

Evolutionarily Conserved Alternative Splicing Across Monocots

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ABSTRACT One difficulty when identifying alternative splicing (AS) events in plants is distinguishing functional AS from splicing noise. One way to add confidence to the validity of a splice isoform is to observe that it is conserved across evolutionarily related species. We use a high throughput method to identify junction-based conserved AS events from RNA-Seq data across nine plant species, including five grass monocots (maize, sorghum, rice, *Brachypodium*, and foxtail millet), plus two nongrass monocots (banana and African oil palm), the eudicot *Arabidopsis*, and the basal angiosperm *Amborella*. In total, 9804 AS events were found to be conserved between two or more species studied. In grasses containing large regions of conserved synteny, the frequency of conserved AS events is twice that observed for genes outside of conserved synteny blocks. In plant-specific RS and RS2Z subfamilies of the serine/arginine (SR) splice-factor proteins, we observe both conservation and divergence of AS events after the whole genome duplication in maize. In addition, plant-specific RS and RS2Z splice-factor subfamilies are highly connected with R2R3-MYB in STRING functional protein association networks built using genes exhibiting conserved AS. Furthermore, we discovered that functional protein association networks constructed around genes harboring conserved AS events are enriched for phosphatases, kinases, and ubiquitylation genes, which suggests that AS may participate in regulating signaling pathways. These data lay the foundation for identifying and studying conserved AS events in the monocots, particularly across grass species, and this conserved AS resource identifies an additional layer between genotype to phenotype that may impact future crop improvement efforts.

KEYWORDS conserved alternative splicing events; monocot; grass family; RS and RS2Z subfamilies; R2R3-MYB

ALTERNATIVE splicing (AS) is an important post-transcriptional process that can produce two or more transcript isoforms from a pre-mRNA. AS occurs in the spliceosome by removing introns and joining exons through the selective use of splice sites (Lee and Rio 2015), and is governed by *cis*-regulatory elements such as splicing enhancers/silencers, and *trans*-regulatory elements including the Serine-Arginine-rich (SR) and Heterogeneous nuclear ribonucleoprotein (hnRNP) protein families (Wang and Burge 2008; Busch and Hertel 2012; Reddy *et al.* 2012, 2013). AS isoforms that are translated can influence proteome diversity, while others that are purposefully non-functional can act to post-transcriptionally modulate protein

levels (Fu *et al.* 2009; Hammond *et al.* 2009). AS participates in many important processes during the lifecycle of plants (Staiger and Brown 2013), and AS occurs in response to many abiotic stresses (Mastrangelo *et al.* 2012), for example red/blue light (Shikata *et al.* 2014; Wu *et al.* 2014), salt stress (Feng *et al.* 2015), drought (Thatcher *et al.* 2016), flooding (Syed *et al.* 2015), and temperature (James *et al.* 2012; Streitner *et al.* 2013).

RNA-Seq has become a standard tool to investigate transcriptomes and AS isoforms. While many studies have identified AS in individual species (Filichkin *et al.* 2010; Li *et al.* 2014; Shen *et al.* 2014; Thatcher *et al.* 2014; Mandadi and Scholthof 2015), there are few reports of conserved AS across multiple plant genomes. Most published studies have focused on identifying conserved AS events between only two species. For example, Severing *et al.* (2009) identified 56 protein-coding conserved AS events between *Arabidopsis* and rice orthologous gene sets, and 30 conserved AS events leading to nonfunctional isoforms subjected to nonsense-mediated decay. Similarly,

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another study detected 537 AS events conserved between *Arabidopsis* and *Brassica* (Darracq and Adams 2013), and 71 conserved AS events were identified between *Populus* and *Eucalyptus* (Xu *et al.* 2014). With respect to comparing more than two species, one study found 16 AS transcripts conserved between *Brachypodium*, rice, and *Arabidopsis* by performing all-vs-all BLAST between EST sequences (Walters *et al.* 2013). Recently, discovery and identification of AS events conserved broadly across eudicots has been reported (Chamala *et al.* 2015). Chuang *et al.* (2015) used available Sanger EST sets to characterize AS in grass species, but did not focus on conserved AS events. There are no studies that leverage the available deep next-generation sequencing resources to characterize and identify conserved AS events across species within monocots and the grass family.

Many monocot species are economically important and grass species are a particularly important source of calories. Within the grass (Poaceae) there are two major clades. The BEP clade is made up of the Bambusoideae, Ehrhartoideae, and Pooideae, including rice and *Brachypodium* (Zhao *et al.* 2013); the PACMAD clade represents the Panicoideae, Arundoideae, Chloridoideae, Micrairoideae, Aristidoideae, and Danthoioideae subfamilies (Cotton *et al.* 2015). Maize, sorghum, and foxtail millet are representatives of Panicoideae. Published whole genome sequences exist for many monocot species, including the grass species maize (Schnable *et al.* 2009), sorghum (Paterson *et al.* 2009), rice (Goff *et al.* 2002), *Brachypodium* (Vogel *et al.* 2010), and foxtail millet (Bennetzen *et al.* 2012), and the nongrass species banana (D'Hont *et al.* 2012) and African oil palm (Singh *et al.* 2013).

A computational method that identifies high confidence isoforms in any species with RNA-Seq data and a reference genome sequence was used to identify and characterize AS events, and a comparative splice junction-based approach identified conserved AS events across multiple species. This analysis focused on seven monocot species that have available reference genome sequences and deep RNA-Seq data sets. Five of these are grasses (maize, rice, sorghum, foxtail millet, and *Brachypodium*) with substantial gene collinearity, which eases the identification of synteny and aids ortholog calls (Schnable *et al.* 2012). The remaining two are banana and African palm oil, which extend the discovery of conserved events into nongrass monocot species. Although there are other nongrass monocot species that have available reference genomes, such as duckweed and orchid, insufficient RNA-Seq data prevented their inclusion in this analysis. Likewise, species representing basal grass lineages were excluded due to lack of reference genome sequences. Finally, the eudicot *Arabidopsis thaliana* and the basal angiosperm *Amborella* were included to provide outgroups for comparison. Therefore, the species studied allow identification of conserved AS events at specific reference points across the grasses and extends into nongrass monocots, eudicots, and the sister species to all angiosperms.

Detecting AS events that are broadly conserved between species is likely to identify functionally important AS isoforms.

Members of the SR proteins and the hnRNP protein families are splicing regulatory proteins that contain RNA binding domains (reviewed in Barbazuk *et al.* 2008). AS has been observed in the hnRNP and SR protein splicing factor gene families (Kalyna *et al.* 2006; Rauch *et al.* 2014; Chamala *et al.* 2015), and has been associated with plant stress (Staiger and Brown 2013). We specifically examined the SR and hnRNP genes for conserved AS events to identify isoforms that may be important for the proper function and regulation of these important splice factors, and to provide a platform to examine differences in AS between species. Similarly, we examined transcription factors (TFs) known to be responsive to five major stresses (Naika *et al.* 2013) for evidence of conserved AS, and applied a STRING functional protein association network analysis (Szklarczyk *et al.* 2015) to identify interaction networks involving the TFs responsive to the five stresses (above) that also have conserved AS events.

The collection of conserved AS events identified also enables an investigation of the extent of positive selection and functional constraints on AS based on the Ka/Ks, and Ks values of pairwise comparisons between splice anchor sequence tags (SASTs) that flank conserved AS events, as well as a test of the functional sharing hypothesis (Su *et al.* 2006) between single-copy vs. nonsingle-copy genes. This hypothesis predicts more instances of conserved AS events will be found in single copy genes than in nonsingle-copy genes. Finally, we also present a STRING functional protein association network analysis based on the *Arabidopsis* protein-protein interaction data to provide evidence of a close association between splicing factors and stress responsive TFs that undergo conserved AS, and between splicing factors and R2R3-MYB TFs.

Materials and Methods

Genome assemblies and annotations

All analyses were performed on publicly available sequence and most reference genome assemblies and annotations were retrieved from Phytozome v10 (Goodstein *et al.* 2012) (Supplemental Material, Table S1) including: foxtail millet 164_v2 (*Setaria italica*), rice 204_v7 (*Oryza sativa* L. *ssp.* *Japonica*), *Brachypodium* 283_v2 (*Brachypodium distachyon*), *Arabidopsis thaliana* 167_TAIR10, and the basal angiosperm *Amborella* 291_v1 (*Amborella trichopoda*), which is a sister taxon to all angiosperms. The Maize RefGen_v2 genome sequence and working gene set annotation were retrieved from MaizeGDB (Lawrence *et al.* 2004). Reference genome sequence and gene annotation for African oil palm v2 (*Elaeis guineensis*) were retrieved from the Malaysian Palm Oil Board (genomsawit.mprob.gov.my). Reference genome and annotation for banana (*Musa acuminata*) were retrieved from the banana genome hub (Droc *et al.* 2013).

