**TITLE:** FREQUENCY OF ANTIRETROVIRAL RESISTANCE MUTATIONS IN PEOPLE LIVING WITH HIV/AIDS (PLHA) IN THE STATE OF MARANHÃO, NORTHEAST BRAZIL, IN 2017.

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## ABSTRACT:

Characterizing Drug Resistance Mutations (DRM) in human immunodeficiency virus (HIV) remains a challenge to overcome the virological failure of people living with HIV/AIDS (PLHA). This is of fundamental importance in the planning of therapeutic measures to combat the early failure of Antiretroviral Therapy (ART). In this study, we propose to determine the frequency of DRM in PLHA in the State of Maranhão (Northeast Brazil), characterizing the mutations for antiretroviral (ARV) classes of Protease Inhibitors (PIs), Nucleoside Reverse Transcriptase Inhibitors (NRTIs) and Non-Nucleoside Reverse Transcriptase Inhibitors (NRTIs), presenting their absolute and relative frequencies. One hundred and three HIV-1 pol-sequences were obtained from the database of the Central Laboratory of Public Health of the State of Maranhão

(LACEN/MA), Northeast Brazil. Sequencing of the entire protease (PR) and part of the reverse transcriptase (RT), with 1029 base pair fragments, was performed by ViroSeq<sup>™</sup> HIV-1 Genotyping System (Abbott Laboratories, US) and TRUGENE® HIV-1 Genotyping Assay (Siemens Diagnostics, US) and analyzed by the ABI PRISM 3100 DNA automated sequencer (Applied Biossytems, US) and the OpenGene® Sequencing System (Siemens Diagnostics, US), respectively. The presence of HIV-1 resistance mutations was determined by submitting the study sequences to the HIV Drug Resistance Database (Stanford University) online platform (http://hivdb.stanford.edu). Two hundred and seventy two DRM were recognized in the 103 sequences analyzed. Reverse Transcriptase (RT) showed 214 DRM and Protease (PR), 58 DRM. The highest percentage was identified in NRTIs (114 mutations, representing 41.9%) followed by NNRTIs (100 mutations, 36.8%) and PIs (58 mutations, 21.3%). Although the PIs had the lowest percentage of DRM, the number of resistance codons identified was higher than all other classes (29 for PIs, 23 for NRTIs and 15 for NNRTIs). The most prevalent mutations were M184V (16.91%), followed by K103N (12.13%) and the I54V and V82A mutations (2.57%). In addition, we identified a large number of codons of IP resistance (29 codons), which may indicate that these genes may be on a higher positive selective pressure, which may have contributed to the virological failure of ART in this group of people.

Keywords: HIV, Drug Resistence Mutations, ART, Genotyping.