Identification of Alternative Variants and Insertion of the Novel Polymorphic AluYl17 in TSEN54 Gene during Primate Evolution

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TSEN54 encodes a subunit of the tRNA-splicing endonuclease complex, which catalyzes the identification and cleavage of introns from precursor tRNAs. Previously, we identified an AluSx-derived alternative transcript in TSEN54 of cynomolgus monkey. Reverse transcription-polymerase chain reaction (RT-PCR) amplification and TSEN54 sequence analysis of primate and human samples identified five novel alternative transcripts, including the AluSx exonized transcript. Additionally, we performed comparative expression analysis via RT-qPCR in various cynomolgus, rhesus monkey, and human tissues. RT-qPCR amplification revealed differential expression patterns. Furthermore, genomic PCR amplification and sequencing of primate and human DNA samples revealed that AluSx elements were integrated in human and all of the primate samples tested. Intriguingly, in langur genomic DNA, an additional AluY element was inserted into AluSx of intron eight of TSEN54. The new AluY element showed polymorphic insertion. Using standardized nomenclature for Alu repeats, the polymorphic AluY of the langur TSEN54 was designated as being of the AluYl17 subfamily. Our results suggest that integration of the AluSx element in TSEN54 contributed to diversity in transcripts and induced lineage- or species-specific evolutionary events such as alternative splicing and polymorphic insertion during primate evolution.

1. Introduction

Alternative splicing (AS) can compensate for the lack of an association between gene number and organismal complexity in the mammal genome [1, 2]. By this mechanism, a single gene can produce various transcripts and proteins, contributing to expanding regulatory and functional complexity, protein diversity, and organismal complexity [2]. Previous studies using high-throughput sequencing have reported that >90% of human genes undergo AS in a tissue- or developmental stage-specific manner [3–5]. AS events are classified into several types: exon skipping, alternative 3’ splice site (3’S), alternative 5′ splice site (5’S), intron retention, mutually exclusive exons, alternative promoter, and poly(A). Exon skipping, 3’S, 5’S, and intron retention events are common types of AS, whereas mutually exclusive exons, alternative promoter, and poly(A) events are less frequent [6–9]. These events can occur when AS sites are recognized or original splicing sites are ignored by the spliceosome [10]. Furthermore, AS events and regulatory mechanisms are highly conserved in mammals [2].

Transposable elements (TEs) are mobile DNA sequences and comprise a large portion of the genome. In humans, TEs comprise 45% of the genome and are contained in introns of about 90% of human genes [11]. TEs provide the AS donor (GT) and acceptor (AG) sites in intron regions, and mature
mRNAs contain fragments of TEs through a splicing process called exonization, even within open reading frames (ORFs) [12]. Alu elements are a common type of TEs in human and nonhuman primate genomes and contribute to new exon creation events [13–16]. The full-length Alu element is about 300 nucleotides long, and Alu elements are divided into three subfamilies according to the evolutionary time of genome insertion. AluI, AluS, and AluY are the oldest, intermediate, and youngest subfamilies, respectively. AluY elements have transposed most recently, and their novel insertion within a specific genomic locus can generate polymorphisms [17]. Older subfamilies of Alu elements commonly lead to exonization. In the human genome, Alu-derived new exons or Alu-containing exons are found in more than 5% of alternatively spliced exons [13]. Alu-derived new exons or Alu-containing exons allow a protein to establish new functions without affecting the original function [18]. However, most cases of Alu exonization occur in UTRs or induce premature transcription termination and do not affect the protein [19]. Nonetheless, the formation of alternative exons from Alu can lead to human genetic diseases [20], and they are associated with lineage- or tissue-specific expression during primate evolution [21].

