Evolution of alternative splicing in primate brain transcriptomes

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Alternative splicing is a predominant form of gene regulation in higher eukaryotes. The evolution of alternative splicing provides an important mechanism for the acquisition of novel gene functions. In this work, we carried out a genome-wide phylogenetic survey of lineage-specific splicing patterns in the primate brain, via high-density exon junction array profiling of brain transcriptomes of humans, chimpanzees and rhesus macaques. We identified 509 genes showing splicing differences among these species. RT–PCR analysis of 40 exons confirmed the predicted splicing evolution of 33 exons. Of these 33 exons, outgroup analysis using rhesus macaques confirmed 13 exons with human-specific increase or decrease in transcript inclusion levels after humans diverged from chimpanzees. Some of the human-specific brain splicing patterns disrupt domains critical for protein–protein interactions, and some modulate translational efficiency of their host genes. Strikingly, for exons showing splicing differences across species, we observed a significant increase in the rate of silent substitutions within exons, coupled with accelerated sequence divergence in flanking introns. This indicates that evolution of cis-regulatory signals is a major contributor to the emergence of human-specific splicing patterns. In one gene (MAGOH), using minigene reporter assays, we demonstrated that the combination of two human-specific cis-sequence changes created its human-specific splicing pattern. Together, our data reveal widespread human-specific changes of alternative splicing in the brain and suggest an important role of splicing in the evolution of neuronal gene regulation and functions.

INTRODUCTION

Despite their close evolutionary relationships, humans and nonhuman primates have notable differences in phenotypic traits and susceptibility to various diseases (1). A long-standing challenge in evolutionary biology is to uncover genomic changes that account for the unique attributes of the human species. It has been proposed that evolution of gene regulation is a driving force for phenotypic divergence between species (2). Consistent with this theory, studies of human and nonhuman primate transcriptomes revealed widespread changes in steady-state transcript levels during recent human evolution (3–8).

In addition to transcriptional regulation, alternative splicing is another predominant mechanism of gene regulation in higher eukaryotes. Alternative splicing occurs among different tissues (9) or developmental states (10,11), during cellular responses to external cues (12,13) and in a wide range of human diseases (14,15). In humans, the vast majority of protein-coding genes are alternatively spliced (16–18). For example, deep RNA sequencing indicates that >90% of multi-exon human genes undergo alternative splicing (18,19). By producing multiple mRNA and protein products from a single gene, alternative splicing is capable of generating tremendous functional and regulatory diversity from a limited repertoire of protein-coding genes in eukaryotic genomes (20,21).

There are numerous examples of genes with species-specific exons or splicing patterns (22,23). Comparative analyses of cDNA and EST data indicate that many alternative splicing events are not conserved between species (24–27). In fact, during evolution, ancient exons undergo creation and loss of alternative splicing patterns (28–30), and new exons are frequently added to existing functional genes (23,24,31,32).

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Thus, evolution could use splicing to create species-specific post-transcriptional regulation of gene expression as well as novel protein function. One well-known example is the primate-specific exon in a human gene ADAR2 (adenosine de-aminase, RNA-specific, B1). This exon is created from an Alu retrotransposon during primate evolution (33). It inserts a new peptide segment into the catalytic domain of ADAR2, altering the catalytic activity of the protein product (34). Even between closely related species, such as humans and chimpanzees, differences in splicing exist (35,36). For example, using a custom Agilent microarray targeting approximately 1700 exon-skipping events and subsequent RT–PCR assays, we and colleagues identified 30 exons with different levels of transcript inclusion in corresponding tissues (frontal cortex or heart) of humans and chimpanzees (35). These data suggest that the splicing patterns of orthologous genes can diverge over relatively short evolutionary timescales [i.e. ~5−7 million years that separate humans and chimpanzees (37)].

In this work, we conducted a systematic survey of splicing differences between human and nonhuman primate brains, particularly lineage-specific changes in splicing after humans diverged from chimpanzees. We carried out a high-throughput microarray analysis of alternative splicing in brain transcriptomes of human, chimpanzee and rhesus macaque, followed by extensive RT–PCR tests in a large panel of tissue samples from all three species. Our study revealed widespread changes of alternative splicing in the brain transcriptome during primate and human evolution.

RESULTS

Comparative analysis of alternative splicing between humans and nonhuman primates using a high-density exon junction array

To study alternative splicing in human and primate brains, we extracted total RNAs from the cerebellum of six chimpanzees, six rhesus macaques and two pooled human cerebellum samples each with 10 or more individual donors (see Materials and Methods). These RNA samples were processed and hybridized to the Affymetrix Human Exon Junction Array (HJAY) for analysis of alternative splicing patterns (38). The HJAY array is a next-generation Affymetrix exon array for genome-wide analysis of alternative splicing. It averages eight probes per probe set for 315 137 exons in the human genome, and also includes probe sets for 15 544 and 10 147 events had sufficient perfect-match microarray probes with mismatches for orthologous chimpanzee/rhesus macaque, using the UCSC pairwise genome alignments of the human genome (hg18) to the genomes of chimpanzee (panTro2) or rhesus macaque (rheMac2) (46–47). Of the 20 815 mRNA/EST-supported human alternative splicing events interrogated by the HJAY array, 15 544 and 10 147 events had sufficient perfect-match probes for orthologous chimpanzee and rhesus transcript isoforms (see definition in Supplementary Material, Methods).

For these events, we used our MADS+ (Microarray Analysis of Differential Splicing) algorithm (38,45) in pairwise comparisons of humans versus chimpanzee or human versus rhesus array profiles to identify differential splicing events. Specifically, we restricted the MADS+ analysis to HJAY probes perfectly matching orthologous transcripts from multiple species. For every alternative splicing event analyzed, MADS+ calculated P-values of multiple probe sets targeting exons and exon–exon junctions (see Fig. 1A for the probe design for exon-skipping events), requiring opposite trends for probe sets targeting competing isoforms as evidence of differential alternative splicing (38). For example, as shown in Figure 1, the exon 2 of GPBP1L1 (GC-rich promoter binding protein 1-like 1) was predicted to be differentially spliced between human and rhesus cerebellums. From the HJAY array data of this exon, we observed significantly higher intensities of the exon inclusion probe sets (i.e. probe sets targeting the upstream exon–exon junction, downstream exon–exon junction and exon) and significantly lower intensities of the exon-skipping probe set in human samples compared with rhesus samples (Fig. 1B; solid blue lines). Meanwhile, the estimated gene expression level of GPBP1L1 was comparable in human and rhesus (Fig. 1B; dashed red lines). These data indicated that this exon was included at a higher level in the human cerebellum. Indeed, our subsequent RT–PCR validation confirmed that this exon was included in human transcripts at intermediate-to-high levels, but almost completely skipped in orthologous rhesus transcripts (Fig. 1C).

