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# Unravelling the Temporal and Geographic Patterns of HIV-1 Cases in Libya: Demographic Trends and Spatial Clustering.

**Mohamed Ali Daw**

mohamedadaw@gmail.com

University of Tripoli, Faculty of Medicine https://orcid.org/0000-0003-1312-5956

**Research Article**

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## Abstract

# Background

The epidemiology of HIV-1 in Libya has evolved substantially since the first major recognized outbreak in Benghazi during the 1990s. Although previous investigations have separately described the national geographic distribution of HIV infection and the molecular diversity of circulating HIV-1 strains, integrating these perspectives provides a broader framework for understanding the changing epidemic landscape. This study aimed to characterize the spatial and temporal distribution of reported HIV-1 infections in Libya and to examine the geographic distribution of major HIV-1 genetic subtypes.

# Methods

A retrospective nationwide analysis was conducted using routinely collected HIV surveillance records covering 1993–2017. A total of 8,015 newly diagnosed HIV cases with geographic information were included in the epidemiological analysis. Temporal changes in regional distribution and demographic characteristics were examined. Molecular findings were integrated from a previously characterized set of 159 HIV-1 strains obtained from 814 HIV-positive individuals across four Libyan regions between 1995 and 2010. HIV-1 subtypes were determined using molecular sequencing and phylogenetic analysis. Spatial patterns were interpreted by comparing regional case concentrations with the geographic distribution of characterized viral subtypes.

# Results

Among the 8,015 reported cases, 5,327 (66.5%) were male and 2,688 (33.5%) were female. Individuals aged 25–34 years represented the largest age group, with 2,965 cases (37.0%), followed by those aged 35–44 years, with 1,892 (23.6%). The geographic distribution changed markedly over the study period. The eastern region represented the major concentration during the earlier period, including 1,180 reported cases during 1998–2002, whereas the western region recorded 1,449 cases during 2010–2017. Central and southern regions also became increasingly represented during the later period. The molecular dataset comprised 117 (73.6%) subtype B strains, 29 (18.2%) CRF02_AG strains, and 13 (8.2%) subtype A strains. Subtype B was detected throughout the country and was particularly represented in the northern region; CRF02_AG was more frequently represented in the eastern region, whereas subtype A was observed particularly in western and southern areas. The combined epidemiological and molecular evidence indicates increasing geographic heterogeneity of HIV-1 across Libya over time.

# Conclusions

The Libyan HIV-1 epidemic demonstrates substantial spatial, temporal, demographic, and molecular heterogeneity. The epidemiological pattern evolved from an early concentration of reported infections in eastern Libya to a broader national distribution, while molecular surveillance demonstrated the circulation of multiple HIV-1 lineages with distinct regional patterns. These findings support the value of integrating molecular surveillance with national epidemiological and spatial monitoring

# BACKGROUND

Human immunodeficiency virus type 1 (HIV-1) exhibits substantial genetic diversity and considerable geographic heterogeneity. The distribution of viral subtypes and circulating recombinant forms varies among populations and can change over time in response to population mobility, transmission networks, healthcare-associated exposures, prevention programs, and other epidemiological factors (1–3). Understanding the geographic distribution of HIV-1 is particularly important in countries where surveillance has identified substantial regional differences in reported infections (4, 5).

Libya provides a distinctive setting for studying HIV-1 spatial-temporal variability due to its large geographic area, highly uneven population distribution, differences in healthcare accessibility, and major political and demographic changes over the past three decades (6–10). The history of HIV-1 in Libya includes the well-documented pediatric outbreak in Benghazi during the 1990s (11–14). Subsequent investigations demonstrated that HIV-1 infections were not restricted to the original outbreak setting and that infections were reported across multiple geographic regions (15–17). A nationwide analysis of 8,015 newly diagnosed HIV cases recorded between 1993 and 2017 identified marked spatial and temporal variation, including four high-frequency clusters occurring during three different periods (18–20).

Molecular surveillance provides an additional dimension to conventional epidemiological surveillance. In a molecular study of HIV-1 in Libya, 159 strains obtained from 814 HIV-positive individuals between 1995 and 2010 were successfully characterized. Subtype B represented 73.6% of characterized strains, CRF02_AG 18.2%, and subtype A 8.2%. Subtype B was reported throughout Libya, with greater representation in the northern region; CRF02_AG was particularly represented in the eastern region, while subtype A was observed particularly in western populations (21, 22).

The combination of geographic surveillance and molecular characterization can therefore provide complementary information. Epidemiological surveillance describes where and when infections are diagnosed, whereas molecular surveillance can identify viral genetic diversity and relationships among sampled infections. Importantly, molecular similarity alone does not establish direct transmission between individuals, and regional subtype frequencies should not be interpreted as definitive transmission pathways (23, 24).

The present study integrates these complementary perspectives to describe the changing spatial and temporal distribution of HIV-1 in Libya and to examine the geographic distribution of major viral subtypes. The primary objective was to determine whether the historical concentration of reported

infections in eastern Libya was followed by broader national geographic dissemination and whether molecular surveillance demonstrated corresponding regional heterogeneity.

## MATERIALS AND METHODS

# 2.1 Study design

A retrospective observational study was undertaken to characterize the spatial, temporal, demographic, and molecular epidemiology of HIV-1 in Libya. The epidemiological component covered the period from 1993 through 2017. The molecular component incorporated HIV-1 sequence data generated from characterized strains collected between 1995 and 2010. The analysis was designed to integrate both the molecular entity and geo-epidemiology of HIV-1 in the four vast regions of Libya.

# 2.2 National HIV surveillance dataset

The national epidemiological component comprised of newly diagnosed HIV cases recorded between 1993 and 2017 for which geographic information was available. The national reporting system was established to collect information on newly diagnosed HIV/AIDS cases from healthcare facilities throughout Libya. Variables included demographic characteristics and geographic information. Geographic distribution was examined using the regional classification employed in the surveillance system. The four broad geographic regions were classified as eastern, western, central, and southern Libya.

# 2.3 Molecular surveillance dataset

The molecular component was based on the previously characterized Libyan HIV-1 molecular dataset comprising 159 successfully genotyped strains obtained from 814 HIV-positive individuals during 1995–2010. Samples were obtained from the four major geographic regions of Libya. HIV-1 molecular characterization was performed using partial polymerase gene sequencing, followed by sequence alignment and phylogenetic analysis. Recombinant analysis was undertaken to distinguish recombinant forms from pure subtypes. The molecular study identified three principal HIV-1 categories among the characterized strains: subtype B, CRF02_AG, and subtype A. The regional distribution of these subtypes was examined in relation to the temporal and geographic distribution of reported HIV infections.

