From sketches of the HERV transcriptome landscape to the clinical evidence of HERV-H specific retroviruses expression in colorectal carcinoma.

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The human genome contains 25,000 genes but also 200,000 endogenous retroviral sequences (HERV) integrated during the evolution and which are nowadays organized into complex multicopy families. Using custom microarrays in Affymetrix format and a panel of normal and tumor tissues, we proposed a first view of the HERV transcriptome. We also showed that the HERV transcriptome follows tropism rules and is sensitive to the state of cell differentiation. In addition, we identified a set of HERV-H loci expressed in colorectal carcinomas (CRC). We sought to validate the microarray findings by characterizing deeply HERV-H reactivations in clinical samples of CRC and integrating expression profiles, molecular patterns as well as clinical data. Expression of several HERV-H loci was analyzed by qRT-PCR in a large cohort of clinical samples from several centers encompassing CRC (n=171), matched normal tissues (n=160), adenomas (n=21) and metastases (n=16). HERV-H expression strongly correlated with microsatellite instability and was maintained throughout disease progression.