Using these computational procedures, our analysis of the HJAY profiles revealed widespread splicing differences between humans and closely related nonhuman primates. In total, we identified 336 alternative splicing differences between human and chimpanzee cerebellums and 415 differences between human and rhesus cerebellums. These events covered all types of alternative splicing patterns, with cassette exons (i.e. exon skipping) being the most prevalent type (Table 1). It should be noted that because of our filtering criteria, in particular
the number of perfect-match probes for orthologous transcripts, a much smaller number of alternative splicing events can be analyzed for human–rhesus differences than for human–chimpanzee differences (1501 versus 2646, see Table 1). Despite this, we identified more alternative splicing events with human–rhesus differences (415) than with human–chimpanzee differences (336), representing 27.6% and 12.7% of all events analyzed between humans and rhesus macaques or between humans and chimpanzees, respectively. This was consistent with the phylogenetic relationship among these three species (37).

The percentage of alternative splicing events with predicted human–chimpanzee differences in the cerebellum (12.7%)
appeared to be higher than the percentage reported for two other tissues (frontal cortex and heart) (6–8%) in our earlier study (35). However, these statistics were not directly comparable, as distinct microarray platforms were used in these two studies. Specifically, in the present work, we used a high-density Affymetrix short oligonucleotide exon junction array, with approximately 32 probes for each exon-skipping event (38). In contrast, the earlier study used a custom Agilent long oligonucleotide array, with six probes designed to interrogate each exon-skipping event (35). Thus, the difference in the percentage of alternative splicing events with predicted human–chimpanzee differences could be largely attributed to the sensitivity of these two microarray platforms. We also noted that in the previous study using the Agilent custom array, we did not observe any significant difference in the rate of splicing evolution in frontal cortex and heart (35).

RT–PCR validation of alternative splicing evolution and human-specific splicing patterns in the brain

To confirm the identified alternative splicing differences between species, we selected 40 cassette exons for experimental validation, from 281 cassette exons predicted to have splicing differences between human and chimpanzee and 340 cassette exons predicted to have splicing differences between human and rhesus. All predicted events in the human versus chimpanzee comparison or the human versus rhesus comparison were ranked according to the overall level of statistical significance summarized from all available exon probes and exon–exon junction probes (see details in Supplementary Material, Methods). The 40 selected exons were analyzed by semi-quantitative RT–PCR in a large panel of cerebellum tissues from all three species. For a subset of these exons with subtle changes in inclusion levels, we also used a highly sensitive fluorescently labeled RT–PCR protocol, which allowed us to accurately quantify the levels of transcript inclusion in different species (see Materials and Methods). To distinguish bona fide inter-species splicing divergence from intra-species splicing variability, our RT–PCR analysis examined all individual samples used for generating the HJAY array profiles, as well as RNAs from additional human/chimpanzee/rhesus tissue samples (see Supplementary Material, Table S1). Of the 40 exons tested, 33 showed splicing differences between species as predicted by the HJAY array, yielding a validation rate of 83%. For most of the RT–PCR confirmed events, the splicing patterns of orthologous exons were consistent within species, while different between species. For example, the exon 2 in the 5′-UTR of GPBP1L1 was predicted according to the HJAY array data to be differentially spliced between humans and rhesus macaques (Fig. 1B). This exon was completely skipped in all eight rhesus cerebellum samples from different animals. In contrast, we observed a consistent pattern of intermediate-to-high levels of exon inclusion in four human cerebellum samples from single or multiple donors, and in eight chimpanzee cerebellum samples from different animals (Fig. 2A).

It should be emphasized that in selecting candidate exons for RT–PCR analysis, we included exons with various levels of statistical significance and did not cherry-pick candidates from the top of our predicted events to achieve a high validation rate. In fact, a primary selection criterion for experimental validation was to facilitate RT–PCR primer design and data interpretation, i.e. the selected cassette exons did not have alternative splice site usage at the upstream and downstream exon–intron boundaries and were flanked by constitutively spliced exons based on the UCSC Genome Browser annotation. All cassette exons analyzed by the HJAY array in the human versus chimpanzee or the human versus rhesus comparison were ranked by a single combined P-value for the overall statistical significance of inter-species splicing difference, which was summarized from individual P-values of all available perfect-match probes targeting orthologous exons and exon–exon junctions as in Shen et al. (38) and Xing et al. (45). Among the 281 predicted cassette exon events in the human versus chimpanzee comparison, the median rank of RT–PCR confirmed events was 65 with an inter-quartile range (IQR) of 9 to 152. The lowest rank of validated events was 239. In the human versus rhesus comparison, among the 340 predicted cassette exon events, the median rank of RT–PCR confirmed events was 80 with an IQR of 43 to 169 and the lowest rank of 320. Thus, based on our validation rate (83%), we expect that the vast majority of our HJAY-predicted events represent real splicing differences between humans and closely related nonhuman primates. The list of validated events and their RT–PCR gel pictures are provided in Supplementary Material, Table S2. The rankings of RT–PCR-validated events among all HJAY-predicted events are provided in Supplementary Material, Table S3. The complete lists of HJAY-predicted cassette exon events are provided in Supplementary Material, Tables S4 and S5.

Our RT–PCR analysis also revealed a number of exons with human-specific changes in splicing compared with both chimpanzee and rhesus orthologous exons. In this phylogenetic analysis, the observed splicing pattern in the rhesus cerebellum was used as the outgroup to infer the direction of splicing changes of the human exon after humans diverged from chimpanzees. For example, in DDX42 (DEAD box protein 42), the exon 2 in its 5′-UTR had different levels of exon inclusion in human, chimpanzee and rhesus cerebellums (Fig. 2B). Based on RT–PCR analysis, this exon was completely skipped in the rhesus transcripts, weakly included in the chimpanzee transcripts and included at an intermediate level in the human transcripts. This suggests that the splicing activity of DDX42 in the cerebellum was gradually strengthened in the lineage leading to humans. Together, of these 33 exons with RT–PCR-validated splicing differences among species, 13 exons (39%) had consistently higher or lower levels of transcript inclusion in the human cerebellum compared with both chimpanzee and rhesus cerebellums, suggesting recent increases or decreases in splicing activities after humans diverged from chimpanzees. These genes covered a broad range of functional categories (Table 2). Extrapolating from the total number of events identified by the HJAY analysis (Table 1), the overall validation rate in our RT–PCR analysis (83%) and the percentage of exons with human-specific splicing changes among all exons with validated splicing differences (39%), we estimated that more than 100 alternative splicing events in our entire data set underwent human-specific splicing changes. These splicing
events represent a group of unique transcriptome signatures in the human brain that can distinguish humans from other closely related primate species.

