) estimates that Sub-Saharan Africa remains the most affected region which carries the heaviest burden of the epidemic with 26 million PLHIV and represents 70% of all deaths related to AIDS in the world [2].

Despite the new recommendations "Test and Treat" adopted by HIV/AIDS control programs in the Democratic Republic of the Congo (National Multisectorial Program to Combat HIV/AIDS-PNMLS and the National HIV/AIDS and National Program ISTS-PNLS) [3] [4], virological (Viral Load) and molecular (circulating strains of the virus) parameters remain important information for Antiretroviral Treatment (ART) and adequate monitoring of patients infected with HIV/AIDS [5] [6]. They, both, are significant parameters for the decision to start ART and of which molecules are suitable according to the molecular diversity of HIV [5]. They are also very important in the epidemiological surveillance, the diagnosis of children under 18 months, and the adherence to treatment at the change of line of treatment [5].

Hence the objective of this study was to present the virological and molecular profile of People Living with HIV starting an Antiretroviral Therapy in Kinshasa in the era of the Dolutegravir.

2. Methods

2.1. Study Design, Patient and Samples Framework

This study is a cross-sectional and descriptive to determine the virological and molecular profile of People Living with HIV (PLHIV) starting an ARV Treatment (ART) in Outpatients Treatment Centers (OTC) for HIV in Kinshasa, Democratic Republic of Congo (DRC). The patient's inclusion period was from October 04, 2021 to February 15, 2022, during which all adult patients initiating an ART in an included OTC were included. Sixteen OTCs had been included for study based on their expertise in the management of PLHIV, their technical tray of care and their accessibility [7].

In the OTCs, 5 ml sample of blood were taken in a tube with EDTA anticoagulant from the vein in the bend of the elbow for molecular biology analyzes (viral load and sequencing) in any positive HIV patient by serology according to The national protocol, after reading and signing informed consent. Patients were included consecutively randomly according to their presence in the OTCs during consultations.

All molecular data has been recorded on the previously tested survey sheets.

2.2. Study Population

The population was made up of adults over the age of 18 during inclusion, infected with HIV and initiating an ART in the OTC during the inclusion period.

2.3. Inclusion Criteria

All the patients coming to initiate ART in the selected centers during the inclusion period were included in the cohort upon signing the informed consent.

2.4. Parameters of Interest

The parameters of interest retained for this study were: sex, age, viral load (VL) and sequencing data.

2.5. Molecular Analyzes

After sampling, the samples were taken, while respecting temperature, at the Molecular Biology laboratory of the Faculty of Medicine, University of Kinshasa for analysis.

DNA was extracted from 200 µl of Buffy Coat using the Qiamp DNA Mini Kit QIIAGEN® for DNA extraction [8]. A Nested PCR in the *gag* and *pol* regions was carried out for confirmation of the serology of all the patients included [9] [10]. A reverse transcription PCR (RT-PCR) and a nesting PCR were made to amplify the regions of interest for the protease and for the Reverse Transcriptase (RT) for sequencing [11] [12].

RNA was extracted from 140 µl of plasma in the Molecular Biology laboratory using the Qiamp RNA Mini Kit QIIAGEN® for RNA extraction [13]. A Quantitative Real-Time PCR (qPCR) was carried out to quantify proviral HIV in the

samples according to the protocols previously described [11] [14] [15].

The extract RNA was also used for sequencing. A Reverse Transcription PCR (RT-PCR) and a Nested PCR were made to amplify the regions of interest for the protease and for the Reverse Transcriptase (RT) for sequencing. The PCRs were carried out under the conditions previously described [11] [12]. These fragments were sequenced by the Sanger sequencing method. The pairing of the fragments obtained (sens and anti-sens) was carried out with the Vector NTI Advance® 11.5 software (Invitrogen, Life Technologies) and compared with the Database of Stanford University (www.hivdb.stanford.edu) [11] [12].

Table 1 presents the different primers and probes used for the different amplifications.

2.6. Ethical Consideration

This study was approved as a whole by the Research Ethics Committee of the School of Public Health, Faculty of Medicine, University of Kinshasa (ESP/CE/115/2021). The authorization to access the OTCs was obtained from the competent authorities of the various institutions included. Before inclusion, the fully written consent was obtained from each patient. The blood samples were taken by the technical teams of the centers. The results of the biochemical analyzes were returned to the centers at the end of the exams.

