



Transcriptional landscape of soybean (*Glycine max*) embryonic axes during germination in the presence of paclobutrazol, a gibberellin biosynthesis inhibitor

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Gibberellins (GA) are key players of plant growth and development process, particularly seed germination. However, the transcriptional changes driven by this phytohormone remain largely unexplored. Here we report time-course transcriptome analysis to identify genes that are transcriptionally regulated by GA during soybean (*Glycine max*) germination in the presence of paclobutrazol (PBZ), a GA biosynthesis inhibitor. Overall, we found 636 and 509 genes that are induced and repressed by PBZ, respectively. Our assumption is that genes down-regulated by PBZ are the targets (direct or otherwise) of endogenous GA. Genes related to cell-cycle, cell wall modification, hormone biosynthesis and signaling were identified as GA-responsive genes during germination. The regulation of hormone biosynthesis and signaling by GA suggest a cross-talk during germination. Moreover, identification of transcription factors (TFs) and their binding sites in promoters of DEGs indicated that GA regulate its downstream targets through the regulation of MYB, bZIP and NAC TFs. Overall, these findings provide insights into the complex molecular mechanism associated with GA regulation of seed germination.

Keywords: gibberellin, transcriptome, germination, soybean, paclobutrazol.

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