Previous studies have suggested a difference in the rate of protein sequence evolution between the human and chimpanzee lineages (48–50). Using our RT–PCR data of 33 exons (Supplementary Material, Table S2), we compared the numbers of exons with human-specific or chimpanzee-specific splicing changes in the brain. To enable an unbiased comparison, we focused on 16 exons predicted by the HJAY array to have splicing differences between humans and chimpanzees and subsequently validated by RT–PCR. Of these 16 exons, 2 exons did not have RT–PCR data in rhesus macaques due to the difficulty of primer design. For the remaining 14 exons, we used the rhesus macaque as the outgroup, we identified 9 exons with human-specific splicing changes and 5 exons with chimpanzee-specific splicing changes. However, we caution that any conclusion on the rate difference of splicing changes in the human and chimpanzee lineages would require a much more extensive set of experimentally validated splicing differences between all three species.

Functional and regulatory implications of alternative splicing evolution in the brain

On all genes with identified splicing differences between human, chimpanzee and rhesus cerebellums, Gene Ontology analysis using the DAVID tool (51) found four strongly enriched GO terms: ‘cytoskeleton organization and biogenesis’ ($P = 0.007$), ‘RNA processing’ ($P = 0.012$), ‘cell–cell adhesion’ ($P = 0.025$) and ‘neurological system process’ ($P = 0.028$) (see the DAVID analysis procedure in Materials and Methods). A previous study of natural selection on protein-coding regions of human genes found cytoskeletal proteins to be under strong negative selection pressure during human evolution (52). Our result thus suggests an intriguing scenario that genes encoding cytoskeletal proteins could experience contrasting modes of selection pressure at the RNA level and at the protein level during recent human evolution.

Next, we investigated potential evidence of positive selection for exons with human-specific splicing changes. Because of the small size of individual exons, methods to detect positive selection using divergence data between
specifies do not have enough power (31). On the other hand, a variety of approaches have been developed to detect signatures of recent positive selection using SNP data (53,54). We compiled the results from 13 genome- or chromosome-wide scans for positive selection in the human genome (55–67). Of the 13 exons with RT–PCR-validated human-specific splicing patterns (Table 2), two exons (in NUPL1 and PTPRZ1) were located within the positively selected genomic regions identified by Tang et al. (65) and Huttley et al. (55), respectively. Notably, Tang et al. (65) used an approach based on contrasting the extended haplotype homozygosity profiles between populations. Huttley et al. (55) was among the earliest scans for positive selection signals using long LD blocks. It is important to note that these SNP-based approaches are only suitable for detecting signals of positive selection during very recent human evolution (i.e. ≤250 kya) (53–54), while the acquisition of a human-specific splicing pattern and the selection pressure acting on such an event could potentially occur any time during the 5–7 million years after humans diverged from chimpanzees.

Interestingly, of the 13 genes showing human-specific changes in brain splicing patterns after humans diverged from chimpanzees, several are implicated in the etiology of human diseases, in particular neurological diseases, including Huntington’s disease [HIP14L (68)], Alzheimer’s disease [GSTM3 (69)] and schizophrenia [PTPRZ1 (70)] (Table 2). For example, HIP14L (Huntingtin-interacting protein 14-related; also referred to as ZDHHC13) encodes a neuronal-specific palmitoyl acyltransferase that interacts with and palmitoylates Huntingtin, a gene when mutated causes Huntington’s disease [HIP14L (68)]. For example, HIP14L (Huntingtin-interacting protein 14-related; also referred to as ZDHHC13) encodes a neuronal-specific palmitoyl acyltransferase that interacts with and palmitoylates Huntingtin, a gene when mutated causes Huntington’s disease [HIP14L (68)].

Another example of human-specific splicing changes with interesting functional implications is the alternative splicing of MAGOH (Mago-nashi homolog, proliferation-associated). MAGOH encodes a key component of the exon junction complex (EJC) and is involved in mRNA nonsense-mediated decay (NMD) (72). The human-specific evolution

### Table 2. Exons with human-specific changes in transcript inclusion levels compared with chimpanzee and rhesus cerebellums

<table>
<thead>
<tr>
<th>Gene symbol</th>
<th>Exon location (hg18)</th>
<th>Phylogenetic patterns of exon inclusion levels</th>
<th>Impact on mRNA/protein</th>
<th>Gene function</th>
</tr>
</thead>
<tbody>
<tr>
<td>MAGOH</td>
<td>chr1:53471801-53471912</td>
<td>Human (medium-major) ≤ chimpanzee (constitutive)/rhesus (constitutive)</td>
<td>Coding</td>
<td>RNA and protein binding, NMD</td>
</tr>
<tr>
<td>PIGX</td>
<td>chr3:19793792-197938039</td>
<td>Human (minor-medium) &gt; chimpanzee (no inclusion)/rhesus (no inclusion)</td>
<td>Coding, exon inclusion introduces premature termination codon</td>
<td>Component of glycosylphosphatidylinositol-mannosyltransferase I</td>
</tr>
<tr>
<td>ZDHHC13/HIP14L</td>
<td>chr11:19121105-19121246</td>
<td>Human (medium) ≤ chimpanzee (almost constitutive)/rhesus (almost constitutive)</td>
<td>Coding, exon 2 skipping causes usage of a downstream ATG start site on exon 5</td>
<td>Palmitoyl transferase, Mg²⁺ transport</td>
</tr>
<tr>
<td>LPHN/CIRL3</td>
<td>chr4:62461031-62461070</td>
<td>Human (medium) ≤ chimpanzee (major)/rhesus (major) (no inclusion)</td>
<td>Coding</td>
<td>G-protein coupled receptor, cell adhesion and signal transduction</td>
</tr>
<tr>
<td>NUPL1</td>
<td>chr13:24781384-24781420</td>
<td>Human (major-constitutive) &gt; chimpanzee (medium)/rhesus (medium-major)</td>
<td>Coding</td>
<td>Component of the nuclear pore complex (NPC); nucleocytoplasmic transporter activity</td>
</tr>
<tr>
<td>DDX42</td>
<td>chr17:59206199-59206270</td>
<td>Human (minor-medium) &gt; chimpanzee (minor) &gt; rhesus (no inclusion)</td>
<td>5'-UTR</td>
<td>ATP-dependent helicase activity, protein displacement and RNA annealing</td>
</tr>
<tr>
<td>CAMTA1</td>
<td>chr1:7738284-7738315</td>
<td>Human (minor-medium) &lt; chimpanzee (medium) &lt; rhesus (medium-major)</td>
<td>Coding, alternative C-terminus</td>
<td>Calmodulin binding, transcription regulator</td>
</tr>
<tr>
<td>GSTM3</td>
<td>chr1:11008397-11008405</td>
<td>Human (major) &lt; chimpanzee (constitutive)/rhesus (constitutive)</td>
<td>Coding, alternative N-terminus</td>
<td>Glutathione S-transferase</td>
</tr>
<tr>
<td>ACSL3</td>
<td>chr2:22347363-22347374</td>
<td>Human (medium) &gt; chimpanzee (minor)/rhesus (minor) (differences confirmed by FAM-labeled RT–PCR)</td>
<td>5'-UTR</td>
<td>Acetate–CoA ligase</td>
</tr>
<tr>
<td>GLS</td>
<td>chr2:19152772-19152778</td>
<td>Human (major) &lt; chimpanzee (major)/rhesus (major) (differences confirmed by FAM-labeled RT–PCR)</td>
<td>Coding, alternative C-terminus</td>
<td>Glutaminase, glutamine catabolic process</td>
</tr>
<tr>
<td>PTPRZ1</td>
<td>chr7:121474963-121475080</td>
<td>Human (minor) &gt; chimpanzee (no inclusion)/rhesus (no inclusion)</td>
<td>Coding</td>
<td>Transmembrane receptor protein tyrosine phosphatase</td>
</tr>
<tr>
<td>KCNJ3/GIRK1</td>
<td>chr2:155274360-155274577</td>
<td>Human (medium) &lt; chimpanzee (constitutive)/rhesus (constitutive)</td>
<td>Coding, truncated protein</td>
<td>G-protein activated inward-rectifier type potassium channel</td>
</tr>
<tr>
<td>NAV2</td>
<td>chr11:19862415-19862484</td>
<td>Human (medium) &gt; chimpanzee (minor)/rhesus (minor-medium)</td>
<td>Coding</td>
<td>ATP-binding helicase</td>
</tr>
</tbody>
</table>
of MAGOH transcripts resulted in pronounced skipping of exon 3 in the human cerebellum, while the orthologous exon was 100% included in chimpanzee and rhesus transcripts (Fig. 2D). Importantly, exon 3 encodes a peptide segment critical for the interaction between MAGOH and the ribosome-associated protein PYM (72). In a previous study, site-directed mutagenesis within exon 3 abolishes MAGOH-PYM interaction, leading to impaired EJC removal and recycling (72). Although the exact functional impact of the exon 3 skipping isoform remains to be determined experimentally, this human-specific splicing event could provide a novel regulatory mechanism to modulate the MAGOH-PYM interaction, thus affecting the NMD pathway in a human-specific manner.