TSEN54 encodes a subunit of the RNA-splicing endonuclease complex, involved in the identification and cleavage of introns from precursor tRNAs. This complex is a heterotrramer composed of TSEN2, TSEN34, TSEN15, and TSEN54. An alternatively spliced variant of TSEN2 is part of a complex with unique RNA endonuclease activity [22]. The tRNA-splicing endonuclease complex is also associated with a pre-mRNA 3’ end processing factor [22]. Additionally, depletion of the tRNA-splicing endonuclease complex causes defects in maturation of pre-tRNA and pre-mRNA. Thus, the tRNA-splicing endonuclease complex is involved in multiple RNA-processing events. Previous studies have shown that the TSEN54 A307S missense mutation is associated with pontocerebellar hypoplasia (PCH) [23, 24]. Homozygous TSEN54 A307S has been identified in PCH type 2 patients, whereas heterozygous TSEN54 A307S and a different nonsense mutation are associated with a more severe phenotype consistent with PCH type 4 [25]. However, functional studies of splicing variants or mutants have not yet been performed.

In this study, we focused on the identification and characterization of alternative splicing and exonization events in TSEN54 in human and nonhuman primates. We performed comparative expression analysis in various cynomolgus, rhesus monkey, and human tissues. Additionally, we analyzed the integration times of Alu elements in TSEN54 during primate evolution.

2. Materials and Methods

2.1. Ethics Statement. Animal preparation and study design were conducted according to the Guidelines of the Institutional Animal Care and Use Committee (KIRBB-AEC-16067) of the Korea Research Institute of Bioscience and Biotechnology (KIRBB). Rhesus and crab-eating monkeys were provided by the National Primate Research Center of Republic of Korea or imported from China using a Convention on International Trade in Endangered Species of Wild Fauna and Flora permit.

2.2. Total RNA and Genomic DNA Samples. Total RNA from pathogen-free, 7-year-old adult, male cynomolgus (Macaca fascicularis) monkey tissues (cerebellum, cerebrum, kidney, colon, liver, lung, pancreas, small intestine, spleen, stomach, and testis) and pathogen-free, 10-year-old adult, female rhesus (Macaca mulatta) monkey tissues (cerebellum, cerebrum, kidney, colon, liver, lung, pancreas, small intestine, spleen, stomach, and ovary) were extracted using RNeasy® Plus Mini kit (Qiagen). RNA samples from human tissues (bone marrow, whole brain, fetal brain, colon, small intestine, heart, kidney, liver, fetal liver, lung, placenta, prostate, skeletal muscle, spinal cord, spleen, stomach, testis, thymus, trachea, and uterus) were purchased from Clontech Laboratories Inc., USA.

Genomic DNA was isolated using a standard protocol from heparinized blood samples from the following species: (1) Hominoid: chimpanzee (Pan troglodytes) and gorilla (Gorilla gorilla); (2) Old world monkey: rhesus monkey (Macaca mulatta), cynomolgus monkey (Macaca fascicularis), African green monkey (Cercopithecus aethiops), colobus (Procolobus badius), and langur (Trachypithecus cristatus); (3) New world monkey: marmoset (Callithrix jacchus), squirrel monkey (Saimiri sciureus), and night monkey (Aotus trivirgatus); (4) Strepsirhini: ring-tailed lemur (Lemur catta). All primate genomic DNA samples used in this study were provided by the late Professor Osamu Takenaka from the Primate Research Institute of Kyoto University of Japan.

2.3. Reverse Transcription-Polymerase Chain Reaction (RT-PCR) and Genomic PCR Amplification. Alternative TSEN54 transcripts were analyzed by RT-PCR. Moloney Murine Leukemia Virus (M-MLV) reverse transcriptase and an RNase inhibitor (Promega) were used for reverse transcription at a reaction temperature of 42°C. To confirm that the total RNA samples did not contain genomic DNA, we performed PCR using a TSEN54 primer pair targeted to an intronic region (Figure S1, in Supplementary Material available online at http://dx.doi.org/10.1155/2016/1679574). The RT-PCR reactions consisted of 35 cycles at 94°C for 30 s, 60°C for 30 s, and 72°C for 30 s. Genomic DNA from various primates was used as the template for PCR amplification. Genomic PCR reactions consisted of 30 cycles at 94°C for 30 s, 57°C for 30 s, and 72°C for 30 s. All primers used in this study and their sequences are listed in Table 1.

