FEBRUARY 2024

PANGEA PUBLICATIONS

In Preparation

1. Otecko N et al. (2024) *Molecular HIV Transmission Cluster Analysis in a Generalised African Epidemic. Manuscript close to completion.*
The study shows that no large clusters can be found in generalised HIV epidemics in Africa, in contrast to concentrated epidemics in Europe. The work has profound implications of how HIV prevention and testing should be conducted in Africa over the coming decade.

2. Hall et al. (2024) *Quantifying the Contribution of Different Aged Men and Women to Onwards Transmission of HIV-1 in Generalised Epidemics In Sub-Saharan Africa: A Modelling and Phylogenetics Approach from the HPTN 071 (PopART) trial. Manuscript undergoing internal review.*
The study compares phylogenetic estimates of transmission patterns by age and sex with modelling results for the HPTN-071 communities in Zambia and finds that they are comparable. Men under 35 contribute most to the generational renewal of the epidemic and more efforts are required to link this group to care.

3. Kim S et al. (2024) *Increasing intra- and inter-subtype HIV diversity despite declining HIV incidence in Uganda. Manuscript undergoing internal review*
The study shows that recombinant viruses increased significantly in Uganda in the last ten years and that genetic diversity in all subtypes is increasing.

4. Di Lauro F et al. (2024) *Existence of a core group of sexually active individuals in HPTN-071 PopART. Manuscript in preparation.*
A model-based analysis of PopART data shows that the existence of a core group of sexually active individuals is necessary to explain a sustained, generalised HIV-epidemic in sub-Saharan Africa.

Submitted

5. Martin M et al. (2023) *Population dynamics of HIV drug resistance among pre-treatment and treatment-experienced persons with HIV during treatment scale-up in Uganda: a population-based longitudinal study.* MedRxiv.
The study found that prevalence of HIV drug resistance among viraemic PLHIV significantly increased with scale-up of ART programs.

6. Igiraneza A et al. (2023) *Learning patterns of HIV-1 co-resistance to broadly neutralizing antibodies with reduced subtype bias using multi-task learning.* Preprint BioRxiv.
The study develops a new machine learning model which can learn patterns of co-resistance between broadly neutralizing antibodies, thus providing tools to predict antibodies' epitopes and to potentially select optimal bnAb combinations.

7. Golubchik T et al. (2022) *HIV-phyloTSI: Subtype-independent estimation of time since HIV-1 infection for cross-sectional measures of population incidence using deep sequence data.* Submitted to Nature Communications. Preprint MedRxiv.
The study presents a new method to estimate time of infection from sequence data alone, which can be used to estimate incidence on population level.

Published

8. Monod M et al (2023) *Longitudinal population-level HIV epidemiologic and genomic surveillance highlights growing gender disparity of HIV transmission in Uganda.* **Nature Microbiology.**
The study suggests that HIV interventions to increase HIV suppression in men are critical to reduce incidence in women, close gender gaps in infection burden and improve men's health in Africa.

9. Hall M et al (2023) *Demographics of sources of HIV-1 transmission in Zambia: a molecular epidemiology analysis in the HPTN 071 PopART study on the demographics of sources of HIV-1 transmission in Zambia.* **Lancet Microbe**.
The study conducted a comprehensive phylogenetic analysis of Zambian HPTN-071 PopART communities during the trial period and found that men aged 25-39 should be a focus of prevention strategies to control HIV transmission in Zambia.

10. Kemp S et al (2023) *HIV transmission dynamics and population-wide drug resistance in rural South Africa*. **Accepted in Nature Communications.**
The study found that whole HIV-1 genome sequencing allowed identification of significant proportions of clusters with multiple individuals, and geospatial analyses suggesting decentralised networks can inform targeting public health interventions to effectively curb HIV-1 transmission.

