Exonization of AluYa5 in the human ACE gene requires mutations in both 3′ and 5′ splice sites and is facilitated by a conserved splicing enhancer

Haixin Lei, Ian N. M. Day and Igor Vořechovský*

University of Southampton School of Medicine, Division of Human Genetics, Duthie Building, Mailpoint 808, Southampton SO16 6YD, UK

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ABSTRACT

Ancient Alu elements have been shown to be included in mature transcripts by point mutations that improve their 5′ or 3′ splice sites. We have examined requirements for exonization of a younger, disease-associated AluYa5 in intron 16 of the human ACE gene. A single G>C transversion in position –3 of the new Alu exon was insufficient for Alu exonization and a significant inclusion in mRNA was only observed when improving several potential splice donor sites in the presence of 3′ CAG. Since complete Alu exonization was not achieved by optimizing traditional splicing signals, including the branch site, we tested whether auxiliary elements in AluYa5 were required for constitutive inclusion. Exonization was promoted by a SELEX-predicted heptamer in Alu consensus sequence 222–228 and point mutations in highly conserved nucleotides of this heptamer decreased Alu inclusion. In addition, we show that Alu exonization was facilitated by a subset of serine/arginine-rich (SR) proteins through activation of the optimized 3′ splice site. Finally, the haplotype- and allele-specific ACE minigenes generated similar splicing patterns in both ACE-expressing and non-expressing cells, suggesting that previously reported allelic association with plasma ACE activity and cardiovascular disease is not attributable to differential splicing of introns 16 and 17.

INTRODUCTION

Splicing removes introns from eukaryotic precursor (pre-)mRNA and joins exons together to form mature transcripts. This step-wise process involves multiple and relatively weak interactions of the pre-mRNA substrate, several small nuclear ribonucleoprotein particles (snRNPs U1, U2, U4/U6 and U5) and a large number of non-snRNP proteins (1–3). In addition to numerous trans-acting factors, splicing requires cis-elements in the pre-mRNA that include the 5′ splice site (5′ss; consensus MAG/GURAGU), branchpoint sequence (BPS; YNCURAY), polypyrimidine tract (PPT) and the 3′ splice site (3′ss; YAG). These sequences are degenerate in higher eukaryotes, but are by no means sufficient for accurate splicing. Efficient intron removal often requires auxiliary sequences, known as exonic and intronic splicing enhancers (ESEs and ISEs) and silencers (ESSs and ISSs), that promote or inhibit splicing, respectively. Splicing enhancers have been identified through mutations or polymorphisms that alter splicing (4–6), through computational comparisons (7–9) and through selection of sequences that activate splicing or bind splicing regulatory factors (10,11), most notably a family of serine/arginine-rich (SR) proteins [reviewed in (12)]. Typically, SR proteins bind to ESEs in both constitutive and alternative exons through one or more N-terminal RNA recognition motifs (RRMs) (12). Unlike more extensively studied ESEs or ESSs, intronic auxiliary splicing signals have been studied in much less detail (13–19).

Human introns contain a large number of repetitive elements that may influence pre-mRNA splicing (20–27). The most abundant class of intronic repeats is represented by short interspersed elements that include Alu sequences. Alus are primate-specific, ~300 nt repeats that constitute ~10% of the human genome in over 10^6 copies. Alu insertions may cause genetic disease (28–30) and can contribute to protein diversity through exonization (31–34). About 5% of alternatively spliced internal exons in the human genome contain an Alu sequence and Alus have recently been shown to be exonized by single point mutations that improve their 5′ or 3′ss (32,33). Alus may therefore provide suitable systems for studying evolutionary aspects of both traditional and auxiliary splicing signals.

