Paying more attention to HIV-1 recombinants among men who have sex with men–Author's reply

We thank Zhenzhou Wan and colleagues for their interest in our Article, wherein we estimated the global genetic diversity of HIV-1 in 2010–21 based on the largest data set collected to date, within the limitations described extensively in the Article.[1] A few studies included in our systematic review contained multiple datasets pertaining to different countries or time periods. However, no duplicate data were included in our analysis. Several methodological differences form the basis for the divergent distributions of HIV-1 variants reported by other researchers, such as an absence of transparency regarding the included studies, undisclosed genome segments and subtyping methods, a substantial portion of the samples being categorised as "unknown or other", and exclusion of subtypes D, F, G, H, and J from the time trend analysis.[2] Further, several regions that are known to harbour divergent subtype distributions (eg, eastern and southern Africa; south, east, and southeast Asia, and the Pacific) were combined without weighting of HIV-1 diversity estimates by country according to the number of people living with HIV in each country.[2] For example, southern Africa, Ethiopia, and India have a predominance (>90%) of HIV-1 subtype C and together account for approximately 46–47% of people living with HIV globally. Our Article reports a global proportion of subtype C of 47·1–50·4%, whereas the study by Williams and colleagues reports a global prevalence of subtype C of 23%, casting doubt on the validity of their methods and estimates.[1,2]

Global surveillance of HIV-1 diversity requires improvement in both generalised and concentrated HIV epidemics. Various key populations play important roles in different settings, and their associations with HIV-1 recombinants show spatiotemporal variations.[3] The sizes of key populations and spread of HIV infection within countries should be accounted for in the estimation of incidence and prevalence of HIV-1 variants.[4] Large sample sizes and recommended sampling strategies will increase external validity.[5] Standardised protocols and validated subtyping methods should be used to ensure internal validity. Near full-length HIV genome sequencing remains the gold standard for HIV subtyping; however, the implementation of near full-length HIV genome sequencing remains challenging in many settings. Complete HIV subtyping results should be reported according to the Strengthening the Reporting of Molecular Epidemiology for Infectious Diseases reporting guideline.[5]

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1 Nair M, Gettins L, Fuller M, Kirtley S, Hemelaar J. Global and regional genetic diversity of HIV-1 in 2010–21: systematic review and analysis of prevalence. *Lancet Microbe* 2024; **5:** 100912.
2 Williams A, Menon S, Crowe M, et al. Geographic and population distributions of human immunodeficiency virus (HIV)-1 and HIV-2 circulating subtypes: A systematic literature review and meta-analysis (2010–2021). *J Infect Dis* 2023; **228:** 1583–91.
3 Nchinda N, Elangovan R, Yun J, et al. Global associations of key populations with HIV-1 recombinants: a systematic review, global survey, and individual participant data meta-analysis. *Front Public Health* 2023; **11:** 1153638.
4 UNAIDS. Key populations atlas. https://kpatlas.unaids.org/dashboard (accessed Nov 26, 2024).
5 Field N, Cohen T, Struelens MJ, et al. Strengthening the Reporting of Molecular Epidemiology for Infectious Diseases (STROME-ID): an extension of the STROBE statement. *Lancet Infect Dis* 2014; **14:** 341–52.

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