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IN BRIEF

The Plant Cell Reviews Alternative Splicing

Most eukaroytic genes contain introns (~90% of protein-coding genes in plants); therefore, an essential step in gene expression is the removal of introns through splicing of precursor mRNA transcripts (pre-mRNAs). Alternative splicing (AS) results in the generation of multiple mRNAs from a single pre-mRNA sequence, mainly by differential regulation of splice site selection. In humans, it is estimated that >95% of intron-containing genes undergo AS, and roughly 15% of genetic diseases are caused by mutations affecting splicing or AS. Recent estimates suggest that over 60% of intron-containing genes in plants undergo AS, producing a vast repertoire of mRNA isoforms. The larger questions are, what is the functional significance of AS, and to what extent and by what mechanisms is the process regulated? Two new review articles in *The Plant Cell* summarize current knowledge of the complexity of the alternative-splicing landscape in plants **(Reddy et al., pages 3657–3683)** and the role of AS in plant growth, development, and responses to external cues **(Staiger and Brown, pages 3640–3656)**.

AS has two major outcomes: It can regulate transcript levels by producing unstable mRNA isoforms, which are either degraded by nonsense-mediated decay, microRNAs, or other RNA decay pathways, or it can produce alternate functional mRNAs (Figure 1A) that give rise to protein isoforms that differ in subcellular localization, stability, or function. Reddy et al. review the extent and complexity of the AS landscape in plants, its regulation, and the roles of AS in gene regulation, as well as recent technological advances that allow large-scale assessment of AS. The review covers the composition and assembly of the spliceosome (a large macromolecular machine containing hundreds of core and auxiliary proteins), experimental and computational approaches for the analysis of AS, and the consequences of AS. The second half of the review offers a detailed update on understanding the splicing code in plants and the effects of chromatin modifications (epigenetic regulation) on AS. The authors emphasize how understanding the regulation of AS and the functions of splice variants can lead to novel ways to regulate gene expression and aid the development of crop plants with novel traits.

Staiger and Brown provide an overview of the pathways of AS and review recent examples of functional AS in plant development and response to external cues. In particular, they highlight the importance of AS in abiotic and biotic stress responses, organ development, flowering time, and the circadian clock. The authors consider how environmental and developmental cues affect gene expression at the level of transcription and AS, leading to an intimate connection between transcription and AS (see figure). The review also underscores the importance of integrating AS information with transcriptional data to arrive at a comprehensive view of functional gene expression.

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REFERENCES

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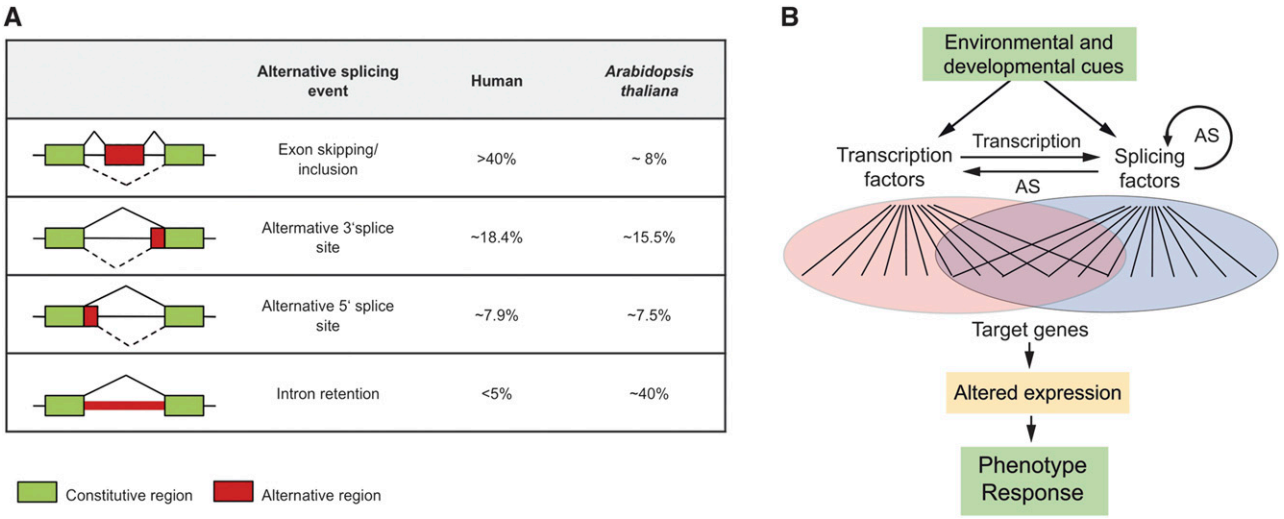

Overview of AS. Proportion of common types of AS events in humans and in *Arabidopsis thaliana* **(A)**. Dynamic regulation of RNA and protein expression by alternative splicing **(B)**. (***[A]*** *and* ***[B]*** *reprinted from Reddy et al. [2013], Figure 1, and Staiger and Brown [2013], Figure 2, respectively*.)

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