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RECEIVED 28 March 2025 ACCEPTED 26 June 2025 PUBLISHED 21 July 2025

CITATION

Kirpich A, Nemira A, Adeniyi AE, Shishkin A, Bunas AS, Kolomiets ND, Glinskaya IN, Gankin Y, Gasich EL and Skums P (2025) Phylodynamics analysis of HIV epidemic history in Belarus in 1987–2022. Front. Epidemiol. 5:1601976. doi: 10.3389/fepid.2025.1601976

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Phylodynamics analysis of HIV epidemic history in Belarus in 1987–2022

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This paper presents the first systematic molecular epidemiology study of the HIV epidemic in Belarus, an Eastern European country that, like much of Eastern Europe and including the Post-Soviet region, has been largely understudied in relation to HIV epidemics. HIV sequences collected nationwide between January 2018 and May 2022 were analyzed using phylogenetic and phylodynamic methods. The findings reveal two distinct epidemic waves spanning 1997–2005 and 2009–2018, each driven by different dominant modes of transmission. The study also identifies potential introductions and intra-country transmission routes, emphasizing the pivotal role of the capital city and eastern industrial hubs within Belarus in shaping the epidemic's trajectory. This work addresses an important gap in understanding HIV dynamics in Eastern Europe.

KEYWORDS

Belarus, HIV, phylodynamics, molecular epidemiology, infectious diseases

1 Introduction

The global Acquired Immunodeficiency Syndrome (AIDS) pandemic, caused by the Human Immunodeficiency Virus (HIV) and first documented in 1981, remains a major public health challenge. Despite substantial efforts to combat HIV, the Joint United Nations Programme on HIV/AIDS (UNAIDS) estimated that by the end of 2023, 36.1–44.6 million people were living with HIV worldwide (1), and 650,000 people died from AIDS-related illnesses in 2021 (1).

Although antiretroviral therapy and preventive measures have reduced new infections in many regions (2), progress has been uneven. In particular, Eastern Europe is one of the few regions where both new HIV infections and AIDS-related deaths continue to rise (3). Along with Sub-Saharan Africa, it has one of the highest HIV incidence rates globally (3), leaving it off track to meet the 2030 AIDS elimination targets (4). Within Eastern Europe, former Soviet Union (FSU) countries account for 92% of all newly registered HIV cases (4)

Despite these concerning trends, Eastern Europe in general and FSU countries in particular remain relatively neglected in HIV epidemiological research. Among the major regions analyzed in a recent global burden of HIV study (3), it has the fewest PubMed-

indexed publications—approximately 19 times fewer than Sub-Saharan Africa and 13 times fewer than North America.

One of FSU countries is the Republic of Belarus, which has a population of 9.155 million (5). Like many nations worldwide, it faces multifaceted challenges associated with HIV pandemic. The country has experienced a steady annual increase in both registered HIV cases and incidence rates, with the latter rising from 9.9 per 100,000 in 1996 to 25.9 per 100,000 in 2017.

HIV infection was first identified in Belarus in 1987, with only 113 recorded cases by 1995, primarily among individuals who had arrived in the country for work or study from abroad (6). However, the epidemiological situation changed dramatically in 1996 with the discovery of a localized outbreak in the southeastern cities of Svietlahorsk and Zlobin. Over six months, 1,021 new cases were registered, 954 (93%) of which were linked to injection drug use (7, 8). Consequently, the incidence rate surged from 0.07 per 100,000 in 1995 to 9.9 per 100,000 in 1996.

Following this outbreak, HIV spread rapidly across the country (9–14). From 1996 to approximately 2004, parenteral transmission i.e., via injection accounted for the majority of new cases, comprising 91.5% of infections in 1996 (15). After 2004, sexual transmission—predominantly through heterosexual contact—became the dominant mode of new infections (12, 16, 17). By 2023, the proportion of parenteral transmission via injection drug use had declined to 14.4%, while sexual transmission accounted for 83.2% of new cases (11, 18, 19).

