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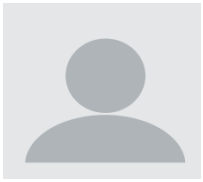

Assessing the HIV-1 epidemic in brazilian drug Users: A molecular epidemiology approach

Monick Zack, Lindenmeyer, Bianca nicon, Reta Marques

[1]*Laboratório de AIDS e Imunologia Molecular, Instituto Oswaldo Cruz- FIOCRUZ, Rio de Janeiro, Brasil*
[2]*Instituto de Comunicação e Informação Científica e Tecnológica em Saúde- FIOCRUZ, Rio de Janeiro, Brasi*

Abstract (600 words limit)

Person who inject illicit substances have an important role in HIV-1 blood and sexual transmission and together with person who uses heavy non-injecting drugs may have less than optimal adherence to anti-retroviral treatment and eventually could transmit resistant HIV variants. Unfortunately, molecular biology data on such key population remain fragmentary in most low and middle-income countries. The aim of the present study was to assess HIV infection rates, evaluate HIV-1 genetic diversity, drug resistance, and to identify HIV transmission clusters in heavy drug users (DUs). For this purpose, DUs were recruited in the context of a Respondent-Driven Sampling (RDS) study in different Brazilian cities during 2009. Overall, 2,812 individuals were tested for HIV, and 168 (6%) of them were positive, of which 19 (11.3%) were classified as recent seroconverters, corresponding to an estimated incidence rate of 1.58%/year (95% CI 0.92–2.43%). Neighbor joining phylogenetic trees from env and pol regions and bootscan analyses were employed to subtype the virus from132 HIV-1-infected individuals. HIV-1 subtype B was prevalent in most of the cities under analysis, followed by BF recombinants (9%-35%). HIV-1 subtype C was the most prevalent in Curitiba (46%) and Itajaí (86%) and was also detected in Brasília (9%) and Campo Grande (20%). Pure HIV-1F infections were detected in Rio de Janeiro (9%), Recife (6%), Salvador (6%) and Brasília (9%).

Clusters of HIV transmission were assessed by Maximum likelihood analyses and were cross-compared with the RDS network structure. Drug resistance mutations were verified in 12.2% of DUs. Our findings reinforce the importance of the permanent HIV-1 surveillance in distinct Brazilian cities due to viral resistance and increasing subtype heterogeneity all over Brazil, with relevant implications in terms of treatment monitoring, prophylaxis and vaccine development Since the start of the AIDS scourge in the mid eighties, 757,042 AIDS cases have been accounted for in Brazil by the Brazilian Ministry of Health. Brazil has a general low broad predominance (0.4%), that is by all accounts stable beginning around 2004, yet pervasiveness is considerably higher in key populaces at higher danger.

As per the UNAIDS rules Brazilian pestilence is concentrated. Different Brazilian overviews led from 1998 to 2009 in key subpopulations were surveyed by a meta-investigation, with the outcomes as follows: men who engage in sexual relations with men [13.6 (95% CI: 8.2-20.2)], female sex laborers [6.2 (95% CI: 4.4-8.3)] and weighty (unlawful) drug clients.In the initial twenty years of the AIDS scourge in Brazil (1980-1997), individuals who infused drugs contributed with 17.3% of the AIDS cases, however starting around 1998, the pervasiveness of HIV disease in this populace has been diminishing. A more articulated decay was seen lately and these days relates to 2.1% of new AIDS cases. This pattern presently can't seem to be completely clarified, however appears to result from a mix of various factors, for example, unconstrained/optional social changes; the convenient execution of preventive measures (for example needles and needles trade programs) combined with various projects meaning to diminish drug-related damage; the exceptionally bad quality of road cocaine, making infusion troublesome and hazardous; and the checked change to non-injectable courses, particularly rocks, just as the inescapable brutality of medication scenes and the related high mortality that wrecked the more established associates of medication clients (large numbers of them injectors) throughout the long term.