2.4. Molecular Cloning and Sequencing. RT-PCR and PCR products were separated on 1.5% agarose gels, purified with the Gel SV extraction kit (GeneAll) and cloned into the TA cloning vector (RBC Bioscience). Cloned DNA was isolated using a Hybrid-Q™ kit (GeneAll). Sequencing of primate DNA samples and alternative transcripts was performed by Macrogen Inc., Republic of Korea. Nucleotide sequences were aligned using the BioEdit program (http://www.mbio.ncsu.edu/BioEdit/bioedit.html).

2.5. Real-Time RT-PCR and Statistical Analyses. TSEN54 genes, including original transcripts and Alu-exonized transcripts,
were analyzed by real-time RT-PCR amplification. All real-time RT-PCR primers used and their sequences, are listed in Table 1. Real-time RT-PCR was performed in a Rotor Gene Q thermocycler (Qiagen) for 40 cycles at 94°C for 10 s, 60°C for 10 s. Melting curve analyses were performed for 5 s at 55–99°C. Each sample (1μL) was added to a 19 μL reaction mixture containing 7 μL H2O, 10 μL QuantiTect SYBR Green PCR Master Mix (Qiagen), and 1μL each of the forward and reverse primers. TSEN54 amplification efficiencies and correlation coefficients (R²) were determined from the slopes of the standard curves obtained using a 10-fold serial dilution series. The amplification efficiency was calculated by the following formula: efficiency (%) = \((10^{-1/slope} - 1) \times 100\). Each primer pair exhibited a single, sharp peak indicating that the primers amplified one specific PCR product. Primer dimers were not observed. All target transcripts were normalized for relative quantification by the normalization factor (NF) derived from geometric means delta-Cq (quantification cycles) of the reference genes. All cynomolgus monkey samples were normalized by ADP-ribosylation factor GTPase activating protein 2 (ARFGAP2) [26]. All rhesus monkey samples were normalized by ribosomal protein L32 (RPL32) and ribosomal protein L13a (RPL13A) [27]. Hydroxymethylbilane synthase (HMBS), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), and PRL32 were used as reference genes in human samples [27]. All samples were amplified in triplicate.

3. Results and Discussion

3.1. Comparative Structure Analysis of the TSEN54 Gene in Humans and Primates. Previously, we analyzed the whole transcriptome of various cynomolgus monkey tissues by RNA sequencing [28] and identified a new AS event, iso1g00002, in cynomolgus monkey TSEN54. This event occurred by the integration of the AluSx element in TSEN54 intron 8 (Figure 1). To compare structural differences in TSEN54 of human, rhesus, and cynomolgus monkey, we analyzed mRNA sequences. Based on the GenBank database, the transcript (NM_207346) of human TSEN54 gene is composed of 11 exons and is transcribed into a 1970 bp mRNA with a 213bp 5' untranslated region (UTR), 1581bp coding region, and 356bp 3' UTR with a consensus polyadenylation signal. The transcript (NM_001261548) of rhesus monkey TSEN54 is also composed of 11 exons and has 94.1% sequence identity and 96.5% amino acid similarity to human TSEN54. TSEN54 of cynomolgus monkey is still registered as a model RefSeq
in the GenBank database. TSEN54 of human, rhesus, and cynomolgus monkey had structural and sequence homology (Figure 1). Therefore, we focused our investigation on exonization events during primate evolution and comparative expression analysis of original and Alu-exonized transcripts.

