Age and HIV Transmission: Insights from Phylogenetic Analysis

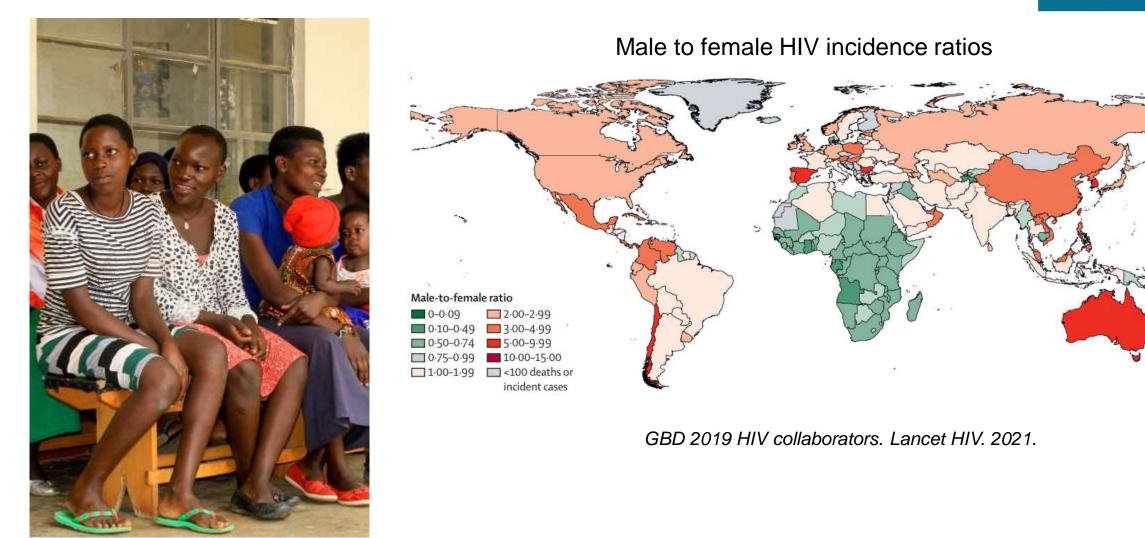
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ANNUAL MEETING 2022

The African HIV epidemic is predominantly female.





Lack of data on sources of female infection

- There is abundant information on risk factors for HIV acquisition among African women.
 - Younger age an historically strong predictor.



- Less is known about male partner sources of female HIV infection.
 - Most data come from longitudinal studies of cohabitating stable couples or self-reported partner data .

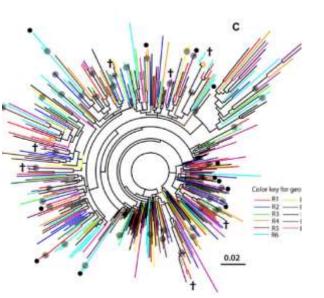






Rakai Health Sciences Program PEPFAR DREAMS program in south central Uganda

- <u>Objective</u>: To characterize sources of HIV transmission by age and gender at the population-level in an African setting with generalized HIV transmission (e.g., what the age profile of male sources of HIV infection to young women?).
- <u>Approach</u>: Molecular epidemiology/HIV phylogenetics



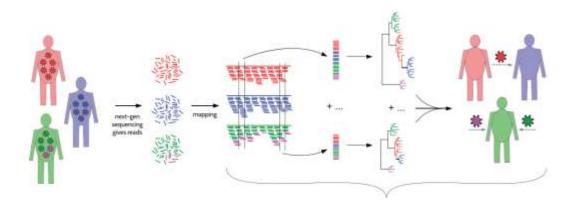


Phylogenetics and Networks for Generalized Epidemics in Africa (PANGEA-HIV)





HIV SHIVER and Phyloscanner



Wymant et al. Virus evolution. 2018 Wymant et al. Mol. Biol. Evo. 2018

Abeler-Dörner et al., Curr Opin HIV/AIDS. 2019 Pillay et al., Lancet, 2015

HIV phylogenetics and ethics



Ethical considerations in global HIV phylogenetic research

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Lancet HIV 2018; 5: e656-66

Published Online August 30, 2018 http://dx.doi.org/10.1016/ \$2352-3018(18)30134-6 *Joint first authors †Joint senior authors ‡Members are listed in the appendix Institute for Global Health (C.E.M.Coltart PhD.

