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 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. Analyze dynamics of HIV-1 transmission.

**Methods**

- **Cross-sectional study:** 8 FCs and 2 GP cohorts.
- **HIV DNA sequencing:**
  - Partial pol gene (1.287 kb).
  - 255 sequences from FCs and 351 from GP.
- **Duplicate sequence removal:**
  - Elimdu tool.
- **Phylogenetic analysis in BEAST v1.8.4**
  - Time-resolved phylogenies.
- **Viral migration patterns between FCs and GPs** reconstructed in SPlREAD.
- **Linking clusters/pairs to socio-demographic data:**
  - Participant records anonymised by assigning unique IDs.

**Results**

- **HIV subtyping:**
  - HIV-1 subtype A1 was the predominant subtype.
  - Other subtypes shown.
  - No significant difference in subtype prevalence.
- **Transmission networks:**
  - 81 cases linked at max pairwise genetic distance (GD) of 4.5%.
  - Many new transmission networks revealed.
- **Number of pairs at GD thresholds:**
  - At 4.5%, 31 pairs were found.
  - 15 pairs were in the GP and 3 in the FCs.
- **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 others (genetic distance >1.5%).
  - Similar mean time depth for transmission pairs in FCs was much shorter (7 months FCs vs 4 years GP).
  - Higher population mobility in the FCs may be responsible.

**Phylogeographic analysis**

- **There was strong support** for viral migration between Rakai, Site A and Site B FCs and Kampala.
- **Significant viral dispersal** was observed between the FCs and the neighboring GP.

**Conclusions**

- Short genetic distance (<1.5%) has surprisingly poor predictive power for recent infection (50%).
- Over longer time scales, HIV-1 transmission was not isolated from networks in the GP.
- Targeted interventions in the FCs could be extended to include the neighboring GP.

**References**