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Human Immunodeficiency Virus Type 1 and Type 2 Co-infection Rate in Kinshasa Patients

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ABSTRACT

Background: Although the two types of HIV essentially cause AIDS; there are major differences between them in terms of phylogeny, pathology, virulence, evolution, transmission, infectivity and epidemiology.

Objective: The objective of this study was to determine the rate of HIV-1 and HIV-2 co-infection in people infected with HIV in Kinshasa.

Methodology: A cross-sectional study performed on 115 randomly selected plasma samples in the archived plasma samples of patients infected with HIV-1. 140µl were used for the extraction of RNA from plasma using the kit QIAamp® RNA Mini Kit in the Molecular Biology Laboratory. A final eluate of 60µl was collected. Different qualitative real-time PCR were performed on all 115 samples to determine HIV-1 and HIV-2 infection.

Results: 113 samples were positive for HIV-1. Four samples of these positive samples also tested positive for HIV-2 giving a rate of HIV-1 and HIV-2 coinfection of 3.54%.

Conclusion: The rate of coinfection HIV-1 and HIV-2 is 3.54% for Kinshasa. This coinfection questions the notions of HIV-2 for the city and even for the Democratic Republic of Congo.

KEYWORDS: Coinfection; HIV-1; HIV-2; Kinshasa.

INTRODUCTION

The Human Immunodeficiency Virus (HIV) is classified into two types (HIV-1 and HIV-2) [1]. Although these two types of HIV (HIV-1 and HIV-2) cause essentially the Acquired Immune Deficiency Syndrome (AIDS); there are major differences between them. Their phylogenies, pathology, virulence, developments, modes of transmission, infectivity and epidemiology differ [2]. Compared to the HIV-1, the HIV-2 has a slower progression to AIDS stage and is hardly transmitted [2]. Coding regions of the two types of HIV vary [2]. The Type 1 is the most common HIV worldwide; it is responsible for over 80% of the global epidemic [1, 3]. The Subtype C of Group M is the most prevalent. It is responsible for over a quarter of the global infection [3, 4]. It is followed by subtype B of the same group; it is found in the industrialized countries of Western Europe and North America [3, 4], while infection with HIV-2 is less spread and is confined mainly in West Africa [2, 5]. Additionally, the HIV-2 AIDS progression is much slower and the virus is hardly transmitted more easily because of its low infectivity and its slow progress; especially as the Viral Loads (VL) in individuals infected with HIV-2 are significantly lower [2, 6, 7].

Currently, no HIV-2 has been documented in Kinshasa or even in the Democratic Republic of Congo (DRC). Hence, the objective of this study was to determine the rate of HIV-1 and HIV-2 co-infection in Kinshasa population.

METHODOLOGY

A Framework

This study was a cross-sectional study on 115 randomly selected plasma samples from the archived plasma samples of newly infected individuals with HIV-1 without Antiretroviral treatment collected between 2013 and 2014 [8, 9]. 500µl of plasma samples were stored at -20°C.

RNA extraction and amplification

140µl were used to extract RNA from plasma using the kit QIAamp® RNA Mini Kit (QIAGEN, Hilden, Germany) in the Laboratory of Molecular Biology to collect a final eluate of 60µl [10]. For confirmation of the infection by HIV-1, a qualitative real-time PCR, based on the previously referred test, was performed on all 115 samples [11]. Each sample (10µl) was analyzed in duplicate.

A qualitative real-time PCR was conducted to determine the HIV-2 infection according to the protocols described previously [12, 13]. Each sample (10µl) was also analyzed in duplicate.

In case of discrepancy between the PCR results, a 3rd Qualitative Real Time PCR (a triplet) was performed.

All analysis were performed at Laboratory of Molecular Biology of the Department of Basic Sciences of the Faculty of Medicine of the University of Kinshasa.

RESULTS

113 samples out of 115 tested were positive for HIV-1, giving an amplification rate of 98.3%. Four samples of the 113 were positive for HIV-2 giving a rate of HIV-1 and HIV-2 coinfection of 4/113 samples or 3.54% for a population newly infected and naive of antiretroviral treatment.

DISCUSSION

113 samples of the 115 analyzed (98.3%) were positive for HIV-1 using qualitative real-time PCR based on a previously described test. Two samples which were previously positive [9], did not amplified even though the PCR tests used were almost same. This difference can be caused by a conservation problem or even thawing and freezing. Indeed, after freezing and thawing, a sample loose close to 1.00 log10 [14]. This means that samples which previously had low VL, i.e., less than this threshold, should not be amplified after thawing and freezing. This justifies the two samples that were not amplified in the collection. These archived plasma samples were previously used in other studies [8, 9, 11].