The human ACE gene encodes angiotensin converting enzyme (ACE; EC 3.4.15.1), which converts inactive...
angiotensin I into a critical vasoconstrictor and blood pressure regulator angiotensin II. Mice lacking ACE have low blood pressure, renal pathology and reduced male fertility (35,36). ACE has been identified as a major component of the genetic variance of highly heritable ACE plasma concentrations (37–41). Closely linked ACE polymorphisms have been associated with cardiovascular diseases, including arterial hypertension, myocardial infarction, left ventricular hypertrophy and coronary arteriosclerosis (42–47), and with Alzheimer’s disease (48). In particular, associations of an insertion/deletion polymorphism (I/D) of antisense AluYa5 in ACE intron 16 with these phenotypes have been reported in a large number of independent studies, with meta-analyses supporting an association of a modest effect (47–51). Detailed linkage disequilibrium studies have attempted to map ACE levels as a quantitative trait locus to a particular polymorphism within ACE, supporting I/D and several intragenic single nucleotide polymorphisms (SNPs) as probable candidates for causal variants (47,52,53). However, genetic mapping of low penetrance genes in regions with high linkage disequilibrium has major limitations in complex traits and a biological mechanism for the proposed allelic and haplotype association needs to be demonstrated. Although several hypotheses have been considered, including a putative influence of I/D haplotypes on transcriptional regulation (54), no reliable evidence has been provided to date.

Here, we have tested if ACE I/D and closely linked SNPs influence pre-mRNA splicing and expression of ACE transcripts using minigene assays. In addition, we have examined the requirements for I/D Alu exonization by modifying both traditional and auxiliary splicing signals. We found that this Alu could not be included in mature transcripts by improving either 3' or 5' ss and that the AluYa5 exonization required at least one mutation in both splice sites. This process was facilitated by a conserved ESE in the new Alu exon. Finally, we show that the Alu I/D inclusion in mRNA was promoted by a subset of SR proteins through increased utilization of the optimized 3'ss.

**MATERIALS AND METHODS**

**Plasmid constructs**

Minigenes A and B (Figure 1A) were cloned into HindIII/EcoRI of pCR3.1 (Invitrogen) using primers 1 (5'-gat caa gct taa gtg caa agg agt aca gct cat tg) and 2 (gat cga att cct cac tca cac tgt ggt ccg tct tt) and a DNA sample heterozygous for the I/D polymorphism. Constructs C–F were made using

![Figure 1](image-url)
heteroduplexes were used as probes to visualize the single-stranded regions. (A) Probe alignment showing the exact position of the heteroduplex motifs. (B) DNA melting curve analysis of the probes. Loss of the bands at 79 °C indicates heteroduplexes. The DNA melting data were consistent with the heteroduplex motif. (C) The heteroduplex formation at the 3’ end of the S/J intron was confirmed by Southern hybridization of the genomic DNA. (D) The length of the probe sequence and the identity of the probe sequence are not shown. The probe sequence contains both the target sequence and the 5’-terminal region of the probe sequence. (E) The sequence alignment of the probes is shown. (F) The sequence alignment of the probes is shown. (G) The sequence alignment of the probes is shown. (H) The sequence alignment of the probes is shown. (I) The sequence alignment of the probes is shown.

RESULTS

A lack of haplotype-specific splicing pattern of \textit{ACE} minigenes

To test the influence of \textit{ACE} variants and \textit{Alu} sequences on pre-mRNA splicing, we prepared minigene constructs carrying predisposing and protective haplotypes (Figure 1A) that have been identified previously in independent human populations (57,58). The constructs contained either full (minigene A, B) or truncated (C, D) intron 16. Since extensive self-complementarity in intronic sequences may influence exon inclusion through modifying secondary RNA structure (20) and intron 16 \textit{Alus} in the opposite orientation would be predicted to create stable stem–loop structures (data not shown), we also deleted tandemly arranged sense \textit{Alu} elements in the latter constructs to create minigenes E and F (Figure 1A).

Examination of the splicing pattern after transfection of the wild-type minigenes with (A, C, E) and without (B, D, F) \textit{Alu}Ya5 into 293T (Figure 1B), HeLa and PANC1 cells (data not shown) revealed a correctly spliced RNA product and a transcript retaining short intron 16, but no exon 17 skipping. Mutations in three SNPs located close to the 3’s of intron 16 (Figure 1A), including IVS16-11G/A in PPT that may weaken 3’s recognition, did not induce exon 17 skipping or intron 16 retention (Figure 1C).