11. Jamrozik E et al (2023) *Public health use of HIV phylogenetic data in sub-Saharan Africa: ethical issues.* **BMJ Global Health.**
By using phylogenetic data to inform the design of HIV diagnosis and treatment programmes for people, more likely to be the source of transmission to others, can produce greater public health benefits per individual treated, but these programmes must avoid exacerbating stigma and injustice.

12. Nakemanya S et al (2023) *Understanding the drivers of preferential migration of people living with HIV to fishing communities of Lake Victoria in Uganda.* **Global Public Health**
The study found that stigma is the major social phenomenon shaping preferential migration to fishing communities in Uganda.

13. Kotokwe K et al (2023) *Prediction of Coreceptor Tropism in HIV-1 Subtype C in Botswana*. **Viruses**
The study showed a significant difference in ART status between participants harboring X4- versus R5-tropic viruses. X4-tropic viruses were more frequent among PLWH receiving ART and suggests that the tools for coreceptor prediction should be used in combination.

14. Abdullahi A et al (2023) *Limited emergence of resistance to integrase strand transfer inhibitors (INSTIs) in ART-experienced participants failing dolutegravir-based antiretroviral therapy: a cross-sectional analysis of a Northeast Nigerian cohort.* **J Antimicrob Chemother**
The study found a low prevalence of resistance to dolutegravir; the data are therefore supportive of the continual rollout of dolutegravir as the primary first-line regimen for ART-naive participants and the preferred switch to second-line ART across the region.

15. Nascimento F et al. (2022) *Evaluating whole genome HIV-1 sequence for estimation of incidence and migration in a rural South African community*. **Wellcome Open Research**
The study found that there was a high probability that new infections were not attributable to endogenous transmission within Hlabisa, suggesting high inter-connectedness between communities in rural South Africa.

16. Bhebhe L et al (2022) *Epidemiological and viral characteristics of undiagnosed HIV infections in Botswana.* **BMC Infectious Diseases.**
The results indicated that those with undiagnosed infections are likely to be young men and women who do not use condoms consistently. Among women, several factors were predictive: being married, educated, and testing frequently increased risk. Men at risk were more difficult to delineate.

17. Xi X et al. (2022) *Inferring the sources of HIV infection in Africa from deep-sequencing data with non-parametric Poisson flow models*. **Journal of the Royal Statistical Society.**
The study presents a semi-parametric Bayesian Poisson model to look at transmission flows in NGS data and shows that adolescent and young women were predominantly infected through age-disparate relationships in Uganda between 2009 and 2015.

18. Barang O et al (2022) *HIV-1 drug resistance mutations among individuals with low-level viraemia while taking combination ART in Botswana.* **J Antimicrob Chemother**.
The study found that a single LLV measurement while on ART strongly predicted the risk of future VF, suggesting the use of VL > 50 copies/mL as an indication for more intensive adherence support with more frequent VL monitoring.

19. Magosi L et al (2022) *Deep-sequence phylogenetics to quantify patterns of HIV transmission in the context of a universal testing and treatment trial - BCPP/Ya Tsie trial.* **Elife**.
The study provides a phylogenetic analysis of the Ya Tsie trial in Botswana, describing age and sex patterns of transmission, clustering, and mobility patterns between partners.

20. Ragonnet-Cronin M et al (2021) *HIV genetic diversity informs stage of HIV-1 infection among patients receiving antiretroviral therapy in Botswana*. **J Infect Dis.**
The results indicate that recency of HIV-1 infection can be inferred from viral sequence diversity even among patients on suppressive ART.

21. Bonsall D et al (2020) *A Comprehensive Genomics Solution for HIV Surveillance and Clinical Monitoring in Low-Income Settings*. **J Clin Microbiol.**
The study showed that viral genetic sequencing can be used to monitor the spread of HIV drug resistance, identify appropriate antiretroviral regimes, and characterize transmission dynamics.