# 2.5 Temporal and Spatial analysis

The temporal analysis was carried out through over the study period and temporal changes were assessed by comparing the absolute number and proportion of reported infections across geographic regions and demographic categories. Spatial distribution was assessed using regional and district-level geographic information available in the national surveillance dataset. The analysis focused on changes in the geographic concentration of reported cases rather than interpreting case counts alone as population-based incidence and spatial-temporal analysis were combined. In the present synthesis, those findings were considered alongside the geographic distribution of molecularly characterized HIV-1

subtypes. The molecular and epidemiological datasets were compared at the regional level all over the country.

## 2.7 Statistical analysis

Categorical variables were summarized using frequencies and percentages. Differences between categorical groups were assessed using chi-square or Fisher's exact tests where appropriate. Logistic regression was used in the molecular study to examine relationships between HIV-1 subtypes and epidemiological characteristics. A *p*-value < 0.05 was considered statistically significant where formal hypothesis testing was performed ( **25, 26**).

# RESULTS

## 3.1 National epidemiological distribution

A total of 8,015 newly diagnosed HIV cases with geographic information were included in the national surveillance analysis as shown in Table 1. Of these studied cases 5,327 (66.5%) were male and 2,688 (33.5%) were female. The largest age group was 25–34 years, accounting for 2,965 cases (37.0%), followed by 35–44 years with 1,892 cases (23.6%). Individuals aged 15–24 years represented 1,188 cases (14.8%), while children younger than 15 years accounted for 640 cases (8.0%). The distribution indicates that reported HIV infections during the complete study period were predominantly recorded among adults, particularly those aged 25–44 years.

Table 1
Demographic characteristics of HIV-1 cases included in the study

| Demographic variables | Number | % of total | 95% CI (%) |
|---|---|---|---|
| **Sex** | | | |
| Male | 5,327 (66.5) | 66.5 | 65.4–67.5 |
| Female | 2,688 | 33.5 | 32.5–34.6 |
| **Age group (years)** | | | |
| <15 | 640 | 8.0 | 7.4–8.6 |
| 15–24 | 1,188 | 14.8 | 14.1–15.6 |
| 25–34 | 2,965 | 37.0 | 35.9–38.1 |
| 35–44 | 1,892 | 23.6 | 22.7–24.5 |
| ≥45 | 1,330 | 16.6 | 15.8–17.4 |
| **Geographic region** | | | |
| Eastern region | 2,895 | 36.1 | 35.1–37.2 |
| Western region | 2,734 | 34.1 | 33.1–35.2 |
| Central region | 1,278 | 15.9 | 15.2–16.8 |
| Southern region | 1,108 | 13.8 | 13.1–14.6 |
| **Total** | **8,015** | 100 | - |
| **Figures: 1–6** | | | |

# 3.2 Demographic and geographic evolution

A substantial demographic difference was observed between the early and later study periods. During 1993–2002, 1,665 of 2,970 cases (56.1%) were male. In comparison, males accounted for 3,662 of 5,045 cases (72.6%) during 2003–2017. The median age increased from 24 years in the early period to 33 years in the later period ($p < 0.001$). The proportion of pediatric cases also declined markedly, from 523/2,970 (17.6%) during 1993–2002 to 117/5,045 (2.3%) during 2003–2017 ($p < 0.001$). Figure 1 shows the demographic and geographic evolution during the study period. The geographic distribution changed substantially across the successive study periods. During 1993–1997, the eastern region represented the major geographic concentration, with 525 reported cases (62.4% of cases recorded during that period. During 1998–2002, the eastern region remained prominent and recorded 1,180 cases. During the later period, the geographic concentration shifted substantially toward western Libya. The western region recorded 1,449 cases during 2010–2017, representing its largest reported concentration during

the study period. Even central and southern Libya also became increasingly represented during the later period.

Figure 2 presents a four-panel visualization of the proposed geographic dissemination of HIV-1 from Benghazi to other Libyan locations, comparing subtype B, CRF02_AG, subtype A, and all three subtypes combined. The figure illustrated how the geographic patterns differ by subtype and how these patterns relate to the wider national distribution of HIV-1. The molecular dataset comprises 159 genotyped strains collected during 1995–2010. Subtype-specific sample sizes were 117 for subtype B, 29 for CRF02_AG, and 13 for subtype A. The number of characterized strains do quantify viral migration events. Benghazi act as a major source of viral migration to other cities and regions. Subtype B shows the highest migration to Tripoli (12.8%) and Misrata (9.4%). Subtype A shows the highest migration to other locations (53.8%) followed by Tripoli (23.1%)

The positive relationship between population density and diversity of HIV-1 was shown in Fig. 3. The density increases from 10 to 85 individuals/km², and genetic-diversity values rise from 22% to 68%. Each blue dot represents one paired example value, and the dashed line is a visual guide to the upward pattern. The number of distinct HIV-1 subtypes was greatest in Eastern region population followed by Western region and to less extent in Southern region.

## 3.4 Spatial and temporal concentration

Figure 4 showed the integrated spatial distribution of HIV-1 at a national level. The highest concentration was reported in Eastern region at an early period (1998–2002) by an annual report of 236 case/year followed Western region on 2010–2017 (181.1/year) followed by Central(67.3/year) and Southern region (66.3/year) at the same period (2010–2017). This shift from an early eastern concentration toward greater representation in western, central, and southern regions indicates increasing geographic heterogeneity of reported HIV infections over the study period. Molecular data comprise 159 HIV-1 genotyped strains successfully characterized during 1995–2010. Subtype B was dominant, accounting for 117 strains (73.6%), CRF02_AG accounted for 29 strains (18.2%), while subtype A accounted for 13 strains (8.2%).

## 3.5 Molecular transmission of HIV-1 subtypes

The molecular transmission network analysis of HIV-1 genotyped strains showed a clustering of HIV-1 strains in each regions. as stated in Fig. 5. These results showed that the three principal HIV-1 genetic categories were not uniformly distributed across the country. Subtype B was identified across the Libyan regions and was the predominant subtype overall. The molecular transmission analysis reported particularly strong representation of subtype B in the northern region. CRF02_AG showed a different geographic pattern and was particularly represented in eastern Libya. Subtype A represented a smaller proportion of characterized strains but was particularly observed in the western region.

## 3.6 Matrix of HIV-1 Transmission

The combined epidemiological and molecular findings demonstrated a changing national HIV-1 landscape in Libya as shown in Fig. 6. The matrix showed a relative strength of inferred transmission connections between cities and regions according to the molecular and epidemiological data from 1995 to 2017 with strength value (0–1). Strength transmission connection were observed within the same region as diagonal blocks Notable interregional connection was evident between Western-Eastern, Eastern-Central, and Central-Southern where Tripoli, Benghazi and Sebha showed a high connectivity with other cities and regions. The early epidemic was characterized by a prominent concentration of reported infections in eastern Libya, particularly Benghazi. Over subsequent years, reported cases became increasingly distributed across western, central, and southern regions. In parallel, molecular surveillance demonstrated the circulation of several HIV-1 genetic forms, with subtype B broadly distributed and CRF02_AG and subtype A showing more pronounced regional representation.

