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Annual Review of Pathology: Mechanisms of Disease Our Conflict with Transposable Elements and Its Implications for Human Disease

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Abstract

Our genome is a historic record of successive invasions of mobile genetic elements. Like other eukaryotes, we have evolved mechanisms to limit their propagation and minimize the functional impact of new insertions. Although these mechanisms are vitally important, they are imperfect, and a handful of retroelement families remain active in modern humans. This review introduces the intrinsic functions of transposons, the tactics employed in their restraint, and the relevance of this conflict to human pathology. The most straightforward examples of disease-causing transposable elements are germline insertions that disrupt a gene and result in a monogenic disease allele. More enigmatic are the abnormal patterns of transposable element expression in disease states. Changes in transposon regulation and cellular responses to their expression have implicated these sequences in diseases as diverse as cancer, autoimmunity, and neurodegeneration. Distinguishing their epiphenomenal from their pathogenic effects may provide wholly new perspectives on our understanding of disease.

1. OUR JUNK-FILLED GENOMES

1.1. Introduction to Mobile Genetic Elements

Like other complex eukaryotic genomes, ours is replete with junk DNA: a fossil record of waves of invasions of mobile genetic elements (1, 2). It appears that our ancestral species contended with these endogenous viruses and other transposons as far back in time as we can perceive by sequence homology. Each successful element type left behind copies of its sequence interspersed in our genome. While many of these insertions were lost, others became fixed through genetic drift and, thus, trapped in the amber of our DNA for millions of years after the loss of their ability to propagate in the genome (3, 4).

In humans and other mammals, this fossil record is dominated by various types of retroelements (also known as class I mobile elements, retrotransposons, or retroposons). This is in contrast to the class II DNA transposons discovered by Barbara McClintock, which excise themselves and reinsert in the genome and are colloquially known as jumping genes or cut-and-paste elements. Retroelements propagate through the reverse transcription of an RNA intermediate. These copy-and-paste elements make up nearly half of the human genome (5) (**Figure 1**).

The most commonly recurrent elements are the so-called short interspersed elements (SINEs), which rely on other retrotransposons to encode the protein functions for their reverse transcription and integration in genomes. *Alu* (6) and mammalian-wide interspersed repeat (7, 8) elements are the most prevalent. Together, they make up 20% of our DNA; *Alu* sequences number nearly 1 million in the human reference genome assembly. Essentially, all ongoing retrotransposition of these sequences stems from a few *AluY* subfamilies (9, 10), the last letter signifying that these are the young remnants in humans of a burst of *Alu* retrotransposition that reached a crescendo 35–40 million years ago in ancestral primates (11–13). *Alu* sequences depend on the endonucle-ase and reverse transcriptase functions of the long interspersed element-1 (LINE-1, L1) for their propagation in genomes (14).

L1 activity has accompanied the evolution of our species from our eutherian mammalian ancestors (15–17). L1 elements are carried in human genomes as \sim 500,000 mostly fragmented copies that make up about 17% of our DNA (5, 18). Today, L1 activity in any individual resides in a small subset of these sequences: 100 or so members of the L1PA1 and L1PA2 subfamilies, or *Homo sapiens*-specific (L1Hs) elements (19, 20). The most active are termed the hot elements. L1 also transposes SVA [SINE/variable number tandem repeat (VNTR)/*Alu*] sequences (21, 22), composite retroelements with SINE, VNTR, and *Alu* sequence homologies. Ongoing germline L1 activity makes L1, *Alu*, and SVA integrations commonplace, and insertions of these sequences represent common structural variants segregating in populations (20, 23–27). We each inherit a unique complement of these mobile element insertions, distinguishing us from other individuals at many hundreds of sites.

Collectively, L1 and the sequences it copies are known as the non-long terminal repeat (LTR) retroelements. This distinguishes them from the endogenous retroviruses, which are flanked by LTRs and have a different mechanism of retrotransposition. In humans, LTR element activity has been extinguished (or all but extinguished) within the past few million years (28), although their sequences persist as about 8% of our genome. Endogenous retroviruses (ERVs) are named for the transfer RNA that primes their reverse transcription reaction, and the most recently active subfamily is HERV-K (HML2, primed by lysine transfer RNA) (**Figure 2**). There remain insertion variants of this type in modern humans—that is, genomic loci where both insertion and preinsertion (or empty) alleles can be found (29). The LTRs that flank full-length proviral insertions have a tendency to recombine, deleting the intervening sequences and reducing an insertion to a solo LTR. Such recombinations have led to structural variants of both ERV-K and older ERVs



