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## **Characterizing the HIV-1 Proviral Reservoir in ART-treated Opioid Users**

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**Background:** People who inject drugs (PWID) are among those with the highest risk for HIV-1 infection and substantially contribute to new infections. There has been considerable progress in understanding the HIV-1 proviral reservoir, yet this understanding has not been extended to PWID.

**Methods:** HIV-1 infected study participants who use opioids (n=9), virally suppressed with ART (median=7 years), were recruited. DNA was subject to single-genome next generation sequencing of near full-length HIV-1. Integration sites were investigated by matched integration site and proviral sequencing (MIP-Seq). HIV patients (n=9) without opioid use were matched based on years of viral suppression.

**Results:** 724 HIV-1 proviral sequences (8% genome-intact), were analyzed in opioid users, while 351 (10% intact) were observed in the comparison cohort. The absolute frequency of intact sequences was similar between both groups (1.88 intact/10<sup>6</sup> PBMC vs 1.99 intact/10<sup>6</sup> PBMC). Thus far, 8 intact sites (4 unique, with 2 clonal clusters of 2 and 4 sequences) and 3 defective sites (2 unique, with one clonal cluster of 2 sequences) were obtained from four opioid users. The sites included 1 intact clone (4 sequence cluster) in a non-genic region, while all other sites occurred in the introns of protein coding regions, predominantly in the opposite orientation of the host genes.

**Conclusion:** Our current data indicate no significant difference between the reservoir composition of ART-suppressed patients who use opioids and those who do not. Our data suggest that opioid users should not be excluded from HIV eradication and cure research.