The only exception in this trend was the mid-2010s period, when the number of new HIV cases has increased from 1,533 cases in 2013 to 2,468 cases in 2017. This has been attributed to the intensification of parenteral transmission routes, and changes in the drug scene. Since 2019, a decrease in the number of newly identified HIV infections has been observed, with the exception of 2022, when the number of newly diagnosed cases slightly increased by 11.3% compared to 2021, which may be attributed to the delayed detection of individuals who were not properly diagnosed during 2020–2021 due to the COVID-19 pandemic the phenomenon observed in several countries (20–22).

Currently, the epidemiological situation regarding HIV infection in Belarus is classified as a concentrated stage of the HIV epidemic, in accordance with internationally accepted criteria (17, 23). The number of people living with HIV (PLHIV) as of January 1, 2024, was 25,038, with an estimated total of 27,000 PLHIV for the same year (24).

In general, the HIV epidemic in Belarus remains concentrated among high-risk groups, including people who inject drugs (PWID), men who have sex with men (MSM), sex workers (SW), and people in detention (PID). Other transmission modes play a relatively minor role; for example, as of January 1, 2018, the vertical transmission rate (mother-to-child) was 1.3% (25, 26).

While traditional epidemiological statistics provide valuable insights, understanding HIV transmission dynamics can be greatly enhanced through molecular epidemiology. In recent decades, particularly during the 2010s, advances in molecular techniques, decreasing sequencing costs (27, 28), and improvements in computational methodologies (29) have established phylogenetic and phylodynamic analyses as essential tools in epidemiological investigations (30). This is especially relevant for HIV, which exhibits extreme genomic heterogeneity due to its rapid replication and the high error rate of reverse transcription (31-36).

Previous molecular epidemiology studies of HIV in Belarus have focused on assessing within-country HIV genomic diversity. These studies identified the A6 sub-subtype of HIV-1 as the dominant lineage circulating in Belarus (37), consistent with trends observed across FSU countries (38–40). Initially, A6 was primarily transmitted among PWID, but over time, heterosexual transmission became the predominant mode of spread (38, 41–43). Additionally, isolated cases of recombinant forms CRF03_AB and CRF02_AG have been reported (42, 44–46).

However, the sequencing data collected by Belarusian epidemiologists over the past decade, combined with existing phylodynamic methodologies, enables more detailed and higher-resolution analysis of the HIV epidemic. These approaches allow for the inference of key epidemiological parameters, transmission routes, and geographical distribution (47).

This study aims to conduct a comprehensive phylogenetic and phylodynamic analysis of HIV epidemiological dynamics in Belarus. Similar studies have been performed in Uzbekistan (48), neighboring Ukraine (49), Poland (50), Russia (51), and more broadly across FSU countries (52–55), as well as in other regions (56–58). However, without epidemiological data from Belarus, the understanding of HIV-1 transmission dynamics in the FSU region and neighboring areas remains incomplete. This analysis will help fill this gap and provide new insights into the molecular epidemiology of HIV in Eastern Europe.

2 Methods

2.1 Data generation and pre-processing

Blood samples were collected by the Republican Center for Hygiene, Epidemiology, and Public Health (RCHEPH) in Minsk, Belarus, between 2018 and May 2022 as part of routine HIV screening and monitoring. Sample processing and sequencing were conducted by the Laboratory for HIV and Opportunistic Infections Diagnosis. The study included both antiretroviral treatment—experienced and treatment-naïve individuals. The geographical distribution of sequences collection regions generally correlates with officially reported HIV prevalence (Pearson's r = 0.79, comparing sequence counts and regional prevalence rates).

Viral RNA was extracted from 1001 of blood plasma using Ribo-Prep following the manufacturer's instructions. Sequencing was performed on a 3,500 Genetic Analyzer (Applied Biosystems, USA), with base calling conducted using the manufacturersupplied sequencing analysis software.

