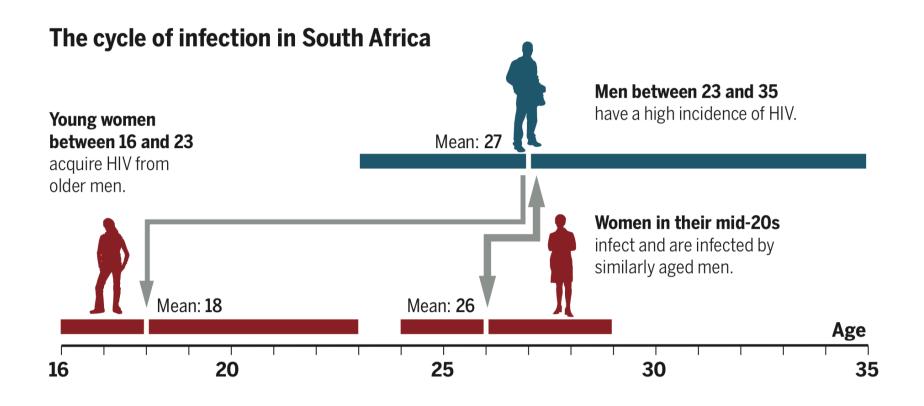
Quantifying HIV transmission by age from cross-sectional viral phylogenetic deep sequence data: a population-based study in Rakai, Uganda

Oliver Ratmann, Xiaoyue Xi, and contributions from Nicholas Bbosa

PANGEA webinar, April 2 2020







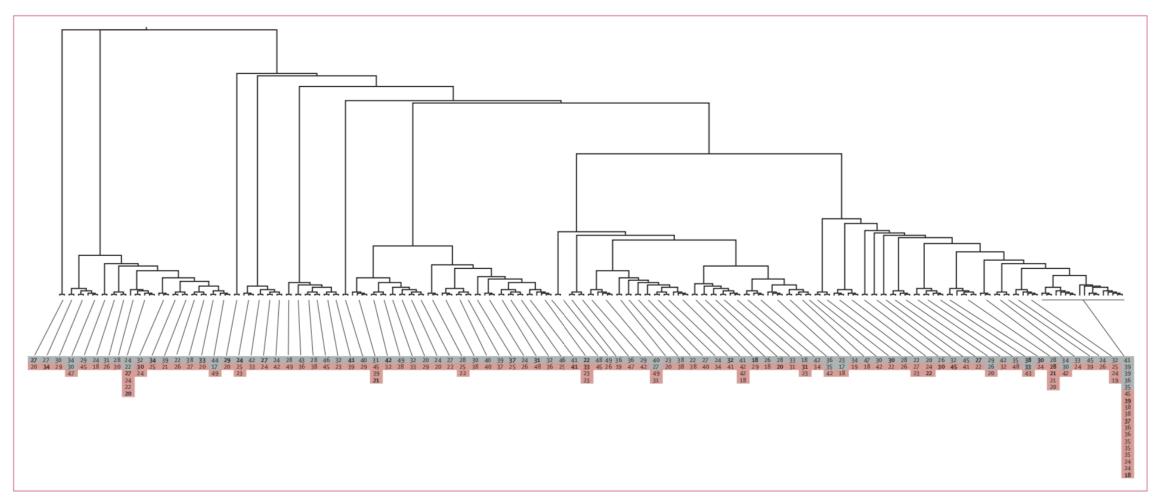


Figure 2: Maximum likelihood tree for 90 heterosexual transmission clusters

Clusters with a bootstrap support higher than 90% and whose sequences had an intraclade genetic distance of 4.5% or less. 123 women were linked to 103 men in the 90 heterosexual clusters. For better visualisation of the clusters, the tree is represented with proportional branch length transformation. The age (years) of the individuals in each transmission cluster is presented inside the boxes. Grey boxes represent men and red boxes represent women.

			Men (n=103)			
			<25 years (7·6%)	25–40 years (40·3%)	41-49 years (47·2%)	
_	Women (n=123)	<25 years (22·3%)	18	37	5	60
		25-40 years (59·8%)	13	58	21	92
		41-49 years (50·1%)	2	24	10	36
1	Total		33	119	36	188

Figure 3: All possible pairings from 90 clusters of men and women stratified by age group

The community-based HIV prevalence in each age group is shown in parentheses.

