

26. HIV-1 Mediated Insertional Mutagenesis Increase the Persistence of Infected T Cells in Patients Under ART by Triggering Their Differentiation Into Long Lived T-Regulatory and T-Central Memory Cells

Daniela Cesana,¹ Francesca R. Santoni de Sio,¹ Laura Rudilosso,¹ Pierangela Gallina,¹ Andrea Calabria,¹ Laura Passerini,¹ Silvia Nozza,² Elisa Vicenzi,³ Guido Poli,³ Giuseppe Tambussi,² Eugenio Montini.¹

¹San Raffaele Telethon Institute for Gene Therapy (HSR-TIGET), San Raffaele Scientific Institute, Milan, Italy; ²Department of Infectious Diseases, San Raffaele Scientific Institute, Milan, Italy; ³AIDS Immunopathogenesis Unit, San Raffaele Scientific Institute, Milan, Italy.

It has been recently suggested that HIV-1 by integrating near cancer-associated genes could promote the expansion and persistence of infected cells in patients under Anti Retroviral Therapy (ART). However, the molecular mechanism/s of insertional mutagenesis used and the physiological impact on the cells harboring these integrations are completely unknown.

Here, we found that in the peripheral blood mononuclear cells from 54 HIV-1 infected patients under ART, BACH2 and STAT5B were targeted by a significant number of integrations compared to other lentiviral integration datasets ($p < 0.0001$) and with the same orientation of gene transcription. Furthermore, we observed that in the blood of 34% of HIV-1 patients under ART (30/87) there are cell clones expressing aberrant chimeric transcripts containing viral sequences fused to the first protein coding exon of BACH2 or STAT5B and predicted to encode for unaltered full-length proteins. However, it is unlikely that the ectopic expression of these transcription factors in T cells per se would trigger cell transformation. Indeed, accordingly with their roles in the regulation of T-cell identity and homeostasis, forced expression of STAT5B and BACH2 in naive CD4+ T-cells significantly skewed their differentiation towards functional T-regulatory cells with a marked immunosuppressive potential. Moreover, STAT5B ectopic expression promoted the IL-2 independent proliferation of T-regulatory cells that was however blocked by TGFB treatment, indicating that these cells are able to respond to external differentiating cues.

Importantly, tracking the expression of HIV-1/STAT5B transcripts in T cell subpopulations and monocytes purified from the blood of patients under ART, we found that, in all patients tested (N=6), chimeric mRNAs were present only in T-regulatory and T-central memory cells but not in CD8+ T-cells, T naïve, T stem cell memory, T effector memory nor monocytes.

Our findings provide novel evidence that HIV-1 takes advantage of insertional mutagenesis to favor its persistence in the host by activating STAT5B and possibly BACH2. However, the selective advantage conferred by these integrations does not involve T-cell transformation but rather their differentiation into functional T-regulatory and T-central memory cells which are long lived, potentially able to diminish the immune surveillance against infected cells thus favoring the escape from the immune system and long-term viral persistence.

Hence, new targeted therapies aimed at interfering with BACH2 and STAT5B regulated pathways could provide the general means for the immunological re-sensitization towards HIV-1 infected cells to reduce long lived cellular reservoirs and the eradication of the viral infection in HIV-1 patients.

27. Aberrant Expression of the Stem Cell microRNA-126 Induces B Cell Malignancy

Silvia Nucera,¹ Francesco Boccalatte,¹ Andrea Calabria,¹ Tiziana Plati,¹ Cristiana Fanciullo,¹ Jose Manteiga,⁴ Fabrizio Benedicenti,¹ Fabio Ciceri,² Maurilio Ponzoni,³ Eugenio Montini,¹ Luigi Naldini,¹ Bernhard Gentner.^{1,3}

¹Division of Regenerative Medicine, Stem Cells and Gene Therapy, San Raffaele Telethon Institute for Gene Therapy, Milano, Italy; ²Department of Hematology and Stem Cell Transplantation, San Raffaele, Milano, Italy; ³Department of Pathology, San Raffaele, Milano, Italy; ⁴Department of Functional Genomics, Vita Salute San Raffaele university, Milano, Italy.

MicroRNAs are essential regulators of normal and malignant hematopoiesis. miRNAs are relevant for gene therapy, since they can be exploited to fine-tune the expression profile of vector constructs or to alter viral tropism (Gentner&Naldini, 2012). We exploited the hematopoietic stem cell (HSC) specific expression of miR-126 to de-target transgene expression from primitive compartment (Gentner et al, 2010; Chiriaco et al, 2014; Escobar et al, 2014) and described the function of miR-126 in HSC where it regulates the balance between quiescence and self-renewal (Lechman et al, 2012). We here report a novel role for miR-126 in the induction and maintenance of high-grade B cell malignancies. By ectopically expressing miR-126 in transplanted BM cells, we observed that up to 60% of mice (n=71) developed B cell malignancies. LV insertion site (IS) analysis revealed that all tumors were monoclonal. We then tracked back leukemic clone to different hematopoietic lineages prospectively purified from the mice 2-6 months before disease onset. IS sharing between normal lineages and leukemic clone suggests stem or multipotent progenitor cell as origin for most tumors. Importantly, we show that miR-126 is the direct cause of genesis and maintenance of leukemia, since leukemogenesis is abolished when miRNA expression is inhibited by doxycycline (doxy) using a tetracycline-repressible miR-126 cassette, and established symptomatic leukemia completely regresses when miR-126 is switched off by doxy through induction of apoptosis. Transcriptional profiling indicated that miR-126 regulates multiple genes in p53 pathway both in murine blasts and in normal human CD34+ cells. Previous work suggested expression of miR-126 in acute lymphoblastic leukemia (ALL) and germinal center lymphoma. To further establish the relevance of miR-126 in human disease, we measured miR-126 expression in blasts from 16 adult patients with ALL. miR-126 was highly expressed in most studied ALL cases (Phil+: n=11, Phil-: n=5), at similar levels as CD34+ cells. We then down-regulated miR-126 in primary blasts from human B-ALL patients (n=5), and we observed increased apoptosis and impaired engraftment in xenograft models after primary and secondary transplantation (miR-126/KD: n=32 mice; Ctrl: n=37 mice), demonstrating the relevance of miR-126 in human B-ALL. In conclusion, we present a novel spontaneous mouse model for high grade B cell malignancies which are addicted to miR-126 expression, provide insight into the dynamic process of leukemogenesis by clonal IS tracking and unveil key tumor signaling pathways controlled by miR-126. Down-regulation of miR-126 could be exploited as therapeutic strategy in ALL, since it would deplete leukemic cells while expanding normal HSC, two ways to restore normal hematopoiesis.