\textit{ACE} intron 16 I/D \textit{Alu} is not exonized by a single mutation at the predicted splice acceptor site

\textit{ACE} intron 16 I/D \textit{Alu} belongs to a young, rapidly accumulating \textit{Ya5} subfamily (59–61), which tends to occupy less \textit{Alu}-dense environment than older relatives of the \textit{Y} subfamily or more ancient \textit{Alu}I/S subfamilies (62). Exonization of old and intermediate \textit{Alus} could be achieved with a single mutation (33,34) and was facilitated by altering concentration of a protein involved in the 3’s selection (33) or U1 snRNA (34). We therefore examined requirements of a polymorphic, recently integrated and disease-associated \textit{Alu} for constitutive inclusion in \textit{ACE} mRNA.

Table 1 shows alignments of the consensus sequences of \textit{AluI/S} subfamilies with \textit{ACE} \textit{Alu}Ya5 at the predicted 3’ss. Unlike the \textit{Alid} subfamily, most \textit{AluS}-derived exons have been spliced via proximal AG as they contain inactivating guanosine in the distal AG (position +3 relative to the proximal AG or −2 relative to the distal AG, Table 1) (33). The proximal 3’ AG is repressed in the presence of guanosine −3 (33). Comparison of \textit{ACE} \textit{Alu}Ya5 with exonized \textit{Alus} showed that this element was more similar to the \textit{Alu}S subfamily (Table 1), suggesting that optimizing position −3 relative to the proximal AG may exonize this sequence. We replaced guanosine −3 with cytosine, which is a preferred nucleotide in competing AG sites (63,64) and the most evolutionarily conserved nucleotide in vertebrates (65), and examined the expression of \textit{Alu}-containing isoforms after transfection (Figures 1A and 2A). However, neither mRNA products transcribed from minigene A (Figure 1A, data not

Table 1. Sequence alignment of the 3’ splice sites of \textit{ACE} I/D \textit{Alu}Ya5 and \textit{AluI/S} consensus sequences

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*Position is relative to the proximal 3’ AG. Sequence variations are in bold. Minigene mutation is indicated in italics. Position in the \textit{Alu} consensus sequence (33) is indicated by a subscript. Proximal (\textit{Alu} position 280 and 281) and distal (276 and 277) AGs are shaded. \textit{PGT} \textit{Alu} was significantly exonized following a single \textit{G}282>C mutation (33).
shown) nor mRNA products transcribed from truncated minigene E (lanes 1–2, Figure 2A) had any detectable exonization of ACE AluYa5.

Exonization of ACE AluYa5 by optimizing several 5’ splice sites in the presence of 3’CAG

