Results from phylogenetic analysis of viral genomes have considerably improved our understanding of HIV epidemics. Although a relatively new scientific technique, HIV phylogenetics is increasingly used in HIV epidemiological research and clinical trials to identify sources and drivers of epidemics as well as to evaluate the impact of prevention interventions. More recently, the technique was successfully used to monitor HIV transmission hotspots in order to guide public health responses. In countries where HIV transmission and exposure is criminalized, forensic evidence has largely relied on this technique.

The utility of HIV phylogenetics analysis cannot, therefore, be underestimated.

However, the procedures involved, inferences made and conclusions drawn present potential ethical challenges and dilemmas as well as add new dimensions to traditional ethics dialogues. To a large extent, these issues have received minimal attention.

To hear more, you are cordially invited to a half-day interactive workshop, which seeks to explore and deliberate on key ethical issues associated with HIV phylogenetic analysis as applied in our understanding of HIV transmission dynamics, particularly in African settings. Keynote presentations will be followed by plenary discussions led by the speakers.

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