Retrovirology

Poster presentation

Repopulation of the Vg2Vd2 Repertoire After Prolonged HAART

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HIV infection leads to a rapid and complete loss of cells expressing the Vg2-Jg1.2 chain of the gd T cell receptor. This cell subset is generally measured by spectratyping and is defined as Vg2 chains encoded by sequences between 990 and 996 nucleotides in length. In a previous cross-sectional study (Bordon, et al. JID 189:1482, 2004) we demonstrated a relationship between the duration of therapy and recovery of Vg2 sequences between 990–996 nucleotides. Now using longitudinal specimens and extensive analysis of Vg2 chains by DNA sequencing, we show that prolonged HAART does indeed reconstitute the repertoire of 990–996 length Vg2 chains, but they are no longer restricted to using the Jg1.2 segment. Instead, we observe Jg1.1 and Jg2.3 sequences with unusual N regions sequences that are rare in healthy individuals. In this unique example, we show that HIV infection exhausts the population of T cell clones capable of expressing the Vg2-Jg1.2 chain, but that strong selection for Vg2 chains in the range of 990–996 nucleotides, forces the expansion of a previously minor population. Within the Vg2Vd2 T cell population, prolonged therapy enabled a functional reconstitution of the Vg2 repertoire. Even though repertoire selection for Vg2 is largely independent of thymic function, there was no evidence that T cell clones could be replaced from hematopoietic stem cells, despite the continued strong selection for Vg2 chains of the appropriate length.