Transposons in the human genome. The schematic shows the structure of different transposable elements and retrotransposition products. Protein-coding ORFs are shown in dark arrows. The full-length LINE-1 (L1) (6 kb) includes an ORF (ORF0) in its 5' untranslated region in a 3' to 5' orientation (132). ORF2p encodes endonuclease and reverse transcriptase activities. Recurrent types of 5' truncated L1 are shown next; these vary in size. *Alu* sequences are about 300 bp. The prototypical SVA insertion is 2 kb, although individual genomic insertions are variable in size. ERV proviral insertions are approximately 10 kb in size. The Pol ORF encodes reverse transcriptase and integrase activities. Abbreviations: Env, envelope; ERV, endogenous retrovirus; FLAM, free left *Alu* monomer; FRAM, free right *Alu* monomer; Gag, group antigen; LINE-1, long interspersed element-1; LTR, long terminal repeat; ORF, open reading frame; ORF2p, ORF2protein; pA, polyA tail; Pol, polymerase; SVA, short interspersed element (SINE)/variable number tandem repeat (VNTR)/*Alu*. Figure adapted from images created with BioRender.

in modern humans—that is, genomic loci where both the proviral sequence and the collapsed (or solo) LTR-containing alleles can be found (30).

Since L1 is the engine behind modern-day mobile element activity, its mechanism of retrotransposition is considered in further detail here (**Figure 3**). The life cycle of L1 begins with its transcription, which is mediated by RNA polymerase II (Pol II) at an internal promoter sequence. The RNA intermediate for retrotransposition must encompass the full 6 kb sequence, the socalled unit or authentic L1 transcript (31, 32), which begins with the L1 promoter and extends up to (or slightly past) the 3' polyA sequence. The overwhelming majority of L1 RNAs in cells



Endogenous retroviral (ERV) retrotransposition. Genomic elements code for RNA (*red*) that is translated to produce viral proteins (*purple*). Functional envelope (Env) protein is produced by the rough endoplasmic reticulum and expressed on the surface of the cell, where it is available to coat viral particles that bud from the cell. ERVs with functional Env can reinfect cells, whereas those without are obligate retrotransposons. Group antigen (Gag) forms the viral capsid. Polymerase (Pol) is responsible for transfer RNA–primed reverse transcription and integration of the double-stranded DNA (dsDNA) into the genome. Reverse transcribed DNA is shown in blue. Figure adapted from images created with BioRender.

do not have this structure (32), but rather are read-through transcripts that variously consist of a short-lived, prespliced mRNA; a long noncoding RNA; or a persistent structural RNA (33). So investigators should not equate the presence of L1 RNA or increases in its level with the potential for retrotransposition.

The unit L1 transcript is bicistronic, coding for two proteins in its regular (sense) orientation, ORF1p and ORF2p. ORF1p is produced in greater quantity, and its expression can be readily detected in human tissues by Western blotting or immunostaining (34–36), where it is a marker of L1 expression and a surrogate for retrotransposition potential. ORF1p encodes an RNA binding protein that forms a homotrimeric complex through interactions of its long coiled-coil domain (37, 38). A hinge in the ORF1p coiled-coil domain gives it the potential to form higher-order oligomers and lattices as well (39, 40). The precise role of ORF1p in retrotransposition is not known, although its presence, RNA binding capacity, and oligomerization all are required for L1 retrotransposition. Dominant negative forms with premature stop codons exist; these retain their coiled-coil domains and presumably suppress retrotransposition in *trans* by interacting with intact ORF1p molecules (41). ORF1p binds to L1 RNA, but its affinity for RNA is not sequence



Long interspersed element-1 (LINE-1, L1) retrotransposition. L1 RNA is transcribed by RNA polymerase II and translated in the cytosol by host ribosomes. The ORF1 protein (ORF1p) is an RNA binding protein and forms ribonucleoprotein (RNP) complexes with ORF2p and L1 RNA. ORF2p encodes endonuclease and reverse transcriptase activities. Upon nuclear entry, ORF2p nicks target DNA and reverse transcribes the L1 RNA. It uses a 3' OH from DNA at the target site to prime the reaction, a mechanism termed target-primed reverse transcription (TPRT). RNA is shown in red; L1-encoded proteins are in blue; and complementary DNA is in black. Figure adapted from images created with BioRender.

specific (42). ORF2p is notoriously difficult to detect. It encodes the enzymatic activities required for retrotransposition, including an apurinic/apyrimidinic endonuclease–like nuclease domain (43, 44) and a telomerase-like reverse transcriptase (45, 46). These effect retrotransposition through a process known as target-primed reverse transcription (47).

