

LINE-1 activity and regulation in cancer

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1. ABSTRACT

LINE-1 retrotransposons are ubiquitous genetic elements interspersed within the primary nuclear genome of modern day humans. Although shorter LINE-1-derived sequences occupy nearly one-in-five nucleotides of our genome, we are just beginning to appreciate the link between these important genetic elements and cancer, perhaps the most well-studied major degenerative disorder affecting humanity today. Herein, I summarize empirical observations linking LINE-1 to tumorigenesis. The work is organized into three major parts. First, I provide an overview of LINE-1 activity in cancer; highlighting major features of LINE-1 life-cycle such as: promoter methylation, transcription, translation, and retrotransposition. Second, I discuss three genetic pathways - epigenetic regulation, interferon signaling, and genome integrity – as they relate to LINE-1 regulation in cancer. Finally, I review most recent body of work linking LINE-1 as not only a diagnostic cancer biomarker, but also a potential therapeutic target.

2. INTRODUCTION

Causal relationships between cancer-related phenotypes and underlying genotype have traditionally been studied using both genetic engineering and epidemiological studies. Because there are likely a couple of hundred retrotransposition-competent active LINE-1 retrotransposons in our genome (1; 2) systematic inactivation of LINE-1 by gene knockout experiments have not been attempted

to date. Given this limitation, epidemiologic studies do show a possible putative role of LINE-1 in cancer; a recent review on the topic finds that there is some evidence linking LINE-1 expression to tumorigenesis in several major human cancer types (3; 4). Of note, for an authoritative recent review on mobile DNA in various diseases, not just cancer, the readership is referred to (5).

To date, 1,057 articles focusing on LINE-1 retrotransposons and cancer are available on Pubmed archive. Of those, I identified and manually curated 35 articles focusing on experimental evidence examining some aspect of LINE-1 biology in cancer. Because of widespread availability of bisulfite-treated DNA-based assays in clinical research, vast majority of published reports are studies focusing on LINE-1 promoter hypomethylation as a proxy biomarker for genome-wide DNA hypomethylation, which is in itself a major hallmark of cancer. Of note, LINE-1 promoter-based studies have recently been reviewed in detail here (6). To arrive at a short list of 35 articles, I asked the following three questions: “Is the body of work contributing to mechanistic insight rather than simply reporting LINE-1 as a cancer biomarker?”, “What are the genes that likely modulate LINE-1 activation in cancer?”, and “Is there any evidence that LINE-1 targeting provides putative therapeutic benefit?”. Small portion, or 9 out of 35 articles, link LINE-1 expression in cancer to a potpourri collection of unique empirical observations, such as: micronuclei formation (7), LINE-1

as pre-diagnostic biomarker within circulating tumor cells/tumor DNA (8; 9; 10), gene expression profiles linked to LINE-1 expression (11), putative mechanism of LINE-1-mediated cellular transformation (12; 13), as well as induction of apoptosis and proliferation following LINE-1 expression in cancer (14; 15). To my mind, these nine studies represent preliminary discovery-based work that may prove to be of interest in the future.

3. ON LINE-1 TRANSCRIPTIONAL ACTIVATION IN CANCER

Recent seminal work by Scott *et al.*, 2016, discovered and documented the actual mechanism of how LINE-1 retrotransposon transcriptional activation can drive, at least in part, colorectal carcinoma (16). Studying only the second reported case of *APC* inactivation by LINE-1 retrotransposition, the authors revealed that LINE-1 insertion in one *APC* allele complements traditional single nucleotide variant-mediated inactivation of the other allele of *APC*. Specifically, one allele was inactivated by introduction of unequivocally deleterious premature stop codon, resulting in premature termination at p.R1450*; whereas the other allele was inactivated by LINE-1 mediated somatic retrotransposition of one *APC* allele by LINE-1 insertion event some 160 bp. By comparing the unique singleton mutation patterns of 295 sequence variants in full-length LINE-1 retrotransposons to that of the LINE-1 insert, the authors identified candidate LINE-1 retrotransposon source, which is located at genome position, chr 17:18776467, of the Hg19 Human Genome assembly. Another important body of work is by Phillippe *et al.*, 2016, identified that only very selected LINE-1 retrotransposons, unique to each individual, contribute to transcriptional activation and subsequently to the bulk of LINE-1 protein expression (17). As high-throughput technology, specifically PacBio-based DNA sequencers, are more widely used in cancer research, we will begin to understand more clearly just when and how LINE-1 transcriptional activation occurs in cancer.