Of the 13 exons whose human-specific changes in splicing activities are confirmed by RT–PCR (Table 2), 11 are located within the protein-coding regions. Alternative splicing of these exons results in either in-frame insertion/deletion of a peptide segment (e.g. MAGOH), alterations of the N-terminus or the C-terminus of the protein product (e.g. HIP14L) or introduction of a premature termination codon and possibly mRNA nonsense-mediated decay (e.g. PIGX). The remaining two exons (DDX42, ACSL3) are located in the 5′-UTR. It is well known that the 5′-UTRs of mRNAs contain regulatory signals for modulating mRNA stability and protein translation (73), and alternative splicing within 5′-UTRs can affect translational efficiency (74,75). Thus, human-specific splicing changes within the 5′-UTR may influence post-transcriptional regulation of gene expression. We also note that the 5′-UTR appears to be a frequent spot for the creation of new exons, based on previous studies on exonization of transposable elements (TEs) during primate evolution (31,76,77).

To further confirm the regulatory impact of human-specific splicing changes in the 5′-UTR, we tested the exon 2 in the 5′-UTR of DDX42 which had a much higher transcript inclusion level in humans compared with chimpanzees and rhesus macaques (Fig. 2B). We performed 5′-UTR luciferase reporter assays (78,79) to assess whether the inclusion of this exon affected translational efficiency of the DDX42 mRNA. Briefly, 5′-UTR isoforms containing or skipping the exon 2 of DDX42 were cloned into the psiCHECK2 luciferase reporter system (Promega). For each 5′-UTR isoform, the resulting reporter construct expressed both the firefly luciferase and the Renilla luciferase fused downstream of the cloned 5′-UTR isoform (Fig. 3A). After transfection into HeLa cells, we measured luciferase activities and mRNA levels. For each 5′-UTR construct, the Renilla luciferase activity and mRNA level were normalized to the firefly luciferase, and the translational efficiency was estimated using the fold change of luciferase activity normalized to mRNA concentration (78,79) (see details in Materials and Methods). We observed a 2-fold reduction in the estimated translational efficiency when the exon 2 of DDX42 was inserted to its 5′-UTR (Fig. 3B). The mRNA concentration remained unchanged (Fig. 3B). Thus, the human-specific increase in the transcript inclusion level of DDX42 exon 2 provides a regulatory mechanism for reducing protein production at the post-transcriptional level without changing the protein-coding sequence.

**Figure 3.** Modulation of translational efficiency by exon 2 in DDX42 5′-UTR with a human-specific splicing change. (A) Schematic diagrams of the DDX42 5′-UTR luciferase reporter constructs. 5′-UTR delta construct: psiCHECK2 vector (Promega) expressing Renilla luciferase under the control of the SV40 promoter and firefly luciferase under the control of the HSV-TK promoter (not shown). 5′-UTR exon-skipping construct: Renilla luciferase downstream of the DDX42 5′-UTR isoform, which skips exon 2. 5′-UTR exon inclusion construct: Renilla luciferase downstream of the DDX42 5′-UTR isoform, which includes exon 2 (black exon). (B) Inclusion of exon 2 into DDX42 5′-UTR results in a 2-fold reduction in translational efficiency according to the luciferase reporter assay. Relative luciferase (LUC) activity: shown as the ratios of Renilla and firefly luciferase activity. The luciferase activity ratio of the control construct 5′-UTR delta (psiCHECK2) was designated as 1 and the values of 5′-UTR exon-skipping/inclusion constructs were normalized accordingly. Relative luciferase (LUC) mRNA levels: shown as the ratios of Renilla and firefly mRNA concentration. The mRNA ratio of the control construct 5′-UTR delta (psiCHECK2) was designated as 1 and the values of 5′-UTR exon-skipping/inclusion constructs were normalized accordingly. Translational efficiency: shown as fold change of luciferase activity normalized to the mRNA level. The fold change of luciferase activity over the mRNA level of the control construct 5′-UTR delta (psiCHECK2) was designated as 1 and the values of 5′-UTR exon-skipping/inclusion constructs were normalized accordingly. In all plots, the mean represents average value from six independent experiments, and the error bar indicates standard error of the mean.

