Supplementary Table. Methodologic details of HIV-1 Molecular Studies from Northern Brazil (2000-2019).

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| --- | --- | --- | --- | --- | --- |
| **Reference**  **State** | **Sample**  **Period (years)** | **HIV-1 region/**  **Sequenced** | **Method** | **Subtyping tool** | **TDR/ADRM tool** |
| VICENTE *et al.*, 2000[8]  AM | Buffy coat DNA  1996-1997 | GAG ( p24), ENV (gp120, C2V3), PR | In house sequencing | RFLP (PR), phylogeny (ENV) | ND |
| MACHADO *et al*., 2009[21]  PA/AP | PBMC DNA  1988-2002 | PR, ENV (gp120 C2V3) | In house sequencing | NCBI, phylogeny | ND |
| CARVALHO *et al*., 2011 [22]  TO | Plasma RNA  2008-2009 | PR/RT | In house sequencing | REGA,  Phylogeny, SimPlot | CPR Stanford |
| CUNHA *et al*., 2012 [23]  AM | Buffy coat DNA  2006-2007 | ENV, GAG, POL | In house sequencing | Phylogeny, SimPlot | ND |
| MACEDO *et al*., 2012[24]  PA/AM  MORAES SOARES et al 2014  AM[25] | Plasma RNA  2002-2006  Dried blood proviral DNA  2009-2010 | PR/RT  PR/RT | ViroSeq®  In house sequencing | Stanford; National STD/AIDS Program algorithm 2004    Phylogeny | ND  WHO algorithm 2009 |
| DOS ANJOS SILVA *et al*., 2015[26]  AP | PBMC DNA  2013-2014 | PR/RT | In house sequencing | REGA  Phylogeny, SimPlot | CPR Stanford |
| LOPES *et al*., 2015[27]  PA | Plasma RNA  2004-2013 | PR/RT | ViroSeq®2004-8  TruGene® 2009-13 | Stanford | Stanford  HIV Drug Resistance Database |
| DA COSTA *et al.,* 2011[28]  AC/AM/PA/RO/RR | PBMC DNA  2010-2011 | PR/RT | TruGene® | REGA, phylogeny, SimPlot | ND |
| ANDRADE *et al*., 2017[29]  AM | Plasma RNA  2010-2015 | PR/RT | TruGene® | REGA,  HIVdb Program/Stanford | CPR, HIVdb Program/ Stanford |
| CORADO *et al*., 2017[30]  RR | Blood DNA  2013-2014 | PR/RT | In house sequencing | REGA,  Phylogeny, SimPlot | CPR; HIVdb Program Stanford |
| MACHADO *et al*., 2017[31]  PA | Blood DNA  2007-2008 | PR/RT | In house sequencing | Stanford, Phylogeny | CPR, Stanford HIVdb Program. |
| REIS *et al*., 2017[19]  TO\* | PBMC DNA  2008-2009 | FGS/NFGS | In house sequencing | Phylogeny, SimPlot | ND |
| ARRUDA *et al.,* 2018[7]  AC/AM/AP/PA/RO/RR/TO | Plasma RNA  2013-2015 | PR/RT | TruGene®  OpenGene® | REGA  HIVdb Program | CPR, HIVdb Program Stanford |
| CRISPIM *et al*., 2019a [32], CRISPIM *et al*., 2019b [33]  AM/RO/RR | Plasma RNA  2011-2017 | PR/RT | In house sequencing | Stanford, Phylogeny,  SimPlot | CPR, HIVdb Program Stanford |

Initials of Northern states AC: Acre , AM: Amazonas, AP: Amapá, PA: Pará, RO: Rondônia, RR: Roraima, TO: Tocantins; PBMC: peripheral blood mononuclear cells; in house sequencing: direct nucleotide sequencing; RFLP: restriction fragment length polymorphism; ENV: C2V3 envelope region; GAG: gag region; PR/RT: protease and reverse transcriptase regions of pol gene; POL:PR/RT regions; NCBI: National Center for Biotechnology Information at http://www.ncbi.nih.gov/retroviruses/subtype/; CPR: Calibrated Population Resistance Tool, Stanford University at http://cpr.stanford.edu/cpr.cgi; Stanford University HIVdb Drug resistance database Genotypic Resistance Interpretation Algorithm at http://sierra2.stanford.edu/sierra/servlet/JSierra; Stanford subtyping tool; ViroSeq® HIV-1 Genotype System (Celera Diagnostics, USA); TruGene® HIV genotyping kit (Siemens, Germany); OpenGene® DNA sequencing system (Siemes, NY, USA); ND: not done; FGS/NFGS: in house full-genome sequencing and near-full-genome sequencing. \*this table included only BF1 samples from TO state (REIS *et al*., 2017).