3.2. Validation of the Alu-Exonized Transcript and Expression Pattern of the TSEN54 Gene. To identify and validate the Alu-exonized transcript, we performed comparative RT-PCR amplification using cerebellum (or whole brain) and testis (or ovary) tissues of human, rhesus, and cynomolgus monkey and sequenced the products. The antisense primer spanned the exon junction between exons 9 and 10, and primer pairs were designed based on the rhesus monkey TSEN54 gene (Figure 2(a)). Unexpected alternative transcript variants AT1 and AT2 were identified in cynomolgus and rhesus monkey, and AT1–AT5 were identified in human (Figure 2(b)). The sequencing data showed that AT1 and AT2 had an extended form of exon 8 and that AT3 had an extended exon 8 that included about 25 bp of intron 8 (Figure 3). AT4 and AT5 included the AluSx sequence as the result of an Alu-exonization event. AT5 showed the same structure as isotig00002 identified from cynomolgus monkey RNA seq data. However, AT5 was not detected in cynomolgus or rhesus monkey. Thus, we performed RT-PCR analysis using a primer that included the AluSx sequence within TSEN54 intron 8 (Figure 2(a)). Using this approach, we confirmed the Alu-exonized transcript (AT5-1) in cynomolgus and rhesus monkey (Figures 2(c) and 3).

Previous studies have shown that intron-rich or ancient genes are associated with higher AS levels in eukaryotic genomes. Furthermore, ancient gene functions such as RNA-binding and mRNA processing show relatively high levels of AS [29]. TSEN54 functions in mRNA processing and RNA-binding and is an intron-rich ancestral gene. Here, we identified the AS variants of TSEN54 in human and in rhesus and cynomolgus monkey. Investigation of AS variants between TSEN54 exons 8 and 9 identified 5 alternative transcripts (Figures 2 and 3). Although identified TSEN54 AS variants result in premature termination of transcripts (Figure S2), they were reasonably varied. It was evident that the AS events were activated in TSEN54.

The exonization event of many transposable elements, including Alu, leads to new exon creation by providing novel splicing sites [12]. Therefore, the alternative splicing machinery contributes to the generation of an abundant transcriptome in primate and human genomes. Recently, Alu exonization was shown to be induced by the U2AF65 splicing factor, which is in competition with RNA-binding protein hnRNP C, binding to Alu elements [30]. Furthermore, TE-derived exons and transcripts are epigenetically regulated, correlating with cell-type specific gene expression [31]. Exonization of intronic Alu elements can induce either cassette exon or exon elongation [32]. In the case of cassette exon, the de novo exon creation occurs by providing both splicing donor and acceptor sites within Alu elements. Depending on the location of elongated exons, exon elongation could be subdivided by the simple elongation of an internal exon or the first/last exon. Alu exonization could change the original character of a functional gene by providing an alternative promoter, coding sequence, or a premature termination. In this study, the AluSx element is exonized in intron 8 of TSEN54 (Figures 2 and 3). However, the exonization mechanism seems to differ between human and primates. In the human genome, AluSx is exonized by two alternative mechanisms of simple elongation and cassette exon (Figure 3). In cynomolgus and rhesus monkey genomes, AluSx is exonized only by the simple elongation mechanism. To trace the human-specific cassette exon mechanism, related splice sites were compared using human, cynomolgus, and rhesus monkey genomic sequences (data not shown). The comparison demonstrated that all splice sites are the same across the three genomes. Therefore, the potential of alternative splicing is the same in human, cynomolgus, and rhesus monkey genomes. We concluded that different alternative splicing observed between human and primates was not due to a primate-specific splicing site mutation. The observed splicing differences might be due to splicing regulatory factors, including epigenetic regulation.

![Figure 1](https://example.com/figure1.png)
Figure 2: RT-PCR analysis of original and alternative transcripts in cerebellum (or whole brain) and testis (or ovary) tissues of human, rhesus, and cynomolgus monkey. (a) Primer location, RT-PCR amplification using primer 1 pair (b) and primer 2 pair (c). GAPDH (120 bp) indicates the positive control. M indicates size marker. AT indicates alternative transcript and NSP is the nonspecific products, confirmed by sequencing.