# DISCUSSION

This study provides an integrated description of the spatial, temporal, and molecular epidemiology of HIV-1 in Libya. The principal finding is that the recorded HIV-1 epidemic changed substantially in geographic distribution over time. The early concentration of reported infections in eastern Libya was followed by increasing representation of western, central, and southern regions. This is in agreement with other studies carried in Africa particularly Central African countries which have the most diverse HIV epidemics that varies greatly from one region to another within the same country (27, 28).

The geographic distribution HIV-1 genetic forms showed a great variability during the study periods. The molecular component analysis demonstrated that subtype CRF02_AG was the highest in the Eastern region (48%) at early study period with a reported cases of 263 case/year in the Eastern region. This subtype migrated through over the period to account for 52% in Southern region followed by Central (46%) and Western (39%) resigns respectively. The concentration of HIV infections in Eastern region represents an important early phase in the epidemiology of HIV-1 in Libya. These findings support that the geographically distributed HIV-1 epidemic was associated to a certain instant with the Benghazi outbreak. However, further phylogenic studies are need to evaluate these results (29, 30).

The nationwide spatial analysis of this study showed substantial increase of reported infections outside eastern region. The western region became particularly prominent during 2010–2017, followed by central and southern regions which also showed increasing numbers of reported cases. This geographic evolution through the four regions illustrated the epidemiological national dissemination of HIV-1 infections in the country. Nevertheless, national dissemination should not be equated with proof of a single continuous transmission chain. Geographic redistribution may reflect several processes, including local transmission, population movement, changes in testing practices, healthcare access, referral patterns, and differences in surveillance completeness (31, 32)

Molecular diversity and geographic heterogeneity are clearly evident in this study. Subtype B accounted for 73.6% of the characterized strains and was detected throughout the country. Its broad distribution is

consistent with a substantial national presence rather than restriction to one geographic focus. CRF02_AG represented 18.2% of characterized strains and was particularly represented in eastern Libya. Subtype A accounted for 8.2% and was particularly observed in western populations. These findings provide important context for interpreting the national HIV-1 epidemic. As the coexistence of these genetic forms demonstrates that the Libyan epidemic is not genetically homogeneous. The regional differences are epidemiologically informative and should be used as a guide line to implant national policy to combat the spread of HIV in country (33, 34).

Molecular surveillance can strengthen conventional epidemiological surveillance by providing information on viral genetic diversity. The present study uses molecular findings to characterize geographic heterogeneity in HIV-1 genetic forms and to follow HIV-1 transmission connections between cities and regions in Libya rather than to infer individual transmission pathways. However, the presence of the same subtype in two geographic regions does not establish direct transmission between those regions (35, 36). Conversely, different subtypes can circulate within the same geographic population. However, to establish probable transmission networks sequence-level phylogenetic analyses should be carried out incorporating sufficient numbers of representative sequences and appropriate reference sequences (37, 38).

The demographic and geographic evolution analysis across the study period showed a marked increase in the proportion of male cases during the later period and the decline in pediatric cases represent another important component of the changing epidemic. The decrease in pediatric cases is particularly notable given the historical importance of the Benghazi pediatric outbreak. In contrast, the later national epidemic was increasingly characterized by adult infections. These findings suggest that the epidemiological characteristics of HIV-1 in Libya changed over time and that risk groups and transmission contexts may differ geographically. Hence, then spatial-temporal variability of HIV-1 in Libyan should be incorporated as a part of the national policy to combat the spread of such contagious life threatening disease (39)

**Public health implications and strengths**

The geographic and molecular heterogeneity demonstrated by this analysis has several implications for HIV surveillance. First, surveillance should remain national rather than focusing exclusively on historical outbreak locations. Second, molecular surveillance can provide an important complement to routine epidemiological monitoring by documenting viral diversity and identifying changes in the distribution of circulating genetic forms. Third, regional differences should be incorporated into HIV testing, prevention, treatment, and harm-reduction planning. Fourth, continued molecular characterization could help identify emerging recombinant forms and changing transmission networks. Finally, the interpretation of surveillance data should avoid stigmatizing particular regions or population groups. Geographic concentration of reported cases may reflect multiple epidemiological and health-system factors rather than characteristics intrinsic to a population.

The major strength of this study is the integration of a large nationwide epidemiological dataset with molecular characterization of HIV-1 strains. The national surveillance dataset provides a long temporal perspective covering 25 years and 8,015 reported cases, while the molecular dataset provides information on viral genetic diversity across four geographic regions. This combination provides a more comprehensive description of the Libyan HIV-1 epidemic than either epidemiological or molecular data alone.

**Study limitations**

Despite that this detailed study was able to show the temporal and geographic patterns of HIV-1 in Libya. Several limitations needed to be highlighted that require consideration. First, the molecular dataset analysis is not sufficient enough to represent every national HIV infection in the country which may have been influenced by availability of specimens, geographic accessibility, clinical characteristics, or other factors. Second, regional case counts do not provide population-based incidence unless appropriate regional denominators are used. Third, surveillance data may be affected by changes in testing practices, healthcare access, reporting completeness, and referral patterns. Fourth, subtype distribution cannot independently establish transmission direction, transmission origin, or direct epidemiological linkage. However further studies are needed.

# CONCLUSIONS AND INTERVENTION POLICIES

The spatial and molecular epidemiology of HIV-1 in Libya demonstrates substantial change over time. The historical concentration of reported infections in eastern Libya was followed by increasingly broad geographic distribution involving western, central, and southern regions. Molecular surveillance demonstrated a predominance of subtype B alongside CRF02_AG and subtype A, with evidence of regional differences in their representation. The integration of epidemiological and molecular surveillance provides a useful framework for understanding the changing Libyan HIV-1 landscape. However, molecular subtype distributions should be interpreted as evidence of genetic diversity and geographic heterogeneity rather than direct proof of transmission pathways. Continued nationwide surveillance, expanded molecular characterization, population-based geographic analyses, and integration of epidemiological and phylogenetic data are warranted to improve understanding of HIV-1 dissemination in Libya(40).

## Declarations

# AUTHOR CONTRIBUTIONS

MAD conceived and designed the study, wrote the article, designed the analysis, analyzed the data, and performed the cartography. FMD and AE-B contributed to the analysis tools. MSM and MA made substantial contributions to conception and design, acquisition of data, or analysis, and interpretation of

data. MAD, MA, and AE-B provided advice and critically reviewed the manuscript. All authors read and approved the final manuscript.


