

Expression of human endogenous retroviruses and associated transcripts in Hodgkin lymphoma cells

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Introduction

During human evolution, germline infections by retroviruses have repeatedly occurred, integrating viral DNA into the host genome. As a result, the human genome consists of approximately 8% human endogenous retroviruses (HERV). Although most of this viral DNA is defective due to mutations, there are sequences with intact open reading frames for the generation of viral transcripts and proteins. In Hodgkin lymphoma (HL) the activation of HERV loci and expression of related transcripts has been observed.

Methods

In order to characterize HL-associated HERV sequences that might play a role in HL biology we analyzed cDNA libraries, DNA microarray data and RNA sequencing data from HL cell lines. With different molecular-biological and computational approaches [1-4] we identified expressed HERV loci that might be relevant for the origin of HL.

Results

We observed increased transcriptional activity of several HERV related sequences in HL cell lines. Among these sequences, we discovered a new HERV-related transcript derived from the chromosomal region immediately upstream of the colony stimulating factor 1 (CSF1) region. The first exon of this Transcript From HL Cells (THOLE) is part of a member of the HUERS-P1/LTR8 family of endogenous retroviruses. High expression of THOLE was observed only in HL cell lines with an exceptionally high expression in the cell line L-1236.

Conclusion

The expression of THOLE in L-1236 cell is an example for HERV/LTR-associated gene expression in HL. The influence of HERV/LTR-associated transcripts on gene expression might explain the characteristic phenotype of human HL and requires further investigations.

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Affix**References**

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