4. ON LINE-1 ENCODED PROTEINS IN CANCER

Work on LINE-1 encoded proteins expression in cancer has largely been based on ORF1p profiling in many human cancer types. Nearly half of all cancers in human support LINE-1 ORF1p expression, which presents pre-diagnostic and/or diagnostic utility in clinical practice today (18). More interestingly, there is evidence that ORF2p encoded reverse transcriptase activity plays a necessary role in *TPR22* and *ETV1* gene fusion (19), and growth of prostate cancer (19). Finally, there is also evidence that ORF1p expression induces hTERT in tumor cells (20).

5. ON LINE-1 RETROTRANSPOSITION IN CANCER

Despite paucity of intronic and intergenic LINE-1 retrotranspositions in several visceral cancers - including pancreatic ductal adenocarcinoma, colorectal carcinoma, esophageal carcinoma, and prostatic carcinoma - there is limited evidence for LINE-1 retrotransposition causing aberrant gene regulation (21; 22; 23; 24). The single example of unequivocal deleterious LINE-1 retrotransposition in cancer has been aforementioned report by Scott *et al.*, 2015 (16), whereby the authors identified that one *APC* allele was inactivated by traditional single nucleotide mutation and the other allele was mutated by LINE-1 insertion; providing evidence for the classic two-hit hypothesis for mutating *APC* gene.

6. ON LINE-1-RELATED GENE REGULATORY NETWORKS

The subgroup of 20 identified research articles collectively identify 18 unique genes whose expression is empirically linked to LINE-1 expression in cancer. The gene symbols representing the genes in question are as follows: *AID*, *APOBEC3D*, *APOBEC3G*, *DNMT1*, *DNMT3B*, *ERCC4*, *ETS1*, *IFNA1R*, *IFNB1*, *IL-6*, *PIWILINE-1*, *RAD21*, *RB*, *RNASEL*, *SIRT6*, *TERT*, *TP53*, and *UHRF1*. To better organize the discussion, I performed a biological pathway analysis using a free online database termed Reactome. The interactive server identified that 9 out of 18 genes belong into two groups of distinct biological pathways. The pathways identified pathways are as follows: (i) epigenetic regulation pathway (*DNMT1*, *DNMT3b*, *UHRF1*, and *ETS1*); and (ii) interferon signaling pathway (*IFNA1R*, *IFNB1*, *RB*, *TERT*, and *IL-6*) (Table 1). Remaining 8 genes were determined to belong to the genome integrity pathway.

6.1. ON LINE-1-related epigenetic regulation pathway

There is compelling empirical evidence that genome-wide LINE-1 promoter methylation is dependent on molecular pathway that entails *MUC1*, *DNMT1*, and *DNMT3B* genes (25). Specifically, Li *et al.*, 2015, performed both loss-of-function experiments (by *MUC1* shRNA) and gain-of-function experiments (by vector expressing *MUC1*) to observe that *MUC1* is transcriptional activator of both *DNMT1* and *DNMT3B* promoters. In turn, *MUC1* expression also causes genome-wide LINE-1 promoter hypomethylation in cultured cancer cells. Nakamura *et al.*, 2016, reported that *UHRF1* overexpression led to genome-wide LINE-1 promoter hypomethylation, as well as that, conversely, siRNA *UHRF1* knockdown increased the global LINE-1 promoter DNA methylation (26).

Table 1. Biological processes related to L1 retrotransposons

Epigenetic Regulation
• DNMT1
• DNMT3B
• UHRF1
• ETS1
Interferon Signaling
• IFNA1R
• IFNB1
• RB
• TERT
• IL-6
Genome Integrity
• AID
• APOBEC3D
• APOBEC3G
• ERCC4
• PIWIL1
• RAD21
• RNASEL
• SIRT6
• TP53

Li *et al.*, 2014, found out that ectopic LINE-1 ORF1p overexpression caused increased RNA expression of ETS1 related genes as well as promoted cell proliferation and anchor-independent growth of LoVo cancer cell line (27). The same group showed that LINE-1 siRNA caused decreased RNA expression of ETS1 related genes as well as reduced the proliferation and anchor-independent growth ability of LoVo cancer cell line. Taken together, there is empirical evidence that genes involved in epigenetic regulation pathway also regulate LINE-1 retrotransposons.

