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 DNA1996-1997 | GAG ( p24), ENV (gp120, C2V3), PR | In house sequencing | RFLP (PR), phylogeny (ENV) | ND |
| MACHADO *et al*., 2009[21]PA/AP | PBMC DNA1988-2002 | PR, ENV (gp120 C2V3) | In house sequencing | NCBI, phylogeny | ND |
| CARVALHO *et al*., 2011 [22] TO | Plasma RNA2008-2009 | PR/RT | In house sequencing | REGA,Phylogeny, SimPlot | CPR Stanford |
| CUNHA *et al*., 2012 [23]AM | Buffy coat DNA2006-2007 | ENV, GAG, POL | In house sequencing |  Phylogeny, SimPlot | ND |
| MACEDO *et al*., 2012[24]PA/AMMORAES SOARES et al 2014AM[25] | Plasma RNA2002-2006Dried blood proviral DNA2009-2010 | PR/RTPR/RT | ViroSeq®In house sequencing | Stanford; National STD/AIDS Program algorithm 2004 Phylogeny | NDWHO algorithm 2009 |
| DOS ANJOS SILVA *et al*., 2015[26]AP | PBMC DNA2013-2014 | PR/RT | In house sequencing | REGAPhylogeny, SimPlot | CPR Stanford |
| LOPES *et al*., 2015[27]PA | Plasma RNA2004-2013 | PR/RT | ViroSeq®2004-8 TruGene® 2009-13 | Stanford  | StanfordHIV Drug Resistance Database |
| DA COSTA *et al.,* 2011[28]AC/AM/PA/RO/RR | PBMC DNA2010-2011 | PR/RT | TruGene® | REGA, phylogeny, SimPlot | ND |
| ANDRADE *et al*., 2017[29]AM | Plasma RNA2010-2015 | PR/RT | TruGene® | REGA,HIVdb Program/Stanford | CPR, HIVdb Program/ Stanford |
| CORADO *et al*., 2017[30]RR |  Blood DNA2013-2014 | PR/RT | In house sequencing | REGA,Phylogeny, SimPlot | CPR; HIVdb Program Stanford |
| MACHADO *et al*., 2017[31]PA | Blood DNA2007-2008 | 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 RNA2013-2015 | 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 RNA2011-2017 | 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).