L1 insertions bear several signature sequences of retrotransposition by ORF2p.

- 1. There is an insertion site preference for the junction between short stretches of thymine (T) and adenine (A) residues (e.g., 5' TTTT-AA 3'), reflecting the preferences of the endonuclease and the need for the L1 RNA to base-pair with the priming DNA strand.
- 2. Many L1 insertions fail to incorporate the full-length element, but rather are 5' truncated; a significant proportion is also 5' inverted (48).
- 3. Occasionally, insertions will incorporate 3' transductions (49)—that is, a reverse transcribed sequence matching the genome immediately downstream of the source element.
- 4. The entire insert is flanked by short (<20 bp) target site duplications; unlike the LTRs of endogenous retroviruses, these do not have a strong tendency to recombine.
- 5. Newly acquired L1 insertions are uniformly members of the L1PA1 and L1PA2 subfamilies, and the originating element encodes intact proteins. ORF2p shows a strong *cis* preference—that is, the tendency of the protein to copy the RNA that templated it (50, 51).

Alu is highly effective at breaking this *cis* preference in the germline. These noncoding RNAs are autonomously transcribed by RNA Pol III and form a highly structured signal recognition particle (52) made up of 7SL-derived *Alu* RNA and SRP9–14 proteins that together stall ORF2p translation on the ribosome (53) and provide an opportunity for *Alu* RNA to interact with ORF2p. While ORF2p is necessary for *Alu* retrotransposition (14), ORF1p appears dispensable. SVA elements use a similar mechanism for retrotransposition via L1-encoded ORF2p (22). Like L1 genomic integration, both *Alu* and SVA elements bear the insertion site preference and target site duplication features described above. However, unlike L1, they are more likely to insert as intact units as opposed to being 5' truncated and rearranged. There are limited numbers of subfamilies of retrotransposition-competent *Alu* and SVA in modern humans (e.g., *AluYa5, AluYb8, AluYb9,* and SVA_E and SVA_F), although these are more diverse than the active human-specific L1Hs elements, which are restricted to the L1PA1 and L1PA2 subfamilies.

Estimates are that 1 person in 100–200 people carries a de novo germline integration of an L1 or SVA element—that is, an insertion that is not inherited (23, 24). The frequency is predicted to be higher for *Alu* insertions: About 1 in 20 individuals is estimated to carry a new insertion (54). Less commonly, ORF2p can interact with mRNAs and generate spliced pseudogene integrations (55) or with U6 RNAs to form integrations consisting of U6–3' L1 chimeras (56, 57).

As is considered in Section 2.1, L1 activity in the germline can be mutagenic, and there is measurable negative selection against full-length, active L1 loci (58), which are relegated to allelic variants in many cases (20). As more complete collections of these active elements and their inheritance patterns become available, it will be interesting to develop combinatorial models to test whether there are limits on the coinheritance of multiple hot L1 loci.

1.2. Mobile Element Silencing and Escape

Retrotransposons contain regions that act as transcriptional activators (i.e., promoters and enhancers), and they rely on these sequences for their expression and, ultimately, their retrotransposition. Because of the threat that this poses to genome integrity, host species have developed epigenetic silencing mechanisms as a counter tactic. These elaborate pathways are most thoroughly studied in experimental models of gametogenesis and early cleavage stage embryogenesis. In these systems, DNA methylation and repressive histone marks are produced by piwi-interacting RNA pathways (59, 60) and various protein complexes, such as the Krüppel-associated box (KRAB) domain-containing zinc-finger proteins with KRAB-associated protein-1 (KAP1, TRIM28) complexes (61–63); human silencing hub (HUSH) complex (64, 65); and Polycomb repressor complex 2 (PRC2) (66, 67). Their combined effects tolerize the genome to the accumulation of retroelements by minimizing transposon transcription.

However, these silencing mechanisms are imperfect, and some elements escape and are transcribed. For older and noncoding mobile elements, the consequences of this may be unimportant. However, at retrotransposition-competent L1 loci, the consequence may be significant, and an example of such an escape was recently reported (68) (**Figure 4***a*). It occurred in a patient with a high-grade mucinous adenocarcinoma of the colon. In this case, the specific L1Hs locus at issue—located on chromosome 17—had an unmethylated promoter sequence and produced RNA in normal tissue samples from the patient. This active element caused a de novo retrotransposon insertion that is inferred to have occurred in the individual's preneoplastic colonic epithelium. The new, somatically acquired L1 insertion disrupted an exon of the adenomatous polyposis coli (*APC*) tumor suppressor gene (chromosome 5) during its integration, producing an early driver mutation that likely contributed to the subsequent colon cancer. The source element on chromosome 17 is a polymorphic structural variant in human populations, and methylation



