RESEARCH ARTICLE

High Prevalence and Onward Transmission of Non-Pandemic HIV-1 Subtype B Clades in Northern and Northeastern Brazilian Regions

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Abstract

The Human immunodeficiency virus type-1 (HIV-1) epidemic in Brazil is mainly driven by the subtype B pandemic lineage (BPANDEMIC), while Caribbean non-pandemic subtype B clades (B_CAR) seem to account for a very low fraction of HIV-infections in this country. The molecular characteristics of the HIV-1 subtype B strains disseminated in the Northern and Northeastern Brazilian regions, however, have not been explored so far. In this study, we estimate the prevalence of the HIV-1 BPANDEMIC and B_CAR clades across different Brazilian regions and we reconstruct the spatiotemporal dynamics of dissemination of the major Brazilian B_CAR clades. A total of 2,682 HIV-1 subtype B pol sequences collected from 21 different Brazilian states from the five country regions between 1998 and 2013 were analyzed. Maximum Likelihood phylogenetic analyses revealed that the B_CAR strains reached 16 out of 21 Brazilian states here analyzed. The B_CAR clades comprise a low fraction (<10%) of subtype B infections in most Brazilian states analyzed, with exception of Roraima (41%), Amazonas (14%) and Maranhão (14%). Bayesian phylogeographic analyses indicate that B_CAR strains originally from the Hispaniola and Trinidad and Tobago were introduced at multiple times into different states from all Brazilian regions and a few of those strains, probably introduced into Roraima, Maranhão and São Paulo between the late 1970s and the early 1980s, established secondary outbreaks in the Brazilian population. These results support that the HIV-1 subtype B epidemics in some Brazilian states from the Northern and Northeastern regions display a unique molecular pattern characterized by the high prevalence of B_CAR lineages, which probably reflects a strong epidemiological link with the HIV-1 epidemics in the Caribbean region.

Introduction

According to estimations of the Brazilian Ministry of Health, about 780,000 people were living with the Human Immunodeficiency Virus Type 1 (HIV-1) in Brazil at 2014 [1]. Most Brazilian
design, data collection and analysis, decision to publish, or preparation of the manuscript.

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AIDS cases notified in the 2000–2015 period were concentrated in the Southeastern region (48%), followed by the Southern (22%), Northeastern (17%), Northern (7%) and Central-Western (6%) regions [1]. The AIDS Brazilian epidemic is primarily driven by the HIV-1 subtype B, followed by subtypes F1, C, and recombinant forms among those subtypes, although the relative prevalence of different HIV-1 genetic variants greatly vary across Brazilian regions [2–7].

Subtype B is the most prevalent HIV-1 lineage circulating in the Americas and its dissemination was probably initiated by the introduction of a founder strain from Central Africa into Haiti around the middle 1960s [8]. Between the late 1960s and the early 1970s, the subtype B seems to have moved out from the island of Hispaniola (shared by Haiti and the Dominican Republic) on several independent occasions, reaching the United States (US) and some neighboring Caribbean countries [8]. One subtype B variant introduced in the US was successfully disseminated within this country and to other countries around the world, establishing a pandemic clade (B_{PANDEMIC}) [8]. Other subtype B variants, by contrast, remained mostly restricted to the Caribbean region and established a number of non-pandemic Caribbean clades (B_{CAR}) [8,9].

The non-pandemic B_{CAR} lineages account for an important fraction of HIV-1 subtype B infections in several American countries including: Haiti and the Dominican Republic (~75%), Jamaica (~50%), Trinidad and Tobago (~95%), other Lesser Antilles (~40–75%), French Guiana (56%) and Suriname (54%) [9,10]. The non-pandemic B_{CAR} strains have been also disseminated from the Caribbean into several Latin American countries [10–12], with evidence of onwards transmission in Argentina, Brazil, Mexico, Panama and Venezuela [10,12]. Those secondary outbreaks established in Latin America, however, were of small size and the B_{CAR} strains only account for a minor fraction (<10%) of HIV-1 subtype B infections in that region [10,12].