Transcriptome data collection

AS in maize (*Zea mays*) and sorghum (*Sorghum bicolor*) was previously identified based on public RNA-Seq data (Mei *et al.* 2017),

and available on figshare (<https://doi.org/10.6084/m9.figshare.4205079.v3>). Transcript sequences and annotations of *Arabidopsis thaliana* were retrieved from Araport11 PreRelease 20151202 (Cheng *et al.* 2017), which presents the updated TAIR10 annotation by inclusion of 113 RNA-Seq data sets. For the remaining six species, Illumina RNA-Seq, 454 and Sanger EST transcript sequences were downloaded from NCBI GenBank. The sequence collections are described in Table S2.

Detection of AS

The process and software parameters used to assemble transcripts from Illumina short reads were described previously (Mei *et al.* 2017). Briefly, three approaches were taken to assemble transcripts from Illumina short reads to maximize isoform detection. The assembly software used was annotation-guided Cufflinks 2.2.1 (Trapnell *et al.* 2012), genome-guided Trinity 2.0.4 (Grabherr *et al.* 2011) and annotation-guided StringTie 1.0.0 (Pertea *et al.* 2015). Isoforms built from Cufflinks were required to have minimal expression FPKM value of 0.1, and required full reads support across the entire isoform.

We masked vector and contaminant sequence in the Sanger ESTs using SeqClean (<http://seqclean.sourceforge.net/>). A total of 454 transcripts was constructed using Newbler v2.8 2010 (Roche) with parameters “-cdna -urt.” Cufflinks, Trinity, and StringTie assembled isoforms were merged with the Newbler 454 assemblies and the cleaned ESTs. Each specific species sequence collection was aligned back to the appropriate reference genome sequence followed by additional assembly and clustering to remove redundancy using the PASA 2.0 package (Haas *et al.* 2003). Isoform quality control steps described in Mei *et al.* (2017) were used on the PASA-generated transcript set to remove isoforms that were poorly supported or potentially poor quality assembled. Briefly, each splice junction in a final retained isoform was required to have a minimum entropy score of two (Sturgill *et al.* 2013). Retained introns that define potential intron-retention isoforms were expected over a minimum of 90% of their length with a minimal median coverage depth of 10, and a minimum intron retention isoform ratio of 10%. The intron retention rate was calculated as described in Marquez *et al.* (2012), where the median coverage of the retained intron was divided by the number of reads supporting the splice junction. Lastly, we required each final isoform to have a minimum FPKM of one and compose at least 5% of the total isoform abundance for that gene in at least one tissue examined.

We performed the above methods to identify and define five AS event-types in rice, foxtail millet, *Brachypodium*, banana, African oil palm, and *Amborella*. The five AS event types considered are Intron retention, Alternative acceptor, Alternative donor, Exon skipping, and Alternate terminal exon; herein designated as IntronR, AltA, AltD, ExonS, AltTE, respectively. The transcripts from Araport11 PreRelease 20151202 for *Arabidopsis* were realigned to the *Arabidopsis* reference genome using PASA to identify and characterize the set of *Arabidopsis* AS events. AS isoforms defined previously

within maize and sorghum Mei *et al.* (2017) were used to complete the AS isoforms sets analyzed in this study.

Orthofinder clustering across nine species

Orthologous sequences were defined and grouped in orthogroups across the nine species by OrthoFinder with default setting (Emms and Kelly 2015). OrthoFinder was designed for plant genome orthogroup identification and accounts for gene length bias.

Identify sets of syntenic genes across five grass species

Syntenic orthologs across five grass species (*Zea mays*, *Sorghum bicolor*, *Setaria italica*, *Oryza sativa*, and *Brachypodium distachyon*) were defined using the methodology employed by Schnable *et al.* (2012). Gene models were updated according to new annotations from Phytozome 10 (Goodstein *et al.* 2012); 11,995 syntenic gene lists across five species (sorghum, rice, foxtail millet, *Brachypodium*, and either maize1/maize2 or both) were used for downstream analysis.

Identification of conserved AS

AS was independently identified in each species (see above). The computational methodology to detect conserved AS relies on the creation of SAST for each AS event and then comparing the SASTs for a given AS event type with the SASTs defining the same AS event type between species. SASTs were generated for each AS event by separately extracting up to 300 bp of sequence from both sides of the splice junction that defines the AS event types described in Figure 1. The tags from both sides of splice junction for a particular AS event (*i.e.*, exon skipping SASTs) from each species were compared to one another using tBLASTx from WU-BLAST (Gish, W. (1996–2003) <http://blast.wustl.edu>) with an *e*-value cutoff of $1e^{-5}$. If the length of two matching tags were both <30 bp, this matching was not considered. In the cases tags being compared were less than 100 bp, the default tBLASTx *E*-value cutoff value was used. To classify conserved AS, Both SASTs flanking a AS event splice junction are required to be conserved separately between genes across species, and those genes must belong to the same orthogroup. Conserved AS events identified by this process were clustered and each cluster may contain conserved AS events identified between orthologous genes across species (1:1) as well as between paralogs. In an ideal setting, one conserved AS cluster represents one ancient conserved AS event across multiple species. However, if a gene within sorghum is present in two copies (homeologs) in maize, and all three genes harbor a conserved AS event, all three events will be assigned to the same event cluster. Therefore, with respect to the gene in sorghum and the two homeologous copies in maize, this cluster identifies one conserved event defined by two homeologous events in maize and one event in sorghum (three genes total). Therefore, the total number of events making up a cluster may be larger than the number of species harboring the conserved AS event. Because we identify these individual events within each species as instances of a conserved event, we generalize each AS event cluster as a

“conserved AS event.” An example illustrating isoform structure, and multiple sequence alignments of conserved events, flanking SASTs and whole transcripts for four randomly picked conserved AS events (two ExonS and two IntronR) are presented in Figure S1 in File S1.

Measure of selection pressure on AS

We looked for evidence of selection pressure on AS events that were conserved by examining the difference between pairwise nonsynonymous substitution rates (K_a) vs. synonymous substitution rates (K_s) for residues defined by exon sequences flanking the conserved AS event in grass species. These are the same regions that were used to construct SASTs (Figure 1). SASTs > 150 bp (50 codons) were used in KaKs analysis, and KaKs ratios of those SASTs alignments with $K_a < 0.5$, $K_s < 5$, and $K_a/K_s < 2$ were retained for further analysis (Quint *et al.* 2012). Since these filtering processes resulted in < 100 SAST alignments associated with AltTE events, we focused only IntronR, ExonS, AltA, and AltD events for this analysis. Selection pressure on AS events at the amino acid level was measured by determining the K_a/K_s ratios using KaKs_Calculator2.0 through model averaging (Wang *et al.* 2010), and functional constraints were measured with K_s value. To minimize errors introduced by alignments, or due to paralogs that may result when comparing loci across large phylogenetic distances, the K_a/K_s evaluation of conserved AS events was limited to those events originating within orthologous grass genome loci that also exhibit conserved synteny (defined above).

Testing the functional sharing hypothesis: whether single copy genes have more conserved AS events

The functional sharing hypothesis predicts that conserved AS events would have a higher incidence in single-copy genes compared to nonsingle-copy genes. We used a set composed of 2717 multi-exon genes identified as “strictly” and “mostly” single copy identified across 20 flowering plant genomes by De Smet *et al.* (2013). We compared the number of single-copy genes exhibiting conserved AS events to the number of nonsingle-copy genes with conserved AS events.

Conserved AS in SR and hnRNP proteins

Maize SR protein genes were retrieved from Rauch *et al.* (2014); Sorghum SR protein genes were retrieved from Richardson *et al.* (2011). Maize hnRNP protein encoding genes were retrieved from PlantGDB (Duvick *et al.* 2008). The primary protein sequences of each SR protein gene in maize and sorghum were used for phylogenetic analysis. Protein sequences were aligned with MUSCLE (version 3.8.31) using default parameters (Edgar 2004). The alignments were used to construct a maximum likelihood phylogenetic tree with RAxML (version 8.1.12) software using a gamma distribution and LG4X model (Le *et al.* 2012; Stamatakis 2014). Conserved AS events in SR families between maize and sorghum exon–intron gene structure were visualized by Fancygene version 1.4 (Rambaldi and Ciccarelli 2009).

