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HIV TYPE 1 GENETIC DIVERSITY, TRANSMISSION NETWORKS AND PHYLOGEOGRAPHY IN FISHING COMMUNITIES OF LAKE VICTORIA AND THE NEIGHBOURING GENERAL POPULATION IN UGANDA

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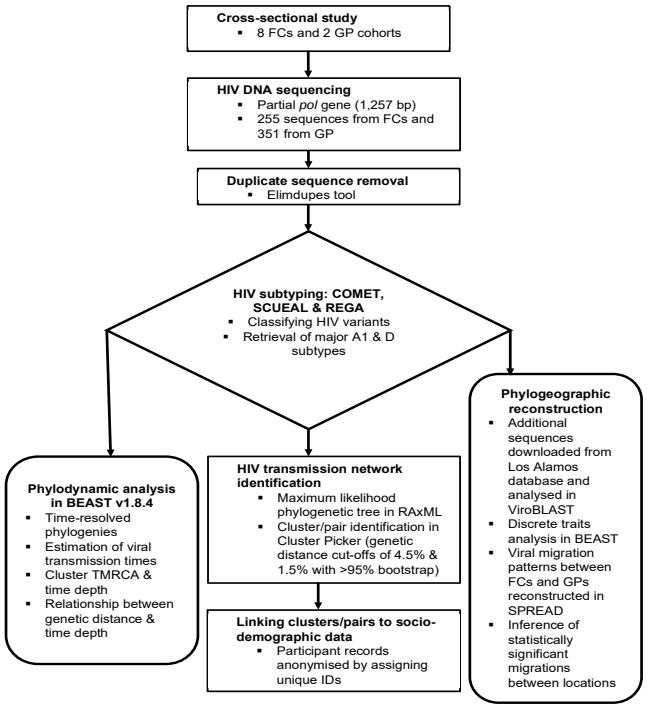
INTRODUCTION

- In fishing communities (FCs) in Uganda, HIV is at high prevalence (29% [1]) and incidence (6/100 PYAR [2]) relative to the general population (GP)
- Understanding transmission dynamics is critical for implementing targeted interventions to avert new infections
- We earlier found most transmissions were within FCs[3]
- Aim:

  Test the hypothesis that HIV-1 transmissions in FCs are isolated from networks in the GP, using viral sequences to

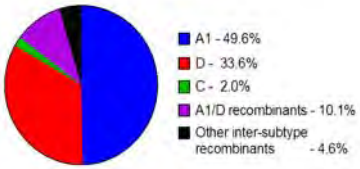
  1. identify HIV-1 transmission networks in FCs and GP
  2. reconstruct geospatial HIV migration patterns
  3. analyse dynamics of HIV-1 transmission

METHODS



RESULTS

HIV subtyping



- HIV-1 subtype A1 was the predominant subtype
- Populations did not differ significantly in subtype prevalence (paired student t-test p=0.2324; p-value>0.05, 95% CI -14.28-46.28)

HIV Subtype	FCs	GP	Total
Subtype A1	118 (46.3%)	177 (50.4%)	295
Subtype D	84 (32.9%)	121 (34.5%)	205
Subtype A1/D	28 (11%)	32 (9.1%)	60
Subtype C	3 (1.2%)	9 (2.6%)	12
Other recombinants	22 (8.6%)	12 (3.4%)	34
Total	**255**	**351**	**606**

Transmission networks

- 81 cases linked at max. pairwise genetic distance (GD) of 4.5%
  - as 35 pairs; 2 triplets and 1 cluster of 5
- 26 (32%) of these were linked at a GD cut-off of 1.5%
  - 13 pairs; 10 from the FCs and 3 from the GP
- More pairs at < 1.5% in FCs than GP but fewer above 1.5%

Number of pairs at GD thresholds of 1.5%-4.5% and <1.5%

Group	No. pairs@ 1.5%-4.5%	No. pairs <1.5%	Total
FC	3	10	13
GP	15	3	18
Total	**18**	**13**	**31**

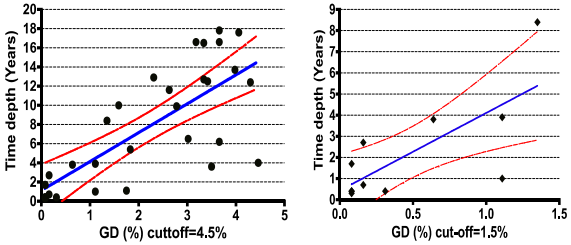
- At a GD cut-off of 4.5%, an additional 18 linked pure viral subtype pairs were found
- 15 were in the GP and only 3 in the FCs showing that any linkage found among individuals in the FCs is more likely to be recent (Fisher's exact test p = 0.0012)

RESULTS

Estimating viral transmission times from time-resolved phylogenies in BEAST

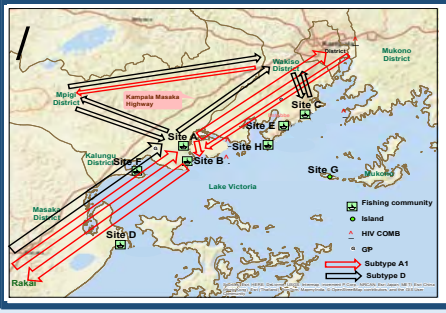
- The time depth (TD) in years for clusters/pairs provides an approximation to time of transmission
- Mean TD for 6 pairs from FCs was 0.53 years (range: 0.3-1) while that of 5 pairs from the GP was 4.1 years (range: 1-8)

Relationship between estimated viral time depth (TD) and genetic distance (GD)



- Th but with poor predictive power: for recent infection (PPV=29.7%; GD= 4.5% & 52.69%; GD=1.5%

Phylogeographic analysis



- There was strong support (BF>10) for viral migration between Rakai, Site A and Site B FCs and Kampala along the Kampala-Masaka highway
- Significant viral dispersal was observed between the FCs and the neighbouring GP

CONCLUSIONS

- Intensive sampling of FCs and the nearby GP has revealed many new transmission networks
- Surprisingly, FCs have more close networks than the GP, but fewer older ones (genetic distance >1.5%)
- Similarly, mean time depth for transmission pairs in was much shorter (7 months FCs vs 4 years GP)
  - Higher population mobility in the FCs may be responsible
- Short genetic distance (<1.5%) has surprisingly poor predictive power for recent infection (50%)
- Over longer time scales, HIV-1 transmission in FCs was not isolated from networks in the GP;
  - targeted interventions in the FCs could be extended to include the neighboring GP

ACKNOWLEDGEMENTS

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