Phylogenetic analysis of pathogens is an increasingly powerful way to reduce the spread of epidemics, including HIV. As a result, phylogenetic approaches are becoming embedded in public health and research programmes, as well as outbreak responses, presenting unique ethical, legal, and social issues that are not adequately addressed by existing bioethics literature. We formed a multidisciplinary working group to explore the ethical issues arising from the design of, conduct in, and use of results from HIV phylogenetic studies, and to propose recommendations to minimise the associated risks to both individuals and groups. We identified eight key ethical domains, within which we highlighted factors that make HIV phylogenetic research unique. In this Review, we endeavoured to provide a framework to assist researchers, public health practitioners, and funding institutions to ensure that HIV phylogenetic studies are designed, done, and disseminated in an ethical manner. Our conclusions also have broader relevance for pathogen phylogenetics.

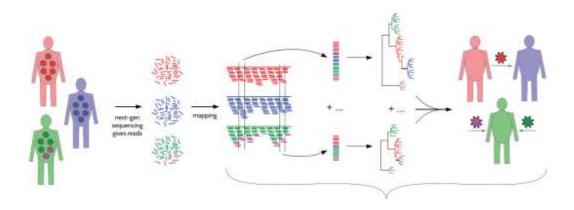
Coltart and Hoppe et al., Lancet HIV. 2018

Phylogenetics and Networks for Generalized Epidemics in Africa (PANGEA-HIV)





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Abeler-Dörner et al., Curr Opin HIV/AIDS. 2019 Pillay et al., Lancet, 2015

The Rakai Community Cohort Study (RCCS)

DR of Congo

Rwanda

Burundi

- Population-based HIV surveillance cohort in south central Uganda conducted by the Rakai Health Sciences Program.
- 28 rural agrarian and semi-urban trading communities under surveillance since 1994
- 4 Lake Victoria fishing communities under surveillance since 2011
- ~20,000 study participants surveyed every 1.5-2 years

Kenya

Lake Victoria

Tanzan

Population census



Biospecimens/biometrics



Survey



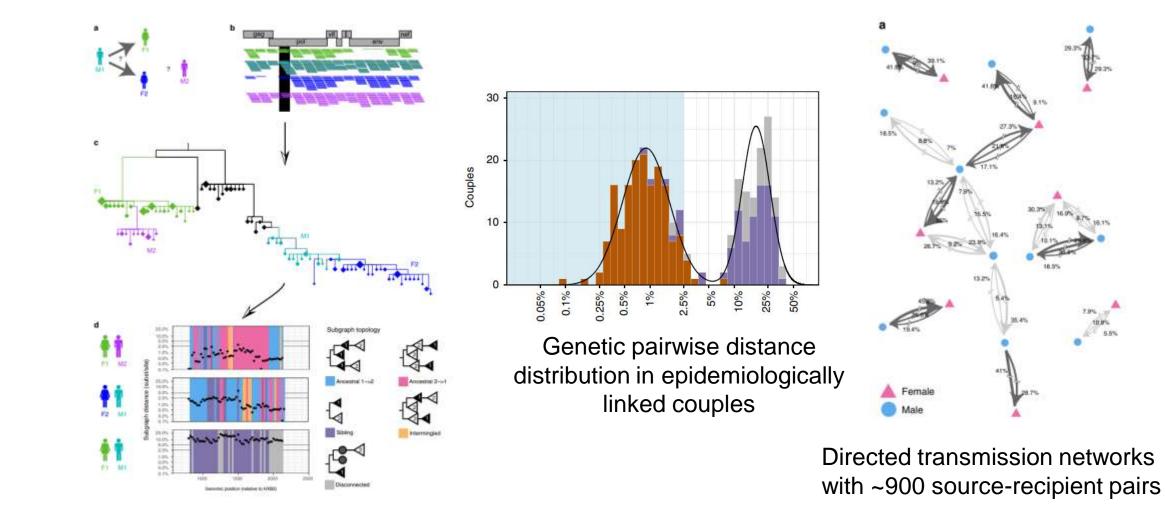
Services





Inferring African HIV transmission networks with deep sequence phylogenetic analysis