Biography (200 words limit)

Dr. Monick zack Lindenmeyer Guimarães Laboratório de AIDS e Imunologia Molecular, Instituto Oswaldo Cruz- FIOCRUZ, Rio de Janeiro, Brasil one of the best professopr of science. He written so many articles. “Experienced (12 y) Clinical Pharmacist with a demonstrated history of working in the Government Administration. Skilled in Infectious Diseases,Drug information, Intensive Care, Pharmacy Benefit Management, Pharmacovigilance, and Pharmacy Automation. Strong healthcare services professional with a Board certified critical care pharmacist focused in Critical care from American collage of clinical Pharmacy, (10 y) Formulary Maker. Professor at the Department of Analytical Chemistry, Faculty of Pharmacy, Istanbul University. She studied Chemical Engineering, had Ph.D. and M.Sc. degrees at Istanbul University, Institute of Health Sciences, Faculty of Pharmacy, Department of Analytical Chemistry on drug analysis in pharmaceutical formulations and biological fluids by spectrophotometric and liquid chromatographic methods. She conducted post-doctoral research at Medical Center of Munich University, Institute of Laboratory Medicine Laboratory of Bio-Separation with a main focus of hyphenation of mass spectrometry with on-line sample processing between the years 2011-2013. She has researches and publications on drug analysis in biological fluids by liquid chromatography mass spectrometry, on-line solid phase extraction coupled liquid chromatography, multidimensional chromatography, spectrophotometry, spectrofluorimetry including validation, degradation and pharmacokinetic studies. She is also serving as reviewer for several reputed journals like Journal of Mass Spectrometry, Journal of Chromatography B, Luminescence, Journal of Fluorescence, Journal of AOAC International, Analytical Methods, Analytical Letters and some others.

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About University: (200 words limit)

The organization started in 1898 as the Federal SeroTherapy Institute with the objective of developing serum and vaccines against the bubonic plague. It was located outside Rio de Janeiro. The institute’s activities, however, changed from simple production into research and experimental medicine, especially after Oswaldo Cruz assumed its leadership in 1902. From there on, the institute became the base for memorable sanitation campaigns in an age of outbreaks and epidemics of the bubonic plague, yellow fever, and smallpox. The Institute, however, was not confined to Rio de Janeiro and collaborated in the occupation of the country’s interior through scientific expeditions, aiding in the development of the country. When Oswaldo Cruz died in 1917, the Institute, which by then already bore his name, was nationally consolidated and important scientific achievements followed, such as Carlos Chagas’ description of the complete cycle of the American trypanosomiasis including the clinical pattern of the disease.

Importance of Research (200 words limit)

Nucleotide sequences were aligned using the Clustal X program implemented in Mega 5.2 program and later manually edited. All positions with alignment gaps were removed, resulting in two alignments, one corresponding to the PR/RT regions of pol gene (nucleotides 2265–3519 relative to HXB2); and the second ones corresponding to the C2-V3 env region (nucleotides 6922–7277 relative to HXB2). References sequences from all CRF_BF circulating in South America which present recombination breakpoint in the regions under study were included in the analysis. The Maximum Likelihood (ML) phylogenetic trees pol and env were inferred under the GTR+I+Γ4 nucleotide substitution model, selected using the jModeltest program. The ML tree was reconstructed with the PhyML program using an online web server. Heuristic tree search was performed using the SPR branch-swapping algorithm and the reliability of the obtained topology was estimated with the approximate likelihood-ratio test (aLRT) based on the Shimodaira-Hasegawa-like procedure. The ML trees were visualized using the FigTree v1.3.1 program available at: http://treebioedacuk/software/figtree.

Recombination analysis was performed by bootscan analysis as implemented in the Simplot version 3.5.1, using representative sequences of HIV-1 subtypes B, C, and F1 as reference. Bootstrap values supporting branching with reference sequences were determined in Neighbor-Joining trees constructed using the K2-parameter model, based on 100 resamplings, with a 200nt sliding window moving in steps of 10 bases.

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