For hosts with multiple samples, the sample with the median collection date was retained for further analysis. This resulted in a dataset of 867 HIV pol gene amplicons. The amplified HIV-1 pol fragment used for the analysis covered positions 4,177–5,211 in relation to HXB2 genome reference. The resulting sequences

were assembled and manually edited using Sequencing Analysis Software v6.0, SeqScape[®] Software v3.0 (Applied Biosystems), and Geneious[®] v8.0 (Biomatters Ltd.). The sequences and associated patient metadata (collection date, place of residence) are publicly available via GenBank (accession numbers OP330328–OP331194).

Nucleotide sequence alignment was carried out using Clustal W (59) and MAFFT (60). Groups of individual sequences were processed using BioEdit v6.1 and Geneious[®] v8.0. The alignment was refined by generating a consensus sequence with EMBOSS Cons (61), realigning sequences to the consensus, and removing those with excessive gaps or poor alignment quality. HIV-1 subtyping was performed using COMET HIV-1 (62) and REGA (63), with sequences with undetermined subtypes further analyzed for recombination using SimPlot (64). After data cleaning and duplicate removal, the final dataset consisted of 640 sequences of subtype A/A6, each 1,032 bp in length, which was then used for further analysis.

All data used in the analysis were depersonalized, and ethical approval was obtained from RCHEPH. Additionally, the study was designated as not human subjects research by the Georgia State University Institutional Review Board (GSU IRB Number: H25158).

2.2 Inference and analysis of HIV introduction pathways and transmission clusters

To infer potential HIV introductions into Belarus, the study dataset was expanded by incorporating globally collected subtype A pol gene sequences downloaded comprehensively from the Los Alamos National Laboratory (LANL) HIV sequence database.

The combined dataset was analyzed using the Nextstrain phylogenetic workflow (65) implemented in augur (version 24.3.0) (66). This included data primary processing (sequence indexing, filtering, and multiple sequence re-alignment), followed by phylogenetic analysis. This second step proceeded in two main stages: first, a maximum likelihood phylogenetic tree was constructed from the aligned sequences using RAxML (67). This initial tree was then refined with TreeTime (68) to generate a time-resolved phylogeny and infer ancestral timing.

Finally, the annotated phylogenetic tree, with leaf traits representing the geographical locations of sequence collection, was analyzed using PastML (69). Ancestral traits representing most likely geographical locations of ancestral HIV variants were reconstructed via maximum likelihood inference using the F81 model of trait evolution (70). The inferred ancestral traits of the most recent common ancestors of intra-Belarusian lineages were interpreted as the likely sources of HIV introduction into the country.

To reconstruct and visualize within-country transmission clusters and potential transmission networks, we used MicrobeTrace (71). This tool builds a genetic relatedness network by connecting sequences whose pairwise genetic distance falls below a predefined threshold. The resulting network serves as an approximation of the underlying transmission network (72). Given the extended temporal and geographic span of our dataset, we used a 2.5% distance threshold, consistent with prior studies of large transmission clusters spanning long time periods (56, 73, 74).

To assess the contribution of local and generalized transmissions, the assortativity coefficient of inferred network with respect to city and region of host residence was calculated. The coefficient measures the tendency of inferred transmission links to connect hosts with the same geolocation traits. For the calculations, we used the script from (75, 76) with Python v3.10.0 and networkx library.

Both external and intra-country transmission networks were visualized using Inkscape v0.92. Base maps were obtained from IGISMAP and SimpleMaps. Transmission links generated by MicrobeTrace were integrated with geolocation data using ArcMap v10.7.