Shiver/Phyloscanner

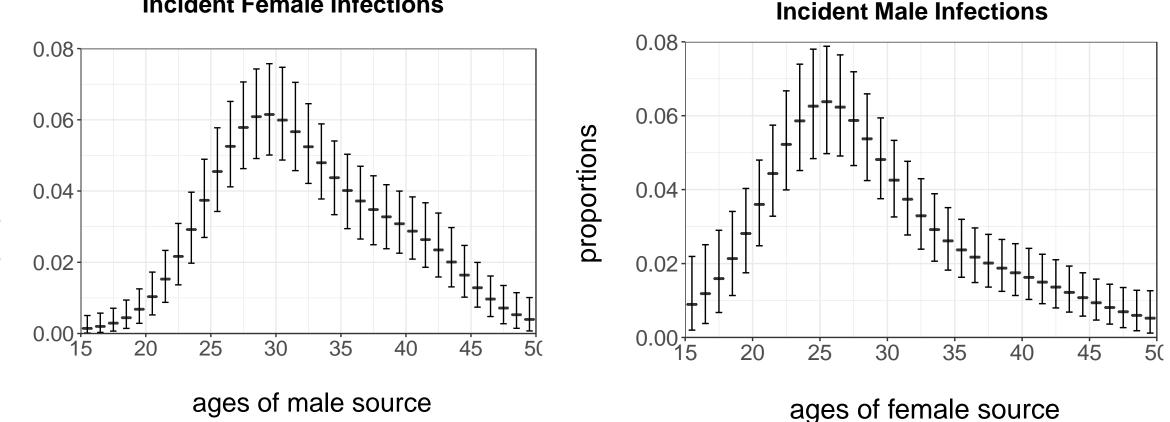
Ratmann et al. Nature Comm. 2019

Sources of transmission by age and gender, 2011-15

Incident Female Infections

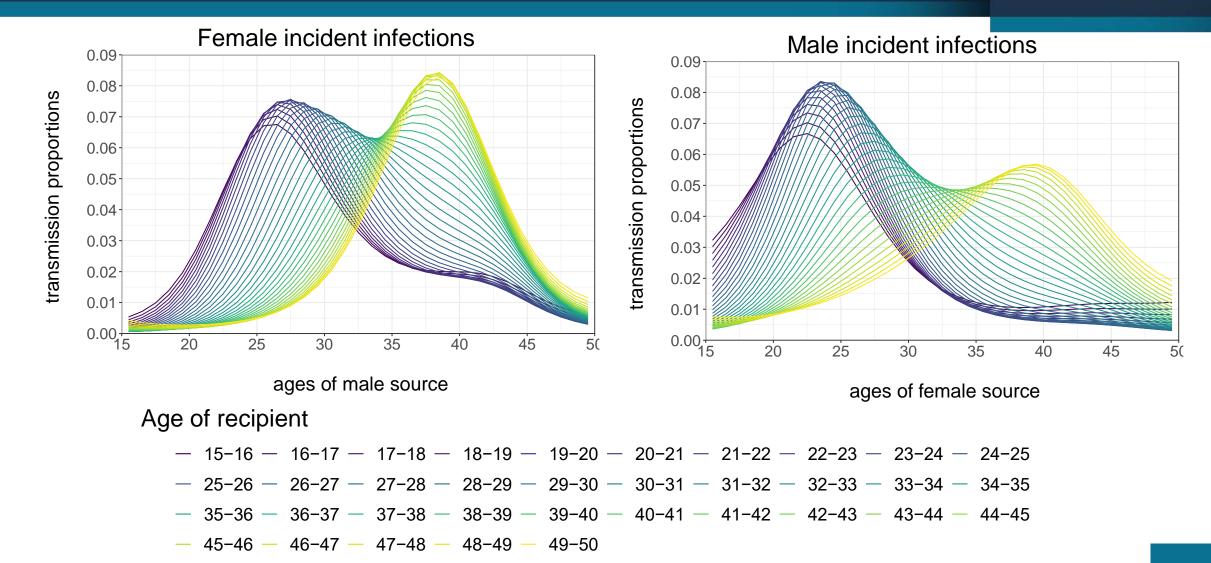


proportions



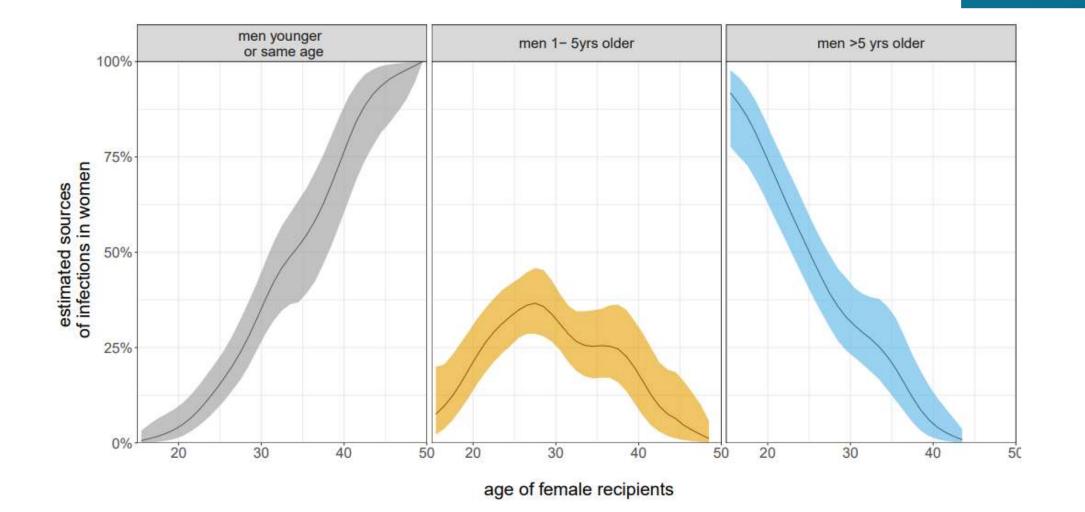
Sources of transmission by age of recipient and transmitter