A previous study conducted by our group, estimated that B_{CAR} strains only explain 1.7% of subtype B infections in Brazil [10]. Most Brazilian subtype B sequences used in that previous study, however, were from the Southeastern, Southern and Central-Western country regions. The objective of this study was to estimate the relative prevalence of the B_{PANDEMIC} and B_{CAR} clades in all Brazilian regions and to reconstruct the spatiotemporal dynamics of dissemination of the HIV-1 B_{CAR} clades circulating in the country. For this, we used a comprehensive dataset of HIV-1 subtype B pol sequences (n = 2,682) isolated from 21 different Brazilian states from the five country regions between 1998 and 2012. Brazilian HIV-1 subtype B sequences were combined with reference sequences of the B_{PANDEMIC} and the B_{CAR} clades and then subjected to Maximum Likelihood and Bayesian phylogeographic analyses.

Materials and Methods

Brazilian HIV-1 subtype B pol sequence dataset

We downloaded all HIV-1 subtype B pol sequences from Brazil with information about sampling state and that covered the entire protease and partial reverse transcriptase (PR/RT) regions (nucleotides 2253–3260 relative to HXB2 clone), available at the Los Alamos HIV Database (http://www.hiv.lanl.gov) by September 2015. Only one sequence per subject was selected and those sequences with incorrect subtype assignment were removed. These sequences were combined with Brazilian HIV-1 subtype B pol sequences from the Northern region recently published (n = 318) [7,13] and others that were newly generated (n = 71). New HIV-1 subtype B pol sequences were obtained from HIV-1-infected persons that attended the Public Health Central Laboratory from Roraima (LACEN-RR) in 2013. Blood samples were transported to the Instituto Leônidas e Maria Deane (FIOCRUZ) in Manaus for HIV
amplification and subtyping as described previously [13]. All patients were informed of the procedures and signed the informed consent. The study was approved by the Ethics Committee of the "Universidade Federal de Roraima" (CAAE 15629013.8.0000.5302). This resulted in a final data set of 2,682 subtype B pol sequences isolated from 21 Brazilian states distributed across the five country regions (Table 1). The subtype assignment of all sequences was confirmed using the REGA HIV subtyping tool v.2 [14] and by performing phylogenetic analyses (see below) with HIV-1 group M subtype reference sequences.

**Phylogenetic analysis**

HIV-1 Brazilian sequences were aligned with subtype B pol (PR/RT) sequences from the US \( (n = 165) \), France \( (n = 135) \) and the Caribbean \( (n = 279) \) representative of the BPANDEMIC and the BCAR clades described previously [9,12]. Sequences were aligned using the Clustal W program [15] and all sites associated with major antiretroviral drug resistance in PR and RT were excluded. Maximum Likelihood (ML) phylogenetic trees were inferred under the GTR+I+Γ nucleotide substitution model selected using the jModeltest program [16]. The ML trees were reconstructed with the PhyML program [17] using an online web server [18]. 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 \( (aLRT) \) [19] based on the Shimodaira-Hasegawa-like procedure. The ML trees were visualized using the FigTree v1.4.0 program [20].

**Analysis of the spatiotemporal dispersion pattern**

The evolutionary rate, the age of the most recent common ancestor \( (T_{MRCA}) \) and the spatial diffusion pattern of HIV-1 BCAR clades circulating in Brazil were jointly estimated using the Bayesian Markov Chain Monte Carlo (MCMC) approach as implemented in BEAST v1.8

<table>
<thead>
<tr>
<th>Region</th>
<th>State</th>
<th>Code</th>
<th>Public database/ Published</th>
<th>Newly generated</th>
<th>Sampling time</th>
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<td>PR</td>
<td>50</td>
<td>-</td>
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</tr>
<tr>
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<td>59</td>
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<td>1997</td>
</tr>
<tr>
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<td>MG</td>
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<td>-</td>
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</tr>
<tr>
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<td>-</td>
<td>1998–2010</td>
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<tr>
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<td>150</td>
<td>-</td>
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<tr>
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<td>-</td>
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</tr>
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<td>Maranhão</td>
<td>MA</td>
<td>70</td>
<td>-</td>
<td>2012</td>
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<tr>
<td></td>
<td>Pernambuco</td>
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<td>97</td>
<td>-</td>
<td>2009–2010</td>
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<td>Piauí</td>
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<tr>
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<td>Acre</td>
<td>AC</td>
<td>11</td>
<td>-</td>
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<tr>
<td></td>
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<td>AP</td>
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<td>-</td>
<td>2013</td>
</tr>
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<td>-</td>
<td>2010–2011</td>
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<tr>
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<td>Tocantins</td>
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<td>46</td>
<td>-</td>
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<td>-</td>
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<td>Roraima</td>
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<td>31</td>
<td>71</td>
<td>2010–2013</td>
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Analyses were performed using the GTR+I+Γ₄ nucleotide substitution model, a relaxed uncorrelated lognormal molecular clock model and a Bayesian Skyline coalescent tree prior. The mean evolutionary rates previously estimated for the subtype B pol gene (2.0–3.0 x 10⁻³ subst/site/year) were incorporated as an informative prior interval. Migration events throughout the phylogenetic history and the most relevant migration pathways were reconstructed using a reversible discrete phylogeography model and the Bayesian stochastic search variable selection (BSSVS) approach, with a CTMC rate reference prior. Three MCMC chains were run for 500 x 10⁶ generations and then combined using LogCombiner v1.8. Convergence and uncertainty of parameter estimates were assessed by calculating the Effective Sample Size (ESS) and 95% Highest Probability Density (HPD) values, respectively, after excluding the initial 10% of each run with Tracer v1.6. The maximum clade credibility (MCC) tree was summarized with TreeAnnotator v1.8 and visualized with FigTree v1.4.0. Migratory events and Bayes factor rates were summarized using the cross-platform SPREAD application.