**Correlation between splicing evolution and sequence divergence of exons and flanking introns**

The large number of identified differential splicing events between human and nonhuman primate brains also allowed us to investigate mechanisms important for the evolution of splicing. It is well-known that cis-elements within exons and flanking introns, such as splice sites and splicing enhancer/silencer elements, play critical roles in the regulation of splicing (80). To assess how evolution of exonic and intronic sequences influenced the evolution of splicing, we analyzed the nucleotide substitution patterns of cassette exons with HJAY-predicted splicing differences among species. As the control, we also analyzed a separate group of cassette exons that passed the same probe-filtering procedure but were not found to have splicing differences among species by the HJAY analysis. Strikingly, for exons showing splicing differences among species, we observed a significant increase in the rate of silent substitutions within exons, coupled with accelerated sequence evolution in flanking introns. Within the region spanning from the 100 nt upstream intron to the 100 nt downstream intron, cassette exons with identified splicing changes between human and chimpanzee cerebellums had an average rate of nucleotide differences of 1.83% (including substitutions and indels), compared with 1.69% for exons without splicing changes ($P = 9.4e^{-4}$, one-sided Fisher’s exact
that these patterns are not artifacts due to sequence of human-specific splicing patterns. It must be emphasized regulatory sequences is a major contributor to the emergence of splicing differences between these two species, the overall was 0.0129. In contrast, for cassette exons without identified splicing changes, the same trend was reproducible in the human versus rhesus comparison (Table 4).

Next, we investigated various types of cis-changes that could contribute to the evolution of splicing. First, small-scale genomic structural changes, including exon duplication and insertion of TEs, have been associated with the creation of new exons during mammalian evolution (23,31). However, as our study focused on exons whose genomic sequences were conserved between humans and nonhuman primates, this mechanism was not an important contributor to the interspecies splicing differences identified in this work. For example, of the 33 exons with RT–PCR-validated splicing differences, only three exons overlapped with TEs, and all three overlapped with TEs in all three species. Therefore, the splicing differences did not result from insertions of TEs during recent human evolution. Next, we investigated evolutionary changes at the 5′ and 3′ splice sites, which were essential signals for exon recognition. For every exon analyzed by the HJAY array, we scored its 5′ and 3′ splice sites in human, chimpanzee and rhesus genomes using MAXENT (86). In the human versus chimpanzee comparison, 16 (5.8%) exons with detected splicing differences had a difference in the 5′ or 3′ splice site scores between humans and chimpanzees of at least 2, compared with 49 (3.0%) exons without detected splicing differences between these two species (P = 0.03, two-sided Fisher’s exact test). However, this trend was not reproduced in the human versus rhesus comparison. Twenty-five (7.5%) exons with detected splicing differences had a difference in the 5′ or 3′ splice site scores between humans and rhesus macaques of at least 2, compared with 56 (7.4%) exons without detected splicing differences between these two species. This was unexpected, as the longer evolutionary distance between humans and rhesus macaques allowed for compensatory cis-changes to occur, which could buffer the changes in the splice site strength.

<table>
<thead>
<tr>
<th>Human versus</th>
<th>Splicing change</th>
<th>Number of synonymous substitutions</th>
<th>Number of synonymous sites</th>
<th>( K_s ) rate (one-sided)</th>
<th>Fisher’s exact test</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chimpanzee</td>
<td>Yes</td>
<td>343</td>
<td>6040</td>
<td>0.0129</td>
<td>2.5e–3</td>
</tr>
<tr>
<td></td>
<td>No</td>
<td>343</td>
<td>38 477</td>
<td>0.0089</td>
<td></td>
</tr>
<tr>
<td>Rhesus</td>
<td>Yes</td>
<td>277</td>
<td>7722</td>
<td>0.0359</td>
<td>5.3e–6</td>
</tr>
<tr>
<td></td>
<td>No</td>
<td>428</td>
<td>16 797</td>
<td>0.0255</td>
<td></td>
</tr>
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</table>

\(^{a}\)Nucleotide differences include substitutions, insertions and deletions.

\(^{b}\)P-value from one-sided Fisher’s exact test on the rate of between-species nucleotide differences of cassette exons with identified splicing changes versus cassette exons without splicing changes.
percentage of all inter-species differences reported. Finally, we investigated the creation and loss of exonic splicing regulatory elements. On a list of exonic splicing enhancers (ESEs) and silencers (ESSs) collected by Burge and colleagues (87,88), we did not observe any overall correlation between splicing differences among species and evolutionary changes that created or disrupted known ESEs and ESSs. Although this could be due to the lack of statistical power, it is more likely that this observation reflects our limited understanding of the tissue-specific ‘splicing code’ in higher eukaryotes (35,89). Indeed, the precise splicing outcomes of individual exons are controlled by a complex array of exonic and intronic regulatory signals (80). Nucleotide changes at any position within the exon or surrounding introns could have the possibility to cause the evolution of splicing patterns. Moreover, these ESEs and ESSs were identified and validated in the HeLa or HEK293 cell lines (87,88), while there are substantial differences in splicing regulation in the brain (90). Additionally, this analysis considered all ESEs or all ESSs as a whole, while the change to a single ESE or ESS may contribute to the evolution of splicing in individual exons.

To further elucidate the molecular mechanisms that could create human-specific splicing patterns, we selected the exon 3 of MAGOH for a detailed case study. This exon was 100% included in chimpanzee and rhesus transcripts, but had a substantial level of exon skipping in the human transcript (Fig. 2D). By comparing the exonic and flanking intronic sequences of this exon in human, chimpanzee and rhesus genomes, we identified two human-specific changes in the flanking intronic sequences. We found a human-specific T-to-G substitution at the sixth intronic nucleotide of the upstream intron–exon boundary, which reduced the score of the 3′ (acceptor) splice site from 8.26 in chimpanzees to 6.13 in humans. Additionally, we identified a human-specific deletion of a 200 bp segment in the downstream intronic region (Fig. 4A). To assess which cis-sequence change(s) contributed to the human-specific evolution of MAGOH exon 3 splicing, we tested the effects of these cis-changes using minigene splicing reporter assays. We cloned the exon and its flanking intronic regions into the minigene reporter pl-11-H3 (see reference (91) and Materials and Methods) and made two minigene constructs corresponding to the wild-type human and chimpanzee genomic sequences (Hs-WT and Pt-WT, see Fig. 4A). The splicing difference between the human and chimpanzee wild-type minigene constructs was consistent with the difference of endogenous splicing patterns in human and chimpanzee tissues. The chimpanzee minigene construct had an exon inclusion level of 97%, while the human minigene construct had a much lower exon inclusion level of 69% (Fig. 4B). We then conducted site-directed mutagenesis of the wild-type chimpanzee minigene construct to introduce the human-specific cis-change(s). The T-to-G change within the 3′ splice site reduced the exon inclusion level of the mutant chimpanzee construct (Pt-T(-6)G) to 84%. However, its inclusion level was still higher than that of the wild-type human construct (Hs-WT, 69%). The deletion of the 200 bp downstream intronic segment reduced the exon inclusion level of the mutant chimpanzee construct (Pt-Del) to 91%. Strikingly, when both cis-changes were introduced simultaneously, the inclusion level of the mutant chimpanzee construct (Pt-T(-6)G-Del) was 70%, almost the same as the inclusion level of the wild-type human minigene construct (69%). These data suggest that both human-specific cis-sequence changes contributed to the evolution of MAGOH exon 3 splicing. This example highlights the complexity of molecular events causing splicing differences between species. Additionally, our sequence and minigene analysis of MAGOH illustrates a general strategy to pinpoint the causal cis-regulatory change(s) responsible for lineage-specific splicing patterns.