To test whether optimized 5’ss can exonerize this Alu in the presence of 3’ CAG or GAG, we mutated positions +2, +3 and +5 of the predicted 5’ss (34). In addition, we improved the match to the 5’ss consensus by introducing single nucleotide mutations in one upstream (position −12 relative to the predicted 5’ss) and two downstream (+136 and +220) potential splice donor sites (Table 2). Furthermore, we created a high Shapiro–Senapathy score 5’ss in position −16 by multiple mutations in both the full-length (A) and truncated (E) constructs. To further improve recognition of the 3’ss, we mutated the closest match (CAGUCA_A19C) to the BPS consensus to the almost invariant BPS of Saccharomyces cerevisiae (UACUAA_A19C), which is also an optimal mammalian BPS (66). Alu-containing isoforms (designated Alu-E for exonized Alu, Figure 1A) were quantified after transfection of mutated constructs into 293T cells. Although mutations at the 5’ss in the presence of 3’ GAG did not exonize Alu (data not shown), combination of a strong 5’ss at position −16 with the 3’ CAG was capable of significant Alu inclusion. The Alu inclusion was further improved in reporters with the optimized BPS (Figure 2A, lanes 3–4, Figure 2B and C). A point mutation of the putative BP [CAGUC(A19>T)] located in the optimal distance from the 3’ AG (67), eliminated Alu from the mRNA (Figure 2A, lane 5), suggesting that A19 is the BP of the new Alu exon. Introduction of uridine at position +2 of the predicted 5’ss, which creates a highly conserved GU
consensus, was insufficient for Alu inclusion (lane 6), but when combined with the 3' CAG, we observed ~11% exonization (lane 7 and Figure 2D). In contrast to position +2U, mutations designed to improve putative base-pairing interactions with U1 snRNA (+3, +5) did not produce any Alu inclusion in the absence of the 5' GU (lanes 8–9 and 12), but further improved exonization when combined with +2U, with adenosine +3 being more efficient than guanosine +5 (Figure 2A, lanes 10–11 and Figure 2D). Triple mutations at the predicted 5'ss producing a good match to the 5' consensus sequence resulted in Alu inclusion levels comparable to those produced by optimal BPS in constructs with 5'ss in position −16 (cf. lanes 13 and 4 in Figure 2A). A C>G transition in position −12 (Table 2) led to activation of the 5'ss in position −16 (lane 14), presumably through improved match in position +5 of the 5'ss. Sequencing of the RNA product generated by the +136C>T mutation showed that ~30% of mature transcripts contained a longer, 256 nt Alu exon (Figure 2E). Finally, a construct mutated in position +220 (Table 2) did not produce any Alu inclusion despite a high-score 5'ss consensus (data not shown), most probably due to a shortened distance between this and downstream 3'ss and/or poor exon definition of a predicted 341 nt exon, which is more than twice the size of an average human exon.

Correlation of the Shapiro and Senapathy scores with Alu inclusion levels produced by minigenes mutated in the predicted 5'ss was significant ($r = 0.73, p = 0.02$, Figure 2A and Table 2). However, a slightly lower Alu inclusion observed for a clone with a high-score 5'ss at position −16 than for an optimized predicted 5'ss (cf. lanes 3 and 13, Figure 2A and Table 2) was indicative of the presence of auxiliary splicing signals outside a 9 nt 5'ss consensus. Thus, despite limitations of the Shapiro–Senapathy scores, such as independence of each position, they provided a reasonably good indicator of splicing outcomes, consistent with their high predictive values for utilization of competing alternative, mutated and cryptic donor sites (68,69).

**Identification of splicing regulatory sequences in exonerized ACE AluYa5**

Strong traditional splicing signals did not result in complete exonization of the new Alu exon (Figure 2A, lane 4), suggesting that a constitutive inclusion requires auxiliary elements in the new Alu exon or in flanking introns. We first used ESE prediction tools that may facilitate identification of putative ESEs in the exonized Alu sequence (Figure 3A), including RESCUE-ESE (7), octamer ESE/ESS (9) and functional systematic evolution of ligands by exponential enrichment (SELEX) implemented in the ESE Finder facility (8). Putative ESEs (shown as segments 1–6, Figure 3A) that did not overlap splice sites were individually deleted in minigene E that was optimized at the 3' and 5'ss (designated E', Figure 3A). Deletion of segment 2 substantially reduced exonization (Figure 3B, lane 2), whereas deletions of segments 3–5 failed to do so (Figure 3B, lanes 3–5). Mutagenesis of each position in this heptamer to reduce Alu inclusion showed that a T>G transversion in position 5 had the strongest effect (Figure 3B, lanes 6–14). This alteration had one of the lowest SRp40 matrix scores (8), although no overall correlation was found between matrix scores and Alu inclusion levels ($P > 0.2$, Figure 3B). Mutation of the last heptamer position, which increased the SRp40 matrix score, did not alter exonization (data not shown). To test whether double mutations with minimized matrix scores can further reduce Alu inclusion, we created constructs containing either mutations 3G/4T (matrix score 0.24) or mutations 1G/5G (matrix score 0.42) in segment 2 (Figure 3C). Mutations 3G/4T had no effect, whereas mutations 1G/5G reduced Alu exonization to a level observed for the segment 2 deletion. Finally, since segments bridging the splice sites could not be deleted, two mutations were introduced at positions 1 and 3 of segment 6 (CCACAGG to GGCAGG, Figure 3A). Alu exonization was reduced to 31% (lane 15, Figure 3B).