Network analysis in stress-responsive TFs and genes with conserved AS

A total of 3150 *Arabidopsis* TFs responsive to 14 diverse stresses were retrieved from STIFDB V2.0 (Naika *et al.* 2013). Specific attention was given to the subset of TFs responsive to ABA, drought, cold, salt (NaCl), and light because a substantial number of these were shown to undergo AS, and many were determined to harbor conserved AS events. Protein–protein interaction networks were built around the TFs with conserved events using STRING v10 (Szklarczyk *et al.* 2015). Additionally, STRING v10 was also used to construct protein–protein interaction networks based around *Arabidopsis* genes demonstrating conserved AS in *Amborella*, *Arabidopsis*, and at least one monocot species. The cluster of constructed networks was identified and analyzed in Cytoscape v3.3.0 (Shannon *et al.* 2003).

Gene ontology (GO) term annotation

Genes harboring conserved AS events between *Amborella*, *Arabidopsis*, and at least one monocot species were further evaluated for functional annotation and GO term enrichment based on the *Arabidopsis* gene name using the agriGO analysis toolkit (Du *et al.* 2010). We use the Fisher’s exact test in singular enrichment analysis, followed by multiple test corrections with the Hochberg FDR test. Only associations with a minimum corrected P -value of 0.05 were considered.

Data availability

AS events table and GFF files for the AS isoforms in seven species (*Setaria italica*, *Oryza sativa* L. ssp. *Japonica*, *Brachypodium distachyon*, *Musa acuminata*, and *Elaeis guineensis*, the eudicot *Arabidopsis thaliana* and the basal angiosperm *Amborella*) are made available to the community via figshare (<https://doi.org/10.6084/m9.figshare.4789153.v2>) and github (https://github.com/wenbinmei/Monocot_conserved_splicing), CoGe, the Comparative Genomics Platform. (<https://www.genomeevolution.org/>). Scripts used in the analysis are available at the same github repository above. The *Zea mays* and *Sorghum bicolor* data are already available to the community at figshare (<https://doi.org/10.6084/m9.figshare.4205079.v3>).

Results

Up to 54.6% of expressed multi-exon genes exhibit evidence of AS among nine species

Five types of AS events were considered during this study: IntronR, AltA, AltD, ExonS, and AltTE (Figure 1); 28.7–54.6% of expressed multi-exon genes exhibit AS across these nine species (Table S3). Although the number of *Amborella* genes that exhibit AS is similar to that of other species examined during this analysis, *Amborella* has a lower proportion of multi-exon genes in the genome relative to other species. Therefore, despite the similar number of multi-exon genes that undergo AS, *Amborella* exhibits the highest fraction

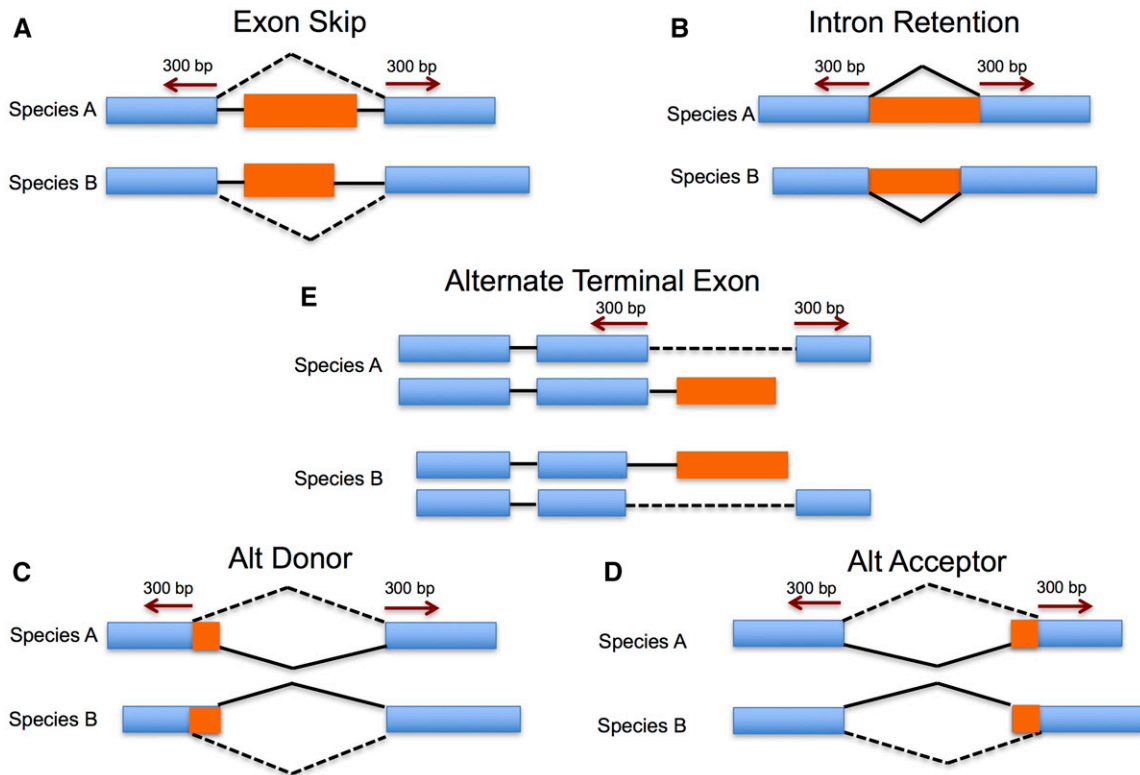


Figure 1 (A)–(E) Pipeline to identify conserved AS events. Up to 300 bp on either side of a splice junction were extracted. These extracted sequences were binned together with all other similarly extracted, and binned sequences flanking the same type of event for each species (e.g., one bin with sequences flanking junctions involved in intron retention, one bin with sequences flanking junctions involved in exon skipping, etc.). Sequences within each bin were compared with tBLASTx to bins of the same event from other species to identify similar tags. Cases where the sequence tags were similar and the parent genes are from different species but represent orthologs as evidenced by being within the same orthogroup (see *Materials and Methods*) defined conserved AS events.

(54.6%) of multi-exon genes that produce AS transcripts compared to the other species considered here. Intriguingly, *Amborella* genes that undergo AS produce the highest average number of isoforms/gene compared to other species (Table S3). Whether this feature reflects the evolutionary position of *Amborella* in angiosperm, or is the result of the absence of lineage specific whole genome duplication events—whereas species with additional lineage specific WGD events have lost or partitioned AS isoforms among paralogues through subfunctionalization (Jiang *et al.* 2013)—remains to be investigated. Maize has the largest collection of RNA-Seq data among the nine species examined, and also has the largest number of AS events, but the percentage of multi-exon genes that undergo AS is similar to other species. The proportions of genes that undergo AS and the total number of AS events are higher than previously reported for many plant species (Campbell *et al.* 2006; *Amborella* Genome Project 2013; Walters *et al.* 2013; Panahi *et al.* 2014; Abdel-Ghany *et al.* 2016). Similar to previous genome-wide AS studies (Li *et al.* 2014; Thatcher *et al.* 2014; Chamala *et al.* 2015; Mandadi and Scholthof 2015), IntronR was the most commonly observed AS event type in monocots. Sorghum and *Amborella* were found to have the lowest percentage of IntronR events, 35.6 and

37.2%, respectively, while African oil palm and *Brachypodium* have the highest proportion of intron retention events, 61.4 and 57.6%, respectively (Table S3). While the data available was successful in identifying several AS events, the sequence data used was collected from public sources, and the tissue representation and sequence depth was not consistent between species studied. Therefore, in many cases, the numbers of AS events identified may under-represent the true extent of AS in these species.