Retroelement insertions and rearrangements implicated in disease. (*a*) A long interspersed element-1 (LINE-1, L1) insertion interrupting the last protein-coding codon in the adenomatous polyposis coli (*APC*) tumor suppressor gene. The adjacent diagram of the colon illustrates that this insertion was somatically acquired, and it contributed a tumor-driving mutation in colon cancer. (*b*) An L1 insertion interrupting a protein-coding sequence in the coagulation factor VIII (*F8*) gene on chromosome X. This and all subsequent loci drawn here are germline (constitutional) alleles. (*c*) A common *Alu* insertion variant promotes exon skipping in the CD58 molecule (*CD58*) gene and appears to contribute to multiple sclerosis risk through this mechanism. (*d*) An intronic short interspersed element/variable number tandem repeat/*Alu* (SVA) insertion in the TATA-box binding protein associated factor 1 (*TAF1*) gene causes X-linked dystonia–parkinsonism. Expansion of the hexanucleotide repeat domain (CCCTCT)_n within the SVA is associated with earlier disease onset. This is predicted to promote G-quadruplex formation (shown). (*e*) An *Alu–Alu* recombination at the ubiquitin conjugating enzyme E2 T (*UBE2T*) gene causing Fanconi anemia (complementation group T). The rearrangement between two *Alu*Ya5 repeats caused deletion of exons 2–6 of the paternal allele and a corresponding duplication of the maternal allele. Figure adapted from images created with BioRender.

studies in other individuals indicate that this specific locus can be effectively silenced. In the patient, the locus was one of ~ 10 expressed L1Hs; all other loci appear to have been silenced.

This case brings into focus many significant knowledge gaps. We do not currently have catalogs of epialleles of active L1 in humans, nor have these loci been systematically evaluated as markers of cancer risk. More fundamentally, we have little insight into the mechanisms that might be responsible for the variation in silencing versus escape among the retrotransposition-competent L1. Why do some individuals silence this same insertion effectively while it was expressed and caused cancer in this patient? Why was this patient able to silence hundreds of nearly identical L1 loci elsewhere in their genome and yet miss this one? Possible scenarios include a stochastic quality to heterochromatin formation in early development, environmental exposures or other changes that affect the maintenance of silencing over time in a locus-specific manner, as well as genetic mechanisms, such as sequence variants within the insertion allele that allow L1 to evade silencing or variations in silencing genes that confer to different individuals distinct competencies for recognizing and silencing different L1. We also have few insights into the frequency of somatic retrotransposition events outside of malignancy. Given that a retrotransposition-competent L1 was left unchecked in this individual, it seems plausible that the person would be prone to acquire other L1 insertions.

1.3. Seeing the Greater Good

Retrotransposons that escape from silencing are not always deleterious to the host. Indeed, transcriptional activity intrinsic to older elements—that is, those that are no longer retrotransposition competent—appears to sometimes be repurposed in the service of gene regulation. Transposition of interspersed repeats widely distributes similarly functioning regulatory sequences in the genome, and this provides an avenue for the evolution of gene networks with coordinated expression. For example, LTR elements have strong promoters, and MER41 and other endogenous retroviral sequences have been co-opted to control interferon-responsive genes (69, 70).

Host genes that have evolved for the purpose of transposon silencing can similarly be used as a substrate for evolutionary innovation. KRAB zinc-finger protein (ZFP)-coding genes are the most abundant type of gene in our species. They have evolved to silence transposable elements in early development (61–63, 71, 72): our stockpiles in the so-called arms race with transposons. With each win, the target retroelements are kept transcriptionally quiescent and eventually become incompetent for retrotransposition, slowly relaxing evolutionary constraints for their cognate ZFPs. Meanwhile, the repertoire of ZFPs that has emerged from this conflict represents a rich collection of DNA sequence-specific regulators in various stages of repurposing for gene regulation (73, 74).

Sometimes, transposable element protein-coding functions are co-opted by a host species, such that the transposon becomes a so-called domesticated host gene. Recombination activating genes (*RAG1* and *RAG2*) were taken from an ancient *Transib* DNA transposable element, and its transposition mechanism now mediates V(D)J recombination in B and T cell precursors (75–79) (**Figure 5**). Mutations in *RAG1* and *RAG2* cause immunodeficiencies. Other ancient cut-and-paste transposons have been co-opted as centromere protein B (*CENPB*) and other pogo-derived genes, and sets of piggyBac- and tigger-derived genes (80–82). Of these, mutations in pogo transposable element derived with ZNF domain (*POGZ*) cause a neurodevelopmental syndrome (83, 84).

