

The 29th Annual Canadian Conference on HIV/AIDS Research Le 29e Congrès annuel canadien de recherche sur le VIH/sida

Session: **BS2**: Friday May 1 – 15:00:17:00 – HIV Latency and Viral Reservoirs

Track: Basic Sciences

Subject: HIV Latency and Viral Reservoirs

Presentation Type: Oral

Title of Abstract: **Characterization of HIV reservoirs in multiple tissues collected post-mortem from two individuals on suppressive ART**

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Abstract

Background: The identification of tissues in which HIV persists during ART is a prerequisite to the development of efficient eradication strategies. Using tissues collected *post-mortem* from two participants on ART who generously gave their body to HIV cure research, we quantified and performed genotypic analysis of infected cells in multiple anatomical sites.

Methods: Participant #1 was enrolled in Ottawa, on ART for 11 years and requested medical assisted death at the age of 67. Participant #2, a 68 years old man from Edmonton, died from B cell lymphoma. A total of 15 tissues including multiple lymph nodes (LNs), gut, liver, spleen, brain and testes were snap frozen in liquid nitrogen. HIV DNA and cell-associated gag RNA were quantified by qPCR. Near-full length HIV sequencing was performed using a modified FLIPS assay.

Results: Participant #1 displayed highest levels of HIV DNA in LNs. HIV transcripts were detected at high levels in LNs and lungs and rarely in other tissues. Proviruses amplified from lungs, colon, rectum, spleen and LNs were all defective. In participants #2, liver and spleen displayed the highest amounts of HIV DNA and HIV transcripts. While most proviruses retrieved from lungs, duodenum, jejunum and LNs were defective, all 5 HIV sequences derived from the spleen were intact. A few identical defective proviruses were found in multiple tissues in both participants.

Conclusion: Although detected in nearly all tissues analyzed, HIV DNA and RNA were more abundant in LNs, spleen, lungs and liver. The majority of the proviruses were defective and some clonally expanded genomes were detected in multiple organs. In one participant, intact proviruses

were primarily detected in the spleen. Our study reveals a large diversity in the frequency of infected cells in different tissues, and highlights interindividual differences in reservoir locations during long-term ART.