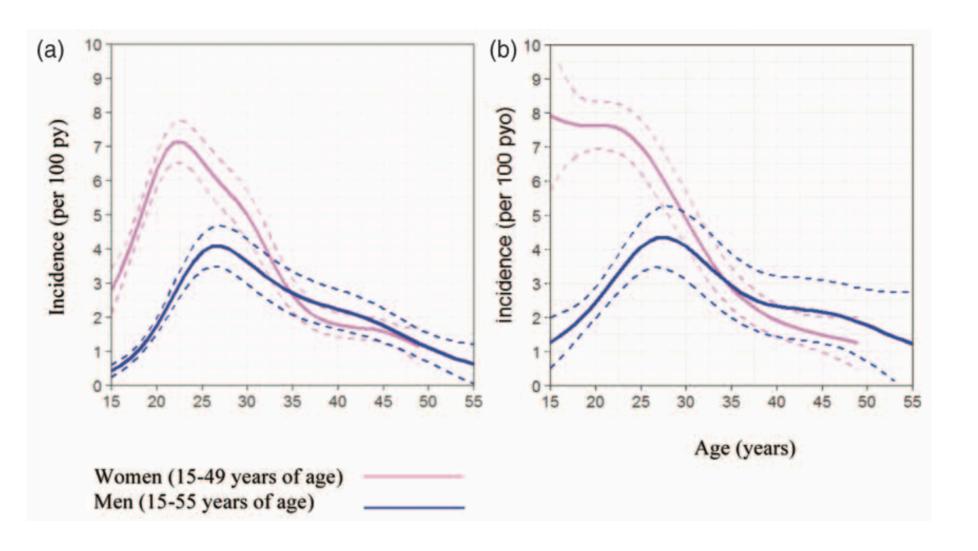
- F<25 linked with M25+: 42/60 = 70% (95% CI 57%-80%)
- F<25 linked with any M: average age difference 8.7 yrs
- Suggesting that such agediscordant pairings may be important driver of epidemic

Association HIV incidence with partner age, primarily Durban area, 2009-2012

	HIV Infections/ Person-Years	HIV Incidence* (95% CI)	Univariate Model† HR (95% CI)	Multivariable Model; HR (95% CI)
Primary analysis				
All participants	243/3343.57	7.27 (6.41 to 8.24)		
Primary partner >5 yrs older				
Yes	67/871.84	7.68 (6.05 to 9.76)	1.10 (0.82 to 1.45)	1.17 (0.88 to 1.56)
Do not know partner age	5/70.36	7.11 (2.96 to 17.07)	0.97 (0.40 to 2.37)	0.98 (0.40 to 2.39)
No	171/2401.37	7.12 (6.13 to 8.27)	1.00	1.00
Primary partner >10 yrs older				
Yes	10/160.43	6.23 (3.35 to 11.58)	0.87 (0.46 to 1.64)	1.01 (0.53 to 1.92)
Do not know partner age	5/70.36	7.11 (2.96 to 17.07)	0.94 (0.39 to 2.29)	0.94 (0.38 to 2.28)
No	228/3112.78	7.32 (6.43 to 8.34)	1.00	1.00
Participants <25 yrs	172/1877.54	9.16 (7.89 to 10.64)		
Primary partner >5 yrs older				
Yes	47/480.43	9.78 (7.35 to 13.02)	1.09 (0.78 to 1.53)	1.13 (0.80 to 1.59)
Do not know partner age	4/35.30	11.33 (4.25 to 30.19)	1.17 (0.43 to 3.18)	1.13 (0.41 to 3.09)
No	121/1361.81	8.89 (7.43 to 10.62)	1.00	1.00

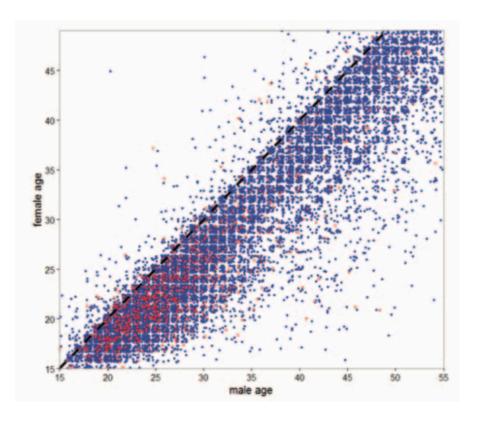
- VOICE trial, South African sites
- 3789 women, 2143 aged <25
- Suggesting agediscordant relationships may not be driver of epidemic among young women