2.7. Statistical Analyzes

The analyses were carried out using the SPSS version 26 software (Statistical Package for Social Sciences, IBM). Only the available data was analyzed, the missing data was considered completely random. The continuous variables were presented on average ± standard deviation and compared using the Student T test. The 95% respective proportions and intervals were calculated for categorical data.

3. Results

One hundred nineteen (119) patients were included in this study in accordance with the inclusion criteria; 67 (56.3%) are of female sex while 52 (43.7%) are male thus giving a sex-ratio of 1.29 in favor of women. Figure 1 presents the above data.

The average age of patients included is 39.87 ± 12.36 years with extremities from 18 to 69 years. The most represented age group is that of 36 to 45 years with 37 patients (31.9%) followed by that from 26 to 35 years with 24 patients (20.7%), that of 46 to 55 years with 22 Patients (19.0%) and that from 18 to 25 years old with 19 patients (16.4%). These data are presented by Figure 2.

All the 119 positive patients per serology were positive by PCR for the "*pol*" region while 115 samples were positive for the "GAG" region. The 4 negative samples on the "*gag*" region were positive on the "*env*" region. Table 2 presents the results of the nested PCR diagnostic.

Table 1. Primers and probes for amplifications.

Types of PCR	Primers	Sequences
Nested PCR for diagnostic on DNA		
HLA	GH26 Forward	5'-GTGCTGCAGGTGTAAACT-3'
	GH27 Reverse	5'-CACGGATCCGGT-3'
Gag	GAG1 Forward	5'-GGTACATCAGGCCATATCACC-3'
	GAG4 Reverse	5'-ACCGGTCTACATAGTCTC-3'
Pol	POLITG1 Forward	5'-CCCTACAATCCCCAAAGTCAAGG-3'
	POLITG4 Reverse	5'-TACTGCCCCTTCACCTTTCCA-3'
Env	ENV1 Forward	5'-GAGGATATAATCAGTTTATGG-3'
	ENV4 Reverse	5'-AATTCCATGTGTACATTGTACTG-3'
Nested gag	GAG2 Forward	5'-GAGGAAGCTGCAGAATGGG-3'
	GAG3 Reverse	5'-GGTCCTTGTCTTATGTCC-3'
Nested pol	POLITG2 Forward	5'-TAAGACAGCAGACAAATGGCAG-3'
	POLITG3 Reverse	5'-GCTGTCCCTGTAATAAACCCG-3'
Nested env	ENV2 Forward	5'-GATCAAAGCCTAAAGCCATG-3'
	ENV3 Reverse	5'-CAATAATGTATGGGAATTGG-3'
Quantitative PCR (qPCR) for Viral Load on RNA		
qPCR	HIV1MG Forward	5'-GCCTCAATAAAGCTTGCCTTGA-3'
	HIV1MG Reverse	5'-GGCGCCACTGCTAGAGATTTT-3'
	HIV1MG Probe	FAM-5'-AAGTAGTGTGTGCCCGTCTGTTRTKTGACT-3'-BHQ1
PCR for Sequencing		
RT-PCR Prot	5' prot 1	5'-TAATTTTTTAGGGAAGATCTGGCCTTCC-3'
	3' prot 1	5'-GCAAATACTGGAGTATTGTATGGATTTTCAGG-3'
Nested PCR Prot	5' prot 2	5'-TCAGAGCAGACCAGAGCCAACAGCCCCA-3'
	3' prot 2	5'-AATGCTTTTATTTTTTCTTCTGTCAATGGC-3'
RT-PCR RT	MJ3	5'-AGTAGGACCTACACCTGTCA-3'
	MJ4	5'-CTGTTAGTGCTTTGGTTCCTCT-3'
Nested PCR RT	A(35)	5'-TTGGTTGCACTTTAAATTTTCCCATTAGTCCTATT-3'
	NE1(35)	5'-CCTACTAACTTCTGTATGTCATTGACAGTCCAGCT-3'
RT-PCR Alt Prot	5' eprB	5'-AGAGCTTCAGGTTTGGGG-3'
	3' eprB	5'-GCCATCCATTCCTGGCTT-3'
Nested PCR Atl Prot	5' prB	5'-GAAGCAGGAGCCGATAGACA-3'
	3' prB	5'-ACTGGTACAGTTTCAATAGG-3'
RT-PCR Atl RT	RT1	5'-CCAAAAGTTAAACAATGGCCATTGACAGA-3'
	RT4	5'-AGTTCATAACCCATCCAAAG-3'
Nested PCR Alt RT	RT18	5'-GGAAACCAAAAATGATAGGGGGAATTGGAGG-3'
	RT21	5'-CTGTATTTCTGCTATTAAGTCTTTTGATGGG-3'