2.3 Phylodynamic analysis

All phylodynamic analyses were conducted using BEAST 2.6.7 (77) with BEAGLE 4.0.0 (78) for computational acceleration. First, temporal signal was evaluated by by regressing root-to-tip genetic divergence against sampling dates using TempEst (79). Next, a non-parametric Bayesian skyline plot (BSP) model (80) was used to reconstruct the HIV phylogeny and estimate the dynamics of the effective population size of the infected population. We employed the GTR nucleotide substitution model, a relaxed molecular clock, and a piecewise constant effective population size (N_e) with n = 10 time intervals. Markov chain Monte Carlo (MCMC) sampling was performed for 20×10^6 iterations, with 20% discarded as burn-in. Convergence of MCMC runs was assessed using Tracer (81), and posterior medians with 95% Highest Posterior Density (HPD) intervals were visualized in R.

We further applied a serial birth-death skyline model (BDSKY) (82) to estimate the effective reproductive number R_e and the becoming uninfectious rate δ . The sampling proportion was also modeled as a piecewise-constant function As in the BSP model, 10 time intervals were used for piecewise constant estimates of model parameters.

We employed the HKY nucleotide substitution model with gamma-distributed rate variation among sites (HKY+ Γ model) and a lognormal relaxed molecular clock. Given the narrow sequence sampling window resulting in a modest root-to-tip divergence correlation (r=0.24), we used a strongly informed prior on the molecular clock rate, with priors on the mean rate set to a lognormal distribution with a mean of 3.5×10^{-3} mutations/site/year and a standard deviation of 5.0×10^{-4} . The standard deviation of the rate also followed a lognormal prior (mean = 5.0×10^{-4} , standard deviation = 5.0×10^{-4}), as suggested by previous studies (49, 83, 84). Different substitution models for BSP and BDSKY models were iused to demonstrate the robustness of conclusions and the consistency of results across methodological frameworks.

Prior distributions for the BDSKY model parameters were set similarly to values used in other studies of Eastern European countries (49):

- A uniform distribution for the date of origin, with an upper bound of 60 years and a lower bound of 19 years.
- A lognormal distribution for the effective reproduction number R_e (mean = 1.0, standard deviation = 1.25), with an upper bound of 5.
- A lognormal distribution for the becoming noninfectious rate δ (mean = 0.0, standard deviation = 1.0 for normal distribution), constrained to the interval [0.05, 6].
- A beta distribution for the sampling proportion $(\alpha = 1.0, \beta = 10.0)$, constrained to the interval [0, 0.001]. These settings were informed by estimates from (49), given a comparable ratio of analyzed sequences to the estimated number of diagnosed PLHIV in both studies.
- A uniform distribution on the interval [0, 1] for the freqParameter.
- An exponential distribution (mean = 1) for the gammaShape parameter.
- A lognormal distribution (mean = 1.0, standard deviation = 1.25) for the kappa parameter.

Markov chain Monte Carlo (MCMC) sampling was performed for 40×10^7 iterations, with 20% discarded as burn-in and with convergence of MCMC assessed using Tracer (81). Effective reproduction numbers inferred using the BDSKY model were visualized with the R package bdskytools.

3 Results

3.1 Phylogenetic analysis of HIV transmission routes

The HIV transmission routes for Belarusian HIV sequences were analyzed at both international and within-country scales.

In the international phylogeny, which included the analyzed Belarusian sequences alongside globally sampled sequences, Belarusian sequences generally clustered with sequences from other FSU countries, as expected. Ancestral phylogeographic reconstruction revealed multiple links to HIV lineages from Russia (average parent and child posterior probabilities for branches indicative of introductions: 0.94 (SD = 0.10), 0.98 (SD = 0.05), respectively), as well as connections with Ukraine [parent = 0.99 (SD = 0.00), child = 0.99 (SD = 0.00)] and Cyprus [parent = 0.82 (SD = 0.03), child = 0.90 (SD = 0.19)]. The latter is the only non-post-Soviet country with such links detected (see the left panel of Figure 1); the presence of 10 Belarusian sequences within the corresponding clade suggests a single introduction followed by limited intra-country transmission.