Nucleotide Sequence Accession Numbers
HIV-1 subtype B pol (PR/RT) sequences from Roraima were deposited in GenBank under accession numbers KX443015-KX443025, KX443027-KX443059 and KX443061-KX443087.

Results
Prevalence of the HIV-1 BPANDEMIC and BCAR clades in Brazil
A total of 2,682 HIV-1 subtype B pol sequences isolated from 21 Brazilian states from the Southeastern (n = 1,512), Northern (n = 457), Northeastern (n = 253), Central-Western (n = 252) and Southern (n = 208) regions were analyzed in this study (Table 1). Brazilian HIV-1 subtype B pol sequences were divided in three subsets and each subset was combined with a reference dataset containing 500 BPANDEMIC sequences from the US and France and 200 BCAR sequences from the Caribbean, selected from a previous study. The ML analyses of all three subsets confirmed that BPANDEMIC reference sequences branched in a highly supported (aLRT > 0.90) monophyletic clade nested within basal BCAR reference sequences (Fig 1). These analyses also showed that BCAR sequences were detected in 16 out 21 Brazilian states here analyzed, although with highly variable prevalence across locations (Fig 2). The BCAR sequences account for a very large proportion (41%) of HIV-1 subtype B infections in the state of Roraima, a relative large/moderate proportion (14%) in the states of Amazonas and Maranhão, and a low proportion (<5%) in the remaining Brazilian states. When analyzed by Brazilian region, the highest proportion of BCAR sequences was observed in the Northern (17%), followed by the Northeastern (4%), Central-Western (1%), Southeastern (1%) and Southern (1%) regions. Analysis of the epidemiological characteristics of the HIV-1 BCAR-infected patients reveals that most individuals were male (58%), and that the heterosexual mode of transmission was the predominant one (65%), followed by men having sex with men (MSM, 23%). Diagnosis of HIV-1 infection ranged between 1995 and 2013 and the country of origin of all individuals was Brazil, with exception of one individual from Guyana that attended the Public Health Central Laboratory from Roraima.

Dispersal pattern of the HIV-1 BCAR strains from the Caribbean into Brazil
The HIV-1 BCAR Pol sequences with known sampling date from Brazil here identified (n = 97) were classified into 15 discrete geographic locations according to the sampling state (S2 Table).
Brazilian BCAR sequences were combined with BCAR pol sequences from the most widely sampled Caribbean islands (Hispaniola, Jamaica and Trinidad and Tobago) previously identified [9,12], and with subtype D pol sequences from the Democratic Republic of Congo (DRC) ($n = 10$) that was pointed as the most probable source location of subtype B strain introduced in the Americas [8] and subsequently subjected to Bayesian phylogeographic reconstructions. The root location of the HIV-1 subtype B ancestor was most probably placed in the island of Hispaniola (Dominican Republic/Haiti) ($PSP = 0.92$) during the

Fig 1. ML phylogenetic tree of HIV-1 subtype B pol PR/RT sequences (~1,000 nt) circulating in Brazil ($n = 2,682$) and representative sequences of the B_{PANDEMIC} ($n = 300$) and the B_{CAR} ($n = 200$) clades. Brazilian subtype B pol sequences were subdivided in three subsets according to their geographic origin: A) sequences from Sao Paulo, B) sequences from the Central-Western/Southern/Southeastern (except Sao Paulo) regions, and C) sequences from the Northern/Northeastern regions. Branches are colored according to the geographic origin/clade classification of each sequence as indicated at the legend at bottom. The B_{PANDEMIC} clade was collapsed for visual clarity. The aLRT support values are indicated at key nodes. Trees were rooted using HIV-1 subtype D reference sequences. The branch lengths are drawn to scale with the bar at the bottom indicating nucleotide substitutions/site.