In summary, while transposable elements pose real risks as endogenous mutagens and may play roles more broadly in disease, their existence also provides benefits to a species over time. Much of the most exciting work in the field today is leveraging advances in genomics and CRISPR-Cas9-enabled functional studies (65, 85) to understand transposable element regulation and how this intersects with critical genome functions.

2. THE DARK SIDE OF MOBILE ELEMENTS

2.1. Disease-Causing Insertion Alleles

The most clear-cut cases of how transposable elements cause disease are those instances in which an insertion in the germline critically affects gene function and creates a characteristic monogenic disease phenotype. The inciting event either can be a de novo insertion (i.e., acquired in the patient



Parallels between V(D)J recombination and DNA transposition. Recombination activating genes RAG1 and RAG2 are derived from a *Transib* DNA transposon. (*Left*) Canonical V(D)J recombination. Juxtaposition of the two recombination signal sequences (RSSs) leads to excision of the intervening sequence. RSSs are tripartite modules made up of partially conserved heptamer (7 bp) and nonamer (9 bp) sequences with an intervening spacer of 12 bp or 23 bp. The ends of the excised fragment are ligated as the signal joint. The rearranged strand is repaired as the coding joint and encodes an immunoglobulin or T cell receptor chain. (*Right*) The alternative to signal joint ligation and loss of the circularized sequence: genomic integration. Figure adapted from images created with BioRender.

or a mosaic parent) or can come from an inherited insertion allele segregating in a population. Highly penetrant insertion alleles are established through genetic drift and are often limited to a founder population (see, e.g., 86–88).

Overall, about 120 examples of transposable element insertions causing genetic disease have been reported (89). There is a widely held expectation that these mutant alleles are being underascertained, as clinical sequencing efforts by and large do not employ tailored pipelines to identify retroelements.

Disease-causing insertions are mostly L1 or *Alu* elements that interrupt a protein-coding exon or land within a few base pairs of an exon so as to directly disrupt mRNA splicing (87, 90). SVA and pseudogene insertions have been described as well, as have insertions that occur deeper within intronic sequences that disrupt normal splicing through an alternative mechanism referred to as

gene trapping, in which the exon 5' of the insertion site is spliced to RNA encoded by the insert (91, 92).

The first—and still a prototypical—example of a disease-causing insertion was discovered in a patient with hemophilia A by investigators at the Johns Hopkins Hospital (90). An L1 was inserted into an exon of the coagulation factor VIII (F8) gene on chromosome X (**Figure 4***b*) and interrupted the F8 open reading frame. The discovery was impactful since it was the first demonstration of an active mobile genetic element in humans. Subsequently, researchers were able to clone elements and develop in vitro assays for retrotransposition, which have been powerful tools to probe transposon and host factor requirements for transposition (20, 65, 93).

2.2. Mobile Element Polymorphisms and the Common Disease Paradigm

Transposable element insertion variants with lesser impact on gene function may play roles in common diseases. Genome-wide association studies (GWASs) have reinforced the observation that these diseases (i.e., diseases traditionally viewed as sporadic) have a genetic basis, and studies have attributed a portion of that heritability to specific haplotypes. We recently identified hundreds of *Alu* element insertion variants occurring at the most well-defined disease risk loci (94). Moreover, in many instances, we see that the mobile element insertion is in linkage disequilibrium (LD) with markers of the disease haplotype (i.e., the trait-associated single nucleotide polymorphisms, or SNPs). In these cases, this is genetic evidence suggesting that the GWAS is identifying functional effects of the mobile element insertion. Although the molecular mechanism at these loci is unproven, our study shows that inherited mobile insertion alleles that are common in all of our genomes may be modifying the risk for developing many types of diseases.

One example is an Alu insertion at the CD58 molecule (CD58) locus on a haplotype that affects multiple sclerosis (MS) susceptibility (Figure 4c). GWASs have identified numerous risk alleles for the disease (95, 96), including one at CD58. The CD58 genotype is one of the strongest genetic indicators of MS risk (odds ratio = 1.3, $p = 3 \times 10^{-10}$) (96, 97). The risk allele reduces CD58 expression in lymphoblastoid cell lines (97), and MS patients in relapse have lower expression of CD58 on peripheral blood mononuclear cells than do MS patients in remission (97). Thus, decreased expression of CD58 is associated with the risk for developing MS and for relapse. Fine-mapping studies, including resequencing of a 76 kb interval at CD58, and targeted SNP genotyping in 1,278 trio families with MS and 3,341 MS cases and controls indicate a single risk allele in LD with SNP rs2300747 is responsible (97). We found perfect LD between rs2300747 and an Alu insertion variant in an intron of CD58. This is a 302 bp insertion that is present in some individuals and absent in others (allele frequency = 0.66). Further, we found that the Alu insertion alters splicing of CD58 mRNA, promoting skipping of exon 3 in splice reporter assays, and associates with this splice event in lymphoblastoid cell lines (98). The resulting transcript is frame-shifted and presumed to be nonfunctional. Together, these data suggest a mechanism by which a commonly occurring Alu insertion compromises CD58 expression, thereby creating an allele that increases susceptibility to MS.