AS events conserved between monocots, *Arabidopsis*, and *Amborella*

Using a junction-based approach (Figure 1 and File S1; *Materials and Methods*) to identify conserved AS within nine species revealed 9804 conserved AS events. Each event is present in two or more orthologous genes, and thus distributes across 19,235 genes (Table 1; *Materials and Methods*). The greatest number of conserved AS events are found in orthologous genes between grasses (Figure 2). Maize had the most (3687) genes harboring conserved AS events, and *Arabidopsis* the least (944), which may reflect its status as the only eudicot under consideration. Of the conserved AS events, 59% are IntronR; ~68.7% of conserved AS events are conserved across two species, 18.6% across

Table 1 Conserved AS across nine species at the gene family level

Number of Species	AltA	AltD	ATE	ExonS	IntronR	Total/%
2	1384	684	201	335	4128	6732/68.7
3	447	181	32	69	1099	1828/18.6
4	218	112	6	26	351	713/7.3
5	117	36	2	21	109	285/2.9
6	58	29	0	10	52	149/1.5
7	22	12	0	3	32	69/0.7
8	7	3	0	4	7	21/0.2
9	2	2	0	1	2	7/0.1
Total/%	2255/23.0	1059/10.8	241/2.5	469/4.8	5780/59.0	9804

Percentage is based on total number of conserved AS clusters.

three species, 7.3% across four species, and 5.4% across five or more species (Table 1). A total of 1816 conserved AS event clusters was found to include *Amborella*. Of these, 1015 involved conserved IntronR, 450 AltA, 205 AltD, 114 ExonS, and 32 AltTE events (Table 2). In addition, we identified 80 AS events conserved only between *Amborella* and *Arabidopsis* and absent from the seven monocot species examined. These 80 AS events likely represent AS events lost after the divergence of eudicots and monocots and include 34 IntronR, 31 AltA, 11 AltD, and four ExonS events (Table 2). As previously mentioned, differences in tissue representation and sequence depth between species make it difficult to ensure that all potential events are discovered. While this does not affect the identification of a conserved event, some will be missed and appear “absent” due to sequence collection coverage and bias.

GO term enrichment analysis was performed on *Arabidopsis* genes with AS events that are conserved within *Amborella*, *Arabidopsis*, and monocots, to determine whether these genes participated in common biological processes. Analysis of 129 AS events representing 64 IntronR, 43 AltA, 11 AltD, 10 ExonS, and one AltTE (Table 2) suggest an over-representation of kinase and phosphorylation activity (Figure S2 in File S1), which is consistent with the proposal that AS impacts protein kinase mediated signaling pathways (Reddy *et al.* 2013) that may modulate the transfer of developmental or environmental cues.

TFIIIA possesses an ExonS event conserved across land plants (Fu *et al.* 2009; Barbazuk 2010). This event was also identified in all species examined in our study. Shikata *et al.* (2014) previously characterized IntronR and AltD events within SPA3—a protein that plays a pivotal role in light signaling as a suppressor of photomorphogenesis (Laubinger and Hoecker 2003). Both splice isoforms harbor premature termination codons resulting in truncated proteins that retain interaction with CONSTITUTIVE PHOTOMORPHOGENIC 1 (COPI) but lose the ability to bind to DAMAGED DNA-BINDING PROTEIN 1 (DDB1). Evidence suggests that phytochrome could mediate the production of AS transcripts of SPA3 in response to some light conditions, thus promoting plant photomorphogenesis (Shikata *et al.* 2014). Both IntronR and AltD events were identified in our analysis: the AltD event is conserved across all nine species examined and the IntronR

event is conserved in four species: maize, foxtail millet, African oil palm, and *Arabidopsis*. The absence of the IntronR event some species examined could be due to limited data depth or tissue sampling. Further investigation is required to determine whether this intron retention is conserved broadly across the angiosperms.

AS events conserved between *Brassica* and *Arabidopsis* are enriched for AltD and AltA events (Darracq and Adams 2013). We found significant enrichment of AltD and AltA events conserved across at least three species relative to events conserved in only two species ($P < 0.0001$, Fisher’s exact test, Table 1); similar enrichment patterns were observed for ExonS events conserved across at least four species relative to clusters conserved in only two species ($P < 0.05$, Fisher’s exact test, Table 1). As expected, there are fewer events conserved across multiple species (>3) than between a pair. Additionally, as the number of species that harbor the conserved AS increase, the proportion of conserved AS events that are intron retention decrease relative to the other event types. This suggests that identifying conserved AS events selects for biologically relevant and important events, and that intron retention suffers a higher proportion of “noisy” or nonrelevant splicing relative to other AS types.

The difference in lengths of conserved retained introns vs. nonconserved retained introns (*i.e.*, unique to only one species) varies across the nine species examined. In *Arabidopsis*, *Brachypodium*, and foxtail millet, the length of conserved retained introns is significantly shorter than that of nonconserved retained introns (Table 3), but the trend is reversed for *Amborella* and African oil palm. There is no significant difference in retained intron length between conserved and nonconserved retained introns in banana, maize, sorghum, and rice (Table 3). A previous report suggested that the lengths of retained introns within *Arabidopsis* that are conserved in *Brassica* are shorter than nonconserved retained introns (Darracq and Adams 2013). We observed the same length trend in *Arabidopsis* and *Brachypodium*, but this is not observed in the other species considered.

Arabidopsis TFs responsive to stress signals were retrieved from STIFDB V2.0 (Naika *et al.* 2013). Some TFs associated with each stress exhibit AS, and those responsive to ABA, NaCl, drought, light, and cold have the highest proportion with conserved events (Table S4). Two TF genes are particularly

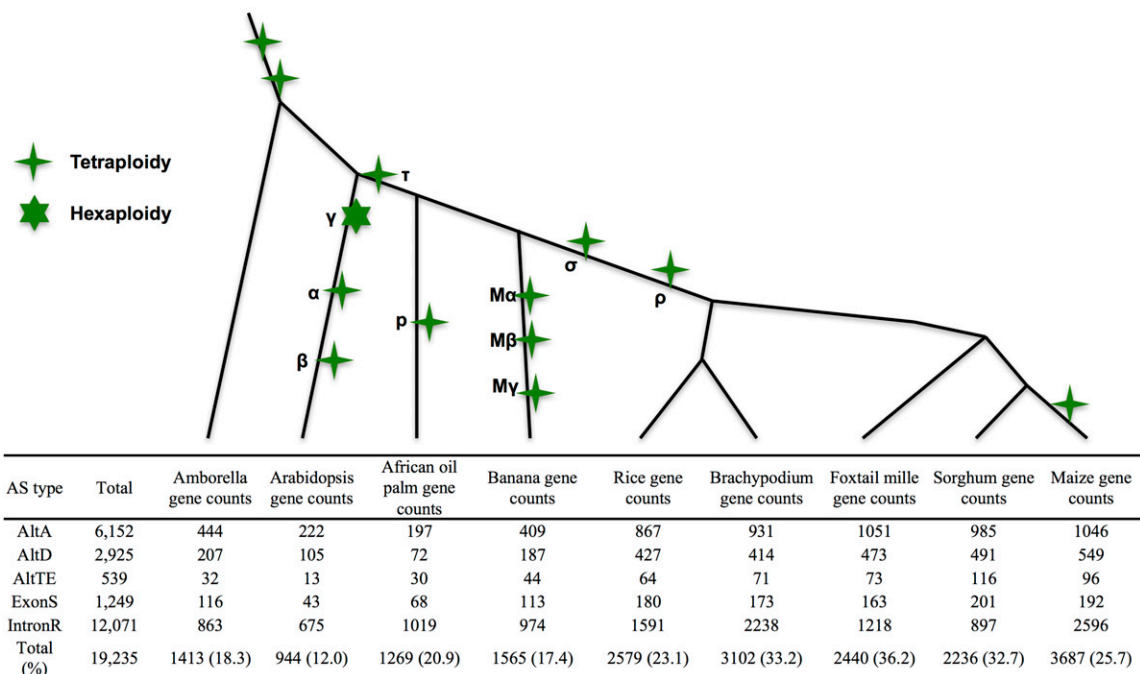


Figure 2 Genes with conserved AS events across nine species. We calculate the number of genes with conserved AS events in each species. Tetraploidy and Hexaploidy are labeled on the phylogenetic trees. The length of the phylogenetic tree is not proportional to the phylogenetic distance.

interesting: AT4G27410 (NAC TF RD26) and AT1G78070 (Transducin/WD40 repeat-like superfamily protein). These two genes have conserved AS events and are responsive to all five stresses listed above (Figure S3 in File S1). RD26 has an IntronR event conserved across seven of the nine species examined (absent in sorghum and *Brachypodium*); AT1G78070 has an AltTE event conserved between sorghum, banana, and *Arabidopsis*. This indicates that there are AS events in stress-response TFs conserved across large phylogenetic distances, and suggests that AS may play an important role in the activity of some TFs during stress response.

