DISTRIBUTION OF HIV-1 VARIANTS IN POPULATION-BASED NATIONAL SURVEYS IN SUB-SAHARAN AFRICA, 2015-2022

1158

Peter D. Ghys[1], Jessica E Justman[2], Andrew C Voetsch[3], Alash'le G Abimiku[4], Sani H Aliyu[5], Hetal K Patel[3], Joshua R DeVos[3], Kristin Brown[3], Faith L Ussery[3], Bharat S Parekh[3], Chéri van der Walt[6,] Vibha Kana[6], Sizulu Moyo[7], Mary I Mahy[8], Joris Hemelaar[9] for the Working Group to characterize HIV-1 variant distributions in national surveys in sub-Saharan Africa.

[1]Independent Consultant, Switzerland, [2]Columbia University, New York, NY, USA; [3]Centers for Disease Control and Prevention, Atlanta, GA, USA; [4]Institute for Human Virology, Abuja, Nigeria, [5]Cambridge University Hospitals, NHS Foundation Trust, Cambridge, UK, [6]National Institute for Communicable Diseases, Sandringham, South-Africa, [7]Human Science Research Council, Pretoria, South-Africa, [8]UNAIDS, Geneva, Switzerland, [9]Oxford Population Health, University of Oxford, Oxford, UK

BACKGROUND

The distribution of HIV-1 genetic variants among people living with HIV (PLHIV) is important for the design of vaccines and broadly neutralising antibodies (bNAbs) as well as for the accuracy of tests for diagnosis and viral load. This study aimed to analyse the distribution of HIV-1 variants from population-based national surveys in sub-Saharan countries.

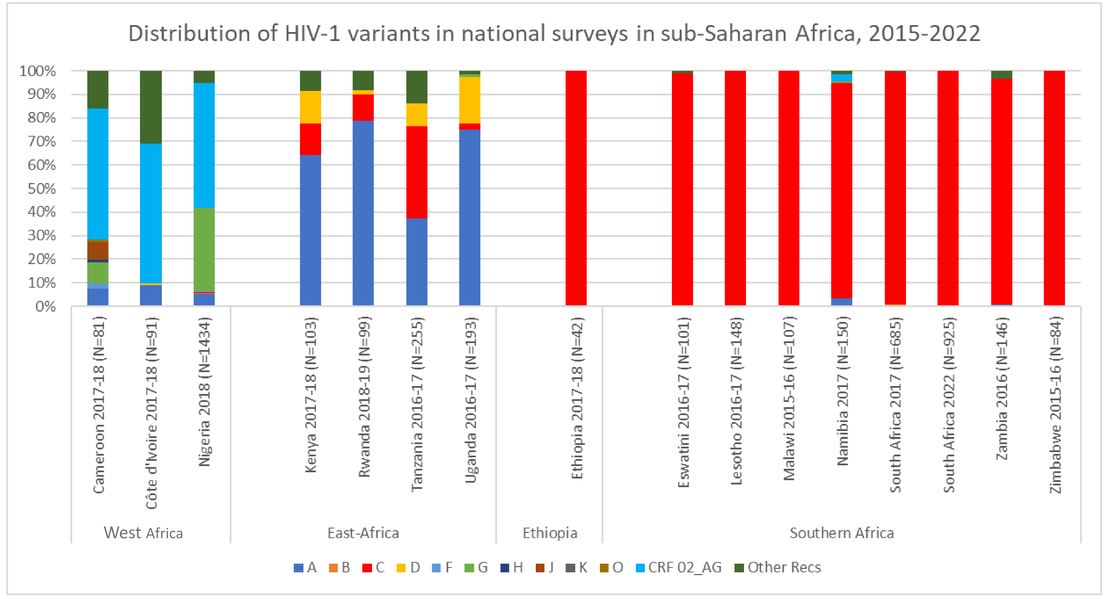
METHODS

Population-based national surveys with HIV-1 subtyping data were available for 15 countries in sub-Saharan Africa during 2015-2022, including Population-based HIV Impact Assessments (PHIAs) in thirteen countries, Nigeria's HIV/AIDS Indicator and Impact Survey (NAIIS) and two South African National HIV Prevalence, Incidence and Behaviour Surveys (SABSSM V and VI). The Ethiopia survey was conducted in urban areas only. Genotyping was performed on the samples selected for resistance testing and in which amplification of HIV RNA/proviral DNA was successful. In most countries, samples from those with a recent HIV infection within the prior 12 months (applying an algorithm that included the Limiting-Antigen Avidity EIA, viral load, and the absence of antiretrovirals), all children younger than 18 months (except for Rwanda), and a country-specific selection of people living with HIV (PLHIV) with a long-standing infection (beyond 12 months) were analysed. In the two SABSSMs, the sampling included PLHIV with >1,000 RNA copies/ml. HIV-1 variants were identified using the REGA HIV-1 & 2 Automated Subtyping Tool. Circulating Recombinant Forms (CRFs) were defined as those listed on the website of the Los Alamos laboratory (https://www.hiv.lanl.gov). Other recombinants were listed as Unique Recombinant Forms (URFs). The unweighted percentage distribution of HIV-1 variants was determined for each survey and the different distributions were compared to each other.

HIV-1 variant distribution, from national surveys conducted during 2015-2022, showed important regional heterogeneity, pointing to a need to consider this variation when developing HIV diagnostics, vaccines, viral load tests, and bNAbs.

RESULTS

Sample sizes of HIV-1 subtyped samples derived from population-based national surveys varied between 42 and 1,434 PLHIV, for a total of 4,644. One sample with subtype O was detected in Cameroon. Comparing country distributions of the main subtypes of HIV-1 and CRF02_AG showed important variation among countries and regions: the dominant variant was the recombinant CRF02_AG in Cameroon, Côte d'Ivoire and Nigeria; subtype A in Kenya, Rwanda and Uganda; subtype C (39%) and subtype A (37%) in Tanzania and subtype C (>90%) in Ethiopia, Eswatini, Lesotho, Malawi, Namibia, South Africa (both surveys), Zambia and Zimbabwe.



No recombinant viruses were detected in the surveys in Ethiopia, Lesotho, South Africa (2022 survey) and Zimbabwe.

In addition to CRF02_AG (see Figure), the following numbers of CRFs were detected: 59x CRF06 (the large majority – 56 - in Nigeria), 9x CRF11, 6x CRF09, 3x CRF10, and 2x CRF37, for a total of 79.

Moreover, the following numbers of URFs were detected: 1x 02_AG/G/A, 1x 02_AG/A, 19x 02_AG/G, 1x 09_cpx/F, 1x D/(10_CD), 19x A/C, 1x A/(A1, A2), 16x A/G, 12x A/D, 1x B/C, 10x C/D, 1x C/G, 1x C/H, 2x C/J, 1x D/G and 1x G/J, for a total of 88. Fifteen viruses were classified as potential recombinants.

CONCLUSIONS

HIV-1 variant distributions from population-based national surveys conducted in countries in West Africa, East Africa, Ethiopia, and Southern Africa showed heterogeneity across these regions, with specific subtypes dominating in each region. In addition to conserved subtypes, a large number of recombinant viruses, both CRFs and URFs, were detected. HIV-1 diversity in sub-Saharan Africa may need to be taken into account for the development of HIV diagnostic and viral load tests, vaccines, and bNAbs.

Author Contact Information: ghysp@hotmail.com

Acknowledgements: We thank all participants of the contributing surveys, the staff responsible for conducting the surveys in-country, and the members of the Working Group to characterize HIV-1 variant distributions in national surveys in sub-Saharan Africa.