6.2. ON LINE-1-related interferon signaling pathway

Aschacher *et al.*, 2016, observed that LINE-1 knockdown decreases TERT function as measured by both telomere dysfunction foci and telomerase activity (20). Conversely, LINE-1 overexpression increased telomerase activity. Yu *et al.*, 2015, discovered that IFNB1 treatment of cancer cell lines inhibits LINE-1 retrotransposition (28). In addition, knockdown of IFNA1R led to increase in LINE-1 retrotransposition. Separate work by Ishak *et al.*, 2016, shows that genetically engineered mice carrying F832A mutation in RB1 causes both genomewide upregulation of LINE-1 RNA in somatic tissues as well as increased

susceptibility to leukemia (29). Taken together, the composite work by Aschacher *et al.*, Yu *et al.*, and Ishak *et al.*, is, to my mind, a collection of the most compelling empirical evidence to date that LINE-1 retrotransposon modify an important aspect of human tumorigenesis. Of note, Gasche *et al.*, 2011, identified that IL-6 treatment of cancer cell line induced genome-wide LINE-1 promoter hypomethylation (30).

6.3. ON LINE-1-related genome integrity pathway

The third group of genes associated with LINE-1 biology belong to genome integrity pathway, whose functions include DNA repair and innate cell immunity against viruses. A series of independent reports document the notion that some members of APOBEC (“apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like”) cytidine deaminases regulate LINE-1 retrotransposition in somatic tissue. Specifically, Servant *et al.*, 2017, showed that ERCC4 limits LINE-1 retrotransposition, suggesting that other core components of the nucleotide excision repair (NER) pathway may also play a similar role (31). Liang *et al.*, 2016, also reported that ectopic expression on both APOBEC3 and APOBEC3DE limit LINE-1 retrotransposition (32). Koyama *et al.*, 2013, showed that APOBEC3G inhibit LINE-1 retrotransposition (33). Similarly, Metzner *et al.*, 2012, also showed that AID

inhibits LINE-1 retrotransposition (34). To conclude, multiple studies show that several cytidine deaminase enzyme isoforms regulate LINE-1 retrotransposition in cancer.

Several other genes involved in repair of DNA double-stranded breaks affect LINE-1 retrotransposition. Two studies support the idea that TP53 protein also limits LINE-1 retrotransposition. First, Haoudi *et al.*, 2004, proposed a dichotomous idea whereby LINE-1 retrotransposition in wild-type TP53 cancer cell line causes apoptosis, but not in cancer cell line carrying mutated TP53 allele (35). More recently, Wyulie *et al.*, 2016, presented multiple lines of empirical evidence including gene complementation studies and genetic fish studies to support an assertion that TP53 restricts LINE-1 retrotransposition (36). Xu *et al.*, 2014, reported that Rad21 expression induces increase in LINE-1 retrotransposition, as well as that Rad21 knockdown by siRNA causes reduction in LINE-1 retransposition (37). Van Meter *et al.*, 2014, discovered that expression of SIRT6 recruits KAP1 to LINE-1 promoters, thus inducing LINE-1 transcriptional silencing (38). In addition, the authors also observed that senescent cells harbor lower SIRT6 levels and comparably higher LINE-1 RNA levels, relative to young cells. Zhang *et al.*, 2014, examined the role of RNASEL on LINE-1 retrotransposition (39). Expression of wild type RNASEL, but not catalytically inactive protein, reduced many aspects of LINE-1 biology including LINE-1 RNA expression, ORF1p and ORF2p expression, and LINE-1 retrotransposition. Wang *et al.*, 2015, made an interesting observation that PIWILINE-1 protein level is decreased in melanoma cell line with metastatic potential (40). Importantly, overexpression of PIWILINE-1 caused LINE-1 promoter hypermethylation (41).

Taken together, biological pathways affecting epigenetic regulation, interferon signaling, and genome integrity play a role in regulating LINE-1 retrotransposon suppression in somatic tissues and aberrations of some of these genes may, at least in part, be the underlying cause of LINE-1 activity in cancer.

7. ON LINE-1 AS PUTATIVE THERAPEUTIC TARGET IN CANCER

The greatest clinical utility/benefit of any biomarker, is not whether or not a given analyte solely provides diagnostic and/or prognostic information, but is knowing if it can be used as a therapeutic target. To broach that question, a hallmark preclinical studies by Sciamanna *et al.*, 2005 uncovered that pharmacologic LINE-1 inhibition by two reverse transcriptase inhibitors slows down the growth of malignant melanoma and prostatic carcinoma cells (19). Follow-up study by Carlini *et al.*, 2010 similarly demonstrated efficacy of reverse transcription inhibition of prostate cancer

growth (42). Most importantly, a clinical trial showed that efavirenz provides therapeutic benefit by increasing progression free survival in a cohort of 53 patients with high-stage castration-resistant prostate cancer (43). The most recent review on the topic suggests that LINE-1 inhibition with reverse transcriptase inhibitors may not only slow down the progression of prostate cancer, but may also play a role in preventing the initiation of tumor growth (44).

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