Xi et al. JRSSC. 2022

Male sources of transmission to women





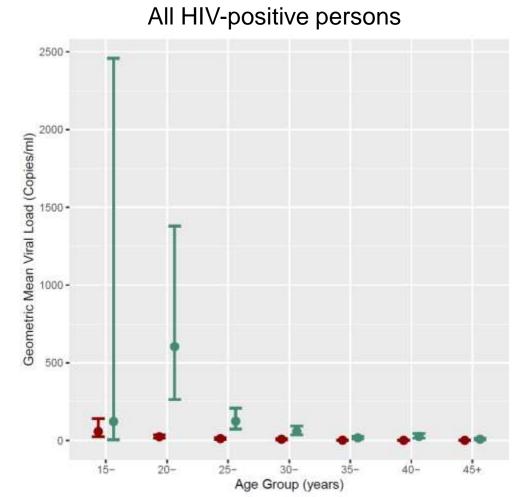
HPTN

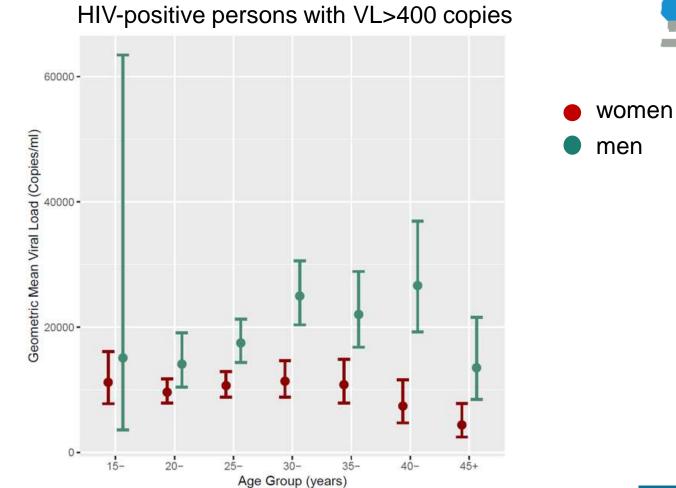
HIV Prevention Trials Network

Xi et al. JRSSC. 2022

HIV viremia in the RCCS, 2016-17





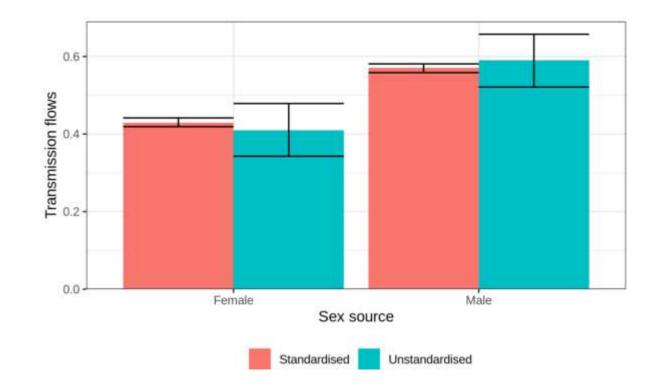


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Transmission cycle