**Impact of alternative splicing evolution on the brain transcriptome**

An intriguing topic of investigation is whether our identified splicing differences preferentially influence the transcriptome of the brain (cerebellum) rather than other tissues. In this study, we chose to analyze a large panel of available human/primate samples from the cerebellum. It must be noted that...
the regulation of gene expression and alternative splicing could be either ubiquitous (92) or tissue specific (3,18,93). Thus, two interesting questions arise. First, do the 509 genes showing splicing differences between human and chimpanzee/rhesus cerebellums tend to exhibit brain-specific expression? Second, what fraction of our reported splicing evolution events are ubiquitous in multiple tissues or reflect changes in tissue-specific patterns of splicing?

To address the first question, we analyzed an RNA-Seq data set of nine human tissues, including cerebellum and eight other tissues: adipose, lymph node, heart, muscle, liver, breast, testes and colon (18). For every human gene, we estimated its overall gene expression levels in these nine tissues by calculating the RPKM value [reads per kilobase of exon model per million mapped reads (18,94)] within its constitutive exons. Not surprisingly, we found that the 509 genes with identified splicing differences exhibited strong tissue-specificity in their gene expression patterns. The median RPKM value of these 509 genes was significantly higher in the cerebellum than in seven other tissues (see Supplementary Material, Fig. S1). The only exception was in the testes, a tissue known to have similar expression profiles as the brain (95,96). Moreover, of the 13 genes showing human-specific changes in brain splicing patterns (Table 2), the expression levels of 12 genes in the cerebellum were higher than their median expression levels in eight tissues (excluding the testes). Ten genes were expressed at the highest level in the cerebellum. These results indicate that our identified splicing evolution events affect genes preferentially expressed in the brain.

The second question is whether our identified splicing evolution events among human and chimpanzee/rhesus cerebellums are ubiquitous in multiple tissues or reflect changes in tissue-specific patterns of splicing. To distinguish these scenarios, from the 13 exons displaying human-specific changes in brain splicing patterns (Table 2), we selected 10 exons whose inter-species splicing differences in the cerebellum were readily identified by semi-quantitative RT–PCR assays, and examined the splicing patterns of these 10 exons in three additional tissues (kidney, liver and muscle) of all three species. Based on the observed inter/intra-species splicing differences in multiple species, these 10 exons could be classified into three major categories. For one exon (PTPRZ1), the evolution of splicing occurred in a gene whose expression was strongly restricted to the cerebellum (Supplementary Material, Fig. S2A). In seven genes (CAMTA1, DDX42, GSTM3, LPHN3, NUPL1, PIGX, ZDHHC13), the splicing of the exon showed tissue specificity within species, and the evolution of splicing in the cerebellum was different from the patterns observed in some other tissues (Supplementary Material, Fig. S2B–H). For example, in PIGX, although the exon was almost completely skipped in all chimpanzee and rhesus tissues, we found varying degrees of human-specific increase in its exon inclusion level in the four tissues. The inclusion level of this exon was the highest in the cerebellum, followed by muscle, kidney and liver (Supplementary Material, Fig. S2G). In the remaining two genes (ACSL3, MAGOH), the splicing pattern of the exon appeared to be identical among all tested tissues within each individual species. There was no detectable difference in the extent of splicing evolution among different tissues (Supplementary Material, Fig. S2I and J).

Together, these experiments provide examples of both tissue-specific and ubiquitous evolution of alternative splicing. It must be noted that even alternative splicing events that ubiquitously affect a wide range of tissues of broadly expressed genes could have significant functional consequences in the brain/nervous system. Two well-known examples are the disease-associated aberrant alternative splicing of SMN in patients with SMA (spinal muscular atrophy) (97) and of MAPT in patients with FTDP-17 (frontotemporal dementia and parkinsonism linked to chromosome 17) (98,99). In both cases, the disease gene is broadly expressed, and the disease mutation causes splicing defects in many tissues. However, the pathological phenotypes of these aberrant alternative splicing events are strongly restricted to neuronal cells (15,100). Thus, it is entirely possible that a splicing evolution event is shared by a broad range of tissues but still has a significant functional impact in the brain.

**DISCUSSION**

This study represents a genome-scale phylogenetic survey of alternative splicing evolution in humans and two closely related nonhuman primate species. Using a new high-density exon junction array with a high accuracy for alternative splicing analysis (38–40), we identified 509 genes with splicing differences in the cerebellums of humans and chimpanzees/rhesus macaques. Semi-quantitative and quantitative RT–PCR analyses of a large panel of cerebellum tissues provided strong experimental evidence for a number of genes with human-specific splicing changes after humans diverged from chimpanzees (Table 2). Of these genes, several were previously implicated in the etiology of human neurological diseases. These data are consistent with the view that alternative splicing provides an important mechanism for the creation of evolutionary novelty and species-specific traits (22,23,35).

Based on published literature and the analysis of resulting protein isoforms, the identified human-specific splicing changes in several genes (HIP14L, MAGOH) may have a significant functional impact, by removing protein domains/segments that modulate key protein–protein interactions. We also experimentally demonstrated the regulatory impact of a human-specific splicing pattern within the 5′-UTR of DDX42 (Fig. 3). Together, these data suggest an important role of splicing in the evolution of neuronal gene regulation and functions and provide a number of intriguing candidates for detailed functional studies.

An important issue in comparative analysis of alternative splicing is whether the identified inter-species splicing divergence could in fact be attributed to artifacts of intra-species splicing variability due to genetic or environmental factors (3,101–103). This is of particular concern to the analysis of primate tissues, due to the scarcity of these samples and the difficulty in matching age, gender and health conditions of corresponding tissues from multiple species. In our study, two independent lines of evidence suggest that the vast majority of our identified events represent bona fide inter-species divergence of splicing. First, in the HJAY array...
profiling and subsequent RT–PCR experiments, we examined
cerebellum tissues from a large number of individuals from all
three species. For most of the RT–PCR-confirmed splicing
differences between human and chimpanzee/rhesus cerebel-
lums, we observed consistent splicing patterns within species
(see Fig. 2 for examples). Second, we found a strong corre-
lation between the evolution of splicing and the sequence
divergence of exons and flanking intronic regions. For exons
showing splicing differences across species, we observed a
significant increase in the rate of silent substitutions within
exons, coupled with accelerated sequence divergence in flank-
ing introns. This was consistent with the role of cis-sequence
signals in the regulation of splicing (15,80). This pattern
would not be expected if our identified splicing differences
between species were significantly contaminated by artifacts
due to intra-species splicing variability.

