# *Drug resistance testing in patients virologically failing first-line antiretroviral therapy in Tanzania.*

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**Background:** The introduction of antiretroviral drugs (ARV) has changed the HIV epidemic into a chronic and manageable disease in many settings, thus reducing HIV infection-associated mortality and morbidity rates. The emergence and spread of viral resistance to ARVs can put antiretroviral therapy (ART) programmes in jeopardy, as it can lead to unexpected poor treatment outcomes such as increased virological failure, morbidity, mortality and infectivity rates. Studies have shown that available therapy regimens (pre-defined triple therapy) in sub-Saharan African countries are compromised by high treatment failure rates at the beginning of ART. Few studies have been done to determine the prevalence of viral resistance to ARVs in virologically failing adult populations on first-line ART in Tanzania. This study determined the prevalence of HIV drug resistance (HIVDR) in patients virologically failing their first-line ART regimen.

**Materials and methods:** A cross sectional study was conducted in 280 patients attending care and treatment services at Bugando Medical Centre in Mwanza Tanzania. HIV-1 RNA was extracted from plasma using the QIAamp Viral RNA kit and the QIAcube automated extraction system according to manufacturer's instructions. The genomic region of the HIV-1 genome targeted for characterization was the *pol* gene, that includes the Protease (PR) and a partial segment of the Reverse Transcriptase (RT) region (HXB2 nucleotides 2082 - 3334), which is important for resistance analyses. Complementary DNA synthesis and first round PCR amplification was done with the Access-RT PCR system, while second round nested PCR amplification was done with the native GoTaq DNA polymerase system following manufacturer's instructions. PCR products were sequenced using the BigDye Terminator v 3.1 Cycle Sequencing Ready Reaction Kit and run on an ABI Prism 3130 Genetic Analyzer, per the manufacturer's instructions. Both strands were sequenced using overlapping primers, sequences were, read, manually edited and assembled into contigs using Sequencher v 5.1. The sequences were then submitted to Stanford's HIV drug resistance database for analysis. **Results:** Twenty five percent (25%, 95%CI 20-30) of the participants had virological failure. Poor adherence was associated with increased risk of virological failure, (OR 2.3, 95%CI 1.2-4.7). sequences obtained from 47 patients and 89% had at least one major mutation with the potential of conferring resistance to ARVs. Of these only two were against protease inhibitors (I54V and V82A) and the rest were against reverse transcriptase inhibitors. Common NRTI mutations were M184V (25%), M41L (12%), D67N (11%) T215 (10%), K70R (9%) and K219K/E). Major NNRTI mutations were K103N (20%), G190A (13%), A98G (11%), Y181C (10%), K101E (8%) and E138A (6%). High-level resistance was against 3TC (73%), FTC (69%), NVP (65%), EFV (64%), AZT (37%), RPV (27%), TDF (15%) and ETR (2%). HIV-1 subtypes found were subtype C (38%), A1 (32%), D (28%) and a recombinant A1/D (2%). **Conclusion and recommendations:** Virological failure and RAMs observed in this study were high and threatens existing and future treatment options. The integration of HIV drug resistance testing into existing HIV treatment and monitoring practices will help achieve the expected health outcomes both at patient and population level. This should go hand in hand with strengthening of other monitoring practices such as adherence counselling and maintaining patient to healthcare practitioner good relationship as they lead into desired health outcomes.