AS conserved between monocot grass and nongrass species

There are 239 AS events conserved between banana, African oil palm, and at least one of the five grass species examined; 34 of these are conserved across all seven monocot species examined (Table 2). A total of 204 conserved AS events exist within the banana and African oil palm lineages but are

absent from the grass species studied, while 224 conserved AS events are conserved across the five grass species examined (Table 2). Within the PACMAD clade, 1544, 1488, and 1323 AS events are conserved between maize vs. sorghum, maize vs. foxtail millet, and sorghum vs. foxtail millet, respectively. In the BEP clade, 1658 conserved AS events are conserved between rice and *Brachypodium*; 4333 conserved AS events are conserved in at least one species in the BEP clade and one species in the PACMAD clade (Table 2). Maize clock genes (*i.e.*, circadian rhythm) GRMZM2G033962 (pseudoresponse regulator protein 37, *PRR37*) and GRMZM2G095727 (pseudoresponse regulator protein 73, *PRR73*) have an IntronR event conserved across rice, *Brachypodium*, and foxtail millet. Our data suggests that this intron retention event is likely specific to members of the grass family; the role of intron retention in *PRR37* and *PRR73* controlling photoperiodic flowering is unknown.

Genes in genomic regions that exhibit synteny between species were more likely to be transcribed and translated than

Table 2 Conserved AS clusters among different species and clades

	Total	IntronR	AltA	AltD	ExonS	ATE
Conserved between <i>Amborella</i> and other species	1816	1015	450	205	114	32
Conserved in <i>Amborella</i> , <i>Arabidopsis</i> , and at least one species of monocots	129	64	43	11	10	1
Conserved between <i>Amborella</i> and <i>Arabidopsis</i> not in monocots	80	34	31	11	4	0
Conserved across <i>Amborella</i> and seven monocot not in <i>Arabidopsis</i>	9	2	3	2	2	0
Conserved in banana, African oil palm and at least one grass species	239	162	44	20	11	2
Conserved across five species in grass	224	60	106	37	21	0
Conserved across seven species in monocots	34	13	12	5	4	0
Conserved between PACMAD and BEP clades ^a	4333	2548	1052	480	177	76

^a Conserved at least one species in PCAMAD clade and one species in BEP clade.

Table 3 A comparison of intron length in the conserved intron retention events vs. nonconserved intron retention events across the species examined

	<i>Amborella</i>	<i>Arabidopsis</i>	Banana	<i>Brachypodium</i>	Foxtail Millet	Maize	Oil Palm	Rice	Sorghum
Conserved AS									
Mean	670	165	329	411	402	440	315	417	409
Median	390	96	143	233	237	207	131	269	256
No evidence for conserved AS									
Mean	651	186	327	474	410	471	287	486	437
Median	316	113	131	245	201	205	121	247	242
Wilcoxon test									
<i>P</i> value	***	***	NS	***	*	NS	*	NS	NS

(NS, Not significant; * $P < 0.05$, *** $P < 0.001$).

those in nonsyntenic regions (Walley *et al.* 2016). We tested the hypothesis that AS and conserved AS is enriched in syntenic vs. nonsyntenic regions across the grass species. There are 11,996 syntenic gene clusters across maize, sorghum, foxtail millet, rice, and *Brachypodium*. In each of five grass species, we compared the proportion of genes within syntenic regions that undergo AS vs. nonsyntenic genes that undergo AS, and the proportion of genes within syntenic regions that have conserved AS events vs. the proportion of nonsyntenic genes that have conserved AS events. The proportion of genes within syntenic regions that exhibit AS is approximately twice that of genes in nonsyntenic regions (Figure 3). This trend is consistent across the grass species analyzed. Similarly, the proportion of genes that have conserved AS events that reside in syntenic regions is approximately twice that of genes with conserved AS events that do not reside within syntenic regions (Figure 3). This suggests that genes residing within conserved syntenic blocks in the grass species studied are enriched in both AS, and conserved AS events.

We examined selection pressure at the amino acid level on AS events conserved within grasses by performing pairwise comparisons of K_a/K_s ratios across the SASTs flanking each conserved AS event (Figure 4). Requiring K_a values of $K_a < 0.5$, $K_s < 5$, and $K_a/K_s < 2$, resulted in a collection of SAST alignments from 886 IntronR, 879 AltA, 424 AltD, and 169 ExonS of remained, respectively. In general, K_a/K_s values of SAST alignments flanking conserved AS events are < 1 across different AS types. There are no significant K_a/K_s differences between IntronR and other types of AS events (Figure 4). There are no single SAST alignments with $K_a/K_s > 1$ that pass a Fisher's exact test for differences from neutrality, indicating that SAST alignments under positive selection were not detected. We did observe that the K_a of IntronR is significantly higher than that of AltA and AltD, but not ExonS. Also, the difference between K_a for IntronR vs. other types of AS events is smaller than the difference between K_s for IntronR vs. other types of AS events (Figure 4), which leads to differences in the K_a/K_s values between IntronR and other types of AS events being nonsignificant.

Conserved AS is more common among single copy genes

We tested the functional sharing hypothesis between single-copy genes vs. nonsingle-copy genes by measuring the number

of genes within each category that exhibit conserved AS events; 2985 single-copy genes, including “strict” and “mostly” single copy, were described in *Arabidopsis* (De Smet *et al.* 2013). Han *et al.* (2014) suggested single-copy genes had increased levels of AS relative to genes from large gene families, and a decreased proportion of AS compared to genes from small gene families. Similarly, Su and Gu (2012) suggested that single copy genes had more isoforms per gene compared to the genes from large gene families, but similar average isoform counts per gene compared to the genes from small gene families.

We compared the number of genes with conserved AS events between single-copy genes vs. nonsingle-copy genes, irrespective of gene family size. Out of 2985 single-copy genes, 2717 (91.0%) are multi-exon genes, and 1113 (40.8%) of these have evidence of AS in *Arabidopsis* based on the Arabidopsis11 transcripts. In contrast, 6751 (34.3%) of the 19,700 nonsingle-copy multi-exon genes exhibit AS. Among multi-exon genes, the single-copy genes have significantly more AS compared to multi-exon genes ($P < 0.0001$, Chi-square with Yates' correction). Among the 944 *Arabidopsis* genes with conserved AS events in our analysis, 173 came from the 1113 (15.5%) single-copy genes that undergo AS, while the remaining 771 came from the 6751 (11.4%) nonsingle-copy genes that undergo AS. Single-copy genes in *Arabidopsis* are also significantly enriched in conserved AS events ($P < 0.0001$, Chi-square with Yates' correction). These results suggest that, among multi-exon genes in *Arabidopsis*, a greater proportion of single copy genes both undergo AS and harbor conserved AS events than do nonsingle-copy genes.

Conserved AS is more common among SR protein genes relative to hnRNP proteins

SR and hnRNP proteins are families of splicing regulatory proteins that contain RNA binding domains (reviewed in Barbazuk *et al.* 2008). AS events were detected in SR proteins, confirming previous observations (Kalyna *et al.* 2006; Rauch *et al.* 2014; Chamala *et al.* 2015). Out of 21 SR proteins in maize, 19 demonstrate AS, and 13 of these have 24 conserved AS events with other species, including 13 IntronR, four AltA, four AltD, and three ExonS events (Table S5). Out of 24 conserved AS events, 10 are present in at least five species. Zm-SCL30 (GRMZM2G065066), previously identified in maize, responds to both cold and heat (Mei *et al.* 2017).