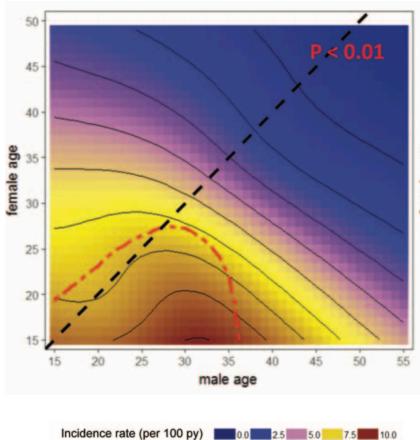
Figure from: Baltus et al. JAIDS 2015



- Africa Centre DSS, 2004-2015
- 10260 women, 7251 reporting age of most recent partner

Association HIV incidence with partner age, KZN, predicted at 2009



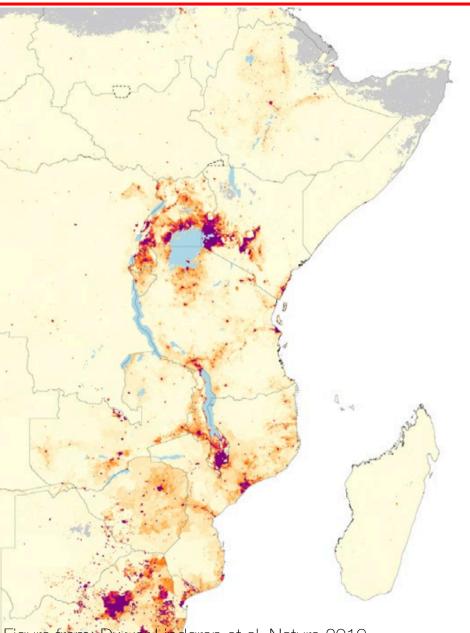


- Africa Centre DSS, 2004-2015
- Considering
 7251women reporting
 age of most recent
 partner

Study objective

- Estimate proportion of infections among women that are attributable to older men using deep-sequence data
- South-eastern Uganda, MRC/UVRI and Rakai

Convenience sample, MRC/UVRI, 2014-2017





Key

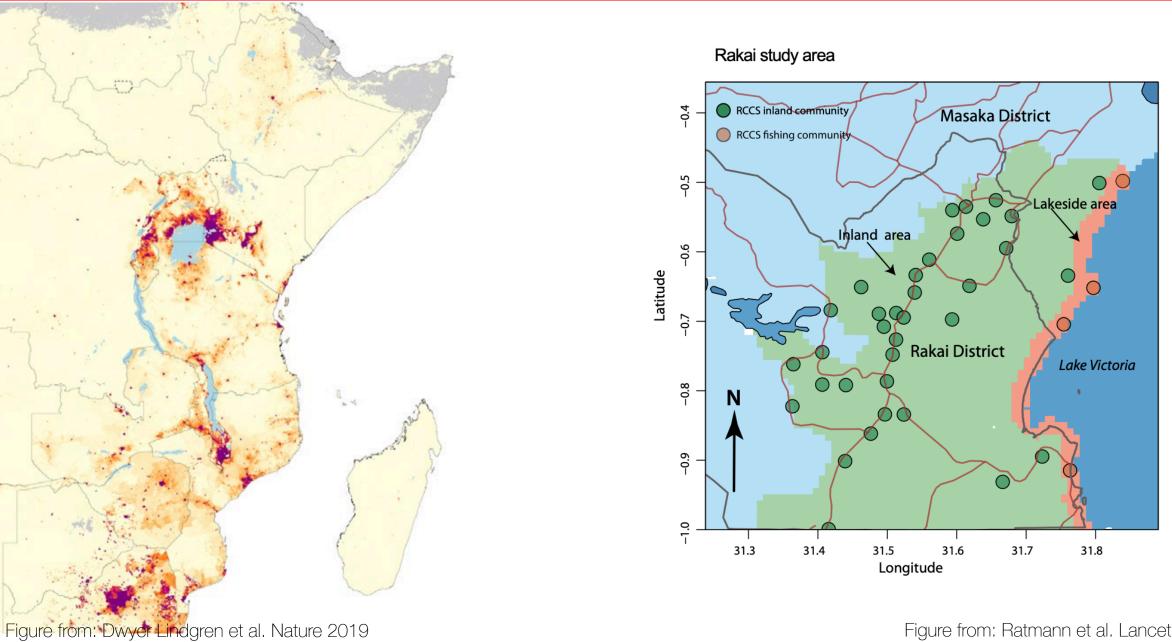
- Fisherfolk communities (Sites 1-10)
- General Population (Locations 1-6)