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1960s (Fig 3A and Table 2), consistent with previous findings [8,9]. The subtype B was then independently disseminated from Hispaniola to Trinidad and Tobago and Jamaica around the early 1970s, where seeded secondary outbreaks that resulted in the origin of the non-pandemic subclades BCAR-TT and BCAR-JM previously described [8,9]. This Bayesian analysis also indicates that BCAR strains were disseminated at multiple times from Hispaniola (n = 11) and Trinidad and Tobago (n = 3) to Brazil (Fig 3). Direct disseminations of BCAR strains from Hispaniola to Brazilian states of the Southern (Rio Grande do Sul), Southeastern (Rio de Janeiro and Sao Paulo), Central-Western (Mato Grosso do Sul), Northeastern (Maranhão) and Northern (Acre, Roraima and Tocantins) regions were detected, as well as dissemination of the BCAR-TT clade from Trinidad and Tobago to Roraima and Sao Paulo states. The Bayes factor tests for significant nonzero rates, however, support epidemiological linkage between Hispaniola and only a few Brazilian states (Acre, Tocantins and Sao Paulo) as well as between Trinidad and Tobago and Roraima (S3 Table).

Dispersal pattern of the Brazilian HIV-1 BCAR clades

Among the 14 BCAR strains introduced into Brazil, four established onward transmission and originated the Brazilian clades here denominated BCAR-BR-I, BCAR-BR-II, BCAR-BR-III and BCAR-BR-IV (Fig 3A), that comprise 51%, 16%, 10% and 8% of the Brazilian BCAR sequences used in this analysis, respectively. All Brazilian non-pandemic subtype B clades displayed a high support (PP > 0.80) with exception of BCAR-BR-III (PP = 0.35). The clade BCAR-BR-I comprises most BCAR sequences detected in Roraima (79%) and all sequences detected in Amazonas. This clade seems to have arisen by the introduction of a BCAR-TT strain into Roraima at around 1978 (Table 2), with later dissemination from Roraima to: Amazonas, Amapá, Piauí and Sao Paulo (Fig 3). The clade BCAR-BR-II comprises all BCAR sequences detected in the state of Maranhão. This clade seems to have arisen by the introduction of a BCAR strain from the Hispaniola into Maranhão at around 1978 (Table 2) and the subsequent dissemination from Maranhão to: Pará, Goiás, Mato Grosso do Sul, Sao Paulo and Espírito Santo (Fig 3). The clade BCAR-BR-III probably arose by the introduction of a BCAR strain from Hispaniola into the state of Sao Paulo at around 1979 (Table 2) and from Sao Paulo it was disseminated to: Rio de Janeiro, Minas Gerais, Rio Grande do Sul and Pará (Fig 3). The clade BCAR-BR-IV probably arose by the introduction of a BCAR strain from Hispaniola into the state of Roraima at around 1982 (Table 2) and from Roraima it was disseminated to Sao Paulo and Espírito Santo (Fig 3). The Bayes factor tests for significant nonzero rates supports epidemiological linkage between most Brazilian locations pairs previously described (S3 Table). Of note, among the 10 Brazilian homosexual/bisexual men infected by BCAR strains here identified, five branched within the clade BCAR-BR-I, three within the clade BCAR-BR-II, one within the clade BCAR-BR-IV, and the remaining one branched outside the major Brazilian clades.

Discussion

This study demonstrates that BCAR strains have been introduced at multiples times into Brazil and circulate in at least 16 out 21 Brazilian states here analyzed. Although subtype B epidemic in most Brazilian states is clearly dominated by the BPANDEMIC clade, the non-pandemic BCAR
strains reach a significant prevalence in a few states from the Northern (Roraima = 41% and Amazonas = 14%) and Northeastern (Maranhão = 14%) regions. The prevalence of BCAR strains detected in Roraima is comparable to that described in some northern South American countries (Suriname and French Guyana), and much higher than that estimated for other continental countries of the Americas [10].