22. Grant H et al. (2020) *Pervasive and non-random recombination in near full-length HIV genomes from Uganda.* **Virus Evolution**.
The study showed that despite similar recombination patterns in many recombinants, no clearly supported circulating recombinant form was found and the vast of the A1/D recombinants appear to be unique recombinant forms.

23. Lamers S et al. (2020) *HIV-1 Subtype Distribution and Diversity Over 18 Years in Rakai, Uganda*. **AIDS Res Hum Retroviruses**.
This study found that genetic diversity in subtypes A and D was increasing before ART rollout and decreasing shortly after.

24. Bbosa N et al. (2020) *Phylogenetic and Demographic Characterization of Directed HIV-1 Transmission Using Deep Sequences from High-Risk and General Population Cohorts/Groups in Uganda.* **Viruses**
More transmissions were observed from the general population to the fisherfolk communities than vice versa, indicating that fishing communities on Lake Victoria are not a net source of transmission flow to neighbouring communities further inland.

25. Ratmann O et al. (2020) *Quantifying HIV transmission flow between high-prevalence hotspots and surrounding communities: a population-based study in Rakai, Uganda*. **Lancet HIV**. The study found that cross-community HIV transmissions between Lake Victoria high-prevalence areas and surrounding inland populations are infrequent and when they occur, virus more commonly flows into rather than out of the fishing villages.

26. Capoferri A et al. (2020) *Recombination Analysis of Near Full-Length HIV-1 Sequences and the Identification of a Potential New Circulating Recombinant Form from Rakai, Uganda*. **AIDS Res Hum Retroviruses**.
The study found a large number of subtype A and D recombinants in Uganda which can be selected for if the combination of subtypes confer a survival advantage.

27. Novitsky V et al. (2020) *Mapping of HIV-1C Transmission Networks Reveals Extensive Spread of Viral Lineages Across Villages in Botswana Treatment-as-Prevention Trial*. **J Infect Dis**.
This study showed a large number of circulating phylogenetically distinct molecular HIV clusters which suggests highly diversified HIV transmission networks across Botswana communities by 2018.

28. Bbosa N et al. (2019) *Phylogeography of HIV-1 suggests that Ugandan fishing communities are a sink for, not a source of, virus from general populations*. **Scientific Reports.**
Phylogeographic analysis showed strong support for viral migration from the general population to fishing communities without evidence of substantial viral dissemination to the general population.

29. Abeler-Dörner L et al. (2019) *PANGEA-HIV 2: Phylogenetics and Networks for Generalised Epidemics in Africa*. **Curr Opin HIV AIDS**
This review gives a brief overview of how the PANGEA 2 consortium will contribute to understanding the HIV epidemics in sub-Saharan Africa.

30. Ratmann O et al. (2019) *Inferring HIV-1 transmission networks and sources of epidemic spread in Africa with deep-sequence phylogenetic analysis*. **Nature Commun**.
The study demonstrate how viral deep-sequencing can be used to reconstruct HIV-1 transmission networks and to infer the direction of transmission in these networks.

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31. Coltart C et al. (2018) *Ethical considerations in global HIV phylogenetic research***. Lancet HIV**.
This review provides a framework to assist researchers, public health practitioners, and funding institutions to ensure that HIV phylogenetic studies are designed, conducted, and disseminated in an ethical manner.

32. Ratmann O et al. (2017) *Phylogenetic Tools for Generalized HIV-1 Epidemics: Findings from the PANGEA-HIV Methods Comparison.* **Mol Biol Evol**.
This study shows that viral phylogenetic tools can be adapted and used to estimate epidemiological quantities of central importance to HIV-1 prevention in sub-Saharan Africa.

33. Ratmann O et al. (2017) *HIV-1 full-genome phylogenetics of generalized epidemics in sub-Saharan Africa: impact of missing nucleotide characters in next-generation sequences*.
AIDS Res Hum Retroviruses.
The study showed that molecular epidemiological analyses of NGS data with variable sequence coverage must proceed cautiously because of a considerable negative impact of missing characters on phylogeny reconstruction.