Four samples out of 113 tested positive for HIV Type 2 by qualitative real-time PCR giving HIV-1 and HIV-2 co-infection rate of 4/113 or 3.54% for samples from a population of newly infected patient's naïve of treatment for HIV in Kinshasa. No study to date has shown that coinfection in Kinshasa; these results challenge the knowledge of the geographical distribution of HIV-2.Our study uncovers the presentation of significant AH in HIV infected individuals who were selected randomly. Further research should be performed to look into histopathological examination and study of the trends of CD4 counts associated with AH.

CONCLUSION

This study was conducted to determine the HIV coinfection rate from patients newly infected, using samples from the archived plasma samples of the Laboratory of Molecular Biology. The rate of coinfection HIV-1 and HIV-2 is of 3.54% for Kinshasa. This coinfection questions the notions of HIV Type 2 for the city of Kinshasa and even the Democratic Republic of Congo.

REFERENCES

1. Kamangu NE, Kabututu Z, Mvumbi LG, Kalala LR, et al. (2013). Genetic Diversity of Human Immunodeficiency Virus Type 1 in the Democratic Republic of Congo: A review of available data. International Journal of Collaborative Research on Internal Medicine & Public Health. 5(5), 295-309.

2. Jeanne-Marie and Amat-Roze. (1993). Les Inégalités géographiques de l'infection à VIH et du SIDA en Afrique Sud Saharienne. Social Science and Medicine. 36(10), 1247-1256.

3. Taylor BS, Sobieszczyk ME, McCutchan FE, Hammer SM, et al. (2008). The challenge of HIV-1 subtype diversity. N Engl J Med. 358(15), 1590-1602.

4. Mc Cutchan FE. (2000). Understanding the Genetic Diversity of HIV Type 1. AIDS. 14(Suppl.3), S31-S44.

5. Jaffar S, Grant AD, Whitworth J, Smith PG, et al. (2004). The natural history of HIV-1 and HIV-2 infections in adults in Africa: a literature review. Bulletin of the World Health Organization. 82(6), 462-469.

6. Berry N, Jaffar S, Ariyoshi K, Harding E, et al. (2002). Low level viremia and high CD4% predict normal survival in a cohort of HIV type-2-infected villagers. AIDS Res Hum Retroviruses. 18(16), 1167-1173.

7. Jaffar S, Vincent T, Ngom P, Meyer AM, et al. (2005). Immunological predictors of survival in HIV type 2-infected rural villagers in Guinea-Bissau. AIDS Res Hum Retroviruses. 21(6), 560-564.

8. Kamangu EN, Chatte A, Susin F, Boreux R, et al. (2015).

Genetic Diversity and Antiretroviral Drug Resistance among Drug-Naïve HIV Type 1 Infected Patients attending Clinics in Kinshasa, Democratic Republic of Congo. J HIV AIDS. 1(1).

9. Kamangu EN, Bulanda BI, Bongenia BI, Botomwito HT, et al. (2015). Virological Profile of Patients Infected with HIV Starting Antiretroviral Treatment in Kinshasa. Open Access Library Journal. 2, e1564.

10. QIAGEN: QIAamp® RNA Blood Mini Handbook. 3rd Edition.

11. Kamangu EN, Chatte A, Boreux R, Kalala RL, et al. (2014). Implementation of an In-House Quantitative Real-Time PCR for Determination of HIV Viral Load in Kinshasa. Open Access Library Journal. 1, e855.

12. Styer LM, Miller TT and Parker MM. (2013). Validation and Clinical use of a sensitive HIV-2 viral load assay that uses a whole virus internal control. J Clin Virol. 58(Suppl 1), e127-133.

13. Youngpairoi AS, Curtis KA, Wells SK, Pau CP, et al. (2014). Reference panel of cloned HIV-2 plasmid DNA for nucleic acid assay development, evaluation and quality monitoring. J Clin Virol. 61(2), 293-297.

14. Adawaye C, Kamangu E, Moussa AM, Tchoumbou B, et al. (2013). Use of Dried Blood Spot to Improve the Diagnosis and Management of HIV in Resource-Limited Settings. World Journal of AIDS. 3, 251-256.