The vast majority of Belarusian sequences formed distinct clades, highlighting the major role of intra-country transmissions. More specifically, we identified six clusters that each have a Belarusian most recent common ancestor (MRCA), contain at least 30 nodes, and are composed of at least 85% Belarusian sequences. Collectively, these clusters represent approximately



FIGURE 1

Left: Phylogenetically reconstructed between-country HIV-1 transmission network. Right: Inferred non-directional HIV intra-country transmission network. Largest transmission clusters are highlighted by circles. The displayed nodes may have multiplicity greater than one, but for simplicity, they are presented as single points.



73% of all Belarusian sequences, with one cluster alone accounting for 54% (see Supplementary Figure S3).

Most inferred potential transmission links were associated with the central (Minsk region) and south-eastern (Homyel region) parts of the country (see the right panel of Figures 1, 2) In particular, three large and highly interconnected clusters were identified, roughly corresponding to:

- 1. the metropolitan area of the capital Minsk,
- 2. the north-western part of the Homyel region, including the cities of Svietlahorsk, Zlobin, and Recyca,
- the southern part of the Minsk region around the city of Salihorsk.

Clusters 2 and 3 correspond to industrial regions with a long history of HIV spread (10). In particular, Svietlahorsk and its surrounding area is considered a hotspot of the HIV epidemic and the location of the largest outbreaks identified in recent decades, most of which have been associated with high prevalence of injection drug use (85).

Significantly fewer within-country transmission links were associated with the western part of the country (Hrodna and Brest regions) compared to the eastern regions(see Figure 1). The main exceptions were a few links involving the city of Hrodna (capital of the Hrodna region) and the vicinity of the town of Luninets, which is adjacent to the Salihorsk cluster. This is consistent with their lower HIV prevalence, which is 1.8-fold and 2.4-fold below the national average, respectively.

The assortativity coefficient (a network parameter that quantifies the tendency of nodes with shared characteristics to connect—ranges from -1 (complete disassortative mixing) to 0 (random mixing) to 1 (perfect assortative mixing)), exhibited different behavior depending on the geographic level of aggregation.

At the regional level, the coefficient was relatively high (r = 0.521), indicating that sequences from the same region were more likely to be linked than sequences from different regions. At the city level, the assortativity coefficient was moderate

(r = 0.345), suggesting that this association was much lower on the settlement level.

3.2 Phylodynamic inference of the effective reproductive number and effective population size

The median estimates of the effective population size, effective reproduction number, and becoming uninfectious rate, along with their 95% highest posterior density (HPD) intervals, are summarized in Figures 3, 4, and the timed phylogeny reconstructed using the Bayesian skyline model is shown in Figure 2.

In general, we observed a clear trend of epidemic growth from the onset of the epidemic through approximately the second half of the 2010s. During this period, the effective reproduction number (R_e) consistently remained above one, beginning in the early 1990s. After that, the trend appears to shift, with the effective population size (N_e) stabilizing and R_e gradually approaching the epidemic threshold toward the end of the study period.

On a finer scale, the analysis revealed three identifiable stages of the HIV epidemic:

- (A) the preliminary stage (roughly before the mid-90s);
- (B) two epidemic waves: the first from the mid-1990s to mid-2000s, and the second during the 2010s.

The preliminary stage was likely driven mostly by external introductions. Its trace, along with that of later isolated introductions, may be reflected in the phylogeny by a small clade of HIV genotypes with most recent common ancestors dating to the 1980s [95% HPD for tMRCA: (39.8903–40.7611)], prior to the first reported HIV cases in the FSU countries (Figure 2).

The start of the first large wave (\sim 1997–2007, according to N_e dynamics; Figure 3) aligns with the first large-scale HIV outbreak detected in the city of Svietlahorsk in mid-1996. Around this time, we observe the beginning of a gradual rise in the effective



infected population size N_e (Figure 3) and a burst in HIV genomic diversity (Figure 2).

