Using dried blood spots collected under field condition to determine HIV-1 diversity and drug resistance mutations in resource limited Tanzania

The Harvard community has made this article openly available. Please share how this access benefits you. Your story matters

Citation

Published Version
doi:10.7448/IAS.17.4.19686

Citable link
http://nrs.harvard.edu/urn-3:HUL.InstRepos:13454670

Terms of Use
This article was downloaded from Harvard University’s DASH repository, and is made available under the terms and conditions applicable to Other Posted Material, as set forth at http://nrs.harvard.edu/urn-3:HUL.InstRepos:dash.current.terms-of-use#LAA
Using dried blood spots collected under field condition to determine HIV-1 diversity and drug resistance mutations in resource limited Tanzania

Kimaro, James; Shao, Elichilia; Nyombi, Balthazar; Kifaro, Emanuel; Maruapula, Dorcas; Gaseitsiwe, Simani and Musonda, Rosemary

1Clinical Laboratory, Kilimanjaro Christian Medical Centre, Moshi, Tanzania. 2HIV Research Lab, Botswana Harvard HIV Research Lab, Gaborone, Botswana.

Introduction: A dried blood spot (DBS) on filter paper has been used for different tests globally and has gained popularities in resource limited settings especially during HIV/AIDS epidemic. We assessed the efficiency of molecular characterization of HIV-1 subtypes using DBS collected under field conditions in northern Tanzania.

Material and Methods: In 2011 and 2012, 60 DBS samples were collected under field conditions from exposed and newly diagnosed HIV-1 infected children from Kilimanjaro (n=20), Arusha (n=20), Tanga (n=10) and Manyara (n=10).

Results and discussion: Of 60 DBS analyzed at both Protease (PR) and Reverse Transcriptase (RT) regions, 45 (75%) were analyzed, including 17 (85%) from Kilimanjaro, 15 (75%) from Arusha, 8 (80%) from Tanga, and 5 (50%) from Manyara region. All 45 DBS characterized had viral load above 1000 copies/mL with mean log10 viral loads of 3.87 copies/mL (SD 0.995). The phylogenetic results indicated presence of subtype and circulating recombinant form (CRF). In which, 24 were subtype A1 (53.33%), 16 were subtype C (35.55%), 3 were subtype D (6.67%) and 2 were CRF10_CD (4.35%). All major mutations were detected in the RT region, none from protease (PR) region. The mutations detected were Y181C (n=8), K103 (n=4) and G190 (n=1), conferring resistance to non-nucleoside reverse transcriptase inhibitors (NNRTIs), and M184V (n=1), conferring resistance to lamivudine and emtricitabine.

Conclusions: Our results indicate that DBS collected from field conditions in resource scarcity areas can be used to determine the phylogeny of the virus and drug resistance mutations in areas with diverse HIV-1 group M subtypes.

Published 2 November 2014

Copyright: © 2014 Kimaro J et al; licensee International AIDS Society. This is an Open Access article distributed under the terms of the Creative Commons Attribution 3.0 Unported (CC BY 3.0) License (http://creativecommons.org/licenses/by/3.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.