HIV-1 A6 Variant Transmissions Poland Are Fuelled by War Refugees From Ukraine & Local MSM Clusters

Authors: Karol Serwin[1], Kaja Schiebe[1], Anna Urbańska[1], Bogusz Aksak-Wąs[1], Magdalena Witak-Jędra[1], Piotr Ząbek[2], Ewa Siwak[2], Iwona Cielniak[3], Elżbieta Jabłonowska[4], Paweł Jakubowski[5], Monika Bociąga-Jasik[6], Elżbieta Mularska[7], Aleksandra Szymczak[8], Bartosz Szetela[8], **Miłosz Parczewski[1]**

[1] *Department of Infectious, Tropical Diseases and Immune Deficiency, Pomeranian Medical University in Szczecin, Poland;* [2] *Department of Adults' Infectious Diseases, Medical University of Warsaw;* [3]*Faculty of Medical Science. Collegium Medicum Cardinal Stefan Wyszynski University in Warsaw;* [4]*Department of Infectious Diseases and Hepatology, Medical University of Łódź, Łódź, Poland;* [5]*Pomeranian Hospitals, Gdańsk, Poland;* [6]*Jagiellonian University Medical College, Department of Infectious and Tropical Diseases, Poland;* [7]*Regional Hospital, Out-Patient's Clinic for Immune Deficiency, Chorzów, Poland;* [8] *Department of Infectious Diseases, Liver Disease and Acquired Immune Deficiencies, Wroclaw Medical University, Wrocław, Poland*

1069

BACKGROUND

- Since February 2022, Poland has become a shelter for over 1.6 million Ukrainian refugees, a number comparable to the total migrant flow of the past decade (Figure 1)
- The HIV-1 A6 lineage, dominant in Eastern Europe, has become the common variant in Poland in the recent years, previously dominated by subtype B infections
- Phylogenetic analysis yields insights into transmission clusters and linkages, offering a deeper understanding of ongoing virus spread
- **In this study we explore the changing epidemic profile of the A6 lineage in Poland in the context of migration and refuge but also local transmissions**

METHODS

- We analyzed **1941 Polish HIV partial *pol*** sequences, including **719 from Ukrainian-born individuals**, supplemented with **11,807 location-annotated A6 sequences**, collected up until November 2023
- Phylogenetic inference and genetic distance-based clustering were employed to identify clusters and genetically linked individuals
- Clusters were classified into singletons and dyads (≤2 sequences), networks (3–13 sequences), or large clusters (≥14 sequences)
- In the Polish cohort, we delineated sequences from individuals born in Poland or Ukraine and analysed transmission routes within clusters.

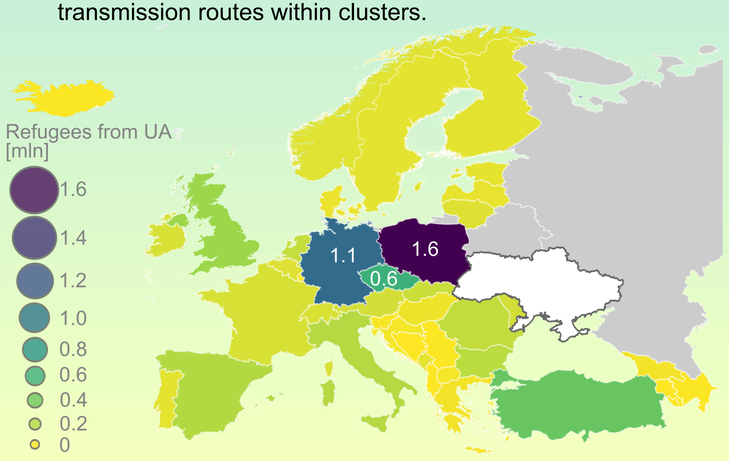

Figure 1. *Refugees from Ukraine registered in Europe*

> The flow of **refugees from Ukraine** to Poland has particularly impacted the national HIV-1 A6 epidemic
>
> Long-lasting **large transmission clusters**, primarily **among MSM**, are also pivotal in evolving A6 variant dissemination in the country
>
> Tailored HIV testing and intervention programs are essential for these two at-risk groups