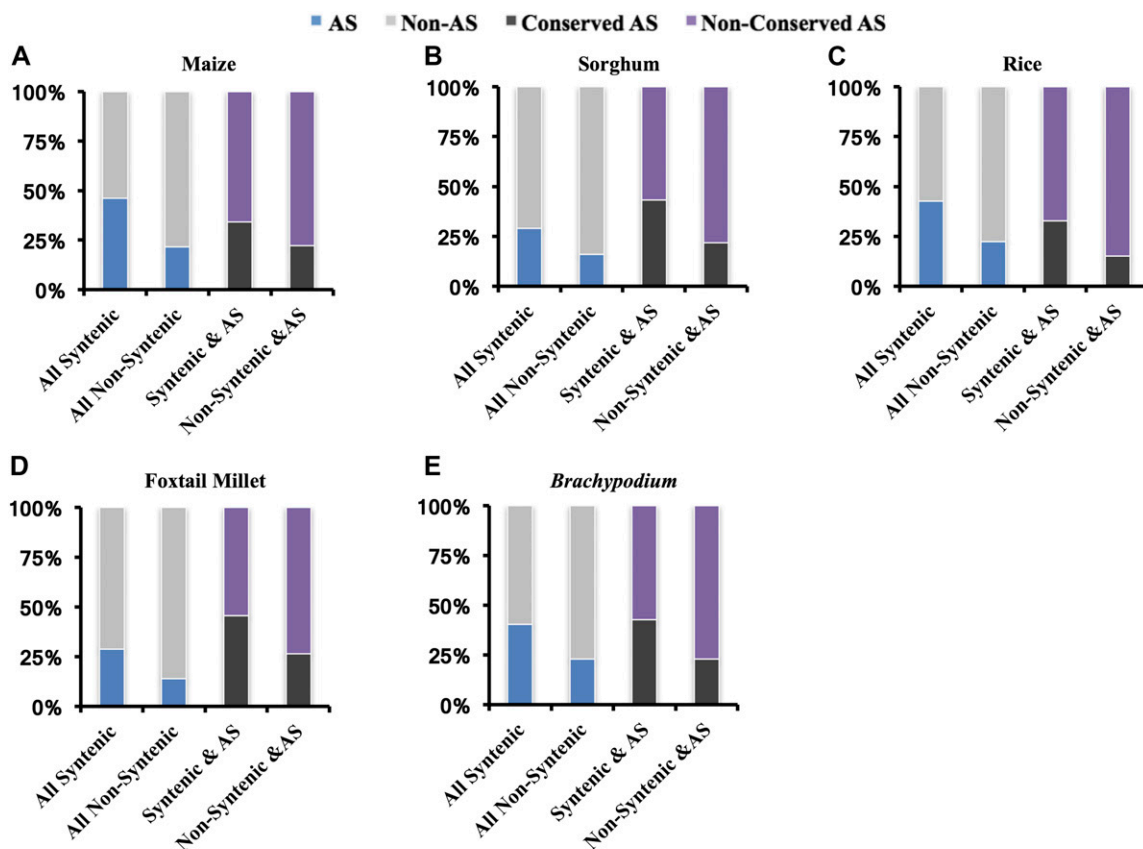


Figure 3 AS and conserved AS enriched across grass syntenic genes in (A) maize, (B) sorghum, (C) rice, (D) foxtail millet, and (E) *Brachypodium*. We calculated the percentage of AS in syntenic and nonsyntenic genes (the percentage of AS genes are labeled in blue). In addition, we calculated the percentage of conserved AS in syntenic AS genes and nonsyntenic AS genes (the percentage of conserved AS genes are labeled in black).

SCL30 has AltA, AltD, and ExonS events conserved across grass species and *Amborella*, as well as two IntronR events only observed within the grass lineage. Altogether, there are four maize SR proteins (two in the RS subfamily, one in the SC subfamily, and one in the SCL subfamily) that demonstrate six conserved AS events with *Amborella* (Table S5) supporting the existence of a deeply conserved splicing mechanism in SR proteins. Out of 40 hnRNP proteins in maize, 10 exhibit evidence of 17 conserved AS events: 10 IntronR, four AltA, two AltD, and one ExonS event (Table S5). None of these 17 AS events are conserved across more than four species. Three of the 17 conserved AS events from three hnRNP genes in maize are conserved with *Amborella* (Table S5), while six out of 24 AS events from four SR proteins in maize are conserved with *Amborella*. These results suggest that the signals for AS within SR protein genes across species are better conserved than those within the hnRNP-protein-encoding genes.

Conservation and divergence of SR proteins and their AS isoforms after whole genome duplication

Conserved AS events across the SR protein subfamilies in maize and sorghum were identified using a phylogenetic approach. An ancestral ExonS event is conserved across all

members of this subfamily in maize and sorghum (Figure 5A). Intriguingly, all three maize SR subfamily genes were reduced to one copy after whole genome duplication; one gene lost a homeologous copy from maize subgenome1, and two genes lost their homeologous copies from subgenome2. The plant-specific RS subfamily also has a shared ExonS event in both maize and sorghum (Figure 5A). The exon skipping isoform generates a complete RNA Recognition Motif (RRM) domain and is known to be conserved between green algae and some angiosperms (Kalyna *et al.* 2006). Our analysis confirms that this exon skipping event is conserved between maize and rice, and is also present within sorghum, *Brachypodium*, foxtail millet, and *Amborella*. Maize maintained both postwhole-genome-duplication copies of the plant-specific RS2Z subfamily genes. Remarkably, two sorghum genes Sobic.009G022100 and Sobic.009G022200 are next to each other but on opposite strands, suggesting one copy may have resulted from tandem duplication. Phylogenetic evidence suggests Sobic.009G022200 is the older copy (Richardson *et al.* 2011). In addition to Sobic.009G022200, and two duplicate genes in maize retaining an ExonS event, they also contain two IntronR events flanking the ExonS event (Figure 5B). Two duplicate genes in maize (GRMZM2G099317 and GRMZM2G474658) apparently gained additional IntronR

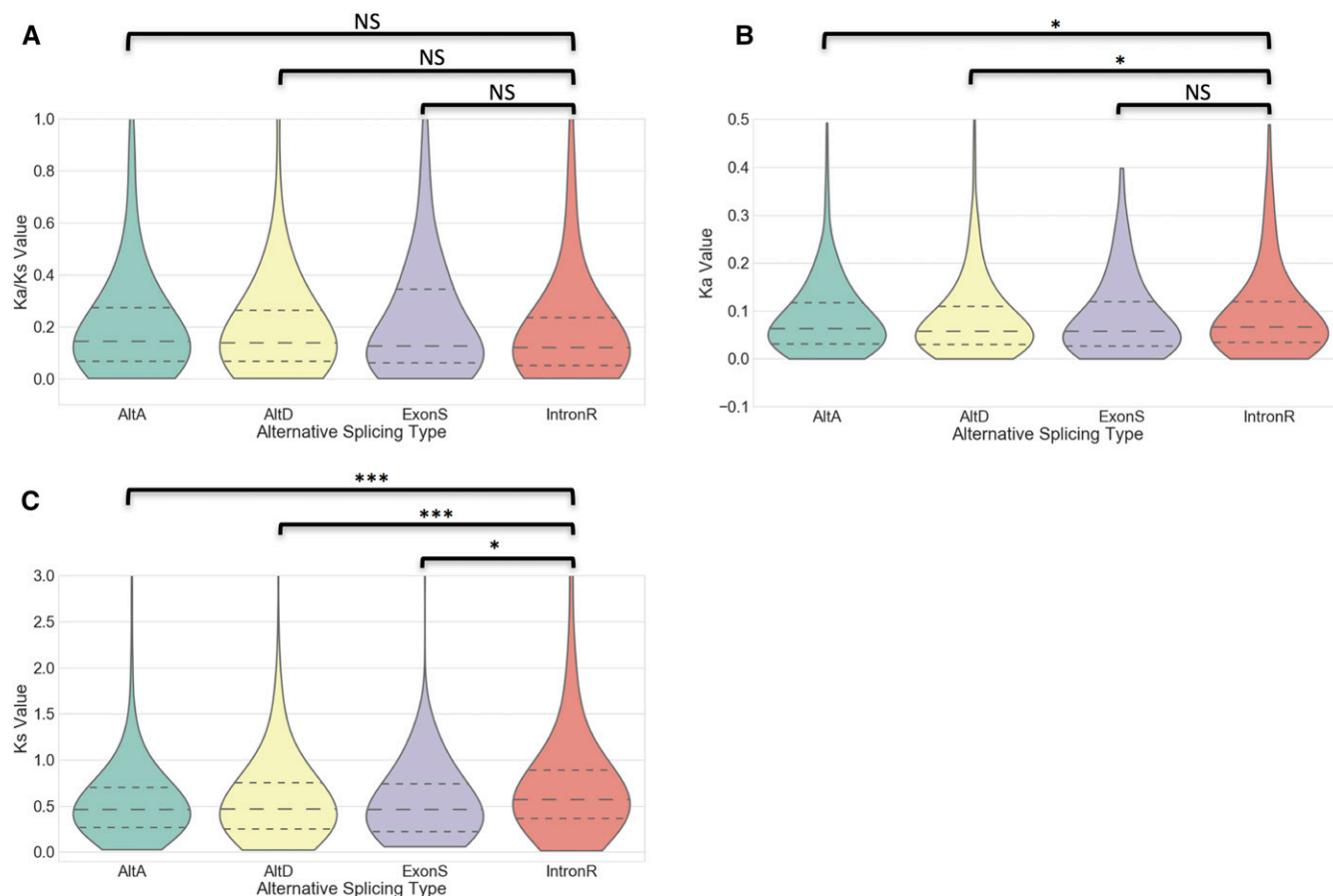


Figure 4 Violinplot of Ka/Ks, Ka, Ks on SASTs in conserved AS events across syntenic genes within grass species. The pairwise Ka/Ks (A), Ka (B), and Ks (C) for SASTs flanking conserved AS events in five grass species were calculated and plotted. Only alignments >150 bp in length with gaps <5% of the total aligned length were considered. We only kept the Ka/Ks results if $Ka < 0.5$, $Ks < 5$ and Ka/Ks ratios < 2. The dotted lines within the violinplots represented the first, second, and third quartile. Wilcoxon Rank-Sum Tests were performed between different splicing event types (NS, Not significant; * $P < 0.05$, *** $P < 0.001$).

and AltA events compared to Sobic.009G022100 (Figure 5B). Sobic.009G022100 preserved only the ExonS isoform, which would generate a complete RRM domain, while GRMZM2G099317 also gained the IntronR and AltA events on the right side of the ExonS event. For the second copy, GRMZM2G474658, the AltA and IntronR events on the left side are gained. There is one additional sorghum gene Sobic.003G064400 without conserved synteny in maize, which suggests that maize might have lost both syntenic copies that had represented orthologs of this sorghum gene. The AS pattern of this gene is similar to that of GRMZM2G474658 (Figure 5B). The alternative long intron in the RS2Z subfamily is also conserved from mosses to angiosperms (Kalyna *et al.* 2006).