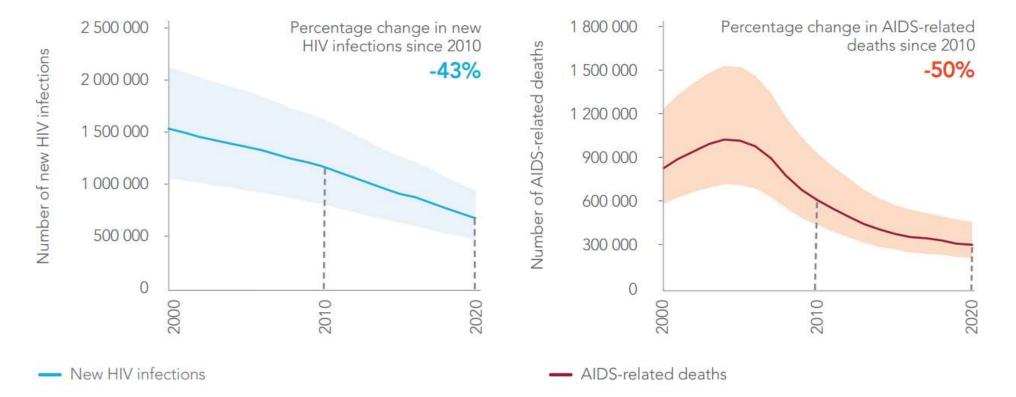




HIV incidence in sub-Saharan Africa is declining



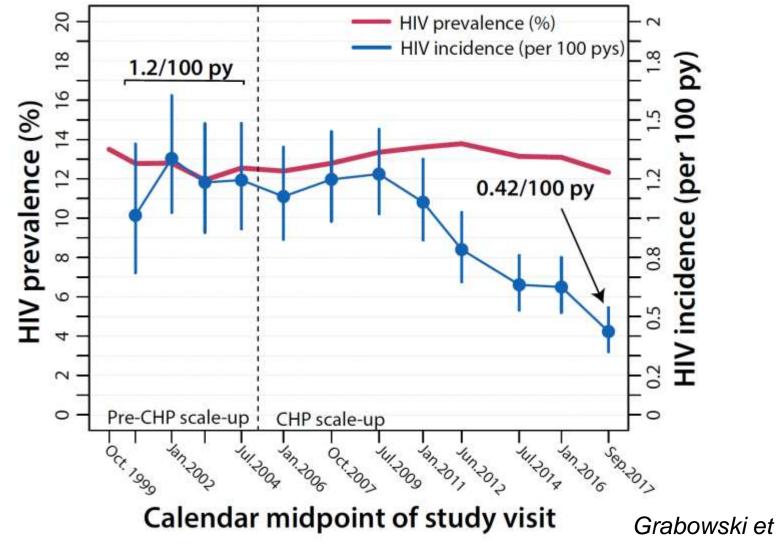
NUMBER OF NEW HIV INFECTIONS AND AIDS-RELATED DEATHS, EASTERN AND SOUTHERN AFRICA, 2000–2020



Source: UNAIDS epidemiological estimates, 2021 (https://aidsinfo.unaids.org/).