Figure 3: Structure of TSEN54 original and alternative transcripts. Open, closed black, and gray boxes represent the untranslated region of exons, protein coding region, and PCR product, respectively. Dashed boxes indicate the predicted TSEN54 gene structure. Arrows indicate primer location.
Figure 4: Real-time RT-qPCR analysis of TSEN54 original and Alu-exonized transcripts in various tissues of cynomolgus, rhesus monkey, and human. Expression pattern of TSEN54 original transcript in cynomolgus monkey (a), rhesus monkey (b), and human (c). Expression pattern of Alu-exonized transcript in cynomolgus monkey (d), rhesus monkey (e), and human (f). Cynomolgus monkey panels: 1, cerebellum; 2, cerebrum; 3, kidney; 4, colon; 5, liver; 6, lung; 7, pancreas; 8, small intestine; 9, spleen; 10, stomach; 11, testis. Rhesus monkey panels: 1, cerebellum; 2, cerebrum; 3, kidney; 4, colon; 5, liver; 6, lung; 7, pancreas; 8, small intestine; 9, spleen; 10, stomach; 11, ovary. Human panels: 1, bone marrow; 2, whole brain; 3, fetal brain; 4, colon; 5, small intestine; 6, heart; 7, kidney; 8, liver; 9, fetal liver; 10, lung; 11, placenta; 12, prostate; 13, skeletal muscle; 14, spinal cord; 15, spleen; 16, stomach; 17, testis; 18, thymus; 19, trachea; 20, uterus.
or differences in the binding efficiency of splicing-associated proteins.

To understand the expression patterns of the transcript variants of the TSEN54 gene including original and Alu-exonized transcripts, we performed transcript-specific RT-qPCR in 11 different cynomolgus and rhesus monkey tissues and 20 different human tissues (Figure 4). Original and Alu-exonized transcripts of TSEN54 were ubiquitously expressed in all examined tissues of cynomolgus and rhesus monkey. The original transcript was more highly expressed in human lung tissue, and the Alu-exonized transcript was highly expressed in human lung and thymus tissues. Overall, the expression patterns of the original and Alu-exonized transcripts were similar. Therefore, we suggested that alternative splicing frequency of original and Alu-exonized transcripts was maintained in various tissues. Also, AluSx insertion in TSEN54 gene leads to exonization by creating an alternative splice site but did not affect the expression changes.

3.3. Evolutionary Analysis of the TSEN54 Intron 8 AluSx Insertion. The majority of Alu elements were inserted into the genome of the primate common ancestor, 35 to 65 million years ago. During primate evolution, these elements have been amplified to extremely high copy numbers (~500,000 copies) [12]. To measure the integration time of AluSx in TSEN54 intron 8, we amplified and sequenced this region in the genomic DNA of various primates. PCR amplification targets were AluSx and MER53, because MER53 is located within intron 8 of AluSx (Figure 5(a)). We identified a 508 bp amplicon containing MER53 and AluSx from the TSEN54 gene in all primate genomic DNA tested, including hominoid (human, chimpanzee, and gorilla), old world monkey (rhesus, cynomolgus monkey, colobus, and langur), new world monkey (marmoset, squirrel, and night monkey), and Strepsirrhini (ring-tailed lemur) (Figure 5(b) and Figure S3).

This indicated that MER53 and AluSx in TSEN54 integrated into the genome of a common ancestor before the divergence of Haplorhini and Strepsirrhini (Figure 5(c)), much earlier than 63 million years. Therefore, the AluSx element integrated into the primate common ancestor genome and could be a source of alternative splicing during TSEN54 evolution.