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## DATA AVAILABILITY STATEMENT

The data presented in this paper are freely available upon request.

## ETHICS STATEMENT

Routinely collected sequence and demographic data on all newly notified HIV-1 infections are linked and irreversibly de-identified to enable public health research in the country as previously described (20, 21). The study was approved by the Libyan National Ethical Committee (Approval No. LY NS, HIV473277). It was conducted under the Helsinki Declaration and the supervision of the Libyan Study Group of Hepatitis & HIV (41).

## References


1. Nair M, Gettins L, Fuller M, Kirtley S, Hemelaar J (2024) Global and regional genetic diversity of HIV-1 in 2010–21: systematic review and analysis of prevalence. Lancet Microbe. ;5(11)
2. Williams A, Menon S, Crowe M, Agarwal N, Biccler J, Bbosa N, Ssemwanga D, Adungo F, Moecklinghoff C, Macartney M, Oriol-Mathieu V (2023) Geographic and population distributions of human immunodeficiency virus (HIV)–1 and HIV-2 circulating subtypes: a systematic literature review and meta-analysis (2010–2021). J Infect Dis 228(11):1583–1591
3. El Bouzidi K *Clinical and HIV determinants of antiretroviral therapy response in a Nigerian subtype G/CRF02_AG epidemic*(Doctoral dissertation, UCL (University College London))
4. Hemelaar J, Elangovan R, Yun J, Dickson-Tetteh L, Kirtley S, Gouws-Williams E, Ghys PD, Agwale S, Archibald C, Avidor B, Barbás MG (2020) Global and regional epidemiology of HIV-1 recombinants in 1990–2015: a systematic review and global survey. lancet HIV 7(11):e772–e781
5. Hemelaar J, Loganathan S, Elangovan R, Yun J, Dickson-Tetteh L, Kirtley S (2020) WHO-UNAIDS Network for HIV Isolation and Characterization. Country level diversity of the HIV-1 pandemic between 1990 and 2015. J Virol 95(2):10–128
6. Daw MA, Daw AM, Sifennasr NE, Draha AM, Daw AA, Daw AA, Ahmed MO, Mokhtar ES, El-Bouzedi AH, Daw IM, Adam SI (2019) Spatiotemporal analysis and epidemiological characterization of the

human immunodeficiency virus (HIV) in Libya within a twenty five year period: 1993–2017. AIDS Res therapy 16(1):14

7. Daw MA, El-Bouzedi AH (2019) Trends and projection of demographic indices of the Libyan population using a fifty-year census data 1954–2016. Afr Popul Stud. ;33(2)
8. Hartley RG *Recent population changes in Libya: economic relationships and geographical patterns*(Doctoral dissertation, Durham University)
9. Blake GH Urbanisation in North Africa: its nature and consequences. InThe City in the Third World 1974(pp. 67–80). London: Macmillan Education UK
10. Salam AA, Bushaala AM (2009) Demographic and health progress in Libya and its implications on population ageing. Bold 19(3):13–18
11. Al-Fraihat E, Irshaid A, Sallam M, Snygg J, Awawdeh R, Al-Shakerchi H, Al-Baidhani S, Sallam M (2026) Phylogenetic Evidence of Local HIV-1 Transmission and Antiretroviral Drug Resistance in the Middle East and North Africa. Viruses 18(8):897
12. Daw MA Tracing a Two-Decade Expansion of HIV-1 Following the Benghazi Pediatric Outbreak in Libya: From a Localized Pediatric Cluster to a Nationally Dispersed Epidemic
13. Hamidi A, Regmi PR, van Teijlingen E (2021) HIV epidemic in Libya: Identifying gaps. J Int Association Providers AIDS Care (JIAPAC) 20:23259582211053964
14. Ronen Y (2007) The HIV/AIDS tragedy and the bulgarian medics affair: A window on state and society in Libya. Middle East Stud 43(3):341–352
15. Bagasra O, Alsayari M (2007) The case of the Libyan HIV-1 outbreak. Libyan J Med 2(1):21–23
16. Bagasra O, Alsayari M, Bullard-Dillard R, Daw MA (2007) The Libyan HIV Outbreak How do we find the truth? Libyan J Med 2(2):57–62
17. Sallam M, Al-Khatib AO, Sabra T, Al-Baidhani S, Al-Mahzoum K, Aleigailly MA, Sallam M (2025) Challenges in elucidating HIV-1 genetic diversity in the Middle East and North Africa: a review based on a systematic search. Viruses 17(3):336
18. Korenromp EL, Sabin K, Stover J, Brown T, Johnson LF, Martin-Hughes R, Ten Brink D, Teng Y, Stevens O, Silhol R, Arias-Garcia S (1999) New HIV infections among key populations and their partners in 2010 and 2022, by world region: a multisources estimation. Journal of acquired immune deficiency syndromes 2024;95(1 Suppl):e34
19. Mumtaz GR, Chemaitelly H, AlMukdad S, Osman A, Fahme S, Rizk NA, El Feki S, Abu-Raddad LJ (2022) Status of the HIV epidemic in key populations in the Middle East and north Africa: knowns and unknowns. Lancet HIV 9(7):e506–e516
20. Daw MA, El-Bouzedi AH, Ahmed MO (2022) The impact of armed conflict on the prevalence and transmission dynamics of HIV infection in Libya. Front public health 10:779778
21. Daw MA, El-Bouzedi A, Ahmed MO, Dau AA (2017) In association with the Libyan Study Group of Hepatitis & HIV. Molecular and epidemiological characterization of HIV-1 subtypes among Libyan patients. BMC Res Notes 10(1):170

