

Article

Changes in RNA Splicing in Developing Soybean (*Glycine max*) Embryos

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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.

Article

Metabolic and Transcriptional Reprogramming in Developing Soybean (*Glycine max*) Embryos

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Abstract: Soybean (*Glycine max*) seeds are an important source of seed storage compounds, including protein, oil, and sugar used for food, feed, chemical, and biofuel production. We assessed detailed temporal transcriptional and metabolic changes in developing soybean embryos to gain a systems biology view of developmental and metabolic changes and to identify potential targets for metabolic engineering. Two major developmental and metabolic transitions were captured enabling identification of potential metabolic engineering targets specific to seed filling and to desiccation. The first transition involved a switch between different types of metabolism in dividing and elongating cells. The second transition involved the onset of maturation and desiccation tolerance during seed filling and a switch from photoheterotrophic to heterotrophic metabolism. Clustering analyses of metabolite and transcript data revealed clusters of functionally related metabolites and transcripts active in these different developmental and metabolic programs. The gene clusters provide a resource to generate predictions about the associations and interactions of unknown regulators with their targets based on “guilt-by-association” relationships. The inferred regulators also represent potential targets for future metabolic engineering of relevant pathways and steps

RESEARCH ARTICLE

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Transcriptome-wide functional characterization reveals novel relationships among differentially expressed transcripts in developing soybean embryos

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Abstract

Background: Transcriptomics reveals the existence of transcripts of different coding potential and strand orientation. Alternative splicing (AS) can yield proteins with altered number and types of functional domains, suggesting the global occurrence of transcriptional and post-transcriptional events. Many biological processes, including seed maturation and desiccation, are regulated post-transcriptionally (e.g., by AS), leading to the production of more than one coding or noncoding sense transcript from a single locus.

Results: We present an integrated computational framework to predict isoform-specific functions of plant transcripts. This framework includes a novel plant-specific weighted support vector machine classifier called CodeWise, which predicts the coding potential of transcripts with over 96 % accuracy, and several other tools enabling global sequence similarity, functional domain, and co-expression network analyses. First, this framework was applied to all detected transcripts (103,106), out of which 13 % was predicted by CodeWise to be noncoding RNAs in developing soybean embryos. Second, to investigate the role of AS during soybean embryo development, a population of 2,938 alternatively spliced and differentially expressed splice variants was analyzed and mined with respect to timing of expression. Conserved domain analyses revealed that AS resulted in global changes in the number, types, and extent of truncation of functional domains in protein variants. Isoform-specific co-expression network analysis using ArrayMining and clustering analyses revealed specific sub-networks and potential interactions among the components of selected signaling pathways related to seed maturation and the acquisition of desiccation tolerance. These signaling pathways involved abscisic acid- and FUSCA3-related transcripts, several of which were classified as noncoding and/or antisense transcripts and were co-expressed with corresponding coding transcripts. Noncoding and antisense transcripts likely play important regulatory roles in seed maturation- and desiccation-related signaling in soybean.

Conclusions: This work demonstrates how our integrated framework can be implemented to make experimentally testable predictions regarding the coding potential, co-expression, co-regulation, and function of transcripts and proteins related to a biological process of interest.

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