Figure 5: Evolutionary investigation of MER54 and AluSx element during primate evolution. (a) Genomic structure of rhesus monkey TSEN54 gene and primer location. (b) PCR amplification of MER54 and AluSx with various primate DNA samples. M indicates the size marker. (c) Schematic representation of the integration events of MER54 and AluSx in TSEN54 during primate evolution. Mya: millions of years ago.
Furthermore, PCR amplification showed an unexpected 838 bp amplicon in langur genomic DNA (Figure 5(b)). Sequencing results indicated that an additional new AluY element was inserted into the AluSx element of TSEN54 intron 8 in langur genomic DNA (Figure S3). We assume that the two different PCR amplicons were caused by polymorphic insertion of the AluY element in langur. To test our hypothesis, we examined AluY element insertion by PCR in two langurs. Two different haplotypes were identified in langur 2371, while two identical haplotypes were identified in langur 2370 (Figure S4). Therefore, we identified the polymorphic insertion of a new AluY element in langur genomic DNA (Figure 5(c)).

The AluY element is the youngest Alu subfamily, and some AluY elements have shown polymorphic insertion in the human population [17]. Polymorphic AluY have been used as valuable genetic markers for population, linkage, and human identification studies [33, 34]. Previously, human-specific polymorphic AluYb8 insertion in WNK1 intron 10 was reported to be associated with blood pressure variation in Europeans [35]. AluYb8 insertion was shown to induce AS events. Here, polymorphic AluY insertion in the langur genome occurred inside the exonized AluSx of TSEN54 intron 8, possibly contributing to transcriptomic diversity and complexity via induced AS events. Most AluY subfamily elements are associated with direct repeats at flanking regions, called target site duplications (TSDs), of 10–20 bp. TSD sequences can be valuable markers for the confirmation of recent classical target-primed reverse transcription-(TPRT-) mediated Alu insertion events [12]. The polymorphic AluY element had TSD sequences (GAAAACCTGTCTC) in direct repeats on either side of the element (Figure S4). We suggest that the polymorphic insertion of the AluY element in the langur TSEN54 gene is not yet fixed and that this element originated from an active master gene via the TPRT machinery.

3.4. Sequence Analysis of Polymorphic AluY Element. Throughout Alu evolution in primate genomes, mutations were accumulated within the master genes and subsequently inherited by their copies [36]. These accumulated mutations created new Alu subfamilies. Therefore, the Alu family is composed of several distinct subfamilies characterized by a hierarchical series of mutations. While the newly amplified AluY family is the youngest, it was able to be subdivided and characterized based on diagnostic sites [37]. To classify the subfamily of the polymorphic AluY in genomic langur TSEN54, we performed sequence analysis. We based our sequence analysis of polymorphic AluY and the AluS, AluS, and AluY subfamilies on Repbase Update (http://www.girinst.org). Polymorphic AluY had diagnostic mutation sites common with the consensus AluY element and showed
94% sequence identity. However, the polymorphic AluY element could not be classified into any existing AluY subfamilies. Therefore, we assumed that the polymorphic AluY could be part of a new Alu subfamily. We found additional 17 specific mutation sites as well as diagnostic mutations of the AluY consensus sequences (Figure 6). Therefore, according to standardized nomenclature for Alu repeats, the polymorphic AluY in langur genomic TSEN54 could be designated as the AluY117 subfamily.

### 4. Conclusions

In this study, we validated and compared exonization derived from AluSx on the TSEN54 gene in human and primate (rhesus and cynomolgus monkey). However, the exonization mechanism seems to differ between human and primates. Next, we confirmed that the AluSx element integrated into an intron of the TSEN54 gene before the divergence of Haplorhini and Strepsirrhini. Furthermore, we identified the polymorphic insertion of a new AluY element in the AluSx element of langur TSEN54 gene. Based on our results, we assume that the AluSx contributed to diversity in transcripts of TSEN54 gene by providing an alternative splicing site and induced species-specific evolutionary event such as polymorphic insertion during primate evolution.

### Competing Interests

The authors declare that there are no competing interests regarding the publication of this paper.

### Authors’ Contributions

Ja-Rang Lee, Young-Hyun Kim, and Sang-Je Park contributed equally to this work.

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