Comparison of segment 2 sequence with exonized Alus (34) showed that this heptamer was invariant ($n = 18$) or had only a single nucleotide change ($n = 12$) in 35 exons that contained the right arms of exonized Alus in antisense orientation. The last heptamer position was least conserved. In contrast, positions 1 and 5, which were most efficient in reducing Alu exonization (Figure 3B), were virtually invariant (Figure 3D), suggesting that they are critical for the splicing enhancement observed for segment 2. Variability of the heptamer was greater in Alu exons derived from Jb subfamilies (13 changes in 12 exons) than those derived

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**Table 2. Minigene mutations at the 5' splice sites**

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<th>+3</th>
<th>+4</th>
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aPosition is relative to the predicted 5'ss. Position in the consensus Alu sequence (33) is subscripted.  
bPosition +220 is downstream of Alu I/D. The 5' GT is shaded. P, clones mutated in predicted 5'ss.
from S subfamilies (11 changes in 19 exons). In addition, the heptamer sequence was invariant in most of over 8000 Alu that were identified as amenable to exonization [(34), data not shown]. Alignment of consensus sequences of major Alu subfamilies (62,70) with ACE Alu Ya5 also showed a high degree of conservation of segment 2 in all Alu subfamilies, except for AluSp. This subfamily typically contains cytosine in position 5, which decreased the SRp40 matrix score, but not Alu inclusion (lane 12, Figure 3B). Interestingly, among 61 Alu-derived exons (34), we found only a single AluSp entry.

SR-mediated inclusion of ACE I/D Alu in mature transcripts

To test whether Alu exonization is influenced by factors known to control RNA processing, we co-transfected the wild-type reporters (data not shown) and minigenes optimized at the 3′ss with plasmids expressing SR proteins. Unlike wild-type constructs, minigenes containing 3′ CAG co-transfected with ASF/SF2, SRp40 and SC35 generated a larger, 1158 bp fragment (Figure 4, lanes 2–4). Sequencing of this RNA product revealed the presence of complete AluYa5, intron 17 and the 3′ end of intron 16 in mature transcripts. This isoform was designated Alu-L (Figure 1A). Minigene A with 3′CAG generated higher amounts of Alu-L as compared to minigene E containing the same 3′CAG mutation (cf. lanes 2 of Figure 4A and B), suggesting that the deleted segment of intron 16 contains sequences that promote utilization of the predicted 3′ss.

Cells that were co-transfected with splicing reporters and identical empty vectors lacked Alu-L (lanes 1 in Figure 4A and B). These results are consistent with promotion of proximal splicing by SR proteins, first observed for ASF/SF2 (71,72).

SR proteins contain one or two N-terminal RRMs and a C-terminal SR domain (73). To test their requirements for the Alu-L activation, we co-transfected the splicing reporters mutated at the 3′CAG with the wild-type and mutated ASF/SF2 plasmids that lacked sequences encoding RRM1, RRM2

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**Figure 3.** Identification of a splicing enhancer element in ACE intron 16 AluYa5. Influence of segments 2–5 deletions and segment 2 point mutations on Alu exonization. (A) Exonized Alu segment (upper case) with putative ESEs (underlined and numbered 1–6). Segments 1, 2 and 6 were predicted by the ESE Finder (8), segments 1 (C allele only), 3 and 4 were significant ESEs identified through octamer sequences (9) and segment 5 was predicted by the RESCUE-ESE (7). Intronic sequence is in lower case. To facilitate mutagenesis, segments 2 through 5 were individually deleted in minigene E′. This minigene contained intron 16 truncation (Figure 1A) and four point mutations optimizing the splice sites (shown below the nucleotide sequence in bold). A segment 2, which was mutated individually in each position, is in the middle of the sequence in bold. (B) Alu inclusion levels following deletions of segments 2–5 and point mutations in segment 2. Transfection of all splicing reporters was into 293T cells. AI, Alu inclusion. (C) Alu inclusion levels in double mutants of minigene E. (D) Consensus sequence of segment 2 heptamer in alternatively spliced exons containing right arms of antisense Alus as identified previously (34). Representation of each heptamer position (numbered above) and flanking sequences was visualized using a pictogram utility available at http://genes.mit.edu/pictogram.html.
and RS domains. In addition, we co-transfected this reporter construct with ASF/SF2 lacking a heptaglycine tract between RRM1 and RRM2 as described (55). Deletion of RRM domains virtually eliminated the Alu-L activation, including the RS domain (Figure 4B, lanes 5 and 6). Similarly, Alu-L could still be induced upon deletion of the RS domain of SRp40 (lanes 7 and 8). Together, these results suggested that interaction of ASF/SF2 RRMs with the pre-mRNA was essential for Alu-L formation and that this process was RS-independent.