22. Giovanetti M, Ciccozzi M, Parolin C, Borsetti A (2020) Molecular epidemiology of HIV-1 in African countries: a comprehensive overview. Pathogens 9(12):1072
23. Zhang J, Xu K, Jiang J, Fan Q, Ding X, Zhong P, Xing H, Chai C, Pan X (2023) Combining molecular network analysis and field epidemiology to quantify local HIV transmission and highlight ongoing epidemics. Int J Infect Dis 128:187–193
24. Hanke K, Rykalina V, Koppe U, Gunsenheimer-Bartmeyer B, Heuer D, Meixenberger K (2024) Developing a next level integrated genomic surveillance: Advances in the molecular epidemiology of HIV in Germany. Int J Med Microbiol 314:151606
25. Bisaso KR, Karungi SA, Kiragga A, Mukonzo JK, Castelnuovo B (2018) A comparative study of logistic regression based machine learning techniques for prediction of early virological suppression in antiretroviral initiating HIV patients. BMC Med Inf Decis Mak 18(1):77
26. Dadi TK, Feyasa MB, Gebre MN (2020) HIV knowledge and associated factors among young Ethiopians: application of multilevel order logistic regression using the 2016 EDHS. BMC Infect Dis 20(1):714
27. Lihana RW, Ssemwanga D, Abimiku AL, Ndembi N (2012) Update on HIV-1 diversity in Africa: a decade in review. Aids Rev 14(2):83–100
28. Alexiev I, Dimitrova R (2025) The origins and genetic diversity of HIV-1: evolutionary insights and global health perspectives. Int J Mol Sci 26(22):10909
29. -Pang X, Tang K, He Q, Ma J, Fang N, Xie H, Zhong G, Liang S (2026) Unraveling HIV-1 spread in Southwest China: a phylogenetic and molecular network approach. Front Microbiol 17:1761072
30. -Brenner BG, Ibanescu RI, Osman N, Cuadra-Foy E, Oliveira M, Chaillon A, Stephens D, Hardy I, Routy JP, Thomas R, Baril JG (2021) The role of phylogenetics in unravelling patterns of HIV transmission towards epidemic control: the Quebec experience (2002–2020). Viruses 13(8):1643
31. - Sullivan PS, Johnson AS, Pembleton ES, Stephenson R, Justice AC, Althoff KN, Bradley H, Castel AD, Oster AM, Rosenberg ES, Mayer KH (2021) Epidemiology of HIV in the USA: epidemic burden, inequities, contexts, and responses. Lancet 397(10279):1095–1106
32. -Lin J, Xu Y, Ren Y, Shen S (2025) Study on the spatial-temporal evolution and influencing factors of AIDS incidence in China from 2006 to 2022. BMC Infect Dis 25(1):1690
33. - Mody A, Sohn AH, Iwuji C, Tan RK, Venter F, Geng EH (2024) HIV epidemiology, prevention, treatment, and implementation strategies for public health. Lancet 403(10425):471–492
34. - Kavanagh MM, Graeden E, Pillinger M, Singh R, Eaneff S, Bendaud V, Gustav R, Erkkola T (2020) Understanding and comparing HIV-related law and policy environments: cross-national data and accountability for the global AIDS response. BMJ global health 5(9):e003695
35. - Günthard HF, Kusejko K, Kouyos RD (2026) Phylogenetics and molecular evolution to understand and curb the HIV pandemic. Nat Rev Microbiol 24(1):76–92
36. - Horsburgh BA, Walker GJ, Kelleher A, Lloyd AR, Bull RA, Giallonardo FD (2024) Next-Generation Sequencing Methods for Near-Real-Time Molecular Epidemiology of HIV and HCV. Rev Med Virol 34(6):e70001

37. - Cai D, Feng Y, Gan M, Li H, Wang D, Hao J, Lin L, Tang Y, Wang Y, Liao L, Wang Z (2026) Integrating haplotype-enhanced HIV surveillance with national databases improves the resolution of transmission networks, drug resistance, and risk assessment. Emerg Microbes Infections 15(1):2678634
38. - Ávila-Ríos S, Parkin N, Swanstrom R, Paredes R, Shafer R, Ji H, Kantor R (2020) Next-generation sequencing for HIV drug resistance testing: laboratory, clinical, and implementation considerations. Viruses 12(6):617
39. -Rutstein SE, Ananworanich J, Fidler S, Johnson C, Sanders EJ, Sued O, Saez-Cirion A, Pilcher CD, Fraser C, Cohen MS, Vitoria M (2017) Clinical and public health implications of acute and early HIV detection and treatment: a scoping review. J Int AIDS Soc 20(1):21579
40. -Rutstein SE, Ananworanich J, Fidler S, Johnson C, Sanders EJ, Sued O, Saez-Cirion A, Pilcher CD, Fraser C, Cohen MS, Vitoria M (2017) Clinical and public health implications of acute and early HIV detection and treatment: a scoping review. J Int AIDS Soc 20(1):21579
41. - General Assembly of the World Medical Association (2014) World Medical Association Declaration of Helsinki: ethical principles for medical research involving human subjects. J Am Coll Dent 81(3):14–18

# Figures

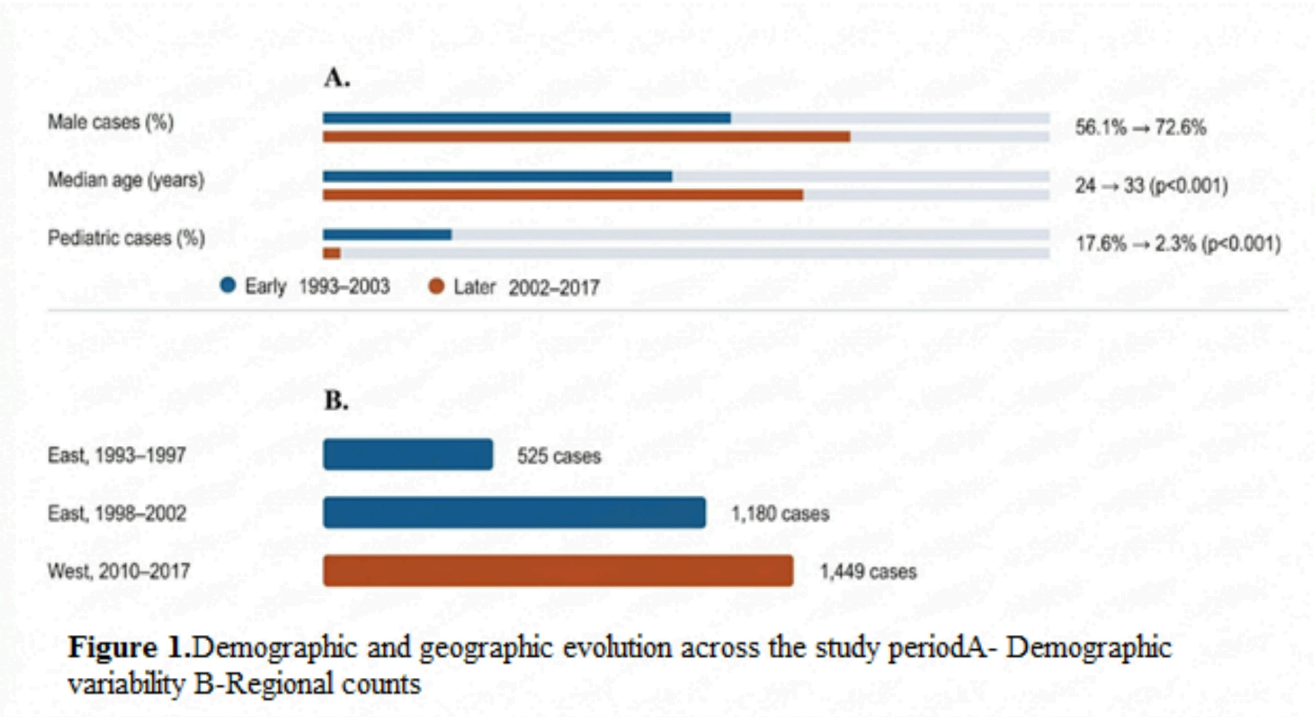



**Figure 1.**Demographic and geographic evolution across the study periodA- Demographic variability B-Regional counts

**Figure 1**

Demographic and geographic evolution of Libyan population across the study period; A-Demographic variability B- Regional counts

