

Association study for determinants of HIV-1 acquisition and viral set point in HIV-1 serodiscordant couples with quantified virus exposure.

[Lingappa JR](#), [Petrovski S](#), [Kahle E](#), [Fellay J](#), [Shianna K](#), [McElrath MJ](#), [Thomas KK](#), [Baeten JM](#), [Celum C](#), [Wald A](#), [de Bruyn G](#), [Mullins JI](#), [Nakku-Joloba E](#), [Farquhar C](#), [Essex M](#), [Donnell D](#), [Kiarie J](#), [Haynes B](#), [Goldstein D](#); [Partners in Prevention HSV/HIV Transmission Study Team](#).

Abstract

BACKGROUND: Host genetic factors may be important determinants of HIV-1 sexual acquisition. We performed a genome-wide association study (GWAS) for host genetic variants modifying HIV-1 acquisition and viral control in the context of a cohort of African HIV-1 serodiscordant heterosexual couples. To minimize misclassification of HIV-1 risk, we quantified HIV-1 exposure, using data including plasma HIV-1 concentrations, gender, and condom use.

METHODS: We matched couples without HIV-1 seroconversion to those with seroconversion by quantified HIV-1 exposure risk. Logistic regression of single nucleotide polymorphisms (SNPs) for 798 samples from 496 HIV-1 infected and 302 HIV-1 exposed, uninfected individuals was performed to identify factors associated with HIV-1 acquisition. In addition, a linear regression analysis was performed using SNP data from a subset ($n = 403$) of HIV-1 infected individuals to identify factors predicting plasma HIV-1 concentrations.

RESULTS: After correcting for multiple comparisons, no SNPs were significantly associated with HIV-1 infection status or plasma HIV-1 concentrations.

CONCLUSION: This GWAS controlling for HIV-1 exposure did not identify common host genotypes influencing HIV-1 acquisition. Alternative strategies, such as large-scale sequencing to identify low frequency variation, should be considered for identifying novel host genetic predictors of HIV-1 acquisition.