R2R3-MYB is tightly connected with a plant-specific SR protein subfamily

We used a network approach to identify the degree of interactivity of TFs with conserved AS in response to five stresses (ABA, drought, cold, NaCl, and light) based on protein–protein interactions in STRING v10 (Szklarczyk *et al.* 2015). Several interesting relationships were identified in the network (Figure S4 in

File S1). Ubiquitin genes such as UBQ10, UBQ11, and UBQ14 are centralized in the network, suggesting that AS may play a role in the susceptibility of translated isoforms to ubiquitin-mediated degradation. Ubiquitin genes are closely associated with splicing related genes (such as RS2Z33, RS41, RS2Z32, RS40, U2AF65A, SR45, and SCL33) via *Glycine Rich Protein 7* (GRP7). GRP7 is part of the circadian clock and negatively autoregulates its own protein abundance by producing a nonproductive AS isoform that is subject to nonsense-mediated decay (Schöning *et al.* 2007, 2008). In addition, we observe an association between R2R3-MYB genes and the splicing factor network through the proline-rich spliceosome-associated protein (AT4G21660) (Figure S4 in File S1). The R2R3-MYB family has undergone expansion in plants (Du *et al.* 2015), and plays many important plant-specific roles. Furthermore, there are many kinase- and phosphatase-related genes in close association with genes responsible for phosphorylation and dephosphorylation of splicing regulators, such as serine-threonine protein kinase (CIPK3), calcium-dependent protein kinase 29 (CPK29), CBL-interacting protein kinase 9 (CIPK9), and calcineurin

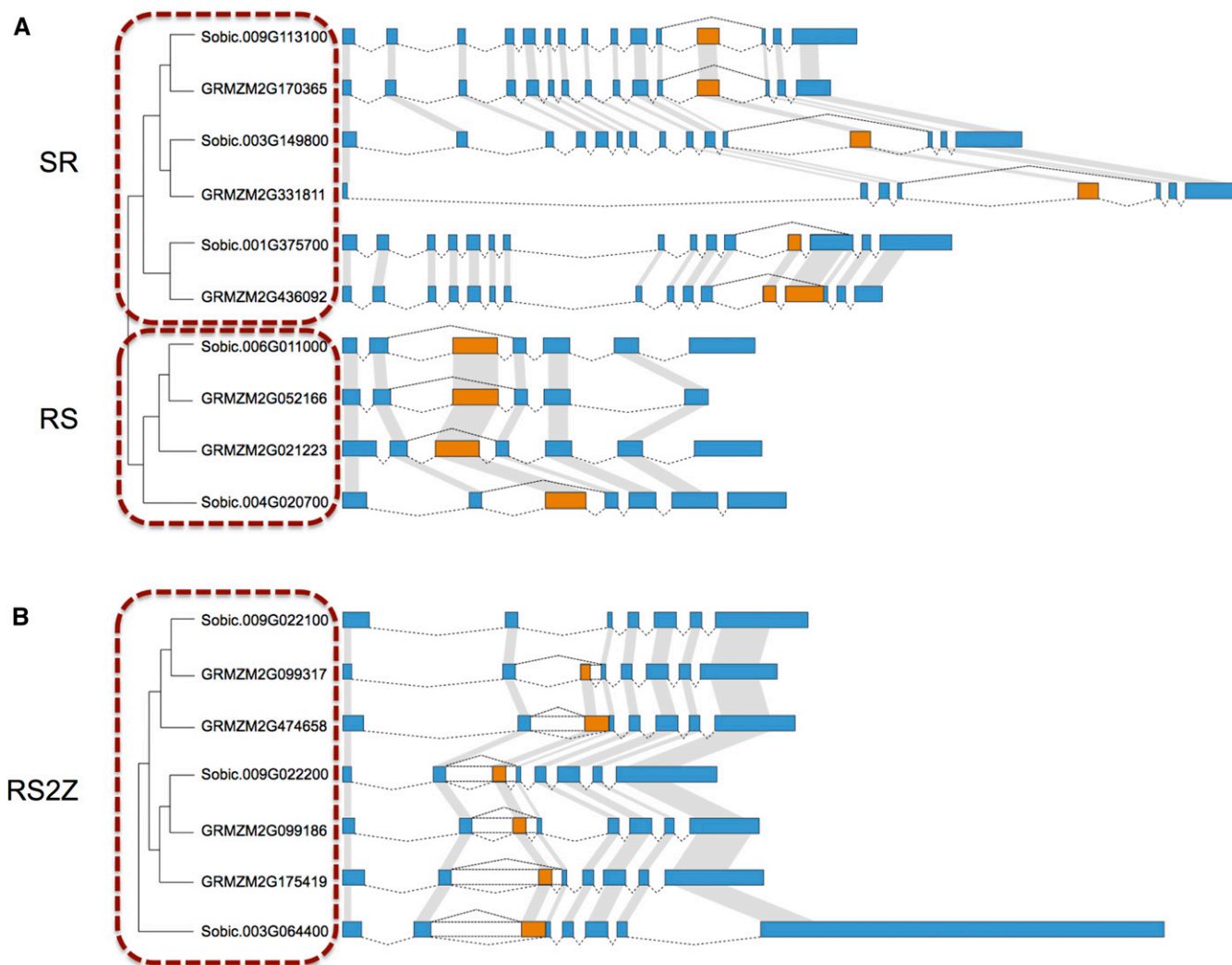


Figure 5 Phylogenetic tree and gene structure of SR, RS, and RS2Z subfamilies in maize and sorghum. (A) Phylogenetic tree representing the relationship of genes from SR and RS subfamilies in maize and sorghum; associated gene structures are illustrated by Fancysgene to the right. Constitutive exons are shaded blue, and alternative regions are indicated with orange. Transcript structure is indicated by exons connected via dashed lines; orthologous exons are indicated with gray lines. (B) Phylogenetic tree and gene structure of RS2Z subfamily in maize and sorghum are illustrated by Fancysgene. Annotation and shading is described above; intron retention regions are indicated in clear boxes.

b-like protein (CBL1). CBL1 is a salt-tolerance gene and connects with components of the spliceosome (Feng *et al.* 2015). CBL2 and CBL3, together with CIPK3 and CIPK9, can form a calcium network to regulate magnesium levels, while CBL1 is a calcium sensor (Tang *et al.* 2015). Here, AS of CBL1 and CIPK3, CIPK9 could potentially contribute in regulating magnesium levels through a feedback loop sensitive to calcium concentration.

We also examined networks containing *Arabidopsis* genes with AS events conserved with *Amborella* and at least one species of monocot. Most of the genes present in the network were from the plant-specific SR protein subfamilies, such as RS2Z, RS, and SR45a. In addition, TFIIA is connected to the splicing protein network via RNA-binding protein (AT4G35785). TFIIA has an ExonS event that is conserved across the land plants (Fu *et al.* 2009; Barbazuk 2010). Similar to the network based on

TFs in response to stress, we identified a close connection between the R2R3-MYB class with a splicing protein network via TFIID-1 (AT3G13445), and proline-rich spliceosome-associated family protein (AT4G21660) (Figure 6). These R2R3-MYBs are involved in many important functions, such as glucosinolate biosynthesis, phenylpropanoid pathway, conical epidermal cell outgrowth, drought, ABA- and JA-mediated pathogens, and cuticular wax biosynthesis (Table S6).