The vast majority of sampled lineages coalesce to a most recent common ancestor around this period. Notably, sequences sampled in Svietlahorsk are distributed across much of the HIV phylogeny, whereas sequences from Salihorsk—despite comparable cluster size —generally form a distinct clade (Figure 2).

Overall, the first wave appears gradual and reflects a common pattern observed in post-Soviet countries, where the epidemic was driven by a combination of nosocomial transmission, sexual transmission, and injection drug use (86, 87). The second wave (\sim 2014–2016, based on N_e dynamics; Figure 3) was more rapid and steep. It is possible that it corresponds to the spread of a new generation of injection drugs that significantly increased transmissions, that is well-documented for other Eastern European countries (88, 89).

Similar trends, though with slightly shifted time frames, are observed in the dynamics of the effective reproductive number R_e (Figure 4). During the first wave, the estimated median \hat{R}_e peaked at 2.98, closely matching the time window suggested by N_e dynamics. For the second wave, the dynamics of R_e peaked at $\hat{R}_e = 3.86$ and points to an earlier start around 2009–2010.

Finally, although strong priors have been used for clock rate due to the narrow sequence sampling window, comparison of the prior and posterior distributions of clock rates (see Supplementary Figure S1) indicates that the posterior clock rate is data-driven.

The becoming uninfectious rate—i.e., the inverse of the average duration of the infectious period—underwent some fluctuations over time. However, the general trend was towards the rate increase, corresponding to a decrease in the average infectious period from approximately \sim 7.7 years in the late 1980s to \sim 1.9 years in the 2020s.

4 Discussion

This study presents findings on the HIV epidemiological dynamics in Belarus, inferred from genomic surveillance data. Eastern European and FSU countries continue to face significant challenges related to the HIV epidemic, while public health and social intervention efforts in the region are still developing—particularly when compared to Western Europe. At the same time, the epidemiological dynamics of HIV in this region remain poorly understood. This study contributes towards filling that knowledge gap and complements several recent studies on HIV transmission dynamics in other FSU countries (48, 49, 52).

The study revealed a complex history of HIV spread in Belarus since the start of the epidemic in 1987. In general, the estimates of the effective reproduction number R_e remained above one throughout most of the analyzed period, indicating sustained transmission (90, 91), and, as discussed above, began to decline only after approximately 2018.

However, the dynamics of HIV transmission were not uniform during this time. The study identified three epidemic waves, separated by transitional periods. The first wave, roughly prior to 1996–1998, was characterized by only minimal growth in the effective infected population size (N_e), and was likely driven by relatively infrequent HIV introductions from abroad.

The next two waves—occurring from the mid-1990s through the early 2000s, and again during the early to late 2010s—can be linked to significant shifts in the epidemiological landscape. The second wave was likely triggered by a large-scale outbreak in the city of Svietlahorsk in mid-1996. This outbreak not only marked a turning point in national transmission dynamics, but also likely served as the source of most of the HIV genetic heterogeneity circulating in Belarus in the subsequent decades. This is supported by the observation that the vast majority of sampled



lineages coalesce to a most recent common ancestor around this period, suggesting that the subsequent epidemic was largely driven by intra-country transmission of a single HIV lineage that rapidly diversified following the Svietlahorsk outbreak. Further evidence comes from the sequence distribution along the phylogeny, with sequences from Svietlahorsk being spread across much of the tree, in contrast with, for instance, sequences from Salihorsk-another HIV infection hotspot—that largely form a distinct clade. (Figure 2).

The third wave is likely associated with the introduction of a new generation of injection drugs and changes in injection practices, which greatly accelerated the pace and extent of HIV transmission (92, 93). Importantly, the dynamics of the effective reproductive number R_e (Figure 4) suggests that this wave began several years before the epidemiologically confirmed events, indicating that the observed outbreaks were merely visible manifestations of underlying epidemiological processes that had already been underway and were not yet detected by traditional surveillance system. Such situations are not uncommon and have been observed in other countries—for example, during the HIV/ HCV epidemic wave in the United States driven by opioid abuse at approximately the same time (93–95).