RESULTS

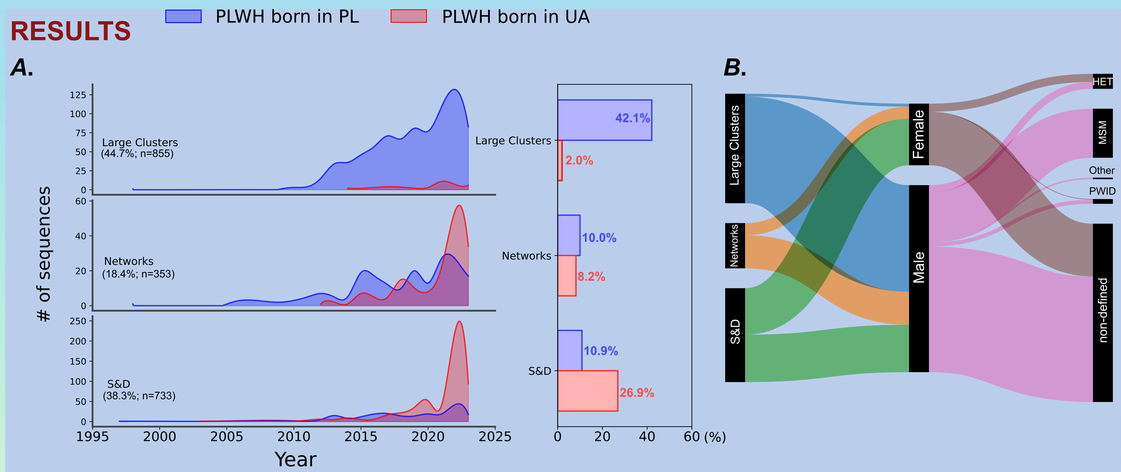

Figure 2. *Sampling density **(A)** and HIV-1 A6 prevalence by cluster size, gender, risk factors **(B);** HET - heterosexual, MSM - men having sex with men, PWID – people who inject drugs, S&D - singletons and dyads, PL – Poland, UA - Ukraine*

- We identified six large clusters (n=855 sequences), 74 networks (n=353), and 590 singletons or dyads (n=733).
- In large clusters dominated internal Polish transmissions among men who have sex with men (MSM) accounting for the total of 41.9% of infections with known transmission route (Figure 2).
- There was also a marked rise in new, late diagnosed (lymphocyte count at baseline < 350 cells/µl) cases observed among Ukrainian male (13.6%) and female (13.3%) migrants since the beginning of 2022.
- Ukrainian-born individuals represent new introductions of the A6 lineage into Poland, primarily as singletons and dyads but without further spreading into larger clusters.

RESULTS CD.

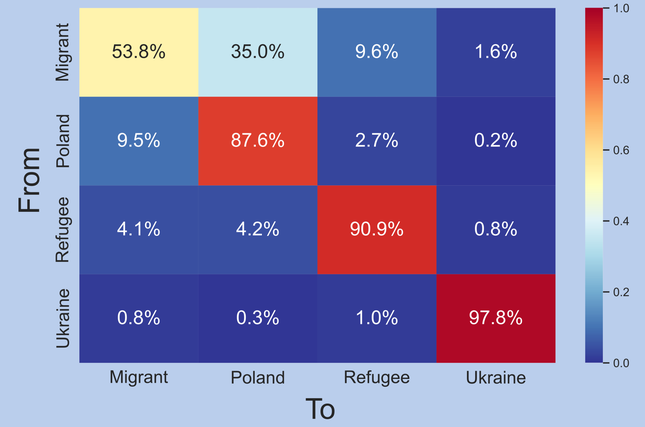

Figure 3. *Normalized fraction of links between different groups of individuals*

- The most common intergroup linkages (35.0% of the normalized links) were observed from Ukrainian migrants diagnosed before 2022 to individuals born in Poland (Figure 3)

CONCLUSIONS

- The influx of war-displaced people from Ukraine notably fuels sub-subtype A6 infections in Poland but majority of introductions resulted in dead-end transmissions.
- On the other hand, large clusters define independently growing national epidemic with this variant in MSM.
- Presented data imply urgent need for targeted HIV testing and intervention programs among key populations

ADDITIONAL KEY INFORMATION

This work was supported by National Science Centre SONATA-BIS Grant UMO-2018/30/E/NZ6/00696

CROI 2024

Author Contact Information:
milosz.parczewski@pum.edu.pl