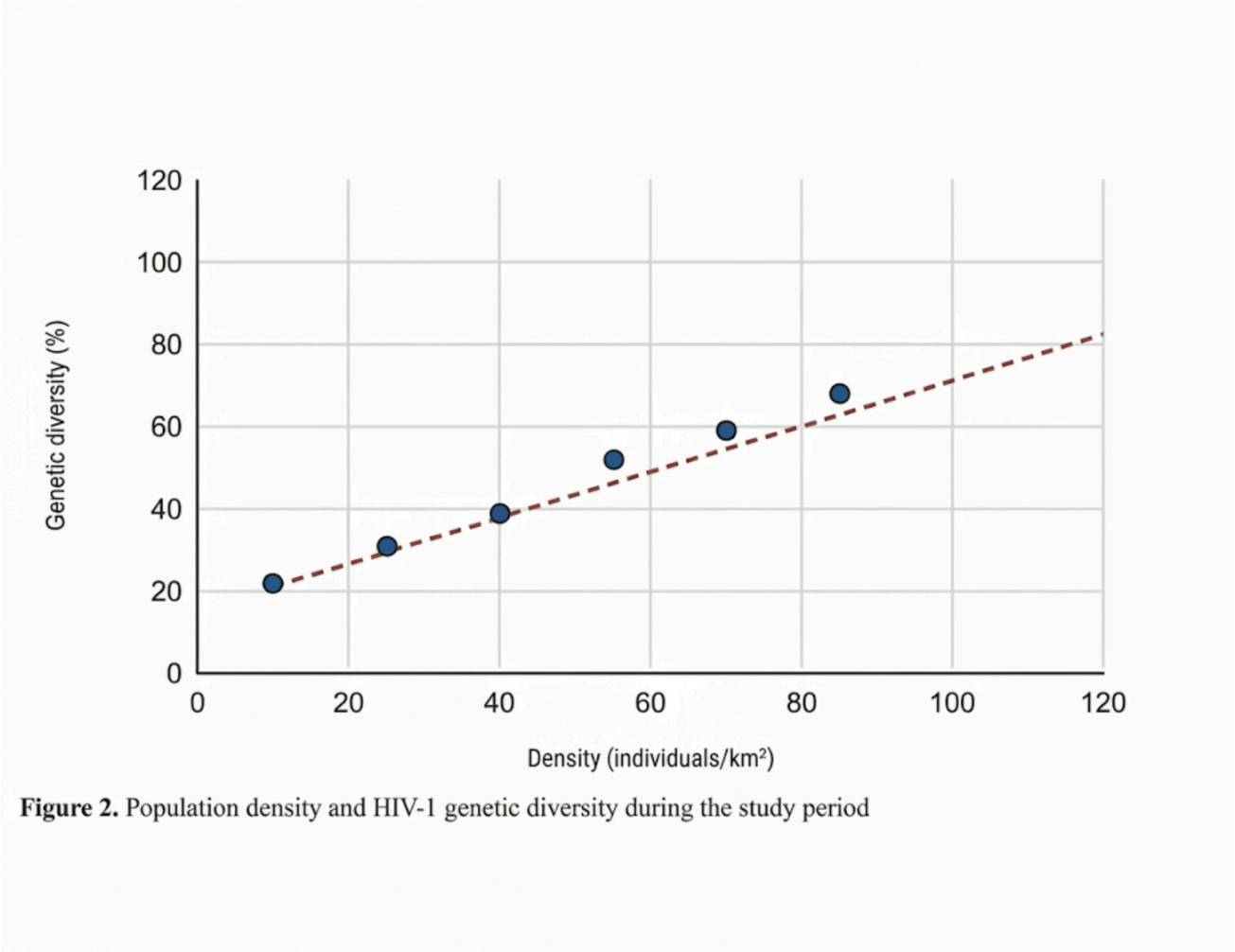



**Figure 2.** Population density and HIV-1 genetic diversity during the study period

## Figure 2

Population density and HIV-1 genetic diversity during the study period

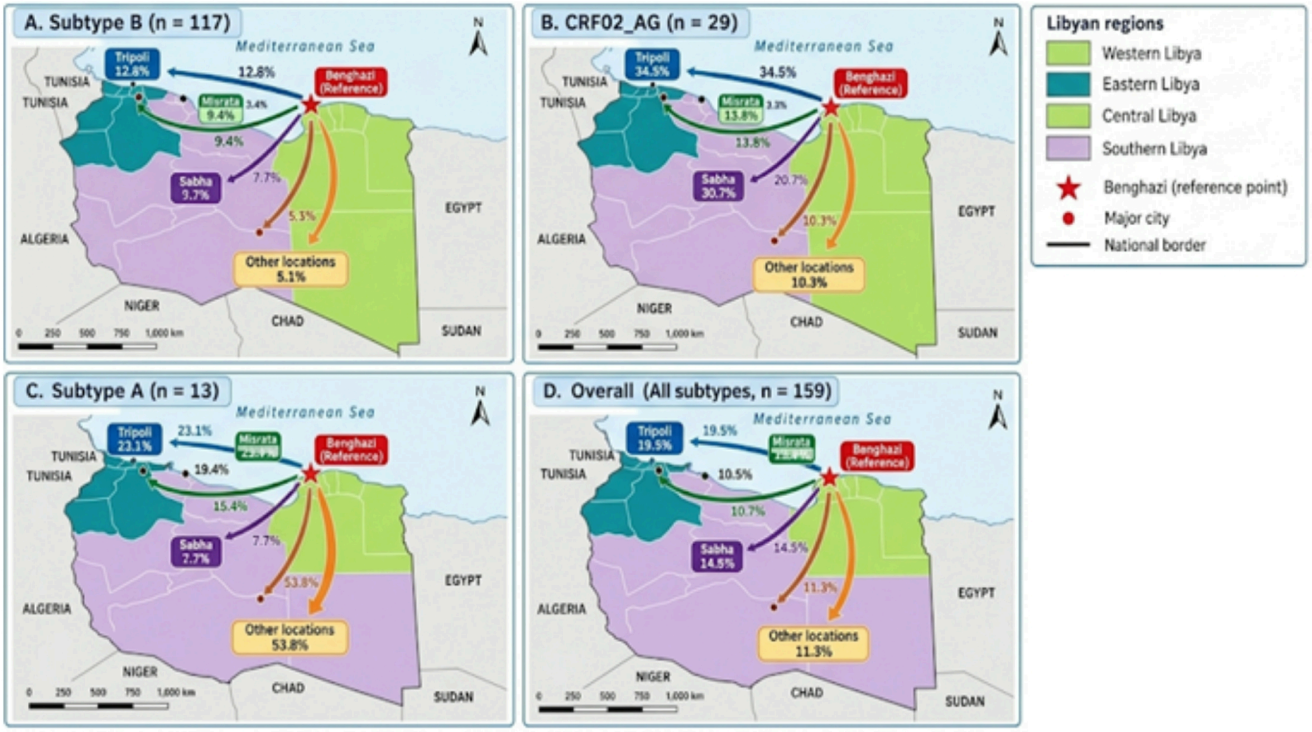



**Figure 3.**Migration events of HIV-1 subtypes through all over the Libyan regions

## Figure 3