The periods of epidemic waves were interspersed with recession periods, which may be partially explained by public health interventions implemented during those periods. The drop in estimated values of Re around 2005 could reflect the delayed effects of multiple governmental efforts, including the UNAIDS intervention program launched in 1997 (10), as well as additional measures introduced in response to the initial outbreak. Similarly, the decline in the estimates of the effective reproduction number Re and infectious period observed since 2018 may be attributed to the implementation of a new clinical protocol, establishing antiretroviral therapy (ART) as a key component of healthcare for individuals living with HIV, and recommending ART for all PLHIV (96). Following this policy change, Belarus has made significant progress toward achieving the UNAIDS 95-95-95 targets (i.e., ensuring that 95% of people living with HIV know their status, 95% of those diagnosed receive antiretroviral therapy, and 95% of those on treatment achieve viral suppression). While in 2018 the percentages were estimated to be 77-58-37, by January 1, 2024, they had improved to 92.7-91.3-85.6 (97).

It is interesting to compare HIV dynamics in Belarus with the dynamics in neighboring Ukraine, also inferred using phylodynamic analysis (49). In particular, the general trend towards the becoming uninfectious rate increase (and, equivalently, decrease in the average infectious period) differs from the dynamics observed in northern Ukraine, where, as demonstrated in (49), the average infectious period has been increasing over time. At the same time, after 2013 the dynamics in Belarus show certain similarities to those observed in the Odessa region of Ukraine, where the estimated average infectious period decreased from \sim 5 years in the 2000s to \sim 1.1 years in 2013-2016, potentially due to the implementation of the transmission reduction intervention project in that region (49). Similarly, several harm reduction programs (such as needle exchange) were implemented in Belarus around the same time, followed by the introduction of the antiretroviral therapy protocol mentioned above. Thus, phylodynamic analyses both here and in (49) highlight the relative effectiveness of such programs in reducing HIV transmission among Eastern European populations.

The reconstruction of HIV introduction routes revealed linkages with neighboring Russia and Ukraine, which is to be expected, given the historically close economic and cultural ties between these regions, as well as largely unrestricted population movement across borders during most of the study period. The only detected link with a non–post-Soviet country was with Cyprus, which is plausibly explained by its longstanding popularity as a tourist destination for the Belarusian population in the decades preceding this study.

Within Belarus, the major regions contributing to HIV spread include the capital city of Minsk—as expected, given its role as a cultural, economic, and demographic hub as well as the Salihorsk and Svietlahorsk–Zlobin metropolitan areas in central and eastern Belarus, respectively where injection drug use has been endemic. This agrees with surveillance data, according to which the Homyel Region, that contains Svietlahorsk and Zlobin, accounts for nearly half of all HIV cases in the country. Both Salihorsk and Svietlahorsk–Zlobin are industrial regions with extensive mining and chemical industries, where limited social and recreational options may contribute to higher rates of HIV spread, in part due to elevated rates of intravenous drug use and associated high-risk behaviors.

Phylogenetically, however, the HIV subpopulations circulating in these regions are distinct (Figure 2) and may play different roles in the overall HIV transmission dynamics. In addition to the likelihood that Svyetlahorsk served as a key source of intra-country HIV diversity as discussed above, various geographical, economic, and environmental factors may also contribute towards the observed phylogenetic patterns. Svyetlahorsk is located along a major transport corridor connecting central and eastern Belarus and is surrounded by several towns of similar size, facilitating regional mobility. It has a legacy of Soviet-era industries, some of which have declined in recent decades, and is known for having one of the poorest ecological conditions in the country. These factors are associated with higher levels of out-migration and population movement, potentially contributing to both inward and outward HIV transmission. In contrast, Salihorsk is more geographically isolated and economically supported by the potash mining sector, which has contributed to population stability. These differences are consistent with the observed phylogenetic patterns: dispersed HIV lineages in Svyetlahorsk vs. more localized clustering in Salihorsk.

