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Transcriptome analysis towards uncovering transcriptional reprogramming during callus formation in soybean

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Callus, a valuable resource in plant genetic engineering, originates from dedifferentiated cells. While extensive studies have investigated transcriptional reprogramming during callus formation in *Arabidopsis thaliana*, our understanding of this process in other species, such as *Glycine max*, remains limited. To bridge this knowledge gap, our study focused on conducting a time-series transcriptome analysis of soybean callus cultured for various durations (0, 1, 7, 14, 28, and 42 days) on a callus induction medium after wounding. Our aim was to identify genes that play crucial roles in callus formation. The results revealed a total of 27,639 gene expression alterations during callus formation, categorized into eight distinct clusters. Gene ontology analysis demonstrated that genes related to hormones, cell wall modification, and cell cycle underwent transcriptional reprogramming throughout callus formation. Furthermore, an in-depth examination of genes associated with hormones, cell cycle, cell wall, and transcription factors showed that auxin, cytokinin, and brassinosteroid signaling pathways activated genes involved in both root and shoot meristem development during callus formation. In conclusion, our transcriptome analysis provides valuable insights into the molecular mechanisms governing callus formation in soybean, enhancing our understanding of this complex process and paving the way for future research in the field.