2.3. Rearrangements of Mobile Element Insertions

Some mobile element sequences are intrinsically unstable, and sequence changes within a repeat or rearrangements between different repeats can have phenotypic consequences. A striking example of this was recently reported by investigators studying a disease-causing SVA insertion in an intron of the TATA-box binding protein associated factor 1 (*TAF1*) gene (**Figure 4***d*). The SVA insertion allele causes X-linked dystonia–parkinsonism, a prevalent movement disorder where the allele was discovered on Panay Island in the Philippines (99). It is now clear that an allelic series exists in the population there, with variably sized expansions of the hexanucleotide repeat domain $(CCCTCT)_n$ within the SVA. Repeat length correlates strongly with disease onset, with longer repeat stretches being associated with earlier manifestations of symptoms (100). The presence of the SVA compromises normal *TAF1* mRNA splicing and results in retention of the intron (101). The precise role of hexanucleotide length as a modifying factor is unclear, although this affects the transcriptional potential of the retroelement and may promote G-quadruplex formation (100). These findings underscore the idea that transposable element insertion polymorphisms should not be considered only in simple biallelic terms—that is, an as an insertion allele versus an empty allele—and that the dynamics of SVA sequences deserve special attention.

Rearrangements between two nonallelic insertions can cause genetic disease. For *Alu* elements, this recombination causes disease alleles as commonly as do de novo retrotransposition events (102). An illustrative example is shown in **Figure 4e**. In that case, an *Alu–Alu* recombination occurred between tandem *Alu*Ya5 insertions at the ubiquitin conjugating enzyme E2 T (*UBE2T*) gene, causing Fanconi anemia (complementation group T). The rearrangement caused an interstitial deletion encompassing exons 2–6 of the paternal allele, with a corresponding duplication of the maternal allele in the patient (103).

3. GOING SLOW TO GO FAST: MOBILE ELEMENT EXPRESSION IN MALIGNANCY

3.1. L1 Expression in Cancer

The previous section focused on how germline insertions of transposable elements can affect surrounding genes and cause genetic disease. For the remainder of this review, the focus is on diseases characterized by the dysregulation of transposable elements and hypotheses about how this may affect pathogenesis.

One of the most straightforward examples of the aberrant expression of transposons in diseased tissues is that of L1 expression in cancers. Large numbers of studies have described hypomethylation of the L1 promoter in human malignancies, and some of these have related the phenomenon to clinical features, including higher histologic grades, more advanced clinical stages, and reduced patient survival (all reviewed in Reference 36). L1 promoter hypomethylation, in turn, is associated with ORF1p expression (34). ORF1p overexpression is recognized as a hallmark of many types of cancers, including ovarian and lung, and many gastrointestinal tract tumors, including colon, pancreatic, and esophageal cancers. All are diseases with significant morbidity and mortality that are frequently diagnosed late in the evolution of the malignancy when curative treatment options are limited. Assays of circulating tumor DNA used to evaluate L1 promoter methylation and assays to detect ORF1p in clinically accessible samples may prove useful for early diagnosis, although these remain to be developed.

The proportion of tumors that become immunoreactive for ORF1p and the timing of L1 ORF1p induction depend on the tumor type. For some diseases, such as high-grade serous ovarian carcinoma, there is nearly uniform upregulation of L1 ORF1p (90% of cases) (34, 104), and aberrant expression is evident early in the disease course. In these cases, L1 induction co-occurs with fixation of tumor protein p53 (*TP53*) tumor suppressor mutations in serous tubal intraepithe-lial carcinoma precursor lesions of the fallopian tube (104). Precursors of pancreatic carcinoma, termed pancreatic intraepithelial neoplasia, progressively accumulate immunoreactive ORF1p (34). In colon carcinoma, L1 ORF1p expression is induced in malignant cells as compared with normal colonic epithelium. However, as was considered earlier, somatic retrotransposition can antedate neoplastic transformation, and somatically acquired L1 insertions may be the mutagenic

mechanism underlying loss of the *APC* tumor suppressor gene, typically ordered as an early event in the series of genetic changes that lead to colon cancer (68, 105). In contrast, glioblastomas express little to no L1 ORF1p and do not support significant numbers of retrotransposition events (106, 107).