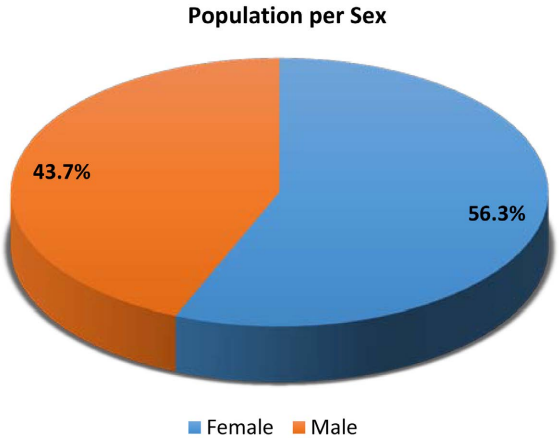

Figure 1. Distribution of the population by gender at the inclusion.

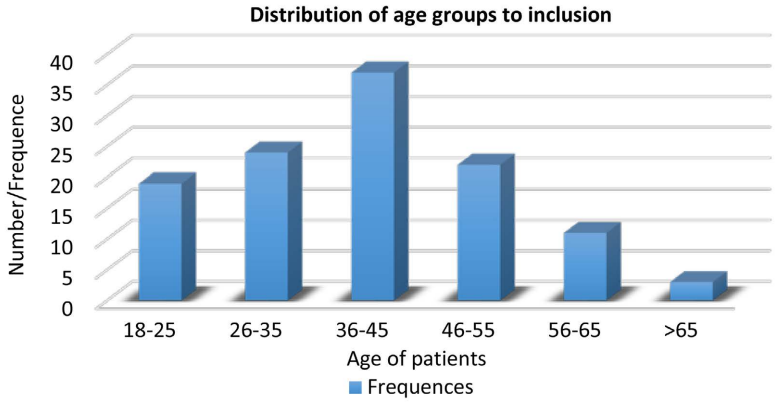

Figure 2. Distribution of age groups to inclusion.

Table 2. Nested PCR results for HIV diagnosis.

Samples	PCR HLA		Region gag		Region pol		Region env	
Positive	Negative	Positive	Negative	Positive	Negative	Positive	Negative	Positive
119	119	0	115	4	119	0	4	0

Out of 119 patients, 21 patients had an undetectable Viral Load (VL) or lower than 50 copies of RNA/ml. The median value of the VL was 4.16 $\log_{10}$ RNA/ml copies (14360.50 RNA/ml copies) with extreme values from 0.0 $\log_{10}$ to 7.11 $\log_{10}$ RNA/ml copies. These data is presented in **Table 3**.

The regions of Reverse Transcriptase (RT) and the Protease were amplified and sequenced respectively for 114 (95.79%) and 111 (93.28%) patients. One hundred and fourteen (114) samples were therefore successfully amplified. Subtype A is dominant with 23 cases (20.2%); followed by the subtype C and CRF02_AG respectively with (14.0%), D (10.5%), G (5.3%), followed by H, CRF01_AE and U respectively (4.4%) as described on **Figure 3** and **Table 4**. No mutation was found for DTG; K65R (1.8%), T69P/N (4.4%), K70R (7.9%) and M184V (7.0%) mutations were listed as existing mutations for nucleotide inhibitors of Reverse Transcriptase (**Table 4**).

Table 3. Values of the viral loads of patients to inclusion.

	Viral Load (copies of RNA/ml)	
	Values	**Log_{10}**
Median	14360.5	4.16
Lower limit	1	0.00
Upper limit	12905352.0	7.11
	Viral Load intervals	
	Values	**Percentage**
Undetermined VL	21	17.65
VL < 3.0 log_{10}	38	31.93
3.0 log_{10} < VL < 5.0 log_{10}	40	33.61
VL > 5.0 log_{10}	20	16.81

Table 4. Molecular data of patients on D0.