Convenience sample, MRC/UVRI, 2014-2017

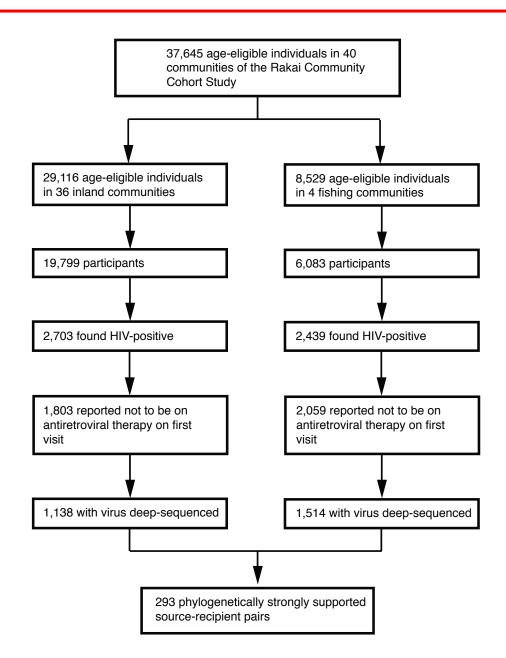
- 72 source-recipient pairs between men and women
- 22 pairs involving female recipient <25 at enrollment

	Estimated sources of infection among study participants, based on data excluding same-sex						
	pairs* (mean, 95% credibility interval of posterior density)						
	Men 18–24 years	Men 25–59 years	Women 18-24 years	Women 25-59 years			
Recipient							
Women 18-24	34.7% (17.1%–55.9%	65.3% (44.1%–82.9%)					
years							
Women 25-59	27.7% (14.1%–45.7%)	72.3% (54.3%–85.9%)					
vears							

Population-based deep-sequence data, Rakai, 2011/08/10-2015/01/30



Population-based deep-sequence data, Rakai, 2011/08/10-2015/01/30



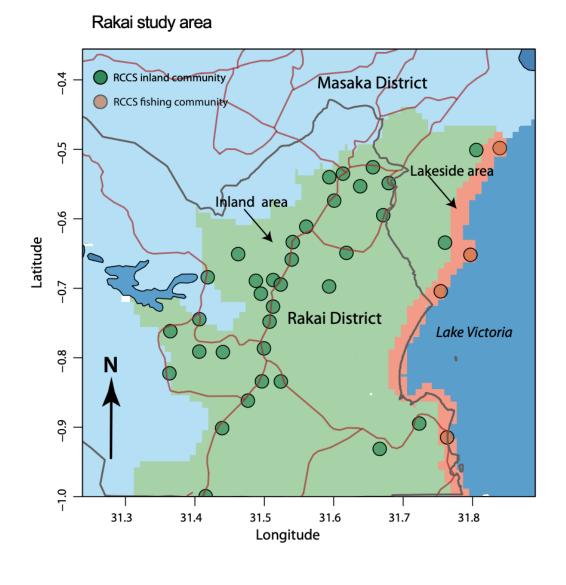
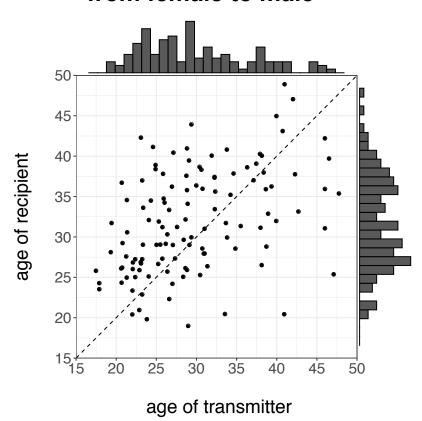