3.2. New L1 Insertions in Cancer

All of the tumor types characterized by ORF1p expression have been shown to support retrotransposition (108–110), although there is no correspondence between the number of genomic L1 insertions and ORF1p levels. Ovarian cancers express high levels of ORF1p and accrue relatively fewer L1 insertions (111, 112), while lung and colon cancers with more moderate ORF1p levels support high levels of retrotransposition (25, 68, 113). Most somatically acquired insertions of transposons in cancers are 5' truncated L1. Many are 5' inverted (114), also a characteristic of germline insertions, and thought to reflect a second priming event during target-primed reverse transcription (48). Others carry 3' transduction events that allow for the identification of source elements (110). Interestingly, unlike germline integrations, somatically acquired insertions in cancers appear to be dominated by L1 itself, with far fewer instances of *Alu*, SVA, and pseudogene retrotransposition (110, 115).

The majority of new insertions in tumors appear to be passenger events, as there is little tendency for the reoccurrence of independent insertions at the same locations in the genome (116). With exceedingly few exceptions, acquired insertions spare exons. This said, it is expected that some mutations in noncoding regions of the genome will be key events in cancer development, and as catalogs of noncoding sequence changes and somatic retrotransposition events mature, it will be important to see whether there is correspondence between the two. Such an observation would suggest that different mutagenic mechanisms disrupt the same key regulatory sequences. It may be that L1 insertions introduce new regulatory sequences to sites as well, but few functions have been ascribed to the 3' end of the L1 element. In summary, there is limited evidence that L1 insertions per se have important roles in tumorigenesis.

As spatiotemporal maps of somatically acquired insertions are refined, though, we can expect that they will provide insights into the timing of L1 expression and activity throughout the evolution of a tumor, inform how well or poorly L1 activity is tolerated as cancers grow, and serve as markers of subclonal phylogenies (110, 112, 114).

3.3. Cellular Effects of Transposon Expression

Could L1 expression impact cancer cell biology in other ways? In experimental systems, L1 expression slows cell growth or is overtly cytotoxic and damages DNA (117–119), and it is hard to envision a scenario in which its expression confers a direct cell growth advantage. However, it is plausible that the DNA damage it exacts transforms cells or that it puts cells in a state analogous to oncogene-induced senescence (120, 121), creating selective advantages for preneoplastic populations of cells with critical tumor suppressor mutations.

The expression of mobile genetic elements in cancers is not limited to L1, although that has been our primary focus up to this point. Because of their relative age and lack of protein-coding capacity, respectively, SINEs and ERV elements are less likely to directly incite DNA damage. However, new studies indicate that their expression may be an important determinant of the immunologic properties of cancerous cells. Both families of retroelements can incite cellular interferon responses (122–124) (**Figure 6**). Excitingly, expression of ERVs can be induced by demethylating agents, an effect that mimics exogenous viral infection (123–125). The same effect



Demonstrated and hypothetical intersections between transposable element (TE) expression and immunity. Activation of TE transcription may directly upregulate interferon-responsive genes (ISGs), given that some long terminal repeat sequences function as promoters or enhancers at these loci. TE-derived RNAs are prevalent and can form double-stranded RNA (dsRNA) in the nucleus. Annealing of these hybrids is relaxed by adenosine (A)-to-inosine (I) editing. ADAR represents adenosine deaminases acting on RNA. Unedited hybrids are prone to come into contact with cytoplasmic dsRNA sensors, such as retinoic acid inducible gene I (RIG-I), melanoma differentiation associated protein 5 (MDA5), and others, for example, endosomal Toll-like receptors (not shown), mimicking viral infection and prompting interferon responses (red arrow). TE-encoded proteins may also play roles as well. TE-encoded endonucleases can damage DNA (red star) and generate nucleic acids that might be sensed through cyclic guanosine monophosphate-adenosine monophosphate (cGAS)/stimulator of interferon genes (STING) and related pathways. TE-encoded reverse transcriptases may generate RNA:DNA hybrids and other complementary DNA forms that feed into the same pathways. TE-encoded peptides may be presented to cytotoxic T cells by major histocompatibility complex I (MHC I) or the proteins handled by antigen presenting cells (not shown). It is unknown whether these proteins are targets of peripheral tolerization in the thymus (i.e., recognized as self or nonself). Figure adapted from images created with BioRender.

can be seen with the inhibition of the lysine-specific demethylase 1A (*LSD1*) gene (126). This provides a rationale for the combination of epigenetic therapies (e.g., demethylating agents and others that promote transposable element expression) with immune checkpoint inhibitors [e.g., targeting programmed cell death 1 (PD-1) and its ligand (PD-L1)].