Discussion

In this study, we utilized a bioinformatics scheme to detect AS events and identify those that are conserved across nine plant species from publicly available RNA-Seq data. In total, across all nine species, 9804 AS events are conserved between two or more species. Newly sequenced plant genomes are published,

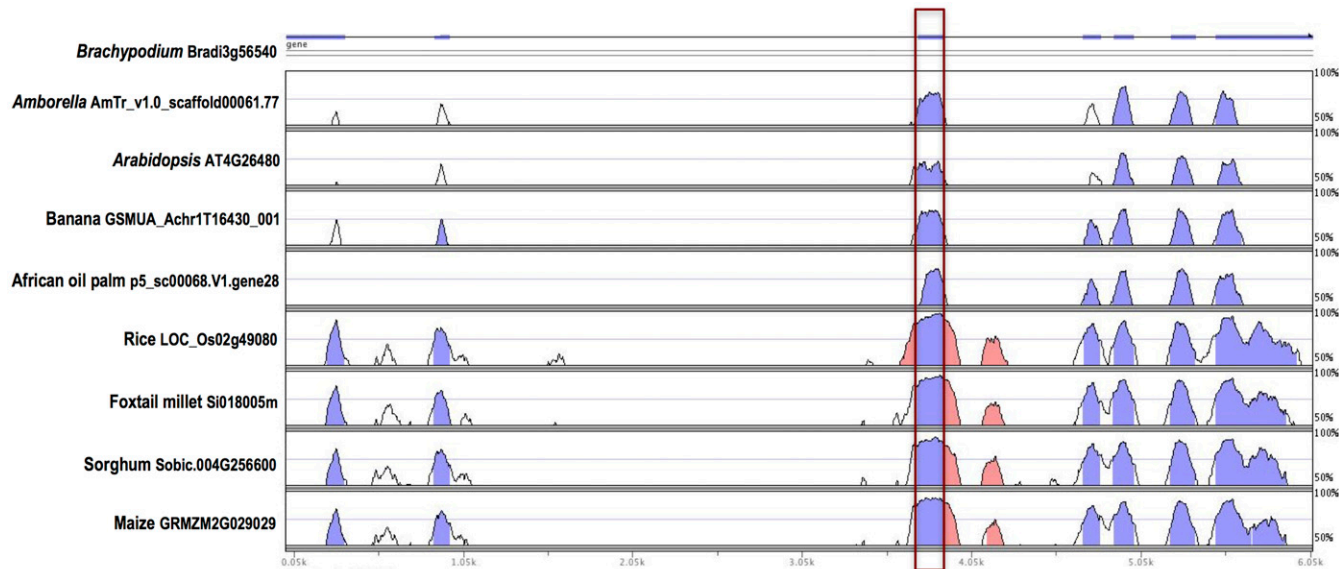


Figure 7 Vista plots illustrating sequence conservation within a gene encoding an RNA-binding KH domain-containing protein that produces an exon skipping event conserved across *Brachypodium*, *Amborella*, *Arabidopsis*, banana, African oil palm, rice, foxtail millet, sorghum, and maize. The exon skipping in *Arabidopsis* is not included in the Araport11, but detected in AtRTD. The alternative exon (boxed in red) is highly conserved between *Brachypodium* and its orthologs across the other plant species examined. Levels of sequence identity between *Brachypodium* and its orthologs in the eight other plants species displayed are depicted as blue peaks. Pink bars signify segments that pass the alignment criteria of 70% identity over a 100 bp window.

genes demonstrating conserved AS with *Amborella* and at least one species of monocots (Figure 6). Many R2R3-MYB genes are represented in this network, and possess plant-specific functions (Table S6). A connection between R2R3-MYB family and splice factors is also detected within networks build around *Arabidopsis* TFs that respond to stress. Li *et al.* (2006) identified conserved AS events within MYB59 and MYB48. Both genes are represented within our network and associate with SR proteins via a proline-rich spliceosome-associated protein AT4G21660 (Figure 6). Together, these results suggest a conserved connection between splicing factors and R2R3-MYB TFs. These two protein classes may cooperate during developmental processes and stress response in plants. In addition, natural variation in *Arabidopsis* contributes to splicing changes in the proline synthesis enzyme (P5CS1) affecting drought-induced proline accumulation. This suggests that AS may play a role in adaptation to environmental challenges (Kesari *et al.* 2012).

Conserved AS events are enriched within grasses

Within monocots, we identified lineage-specific conserved AS events. There are 239 AS events conserved between banana, African oil palm, and at least one grass species, while an additional 204 AS events conserved between banana and African oil palm are absent in the grass species examined and were likely lost. The number of conserved AS between two species in the PACMAD clade (maize, sorghum, and foxtail millet) is similar to the number of conserved AS events between two species within the BEP clade (rice and *Brachypodium*). There were 224 conserved AS events found conserved across five grass species

examined. In addition, the proportion of genes within syntenic blocks with AS events in the grasses is approximately twice that compared to those outside of syntenic blocks, and this trend is also mirrored across those genes with conserved AS events (Figure 3).

While KaKs analysis on regions flanking conserved AS revealed no evidence of positive selection, we did observe elevated Ks values associated with regions flanking IntronR compared to other AS types. This suggests that these regions may be functionally constrained and undergoing purifying selection, perhaps to maintain *cis*-regulatory signals required for AS. Some conserved intron retention events exhibit high cross-species sequence conservation based on multiple sequence alignments (Figure S1 in File S1). These retained introns may have conserved RNA structure that participates in the switch between splicing and retention analogous to the situation seen for TFIID (Fu *et al.* 2009), or may play a role in proteome plasticity. Previous studies have suggested only moderate selection pressure on the alternative vs. the constitutive regions (Xing and Lee 2005, 2006; Chen *et al.* 2006). However, the selection on the regions flanking conserved AS events is less explored, particularly in plants. Our study reveals the flanking exonic regions of conserved AS events are under purifying selection, perhaps preserving splicing regulatory elements.

We observed both conserved and divergent patterns of AS within SR-protein-encoding genes after the whole genome duplication event in the maize lineage. The plant-specific RS subfamily in maize and sorghum harbor conserved ExonS events, although the maize ortholog has been reduced to a

single copy after whole genome duplication (Figure 5A). In the RS2Z family, maize has retained both homeologous copies of the RS2Z subfamily genes. In one case, it has maintained the conserved AS events in both maize homeologues including ExonS and IntronR events (Figure 5B); however, in another case, the AS events have diverged between the sorghum gene and its two maize homeologues (Figure 5B). Whether these divergent patterns are truly indicative of sub or neofunctionalized genes needs to be experimentally confirmed.

Important functional conserved AS in SR protein in response to environmental stress

Many TFs that respond to ABA, salt (NaCl), drought, light, and cold stress have conserved AS. Two genes—AT1G78070 (Transducin/WD40 repeat-like superfamily protein) and AT4G27410 (RD26)—are expressed during all five stresses. RD26 encodes a NAC TF induced in response to desiccation. In our data, RD26 has conserved AS in seven out of the nine species we examined (except sorghum and *Brachypodium*). As illustrated in Figure S5 in File S1, the exonic flanking sequences of this IntronR event are the sites of the highest sequence conservation within this gene across the nine species examined. This conserved IntronR event may be broadly conserved across angiosperms.

The protein–protein interaction network based on *Arabidopsis* stress response TFs with conserved AS events places phosphatases, kinases, and several ubiquitin genes in the center of the network (Figure S4 in File S1). This result is in line with the recent discovery that alternative exons and exons (exon-like introns) have more phosphorylation sites and ubiquitination sites compared to constitutive exons (Marquez *et al.* 2015). In these genes with conserved AS across the angiosperms, AS may be involved in signaling pathways responsible for de/phosphorylation and protein degradation pathways, which suggests an important regulatory role in plants. Another interesting finding in the network is SPA3 (Figure 6). In moss, red and blue light photoreceptors were shown to regulate AS, and intron retention was misregulated in moss mutants defective in red light sensing phytochromes (Wu *et al.* 2014), which suggests an ancient connection between light regulation and conserved AS in land plants. We found both conserved alternative donor and intron retention events in SPA3, which acts as a negative regulator during light signaling via suppression of photomorphogenesis (Laubinger and Hoecker 2003). SPA3 is connected to nine additional kinase genes in the network, all of which have conserved AS across the angiosperms (Figure 6). This suggests that AS of kinases might play an important role in the regulation of the light signal, perhaps by affecting a kinase-mediated signal cascade linked to SPA3.

The conserved AS landscape in plants is complex, but likely identifies events of functional significance. Collections of evolutionarily conserved AS events provide a foundation for additional efforts to link functions and phenotypes to these ancient events and will aid in identifying sequence that participate in the regulation of these events.

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