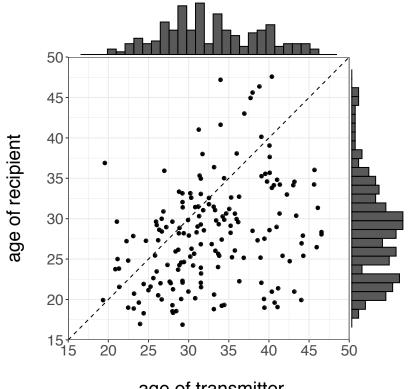
Figure from: Ratmann et al. Lancet HIV 2020



from male to female

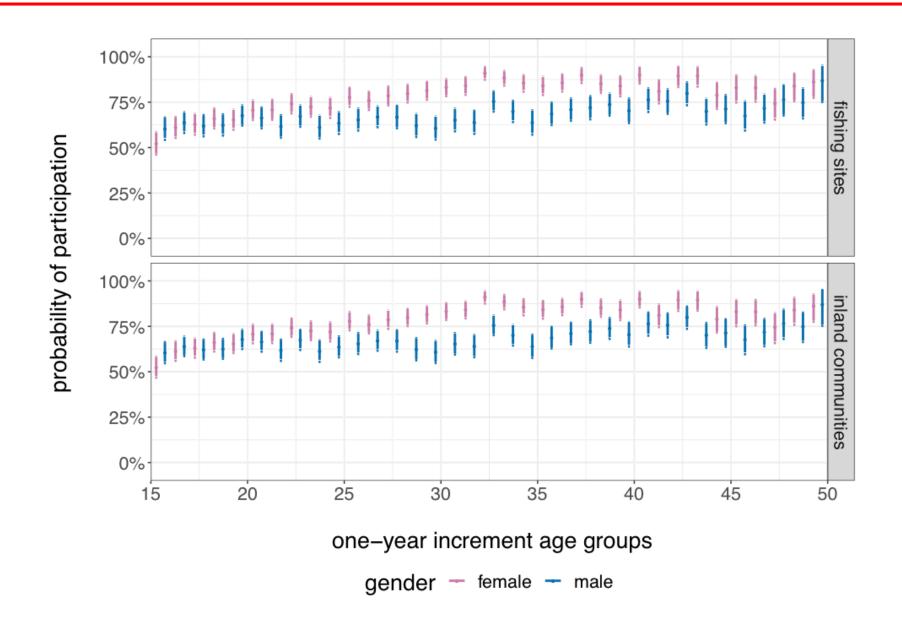
from female to male

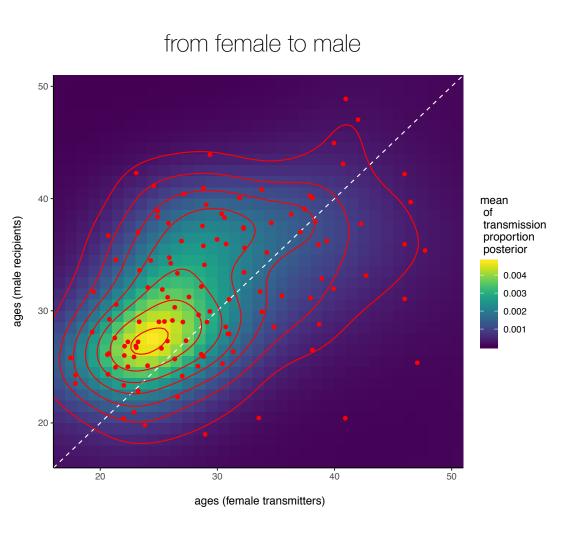