Migration events of HIV-1 subtypes through all over the Libyan regions

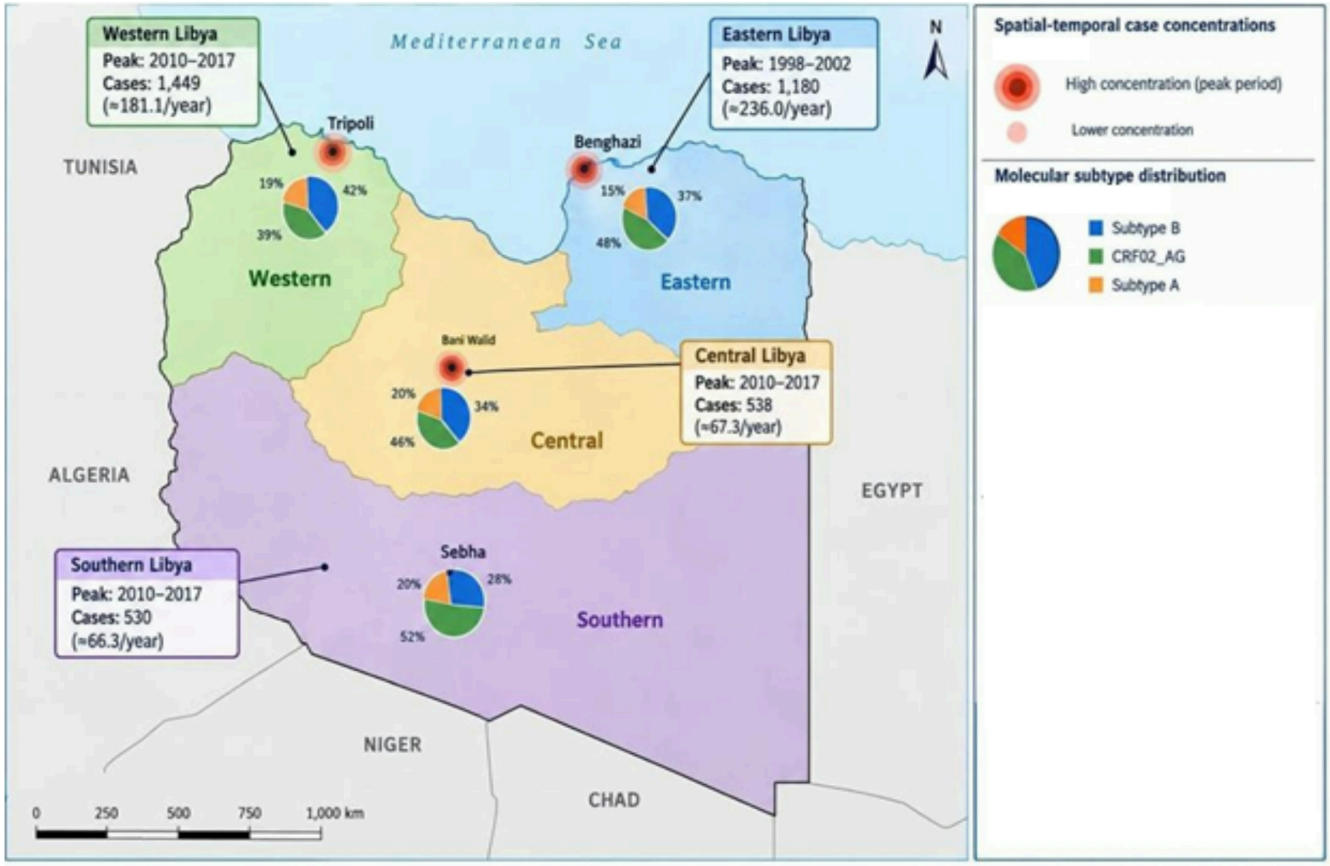



**Figure 4.** Integrated spatial distribution of HIV-1 in Libya: national case concentrations and molecular subtype patterns

## Figure 4

Integrated spatial distribution of HIV-1 in Libya: national case concentrations and molecular subtype patterns