Molecular data of patients on D0		
Prevalence of circulating subtypes		
Subtypes	**Number**	**Percent**
A	23	20.2
B	3	2.6
C	16	14.0
D	12	10.5
E	1	0.9
F	2	1.8
G	6	5.3
H	5	4.4
J	3	2.6
K	4	3.5
CRF01	5	4.4
CRF02	16	14.0
CRF05	2	1.8
CRF06	2	1.8
CRF11	1	0.9
CRF25	3	2.6
CRF45	3	2.6
CRF56	2	1.8
U	5	4.4
Total	**114**	**100.0**

Continued

Prevalence of mutations of interest		
INTR	**Number**	**Percent**
K65R	2	1.8
T69P	5	4.4
K70E/R	9	7.9
M184V	8	7.0

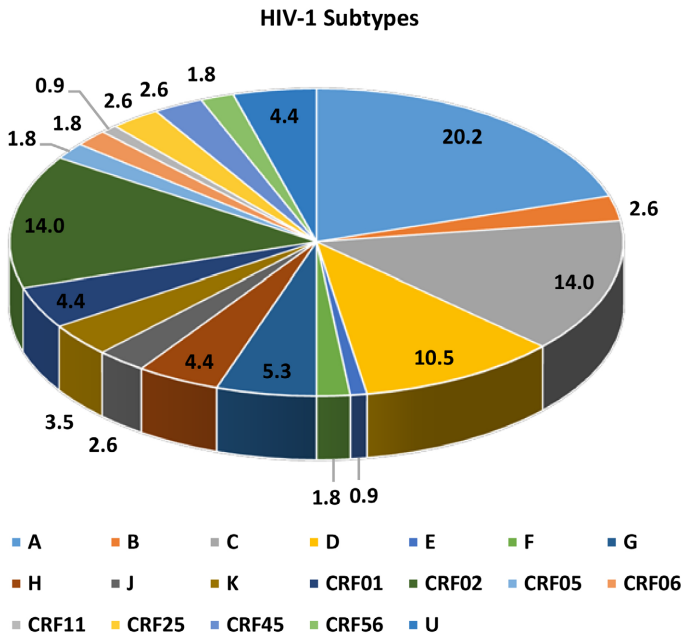

Figure 3. Distribution of HIV-1 subtypes in Kinshasa.

4. Discussion

The objective of this work was to present the virological and molecular profile of People Living with HIV (PLHIV) starting Antiretroviral Treatment (ART) in Kinshasa in the era of the Dolutegugal. A total of 119 PLHIV had been included, in accordance with the criteria, for this study starting ART in 16 Outpatient Treatment Centers (OTC) disseminated in the 4 districts of Kinshasa, Democratic Republic of Congo.

Sixty-seven (67) patients, or 56.3%, are of female sex while 52 (43.7%) are male thus giving a sex-ratio of 1.29 in favor of women. These results presenting a sex-ratio in favor of the female sex are similar to the trend related to the various studies published for Kinshasa in recent years which tend to feminize HIV infection in Kinshasa and even in Central Africa [5] [7] [11] [12] [16].

The average age of patients included is 39.87 ± 12.36 years with extremities from 18 to 69 years. The most represented age group is that of 36 to 45 years with 37 patients (31.9%) followed by that from 26 to 35 years with 24 patients (20.7%), that of 46 to 55 years with 22 Patients (19.0%) and that from 18 to 25

years old with 19 patients (16.4%). These values, which present the age group of 36 to 45, are shared by the various authors who have published on PLHIV in Kinshasa in recent years [5] [7] [11] [12] [16].

All the 119 positive patients per serology were positive by PCR for the "pol" region while 115 samples were positive for the "gag" region. The 4 negative samples on the "gag" region were positive on the "env" region. Diagnostic PCR was used later to confirm the positivity of questionable and indeterminate samples [9] [10].

Twenty-one (21) patients out of the 119 patients included, 17.65%, had an undetectable VL or lower than 50 copies of RNA/ml. This brings into question the concept and definition of "patients starting treatment" or even "patient naive of treatment". It has been shown that, in precarious situations, patients change treatment centers without notice; they leave an OTC to register as a naive patient in another center which has a better tray of management of PVVIH [17].