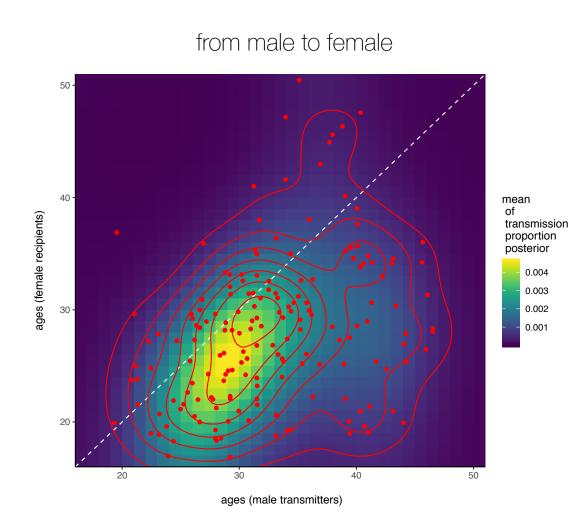


- age of transmitter
- n=120n=173

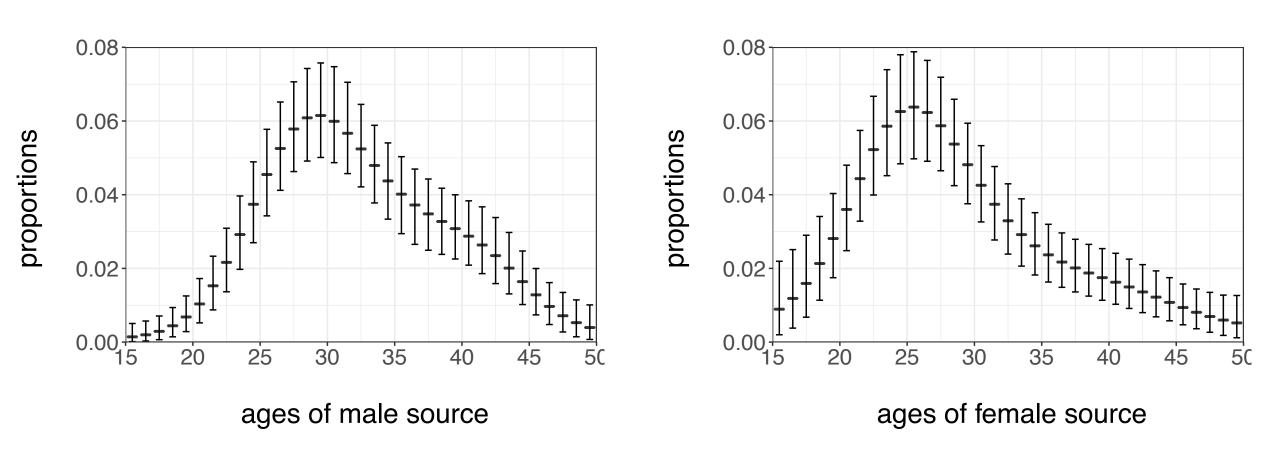
- 96 source-recipient pairs involving women <25
- 57 source-recipient pairs with female recipient <25



