

# Changes in RNA Splicing in Soybean Seed Embryos

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**Short Abstract** — Developing soybean seeds accumulate oils, proteins, and carbohydrates that are used as oxidizable substrates providing metabolic precursors and energy during seed germination. The accumulation of these storage compounds in developing seeds is highly regulated at multiple levels, including at transcriptional and post-transcriptional regulation. RNA sequencing was used to provide comprehensive information about transcriptional and post-transcriptional events that take place in developing soybean embryos. Bioinformatics analyses lead to the identification of different classes of alternatively spliced isoforms and corresponding changes in their levels on a global scale during soybean embryo development. Alternative splicing was associated with transcripts involved in various metabolic and developmental processes, including central carbon and nitrogen metabolism, induction of maturation and dormancy, and splicing itself. Detailed examination of selected RNA isoforms revealed alterations in individual domains that could result in changes in subcellular localization of the resulting proteins, protein-protein and enzyme-substrate interactions, and regulation of protein activities. Different isoforms may play an important role in regulating developmental and metabolic processes occurring at different stages in developing oilseed embryos.

**Keywords** — abscisic acid, alternative splicing, auxin, central carbon and nitrogen metabolism, desiccation tolerance, dormancy induction, post-transcriptional regulation, seed and embryo development, soybean

## I. PURPOSE

Seed filling, the induction of dormancy, and the acquisition of desiccation tolerance constitute essential events in soybean seed development. Seed storage compounds (oil, protein, and carbohydrates) accumulating during seed filling provide substrates and energy in germinating, photosynthetically incompetent seedlings. In soybean, seed storage compounds are synthesized through pathways of central carbon and nitrogen metabolism.

Alternative splicing (AS) is a post-transcriptional regulatory

process contributing to transcriptome and proteome diversities by enabling the production of multiple mRNA and protein molecules from a single gene. Different splice isoforms, originating from the same gene, may contain or lack specific sequences, including functional, regulatory, and interaction domains, as well as organelle localization sequences. As such, the resulting mRNA and protein molecules may be affected in terms of stability, subcellular localization, structure, protein-molecule interactions, regulation, and function.

We have performed a detailed time-course of soybean embryo development, involving ten time points with three replicates. RNA-sequencing in conjunction with several computational and clustering tools allowed us to identify and explore alternative splicing events during soybean seed development. We have identified a set of novel splice variants as well as known ones that may play a role at different stages of regulation during embryo development.

## II. CONCLUSION

Current research shows how RNA-sequencing can be utilized to investigate multiple ongoing aspects of transcriptional regulation such as alternative splicing in developing soybean embryos.

## REFERENCES

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