**DISCUSSION**

Antisense Alu are amenable to exonization since they contain strong PPTs and several potential 5's and 3's (32–34). A single, 3' GAG to 3' CAG mutation in an Alu in the PGT gene, which has the 3's identical to the ACE AluYa5 (Table 1), resulted in almost constitutive inclusion in mRNA (33). In contrast, an identical mutation in ACE AluYa5 did not result in any inclusion in mature transcripts (Figure 2A). Differential effects of this mutation on Alu inclusion could explain a less significant contribution of the younger AluY subfamily to protein diversity as there are only few examples of AluY-containing exons (32).

Proximal 3' AG (positions 280/281, Table 1) is selected in most exonized Alu that were derived from S subfamilies, whereas the distal AG (positions 276/277) is preferred by exonized Alu J sequences (33). The proximal 3'CAG was essential for successful exonization of this element, as we observed no Alu inclusion with the 3' GAG minigenes carrying strong 5'ss at position −16 (Table 2, data not shown). This is consistent with an unproductive use of the proximal 3'CAG in most Alu-derived exons (33) and with a general C ~ T > A > G hierarchy in the 3's utilization (63,64). An apparently inefficient use of the 3'CAG (Figure 2A, lane 2) could be due to a shorter PPT in our constructs (14 uninterrupted Ts) as compared with, on average, 19 ± 3 Ts in exonized Alus (33). The mean size of poly(A) tail of Alu S/J and the younger Ya5 was ~21 and ~26 nt, respectively, whereas the size range of recent, disease-causing Alu insertions was between 40 and 97 nt (74), suggesting that the size of poly(A) tails determines retropositional capability. If in antisense orientation, the 3'ss that contain longer tracts may be recognized more efficiently by the spliceosome than Alus with shorter tracts.

Since the BPS of the new Alu exon is located in a flanking intronic sequence, branch site variability may contribute to diverse exonization potential of similar Alu elements. This is supported by the observed increase of Alu inclusion in minigenes with optimized BPS consensus (lane 2, Figure 2A) and its elimination in a construct with A19>T mutation (lane 5), suggesting that a poor BPS consensus limits exonization of weakly included Alus. Although we did not test if improvement of the 5'ss coupled with the optimal BPS would suffice for Alu inclusion in constructs containing 3'GAG, the enhancement mediated by the S.cerevisiae BPS was only minor (Figure 2A, lane 4).

Although the predicted 5'ss in ACE Alu (Table 2) was not used in the presence of the 3'CAG, creation of the 5'ss GT consensus resulted in 11% Alu inclusion, which was further improved by optimizing 5'ss in positions 3 and 5 (Figure 2, lanes 7, 10, 11 and 13). The GT dinucleotide was essential for Alu inclusion, because mutations in these positions did not exonize Alus in constructs lacking the GT consensus (lanes 8 and 9, Figure 2A). The enhancement of Alu inclusion is likely to be mediated by optimized pairing with U1 snRNA, as shown earlier (34).