4. CELLULAR RESPONSES TO TRANSPOSON EXPRESSION IN INFLAMMATORY DISEASES

The paradigm that endogenous transposon expression can elicit the same interferon responses that have been associated with viral infections has implications for many other diseases. For example, Alu, L1, and other repeats have been proposed as central components of the pathogenesis of Aicardi-Goutières syndrome (AGS) diseases, a spectrum of inflammatory disorders characterized by severe neurologic impairment. AGS is caused by loss-of-function mutations in genes that normally limit the feeding of nucleic acids into the viral sensor pathways, including three prime repair exonuclease 1 (TREX1), ribonuclease H2 endonuclease complex components, adenosine deaminase acting on RNA 1 (ADAR1) double-stranded RNA (dsRNA) adenosine-to-inosine editing enzymes, and others. Gain-of-function mutations in melanoma differentiation associated protein 5 (MDA5), encoded by interferon induced with helicase C domain 1 (IFIH1), that make it hypersensitive to Alu dsRNAs (127) also cause AGS and a heritable form of systemic lupus erythematosus. Independent investigators have pointed to different types of retroelement-derived nucleic acids including dsRNA, RNA:DNA hybrids, and extrachromosomal DNA-and described models for AGS that converge on sensors of these products [i.e., retinoic acid inducible gene I (RIG-I) and MDA5 or cyclic guanosine monophosphate-adenosine monophosphate (cGAS)/stimulator of interferon genes (STING)] and the triggering of interferon signaling (127-129) (Figure 6). Similarly, interferon signaling prompted by L1 reverse transcriptase activity in senescent cells has been suggested recently to be an underlying basis for aging-associated inflammation (130).

Together, these studies point toward a need to better characterize transposable element insertion variants and their expression in sporadic inflammatory diseases and in heritable epigenetic disorders (131) and to identify cellular responses to these RNAs and proteins.

5. CONCLUSIONS AND FUTURE PERSPECTIVES

We are at an exciting time when advances in concepts of transposable element biology will inform perspectives on disease pathogenesis. We are more capable and curious than ever to learn more about these elements: If they were previously dismissed as junk DNA and intractable to experimentation, this is less true today.

As more genomes are sequenced, comparative genomics will likely point to functional elements. Structural and sequence variants within human populations will associate with specific diseases, and new insertions responsible for clinical phenotypes will allow for a molecular accounting of more occurrences of genetic disease.

Single-cell advances will give us the chance to probe for somatic retrotransposition in noncancerous tissues in disease contexts and to build more comprehensive maps of cancer cell lineages. New sequencing technologies, including long-read single-molecule sequencing, and tailored informatics for RNA expression profiling will allow us to better map expressed transposons and distinguish read-through transcription from authentic transcription. Transcript structure will be an important determinant of, for example, protein-coding capacity or *Alu–Alu* dsRNA hybrid formation. As disease-specific experimental systems are established, CRISPR-Cas9-based tools for transcriptional activation and silencing will enhance our ability to interrogate the functions of specific elements. The field will need additional reagents to detect and pharmacologically inhibit specific activities of transposon-encoded proteins.

Conclusions that a retroelement is important to disease should become less reliant on quantitative measures of transcripts or DNA copy number changes that cannot be traced unambiguously to their origins or on nonspecific nucleoside analog inhibitors of reverse transcriptase. If the field can avoid pitfalls and continue to find creative and rigorous ways to interrogate the effects of mobile elements, we are certain to discover fascinating biology and make meaningful inroads into understanding disease.

SUMMARY POINTS

- 1. Much of our genome is derived from mobile genetic elements, and this reflects a rich evolutionary history of many diverse, self-propagating sequences.
- 2. Most elements in the genome today are no longer competent as mobile DNAs, but a subset of L1 and the sequences it mobilizes remain active.
- 3. New insertions can cause genetic disease by disrupting critical functional sequences, and insertions with lesser effects may contribute to common disease risk.
- 4. L1 is highly expressed in many human cancers, where it functions as an endogenous mutagen.
- 5. Transposable element expression triggers cellular interferon responses in experimental systems, an observation with implications for tumor immunotherapy, inflammatory diseases, and potentially for other pathologies.

DISCLOSURE STATEMENT

Johns Hopkins University has licensed LINE-1 ORF1p antibodies to EMD Millipore. K.H.B. receives royalty payments from these sales.

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