Our phylogeographic analysis indicates that the islands of Hispaniola and Trinidad and Tobago were probably the major sources of BCAR lineages introduced into Brazil, although direct epidemiological linkages between the Caribbean islands and several Brazilian states were not significantly supported. It is highly probable that Suriname, French Guyana and Guyana may have also played a crucial role in such dissemination process, acting as a staging post between the Caribbean islands and Brazil. Those South American countries displayed a high prevalence of BCAR strains [10] and have maintained a high human flux with both Caribbean islands and Brazil. Interestingly, the number of subtype B pol (PR/RT) sequences from those South American countries currently available in public database is too small to obtain robust phylogeographic reconstructions of the viral migrations pathways in the northernmost South American region.

Irrespective of the precise location of the source, our phylogeographic analysis clearly showed that several Brazilian states from the Northern (Roraima, Acre and Tocantins),

**Table 2. Bayesian TMRCA estimates for major BCAR clades from Brazil and the Caribbean.**

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<thead>
<tr>
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<tbody>
<tr>
<td>BCAR-BR-I</td>
<td>1978 (1975–1981)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>BCAR-BR-II</td>
<td>1978 (1974–1982)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>BCAR-BR-III</td>
<td>1979 (1974–1983)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>BCAR-BR-IV</td>
<td>1982 (1977–1986)</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

The mean estimated evolutionary rate of the HIV-1 BCAR/D pol dataset was $2.1 \times 10^{-3}$ substitutions/site per year (95% HPD $2.0 \times 10^{-3}$–$2.2 \times 10^{-3}$ substitutions/site per year), whereas the corresponding median coefficient of rate variation was 0.31 (95% HPD: 0.27–0.35), supporting the selection of a relaxed molecular clock model.

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Northeastern (Maranhão), Southeastern (Rio de Janeiro and Sao Paulo), Central-Western (Mato Grosso do Sul) and Southern (Rio Grande do Sul) regions acted as an entry point of BCAR strains. Most Brazilian individuals infected with BCAR strains were heterosexual (65%), although the proportion of individuals infected by heterosexual (44%) and homosexual/bisexual (40%) contacts was roughly similar among men caring BCAR strains. These results revealed that the BCAR strains are being introduced into both heterosexual and MSM networks from different Brazilian states. Most introductions seem to have resulted in dead-end infections that were not further disseminated in the Brazilian population. Four BCAR strains, however, established onward transmission in the Brazilian population and originated local non-pandemic subtype B clades here designated from BCAR-BR-I to BCAR-BR-IV, according to their relative prevalence.

Roraima not only display the highest prevalence of BCAR strains among all Brazilian states, but was also pointed as the most probable source location of BCAR-BR-I and BCAR-BR-IV clades. The clade BCAR-BR-I probably evolved from the clade BCAR-TT circulating in Trinidad and Tobago, while the clade BCAR-BR-IV was more closely related to BCAR strains from the Hispaniola. The clade BCAR-BR-I was successfully spread within Roraima and disseminated to Amazonas at multiple times, and also to Amapá, Piauí and Sao Paulo. The pervasive dissemination of the clade BCAR-BR-I from Roraima into Amazonas is expected considering that these two neighboring states maintain a very intense population flux through the BR-174 highway that connects both states and is the only accession route by land to Roraima from Brazil. The clade BCAR-BR-IV displayed a more restricted spread in Roraima, but was also disseminated over long distances reaching Sao Paulo and Espírito Santo.

The estimated median TMRCA of clades BCAR-BR-I (1978) BCAR-BR-IV (1982) coincides with a period of fast population growth and increasing geographical accessibility in Roraima. The population in Roraima increased from 41,000 to nearly 220,000 inhabitants between 1970 and 1990 [41,42]. This population growth was fueled by the creation of incentives to immigration and the inauguration of important highways that gave access to large areas of the state, including some at the border with Guyana [41,42]. Many Brazilian migrants initially attracted by the rise of legal/illegal mining activities in Roraima later migrated to Guyana, and Brazil is (together with Suriname and Venezuela) one of the major migrants exporting countries to Guyana [33,37,38]. The economic crisis in Guyana also produced an increasing migration flux of Guyanese people to Roraima since the 1960s onwards, particularly to the neighboring district of Bonfim and the state capital Boa Vista [33,37,38]. These drastic changes in the demographic structure and population mobility may have fueled the introduction and dissemination of Guyanese BCAR strains into Roraima.