A related question is whether genes showing splicing differ-
ces among human, chimpanzee and rhesus cerebellums display sex-biased splicing. Recent studies of primate and
rodent tissues have identified evolutionarily conserved sex-
biasied splicing events (36,104). However, whether the evol-
utionary divergence of splicing patterns could be sex-specific
has not been investigated before. For the 33 exons with
RT–PCR data in our work, we compared their splicing pat-
terns in samples from male and female donors. We found
only one exon (in \textit{FACE2}) whose exon inclusion level
appeared to be slightly higher in female chimpanzees than in
male chimpanzees. However, even in this case, the difference
in splicing between male and female chimpanzees was very
minor compared with the inter-species difference, which was
shared by all single-donor male and female samples
from humans and chimpanzees (Supplementary Material,
Table S2). It must be emphasized that the goal of this study
is to identify robust inter-species differences of splicing,
regardless of other factors (including sex) that could contribute
to intra-species splicing variability. Therefore, we designed
our HJAY array experiments to profile multi-donor human
RNAs mixed with male and female samples, as well as single-
donor chimpanzee/rhesus samples of both sexes. It is possible
that certain splicing events could evolve differently in males
and females. However, to identify sex-specific evolution of
splicing and possibly compare the rate of such events in
males and females, it is necessary to perform genomic profil-
ing and extensive RT–PCR analysis of a much larger panel of
samples from both sexes of all three species.

Although we have already identified over 500 genes with
differential splicing between human and chimpanzee/rhesus
cerebellums, we expect that they constitute only a subset of
all splicing differences among these tissues. Despite the high
validation rate for the new HJAY array in detecting differen-
tial splicing events (38), our approach has several sources of
false negatives. First, array-based analysis of alternative spli-
cing is best at the detection of known alternative splicing
events. Novel alternative splicing events that are not interro-
gated by the initial array design will be missed by this analy-
sis. Second, as the HJAY array is designed from human exon
annotations, it cannot identify lineage-specific exon loss in
humans or lineage-specific exon creation in chimpanzees
or rhesus macaques. Third, in order to accurately assess
alternative splicing patterns in nonhuman primate tissues, it
is necessary to restrict the analysis of HJAY profiles to
probes that perfectly match orthologous transcripts from mul-
tiple species (41,105,106). Thus, exons with a high rate of
sequence divergence between humans and nonhuman pri-
mates, which could be hotspots for splicing evolution (35),
are less likely to have sufficient perfect-match probes allowing
comparative analysis by the HJAY array. These limitations in
the array-based approach may be addressed by other genomic
technologies for high-throughput splicing analysis. For
example, RNA-Seq has emerged as a powerful tool for tran-
scripome profiling (18,19,107,108). RNA-Seq can detect
novel transcripts, exons and splice junctions independent of
prior annotations, which is an attractive feature for comparing
transcriptomes of closely related species. However, for
RNA-Seq to obtain quantitative sampling of alternative spli-
cing events in the entire transcriptome, the sequencing has
to go extremely deep. Differential splicing events of genes
with intermediate or low expression levels could be missed
by RNA-Seq (107). As a result, currently RNA-Seq analysis of
alternative splicing is strongly biased towards events in
highly expressed genes. For example, in our ongoing study
of the epithelia-specific splicing regulator ESRP1/2
(38,91,109), using 76 bp RNA-Seq with over 60 million
reads per sample, we can detect only <30\% of known ESRP-
dependent splicing events previously identified by the HJAY
array and confirmed by RT–PCR (Xing Y and Carstens
RP, unpublished data). Thus, we anticipate that studies
using RNA-Seq may generate a complementary list of
splicing differences among these species. In the future, the
integration of array and sequencing-based results and further
improvement in these technologies could provide a more
complete picture of splicing evolution in the primate brain
transcriptomes.

Among the 33 events validated by RT–PCR, we observed
both exons with substantial changes in splicing patterns
between species (e.g. \textit{HIP14L}, \textit{MAGOH}, \textit{DDX42}), and exons
with consistent but subtle inter-species differences in exon
inclusion levels (see Supplementary Material, Table S2). For
subtle differences in splicing between species, there could be
several possible evolutionary implications. Some of these
events may result from minor, nonfunctional changes in spli-
cing activities that have been tolerated during evolution.
These may include evolutionary intermediates that have the
potential to evolve into novel functions, as hypothesized
by Lee and colleagues (22–24). On the other hand, we note
that minor changes in exon inclusion levels (as low as a few
percent) sometimes could have significant functional impacts
in the brain, as highlighted by studies of several neurological
diseases caused by splicing defects (100,110).

MATERIALS AND METHODS

Total RNA preparation and HJAY array profiling of
human, chimpanzee and rhesus cerebellum tissues

Postmortem cerebellum samples of eight adult chimpanzees
(four males and four females) and eight adult rhesus macaques
(two males and six females) were generously provided by the
Southwest National Primate Research Center (San Antonio,
TX, USA). These animals died of natural causes or
Identification of differential splicing events between human, chimpanzee and rhesus cerebellums from the HJAY profiles

We have developed a series of statistical methods for the detection of differential splicing events from the Affymetrix HJAY array data (38–41). In this work, these methods were applied to HJAY array data of human, chimpanzee and rhesus cerebellums, after modifications to enable comparisons of splicing patterns between species. Briefly, we identified HJAY array probes perfectly matching exons or exon–exon junctions of orthologous human, chimpanzee and rhesus mRNA transcripts. We then used microarray signals of these probes to identify differential splicing events between human and chimpanzee or between humans and rhesus macaques. A detailed description of our HJAY array analysis procedure is provided in the Supplementary Material, Methods.

RT–PCR validation of differentially spliced exons between human, chimpanzee and rhesus cerebellums

Single-pass cDNA was synthesized using the High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems, Foster City, CA, USA) according to manufacturer’s instructions. Two micrograms of total RNA were used for each 20 μl cDNA synthesis reaction. For each tested exon, a pair of forward and reverse PCR primers targeting flanking constitutive exons were designed using PRIMER3 (111). Primer sequences are described in Supplementary Material, Table S6. For each RT–PCR reaction, 15 ng of total RNA equivalent of cDNA were used for the amplification in a 10 μl PCR reaction using the Phire® Hot Start DNA Polymerase (NEB, Ipswich, MA, USA). PCR reactions were run between 25 and 35 cycles (depending on target transcript abundance; optimized for each exon) in a Bio-Rad thermocycler with an annealing temperature of 62–66°C (optimized for each exon). The reaction products were resolved on 5% TBE polyacrylamide gels and visualized by ethidium bromide staining. Each gel picture shown in Supplementary Material, Table S2 was a representation of three to six RT–PCR replicates.