34. Yebra G et al. (2016) *Using nearly full-genome HIV sequence data improves phylogeny reconstruction in a simulated epidemic*. **Sci Rep**.
The study concluded that using longer sequences derived from nearly whole genomes improves the reliability of phylogenetic reconstruction.

35. Pillay D et al. (2015) *PANGEA-HIV: phylogenetics for generalised epidemics in Africa.*
Lancet Infect Dis.
This review provides a concise summary of the ways in which the PANGEA consortium aims to enhance the understanding of HIV epidemics in sub-Saharan Africa.

36. Yebra G et al. (2015) *Analysis of the history and spread of HIV-1 in Uganda using phylodynamics*. **J Gen Virol.**
The sequence analysis shows both the subtype A and the subtype D epidemic grew exponentially during the 1970s-1980s and decreased from 1992, which agrees with HIV prevalence reports in Uganda.

37. Dennis A et al. (2014) *Phylogenetic studies of transmission dynamics in generalized HIV epidemics: an essential tool where the burden is greatest*? **J Acquir Immune Defic Syndr**.
This study describes the current uses for phylogenetics in generalized epidemics and discusses their promise for elucidating transmission patterns and informing prevention trials.

Contact

For feedback, partnerships, or further information, please feel free to contact us at

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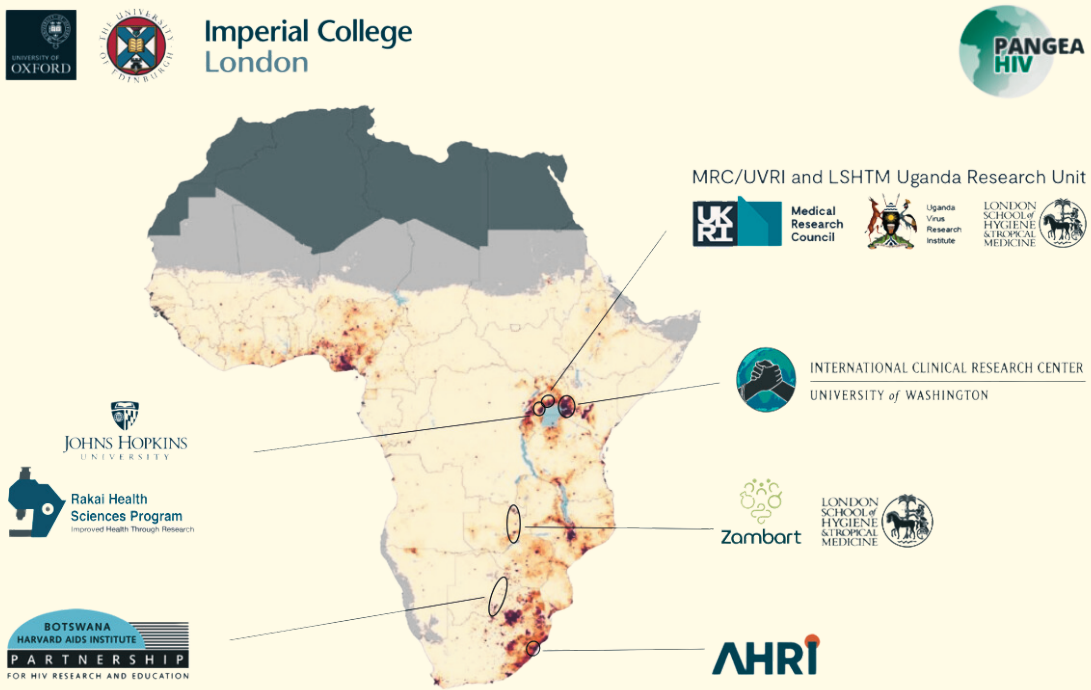

PANGEA is a network of African, European and American researchers identifying individual and population-level factors that drive HIV transmission in Sub-Saharan Africa by using viral genetics and epidemiology