It is important to acknowledge that the findings presented in this study are subject to several limitations. First, the analysis covers the period only up to 2022, and therefore does not account for potential changes in epidemiological dynamics resulting from the demographic and social impacts of recent geopolitical events in the region. The analysis of such effects will only be possible once sufficient post-2022 data becomes available, and should be the focus of a separate, dedicated study. The same applies to the assessment of recently introduced HIV containment policies.

It should also be acknowledged that any analysis of HIV data may be influenced by under-reporting, delays in reporting due to the long incubation period of the virus (98), and sampling biases related to the social stigma surrounding HIV (99–101) and uneven sequencing capabilities among different regions. In particular, sequencing costs in non-Western countries remain high, and sequencing technologies are not yet as widely accessible to public health researchers as they are in Western Europe or North America. As pertains this study, only samples deemed to be of certain priority have been sequenced in Belarus and were thus available for this analysis. This may have introduced certain selection bias, as sequencing at the RCHEPH has been routinely performed only for patients with suspected drug resistance. Similarly, sampling biases could potentially have an impact on the global transmission analysis results.

As of September 2024, the Belarusian Ministry of Health and RCHEPH are actively working to expand sequencing capacity and increase funding to support comprehensive sequencing of all HIV samples from newly diagnosed individuals. This initiative is planned to be implemented in stages starting in 2025, and is expected to generate a larger dataset with more uniform coverage in the coming years. These expanded data will offer valuable insights into HIV dynamics in Eastern Europe, with the ultimate goal of enabling more targeted intervention strategies and optimizing resource allocation.

Data availability statement

Publicly available datasets were analyzed in this study. This data can be found here: The Belarusian HIV pol gene amplicons used in this study are publicly available on GenBank (accession numbers OP330328–OP331194).

Ethics statement

The studies involving human participants were approved by the Georgia State University Institutional Review Board (IRB Number: H25158) and were conducted in accordance with applicable local legislation and institutional requirements. The human samples used in this study were obtained prior to the presented work was conducted as byproducts of routine care or industry, and the depersonalized sequences analyzed were already publicly available. Informed consent for participation was not required from the participants or their legal guardians/next of kin, in accordance with national legislation and institutional guidelines.

Author contributions

AK: Methodology, Data curation, Writing – original draft, Investigation, Visualization, Formal analysis, Supervision, Conceptualization, Writing – review & editing, Project administration. AN: Writing - original draft, Data curation, Visualization, Investigation, Writing - review & editing, Formal AEA: Writing - original draft, Investigation, analysis. Visualization, Formal analysis, Data curation. AS: Data curation, Writing - original draft, Investigation, Writing - review & editing, Formal analysis. ASB: Writing - original draft, Data curation, Investigation. NDK: Conceptualization, Investigation, Writing - original draft, Data curation, Methodology. ING: Investigation, Methodology, Conceptualization, Writing - original draft, Data curation. YG: Conceptualization, Methodology, Investigation, Writing – original draft. ELG: Project Writing – original draft, Investigation, administration, Supervision, Conceptualization, Writing - review & editing, Methodology. PS: Writing - review & editing, Supervision, Methodology, Writing - original draft, Conceptualization, Investigation, Project administration, Data curation.

Funding

The author(s) declare that financial support was received for the research and/or publication of this article. PS was supported by the NSF grant CCF-2415564.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Generative AI statement

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Supplementary material

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fepid.2025. 1601976/full#supplementary-material

Phylodynamics Analysis of HIV Epidemic History in Belarus in 1987–2022 by Kirpich et al.

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