HIV incidence trends in Rakai, 1999-2017

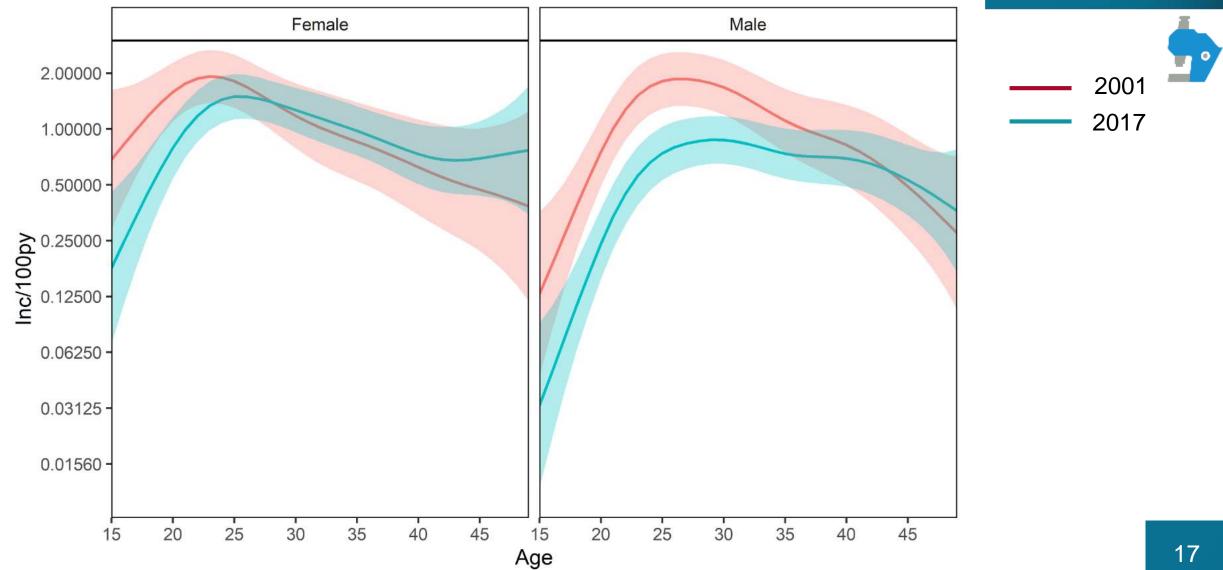




CHP=combination HIV prevention

Grabowski et al. NEJM. 2017 Grabowski et al. CROI. 2020

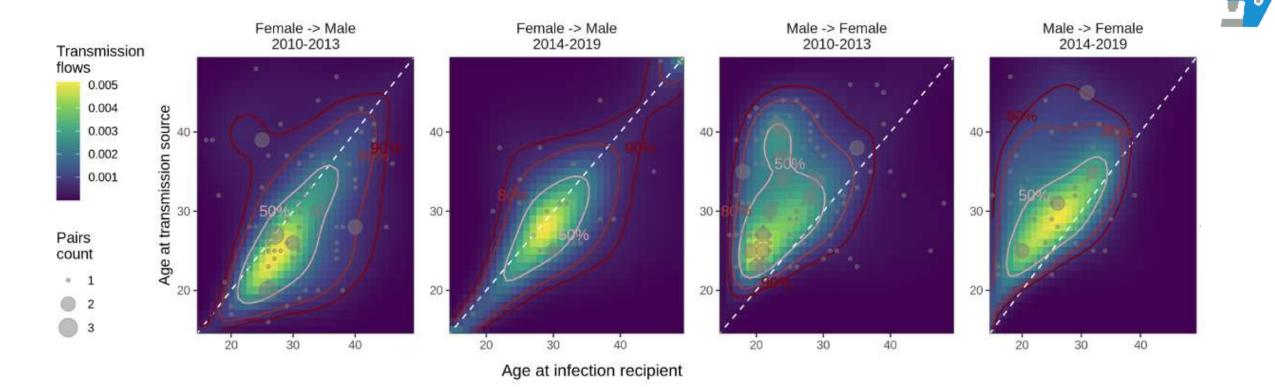
HIV incidence in Rakai by age, 2001 vs. 2017