The median value of the VL was 4.16 $\log_{10}$ RNA/ml copies (14,360.50 RNA/ml copies) with extreme values from 0.0 $\log_{10}$ to 7.11 $\log_{10}$ RNA/ml copies. Despite the various awareness of different programs, patients are still starting their treatment with high VLs. Twenty (20) patients, or 16.81%, started the ART with a higher VL at 5.00 $\log_{10}$ RNA/ml copies; this is already synonymous with a poor prognosis for treatment [5] [17] [18] [19]. The majority (33.61%) of patients started the ART with a VL included between 3.00 $\log_{10}$ and 5.00 $\log_{10}$ RNA/ml copies; This is a mitigated prognosis for good management of PVVIH [5] [17] [18] [19]. Only 38 patients (31.93%) started the ART with a positive prognosis. These data corroborate those of the literature on the profile of PLHIVs starting an ART in Kinshasa and even in some cases in Central Africa [5] [11] [20].

The regions of Reverse Transcriptase (RT) and the Protease were amplified and sequenced respectively for 114 (95.79%) and 111 (93.28%) patients. One hundred and fourteen (114) samples were therefore successfully amplified. The amplification rate of the two regions was almost 96% for samples. The differences in amplification between Protease and RT are mainly in the sizes of regions of interest to amplify and diversity that exists [12] [21] [22]. Similar data has been presented in different literatures [12] [21] [22].

Subtype A is dominant with 23 cases (20.2 %); followed by the subtype C and CRF02_AG respectively with (14.0%), D (10.5%), G (5.3%), followed by H, CRF01_AE and U respectively (4.4%). These results are similar to the various subtypes found in the literature for Kinshasa where subtype A maintains itself dominant compared to other subtypes C, D and G [11] [12]. The presence of recombined forms is explained by the dynamism of HIV infection in Kinshasa, the possibilities of crossed infections due to the population movement of villages to metropolitan areas, but also by the return of expatriates and immigrants to the capital [23].

No mutation was found associated with resistance to the DTG; K65R (1.8%), T69P/N (4.4%), K70E/R (7.9%) and M184V (7.0%) mutations were listed as existing mutations associated with resistance to Nucleotide Inhibitors of Reverse

Transcriptase (NIRT). The K65R mutation (1.8%) is associated with resistance against Lamivudine (3TC) and Tenofovir (TDF); The T69P/N mutation (4.4%) is associated with resistance to all NIRT; The K70E/R (7.9%) is associated with TDF; The M184V (7.0%) at 3TC [11] [12] [23]. Almost 8% of naive patients start the first -line TARV with a predisposition to failure for treatment such as recommended for the DRC since 2019 (Tenofovir + Lamivudine + Dolutegravir) [24] [25].

Limitation of the Study

This present study was limited to some centers of Kinshasa. Therefore, generalization of the results should be done carefully. However, being the first study in the era of Dolutegravir transition, this does not take any value out of the findings.

5. Conclusion

Thirty-eight (38) patients (31.93%) started the ART with a positive virological prognosis. The subtype a remains dominant in Kinshasa with 23 cases (20.2%); followed by C and CRF02_AG subtype respectively with (14.0%). No mutation was found associated with resistance to the Dolutegravir. For Nucleotide Inhibitors of Reverse Transcriptase; K65R (1.8%), T69P/N (4.4%), K70E/R mutations (7.9%) and M184V (7.0%) were found in naive treatment patients.

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Conflicts of Interest

The authors do not declare any conflict of interest for this study.

References

[1] United Nations AIDS Program (UNAIDS) (2020) Country Factsheets: Democratic Republic of the Congo. https://www.unaids.org/en/regionscountries/countries/democraticrepublicofthecongo

[2] Organisation Mondiale de la Santé (OMS) (2016) Mettre fin au VIH/SIDA d'ici 2030: Cadre d'action dans la région Africaine de l'OMS 2016-2022. Organisation mondiale de la Santé, Geneva.

[3] Programme National de Lutte contre le VIH/SIDA et les Infections Sexuellement Transmissibles (PNLS), Ministère de la Santé publique et Hygiène, République Démocratique du Congo (2017) Guide de Prise en charge intégrée du VIH en République Démocratique du Congo. https://www.pnls-rdc.org/

[4] World Health Organization (WHO) (2015) Guideline on When to Start Antiretroviral Therapy and on Pre-Exposure Prophylaxis for HIV. World Health Organization, Geneva.

