Special Issue

Epigenetics of Alternative Splicing in Plants

Message from the Guest Editors

Alternative splicing is widespread in humans and plants. Evidence suggests that the process of splicing is co-transcriptional, and introns are spliced when pre-mRNA is attached to DNA by RNA polymerase II. Since DNA is packaged into chromatin, it provides a barrier to the RNAPII and influences the splicing process. Exons are GC-rich, and transcription through nucleosome-rich regions with compact chromatin tends to be slower. Nucleosome occupancy is lower in alternatively spliced exons compared to those that are constitutively spliced. DNA methylation affects exon recognition and is influenced by the GC architecture of exons and flanking introns in humans. Recent evidence suggests that histone modifications affect AS in humans. Such evidence in plants is lacking; similar mechanisms may be involved, as the majority of Arabidopsis genes exhibit similar gene body methylation to other organisms. Novel findings in plants have shown that the splicing process is indeed co-transcriptional; the mechanistic remain to be elucidated. This Special Issue aims to address how differences in DNA methylation, chromatin architecture, histone modification and RNA modifications influence splicing.

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Message from the Editor-in-Chief

Plants is an open access journal which provides an advanced forum for research findings in areas related to plant function, its physiology, biology, taxonomy, stresses, and its interactions with other organisms. It publishes original research articles, reviews, reports, conference proceedings (peer reviewed full articles) and communications. In original research papers, it is important that full experimental details are provided. We also encourage timely reviews and commentaries on topics of interest to the plant research community.

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