HPTN

Prevention Trials Network

Shifting sources of transmission

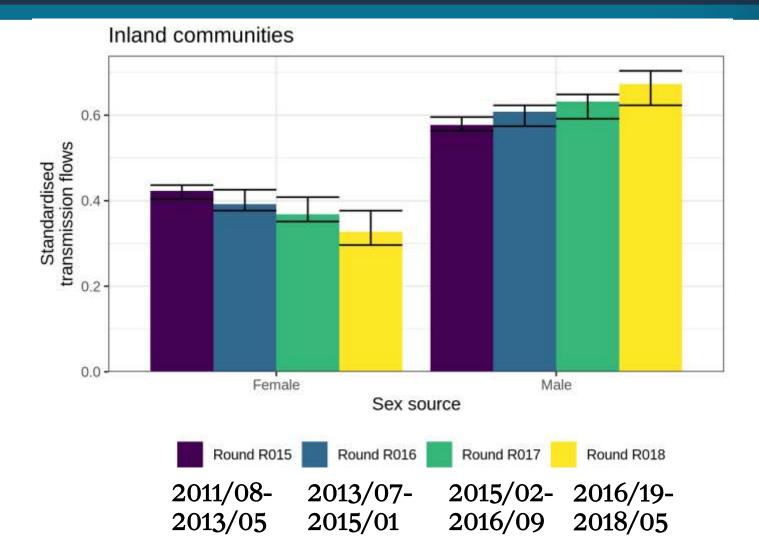


HPTN

HIV Prevention Trials Network

Increasingly male driven transmission flows

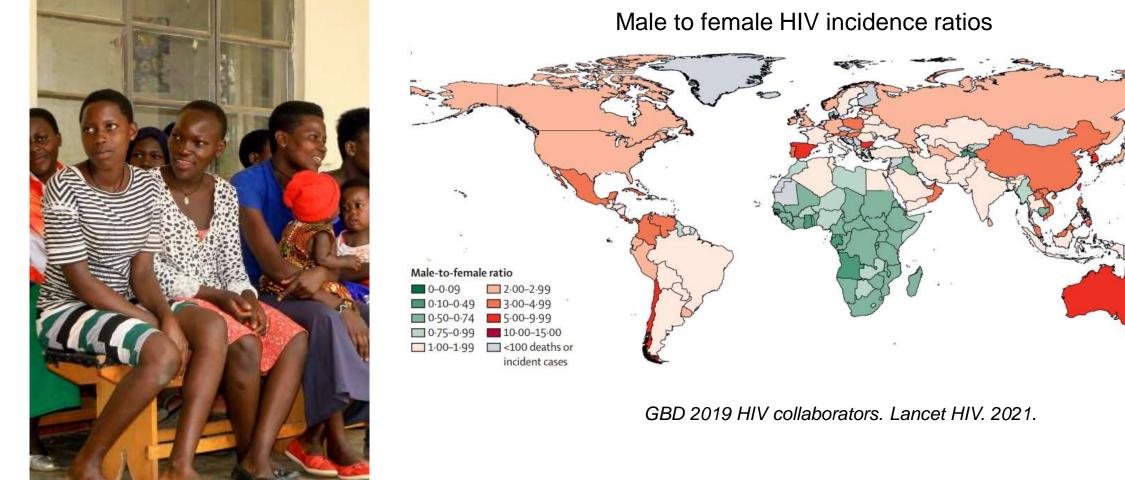






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- 1. Young, unsuppressed HIV-positive men, ages 25-34, are linked disproportionately to many transmission events.
- 2. Adolescent girls and young women, 15-24 years, are typically infected by men many years (5+) older than them.
- 3. As women age, their transmitting partners tend to be the same age or younger.
- 4. The HIV epidemic is aging, with incidence becoming more concentrated in older age groups, increasingly male driven transmission flows, and age-disparate partnerships contributing less to virus transmission.
- 5. Viral phylogenetics are a powerful tool for understanding HIV transmission patterns at a population-level.



Thank you!

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Acknowledgments



Rakai Health Sciences Program David Serwadda Fred Nalugoda Joseph Kagaayi * Godfrey Kigozi Gertrude Nakigozi Tom Lutalo Robert Ssekubugu* Grace Kigozi **Ronald Galiwango*** Anthony Ndyanabo

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Johns Hopkins School of Medicine Kate Grabowski Aaron Tobian Larry Chang

National Institute of Allergy and Infectious Diseases Thomas Quinn Andrew Redd Oliver Laeyendecker Steve Reynolds

Oxford University Christophe Fraser* Matthew Hall Chris Wymant Tanya Golubchik Locie Abeler Dorner* Rafael Sauter Francois Blanguart Will Probert



Modeling

Imperial College Rakai Health Science Program Staff and Study participants

Uganda Ministry of Health

National Institutes of Health

Centers for Disease Control

Bill and Melinda Gates Foundation



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