[5] Kamangu, N.E., Bulanda, I.B., Bongenya, I.B., Botomwito, T.H., Mvumbi, L.G., De Mol, P., Vaira, D., Hayette, M.-P. and Kalala, L.R. (2015) Virological Profile of Patients Infected with HIV Starting Antiretroviral Treatment in Kinshasa. *Open Access Library Journal*, **2**, e1564. https://doi.org/10.4236/oalib.1101564

[6] Girum, T., Yasin, F., Wasie, A., Shumbej, T., Bekele, F. and Zeleke, B. (2020) The Effect of "Universal Test and Treat" Program on HIV Treatment Outcomes and Patient Survival Among a Cohort of Adults Taking Antiretroviral Treatment (ART) in Low Income Settings of Gurage Zone, South Ethiopia. *AIDS Research and Therapy*, **17**, Article No. 19. https://doi.org/10.1186/s12981-020-00274-3

[7] Losenga, L.O., Dikati, N.M., Bongenya, B.I., Ntumba, T.K., Booto, G.I., Dembo, R.D., Selenge, S.M., Nonga, J.E., Kabamba, C.A., Sombo, M.-T.A.S., Bumoko, G.M.M. and Kamangu, E.N. (2022) Sociodemographic and Anthropometric Profile of People Living with Human Immunodeficiency Virus Starting Treatment in Kinshasa, Democratic Republic of the Congo. *Open Access Library Journal*, **9**, e9056. https://doi.org/10.4236/oalib.1109056

[8] QIAGEN (2010) QIAamp® DNA Mini and Blood Mini Handbook. 3rd Edition, QIAGEN, Venlo.

[9] Kamangu, N.E., Mayemba, C., Mbikayi, S., Ndarabu, A., Kalala, R.L., Mvumbi, G.L. and Vaira, D. (2014) Implementation of a Classic Nested PCR DNA for HIV Diagnosis in Kinshasa. *International Journal of Collaborative Research on Internal Medicine and Public Health* (*IJCRIMPH*), **6**, 145-151.

[10] Bongenya, B.I., Bulanda, B.I. and Kamangu, E.N. (2020) Comparison of Rapid Diagnosis Test and Nested PCR for HIV Diagnosis in Kinshasa. *Open Access Library Journal*, **7**, e6325. https://doi.org/10.4236/oalib.1106325

[11] Kamangu, N.E. (2022) Caractérisation Moléculaire du VIH-1 à Kinshasa: Caractérisation Moléculaire du Virus de l'Immunodéficience Humaine de Type 1 et Suivi Thérapeutique des patients pris en charge à Kinshasa/République Démocratique du Congo. Editions Universitaires Européennes, Republic of Moldova.

[12] Kamangu, N.E., Wumba, D.M.R., Situakibanza, N.T.S., Lukusa, T.P., Kapend, K.L., Mvumbi, L.G., Hayette, M.P. and Kalala, L.R. (2018) Molecular Epidemiology of Human Immunodeficiency Virus Type 1 and Therapeutic Monitoring of Patients treated in Kinshasa/Democratic Republic of the Congo. *International Journal of HIV and Aids Research*, **2**, 6-11.

[13] QIAGEN (2010) QIAamp® RNA Mini and Blood Mini Handbook. 3rd Edition, QIAGEN, Venlo.

[14] Kamangu, N.E., Chatté, A., Boreux, R., Kalala, L.R., Mvumbi, L.G., De Mol, P., Vaira, D. and Hayette, M.P. (2014) Implementation of an In-House Quantitative Real-Time PCR for Determination of HIV Viral Load in Kinshasa. *Open Access Library Journal*, **1**, e855. https://doi.org/10.4236/oalib.1100855

[15] Kamangu, N.E., Chatté, A., Boreux, R., Susin, F., Kalala, L.R., Mvumbi, L.G., De Mol, P., Hayette, M.P. and Vaira, D. (2015) Comparison of an In-House Quantitative PCR and COBAS Ampliprep/TaqMan Roche for Determination of Viral Load for HIV Type 1 Non-B. *Open Access Library Journal*, **2**, e1402. https://doi.org/10.4236/oalib.1101402

[16] Bongenya, B.I., Bukongo, R.N., Bulanda, B.I., Chuga, D., Kabasele, J.Y.K., Okonda, M.O., Tshisumbu, C. and Kamangu, N.E. (2018) Gender Difference in Early Treat-

ment Patients for Human Immunodeficiency Virus Type 1 Infection in Kinshasa, Democratic Republic of Congo. *Mathews Journal of HIV/AIDS*, **3**, Article No.18.