For exons with subtle changes in inclusion levels, a fluorescently labeled RT–PCR protocol was used to accurately quantify exon inclusion levels. This protocol was modified from the method described in Schuelke (112). Briefly, a 22 nt universal tag sequence (designated as ‘GFPN’), 5′-CGTCGCCGTCC AGCTCGACCAG-3′ derived from GFP N-terminal region, was added to the 5′ end of the forward or reverse primer during oligo synthesis, while the other primer remained un-tagged. A fluorescently labeled universal primer 5′-FAM-CGTCGCCGTCCAGCTGACCAG-3′ was added as a third primer in the RT–PCR reaction. The reaction products were resolved on 5% TBE-urea polyacrylamide gels and visualized using a Typhoon 9200 phosphorimager (GE Healthcare, Piscataway, NJ, USA). Bands were quantified using the Quantity One software (Bio-Rad, Hercules, CA, USA). The exon inclusion level of each exon was calculated as the intensity of the exon inclusion band divided by the total intensity of the exon inclusion and skipping bands.

GO term enrichment analysis of genes with identified splicing differences between human, chimpanzee and rhesus cerebellums

We used the online tool DAVID (113,114) to identify significantly enriched GO terms in genes with splicing differences between human, chimpanzee and rhesus cerebellums as identified by our HJAY array analysis. Of all the cassette exons queried by the HJAY array, 1842 exons passed our filters for gene expression level in the cerebellum, probe intensity and number of perfect-match probes for orthologous chimpanzee/rhesus transcripts (see Supplementary Material, Methods). These 1842 cassette exons were included in our pairwise comparisons of splicing patterns between humans and nonhuman primates. From these 1842 exons, we collected 1056 genes with GO terms and used these genes as our background set in the GO term analysis. Using MADS+, we identified a total of 567 cassette exons with substantial splicing changes between humans and chimpanzees or humans and rhesus macaques. From these 567 exons, we collected 389 genes with GO terms. These 389 genes were analyzed by DAVID for the enrichment of GO terms against our background set of 1056 genes as the control.
Analysis of exon–intron nucleotide differences between human, chimpanzee and rhesus genomes

For all the cassette exons included in our HJAY array analysis, we calculated the rates of nucleotide differences between the human, chimpanzee and rhesus genomes within the exons, 100 nt upstream intronic regions and 100 nt downstream intronic regions. Orthologous exonic and intronic regions between these species were identified using the UCSC pairwise genome alignments of the human genome (hg18) to the genomes of chimpanzee (panTro2) and rhesus macaque (rheMac2) (46,47). For each exon, the rates of nucleotide differences (including substitutions and indels) were calculated separately for exonic and flanking intronic regions using the global alignment program NEEDLE from the EMBOSS package (115).

Calculation of exonic synonymous substitution rate ($K_s$ rate)

For all the cassette exons included in our HJAY array analysis, we calculated their exonic synonymous substitution rate ($K_s$ rate) between the human, chimpanzee and rhesus genomes. We computed the $K_s$ rate between orthologous exon pairs following the approach that we used previously (116). Briefly, orthologous exon sequences from human and chimpanzee (or human and rhesus macaque) were retrieved from the UCSC genome alignments and translated in all three possible reading frames. Translations containing stop codons were removed, and the resulting protein sequences were aligned in all possible combinations of reading frames. We computed sequence identities in all resulting alignments using the global sequence alignment program NEEDLE (115). After removing alignments with <50% protein sequence identity, we selected the reading-frame pair with the highest sequence identity and re-aligned these two protein sequences using CLUSTALW (117,118) under default parameters. The resulting CLUSTALW alignment was used to align corresponding nucleotide sequences (codons), and gaps in the alignment were trimmed. We calculated $K_s$ from the codon-based nucleotide sequence alignment using the Yang– Nielsen maximum-likelihood method (119) implemented in the yn00 program of the PAML package (120). For each group of exons (i.e. exons with or without identified splicing changes between species), we summed up the total numbers of synonymous substitutions/sites over all sequences to calculate its overall $K_s$ rate.

Vector construction for luciferase reporter assay

The psiCHECK2 (Promega, Madison, WI, USA) plasmid was linearized through NheI restriction digestion. The exon 2 inclusion and skipping isoforms of DDX42 5′-UTR were cloned into the NheI-linearized psiCHECK2 vector through homologous recombination using the In-Fusion PCR Cloning System (Clontech) according to the manufacturer’s protocol. The resulting final constructs contained the DDX42 5′-UTR region directly upstream of the Renilla luciferase start codon without the linker sequence. Structures of the tested vectors are illustrated in Figure 3A.

Quantitative real-time PCR assay

Total RNA was prepared from transfected cells using the TRizol (Invitrogen) according to manufacturer’s instructions. Single-pass cDNA was synthesized using High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems) according to manufacturer’s instructions. Quantitative real-time polymerase chain reaction (qRT-PCR) was performed using Power SYBR Green PCR Master Mix (Applied Biosystems) for the luciferase mRNA level. Primers used for the qRT-PCR analysis are Renilla luciferase: forward: 5'-ACAAGTACCTCACCCTGG-3', reverse: 5' CGAT GCCTGTATCTGTGT-3'; firefly luciferase: forward: 5'-GGACATCACTATGCGGAGT-3', reverse: 5'-GGTTC CAGAACACACCAGA-3'. Using a mathematical method described by Pfaffl (121), we calculated the average expression fold change of Renilla luciferase and used mRNA concentrations of firefly luciferase for normalization.

Minigene construction and site-directed mutagenesis

Exon 3 of MAGOH gene homologs and its partial flanking introns were amplified from the human and chimpanzee genomic DNAs using PfuUltra Fusion II HS DNA polymerase (Stratagene, La Jolla, CA, USA). PCR products were subcloned into the NheI site of the pI-11-H3 minigene vector (91) (kindly provided by Dr Russ P. Carstens, University of Pennsylvania, Philadelphia, PA, USA) using the In-Fusion Advantage PCR Cloning Kit (Clontech). Site-directed mutagenesis was done using PfuUltra Fusion II HS DNA polymerase. All sequences and mutations were verified by DNA sequencing.

In vitro minigene splicing reporter assay

HeLa cells were grown in DMEM (Invitrogen) with 10% FBS (Invitrogen). Cells were plated in 24-well plates and transfected using Lipofectamine 2000 (Invitrogen) according to the manufacturer’s protocol. RNA was purified 16 h after transfection and reverse-transcribed into single-pass cDNA. Fluorescently labeled RT–PCR was done as described in the previous section. The pl-11-H3 minigene-specific primer sequences were pl11-F: 5'-GCTGTCCCTCACGAGTACCCA-3'; pl11-R: 5'-CAGCTCGCCAGGCTCAGCAGCGGTTG CATAGA-3'.
SUPPLEMENTARY MATERIAL

Supplementary Material is available at HMG online.

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Conflict of Interest statement. None declared.

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