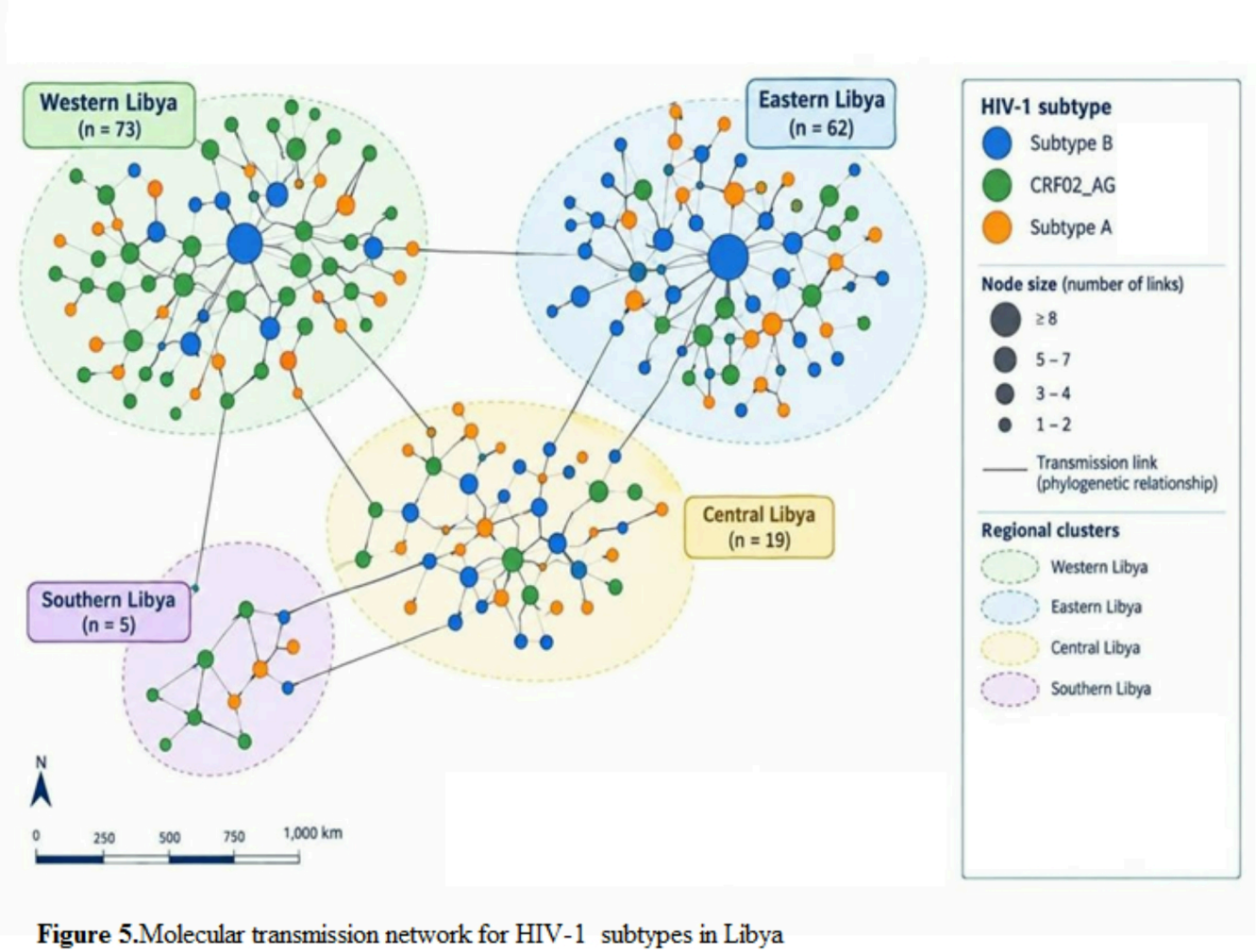



**Figure 5.**Molecular transmission network for HIV-1 subtypes in Libya

## Figure 5

Molecular transmission network for HIV-1 subtypes in Libya

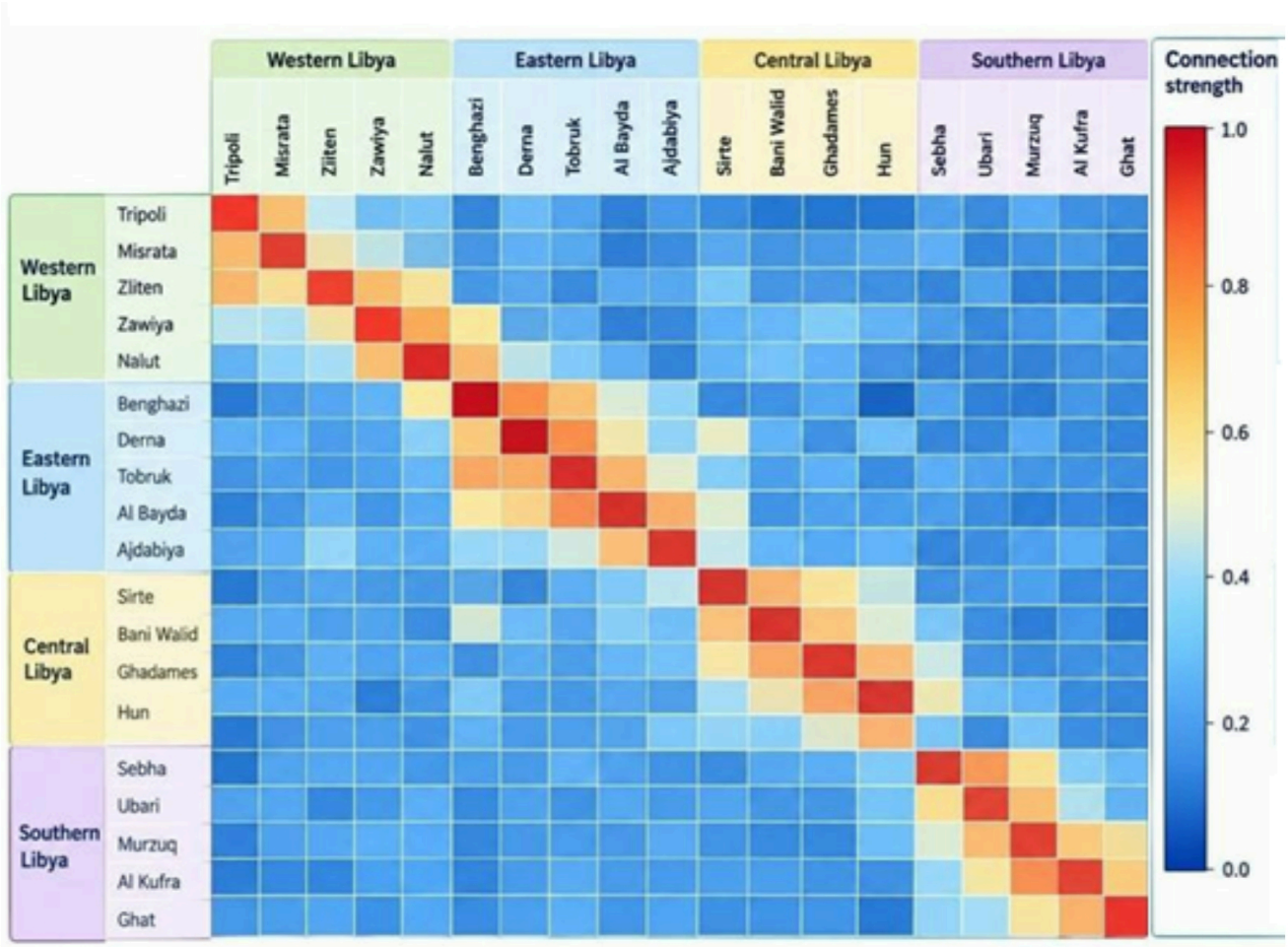



**Figure 6.** Strength matrix of HIV-1 transmission connections between cities and regions in Libya

## Figure 6

Strength matrix of HIV-1 transmission connections between cities and regions in Libya