However, the presence of strong traditional splicing signals, including a long PPT, the preferred BPS and optimized 3' and 5'ss, did not result in complete inclusion of the new Alu exon (lane 4 in Figure 2A). This suggested that auxiliary splicing signals, such as the presence of enhancers or a lack of silencers, or both (7,8,75), were essential for constitutive Alu derepression. Consistent with this assumption, deletion of a predicted enhancer element in Alu positions 222–228 diminished exonization in the presence of optimized 3' and 5'ss and
mutations in positions conserved in exonized Alus contributed most to Alu exclusion (Figure 3B). This segment was predicted by the ESE Finder (8) as a putative SRp40 binding site with a significant matrix score of 5.2, suggesting that it might be a binding site for this protein, although novel regulatory features in sequences created by deletions could not be excluded (Figure 3A). Although testing of putative ESEs in the exonized Alu of the ADAR2 gene did not identify any splicing auxiliary sequences (34), this heptamer is present in the ADAR2 Alu exon and it will be interesting to examine its activity in other exonized Alus and in a heterologous context. The presence of sequences that strongly repress splicing in sense Alus (55) may contribute to a low exonization potential of these elements. Since antisense Alus also contain sequences that repress splicing (14), it will be interesting to compare their inhibitory activities in future studies.

In addition to exonization of ACE Alu by optimizing both 3′ and 5′ss, we have shown that this element can be included in mature transcripts in cells over-expressing three SR proteins in the presence of a single point mutation G29G>C. This effect, which depends critically on the interaction between ASF/SF2 RRM with the pre-mRNA (Figure 4B), can be explained by promotion of proximal splicing (6,71,72,76) or could be attributed to altered mRNA export or translation in co-transfected cells. Future studies should test to what extent, if any, the promotion of proximal splicing depends on the sequences contributed by the ID Alu. Together, these results suggest that ~238 000 antisense Alus in human introns (33), which may represent a reservoir of ready-to-use segments expanding protein diversity (31), have a differential exonization potential and that trans-acting factors controlling coupled processes of transcription, splicing and mRNA export play an important role in this process.

Altered splicing contributes to aberrant expression of genes that may predispose to cardiovascular diseases, including LDLR, LPL, LIPA, LCAT, APOB and APOAI [reviewed in (77)]. The variability of ACE mRNA expression, its sensitivity to external signals and inaccessibility of relevant patient tissues makes it difficult to study the importance of ACE SNPs in functional assays. Here, we have tested the hypothesis that ACE haplotypes and several SNPs flanking the 3′ss of intron 16, including IVS16-11C/A, result in differential exon 17 skipping, alter the amounts of natural transcripts and explain putative allelic association with disease. Purine residues around position IVS-11 show a great depletion in the PPTs of several mammals, zebrafish, fugu, ciona and other species (65), suggesting that this conserved position is important in evolution. As the IVS16-11C>A transversion may weaken the PPT by reducing interaction with the 65 kDa subunit of auxiliary factor of U2 snRNP and other polypyrimidine-binding proteins, carriers of the A allele would be predicted to show increased exon skipping and/or lower expression of natural transcripts. However, the absence of ACE AluYa5, which is in tight linkage disequilibrium with the IVS16-11A allele (Figure 1A), has been associated with a higher ACE activity in plasma and a higher risk of coronary disease (47,48,58). Intron 16 has a strong 5′ss (the Shapiro and Senapathy score 89.3) and was spliced out efficiently in our reporter assay (Figure 1B). A small reduction in the strength of the 3′ss scores (71.0 in minigenes A, C and E down to 68.5 in minigenes B, D and F, Figure 1A) due to IVS16-11A may not lead to recognizable differences in ACE expression. Although neither the exonic SNP nor PPT variants altered splicing (Figure 1C) and minigene assays generally show good reproducibility of the splicing patterns in vivo, we cannot formally exclude that the tested SNPs exert differential effect on mRNA expression in relevant tissues or distinct developmental stages. Taken together, our results do not support a role of allele-specific pre-mRNA splicing patterns generated by putative predisposing and protective ACE haplotypes in the analyzed gene segment. Future studies should address putative involvement of other ACE polymorphisms in mRNA processing, such as the recently implicated SNP rs4362 in a downstream exon (47).

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