

Genome-wide comparative analysis of alternative splicing in plants

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Abstract

Alternative splicing (AS) has been extensively studied in mammalian but not in plants. Here we report AS events deduced from EST/cDNA analysis in two model plants: Arabidopsis and rice. In Arabidopsis, 4,768 (22%) of the genes with EST/cDNA evidence show 8,423 AS events. About 56% of these events are intron retention (IntronR), and only 8% are exon skipping (ExonS). In rice, 6,638 (21.5%) of the expressed genes display 14,825 AS events, of which 54% are IntronR and 13.5% are ExonS. The consistent high frequency of IntronR indicates the deployment of intron definition mechanism in plants. 14-16% of plant AS events can be read-through and 22%-30% AS events occur in untranslated region (UTR). The remaining AS events will change the stop or/and start codon position. By applying the 50-55 bp nonsense-mediated decay (NMD) rules, more than one third (36%-43%) of plant AS events were found to generate NMD candidates, which will be degraded rapidly. Gene ontology analysis revealed that genes targeted to golgi apparatus have higher AS ratio, while cell wall have lower AS ratio. 40% of Arabidopsis AS genes are also alternative spliced in rice, indicating the importance of AS in plants as a post-transcriptional regulation. Non-functional AS events are probably just splicing error, which may have similar roles as DNA mutations in evolution. We created the first comprehensive web-interfaced database to summarize the evidence for alternative splicing in plants (ASIP, available at: <http://www.plantGDB.org/ASIP/>).