

## **ABSTRACT**

### **BACKGROUND:**

HIV-1 subtype C has emerged as the most prevalent strain of HIV-1 worldwide, leading to speculation that subtype C may be more transmissible than other subtypes. We compared the risk of HIV-1 transmission for subtype C versus non-C subtypes (A, D, G and recombinant forms) among heterosexual African HIV-1 serodiscordant couples.

### **METHODS:**

We conducted a nested case-control analysis using data from two prospective cohort studies of heterosexual HIV-1 serodiscordant couples from six countries in eastern and southern Africa. Cases (N=121) included incident HIV-1 transmissions that were established as linked within the serodiscordant partnership by viral sequencing; controls (N=501) were nontransmitting HIV-1-infected partners. Subtype was determined for partial env and gag genes. Multiple logistic regression controlled for age and gender of the HIV-1-infected partner and self-reported unprotected sex. Plasma and genital HIV-1 RNA concentrations were compared between subtype C and non-C subtypes using generalized estimating equations.

### **RESULTS:**

HIV-1 subtype C was not associated with increased risk of HIV-1 transmission compared with non-C subtypes: env adjusted odds ratio (adjOR) 1.14 [95% confidence interval (CI) 0.74-1.75, P=0.6] and gag adjOR 0.98 (95% CI 0.63-1.52, P=0.9). Plasma and genital HIV-1 RNA levels did not differ significantly for subtype C versus non-C.

### **CONCLUSION:**

In a geographically diverse population of heterosexual African HIV-1 serodiscordant couples, subtype C was not associated with greater risk of HIV-1 transmission compared with non-C subtypes, arguing against the hypothesis that subtype C is more transmissible compared with other common subtypes.