HIV nearly full-genome sequencing is still unusual in sub-Saharan Africa. The PANGEA HIV project is generating HIV full-genomes in Ugandan sites, including [1]. Two HIV subtypes (A1 and D) co-circulate in Uganda, with the consequent emergence of many recombinants. We collected 485 contemporary (2009-2014) samples from three Ugandan populations:

- A rural cohort in Masaka district, SW Uganda
- Lake Victoria fishing communities (“fishing villages”), from Entebbe, Masaka district and Nasi island
- Female sex workers from Kampala and 53 historical samples taken in Kampala in 1986 from AIDS patients.

Illimuna MiSeq sequencing produced consensus sequences ±1kb for 609 samples (565 contemporary, 44 historical). Half of them (320, 52%) were full-genomes.

**Drug-resistance mutations & co-receptor tropism**

- Contemporary sequences had low DRM rates at PI-HIV (3.3%) and integrase (0.5%).
- Historical sequences had no significant DRM.
- Usage of C31AR co-receptor, which confers resistance to entry inhibitors, was rare in contemporary samples (0.5%) but frequent (47.4%) in historical ones, probably due to an advanced infection stage.

**Drug-resistance mutations**

- NRTI: d4T = 5.1% & 1.2% contemporary and historical.
- NNRTI: maraviroc = 2.4% & 1.7%.
- PI: darunavir = 1.3% & 1.3%.
- TR: VXCAVIAV = 0.5% & 0.5%.

**Conclusions**

- HIV A1/D recombinants dominate in Uganda. Their prevalence analysing full genomes was higher than in previous studies of partial sequences.
- We found low levels of resistance, as expected in low-income settings.
- We also obtained a low rate of phylogenetic clustering, with most clusters restricted to one population.
- However, almost 40% of the clusters involved geographical mobility.
- Methods for cluster detection need to be adapted and standardised to analyse full genomes.

**References**

5. Stanford University, HIV Drug Resistance Database. [http://hivdb.stanford.edu/]