

Publication

Assessing the danger of self-sustained HIV epidemics in heterosexuals by population based phylogenetic cluster analysis

JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)**ID** 4267050**Author(s)** Turk, Teja; Bachmann, Nadine; Kadelka, Claus; Böni, Jürg; Yerly, Sabine; Aubert, Vincent; Klimkait, Thomas; Battegay, Manuel; Bernasconi, Enos; Calmy, Alexandra; Cavassini, Matthias; Furrer, Hansjakob; Hoffmann, Matthias; Günthard, Huldrych F.; Kouyos, Roger D.; Swiss HIV Cohort Study,**Author(s) at UniBasel** [Bucher, Heiner](#) ; [Klimkait, Thomas](#) ;**Year** 2017**Title** Assessing the danger of self-sustained HIV epidemics in heterosexuals by population based phylogenetic cluster analysis**Journal** eLife**Volume** 6**Pages / Article-Number** e28721**Mesh terms** Basic Reproduction Number; Cluster Analysis; Disease Transmission, Infectious; Epidemics; Female; HIV Infections, virology; Heterosexuality; Humans; Male; Models, Statistical; Molecular Epidemiology; Phylogeny; Switzerland, epidemiology

Assessing the danger of transition of HIV transmission from a concentrated to a generalized epidemic is of major importance for public health. In this study, we develop a phylogeny-based statistical approach to address this question. As a case study, we use this to investigate the trends and determinants of HIV transmission among Swiss heterosexuals. We extract the corresponding transmission clusters from a phylogenetic tree. To capture the incomplete sampling, the delayed introduction of imported infections to Switzerland, and potential factors associated with basic reproductive number R_0 , we extend the branching process model to infer transmission parameters. Overall, the R_0 is estimated to be 0.44 (95%-confidence interval 0.42-0.46) and it is decreasing by 11% per 10 years (4%-17%). Our findings indicate rather diminishing HIV transmission among Swiss heterosexuals far below the epidemic threshold. Generally, our approach allows to assess the danger of self-sustained epidemics from any viral sequence data.

Publisher eLife Sciences Publications**ISSN/ISBN** 2050-084X**URL** <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5650480/>**edoc-URL** <https://edoc.unibas.ch/62096/>**Full Text on edoc** No;**Digital Object Identifier DOI** 10.7554/eLife.28721**PubMed ID** <http://www.ncbi.nlm.nih.gov/pubmed/28895527>**ISI-Number** 000411487000001**Document type (ISI)** Journal Article