[17] Wateba, I.N.M., Patassi, A.A., Balaka, A. and Tidjani, O. (2013) Viral Characteristic of HIV Infected Patients Naïf of Anti-Retroviral Therapy with CD4+ T Lymphocytes Rate Greater than 350 per Microliter of Blood in Lomé Togo. *World Journal of AIDS*, **3**, 364-366. https://doi.org/10.4236/wja.2013.34047

[18] Egger, M., May, M., Chêne, G., Phillips, A.N., Ledergerber, B., *et al.* (2002) Prognosis of HIV-1-Infected Patients Starting Highly Active Therapy: A Collaborative Analysis of Prospective Studies. *The Lancet*, **360**, 119-129. https://doi.org/10.1016/S0140-6736(02)09411-4

[19] Phair, J.P., Mellors, J.W., Detels, R., Margolick, J.B. and Muñoz, A. (2002) Virologic and Immunologic Values Allowing Safe Deferral of Antiretroviral Therapy. *AIDS*, **16**, 2455-2459. https://doi.org/10.1097/00002030-200212060-00011

[20] Bulanda, B.I., Bongenya, B.I., Chatte, A., Kateba, E.T., Kabasele, J.-Y.D., Omakoy, M.O., Chuga, D., Tshibumbu, C., Mwanaut, I. and Kamangu, E.N. (2020) Molecular Diversity of the Human Immunodeficiency Virus Type 1 in Metropolitan Cities in Central Africa: An Update of Data. *World Journal of AIDS*, **10**, 80-93. https://doi.org/10.4236/wja.2020.102007

[21] Jordan, M.R., Winsett, J., Tiro, A., Bau, V., Berbara, R.S., Rowley, C., Bellosillo, N., Wanke, C. and Coakley, E.P. (2013) HIV Drug Resistance Profiles and Clinical Outcomes in Patients with Viremia Maintained at Very Low Levels. *World Journal of AIDS*, **3**, 71-78. https://doi.org/10.4236/wja.2013.32010

[22] Guillaume, L.Y., Yessé, Z.N., Hortense, K., Laurent, D., Arsher, C.M., Joseph, L.S. and Marie-Chantal, A.K. (2012) Genetic Diversity and Antiretroviral Drug Resistance among Drug-Naïve HIV-1 Infected Pregnant Women Attending Antenatal Clinics in Abidjan, Côte d'Ivoire. *World Journal of AIDS*, **2**, 57-63. https://doi.org/10.4236/wja.2012.22008

[23] Kamangu, E.N. (2020) Diversité Génétique du VIH à Kinshasa, République Démocratique du Congo: Défis d'une dynamique évolutive. Editions Universitaires Européennes, Republic of Moldova.

[24] Programme National de Lutte Contre le VIH/SIDA et les IST (PNLS), Ministère de la Santé Publique, République Démocratique du Congo (2019) Révision du Guide National de Prise en Charge. https://www.pnls-rdc.org/

[25] Bongenya, B.I., Sombo, M.-T.A.S., Bumoko, G.M.M., Kabengele, B.O., Lusakibanza, M.M., Mesia, G.K. and Kamangu, E.N. (2023) Compliance with First-Line Antiretroviral Treatment (ART) for HIV Infection in the Era of Dolutegravir in Kinshasa, Democratic Republic of Congo. *World Journal of AIDS*, **13**, 11-17. https://doi.org/10.4236/wja.2023.131002

List of Abbreviations and Acronyms

ART: Antiretroviral Treatment; **ARV:** Antiretroviral; **DRC:** Democratic Republic of Congo; **DTG:** Dolutegravir; **HIV:** Human Immunodeficiency Virus; **OTC:** Outpatient Treatment Center; **PLHIV:** Person Living with the Human Immunodeficiency Virus.