Maranhão display the highest prevalence of BCAR strains outside the Northern Brazilian region and was pointed as the most probable source location of clade BCAR-BR-II at around 1978. This clade was disseminated within Maranhão and from this state to Pará, Goiás, Mato Grosso do Sul, Sao Paulo and Espírito Santo. Most people that migrate to Roraima during the 1970s and 1980s were from Maranhão [33,41,42], which creates a potential link for the direct dissemination of BCAR strains from Roraima to Maranhão. The clade BCAR-BR-II, however, is not closely related to the clade BCAR-BR-I, supporting an independent origin. We propose that the clade BCAR-BR-II probably arose by the introduction of a BCAR strain from Suriname or French Guiana that host about 15,000 and 20,000 Brazilian immigrants, particularly from Maranhão, Amapá and Pará states [33–36,39,40]. Many of those immigrants are female sex workers and gold-diggers (populations typically associated with a high risk of acquisition of HIV) that come back to Brazil from time to time and may thus introduce new BCAR strains in the Northern and Northeastern regions.
The high prevalence of BCAR strains detected in Roraima and Maranhão correlates with an intense migratory flux to Northern South American countries, but that association was not observed in other Brazilian states. Many individuals from the Northern Brazilian states of Amapá and Pará have migrated to the French Guyana since the middle 1960s and the social conditions in the border region between Amapá and French Guyana are certainly favorable for the spread of HIV [33–36]. Despite this, we detected a low proportion (3–4%) of BCAR strains and no evidence of direct viral migrations from the Caribbean into Amapá or Pará. The BCAR sequences detected in Amapá branched within the clade BCAR-BR-I, and the BCAR sequences detected in Pará branched within clades BCAR-BR-II and BCAR-BR-III. Thus, the BCAR strains circulating in Amapá and Pará probably originated from other Brazilian states, rather than from neighboring Caribbean countries.

The clade BCAR-BR-III was the only Brazilian non-pandemic subtype B lineage that originates outside the Northern/Northeastern region. This clade was most probably introduced from the Caribbean into the state of Sao Paulo at around 1979 and from there it was disseminated to Rio de Janeiro, Minas Gerais, Rio Grande do Sul and Pará. A previous study conducted by our group indicates that this clade (formerly named BCAR-BR-I) was also disseminated from Brazil to Argentina [10]. Sao Paulo is a potential hub for introduction and dissemination of new HIV-1 strains because it hosts the largest Brazilian international airport as well as a large number of international visitors and immigrants [43]. Although these results point to the existence of a BCAR lineage mostly circulating in the southern area of South America, this should be interpreted with caution because the low branch support of the clade BCAR-BR-III.

In summary, this study demonstrates that non-pandemic HIV-1 BCAR strains have been introduced at multiple times from the Caribbean into Brazil and reach a significant prevalence in some states from Northern (Roraima and Amazonas) and Northeastern (Maranhão) regions. Several Brazilian states from all country regions acted as an entry point of BCAR strains, but only a few BCAR strains, particularly those introduced into Roraima and Maranhão, established local outbreaks of relative large size. The molecular epidemiological surveillance of HIV-infected individuals from Guyana, French Guiana, and Suriname as well as of mobile populations migrating between Brazil and those neighboring countries will be of paramount importance to reconstruct the precise dissemination routes of BCAR strains in the northernmost region of South America.

Supporting Information

S1 Table. HIV-1 subtype B pol (PR/RT and RT) sequences from Brazil, the Caribbean, US and France used for ML phylogenetic analyses. aAntigua and Barbuda (n = 4), Bahamas (n = 5), Dominica (n = 1), Grenada (n = 2), Montserrat (n = 1), Saint Lucia (n = 4) and Saint Vincent and the Grenadines (n = 4).

S2 Table. HIV-1 BCAR pol (PR/RT) sequences from Brazil and the Caribbean used for Bayesian phylogeographic analysis. aIdentified in a previous study [9]. bSubtype D sequences from the Democratic Republic of Congo (DRC).

S3 Table. Bayes factor (BF) rates of epidemiological links between Caribbean and Brazilian locations for dispersal of non-pandemic BCAR lineages. BF > 100 indicates decisive support, 30 ≤ BF ≤ 100 indicates very strong support, 10 ≤ BF ≤ 30 indicates strong support, and 6 ≤ BF ≤ 10 indicates substantial support for migration between locations.
Author Contributions
Conceived and designed the experiments: GB.
Performed the experiments: FD ALGC.
Analyzed the data: FD ALGC FGN MMAS GB.
Contributed reagents/materials/analysis tools: ALGC FGN MMAS.
Wrote the paper: GB FD.

References


