

1. **Oyugi JO**, Vouriot FC, Alimonti J, Wayne S, Luo M, Land AM, Ao Z, Yao X, Sekaly RP, Elliott LJ, Simonsen JN, Ball TB, Jaoko W, Kimani J, Plummer FA, Fowke KR. A Common CD4 Gene Variant Is Associated with an Increased Risk of HIV-1 Infection in Kenyan Female Commercial Sex Workers. *J Infect Dis.* 2009 May 1;199 (9):1327-1334.

Abstract

BACKGROUND:

It has been predicted that CD4 C868T, a novel CD4 single-nucleotide polymorphism (SNP) that has been found to be highly prevalent among Africans, changes the tertiary structure of CD4, which may alter susceptibility to human immunodeficiency virus (HIV) infection.

METHODS:

Participants were from a Kenyan cohort and included 87 uninfected and 277 HIV-1-infected individuals. DNA sequencing was used to determine CD4 genotype. A2.01 cells expressing similar levels of either wild-type CD4 or CD4-Trp240 as well as peripheral blood mononuclear cells from uninfected donors were infected with HIV-1(IIB) or a Kenyan primary HIV-1 isolate. HIV-1 p24 enzyme-linked immunosorbent assay was used to determine the outcome of infection.

RESULTS:

CD4 C868T was found to be significantly more prevalent among HIV-1-infected participants than among HIV-1-uninfected participants ($P = .002$), and C868T was associated with an increased incidence of HIV-1 infection as well ($P = .005$, log-rank test; $P = .009$, Wilcoxon test), with an odds ratio of 2.49 ($P = .009$). Both in vitro and ex vivo models demonstrated a significant association between CD4 C868T and susceptibility to HIV-1 infection ($P < .001$ and $P = .003$, respectively).

CONCLUSION:

Overall, the present study found a strong correlation between CD4 C868T and increased susceptibility to HIV-1 infection. Given the high prevalence of both HIV infection and CD4 C868T in African populations, the effect of this SNP on the epidemic in Africa could be dramatic.