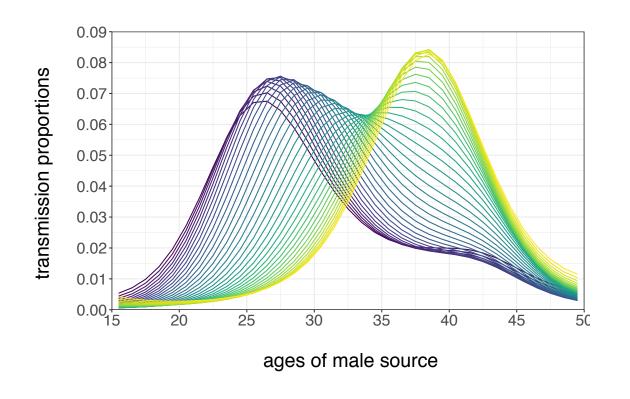


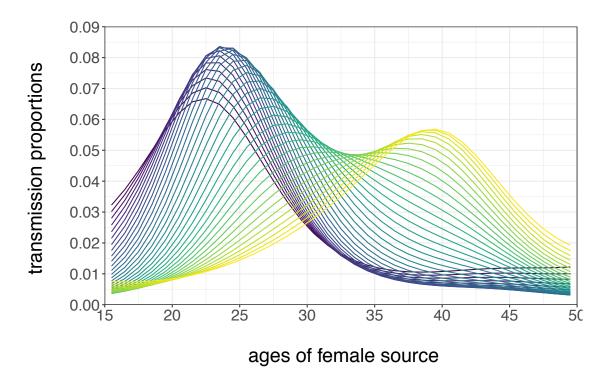


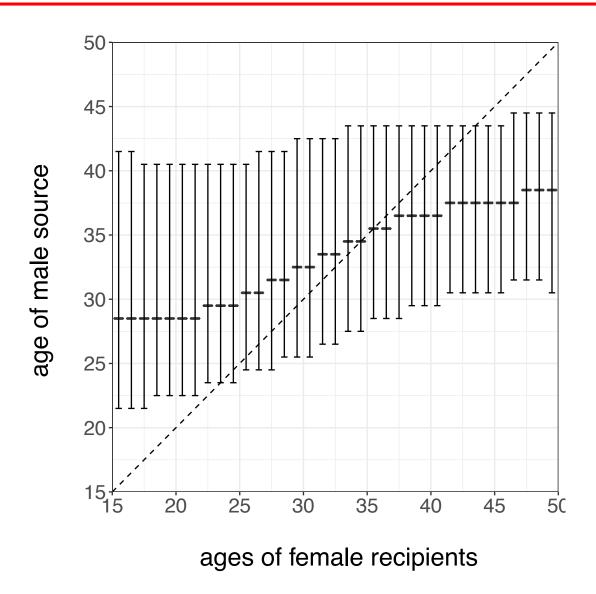
n=120 n=173

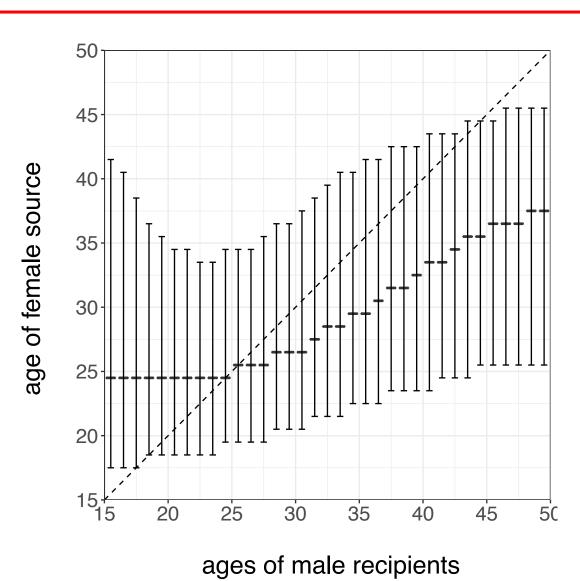


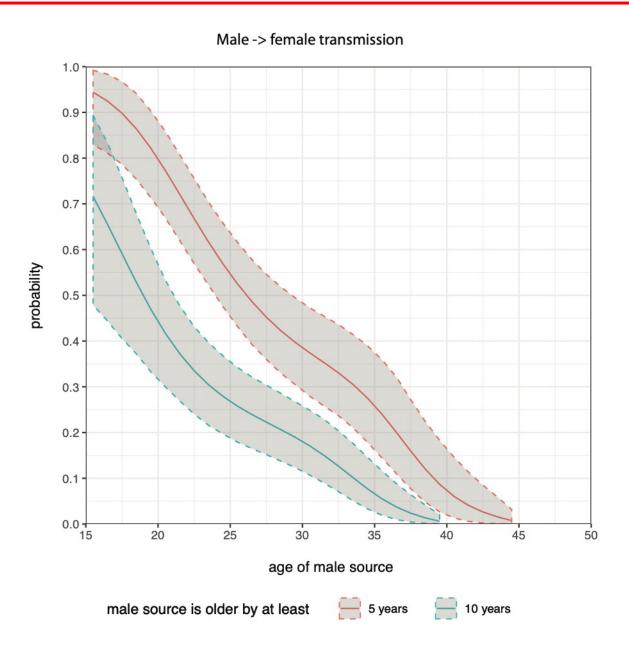
50% of infections in women attributed to men aged 26-37 50% of infections in men attributed to women aged 23-34







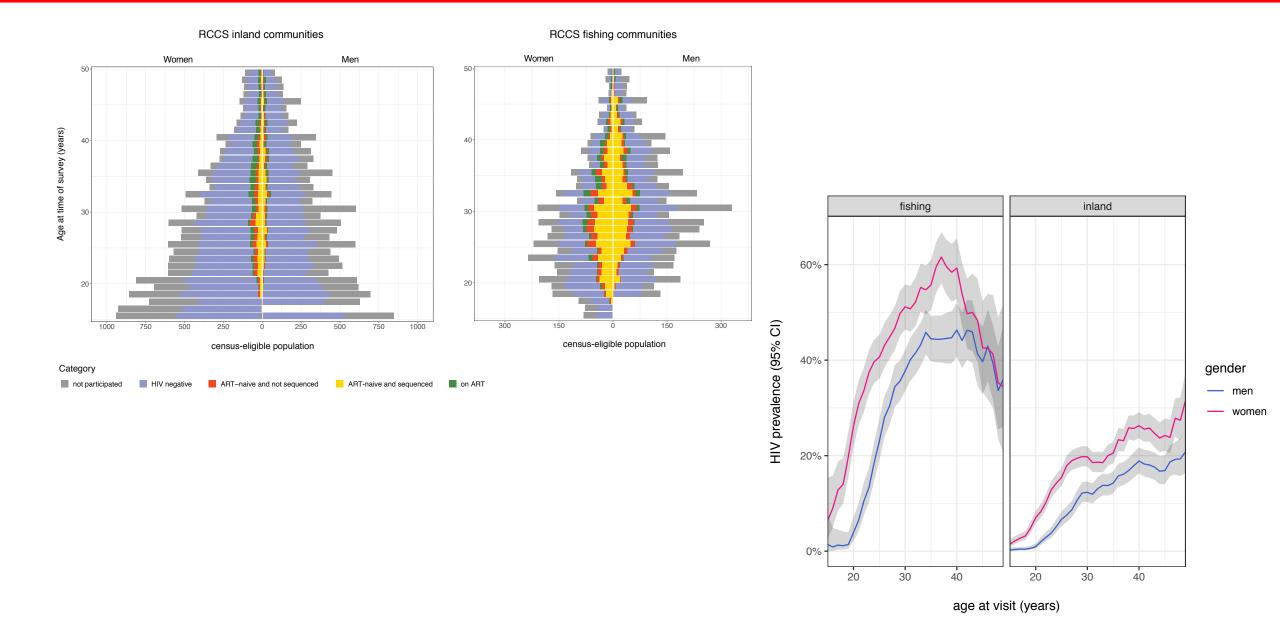




Summary of findings

- Overall, half of all infections among women were attributed to men aged 26-37, whereas half of all infection among men were attributed to women aged 23-34.
- However the mean age of the source case depended on the age of the recipient, and on gender. Women aged >35 were typically infected by younger men. Men aged >25 were typically infected by younger women.
- Most young women (aged 15-24) were infected by men who are >5 years older. An estimated 91% of women aged 15 were infected by men >5 years older, which declined to 73% at age 20, and 51% at age 25.

Youth bulge + rapid increases in prevalence among men and women



Rakai Health **Sciences Program**

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Johns Hopkins School of Medicine

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PANGEA-HIV-II consortium

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Rakai Health Science **Program Staff and Study** participants

MRC/UVRI Program Staff and Study participants









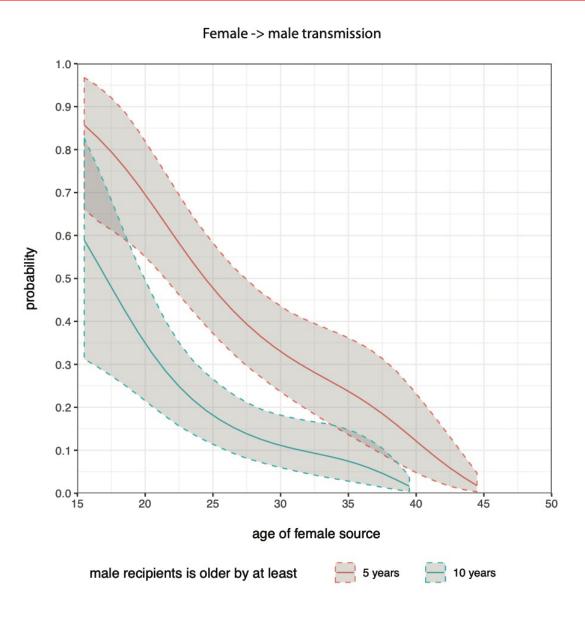






Thank you

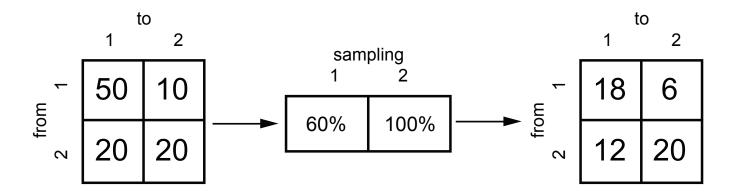
Contribution of age-discordant relationships, female -> male



An intuitive example (1)

actual transmissions

observed transmissions



An intuitive example (2)

